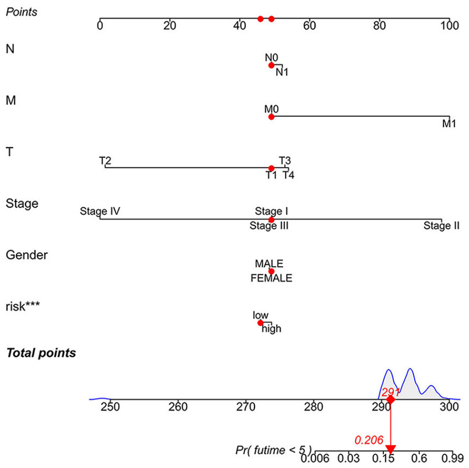
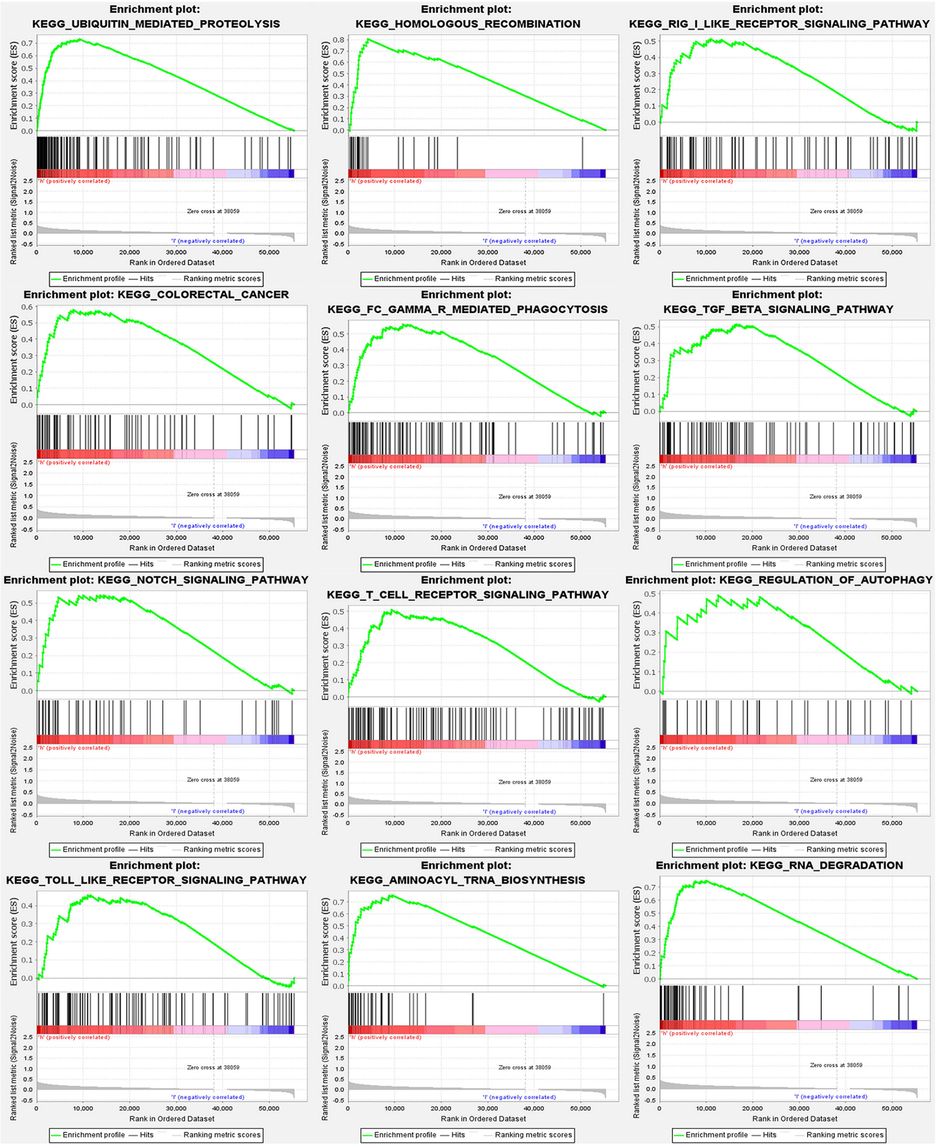
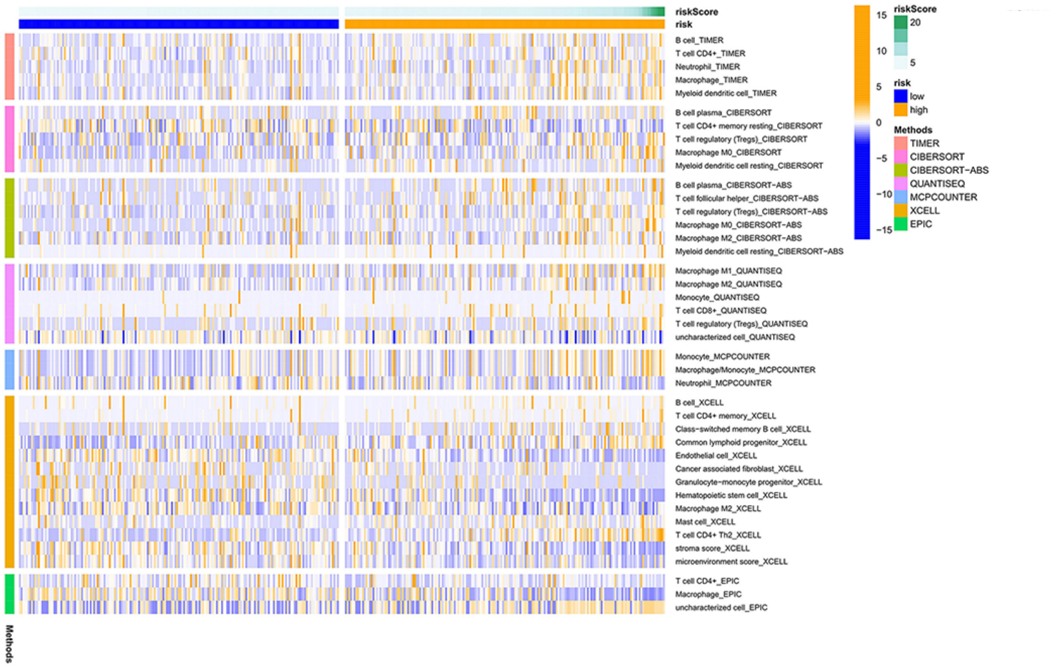
Supplementary Figure 1. Showing the combined nomogram.



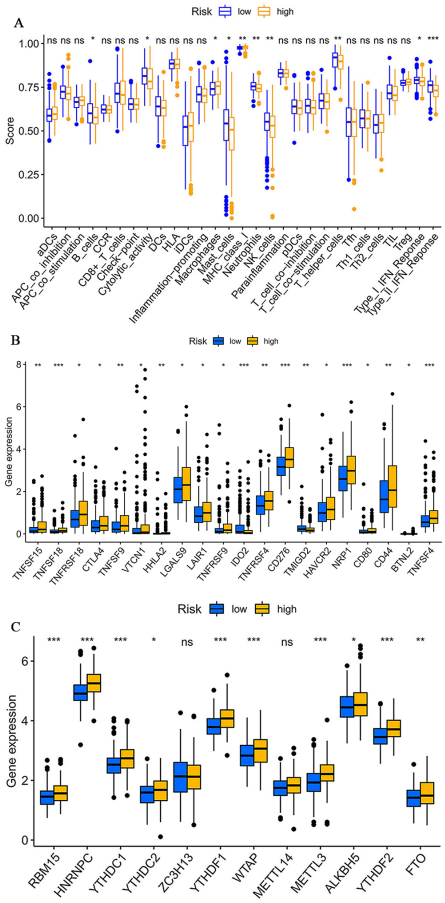
Supplementary Figure 2. Showing the majority of prognostic features of lncRNAs associated with ferroptosis regulate immune and tumor-related pathways.



Supplementary Figure 3. Showing the heatmap indicated the B cells, T cells, neutrophils granulocytes, macrophages, and medullary dendritic cells.



Supplementary Figure 4. Showing the correlation analysis of immune cell subpopulations and related functions in ssGSEA using the TCGA-LIHC database revealed that immune cells.



Supplementary Table 1. An overview of relevant clinical aspects of HCC patients.

An overview of relevant clinical aspects of HCC patients									
ID	futime	fustat	Age	Gender	Grade	Stage	T	M	N
TCGA-5R-AA1D	449	0	17	FEMALE	G3	Stage IIIA	T3a	M0	N0
TCGA-DD-A1EC	602	0	20	FEMALE	G3	Stage I	T1	M0	N0
TCGA-ED-A7PY	390	0	20	FEMALE	G3	Stage II	T2	M0	NX
TCGA-RC-A6M5	15	0	20	FEMALE	G2	Stage IVA	T1	M0	N1
TCGA-CC-A123	219	0	24	FEMALE	G1	Stage IIIA	T3	M0	N0
TCGA-BW-A5NP	0	0	26	FEMALE	G3	Stage IV	T2	M1	N0
TCGA-DD-A39W	827	1	29	FEMALE	G2	Stage III	T3	M0	N0
TCGA-WX-AA47	556	1	33	FEMALE	G2	Stage IIIA	T3a	MX	NX
TCGA-FV-A3R3	366	1	38	FEMALE	G2	Stage I	T1	MX	NX
TCGA-CC-A8HU	344	1	39	FEMALE	G3	Stage IIIA	T3	M0	N0
TCGA-XR-A8TC	1339	0	43	FEMALE	G2	Stage I	T1	MX	NX
TCGA-DD-AADI	1085	0	43	FEMALE	G3	Stage I	T1	M0	N0
TCGA-DD-A39Z	601	1	43	FEMALE	G2	Stage II	T2	M0	NX
TCGA-DD-AAE0	555	0	45	FEMALE	G4	Stage IIIA	T3a	M0	N0
TCGA-G3-A25T	1553	0	45	FEMALE	G2	Stage IIIA	T3	M0	N0
TCGA-EP-A2KB	596	1	46	FEMALE	G2	Stage I	T1	MX	NX
TCGA-RC-A7S9	640	0	47	FEMALE	G3	Stage I	T1	M0	N0
TCGA-ED-A7PX	6	0	48	FEMALE	G3	Stage II	T2	M0	NX
TCGA-XR-A8TD	1030	0	49	FEMALE	G3	Stage IIIB	T3	M0	N0
TCGA-DD-AAE4	608	0	49	FEMALE	G1	Stage I	T1	M0	N0
TCGA-ED-A8O6	56	1	50	FEMALE	G3	Stage IIIA	T3a	M0	N0
TCGA-FV-A495	1	0	51	FEMALE	G2	Stage II	T2	M0	NX
TCGA-DD-AAD1	564	0	51	FEMALE	G4	Stage I	T1	M0	N0
TCGA-BC-A110	2116	1	51	FEMALE	G1	unknow	T1	MX	NX
TCGA-ED-A66Y	296	1	51	FEMALE	G3	Stage IIIA	T3a	M0	N0
TCGA-CC-A8HV	279	1	51	FEMALE	G2	Stage II	T2	M0	N0
TCGA-CC-A9FU	0	0	52	FEMALE	G2	Stage IIIA	T3a	M0	N0
TCGA-EP-A2KA	627	1	52	FEMALE	G3	Stage IIIA	T3a	MX	NX
TCGA-G3-A25Y	452	1	52	FEMALE	G3	Stage I	T1	M0	N0
TCGA-BC-A10X	770	1	52	FEMALE	G2	Stage IIIA	T3a	MX	N0
TCGA-ED-A7XP	400	0	53	FEMALE	G3	Stage II	T2	M0	N0
TCGA-G3-AAV6	65	1	53	FEMALE	G3	Stage IIIA	T3a	M0	N0
TCGA-DD-A4NJ	928	0	54	FEMALE	G2	Stage II	T2	M0	N0
TCGA-2Y-A9GV	2532	1	54	FEMALE	G1	Stage I	T1	MX	NX
TCGA-DD-A113	2425	0	55	FEMALE	G3	Stage II	T2	M0	N0
TCGA-2Y-A9GU	1939	0	55	FEMALE	G2	Stage I	T1	MX	NX
TCGA-DD-AADY	555	0	55	FEMALE	G2	Stage I	T1	M0	N0
TCGA-ZP-A9D1	21	0	56	FEMALE	G2	unknow	T1	MX	NX
TCGA-DD-A4ND	2746	0	56	FEMALE	G3	Stage I	T1	M0	N0
TCGA-DD-A4NN	899	1	56	FEMALE	G3	Stage I	T1	M0	N0
TCGA-DD-A1EF	394	1	57	FEMALE	G3	Stage I	T1	M0	N0
TCGA-DD-A11D	1560	1	57	FEMALE	G2	Stage I	T1	M0	N0
TCGA-G3-AAV3	412	0	58	FEMALE	G2	Stage II	T2	M0	N0

TCGA-PD-A5DF	639	1	58	FEMALE	G2	Stage IIIB	T4	M0	N0
TCGA-DD-AAE6	141	0	59	FEMALE	G2	Stage I	T1	M0	N0
TCGA-DD-AAEG	719	0	59	FEMALE	G3	Stage I	T1	M0	N0
TCGA-ED-A8O5	406	0	59	FEMALE	G3	Stage IIIA	T3a	M0	N0
TCGA-2Y-A9H5	555	1	59	FEMALE	G3	Stage I	T1	MX	N0
TCGA-ED-A5KG	854	0	60	FEMALE	G2	Stage II	T2	M0	N0
TCGA-CC-5259	250	0	60	FEMALE	G2	Stage IIIC	T4	M0	N0
TCGA-ED-A82E	408	0	60	FEMALE	G2	Stage IIIA	T3a	M0	N0
TCGA-G3-A7M6	632	0	60	FEMALE	G3	Stage I	T1	MX	NX
TCGA-KR-A7K7	951	0	61	FEMALE	G1	Stage II	T2	M0	N0
TCGA-DD-A4NS	2456	1	61	FEMALE	G2	Stage I	T1	M0	N0
TCGA-CC-5260	87	1	61	FEMALE	G1	Stage IIIC	T4	M0	N0
TCGA-UB-A7MA	848	0	62	FEMALE	G2	Stage II	T2b	M0	N0
TCGA-BC-A216	1351	0	62	FEMALE	G2	Stage IIIA	T3	M0	NX
TCGA-BC-A10Z	34	1	62	FEMALE	G2	Stage I	T1	MX	N0
TCGA-G3-A25U	1636	0	63	FEMALE	G3	Stage I	T1	M0	N0
TCGA-DD-AACZ	171	1	63	FEMALE	G4	Stage I	T1	M0	N0
TCGA-2Y-A9H2	1731	0	64	FEMALE	G3	Stage I	T1	MX	N0
TCGA-ZP-A9D4	395	0	64	FEMALE	G1	unknow	T1	MX	NX
TCGA-WX-AA44	615	0	64	FEMALE	G3	Stage I	T1	MX	NX
TCGA-DD-A1EK	558	1	64	FEMALE	G2	Stage IVB	T4	M1	N0
TCGA-DD-A3A9	931	1	64	FEMALE	G2	Stage IVB	T4	M1	N0
TCGA-2Y-A9GY	757	1	64	FEMALE	G3	Stage II	T2	MX	NX
TCGA-DD-AADF	115	1	64	FEMALE	G4	Stage I	T1	M0	N0
TCGA-DD-A73C	701	0	65	FEMALE	G1	Stage IIIA	T3a	M0	N0
TCGA-DD-A4NH	917	0	65	FEMALE	G3	Stage IIIB	T3b	M0	N0
TCGA-5R-AAAM	46	1	65	FEMALE	G2	Stage II	T2	M0	N0
TCGA-BC-A8YO	562	0	66	FEMALE	G3	Stage IIIC	T4	M0	N0
TCGA-ZP-A9CY	782	0	66	FEMALE	G1	unknow	T1	MX	NX
TCGA-BC-A3KF	8	0	66	FEMALE	G2	Stage I	T1	M0	NX
TCGA-DD-AADA	1233	0	66	FEMALE	G3	Stage I	T1	M0	N0
TCGA-DD-AACL	107	1	66	FEMALE	G3	Stage I	T1	M0	N0
TCGA-DD-A3A5	3125	1	66	FEMALE	G2	Stage III	T3	M0	N0
TCGA-BC-A10R	308	1	66	FEMALE	G2	unknow	T3	MX	NX
TCGA-DD-A4NA	1008	0	67	FEMALE	G3	Stage IIIC	T2	M0	N1
TCGA-ZP-A9D0	1091	0	67	FEMALE	G1	unknow	T1	MX	NX
TCGA-2Y-A9H6	357	0	68	FEMALE	G2	Stage I	T1	MX	NX
TCGA-BC-A3KG	680	0	68	FEMALE	G3	Stage II	T2	M0	N0
TCGA-DD-A73D	693	0	68	FEMALE	G1	Stage II	T2	MX	NX
TCGA-DD-AADK	1049	0	68	FEMALE	G3	Stage II	T2	M0	N0
TCGA-WJ-A86L	345	0	68	FEMALE	G2	Stage I	T1	MX	NX
TCGA-UB-AA0V	314	0	69	FEMALE	G1	Stage I	unknow	MX	NX
TCGA-DD-AACT	1562	0	69	FEMALE	G2	Stage I	T1	M0	N0
TCGA-DD-AADJ	1066	0	70	FEMALE	G3	Stage I	T1	M0	N0
TCGA-FV-A23B	1852	1	70	FEMALE	unknow	Stage II	T2	M0	N0
TCGA-WQ-A9G7	30	0	71	FEMALE	G3	unknow	T3a	M0	NX
TCGA-DD-A1EJ	1005	1	71	FEMALE	G2	Stage IIIC	T1	M0	N1

TCGA-DD-A1EB	2017	0	72	FEMALE	G2	Stage I	T1	M0	N0
TCGA-DD-A73B	283	1	72	FEMALE	G2	Stage I	T1	M0	N0
TCGA-DD-A3A6	3258	1	72	FEMALE	G2	Stage II	T2	M0	N0
TCGA-BC-A10Q	1135	1	72	FEMALE	unknow	unknow	T2	MX	NX
TCGA-DD-AAD0	137	0	73	FEMALE	G2	Stage I	T1	M0	N0
TCGA-DD-A73G	3478	0	73	FEMALE	G3	Stage I	T1	M0	N0
TCGA-DD-AAD8	1219	0	73	FEMALE	G2	Stage I	T1	M0	N0
TCGA-DD-AACB	2324	0	74	FEMALE	G3	Stage I	T1	M0	N0
TCGA-RC-A6M4	22	0	74	FEMALE	G2	Stage IIIA	T3	MX	NX
TCGA-BC-4072	1490	1	74	FEMALE	G3	Stage IIIA	T3	M0	N0
TCGA-BD-A3EP	409	0	75	FEMALE	G2	Stage I	T1	M0	N0
TCGA-DD-A4NE	660	1	75	FEMALE	G3	Stage IIIA	T3a	M0	N0
TCGA-BC-A217	1397	1	75	FEMALE	G3	Stage II	T2	M0	NX
TCGA-GJ-A6C0	31	1	75	FEMALE	G2	Stage II	T2	MX	NX
TCGA-FV-A3I0	848	0	76	FEMALE	G2	Stage II	T2	M0	NX
TCGA-DD-A3A2	2131	1	76	FEMALE	G1	Stage I	T1	M0	N0
TCGA-DD-A73F	1085	0	77	FEMALE	G1	Stage I	T1	M0	N0
TCGA-DD-A118	3437	0	77	FEMALE	G2	Stage II	T2	M0	N0
TCGA-DD-A39X	1694	1	78	FEMALE	G2	Stage I	T1	M0	NX
TCGA-ZS-A9CE	1241	0	79	FEMALE	G1	Stage II	T2	MX	NX
TCGA-LG-A6GG	387	0	79	FEMALE	G2	Stage II	T2	M0	NX
TCGA-G3-A25W	935	0	79	FEMALE	G2	Stage IIIB	T3b	M0	N0
TCGA-DD-A4NK	1210	1	80	FEMALE	G2	Stage IIIA	T3	M0	N0
TCGA-2Y-A9H7	1168	0	81	FEMALE	G2	Stage I	T1	MX	N0
TCGA-DD-AA3A	410	1	81	FEMALE	G4	Stage I	T1	MX	N0
TCGA-FV-A3I1	247	1	81	FEMALE	G2	Stage II	T2	MX	N0
TCGA-2Y-A9GZ	848	1	82	FEMALE	G2	Stage II	T2	MX	NX
TCGA-G3-AAV4	27	1	83	FEMALE	G1	Stage I	T1	M0	N0
TCGA-FV-A496	10	0	84	FEMALE	G2	Stage I	T1	M0	NX
TCGA-DD-A4NR	9	1	85	FEMALE	G3	Stage I	T1	M0	N0
TCGA-2Y-A9H8	633	1	85	FEMALE	G2	unknow	T1	MX	NX
TCGA-HP-A5N0	752	1	90	FEMALE	unknow	unknow	TX	M0	NX
TCGA-XR-A8TE	925	0	16	MALE	G1	Stage IIIA	T3	MX	N0
TCGA-CC-A8HS	300	1	18	MALE	G1	Stage IIIC	T3	M0	N1
TCGA-DD-A1EH	1495	0	23	MALE	G3	Stage III	T3	M0	N0
TCGA-DD-A1EL	415	1	23	MALE	G3	Stage II	T2	M0	N0
TCGA-RC-A6M3	0	0	24	MALE	G3	Stage II	T2	M0	N0
TCGA-UB-A7MB	601	0	24	MALE	G3	Stage II	T2	MX	NX
TCGA-DD-A4NB	989	0	25	MALE	G2	Stage I	T1	M0	N0
TCGA-ED-A7XO	427	0	29	MALE	G2	Stage IIIA	T3a	M0	N0
TCGA-G3-A7M8	430	0	31	MALE	G1	Stage I	T1	MX	NX
TCGA-DD-A4NP	3308	0	32	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AACN	1302	0	32	MALE	G3	Stage I	T1	M0	N0
TCGA-MR-A8JO	330	0	34	MALE	G3	Stage I	T1	MX	N0
TCGA-ED-A66X	406	0	35	MALE	G3	Stage IIIA	T3a	M0	N0
TCGA-DD-AAVW	2317	0	35	MALE	G2	Stage I	T1	M0	N0
TCGA-CC-5263	129	1	35	MALE	G1	Stage IIIA	T3	M0	N0

TCGA-CC-A3MB	315	1	36	MALE	G1	Stage IIIA	T3	M0	N0
TCGA-DD-A3A4	612	1	37	MALE	G3	Stage IIIA	T3	M0	N0
TCGA-G3-AAV7	361	0	38	MALE	G2	Stage II	T2	M0	N0
TCGA-DD-AAVX	1718	0	38	MALE	G2	Stage II	T2	M0	N0
TCGA-DD-AAVZ	1900	0	38	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AAVQ	2728	0	38	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AACS	1804	0	39	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AACO	1876	0	40	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-A119	223	1	40	MALE	G3	Stage IV	T3a	M1	N0
TCGA-RC-A7SH	468	0	42	MALE	G3	Stage II	T2	M0	N0
TCGA-DD-A114	1149	1	42	MALE	G3	Stage II	T2	M0	unknow
TCGA-DD-AAD3	1295	0	43	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AACW	1424	0	43	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AAVR	2513	0	44	MALE	G2	Stage I	T1	M0	N0
TCGA-CC-5261	97	1	44	MALE	G2	Stage II	T2	M0	N0
TCGA-G3-A5SI	768	1	44	MALE	G2	Stage II	T2	M0	N0
TCGA-DD-AADP	458	0	45	MALE	G3	Stage I	T1	M0	N0
TCGA-2Y-A9H3	1516	0	45	MALE	G1	Stage II	T2	MX	NX
TCGA-DD-AAE8	664	0	45	MALE	G3	Stage I	T1	M0	N0
TCGA-CC-A3M9	300	1	45	MALE	G3	Stage IIIA	T3a	M0	N0
TCGA-CC-A5UD	304	1	45	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-DD-A3A3	535	1	45	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-A4NL	1711	0	46	MALE	G1	Stage I	T1	M0	N0
TCGA-DD-AAVU	2202	0	46	MALE	G2	Stage II	T2	M0	N0
TCGA-DD-A1EI	183	0	46	MALE	G2	Stage I	T1	M0	N0
TCGA-ED-A459	910	0	47	MALE	G2	Stage II	T2	M0	N0
TCGA-CC-A7IG	299	1	47	MALE	G2	Stage II	T2	M0	N0
TCGA-LG-A9QC	425	0	48	MALE	G2	Stage I	T1	M0	NX
TCGA-G3-AAUZ	480	0	48	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AACM	1769	0	48	MALE	G3	Stage II	T2	M0	N0
TCGA-QA-A7B7	94	0	48	MALE	G2	Stage II	T2	MX	NX
TCGA-DD-AAVP	2752	0	48	MALE	G1	Stage I	T1	M0	N0
TCGA-DD-AADW	587	0	48	MALE	G3	Stage I	T1	M0	N0
TCGA-CC-A5UE	272	1	48	MALE	G2	Stage IIIB	T4	M0	N0
TCGA-CC-5258	129	1	48	MALE	G2	Stage II	T2	M0	N0
TCGA-DD-AACD	381	1	48	MALE	G4	Stage I	T1	M0	N0
TCGA-2Y-A9H0	3675	0	49	MALE	G1	Stage IIIA	T3	M0	N0
TCGA-G3-AAV2	372	0	50	MALE	G1	Stage I	T1	M0	N0
TCGA-BW-A5NO	20	0	50	MALE	G2	Stage IIIA	T3a	MX	NX
TCGA-DD-AAE3	566	0	50	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AADE	1202	0	50	MALE	G4	Stage I	T1	M0	N0
TCGA-DD-AADV	574	0	50	MALE	G3	Stage I	T1	M0	N0
TCGA-CC-A1HT	101	1	50	MALE	G3	Stage IIIA	T3	M0	N0
TCGA-BC-A10W	91	1	50	MALE	G3	unknow	T4	MX	NX
TCGA-DD-AACQ	432	1	50	MALE	G3	Stage II	T2	M0	N0
TCGA-DD-AAED	763	0	51	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AADB	1242	0	51	MALE	G4	Stage I	T1	M0	N0

TCGA-UB-A7ME	486	0	51	MALE	G2	Stage I	T1	MX	NX
TCGA-DD-AAE2	638	0	51	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AADD	1231	0	51	MALE	G4	Stage I	T1	M0	N0
TCGA-DD-AAEK	1067	0	51	MALE	G3	Stage II	T2	M0	N0
TCGA-DD-AAC9	347	0	51	MALE	G2	Stage I	T1	M0	N0
TCGA-G3-AAV1	359	1	51	MALE	G3	Stage IIIC	T4	M0	N0
TCGA-ZP-A9D2	765	1	51	MALE	G2	unknow	T2	MX	NX
TCGA-2Y-A9GT	1624	1	51	MALE	G2	Stage I	T1	MX	NX
TCGA-G3-A3CJ	594	0	52	MALE	G2	Stage II	T2	M0	N0
TCGA-FV-A4ZQ	12	0	52	MALE	G2	Stage I	T1	M0	NX
TCGA-DD-AAE1	552	0	52	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AACG	469	1	52	MALE	G4	Stage II	T2	M0	N0
TCGA-G3-A3CH	780	0	53	MALE	G2	Stage IIIA	T3a	M0	N0
TCGA-RC-A7SB	588	0	53	MALE	G2	Stage II	T2	M0	N0
TCGA-DD-AACV	1531	0	53	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-A115	2542	1	53	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-DD-AADC	425	1	53	MALE	G3	Stage I	T1	M0	N0
TCGA-ED-A97K	6	0	54	MALE	G2	Stage IIIA	T3a	M0	N0
TCGA-CC-A7II	399	0	54	MALE	G3	Stage IIIA	T3	M0	N0
TCGA-CC-A3MC	363	0	54	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-DD-AAD5	1345	0	54	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AAW0	2015	0	54	MALE	G2	Stage I	T1	M0	N0
TCGA-O8-A75V	538	0	54	MALE	G2	Stage I	T1	MX	NX
TCGA-ES-A2HT	438	1	54	MALE	G2	Stage I	T1	MX	NX
TCGA-DD-AAW1	1989	0	55	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-DD-AAEE	810	0	55	MALE	G4	Stage I	T1	M0	N0
TCGA-CC-A9FS	211	0	55	MALE	G2	Stage II	T2	M0	N0
TCGA-ZS-A9CG	341	0	55	MALE	G2	Stage II	T2	MX	NX
TCGA-DD-AAD0	453	0	55	MALE	G3	Stage I	T1	M0	N0
TCGA-CC-A7IJ	382	0	56	MALE	G3	Stage II	T2	M0	N0
TCGA-DD-AAVS	1823	0	56	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AAVV	2455	0	56	MALE	G3	Stage II	T2	M0	N0
TCGA-DD-AAVY	1970	0	56	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-UB-A7MF	214	1	56	MALE	G2	Stage IIIA	T3a	MX	NX
TCGA-5R-AA1C	520	0	57	MALE	G2	Stage II	T2	M0	N0
TCGA-CC-A9FV	0	0	57	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-KR-A7K8	906	0	57	MALE	G1	Stage I	T1	M0	N0
TCGA-CC-A7IE	217	1	57	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-XR-A8TG	898	0	58	MALE	G2	Stage I	T1	M0	NX
TCGA-G3-A25Z	655	0	58	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AADR	2028	0	58	MALE	G3	Stage I	T1	M0	N0
TCGA-ED-A4XI	819	0	58	MALE	G3	Stage II	T2	M0	N0
TCGA-DD-AADL	636	0	58	MALE	G4	Stage I	T1	M0	N0
TCGA-G3-A5SM	520	0	58	MALE	G3	Stage II	T2	M0	NX
TCGA-G3-AAV0	476	0	58	MALE	G2	Stage I	T1	M0	N0
TCGA-MR-A520	229	0	58	MALE	G1	Stage I	T1	MX	NX
TCGA-5C-A9VG	328	0	58	MALE	G2	Stage II	T2	M0	N0

TCGA-CC-A7IH	365	0	58	MALE	G1	Stage IIIA	T3	M0	N0
TCGA-G3-A5SK	744	0	58	MALE	G1	Stage I	T1	M0	NX
TCGA-DD-AADM	12	1	58	MALE	G3	Stage II	T2	M0	N0
TCGA-2Y-A9H1	1229	1	58	MALE	G2	Stage I	T1	MX	NX
TCGA-2Y-A9GS	724	1	58	MALE	G2	unknow	T2	MX	NX
TCGA-UB-A7MC	500	0	59	MALE	G3	Stage IIIA	T3a	MX	N0
TCGA-DD-AADQ	436	0	59	MALE	G3	Stage II	T2	M0	N0
TCGA-GJ-A3OU	879	0	59	MALE	G2	Stage I	T1	MX	NX
TCGA-DD-AADN	898	0	59	MALE	G4	Stage I	T1	MX	NX
TCGA-RC-A7SK	472	0	59	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AACU	1567	0	59	MALE	G3	Stage I	T1	M0	N0
TCGA-G3-A5SJ	698	0	59	MALE	G2	Stage I	T1	M0	NX
TCGA-CC-A7IF	649	1	59	MALE	G1	Stage IIIA	T3	M0	N0
TCGA-CC-A7IK	262	1	59	MALE	G3	Stage IIIA	T3	M0	N0
TCGA-ZP-A9CV	1088	1	59	MALE	G1	unknow	T1	MX	NX
TCGA-UB-AA0U	327	0	60	MALE	G2	Stage II	T2	MX	NX
TCGA-DD-AADU	554	0	60	MALE	G3	Stage II	T2	M0	N0
TCGA-DD-AAEB	478	0	60	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-A4NQ	373	1	60	MALE	G3	Stage II	T2	M0	N0
TCGA-5C-AAPD	20	0	61	MALE	G1	Stage II	T2	M0	N0
TCGA-MI-A75I	630	0	61	MALE	G1	unknow	T2	MX	NX
TCGA-DD-A4NV	2398	0	61	MALE	G1	Stage IIIA	T3	M0	N0
TCGA-ED-A7PZ	6	0	61	MALE	G2	Stage II	T2	M0	NX
TCGA-MI-A75E	507	0	61	MALE	G2	Stage IIIC	T4	M0	N0
TCGA-DD-AACY	1450	0	61	MALE	G3	Stage I	T1	M0	N0
TCGA-K7-AAU7	359	0	61	MALE	G2	Stage II	T2a	MX	NX
TCGA-WX-AA46	756	0	61	MALE	G1	Stage II	T2	MX	NX
TCGA-G3-A3CK	585	0	61	MALE	G2	Stage I	T1	M0	N0
TCGA-CC-A7IL	278	1	61	MALE	G1	Stage IIIA	T3	M0	N0
TCGA-DD-AACC	1685	1	61	MALE	G2	Stage I	T1	M0	N0
TCGA-CC-A3MA	303	1	61	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-DD-AACE	2184	0	62	MALE	G3	Stage I	T1	M0	N0
TCGA-WQ-AB4B	395	0	62	MALE	G2	Stage II	T2	M0	NX
TCGA-BD-A3ER	1115	0	62	MALE	G2	Stage II	T2	MX	NX
TCGA-EP-A12J	570	0	62	MALE	G1	Stage I	T1	MX	NX
TCGA-EP-A2KC	19	1	62	MALE	G3	Stage I	T1	MX	NX
TCGA-MI-A75G	698	0	63	MALE	G2	Stage II	T2	M0	N0
TCGA-DD-AADS	474	0	63	MALE	G2	Stage I	T1	M0	N0
TCGA-BW-A5NQ	0	0	63	MALE	G3	Stage I	T1	MX	NX
TCGA-CC-A5UC	347	1	63	MALE	G3	Stage IIIA	T3	M0	N0
TCGA-ZS-A9CF	2412	0	64	MALE	G2	Stage II	T2	MX	NX
TCGA-BC-A69H	444	0	64	MALE	G3	Stage II	T2	M0	NX
TCGA-MI-A75C	291	0	64	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AACP	415	0	64	MALE	G3	Stage I	T1	M0	N0
TCGA-K7-A5RF	631	0	64	MALE	G1	Stage I	T1	MX	NX
TCGA-KR-A7K2	829	0	64	MALE	G1	Stage I	T1	M0	N0
TCGA-2Y-A9GW	1271	1	64	MALE	G2	Stage I	T1	MX	N0

TCGA-G3-A25S	416	1	64	MALE	G2	Stage I	T1	M0	N0
TCGA-G3-A6UC	671	0	65	MALE	G2	Stage IIIB	T3b	M0	N0
TCGA-DD-AACA	2301	0	65	MALE	G3	Stage I	T1	M0	N0
TCGA-3K-AAZ8	396	0	65	MALE	G1	Stage IIIB	T3b	MX	NX
TCGA-DD-AAEA	575	0	65	MALE	G3	Stage I	T1	M0	N0
TCGA-G3-A7M7	361	0	65	MALE	G1	Stage I	T1	MX	NX
TCGA-DD-A4NO	2245	0	65	MALE	G1	Stage I	T1	M0	N0
TCGA-KR-A7K0	65	1	65	MALE	G1	Stage I	T1	M0	N0
TCGA-DD-A3A1	233	1	65	MALE	G2	Stage IIIA	T3b	M0	N0
TCGA-K7-A6G5	512	0	66	MALE	G2	Stage I	T1	MX	N0
TCGA-DD-AACX	170	0	66	MALE	G3	Stage II	T2	M0	N0
TCGA-DD-A73E	44	0	66	MALE	G1	Stage I	T1	M0	N0
TCGA-RC-A7SF	579	0	66	MALE	G2	Stage I	T1	M0	N0
TCGA-2Y-A9HB	260	0	66	MALE	G2	Stage I	T1	MX	NX
TCGA-DD-AAD2	658	0	66	MALE	G2	Stage I	T1	M0	N0
TCGA-K7-A5RG	519	0	66	MALE	G1	Stage I	T1	MX	NX
TCGA-DD-AAD6	672	0	66	MALE	G3	Stage IIIA	T3a	M0	N0
TCGA-4R-AA8I	262	1	66	MALE	G2	Stage II	T2	MX	NX
TCGA-DD-A4NI	816	0	67	MALE	G2	Stage II	T2	M0	NX
TCGA-DD-A11A	79	0	67	MALE	G3	Stage I	T1	M0	N0
TCGA-G3-AAV5	354	0	67	MALE	G2	Stage II	T2	M0	N0
TCGA-UB-A7MD	52	1	67	MALE	G3	Stage I	T1	MX	N0
TCGA-DD-A39Y	171	1	67	MALE	G3	Stage I	T1	M0	NX
TCGA-CC-5262	103	1	67	MALE	G1	Stage IIIC	T4	M0	N0
TCGA-DD-A3A7	419	1	67	MALE	G3	Stage IIIB	T3b	M0	N0
TCGA-DD-A1EA	2415	0	68	MALE	G2	Stage II	T2	M0	N0
TCGA-G3-A25V	860	0	68	MALE	G2	Stage I	T1	M0	N0
TCGA-T1-A6J8	23	0	68	MALE	G2	unknow	T1	M0	NX
TCGA-CC-A9FW	248	0	68	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-2Y-A9H4	1452	0	68	MALE	G2	Stage I	T1	MX	N0
TCGA-LG-A9QD	366	0	68	MALE	G2	Stage IIIA	T3a	M0	N0
TCGA-2Y-A9GX	2442	0	68	MALE	G2	Stage I	T1	MX	NX
TCGA-DD-A1ED	2301	0	68	MALE	G1	Stage I	T1	M0	N0
TCGA-GJ-A9DB	67	1	68	MALE	G2	Stage I	T1	MX	N0
TCGA-DD-A116	1622	1	68	MALE	G3	Stage IIIA	T3	M0	N0
TCGA-DD-AACF	365	1	68	MALE	G3	Stage I	T1	M0	N0
TCGA-YA-A8S7	412	1	68	MALE	G3	Stage IIIA	T3a	MX	N0
TCGA-DD-AAW2	1855	0	69	MALE	G2	Stage I	T1	M0	N0
TCGA-BC-A69I	387	0	69	MALE	G1	Stage I	T1	M0	N0
TCGA-RG-A7D4	1098	0	69	MALE	G2	Stage II	T2	M0	N0
TCGA-BD-A2L6	1363	0	69	MALE	G2	unknow	T2	MX	NX
TCGA-DD-AAW3	1633	0	69	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AACI	1618	0	69	MALE	G3	Stage II	T2	M0	N0
TCGA-DD-A11C	662	0	69	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AAE9	722	0	69	MALE	G3	Stage I	T1	M0	N0
TCGA-BC-A10U	837	1	69	MALE	G2	unknow	T2	MX	NX
TCGA-BC-A5W4	547	1	69	MALE	G3	Stage IIIA	T3a	M0	NX

TCGA-DD-AACH	195	1	69	MALE	G3	Stage II	T2	M0	N0
TCGA-2Y-A9H9	697	0	70	MALE	G2	Stage I	T1	MX	N0
TCGA-5C-A9VH	322	0	70	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AACK	9	0	70	MALE	G2	Stage I	T1	M0	N0
TCGA-G3-A5SL	621	0	70	MALE	G2	Stage II	T2	M0	NX
TCGA-DD-AADG	1145	0	70	MALE	G3	Stage IIIA	T3a	M0	N0
TCGA-EP-A26S	608	0	70	MALE	G2	Stage I	T1	MX	N0
TCGA-DD-A1E9	2759	1	70	MALE	G2	Stage I	T1	M0	N0
TCGA-2Y-A9HA	36	1	70	MALE	G2	Stage II	T2	MX	NX
TCGA-G3-A7M9	56	1	70	MALE	G2	Stage IIIB	T3b	MX	NX
TCGA-DD-A3A0	785	1	70	MALE	G2	Stage I	T1	M0	NX
TCGA-DD-A73A	728	0	71	MALE	G2	Stage I	T1	M0	N0
TCGA-G3-A3CI	180	0	71	MALE	G2	Stage I	T1	M0	N0
TCGA-CC-5264	102	1	71	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-NI-A4U2	1791	1	71	MALE	G1	Stage IIIA	T3	MX	NX
TCGA-DD-AAE7	644	0	72	MALE	G2	Stage I	T1	M0	N0
TCGA-ZP-A9CZ	706	0	72	MALE	G1	unknow	T1	MX	NX
TCGA-DD-AAEI	1531	0	72	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-A4NF	942	0	72	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-AAC8	16	1	72	MALE	G3	Stage I	T1	M0	N0
TCGA-DD-AAEH	784	0	73	MALE	G2	Stage I	T1	M0	N0
TCGA-G3-A25X	1779	0	73	MALE	G3	Stage II	T2	M0	N0
TCGA-EP-A3RK	363	0	73	MALE	G2	Stage IIIA	T3a	MX	NX
TCGA-BC-4073	849	0	73	MALE	G3	Stage IIIA	T3	MX	N0
TCGA-ZS-A9CD	1386	1	73	MALE	G2	Stage II	T2	MX	NX
TCGA-DD-A11B	14	1	73	MALE	G2	Stage I	T1	M0	N0
TCGA-DD-A1EE	349	1	73	MALE	G3	Stage IIIA	T3	M0	N0
TCGA-ED-A627	423	0	74	MALE	G2	Stage I	T1	M0	NX
TCGA-NI-A8LF	799	0	74	MALE	G3	Stage I	T1	MX	NX
TCGA-XR-A8TF	693	1	74	MALE	G1	Stage I	T1	MX	NX
TCGA-CC-A8HT	140	1	74	MALE	G2	Stage IIIA	T3	M0	N0
TCGA-RC-A6M6	9	0	75	MALE	G3	Stage II	T2	M0	NX
TCGA-DD-AACJ	2102	0	75	MALE	G2	Stage II	T2	M0	N0
TCGA-FV-A3R2	194	1	75	MALE	unknow	Stage I	T1	MX	NX
TCGA-FV-A2QR	581	1	75	MALE	G1	Stage I	T1	M0	N0
TCGA-DD-A3A8	11	1	75	MALE	G2	Stage II	T2	M0	N0
TCGA-EP-A3JL	303	0	76	MALE	G2	Stage I	T1	MX	NX
TCGA-G3-A7M5	447	0	76	MALE	G2	Stage I	T1	MX	NX
TCGA-BC-A10Y	711	1	76	MALE	G3	unknow	T4	MX	NX
TCGA-BC-A10T	837	1	76	MALE	G1	unknow	T4	MX	NX
TCGA-DD-A1EG	1372	1	76	MALE	G3	Stage I	T1	M0	N0
TCGA-MI-A75H	747	0	77	MALE	unknow	unknow	unknow	MX	NX
TCGA-DD-A39V	643	1	77	MALE	G3	Stage II	T2	M0	NX
TCGA-DD-A4NG	802	1	77	MALE	G2	Stage IIIA	T3a	M0	NX
TCGA-HP-A5MZ	91	1	78	MALE	G2	Stage I	T1	M0	NX
TCGA-FV-A4ZP	2486	1	78	MALE	G2	Stage IIIA	T3	M0	NX
TCGA-G3-A3CG	673	0	80	MALE	G2	Stage I	T1	M0	N0

TCGA-FV-A2QQ	729	0	80	MALE	G2	Stage I	T1	MX	N0
TCGA-ES-A2HS	688	1	80	MALE	G2	Stage I	T1	MX	NX
TCGA-BC-A112	153	1	80	MALE	G2	unknow	T3	MX	NX
TCGA-BC-A10S	1423	1	81	MALE	G1	unknow	T3	MX	NX
TCGA-2V-A95S	-	0	unknow	MALE	G3	Stage II	T2	MX	NX

Supplementary Table 2. Ferroptosis-related genes.

Ferroptosis-related genes													
Driver													
Symbol	**Name**	**HGNC_ID**	**Evidence**	**Test method**	**Test in**	**Test setting**	**Pathway**	**Confidence**	**Caution**	**Protein encoded**	**UniProtKB**	**PMID**	**Remark**
RPL8	Ribosomal protein L8	HGNC:10368	Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced ferroptosis.	shRNA screening, qPCR, gene silencing	Human	NRAS mutant HT-1080 fibrosarcoma cells; KRAS mutant Calu-1 non small cell lung cancer cell	RPL8:+:Ferroptosis	Validated	_NA_	60S ribosomal protein L8	P62917 (RL8_HUMAN)	####	_NA_
IREB2	Iron response element binding protein 2	HGNC:6115	Required in erastin-induced ferroptosis. Silencing of it conferred against erast	shRNA screening, qPCR, gene silencing	Human	NRAS mutant HT-1080 fibrosarcoma cells; KRAS mutant Calu-1 non small cell lung	IREB2:+:Ferroptosis	Validated	_NA_	Iron-responsive element-binding protein 2	P48200 (IREB2_HUMAN)	####	_NA_

			in-induced ferroptosis.			cancer cell							
ATP5MC3	ATP synthase membrane subunit c locus 3	HGNC:843	Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced ferroptosis.	shRNA screening, qPCR, gene silencing	Human	NRAS mutant HT-1080 fibrosarcoma cells; KRAS mutant Calu-1 non small cell lung cancer cell	ATP5MC3 :+: Ferroptosis	Validated	_NA_	ATP synthase F(0) complex subunit C3	P48201 (AT5G3_HUMAN)	####	ATP5G3 in article
CS	Citrate synthase	HGNC:2422	Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced	shRNA screening, qPCR, gene silencing	Human	NRAS mutant HT-1080 fibrosarcoma cells; KRAS mutant Calu-1 non small cell lung cancer cell	CS :+: Ferroptosis	Validated	_NA_	Citrate synthase	O75390 (CISY_HUMAN)	####	_NA_

			ferroptosis.										
EMC2	ER membrane protein complex subunit 2	HGNC:28963	Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced ferroptosis.	shRNA screening, qPCR, gene silencing	Human	NRAS mutant HT-1080 fibrosarcoma cells; KRAS mutant Calu-1 non small cell lung cancer cell	EMC2 :+: Ferroptosis	Validated	_NA_	ER membrane protein complex subunit 2	Q15006 (EMC2_HUMAN)	####	TTC35 in article
ACSF2	Acyl-CoA synthetase family member 2	HGNC:26101	Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced	shRNA screening, qPCR, gene silencing	Human	NRAS mutant HT-1080 fibrosarcoma cells; KRAS mutant Calu-1 non small cell lung cancer cell	ACSF2 :+: Ferroptosis	Validated	_NA_	Medium-chain acyl-CoA ligase ACSF2	Q96CM8 (ACSF2_HUMAN)	####	_NA_

			ferroptosis.										
NOX1	Nicotinamide adenine dinucleotide phosphate (NADPH) oxidase (NOX) 1	HGNC:7889	Suppresses erastin-induced ferroptosis when inhibited by inhibitor.	Inhibition test by diphenylene iodonium (DPI) and GKT137831.	Human	KRAS mutant Calu-1 non small cell lung cancer cell	NOX1 :+: Ferroptosis	Deduced	The presented inhibition study is not sufficient to confirm its role in ferroptosis.	NADPH oxidase 1	Q9Y5S8 (NOX1_HUMAN)	####	_NA_
CYBB	Cytochrome b-245 beta chain	HGNC:2578	Suppresses erastin-induced ferroptosis when inhibited by inhibitor.	Inhibition test by diphenylene iodonium (DPI).	Human	KRAS mutant Calu-1 non small cell lung cancer cell	CYBB :+: Ferroptosis	Deduced	The presented inhibition study is not sufficient to confirm its role in ferroptosis.	Cytochrome b-245 heavy chain	P04839 (CY24B_HUMAN)	####	NOX2 in article
NOX3	Nicotinamide adenine dinucleotide phosphate (NADPH) oxidase (NOX) 3	HGNC:7890	Suppresses erastin-induced ferroptosis when inhibited	Inhibition test by diphenylene iodonium (DPI).	Human	KRAS mutant Calu-1 non small cell lung cancer cell	NOX3 :+: Ferroptosis	Deduced	The presented inhibition study is not sufficient to confirm its role in	NADPH oxidase 3	Q9HBY0 (NOX3_HUMAN)	####	_NA_

			by inhibitor.						ferroptosis.			
NOX4	Nicotinamide adenine dinucleotide phosphate (NADPH) oxidase (NOX) 4	HGNC:7891	Suppresses erastin-induced ferroptosis when inhibited by inhibitor.	Inhibition test by diphenylene iodonium (DPI) and GKT137831.	Human	KRAS mutant Calu-1 non small cell lung cancer cell	NOX4 :+: Ferroptosis	Deduced	The presented inhibition study is not sufficient to confirm its role in ferroptosis.	NADPH oxidase 4	Q9NPH5 (NOX4_HUMAN)	####	_NA_
NOX5	Nicotinamide adenine dinucleotide phosphate (NADPH) oxidase (NOX) 5	HGNC:14874	Suppresses erastin-induced ferroptosis when inhibited by inhibitor.	Inhibition test by diphenylene iodonium (DPI).	Human	KRAS mutant Calu-1 non small cell lung cancer cell	NOX5 :+: Ferroptosis	Deduced	The presented inhibition study is not sufficient to confirm its role in ferroptosis.	NADPH oxidase 5	Q96PH1 (NOX5_HUMAN)	####	_NA_
DUOX1	Dual oxidase 1	HGNC:3062	Suppresses erastin-induced ferroptosis when inhibited by inhibitor.	Inhibition test by diphenylene iodonium (DPI).	Human	KRAS mutant Calu-1 non small cell lung cancer cell	DUOX1 :+: Ferroptosis	Deduced	The presented inhibition study is not sufficient to confirm its role in ferroptosis.	Dual oxidase 1	Q9NRD9 (DUOX1_HUMAN)	####	_NA_

DUOX2	Dual oxidase 2	HGNC:13273	Suppresses erastin-induced ferroptosis when inhibited by inhibitor.	Inhibition test by diphenylene iodonium (DPI).	Human	KRAS mutant Calu-1 non small cell lung cancer cell	DUOX2 :+: Ferroptosis	Deduced	The presented inhibition study is not sufficient to confirm its role in ferroptosis.	Dual oxidase 2	Q9NRD8 (DUOX2_HUMAN)	####	_NA_
G6PD	Glucose-6-phosphate dehydrogenase	HGNC:4057	Required in erastin-induced ferroptosis.	shRNA silencing, RT-qPCR	Human	KRAS mutant Calu-1 non small cell lung cancer cell	G6PD :+: Ferroptosis	Validated	_NA_	Glucose-6-phosphate 1-dehydrogenase	P11413 (G6PD_HUMAN)	####	_NA_
PGD	Phosphoglycerate dehydrogenase	HGNC:8891	Required in erastin-induced ferroptosis.	shRNA silencing, RT-qPCR	Human	KRAS mutant Calu-1 non small cell lung cancer cell	PGD :+: Ferroptosis	Validated	_NA_	6-phosphogluconate dehydrogenase	P52209 (6PGD_HUMAN)	####	_NA_
VDAC2	Valtage-dependent anion channels 2	HGNC:12672	Required in erastin-induced ferroptosis.	shRNA silencing, RT-qPCR	Human	KRAS mutant Calu-1 non small cell lung cancer cell	VDAC2 :+: Ferroptosis	Validated	_NA_	Voltage-dependent anion-selective channel protein 2	P45880 (VDAC2_HUMAN)	####	_NA_

PIK3CA	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha	HGNC:8975	Inhibitor blocked ferroptotic cell death.	Cell survival assays	Mice	HT22 cells	PIK3CA :-: GSH, GSH :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	Also involved in necrosis and apoptosis.	Phosphatidylinositol 4	P42336 (PK3CA_HUMAN)	####	PI3K alpha in article
FLT3	Fms related tyrosine kinase 3	HGNC:3765	Inhibitor blocked ferroptotic cell death.	Cell survival assays	Mice	HT22 cells	FLT3 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	Also involved in necrosis and apoptosis.	Receptor-type tyrosine-protein kinase FLT3	P36888 (FLT3_HUMAN)	####	_NA_
SCP2	Sterol carrier protein 2	HGNC:10606	SCP-2 inhibitors showed anti-ferroptotic activity, which was substantiated by knocking down SCP-2 in Gpx4 −/− cells.	Cell viability test, siRNA-mediated knockdown.	Mice	PZL cells	SCP2 :+: Ferroptosis	Validated	Transient effect. Other translocases may work in parallel.	Non-specific lipid-transfer protein	P22307 (NLTP_HUMAN)	####	_NA_

TP53	Tumor protein p53	HGNC:11998	Inhibits cystine uptake and sensitizes cells to ferroptosis. Erastin induced high levels of cell death in p53 +/+ MEFs.	Cell death kinetics, shRNA, western blotting, RT-PCR, ChIP assay, cystine uptake assay	Human, mice	H1299, U2OS and MCF7 cells, mouse embryonic fibroblasts	TP53 :-: SLC7A11, SLC7A11 :+: Cystine, Cystine :-: Ferroptosis	Validated	The acetylation-defective mutant (p53[3KR]) also retains the ability to induce ferroptosis upon reactive oxygen species (ROS)-induced stress.	Cellular tumor antigen p53	P04637 (P53_HUMAN)	####	_NA_
ACSL4	Acyl-CoA synthetase long chain family member 4	HGNC:3571	Deletion of this gene likely suppress ferroptosis by limiting the membrane-resident pool of oxidation-sensitive fatty acids.	Retroviral-mediated insertional mutagenesis and sequencing	Human	Chronic myeloid leukemia cell line KBM7	ACSL4 :+: Ferroptosis	Predicted	Author prediction based on gene function.	Long-chain-fatty-acid--CoA ligase 4	O60488 (ACSL4_HUMAN)	####	_NA_

LPCAT3	Lysophosphatidylcholine acyltransferase 3	HGNC:30244	Deletion of this gene likely suppress ferroptosis by limiting the membrane-resident pool of oxidation-sensitive fatty acids.	Retroviral-mediated insertional mutagenesis and sequencing	Human	Chronic myeloid leukemia cell line KBM7	LPCAT3 :+: Ferroptosis	Predicted	Author prediction based on gene function.	Lysophospholipid acyltransferase 5	Q6P1A2 (MBOA5_HUMAN)	####	_NA_
NRAS	NRAS proto-oncogene, GTPase	HGNC:7989	NRAS S12V mutant protects RMS13 cells from ferroptotic cell death.	Cell viability assessed by MTT assay, western blot	Human	RMS13 cells	NRAS :+: Ferroptosis	Deduced	Inferred as a promoter because RAS mutant is resistant to ferroptosis.	GTPase NRas	P01111 (RASN_HUMAN)	####	_NA_
KRAS	KRAS proto-oncogene, GTPase	HGNC:6407	KRAS S12V mutant protects RMS13 cells from ferroptotic cell death.	Cell viability assessed by MTT assay, western blot	Human	RMS13 cells	KRAS :+: Ferroptosis	Deduced	Inferred as a promoter because RAS mutant is resistant to ferroptosis.	GTPase KRas	P01116 (RASK_HUMAN)	####	_NA_

HRAS	HRas proto-oncogene, GTPase	HGNC:5173	HRAS S12V mutant protects RMS13 cells from ferroptotic cell death.	Cell viability assessed by MTT assay, western blot	Human	RMS13 cells	HRAS :+: Ferroptosis	Deduced	Inferred as a promoter because RAS mutant is resistant to ferroptosis.	GTPase HRas	P01112 (RASH_HUMAN)	####	_NA_
TF	Transferrin	HGNC:11740	Essential for the induction of ferroptotic cell death. Transferrin can only interact with transferrin receptor and be transported into the cell when it is loaded with iron.	Killing activity	Mice	Mouse embryonic fibroblasts	TF :+: Ferroptosis	Validated	_NA_	Serotransferrin	P02787 (TRFE_HUMAN)	####	Transferrin in article
TFRC	Transferrin receptor	HGNC:11763	RNAi of transferrin receptor (TfR) inhib	RNAi	Mice	Mouse embryonic fibroblasts	TFRC :+: Ferroptosis	Validated	_NA_	Transferrin receptor protein 1	P02786 (TFR1_HUMAN)	####	Tfr in article

			ited ferroptosis.									
TFR2	Transferrin receptor 2	HGNC:11762	RNAi of transferrin receptor (TfR) inhibited ferroptosis.	RNAi	Mice	Mouse embryonic fibroblasts	TFR2 :+: Ferroptosis	Validated	_NA_	Transferrin receptor protein 2	Q9UP52 (TFR2_HUMAN)	####	Tfr in article
SLC38A1	Solute carrier family 38 member 1	HGNC:13447	RNAi knockdown markedly blocked ferroptosis.	RNAi knockdown, cell survival analysis	Mice	Mouse embryonic fibroblasts	SLC38A1 :+: Glutamine, Glutamine :+: Glutamate, Glutamate :+: alpha-Ketoglutarate, alpha-Ketoglutarate :+: Ferroptosis	Validated	_NA_	Sodium-coupled neutral amino acid transporter 1	Q9H2H9 (S38A1_HUMAN)	####	_NA_

SLC1A5	Solute carrier family 1 member 5	HGNC:10943	Pharmacological inhibition by L-g-glutamyl-p-nitroanilide or RNAi knockdown markedly blocked ferroptosis.	RNAi knockdown, cell survival analysis	Mice	Mouse embryonic fibroblasts	SLC1A5 :+: Glutamine, Glutamine :+: Glutamate, Glutamate :+: alpha-Ketoglutarate, alpha-Ketoglutarate :+: Ferroptosis	Validated	_NA_	Neutral amino acid transporter B(0)	Q15758 (AAAT_HUMAN)	####	_NA_
GLS2	Glutaminase 2	HGNC:29570	Both inhibitor inhibition and gene knockdown inhibit ferroptotic cell death.	shRNA, western blot, cell viability	Mice	Mouse embryonic fibroblasts	GSL2 :+: Glutamate, Glutamate :+: Ferroptosis	Validated	_NA_	Glutaminase liver isoform	Q9UI32 (GLSL_HUMAN)	####	_NA_
GOT1	Glutamic-oxaloacetic transaminase 1	HGNC:4432	RNAi reduced ferroptosis.	shRNA, qPCR, cell viability	Mice	Mouse embryonic fibroblasts	GOT1 :+: alpha-Ketoglutarate, alpha-Ketoglutarate :+: Ferroptosis	Validated	_NA_	Aspartate aminotransferase	P17174 (AATC_HUMAN)	####	_NA_

CARS1	Cysteinyl-tRNA synthetase 1	HGNC:1493	Required for ferroptosis in diverse cell contexts. Knockdown of CARS inhibited erastin-induced death by preventing the induction of lipid reactive oxygen species, without altering iron homeostasis.	siRNA screen, shRNA, western blot, cell viability	Human, rat	HT-1080 fibrosarcoma cells, BJeLR fibroblast cells, Panc1 cells, A673 (Ewing’s sarcoma) and 143B (osteosarcoma) cells, PC12 cells	CARS1 :-: Transsulfuration pathway, Transsulfuration pathway :-: Ferroptosis	Validated	_NA_	Cysteine--tRNA ligase	P49589 (SYCC_HUMAN)	####	CARS in article
TP53	Tumor protein p53	HGNC:11998	Wild type p53 can induce ferroptosis upon reactive oxygen species	Cell death quantification, western blot	Human	H1299 cells	TP53 :-: SLC7A11, SLC7A11 :-: Ferroptosis	Validated	_NA_	Cellular tumor antigen p53	P04637 (P53_HUMAN)	####	p53 in article

			(ROS)-induced stress.										
ALOX5	Arachidonate 5-lipoxygenase	HGNC:435	The 5-Lipoxygenase inhibitor zileuton protected HT22 neuronal cells from erastin-induced ferroptosis.	Cell Viability Assay, ROS measurement	Mice	HT22 mouse neuronal cell line	ALOX5 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Arachidonate 5-lipoxygenase	P09917 (LOX5_HUMAN)	####	5-LOX in article

KEAP1	Kelch like ECH associated protein 1	HGNC:23177	Knockdown of Keap1 reversed loss of p62-increased degradation of NRF2 in ferroptosis. Keap1 knockdown led to resistance to erastin-induced and sorafenib-induced growth inhibition with decreased ferroptotic events in the absence or presence of p62 knoc	Western blot, shRNA knockdown, cell viability	Human, mice	HepG2, Hepa1-6, Hep3B, and SNU-182 cells	KEAP1 :-: NFE2L2, NFE2L2 :-: Ferroptosis	Validated	_NA_	Kelch-like ECH-associated protein 1	Q14145 (KEAP1_HUMAN)	####	_NA_

			kdown.										
HMOX1	Heme oxygenase 1	HGNC:5013	Zinc protoporphyrin IX, a HO-1 inhibitor, prevented Erastin-triggered ferroptotic cancer cell death. Overexpr	Cell viability assay, qRT-PCR, western blot	Human, mice	HT-1080 fibrosarcoma cells, mice lung fibroblastic cells	HMOX1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	Other articles (PMID 26403645, 28515173) suggest it a suppressor.	Heme oxygenase 1	P09601 (HMOX1_HUMAN)	####	HO-1 in article

			ession accelerates erastin-induced cell death.										
TP53	Tumor protein p53	HGNC:11998	p53^3KR/3KR Xrcc4^-/- MEF cells are very sensitive to ferroptosis. Stabilized in the spleens of p53^3KR/3KR Xrcc4^-/- mice which enables to prevent the development of pro-B-	Western blot, qRT-PCR, cell viability	Mice	p53^3KR/3KR Xrcc4^-/- MEF cells, p53^3KR/3KR Xrcc4^-/- mice	TP53 :-: SLC7A11, SLC7A11 :-: Ferroptosis	Validated	_NA_	Cellular tumor antigen p53	P04637 (P53_HUMAN)	####	p53 in article

			cell lymphomas.										
TP53	Tumor protein p53	HGNC:11998	Incubation with erastin led to profound cell death in wild-type MEFs.	Cell viability assay, phase-contrast microscopy	Human, mice	Mouse embryonic fibroblasts, lymphoblastoid cell lines	TP53 :-: SLC7A11, SLC7A11 :-: Ferroptosis	Validated	_NA_	Cellular tumor antigen p53	P04637 (P53_HUMAN)	####	p53 in article

GLS2	Glutaminase 2	HGNC:29570	Upregulated in erastin-treated wild-type MEFs, and silencing Gls2 exihibits cell death defect in wild-type MEFs treated with erastin.	Cell viability assay,western blot	Mice	Mouse embryonic fibroblasts	GLS2:+:Ferroptosis	Validated	_NA_	Glutaminase liver isoform	Q9UI32 (GLSL_HUMAN)	####	_NA_
ATG5	Autophagy related 5	HGNC:589	Knockout or knockdown limited erastin-induced ferroptosis.	shRNA	Human, mice	Mouse embryonic fibroblasts, human pancreatic cancer cell lines (PANC1 and PANC2.03), and the human fibrosarcoma cell line	ATG5:+:Ferroptosis	Validated	_NA_	Autophagy protein 5	Q9H1Y0 (ATG5_HUMAN)	####	_NA_

						HT-1080							
ATG7	Autophagy related 7	HGNC:16935	Knockout or knockdown limited erastin-induced ferroptosis.	shRNA	Human, mice	Mouse embryonic fibroblasts, human pancreatic cancer cell lines (PANC1 and PANC2.03), and the human fibrosarcoma cell line HT-1081	ATG7:+:Ferroptosis	Validated	_NA_	Ubiquitin-like modifier-activating enzyme ATG7	O95352 (ATG7_HUMAN)	####	_NA_

NCOA4	Nuclear receptor coactivator 4	HGNC:7671	Inhibition suppressed ferroptosis, and overexpression promoted ferroptosis.	shRNA, gene transfection	Human	PANC1 or HT-1080 cells	NCOA4 :-: FTH1, FTH1 :-: Ferroptosis	Validated	_NA_	Nuclear receptor coactivator 4	Q13772 (NCOA4_HUMAN)	####	_NA_
TF	Transferrin	HGNC:11740	Involved in siramesine and lapatinib-induced ferroptotic cell death. Increased following treatment with lapatinib alone or in combination with siramesine. Knocking down of transferrin resulted	Western blot, densitometry quantification, siRNA, gene transfection, cell death test	Human	MDA MB 231 and SKBr3 cells	TF :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Serotransferrin	P02787 (TRFE_HUMAN)	####	Transferrin in article

			in decreased cell death and ROS after treatment.										
ALOX5	Arachidonate 5-lipoxygenase	HGNC:435	Silencing ALOX genes made cells resistant to ferroptosis.	qPCR	Human	G-401 cells	ALOX5 :+: PUFAs peroxidation, PUFAs peroxidation :+: Ferroptosis	Validated	_NA_	Arachidonate 5-lipoxygenase	P09917 (LOX5_HUMAN)	####	_NA_
ALOX12	Arachidonate 12-lipoxygenase, 12S type	HGNC:429	Silencing ALOX genes made cells resistant to	qPCR	Human	G-401 cells	ALOX12 :+: PUFAs peroxidation, PUFAs peroxidatio	Validated	_NA_	Arachidonate 12-lipoxygenase	P18054 (LOX12_HUMAN)	####	_NA_

			ferroptosis.				n :+: Ferroptosis						
ALOX12B	Arachidonate 12-lipoxygenase, 12R type	HGNC:430	Silencing ALOX genes made cells resistant to ferroptosis.	qPCR	Human	G-401 cells	ALOX12B :+: PUFAs peroxidation, PUFAs peroxidation :+: Ferroptosis	Validated	_NA_	Arachidonate 12-lipoxygenase	O75342 (LX12B_HUMAN)	####	_NA_
ALOX15	Arachidonate 15-lipoxygenase	HGNC:433	Silencing ALOX genes made cells resistant to ferroptosis.	qPCR	Human	G-401 cells	ALOX15 :+: PUFAs peroxidation, PUFAs peroxidation :+: Ferroptosis	Validated	_NA_	Arachidonate 15-lipoxygenase	P16050 (LOX15_HUMAN)	####	_NA_

ALOX15B	Arachidonate 15-lipoxygenase type B	HGNC:434	Silencing ALOX genes made cells resistant to ferroptosis. Erastin-induced cell death was rescued by silencing either ALOX15B or ALOXE3, which supported the hypothesis that lipoxygenases are required for ferroptosis.	qPCR, siRNA	Human	G-401, BJeLR and HT-1080 cells	ALOX15B :+: PUFAs peroxidation, PUFAs peroxidation :+: Ferroptosis	Validated	_NA_	Arachidonate 15-lipoxygenase B	O15296 (LX15B_HUMAN)	####	_NA_

ALOXE3	Arachidonate lipoxygenase 3	HGNC:13743	Silencing ALOX genes made cells resistant to ferroptosis. Erastin-induced cell death was rescued by silencing either ALOX15B or ALOXE3, which supported the hypothesis that lipoxygenases are required for ferroptosis.	qPCR, siRNA	Human	G-401, BJeLR and HT-1080 cells	ALOXE3 :+: PUFAs peroxidation, PUFAs peroxidation :+: Ferroptosis	Validated	_NA_	Hydroperoxide isomerase ALOXE3	Q9BYJ1 (LOXE3_HUMAN)	####	_NA_

PHKG2	Phosphorylase kinase catalytic subunit gamma 2	HGNC:8931	U-2-OS cells became resistant to erastin upon PHKG2 silencing. Erastin-treated HT-1080 cells were rescued by shPHKG2.	shRNA suppressor screen, qPCR, cellular iron staining, cell viability	Human	U-2-OS, HT-1080 cells	PHKG2 :+: PUFAs peroxidation, PUFAs peroxidation :+: Ferroptosis	Validated	_NA_	Phosphorylase b kinase gamma catalytic chain	P15735 (PHKG2_HUMAN)	####	_NA_
TFRC	Transferrin receptor	HGNC:11763	The gene targets of the enriched shRNAs are potential genes that positively regulate ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	TFRC :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Transferrin receptor protein 1	P02786 (TFR1_HUMAN)	####	_NA_

ACO1	Aconitase 1	HGNC:117	The gene targets of the enriched shRNAs are potential genes that positively regulate ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	ACO1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Cytoplasmic aconitate hydratase	P21399 (ACOC_HUMAN)	####	_NA_
IREB2	iron responsive element binding protein 2	HGNC:6115	The gene targets of the enriched shRNAs are potential genes that positively regulate ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	IREB2 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Iron-responsive element-binding protein 2	P48200 (IREB2_HUMAN)	####	_NA_
SLC38A1	Solute carrier family 38 member 1	HGNC:13447	The gene targets of the enriched shRNAs are potential genes that positively	RNAi screening	Mice	Mouse embryonic fibroblasts	SLC38A1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Sodium-coupled neutral amino acid transporter 1	Q9H2H9 (S38A1_HUMAN)	####	_NA_

			regulate ferroptosis.										
GLS2	Glutaminase 2	HGNC:29570	The gene targets of the enriched shRNAs are potential genes that positively regulate ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	GLS2 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Glutaminase liver isoform	Q9UI32 (GLSL_HUMAN)	####	_NA_
G6PDX	_NA_	_NA_	The gene targets of the enriched shRNAs are potential genes that positively regulate ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	G6PDX :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	_NA_	_NA_	####	Not found in HGNC

ULK1	Unc-51 like autophagy activating kinase 1	HGNC:12558	Potential positive regulators of ferroptosis. Knockout of ULK1 led to significantly lower levels of erastin-induced ferroptosis in a dose- and time-dependent manner.	RNAi screening, gene knockout	Mice	Mouse embryonic fibroblasts	ULK1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Serine/threonine-protein kinase ULK1	O75385 (ULK1_HUMAN)	####	_NA_

ATG3	Autophagy related 3	HGNC:20962	Potential positive regulators of ferroptosis. Knockout of ATG3 greatly reduced the sensitivity of MEFs to ferropotosis, and reconstituting ATG3 back to these cells restored the ferroptosis sensitivity.	RNAi screening, gene knockout	Mice	Mouse embryonic fibroblasts	ATG3 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Ubiquitin-like-conjugating enzyme ATG3	Q9NT62 (ATG3_HUMAN)	####	_NA_
ATG4D	Autophagy related 4D cysteine peptidase	HGNC:20789	Potential positive regulators of ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	ATG4D :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Cysteine protease ATG4D	Q86TL0 (ATG4D_HUMAN)	####	_NA_

ATG5	Autophagy related 5	HGNC:589	Potential positive regulators of ferroptosis. Knockout of ATG5 led to significantly lower levels of erastin-induced ferroptosis in a dose - and time-dependent manner.	RNAi screening	Mice	Mouse embryonic fibroblasts	ATG5 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Autophagy protein 5	Q9H1Y0 (ATG5_HUMAN)	####	_NA_
BECN1	Beclin 1	HGNC:1034	Potential positive regulators of ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	BECN1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Beclin-1	Q14457 (BECN1_HUMAN)	####	_NA_
MAP1LC3A	Microtubule associated protein 1 light chain 3 alpha	HGNC:6838	Potential positive regulators of ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	MAP1LC3A :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Microtubule-associated proteins 1A/1B light chain 3A	Q9H492 (MLP3A_HUMAN)	####	_NA_

GABARAPL2	GABA type A receptor associated protein like 2	HGNC:13291	Potential positive regulators of ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	GABARAPL2 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Gamma-aminobutyric acid receptor-associated protein-like 2	P60520 (GBRL2_HUMAN)	####	_NA_
GABARAPL1	GABA type A receptor associated protein like 1	HGNC:4068	Potential positive regulators of ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	GABARAPL1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Gamma-aminobutyric acid receptor-associated protein-like 1	Q9H0R8 (GBRL1_HUMAN)	####	_NA_
ATG16L1	Autophagy related 16 like 1	HGNC:21498	Potential positive regulators of ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	ATG16L1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Autophagy-related protein 16-1	Q676U5 (A16L1_HUMAN)	####	_NA_
WIPI1	WD repeat domain, phosphoinositide interacting 1	HGNC:25471	Potential positive regulators of ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	WIPI1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	WD repeat domain phosphoinositide-interacting protein 1	Q5MNZ9 (WIPI1_HUMAN)	####	_NA_
WIPI2	WD repeat domain, phosphoinositide interacting 2	HGNC:32225	Potential positive regulators of ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	WIPI2 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	WD repeat domain phosphoinositide-interacting protein 2	Q9Y4P8 (WIPI2_HUMAN)	####	_NA_
SNX4	Sorting nexin 4	HGNC:11175	Potential positive regulators of ferroptosis.	RNAi screening	Mice	Mouse embryonic fibroblasts	SNX4 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Screened	_NA_	Sorting nexin-4	O95219 (SNX4_HUMAN)	####	_NA_

ATG13	Autophagy related 13	HGNC:29091	Knockout of ATG13 greatly reduced the sensitivity of MEFs to ferroptosis, and reconstituting ATG13 back to these cells restored the ferroptosis sensitivity.	Gene knockout	Mice	Mouse embryonic fibroblasts	ATG13 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Autophagy-related protein 13	O75143 (ATG13_HUMAN)	####	_NA_
ULK2	Unc-51 like autophagy activating kinase 2	HGNC:13480	Knockout of ULK2 led to significantly lower levels of erastin-induced ferroptosis in a dose- and time-dependen	Gene knockout	Mice	Mouse embryonic fibroblasts	ULK2 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Serine/threonine-protein kinase ULK2	Q8IYT8 (ULK2_HUMAN)	####	_NA_

			t manner.										
NCOA4	Nuclear receptor coactivator 4	HGNC:7671	Elimination of NCOA4 expression by RNAi knockdown significantly block ferroptosis	RNAi knockdown, western blot	Human, mice	Mouse embryonic fibroblasts and HT1080 cells	NCOA4 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Nuclear receptor coactivator 4	Q13772 (NCOA4_HUMAN)	####	_NA_

ACSL4	Acyl-CoA synthetase long chain family member 4	HGNC:3571	Knockdown inhibited erastin-induced ferroptosis, whereas overexpression restored ferroptosis sensitization.	shRNA, gene transfection, western blot	Human	LNCaP (human prostate cancer cells), K562 (human erythromyeloblastoid leukemia cell line), HepG2 (human hepatocellular cells), and HL60 (human promyelocytic leukemia cells)	ACSL4 :+: 5-HETE, 5-HETE :+: Ferroptosis	Validated	_NA_	Long-chain-fatty-acid--CoA ligase 4	O60488 (ACSL4_HUMAN)	####	_NA_

TP53	Tumor protein p53	HGNC:11998	p53 acetylation has a critical role in ferroptotic responses. Simultaneous loss of K98/117/161/162 acetylations is unable to induce ferroptosis, and its ability to thwart cancer growth is also abrogated.	Mass spectrometry screening, western blot, cell death assay	Human, mice	H1299 cells, mouse xenograft models	TP53 :-: SLC7A11, SLC7A11 :-: Ferroptosis	Validated	_NA_	Cellular tumor antigen p53	P04637 (P53_HUMAN)	####	_NA_

SAT1	Spermidine/spermine N1-acetyltransferase 1	HGNC:10540	p53-mediated activation of SAT1 contributes to ferroptotic cell death in the presence of ROS stress. Knockdown of Sat1 partially rescued ROS-induced ferroptosis.	qRT-PCR, siRNA, CRISPR-cas9, western blot	Human, mice	H1299, U2OS cells, mouse embryonic fibroblasts, mouse xenograft	SAT1 :+: ALOX15, ALOX15 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	Activated by p53.	Diamine acetyltransferase 1	P21673 (SAT1_HUMAN)	####	_NA_
ALOX15	Arachidonate 15-lipoxygenase	HGNC:433	SAT1- and ROS-induced ferroptosis was completely abrogated by PD146176, an ALOX15-specific inhibitor.	Cell death count, qRT-PCR, siRNA	Human	H1299, U2OS cells	ALOX15 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Arachidonate 15-lipoxygenase	P16050 (LOX15_HUMAN)	####	_NA_

ACSL4	Acyl-CoA synthetase long chain family member 4	HGNC:3571	Inhibition of ACSL4 was effective in protecting against RSL3-induced cell death. Acsl4 KO cells are resistant to ferroptosis.	Cell death count, LC-MS/MS, fluorescence imaging	Mice	Mouse embryonic fibroblasts (Pfa1 cells)	ACSL4 :+: PE, PE :+: Ferroptosis	Validated	_NA_	Long-chain-fatty-acid--CoA ligase 4	O60488 (ACSL4_HUMAN)	####	_NA_
LPCAT3	Lysophosphatidylcholine acyltransferase 3	HGNC:30244	Knockdown of Lpcat3 increased resistance to ferroptosis triggered by RSL3.	shRNA	Mice	Mouse lung epithelial (MLE) and embryonic cells	LPCAT3 :+: Ferroptosis	Validated	_NA_	Lysophospholipid acyltransferase 5	Q6P1A2 (MBOA5_HUMAN)	####	_NA_

ALOX15	Arachidonate 15-lipoxygenase	HGNC:433	Liproxstatin-1 inhibited the 15-LOX enzymatic activity and suppressed ferroptosis.	Identification of oxygenated PE	Mice	Kidney of GPX4-deficient mice	ALOX15 :+: PE, PE :+: Ferroptosis	Validated	_NA_	Arachidonate 15-lipoxygenase	P16050 (LOX15_HUMAN)	####	15-LOX in article
ACSL4	Acyl-CoA synthetase long chain family member 4	HGNC:3571	An essential proferroptotic gene. Re-expression of Flag-tagged human wild-type (WT) ACSL4 (ACSL4-Flag) in Acsl4 KO Pfa1 cells restored full sensitivity to ferroptosis induction.	Cell viability, immunoblot, lipid peroxidation assessment, CRISPR–Cas9, qPCR, microarray, RNA-seq	Human, mice	Mouse embryonic fibroblasts (Pfa1 cells), human breast cancer cell lines, Gpx4 KO mice	ACSL4 :+: Ferroptosis	Validated	_NA_	Long-chain-fatty-acid--CoA ligase 4	O60488 (ACSL4_HUMAN)	####	_NA_

			Inhibition showed significantly prolonged survival compared to vehicle-treated mice.										
KEAP1	Kelch like ECH associated protein 1	HGNC:23177	Keap1 silencing decreased ferroptosis.	Cell viability assay, western blot, siRNA	Mice	Head and neck cancer cells, nude mice	KEAP1 :-: NFE2L2, NFE2L2 :-: Ferroptosis	Validated	_NA_	Kelch-like ECH-associated protein 1	Q14145 (KEAP1_HUMAN)	####	_NA_

EGFR	Epidermal growth factor receptor	HGNC:3236	Cell death in activated EGFR mutant cells occurs by ferroptosis. Inhibiting EGFR and MAPK signaling rescued cell viability following cystine withdrawal.	Fluorescence-activated cell sorting (FACS) analysis, cell viability	Human	Human mammary epithelial) cells	EGFR:+: MAPK, MAPK:+: Ferroptosis	Validated	_NA_	Epidermal growth factor receptor	P00533 (EGFR_HUMAN)	####	_NA_
NOX4	NADPH oxidase 4	HGNC:7891	Inhibition of NADPH oxidase 4 (NOX4) blocked ferroptosis.	Fluorescence-activated cell sorting (FACS) analysis, cell viability	Human	Human mammary epithelial) cells	NOX4:+: Lipid ROS, Lipid ROS:+: Ferroptosis	Validated	_NA_	NADPH oxidase 4	Q9NPH5 (NOX4_HUMAN)	####	_NA_

MAPK3	Mitogen-activated protein kinase 3	HGNC:6877	Inhibiting EGFR and MAPK signaling rescued cell viability following cystine withdrawal.	Immunoblots, lucifer yellow infiltration, cell viability, fluorescence-activated cell sorting (FACS) analysis	Human	Human mammary epithelial) cells	MAPK :-: GPX4, GPX4 :-: Lipid ROS, MAPK :+: NOX4, NOX4 :+: H2O2, H2O2 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Mitogen-activated protein kinase 3	P27361 (MK03_HUMAN)	####	ERK1 in article
MAPK1	Mitogen-activated protein kinase 1	HGNC:6871	Inhibiting EGFR and MAPK signaling rescued cell viability following cystine withdrawal.	Immunoblots, lucifer yellow infiltration, cell viability, fluorescence-activated cell sorting (FACS) analysis	Human	Human mammary epithelial) cells	MAPK :-: GPX4, GPX4 :-: Lipid ROS, MAPK :+: NOX4, NOX4 :+: H2O2, H2O2 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Mitogen-activated protein kinase 1	P28482 (MK01_HUMAN)	####	ERK2 in article

BID	BH3 interacting domain death agonist	HGNC:1050	BID deletion prevents erastin- and glutamate-induced cell death. BID inhibition inhibited erastin-induced ferroptosis.	Cell viability, western blot, CRISPR/Cas9, gene transfection	Mice	HT-22 cells, mouse embryonic fibroblasts	BID :+: Ferroptosis	Validated	_NA_	BH3-interacting domain death agonist	P55957 (BID_HUMAN)	####	_NA_
ACSL4	Acyl-CoA synthetase long chain family member 4	HGNC:3571	Knockout of Acsl4 in ferroptosis-sensitive cells conferred protection from erastin- and RSL3-induced cell death.	CRISPR/Cas9, western blotting, cell death assessment	Human, mice	NIH3T3, HT-29, HT-1080 and L929 cells	ACSL4 :+: Ferroptosis	Validated	_NA_	Long-chain-fatty-acid--CoA ligase 4	O60488 (ACSL4_HUMAN)	####	_NA_

ZEB1	Zinc finger E-box binding homeobox 1	HGNC:11642	Knockout of ZEB1 prevents cell death induced by GPX4 inhibition.	sgRNA, cell viability	Human	KP4 pancreatic cancer cells	ZEB1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Zinc finger E-box-binding homeobox 1	P37275 (ZEB1_HUMAN)	####	_NA_
KEAP1	Kelch like ECH associated protein 1	HGNC:23177	Keap1 inhibition promotes resistance to ferroptosis.	Cell viability analysis	Human, rat	F98, U87 glioma cells	KEAP1 :+: Ferroptosis	Validated	_NA_	Kelch-like ECH-associated protein 1	Q14145 (KEAP1_HUMAN)	####	_NA_
DPP4	Dipeptidyl peptidase 4	HGNC:3009	Required for ferroptosis in TP53-deficient CRC cells.	Cell death, RNAi, western blot, enzyme activity	Human, mice	TP53 -/- HCT116 cells, athymic nude mice	DPP4 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Dipeptidyl peptidase 4	P27487 (DPP4_HUMAN)	####	_NA_

ALOX15	Arachidonate 15-lipoxygenase	HGNC:433	Suppression of ferroptosis following ALOX15 silencing was detected in cancer cells. Cells with exogenous expression of ALOX15 had an increased cell death rate following RSL3 treatment.	siRNA, transfection, western blot, cellular lipoxygenase assay	Human	HT1080, Panc-1, Calu-1 cells	ALOX15 :+: Ferroptosis	Validated	_NA_	Arachidonate 15-lipoxygenase	P16050 (LOX15_HUMAN)	####	_NA_

ALOX12	Arachidonate 12-lipoxygenase, 12S type	HGNC:429	12-LOX inhibitors prevented cell death, whereas ALOX12 overexpression significantly enhanced cell death. ALOX12 expression was gradually elevated during the erastin or RSL3 treatments, and was stable in the late stage of ferroptosis.	siRNA, transfection, western blot, cellular lipoxygenase assay	Human	HT1080, Panc-1, Calu-1 cells	ALOX12 :+: Ferroptosis	Validated	_NA_	Arachidonate 12-lipoxygenase	P18054 (LOX12_HUMAN)	####	_NA_

CDKN2A	Cyclin dependent kinase inhibitor 2A	HGNC: 1787	Combination of ARF induction and ROS treatment induced ferroptotic cell death. Knockdown of endogenous ARF protected cells from ROS-induced cell death.	RNAi, immunoblot, phase-contrast image, cell death quantification	Human, mice	H1299, SaoS2, U2OS cells, mouse embryonic fibroblasts	CDKN2A :-: NFE2L2, NFE2L2 :+: SLC7A11, SLC7A11 :-: Ferroptosis, CDKN2A :+: p53, p53 :-: SLC7A11, SLC7A11 :-: Ferroptosis	Validated	_NA_	Cyclin-dependent kinase inhibitor 2A	P42771 (CDN2A_HUMAN)	####	ARF in article

PEBP1	Phosphatidylethanolamine binding protein 1	HGNC:8630	Elevated levels of PEBP1 resulted in increased sensitivity of HK2 cells to RSL3 whereas lowered contents of PEBP1 in HAEC and HT22 cells were associated with decreased sensitivity to ferroptosis.	Western blot, siRNA, cell death assay	Human, mice	HK2, HAEC and HT22 cells	(PEBP1/15LO) :+: Ferroptosis	Validated	_NA_	Phosphatidylethanolamine-binding protein 1	P30086 (PEBP1_HUMAN)	####	_NA_

SOCS1	Suppressor of cytokine signaling 1	HGNC:19383	Expression of SOCS1 sensitized cells to ferroptosis inducer. This effect of SOCS1 was efficiently blocked by ferroptosis inhibitor. Expression of SOCS1 reduced the levels of GSH, explaining in part its ability to sensitize cells to ferroptosis.	Cell death assay, cell viability assay, qPCR	Human	U2OS or IMR90 cells	SOCS1 :+: p53, p53 :-: SLC7A11, SLC7A11 :+: GSH, GSH :-: Ferroptosis	Validated	_NA_	Suppressor of cytokine signaling 1	O15524 (SOCS1_HUMAN)	####	_NA_

CDO1	Cysteine dioxygenase type 1	HGNC:1795	CDO1 suppression contributes to ferroptosis resistance.	siRNA, western blot, MTT assay	Human	Gastric cancer cells AGS, BGC823, athymic nude mice	CDO1 :-: GPX4, GPX4 :-: Ferroptosis	Validated	_NA_	Cysteine dioxygenase type 1	Q16878 (CDO1_HUMAN)	####	_NA_
MYB	MYB proto-oncogene, transcription factor	HGNC:7545	Erastin-induced ferroptosis was restrained when c-Myb was suppressed.	Western blot, siRNA, qRT-PCR, MTT assay	Human	Gastric cancer cells AGS, BGC823, MKN45, SGC7901, and MGC803	MYB :+: CDO1, CDO1 :-: GPX4, GPX4 :-: Ferroptosis	Validated	_NA_	Transcriptional activator Myb	P10242 (MYB_HUMAN)	####	C-Myb in article
HMOX1	Heme oxygenase 1	HGNC:5013	Inhibiting HO-1 effectively attenuated BAY-induced ferroptotic cell death. Defective HO-1 expression significantly rescued cell survi	Cell viability assay, qRT-PCR, shRNA, gene overexpression, western blot	Human	MDA-MB-231, MDA-MB-468	HMOX1 :+: Ferroptosis	Validated	_NA_	Heme oxygenase 1	P09601 (HMOX1_HUMAN)	####	HO-1 in article

			val suppressed by BAY.										
MAPK8	Mitogen-activated protein kinase 8	HGNC:6881	JNK1/2 inhibitors inhibited t-BHP-induced ferroptosis. t-BHP treatment significantly increased the protein expression of p-JNK.	MitoSOX probe, luminometer kit, C11-BODIPY probe, western blot	Rat	PC12 cells	MAPK8 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Mitogen-activated protein kinase 8	P45983 (MK08_HUMAN)	####	JNK1 in article

MAPK9	Mitogen-activated protein kinase 9	HGNC:6886	JNK1/2 inhibitors inhibited t-BHP-induced ferroptosis. t-BHP treatment significantly increased the protein expression of p-JNK.	MitoSOX probe, luminometer kit, C11-BODIPY probe, western blot	Rat	PC12 cells	MAPK9 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Mitogen-activated protein kinase 9	P45984 (MK09_HUMAN)	####	JNK2 in article
MAPK1	Mitogen-activated protein kinase 1	HGNC:6871	ERK1/2 inhibitors inhibited t-BHP-induced ferroptosis. t-BHP treatment significantly increased the protein expression of p-ERK.	MitoSOX probe, luminometer kit, C11-BODIPY probe, western blot	Rat	PC12 cells	MAPK1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Mitogen-activated protein kinase 1	P28482 (MK01_HUMAN)	####	ERK2 in article

MAPK3	Mitogen-activated protein kinase 3	HGNC:6877	ERK1/2 inhibitors inhibited t-BHP-induced ferroptosis. t-BHP treatment significantly increased the protein expression of p-ERK.	MitoSOX probe, luminometer kit, C11-BODIPY probe, western blot	Rat	PC12 cells	MAPK3 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Mitogen-activated protein kinase 3	P27361 (MK03_HUMAN)	####	ERK1 in article
SLC1A5	Solute carrier family 1 member 5	HGNC:10943	Overexpression of SLC1A5 restored miR-137-mediated ferroptosis suppression.	Cell viability assay, lipid ROS assay, western blot, gene overexpression, shRNA	Human	Melanoma cell lines A375 and G-361	SLC1A5 :+: Glutaminolysis, Glutaminolysis :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Neutral amino acid transporter B(0)	Q15758 (AAAT_HUMAN)	####	_NA_
CHAC1	ChaC glutathione specific gamma-glutamylcyclotransferase 1	HGNC:28680	CHAC1 degradation of GSH might enhance cystine-starvation	Western blot, real-time PCR, cell viability assay, siRNA, GSH assay kit	Human	MDA-MB-231, Hs 578T, and HCC1937 cells	CHAC1 :-: GSH, GSH :-: Ferroptosis	Validated	_NA_	Glutathione-specific gamma-glutamylcyclotransferase 1	Q9BUX1 (CHAC1_HUMAN)	####	_NA_

			-induced cell death.										
MAPK14	Mitogen-activated protein kinase 14	HGNC:6876	Ferroptosis was blocked by inhibiting p38 MAPK activation.	Cell viability assay, lipid ROS measurement, RT-qPCR, western blot	Mice	TM4 Sertoli cells	MAPK14 :+: Ferroptosis	Validated	_NA_	Mitogen-activated protein kinase 14	Q16539 (MK14_HUMAN)	####	p38 MAPK in article
LINC00472	Long intergenic non-protein coding RNA 472	HGNC:21380	Increases erastin-induced growth inhibition, whereas depletion of P53RRA decreased erastin-induced growth inhibition.	Bisulfite sequencing, RNA pull-down, mass spectrometry, RNA immunoprecipitation, qRT-PCR, cell viability assay	Human	Lung cancer A549, SPCA1, and H522 cells	LINC00472 :+: p53, p53 :+: Ferroptosis	Validated	Also triggers apoptosis.	Putative uncharacterized protein encoded by LINC00472	Q9H8W2 (CF155_HUMAN)	####	P53RRA in article

NOX4	NADPH oxidase 4	HGNC:7891	Activated Nox4 contributes to PAB-induced ferroptotic cell death. knockdown made cells resistant to PAB-induced death.	Western blot, LDH release assay, siRNA, cell death, siRNA	Human, rat	Rat C6, human SHG-44, U87 and U251 glioma cells	NOX4 :+: H2O2, H2O2 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	NADPH oxidase 4	Q9NPH5 (NOX4_HUMAN)	####	_NA_
GOT1	Glutamic-oxaloacetic transaminase 1	HGNC:4432	Overexpression of miR-9 suppressed GOT1, which subsequently reduced ferroptosis. Overexpression of GOT1 restored miR-9 mediated	Immunoblotting, luciferase reporter assay, qPCR, cell viability assay, MDA assay, iron assay, glutamate assay	Human	A375 and G-361 cells	GOT1 :+: alpha KG, alpha KG :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Aspartate aminotransferase	P17174 (AATC_HUMAN)	####	_NA_

			ferroptosis suppression.										
BECN1	Beclin 1	HGNC:1034	Knockdown inhibits ferroptosis. Overexpression increases ferroptotic cancer cell death.	shRNA, western blot, cell viability assay, gene overexpression	Human, mice	HCT116, CX-1, PANC1, HT1080, and Calu-1 cells, athymic nude immunodeficient mice	BECN1 :-: System Xc-, System Xc- :+: GSH, GSH :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Beclin-1	Q14457 (BECN1_HUMAN)	####	_NA_
PRKAA2	Protein kinase AMP-activated catalytic subunit alpha 2	HGNC:9377	Inhibition of PRKAA/AMPK alpha diminishes ferroptosis.	siRNA, western blot, cell viability assay, GSH assay, lipid peroxidation assay, iron assay	Human	HCT116 and CX-1 cells	PRKAA2 :+: (BECN1/SLC7A11), (BECN1/SLC7A11) :+: Ferroptosis	Validated	_NA_	5'-AMP-activated protein kinase catalytic subunit alpha-2	P54646 (AAPK2_HUMAN)	####	PRKAA in article

PRKAA1	Protein kinase AMP-activated catalytic subunit alpha 1	HGNC:9376	Inhibition of PRKAA/AMPK alpha diminishes ferroptosis.	siRNA, western blot, cell viability assay, GSH assay, lipid peroxidation assay, iron assay	Human	HCT116 and CX-1 cells	PRKAA1 :+: (BECN1/SLC7A11), (BECN1/SLC7A11) :+: Ferroptosis	Validated	_NA_	5'-AMP-activated protein kinase catalytic subunit alpha-1	Q13131 (AAPK1_HUMAN)	####	AMPK alpha in article
ELAVL1	ELAV like RNA binding protein 1	HGNC:3312	ELAVL1 siRNA led to ferroptosis resistance, whereas ELAVL1 plasmid contributed to classical ferroptotic events.	Immunohistochemistry, hydroxyproline assay, immunofluorescence, cell viability assay, western blot, qPCR, iron assay, ROS assay, RNAi	Human, mice	Human liver specimens and hepatic stellate cell; C57BL/6 mice; mouse hepatocyte and hepatic stellate cell; HSC-LX2 and HSC-T6 cells	ELAVL1 :+: Ferroptosis	Validated	_NA_	ELAV-like protein 1	Q15717 (ELAV1_HUMAN)	####	_NA_

BAP1	BRCA1 associated protein 1	HGNC:950	Suppresses SLC7A11-mediated cystine uptake and promotes ferroptosis. BAP1 mutants lose their abilities to repress SLC7A11 and to promote ferroptosis.	Flow cytometry, cell viability assay, cell death assay, western blot, gene knockout, lipid peroxidation assay, cystine uptake assay, GSH assay, RT-PCR, ChIP-qPCR, luciferase reporter assay, immunoprecipitation, IHC, ChIP-seq	Human	HEK-293T, Caki 1, 786-O, 769-P, ACHN and NCI-H226 cell lines; RCC4, UMRC2, SLR20, and UMRC6 cell lines; TK10 cell line; athymic nude mice	BAP1 :-: SLC7A11, SLC7A11 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Ubiquitin carboxyl-terminal hydrolase BAP1	Q92560 (BAP1_HUMAN)	####	_NA_
TP53	Tumor protein p53	HGNC:11998	Facilitates ART-induced ferroptosis. Conversely, knockdown of P53 blocked ART-induced ferroptosis.	Western blot, immunofluorescence, siRNA	Rat	Hepatic stellate cell HSC-T6	TP53 :+: Ferroptosis	Validated	_NA_	Cellular tumor antigen p53	P04637 (P53_HUMAN)	####	P53 in article

ABCC1	ATP binding cassette subfamily C member 1	HGNC:51	Accelerates ferroptosis. Disruption of MRP1 inhibited ferroptosis potently.	Western blot, GSH assay, dead cell counts, gene transfection, CRISPR/Cas9, cell viability assay, RT-qPCR	Human	HAP1, H1299, U-2 OS cells	ABCC1 :-: GSH, GSH :-: Ferroptosis	Validated	_NA_	Multidrug resistance-associated protein 1	P33527 (MRP1_HUMAN)	####	MRP1 in article
ACSL4	Acyl-CoA synthetase long chain family member 4	HGNC:3571	Inhibition suppresses ferroptosis.	siRNA, western blot, microscopy imaging, fluorescence microscopy, real-time PCR	Human, mice	Male C57BL/6 mice, Caco-2 cells	ACSL4 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Long-chain-fatty-acid--CoA ligase 4	O60488 (ACSL4_HUMAN)	####	_NA_
MIR6852	microRNA 6852	HGNC:49993	Promotes ferroptosis. Binds to LINC0033 and serves as a negative upstream regulator of CBS-mediated ferroptosis inhibition.	qRT-PCR, gene knockdown, luciferase assay, gene overexpression, MTT assay, colony-formation assay	Human	A549 and SPC-A-1 cells	MIR6852 :-: CBS, CBS :-: Ferroptosis	Validated	_NA_	_NA_	_NA_	####	_NA_

ACVR1B	Activin A receptor type 1B	HGNC:172	Inhibition attenuated erastin-induced ferroptosis.	Western blot, siRNA, glutathione assay, RT-PCR, cell viability assay	Human	HK-2 cells	ACVR1B :-: NFE2L2, NFE2L2 :-: Ferroptosis	Validated	_NA_	Activin receptor type-1B	P36896 (ACVR1B_HUMAN)	####	ALK4 in article
TGFBR1	Transforming growth factor beta receptor 1	HGNC:11772	Inhibition attenuated erastin-induced ferroptosis.	Western blot, siRNA, glutathione assay, RT-PCR, cell viability assay	Human	HK-2 cells	TGFBR1 :-: NFE2L2, NFE2L2 :-: Ferroptosis	Validated	_NA_	TGF-beta receptor type-1	P36897 (TGFR1_HUMAN)	####	ALK5 in article
BAP1	BRCA1 associated protein 1	HGNC:950	Promotes ferroptosis induced by class I ferroptosis inducer.	Immunoprecipitation, western blotting, cell death, cell viability, RT-PCR	Human	HEK 293T cells	BAP1 :-: SLC7A11, SLC7A11 :-: Ferroptosis	Validated	_NA_	Ubiquitin carboxyl-terminal hydrolase BAP1	Q92560 (BAP1_HUMAN)	####	_NA_

EPAS1	Endothelial PAS domain protein 1	HGNC:3374	A driver of ferroptosis susceptibility. Ablation reduced susceptibility to ferroptosis.	CRISPR, sgRNA, shRNA, immunoblot, cell viability, western blot	Mice	786-O cells	EPAS1 :+: HILPDA, EPAS1 :+: PLIN2, HILPDA :+: PUFA, PLIN2 :+: PUFA, PUFA :+: PUFA-phospholipid hydroperoxides, PUFA-phospholipid hydroperoxides :+: Ferroptosis	Validated	_NA_	Endothelial PAS domain-containing protein 1	Q99814 (EPAS1_HUMAN)	####	HIF-2alpha in article
HILPDA	Hypoxia inducible lipid droplet associated	HGNC:28859	Promotes ferroptosis sensitivity downstream of HIF-2alpha.	RNA-Seq, western blot, qRT-PCR, shRNA, cell viability, immunoblot	Mice	786-O cells	HILPDA :+: PUFA, PUFA :+: PUFA-phospholipid hydroperoxides, PUFA-phospholipid hydroperoxides :+: Ferroptosis	Validated	_NA_	Hypoxia-inducible lipid droplet-associated protein	Q9Y5L2 (HLPDA_HUMAN)	####	_NA_

HIF1A	Hypoxia inducible factor 1 subunit alpha	HGNC:4910	Re-sensitized HIF-2alpha-null cells to ferroptosis. Induce ferroptosis sensitivity in cancer cells.	cDNA screening, cell viability	Mice	786-O cells	HIF1A :+: HILPDA, HIF1A :+: PLIN2, HILPDA :+: PUFA, PLIN2 :+: PUFA, PUFA :+: PUFA-phospholipid hydroperoxides, PUFA-phospholipid hydroperoxides :+: Ferroptosis	Validated	_NA_	Hypoxia-inducible factor 1-alpha	Q16665 (HIF1A_HUMAN)	####	HIF-1alpha in article
ALOX12	Arachidonate 12-lipoxygenase, 12S type	HGNC:429	An essential factor of p53-dependent ferroptosis. Loss of one Alox12 allele is sufficient to abrogate p53-mediated ferro	RNAi, qRT-PCR, western blot, CRISPR, cell death assay, GSH measurement, flow cytometer	Human, mice	H1299 cells, U2OS cells, mouse embryonic fibroblasts, mice	ALOX12 :+: PUFAs-OOH, PUFAs-OOH :+: Ferroptosis	Validated	_NA_	Arachidonate 12-lipoxygenase	P18054 (LOX12_HUMAN)	####	_NA_

			ptosis.										
ACSL4	Acyl-CoA synthetase long chain family member 4	HGNC:3571	Required for ferroptosis induced by erastin. ACSL4-null cells are resistant to ferroptosis induced by either erastin.	Western blot, cell death assay, CRISPR	Human	U2OS	ACSL4 :+: Ferroptosis	Validated	_NA_	Long-chain-fatty-acid--CoA ligase 4	O60488 (ACSL4_HUMAN)	####	_NA_

HMOX1	Heme oxygenase 1	HGNC:5013	Enhances the ferroptotic process in PRDX6-silenced cells by promoting cellular accumulation of ferrous ions. Overexpression increases both erastin and RSL-3-induced lipid ROS.	Gene transfection, western blot, qRT-PCR, LOOH quantification	Human	H1299 cells	HMOX1 :+: Ferroptosis	Validated	_NA_	Heme oxygenase 1	P09601 (HMOX1_HUMAN)	####	_NA_

IFNG	Interferon gamma	HGNC: 5438	Interferon gamma released from CD8+ T cells downregulates the expression of SLC3A2 and SLC7A11, and as a consequence, promotes tumour cell lipid peroxidation and ferroptosis.	BODIPY-C11, liperfluo staining, cell death measurement, FACS, cell proliferation and viability assay, qPCR, immunoblotting, glutathione quantification, MDA assay, glutamate assay	Human, mice	HT-1080, A375, B16-F0, ID8 cells, female NSG and C57BL/6 mice	IFNG :-: SLC3A2, IFNG :-: SLC7A11, SLC3A2 :+: System Xc-, SLC7A11 :+: System Xc-, System Xc- :+: Cystine, Cystine :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Interferon gamma	P01579 (IFNG_HUMAN)	####	IFNgamma in article
ANO6	Anoctamin 6	HGNC: 25240	Essential for ferroptosis. Inhibition blocked ferroptotic cell death induced by RSL3/erastin.	Immunocytochemistry, RT-PCR, TUNEL Assay, flow Cytometry, LDH assay, gene knockout, siRNA	Human, mice	A549, Cal27, HT29 and MG-63 cells, Cx3cr1-Cre mice	ANO6 :+: Ferroptosis	Validated	_NA_	Anoctamin-6	Q4KMQ2 (ANO6_HUMAN)	####	_NA_

LPIN1	Lipin 1	HGNC:13345	Overexpression of adipose lipin-1 in mice facilitated the onset of hepatic ferroptosis.	Enzyme-linked immunosorbent assay, lipid peroxidation assay, iron assay, MDA assay, qPCR, GSH assay	Mice	C57BL/6 mice	LPIN1 :+: Ferroptosis	Validated	_NA_	Phosphatidate phosphatase LPIN1	Q14693 (LPIN1_HUMAN)	####	_NA_
HMGB1	High mobility group box 1	HGNC:4983	Required for erastin-induced ferroptosis. Knockdown of HMGB1 decreased erastin-induced cell death.	Gene transfection, RNAi, cell viability assay, ELISA, LDH assay, flow cytometry, qPCR, western blot, electron microscopy	Human, mice	HL-60 cell, male NOD/SCID mice	HMGB1 :+: Ferroptosis	Validated	_NA_	High mobility group protein B1	P09429 (HMGB1_HUMAN)	####	_NA_

TNFAIP3	TNF alpha induced protein 3	HGNC:11896	Overexpression increased ROS generation and enhanced erastin-induced ferroptosis, whereas knockdown inhibited erastin-induced ferroptosis.	Lentivirus transduction, CCK-8 assay, DYE670 staining assay, ROS staining assay, RT-qPCR, western blot	Human	HUVEC cells	TNFAIP3 :+: ACSL4, ACSL4 :+: Lipid ROS, TNFAIP3 :-: GPX4, GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Tumor necrosis factor alpha-induced protein 3	P21580 (TNAP3_HUMAN)	####	Zinc lipoprotein A20 in article
TLR4	Toll like receptor 4	HGNC:11850	Knockdown inhibited ferroptosis.	Immunohistochemistry, western blot, cell death assay, siRNA	Rat	Sprague Dawley rats	TLR4 :+: Ferroptosis	Validated	_NA_	Toll-like receptor 4	O00206 (TLR4_HUMAN)	####	_NA_
NOX4	NADPH oxidase 4	HGNC:7891	Knockdown inhibited ferroptosis.	Immunohistochemistry, western blot, cell death assay, siRNA	Rat	Sprague Dawley rats	NOX4 :+: Ferroptosis	Validated	_NA_	NADPH oxidase 4	Q9NPH5 (NOX4_HUMAN)	####	_NA_

ATF3	Activating transcription factor 3	HGNC:785	Promotes ferroptosis induced by erastin.	Cell viability assay, transfection, lentiviral infection, qRT-PCR, western blot	Human	HT1080 cells, retinal pigment epithelial cells	ATF3 :-: SLC7A11, SLC7A11 :+: System Xc-, System Xc- :+: GSH, GSH :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Cyclic AMP-dependent transcription factor ATF-3	P18847 (ATF3_HUMAN)	####	_NA_
ATM	ATM serine/threonine kinase	HGNC:795	Essential for ferroptosis. Genetic knockdown and chemical inhibition of ATM both suppress ferroptotic cell death.	siRNA, western blot, nuclear/cytosol fraction, cell viability, cell death, GSH assay, kinome screen, qRT-PCR, immunofluorescence assay	Human	MDA-MB-231, RCC4, 293T, and HT-1080 cell lines	ATM :-: MTF1, MTF1 :+: FTL, MTF1 :+: FTH1, FTL :-: Ferroptosis, FTH1 :-: Ferroptosis	Validated	_NA_	Serine-protein kinase ATM	Q13315 (ATM_HUMAN)	####	_NA_

YY1AP1	YY1 associated protein 1	HGNC:30935	Makes cells more sensitive to ferroptosis. Cells lacking YAP were no longer sensitised to ferroptosis.	Cell death, cell viability, lipid peroxidation, immunoblotting, CRISPR/Cas9, ChIP assay, qRT-PCR	Human, mice	Mouse embryonic fibroblasts, NF639 cells, human epithelial tumour cells, human mesothelioma cells, xenograft mouse	YAP :+: ACSL4, ACSL4 :+: Ferroptosis, YAP :+: TFRC, TFRC :+: Ferroptosis	Validated	_NA_	YY1-associated protein 1	Q9H869 (YYAP1_HUMAN)	####	YAP in article
EGLN2	Egl-9 family hypoxia inducible factor 2	HGNC:14660	Inhibiting EGLN2 activation diminished ferroptotic tumor cell death.	Cytotoxicity assays, western blot, immunoprecipitation, RNA interference, gene transfection, qPCR, MDA assay	Human, mice	Calu-1, THP1, HT1080, and HL-60 cells, athymic nude mice	EGLN2 :-: HIF1A, HIF1A :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Egl nine homolog 2	Q96KS0 (EGLN2_HUMAN)	####	_NA_

MIOX	Myo-inositol oxygenase	HGNC:14522	Overexpression exacerbates cell death, knockdown inhibits its ferroptosis.	MTT assay, measurement of GPX4 activity, labile iron pool assay, evaluation of cell death and cell morphology, immunohistochemical staining	Human, mice	HK-2 cells, C57BL/6J mice	MIOX :-: GPX4, GPX4 :-: Ferroptosis, MIOX :-: GSH, GSH :-: Ferroptosis	Validated	_NA_	Inositol oxygenase	Q9UGB7 (MIOX_HUMAN)	####	_NA_
TAZ	Tafazzin	HGNC:11577	TAZ removal confers ferroptosis resistance, whereas overexpression of TAZS89A sensitizes cells to ferroptosis.	Cell viability, cell death, western blot, siRNA, qRT-PCR, microarray, immunofluorescence staining, ChIP-seq, Lipid ROS assay	Human, mice	RCC4, 786O cells, JAX NOD.CB17-PrkdcSCID-J mice	TAZ :+: EMP1, EMP1 :+: NOX4, NOX4 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Tafazzin	Q16635 (TAZ_HUMAN)	####	_NA_

MTDH	Metadherin	HGNC:29608	Can enhance sensitivity to inducers of ferroptosis. Enhances the vulnerability of cancer cells to ferroptosis.	Cell viability, qRT-PCR, western blotting, GSH assay, GPx4 activity assay, tumor xenograft model	Human, mice	Cell lines A549, H1975, DMS53, DMS273, KLE, AN3CA, RL95, Hec1A, Ishikawa, MDA-MB-231, MCF-7, Hec50, immunodeficient mice	MTDH :-: Cysteine, Cystein :-: Ferroptosis, MTDH :-: SLC3A2, SLC3A2 :-: Ferroptosis, MTDH :-: GPX4, GPX4 :-: Ferroptosis, MTDH :-: GSH, GSH :-: Ferroptosis, MTDH :+: Glutamate, Glutamate :+: Ferroptosis	Validated	_NA_	Protein LYRIC	Q86UE4 (LYRIC_HUMAN)	####	_NA_

IDH1	Isocitrate dehydrogenase (NADP(+)) 1	HGNC:5382	Deletion of the mutant IDH1 allele or pharmacological inhibition of mutant IDH1 confers resistance to erastin-induced ferroptosis. Ectopic expression of mutant IDH1 promotes ferroptosis.	Cell transfection, cell viability, GSH assay, lipid ROS assay	Human	HEK293T, HT-1080 and KYSE-170 cells	IDH1 :-: GPX4, GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis, IDH1 :-: GSH, GSH :-: Ferroptosis	Validated	_NA_	Isocitrate dehydrogenase [NADP] cytoplasmic	O75874 (IDHC_HUMAN)	####	_NA_
SIRT1	Sirtuin 1	HGNC:14929	Knockout partially mitigates ferroptosis.	Lipid peroxidation, iron and GSH assay, qRT-PCR, western blot	Mice	Mice in C57BL/6 background	SIRT1 :+: Ferroptosis	Predicted	_NA_	NAD-dependent protein deacetylase sirtuin-1	Q96EB6 (SIR1_HUMAN)	####	_NA_

TAZ	Tafazzin	HGNC:11577	TAZ removal confers ferroptosis resistance, while TAZS89A overexpression sensitizes cells to ferroptosis.	siRNA, qRT-PCR, western blot, cell viability, lipid ROS assay	Human	TOV-21G, CAOV2, CAOV2R, MDA-MB-231 cells	TAZ :+: ANGPTL4, ANGPTL4 :+: NOX2, NOX2 :+: Ferroptosis	Validated	_NA_	Tafazzin	Q16635 (TAZ_HUMAN)	####	_NA_
BECN1	Beclin 1	HGNC:1034	Overexpression aggravated isoflurane-induced cell damage by upregulating ferroptosis. This phenomenon was significantly attenuated by silencing of	Cell viability, RNAi, RT-qPCR, western blot, lipid peroxidation, iron, GSH and glutamate release assays	Human	SH-SY5Y cells	(Beclin1/SLC7A11) :-: System Xc-, System Xc- :-: Ferroptosis	Validated	_NA_	Beclin-1	Q14457 (BECN1_HUMAN)	####	Beclin1 in article

			Beclin1.										
FBXW7	F-box and WD repeat domain containing 7	HGNC:16712	FBXW7 plasmid induces ferroptosis.	Cell viability, lipid peroxidation, iron, GSH and ROS assays, western blot, RT-PCR, RNA-seq	Human, mice	Hepatic stellate cells, C57BL/6 mice	FBXW7 :+: Ferroptosis	Deduced	_NA_	F-box/WD repeat-containing protein 7	Q969H0 (FBXW7_HUMAN)	####	_NA_

PANX1	Pannexin 1	HGNC:8599	Deletion protects against ferroptotic cell death. Silenced Panx1 expression significantly attenuated ferroptotic lipid peroxidation and iron accumulation induced by the ferroptosis inducer erastin.	Cell viability, cell death, qRT-PCR, western blot, lipid peroxidation detection, shRNA	Human, mice	HK-2 cells, C57BL/6 mice	PANX1 :-: HMOX1, HMOX1 :-: Ferroptosis, PANX1 :+: MAPK/ERK, MAPK/ERK :+: Ferroptinophagy, Ferroptinophagy :+: Ferroptosis	Validated	_NA_	Pannexin-1	Q96RD7 (PANX1_HUMAN)	####	_NA_

DNAJB6	DnaJ heat shock protein family (Hsp40) member B6	HGNC:14888	Promotes ferroptosis in esophageal squamous cell carcinoma.	Western blot, immunohistochemistry,lentivirus infection, colony-forming, RT-qPCR, CCK-8, transwell and mouse xenograft assays	Human, mice	Cell lines TE-1, Eca9706, Eca109, KYSE 150, and KYSE 450, BALB/c athymic nude mice	DNAJB6 :-: GPX4, GPX4 :-: Ferroptosis	Predicted	_NA_	DnaJ homolog subfamily B member 6	O75190 (DNJB6_HUMAN)	####	_NA_
BACH1	BTB domain and CNC homolog 1	HGNC:935	Promotes ferroptosis by repressing the transcription of a subset of the erastin-induced protective genes.	Western blotting, qPCR, cell death, labile iron detection, RNA-seq	Mice	C57BL/6J mice, mouse embryonic fibroblasts	BACH1 :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Transcription regulator protein BACH1	O14867 (BACH1_HUMAN)	####	_NA_
ACSL4	Acyl-CoA synthetase long chain family member 4	HGNC:3571	Overexpression induced ferroptosis. The opposite results were observed when ACSL	Western blotting, immunofluorescence, 5-HETE, LDH and CCK-8 cell viability assay	Human	HEB, T98G, U87MG and U251 cells	ACSL4 :-: GPX4, GPX4 :-: Ferroptosis	Validated	_NA_	Long-chain-fatty-acid--CoA ligase 4	O60488 (ACSL4_HUMAN)	####	_NA_

			4 was silenced.										
LONP1	Lon peptidase 1, mitochondrial	HGNC:9479	Inhibition of LONP1 negatively regulates erastin-induced cell death.	Cell viability, western blot, qRT-PCR, lipid peroxidation assay, glutathione assay	Human	PANC1, BxPC3 cells	LONP1 :-: Nrf2/Keap1 pathway, Nrf2/Keap1 pathway :-: Ferroptosis, LONP1 :-: GPX4, GPX4 :-: Ferroptosis	Validated	_NA_	Lon protease homolog, mitochondrial	P36776 (LONM_HUMAN)	####	_NA_
Suppressor													
Symbol	Name	HGNC_ID	Evidence	Test method	Test in	Test setting	Pathway	Confidence	Caution	Protein encoded	UniProtKB	PMID	Remark

SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Silencing of SLC7A11 sensitized HT-1080 cells to erastin-induced death, whereas transfection of HT-1080 cells with a plasmid encoding SLC7A11 conferred protection from erastin- and sulfasalazine-induced death.	RT-qPCR, siRNA, gene transfection, cell viability	Human	HT-1080 cells	SLC7A11 :+: Cystine, Cystine :-: Ferroptosis	Validated	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	####	_NA_

GPX4	Glutathione peroxidase 4	HGNC:4556	RNAi-mediated GPX4 knockdown induces ferroptosis.	Affinity-based chemoproteomics, western blotting, and RNAi	Human, mice	HRAS mutant BJeLR-engineered tumor cells, HT-1080 cells, xenograft mouse model (athymic nude mice injected with four million HT-1080 cells)	GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_

AKR1C1	Aldo-keto reductase family 1 member C1	HGNC:384	Up-regulated in DU-145 erastin-resistant clones. Participate in the detoxification of toxic lipid metabolites. May confer partial resistance to erastin by enhancing the detoxification of reactive aldehydes generated downstream of the oxidative destruction of the plasma	RNA-seq, glutamate release assay, cell growth, flow cytometry	Human	DU-145 prostate cancer cells	AKR1C1 :-: Ferroptosis	Validated	_NA_	Aldo-keto reductase family 1 member C1	Q04828 (AK1C1_HUMAN)	####	_NA_

			membrane during ferroptosis.										

AKR1C2	Aldo-keto reductase family 1 member C2	HGNC:385	Up-regulated in DU-145 erastin-resistant clones. Participate in the detoxification of toxic lipid metabolites. May confer partial resistance to erastin by enhancing the detoxification of reactive aldehydes generated downstream of the oxidative destruction of the plasma	RNA-seq, glutamate release assay, cell growth, flow cytometry	Human	DU-145 prostate cancer cells	AKR1C2 :-: Ferroptosis	Validated	_NA_	Aldo-keto reductase family 1 member C2	P52895 (AK1C2_HUMAN)	####	_NA_

			membrane during ferroptosis.										

AKR1C3	Aldo-keto reductase family 1 member C3	HGNC:386	Up-regulated in DU-145 erastin-resistant clones. Participate in the detoxification of toxic lipid metabolites. May confer partial resistance to erastin by enhancing the detoxification of reactive aldehydes generated downstream of the oxidative destruction of the plasma	RNA-seq, glutamate release assay, cell growth, flow cytometry	Human	DU-145 prostate cancer cells	AKR1C3 :-: Ferroptosis	Validated	_NA_	Aldo-keto reductase family 1 member C3	P42330 (AK1C3_HUMAN)	####	_NA_

			membrane during ferroptosis.										

GPX4	Glutathione peroxidase 4	HGNC: 4556	Knockout of glutathione peroxidase 4 (Gpx4) causes cell death in a pathologically relevant form of ferroptosis. Knockdown renders cells more sensitive to ferroptosis-inducing agents.	Cell viability assessment, siRNA	Human, mice	Mouse embryonic fibroblast (MEF) cells (Pfa1 cells), Gpx4 −/− cells and mice, HK-2 cells	GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_

RB1	RB transcriptional corepressor 1	HGNC:9884	Rb knock-down cells exposed to sorafenib encounter ferroptosis. Lack of Rb sensitized HCC cells to the induction of ferroptosis.	RNA interference, cell viability assay, oxidative stress measurement	Human, mice	HCC cell lines Huh7 and PLC/PRF5; Balb/c nude mice received tumour xenografts derived from HCC cells.	RB1 :-: Ferroptosis	Validated	_NA_	Retinoblastoma-associated protein	P06400 (RB_HUMAN)	####	_NA_
HSPB1	Heat shock protein family B (small) member 1	HGNC:5246	Knockdown of HSF1 and HSPB1 enhances erastin-induced ferroptosis, whereas heat shock pretreatment and overexpression of HSPB1	RNAi, RT-qPCR, western blot, cell viability	Human, mice	HeLa and U2OS cells, human xenograft mouse tumor derived from HeLa (#CCL-2) cells.	HSPB1 :-: Ferroptosis	Validated	_NA_	Heat shock protein beta-1	P04792 (HSPB1_HUMAN)	####	_NA_

			inhibits erastin-induced ferroptosis.										
HSF1	Heat shock transcription factor 1	HGNC: 5224	Knockdown of HSF1 and HSPB1 enhances erastin-induced ferroptosis, whereas heat shock pretreatment and overexpression of HSPB1 inhibits erast	RNAi, RT-qPCR, western blot, cell viability	Human, mice	HeLa and U2OS cells, human xenograft mouse tumor derived from HeLa (#CCL-2) cells.	HSF1 :-: Ferroptosis	Validated	_NA_	Heat shock factor protein 1	Q00613 (HSF1_HUMAN)	####	_NA_

			in-induced ferroptosis.										
SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Overexpressed in human cancer specimens. Overexpression inhibits ROS-induced ferroptosis.	Western blot, cell death test, ChIP assay, RT-PCR, immunofluorescence staining, colony formation assay, TUNEL and BrdU assay	Human, mice	H1299 cells, mouse embryonic fibroblasts, transgenic mice; colon, liver and kidney tumour samples; mouse xenograft	SLC7A11 :+: Cystine, Cystine :-: Ferroptosis	Validated	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	####	_NA_

GPX4	Glutathione peroxidase 4	HGNC:4556	Ex vivo, Gpx4-deficient T cells rapidly accumulated membrane lipid peroxides and concomitantly underwent cell death driven by ferroptosis.	Viability assays, flow cytometry, lipid peroxidation assay	Mice	T cells	GPX4 :-: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_
GCLC	Glutamate-cysteine ligase catalytic subunit	HGNC:4311	RNAi knockdown sensitized cell death induced by cystine starvation.	RNAi, qPCR	Mice	Mouse embryonic fibroblasts	GCLC :+: GSH, GSH :-: Ferroptosis	Validated	_NA_	Glutamate–cysteine ligase catalytic subunit	P48506 (GSH1_HUMAN)	####	_NA_
SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Overexpression of SLC7A11 considerably abrogated	Cell death quantification, gene transfection, western blot	Human	H1299 cells	SLC7A11 :-: Ferroptosis	Validated	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	####	_NA_

			ferroptosis.										
NFE2L2	Nuclear factor, erythroid 2 like 2	HGNC:7782	NRF2 plays a central role in protecting hepatocellular carcinoma (HCC) cells against ferroptosis	Cell Viability Analysis, western blot, RNAi, qRT-PCR	Human, mice	HepG2, Hepa 1-6, Hep3B, and SNU-182 cells, C57BL/6 mice	NFE2L2 :+: (NQO1/HMOX1/FTH1), (NQO1/HMOX1/FTH1) :-: Ferroptosis	Validated	_NA_	Nuclear factor erythroid 2-related factor 2	Q16236 (NF2L2_HUMAN)	####	NRF2 in article

SQSTM1	Sequestosome 1	HGNC:11280	The interaction between p62 and Keap1 increased following erastin and sorafenib treatment. Knockdown of p62 suppressed NRF2 expression and promoted growth inhibition with increased ferroptotic events including GSH depletion, lipid ROS production, and an	Immunoprecipitation assay, shRNA knockdown, iron assay, lipid peroxidation assay, glutathione assay, cell viability	Human, mice	HepG2, Hepa 1-6, Hep3B, and SNU-182 cells	SQSTM1 :-: KEAP1, KEAP1 :-: NFE2L2, NFE2L2 :-: Ferroptosis	Validated	_NA_	Sequestosome-1	Q13501 (SQSTM_HUMAN)	####	p62 in article.

			increase of iron levels.										

NQO1	NAD(P)H quinone dehydrogenase 1	HGNC:2874	Knockdown of p62, quinone oxidoreductase-1, heme oxygenase-1, and ferritin heavy chain-1 by RNA interference in HCC cells promoted ferroptosis in response to erastin and sorafenib.	qRT-PCR, RNA interference	Human, mice	HepG2, Hepa1-6, Hep3B, and SNU-182 cells	NQO1 :-: Ferroptosis	Validated	_NA_	NAD(P)H dehydrogenase [quinone] 1	P15559 (NQO1_HUMAN)	####	_NA_

HMOX1	Heme oxygenase 1	HGNC:5013	Knockdown of p62, quinone oxidoreductase-1, heme oxygenase-1, and ferritin heavy chain-1 by RNA interference in HCC cells promoted ferroptosis in response to erastin and sorafenib.	qRT-PCR, RNA interference	Human, mice	HepG2, Hepa1-6, Hep3B, and SNU-182 cells	HMOX1 :-: Ferroptosis	Validated	Article (PMID 26405158) suggests it a driver.	Heme oxygenase 1	P09601 (HMOX1_HUMAN)	####	HO1 in article

FTH1	Ferritin heavy chain 1	HGNC:3976	Knockdown of p62, quinone oxidoreductase-1, heme oxygenase-1, and ferritin heavy chain-1 by RNA interference in HCC cells promoted ferroptosis in response to erastin and sorafenib.	qRT-PCR, RNA interference	Human, mice	HepG2, Hepa 1-6, Hep3B, and SNU-182 cells	FTH1 :-: Ferroptosis	Validated	_NA_	Ferritin heavy chain	P02794 (FRIH_HUMAN)	####	_NA_
MUC1	Mucin 1, cell surface associated	HGNC:7508	MUC1-C (C-terminal subunit) blocks erastin-induced ferroptosis and induces	shRNA, GSH level measurement, cell death test	Human	MDA-MB-468, BT-20 cells	MUC1 :+: System Xc-, System Xc- :+: GSH, GSH :-: Ferroptosis	Validated	_NA_	Mucin-1	P15941 (MUC1_HUMAN)	####	_NA_

			increases in GSH.										
SLC3A2	Solute carrier family 3 member 2	HGNC:11026	Required for in vitro cell survival because of its role in protecting cells from ferroptosis.	Cell survival test	Mice	Mouse ES-derived fibroblasts	SLC3A2 :+: System Xc-, System Xc- :-: Ferroptosis	Validated	_NA_	4F2 cell-surface antigen heavy chain	P08195 (4F2_HUMAN)	####	CD98hc in article

MT1G	Metallothionein 1G	HGNC:7399	A negative regulator of ferroptosis in HCC cells. Knockdown of MT-1G by RNA interference increases glutathione depletion and lipid peroxidation, which contributes to sorafenib-induced ferroptosis.	RNA interference, cell viability assay, colony formation assay, western blot, qRT-PCR, glutathione assay, lipid peroxidation assay	Human, mice	HCC cells (HepaG2, Hep3B, and Huh7 cells), nude mice.	MT1G :-: Ferroptosis	Validated	_NA_	Metallothionein-1G	P13640 (MT1G_HUMAN)	####	MT-1G in article
NFE2L2	Nuclear factor, erythroid 2 like 2	HGNC:7782	Required for sorafenib-induced expression of MT-1G which is a ferroptosi	shRNA, qRT-PCR, western blot	Human	Huh7 and/or HepG2 cells	NFE2L2 :+: MT1G, MT1G :-: Ferroptosis	Deduced	Its ability to induce MT1G was validated, but its role in ferroptosis needs validation.	Nuclear factor erythroid 2-related factor 2	Q16236 (NF2L2_HUMAN)	####	NRF2 in article

			s suppressor.										
SLC40A1	Solute carrier family 40 member 1	HGNC:10909	Involved in siramesine and lapatinib-induced ferroptotic cell death. Its expression is decreased after treatment with siramesine alone or in combination with lapatinib. Overexpression FPN resulted in decr	Western blot, densitometry quantification, siRNA, gene transfection, cell death test	Human	MDA MB 231 and SKBr3 cells	SLC40A1 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Solute carrier family 40 member 1	Q9NP59 (S40A1_HUMAN)	####	Ferroportin-1 (FPN) in article

			eased ROS and cell death whereas knockdown of FPN increased cell death after siramesine and lapatinib treatment.										
SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Knockdown increased cell death.	siRNA, western blot, cell death test	Human	MDA MB 231 cells	SLC7A11 :+: GSH, GSH :-: Ferroptosis	Validated	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	####	_NA_
GPX4	Glutathione peroxidase 4	HGNC:4556	Knockdown increased cell death.	siRNA, western blot, cell death test	Human	MDA MB 231 and SKBr3 cells	GPX4 :-: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_

SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Inhibition induces ferroptosis. Silencing of the SLC7A11 gene increases the cisplatin sensitivity of resistant HNC cells.	Cell viability, western blot, siRNA or shRNA, glutathione and ROS production measurements	Human, mice	AMC-HN3R, -HN4R, and -HN9R head and neck cancer cells, BALB/c male nude mice	SLC7A11 :-: Ferroptosis	Validated	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	####	_NA_
CISD1	CDGSH iron sulfur domain 1	HGNC:30880	Genetic inhibition of CISD1 contributes to erastin-induced ferroptosis. Stabilization of the iron sulfur cluster of CISD1 inhibits ferroptosis.	Cytotoxicity assays, western blot, q-PCR, RNAi	Human	HepG2 and Hep3B cells	CISD1 :-: Mitochondrial lipid ROS, Mitochondrial lipid ROS :+: Ferroptosis	Validated	_NA_	CDGSH iron-sulfur domain-containing protein 1	Q9NZ45 (CISD1_HUMAN)	####	_NA_

SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Elevated levels of expression are resistant to erastin-induced ferroptosis. Repression of SLC7A11 expression by p53 sensitized cells to undergo erastin-induced ferroptosis.	Western blot, cell death assay, qPCR	Human	H1299 cells	SLC7A11 :-: Ferroptosis	Validated	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	####	_NA_
FANCD2	FA complementation group D2	HGNC:3585	Inhibits erastin-induced ferroptosis. Plays a novel role in the negative regulation of ferro	Cell viability assay, Q-PCR, western blot, iron assay, lipid peroxidation assay, glutathione assay	Mice	Bone marrow stromal cells	FANCD2 :-: Ferroptosis	Validated	_NA_	Fanconi anemia group D2 protein	Q9BXW9 (FACD2_HUMAN)	####	_NA_

			ptosis.										
GPX4	Glutathione peroxidase 4	HGNC: 4556	Protects lipid peroxidation. Cell damage induced by GPx4 ablation is involved in ferroptosis.	RT-PCR, western blot, cytotoxicity assay, cell proliferation assay, siRNA	Human	Umbilical vein endothelial cell	GPX4 :-: LDH, LDH :+: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_
NFE2L2	Nuclear factor, erythroid 2 like 2	HGNC: 7782	Nrf2 activation contributes to the resistance of HNCs to artesunate-induced ferroptosis. Nrf2 inhibition sensitizes head	Cell viability assay, RNAi, gene transfection, western blot	Mice	Head and neck cancer cells (HN2−10), nude mice	NFE2L2 :-: Ferroptosis	Validated	_NA_	Nuclear factor erythroid 2-related factor 2	Q16236 (NF2L2_HUMAN)	####	NRF2 in article

			and neck cancer cells to artesunate-induced ferroptosis.										
FTMT	Ferritin mitochondrial	HGNC:17345	Overexpression significantly inhibited erastin-induced ferroptosis.	Cell viability assay, western blot	Mice, fly	SH-SY5Y cells, drosophila melanogasters W1118, elav-Gal4 and UAS-Fer3HCH	FTMT :-: Labile iron pool, Labile iron pool :+: Ferroptosis	Validated	_NA_	Ferritin	Q8N4E7 (FTMT_HUMAN)	####	_NA_

HSPA5	Heat shock protein family A (Hsp70) member 5	HGNC:5238	Negatively regulates ferroptosis. Suppression of HSPA5 expression increased erastin-induced death. Overexpressed HSPA5 inhibited erastin-induced ferroptotic cell death.	Cell viability assay, western blot, shRNA, gene transfection	Human, mice	Pancreatic ductal adenocarcinoma cell lines (PANC1, CFPAC1, MiaPaCa2), nude mice, B6 mice	HSPA5 :+: GPX4, GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Endoplasmic reticulum chaperone BiP	P11021 (BIP_HUMAN)	####	_NA_

ATF4	Activating transcription factor 4	HGNC:786	Inhibition of ATF4 expression increased erastin-induced cell death. ATF4 results in the induction of HSPA5, which in turn protects against GPX4 protein degradation and subsequent ferroptosis.	CCK8 cell viability assay, clonogenic cell survival assay, western blot, q-PCR, RNAi	Human	Pancreatic ductal adenocarcinoma cells (e.g., PANC1, CFPAC1, MiaPaCa2, and Panc2.03)	ATF4 :+: HSPA5, HSPA5 :+: GPX4, GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Cyclic AMP-dependent transcription factor ATF-4	P18848 (ATF4_HUMAN)	####	_NA_
SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Slc7a11 deletion increases susceptibility to iron overload-induced	Cell viability, RNAi, RT-PCR	Mice	Mice, hepatocytes, bone marrow–derived macrophages	SLC7A11 :-: Ferroptosis	Validated	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	####	_NA_

			ferroptosis.										
GPX4	Glutathione peroxidase 4	HGNC: 4556	Ferroptosis drives neurodegeneration in Gpx4 BIKO mice.	RT-qPCR, behavior test, western blot	Mice	Forebrain neurons of Gpx4 BIKO mice and Gpx4 (f/f) mice	GPX4 :-: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_
GPX4	Glutathione peroxidase 4	HGNC: 4556	Downregulation conferred increased sensitivity to ferroptosis following cystine deprivation.	Immunoblotting, cell viability	Human	Human mammary epithelial cells	GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_
HMOX1	Heme oxygenase 1	HGNC: 5013	Demonsrates antiferroptotic role. HO-1 deficiency promotes erastin-induced	RT-PCR, western blot, cell viability, siRNA	Mice	Renal proximal tubule cells	HMOX1 :-: Ferroptosis	Validated	Article (PMID 26405158) suggests it a driver.	Heme oxygenase 1	P09601 (HMOX1_HUMAN)	####	HO-1 in article

			ferroptosis.										
ATF4	Activating transcription factor 4	HGNC:786	ATF4 expression induces acquired cell death resistance. ATF4 knockdown renders cells susceptible for ferroptosis.	siRNA, cell transfection, cell viability assay, RT-PCR, immunoblotting	Human	U87 and U251 glioblastoma cells	ATF4 :+: xCT, xCT :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Cyclic AMP-dependent transcription factor ATF-4	P18848 (ATF4_HUMAN)	####	_NA_
NFE2L2	Nuclear factor, erythroid 2 like 2	HGNC:7782	Nrf2 overexpression promotes resistance to ferroptosis.	Cell growth assay	Human, rat	F98, U87 glioma cells	NFE2L2 :+: xCT, xCT :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Nuclear factor erythroid 2-related factor 2	Q16236 (NF2L2_HUMAN)	####	Nrf2 in article

TP53	Tumor protein p53	HGNC:11998	Inhibits ferroptosis in human colorectal cancer (CRC) cells. Loss of TP53 restored erastin sensitivity. Inhibits cell death induction by erastin in human CRC cells.	RNAi, live-cell imaging, cell viability, qPCR, western blot	Human, mice	HCT116, athymic nude mice	TP53:+:Nucleus DPP4, Nucleus DPP4:+:SLC7A11, SLC7A11:-:Ferroptosis	Validated	Promotes ferroptosis via a transcription-dependent mechanism in non-CRC cells.	Cellular tumor antigen p53	P04637 (P53_HUMAN)	####	_NA_
SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Knockdown sensitized cells to erastin.	shRNA, cell viability	Human	HCT116	SLC7A11:-:Ferroptosis	Validated	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	####	_NA_

HELLS	Helicase, lymphoid specific	HGNC:4861	LSH inhibits ferroptosis by decreasing the intracellular levels of iron and lipid ROS.	Plate-colony formation assay; measurement of total ROS, Lipid ROS, and intracellular iron	Human, mice	Lung cancer H358 and PC9 cells, SCID Mice	HELLS :+: GLUT1, HELLS :+: SCD, HELLS :+: FADS2, GLUT1 :-: Ferroptosis, SCD :-: Ferroptosis, FADS2 :-: Ferroptosis	Validated	_NA_	Lymphoid-specific helicase	Q9NRZ9 (HELLS_HUMAN)	####	LSH in article
SCD	Stearoyl-CoA desaturase	HGNC:10571	Depletion of the SCD1 and FADS2 metabolic genes induces ferroptosis.	shRNA, RT-qPCR, MTT assay, total iron detection, lipid ROS detection	Human	A549 cancer cells	SCD :-: Ferroptosis	Validated	_NA_	Acyl-CoA desaturase	O00767 (ACOD_HUMAN)	####	SCD1 in article
FADS2	Fatty acid desaturase 2	HGNC:3575	Depletion of the SCD1 and FADS2 metabolic genes induces ferroptosis.	shRNA, RT-qPCR, MTT assay, total iron detection, lipid ROS detection	Human	A549 cancer cells	FADS2 :-: Ferroptosis	Validated	_NA_	Acyl-CoA 6-desaturase	O95864 (FADS2_HUMAN)	####	_NA_

SRC	SRC proto-oncogene, non-receptor tyrosine kinase	HGNC:11283	Src-STAT3 activation renders the cell unable to undergo to ferroptosis. Src inhibition decreased cell viability significantly, and that loss of viability was rescued by ferroptosis inhibitors.	Immunoblotting, RNAi, qPCR, western blot, cell viability	Human	MCF-10A and SUM-159 cells	SRC :+: STAT3, STAT3 :-: ACSL4, ACSL4 :+: Ferroptosis	Validated	_NA_	Proto-oncogene tyrosine-protein kinase Src	P12931 (SRC_HUMAN)	####	_NA_
STAT3	Signal transducer and activator of transcription 3	HGNC:11364	Src-STAT3 activation renders the cell unable to undergo to ferroptosis.	Immunoblotting, RNAi, qPCR, western blot, cell viability	Human	MCF-10A and SUM-159 cells	STAT3 :-: ACSL4, ACSL4 :+: Ferroptosis	Validated	_NA_	Signal transducer and activator of transcription 3	P40763 (STAT3_HUMAN)	####	_NA_

NFE2L2	Nuclear factor, erythroid 2 like 2	HGNC:7782	ARF-mediated ferroptosis was largely abrogated by co-expression of NRF2.	Gene transfection, cell death quantification	Human, mice	H1299, SaoS2, U2OS cells, nude mice	NFE2L2 :+: SLC7A11, SLC7A11 :-: Ferroptosis	Validated	_NA_	Nuclear factor erythroid 2-related factor 2	Q16236 (NF2L2_HUMAN)	####	NRF2 in article
PML	Promyelocytic leukemia	HGNC:9113	PML expression turned cells highly resistant to ferroptosis.	Cell death assessment	Human	IMR90 cells	PML :-: Ferroptosis	Validated	_NA_	Protein PML	P29590 (PML_HUMAN)	####	_NA_
MTOR	Mechanistic target of rapamycin kinase	HGNC:3942	Necessary and sufficient to protect cardiomyocyte cells against ferroptotic cell death. mTOR overexpression suppressed	Cell viability assay, ROS production assay, western blot	Mice	Cardiomyocyte cell, C57BL/6 mice	MTOR :-: Ferroptosis	Validated	_NA_	Serine/threonine-protein kinase mTOR	P42345 (MTOR_HUMAN)	####	_NA_

			ferroptotic cell death, whereas mTOR deletion exaggerated cell death.										
NFS1	NFS1 cysteine desulfurase	HGNC:15910	Suppression of NFS1 cooperates with inhibition of cysteine transport to trigger ferroptosis in vitro and slow tumour growth. Suppression of NFS1 predi	RNAi, cell viability assay,flow cytometry	Human	MDA-MB-231 cells, NOD.CB17 Scid/J mice	NFS1 :-: TFRC, TFRC :+: Ferroptosis	Validated	_NA_	Cysteine desulfurase	Q9Y697 (NFS1_HUMAN)	####	_NA_

			sposes cancer cells to ferroptosis.										
TP63	Tumor protein p63	HGNC:15979	DeltaNp63 alpha can inhibit ferroptosis independent of p53. Overexpression protects cells from ferroptosis-inducing agents.	siRNA, cell death quantification	Human	ME-180 cells	TP63 :-: Ferroptosis	Validated	_NA_	Tumor protein 63	Q9H3D4 (P63_HUMAN)	####	DeltaNp63 alpha in article

SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Overexpression of SLC7A11 attenuated BAY-inhibited cell viability by ferroptosis.	Cell viability assay, qRT-PCR, shRNA, gene overexpression, western blot	Human	MDA-MB-231, MDA-MB-468, DBTRG-05MG	SLC7A11 :-: Ferroptosis	Validated	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	####	_NA_
TP53	Tumor protein p53	HGNC:11998	p53 stabilization suppresses ferroptosis. p53 suppresses metabolic stress-induced ferroptosis.	Immunoblotting, cell death quantification, time-lapse imaging	Human	HT-1080 cells	TP53 :+: CDKN1A, CDKN1A :+: GSH, GSH :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	Found to promote ferroptosis by other studies.	Cellular tumor antigen p53	P04637 (P53_HUMAN)	####	p53 in article
CDKN1A	Cyclin dependent kinase inhibitor 1A	HGNC:1784	Required to suppress ferroptosis.	CRISPR, shRNA, immunoblotting, cell-cycle profile, cell death quantification	Human	HT-1080 cells	CDKN1A :+: GSH, GSH :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Cyclin-dependent kinase inhibitor 1	P38936 (CDN1A_HUMAN)	####	Encoding p21

MIR137	microRNA 137	HGNC:31523	Suppresses ferroptosis both in vitro and in vivo.	Immunoblotting, luciferase reporter assay, qRT-PCR, cell viability assay, colony formation assay, malondialdehyde assay, iron assay, flow cytometer, shRNA, xenograph mouse model	Human, mice	Melanoma cell lines A375 and G-361, C57BL/6 mice	MIR137 :-: SLC1A5, SLC1A5 :+: Glutaminolysis, Glutaminolysis :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	_NA_	_NA_	####	_NA_
SLC40A1	Solute carrier family 40 member 1	HGNC:10909	Overexpression of Fpn inhibited ferroptosis.	Cell viability assay, lipid ROS measurement, RT-qPCR, western blot	Mice	TM4 Sertoli cells	SLC40A1 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Solute carrier family 40 member 1	Q9NP59 (S40A1_HUMAN)	####	Fpn in article
GPX4	Glutathione peroxidase 4	HGNC:4556	Activation blocked ferroptosis.	Cell viability assay, lipid ROS measurement, RT-qPCR, western blot	Mice	TM4 Sertoli cells	GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_

GPX4	Glutathione peroxidase 4	HGNC:4556	GPX4-overexpressing cells were resistant to reactive oxygen species-induced cell death. Conversely, GPX4-knockdown cells were sensitive to reactive oxygen species-induced cell death.	Immunohistochemistry, qRT-PCR,lentiviral transduction, shRNA, flow cytometry, cell viability assay	Human	LCL-K cell	GPX4 :-: 8-OHdG , 8-OHdG :+: Ferroptosis	Deduced	The authors did not determine wether the ROS-induced cell death is related to ferroptosis or not.	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_

ENPP2	Ectonucleotide pyrophosphatase/phosphodiesterase 2	HGNC:3357	Overexpression modestly promotes migration and proliferation and significantly inhibits erastin-induced ferroptosis.	Cell viability assay, qRT-PCR, western blot, ROS measurement, ELISA	Rat	H9c2 cells	ENPP2 :-: Ferroptosis	Validated	_NA_	Ectonucleotide pyrophosphatase/phosphodiesterase family member 2	Q13822 (ENPP2_HUMAN)	####	_NA_
VDAC2	Voltage dependent anion channel 2	HGNC:12672	Overexpression could partially protect cells from ferroptosis.	Western blot, cell viability assay	Human	HT1080 cells	VDAC2 :-: Ferroptosis	Validated	_NA_	Voltage-dependent anion-selective channel protein 2	P45880 (VDAC2_HUMAN)	####	_NA_
FH	Fumarate hydratase	HGNC:3700	FH inactivation (FH-/-) proves synthetic lethal with inducers of ferroptosis. FH-/-	CRISPR/Cas9, sgRNA, cell viability assay, immunoblotting, qPCR,	Human	UOK262, HT1080, HK2, A498 cells	FH :+: GPX4, GPX4 :-: Ferroptosis	Validated	_NA_	Fumarate hydratase	P07954 (FUMH_HUMAN)	####	_NA_

			sensitizes cells to multiple ferroptosis inducers.										
CISD2	CDGSH iron sulfur domain 2	HGNC:24212	Overexpression conferred resistance to ferroptosis. Inhibition blocked resistance to ferroptotic cell death.	Cell viability and death assay, GSH and ROS levels and lipid peroxidation assays, RNAi, gene transfection, immunoblotting	Human	Head and neck cancer cells	CISD2 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	CDGSH iron-sulfur domain-containing protein 2	Q8N5K1 (CISD2_HUMAN)	####	_NA_

SLC40A1	Solute carrier family 40 member 1	HGNC:10909	A negative regulator of ferroptosis by reducing intracellular iron concentration. Knockdown accelerates erastin-induced ferroptosis.	Cell viability, qRT-PCR, western blot, siRNA	Human	SH-SY5Y cells	SLC40A1 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Solute carrier family 40 member 1	Q9NP59 (S40A1_HUMAN)	####	Ferroportin in article
MIR9-1	microRNA 9-1	HGNC:31641	Overexpression of miR-9 suppressed GOT1, which subsequently reduced ferroptosis. Suppression of miR-9 increased the sensi	Immunoblotting, luciferase reporter assay, qPCR, cell viability assay, MDA assay, iron assay, glutamate assay	Human	A375 and G-361 cells	MIR9 :-: GOT1, GOT1 :+: alpha KG, alpha KG :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	_NA_	_NA_	####	miR-9 in article

			tivity of melanoma cells to ferroptosis inducers.										
MIR9-2	microRNA 9-2	HGNC:31642	Overexpression of miR-9 suppressed GOT1, which subsequently reduced ferroptosis. Suppression of miR-9 increased the sensitivity of melanom	Immunoblotting, luciferase reporter assay, qPCR, cell viability assay, MDA assay, iron assay, glutamate assay	Human	A375 and G-361 cells	MIR9 :-: GOT1, GOT1 :+: alpha KG, alpha KG :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	_NA_	_NA_	####	miR-9 in article

			a cells to ferroptosis inducers.										
MIR9-3	microRNA 9-3	HGNC:31646	Overexpression of miR-9 suppressed GOT1, which subsequently reduced ferroptosis. Suppression of miR-9 increased the sensitivity of melanom	Immunoblotting, luciferase reporter assay, qPCR, cell viability assay, MDA assay, iron assay, glutamate assay	Human	A375 and G-361 cells	MIR9 :-: GOT1, GOT1 :+: alpha KG, alpha KG :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	_NA_	_NA_	####	miR-9 in article

			a cells to ferroptosis inducers.										
CBS	Cystathionine beta-synthase	HGNC:1550	Inhibition triggers ferroptosis in hepatocellular carcinoma.	Cell viability, western blotting, LC/ESI-MS/MS, flow cytometry, xenograft mice	Human, mice	HepG2 cells, female ICR mice	CBS :-: Ferroptosis	Validated	_NA_	Cystathionine beta-synthase	P35520 (CBS_HUMAN)	####	_NA_
NFE2L2	Nuclear factor, erythroid 2 like 2	HGNC:7782	Associated with resistance to ferroptosis. Inhibition of Nrf2 sensitized cells to ferroptosis.	Cell viability and cell death assays, ROS production measurement, RNAi, gene transfection, immunoblotting	Human, mice	HNC cell line (AMC-HN2−11), SNUcell lines (SNU-1041, -1066, and -1076), athymic BALB	NFE2L2 :+: FTH1, FTH1 :-: Ferroptosis, NFE2L2 :+: FPN, FPN :-: Ferroptosis, NFE2L2 :+: HO-1, HO-1 :-:	Validated	_NA_	Nuclear factor erythroid 2-related factor 2	Q16236 (NF2L2_HUMAN)	####	Nrf2 in article

						/c male nude mice	Ferroptosis						
SQSTM1	Sequestosome 1	HGNC:11280	Inhibition of the p62 gene significantly reduced cell viability and increased cellular lipid ROS levels in HN3R cells; this was reversed by treatment with ferrostatin-1, a ferroptosis	siRNA, qPRC, fluorescent microscopy and flow cytometry, ROS production measurement	Human	HN3 cells	SQSTM1 :+: NFE2L2, NFE2L2 :+: FTH1, FTH1 :-: Ferroptosis, NFE2L2 :+: FPN, FPN :-: Ferroptosis, NFE2L2 :+: HO-1, HO-1 :-: Ferroptosis	Validated	Not test cell death or cell viability.	Sequestosome-1	Q13501 (SQSTM_HUMAN)	####	p62 in article.

			inducer.										
GPX4	Glutathione peroxidase 4	HGNC:4556	Overexpression GPX4 resulted in decreased cell death after RSL3 treatment. Moreover, this effect was able to be reversed by overexpression of	Cell viability, cell death, ROS determination, western blot	Human	HCT116, LoVo, and HT29 CRC cells	GPX4 :-: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_

			GPX4.										
ISCU	Iron-sulfur cluster assembly enzyme	HGNC:29882	Overexpression significantly attenuated DHA induced ferroptosis.	Cell viability, cell cycle, ROS determination, western blot, immunofluorescence, ectopic expressing, lentiviral transduction	Human	HL60, KG1, THP-1 cells	ISCU :+: GSH, GSH :-: Ferroptosis	Validated	_NA_	Iron-sulfur cluster assembly enzyme ISCU	Q9H1K1 (ISCU_HUMAN)	####	_NA_

FTH1	Ferritin heavy chain 1	HGNC: 3976	FTH reconstituted cells exhibited the reduced lipid peroxides content and restored the DHA-induced ferroptosis.	Cell viability, cell cycle, ROS determination, western blot, immunofluorescence, ectopic expressing, lentiviral transduction	Human	HL60, KG1, THP-1 cells	FTH1 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Ferritin heavy chain	P02794 (FRIH_HUMAN)	####	FTH in articicle
ACSL3	Acyl-CoA synthetase long chain family member 3	HGNC: 3570	Required for exogenous monounsaturated fatty acids to protect cells against ferroptosis. Negatively correlates with ferroptosis sensitivity.	Dead cell count, gene knockout, confocal imaging, thin-layer chromatography, BODIPY 493/503 imaging, CRISPR/Cas9, RT-qPCR, western blot	Human	HEK 293, HT-1080 cells	ACSL3 :-: Ferroptosis	Validated	_NA_	Long-chain-fatty-acid--CoA ligase 3	095573 (ACSL3_HUMAN)	####	_NA_

OTUB1	OTU deubiquitinase, ubiquitin aldehyde binding 1	HGNC:23077	Inactivation promotes ferroptosis by down-regulating SLC7A11 levels. Overexpression is critical for tumor growth.	CRISPR/Cas9, RNAi, cell death, western blot, qRT-PCR	Human, mice	H1299, SK-N-BE(2)C, T24, UM-UC-3, SW780 cells, nude mice	OTUB1 :+: SLC7A11, SLC7A11 :-: Ferroptosis	Validated	_NA_	Ubiquitin thioesterase OTUB1	Q96FW1 (OTUB1_HUMAN)	####	_NA_
CD44	CD44 molecule (Indian blood group)	HGNC:1681	Knockdown sensitizes cells to ferroptosis.	Western blot, siRNA, cell death	Human	H1299 cells	CD44 :+: SLC7A11, SLC7A11 :-: Ferroptosis	Validated	_NA_	CD44 antigen	P16070 (CD44_HUMAN)	####	_NA_
LINC00336	Long intergenic non-protein coding RNA 336	HGNC:33813	Overexpression inhibits ferroptosis. Knockdown promotes ferroptosis.	qRT-PCR, MTT assay, colony-formation assay, lipid ROS assays, iron assay, immunoblotting	Human	A549 and SPC-A-1 cells	(LINC00336/ELAVL1) :-: Ferroptosis	Validated	_NA_	Putative uncharacterized protein encoded by LINC00336	Q6ZUF6 (NC336_HUMAN)	####	_NA_

STAT3	Signal transducer and activator of transcription 3	HGNC:11364	Upregulated in ferroptosis resistant cells. Inhibition increases ferroptosis.	Cell viability tests, ROS and lipid peroxidation measures, MDA measurement, western blot	Human	Osteosarcoma cells MG63 and Saos-2	STAT3 :-: Ferroptosis	Validated	_NA_	Signal transducer and activator of transcription 3	P40763 (STAT3_HUMAN)	####	_NA_
BRD4	Bromodomain containing 4	HGNC:13575	Inhibition induces ferroptosis.	Cell proliferation assay, migration and invasion assays, RT-PCR, western blot, immunohistochemistry, iron assay	Human	MDA-MB-231, Hs578T, H1299, A549 and MCF-10A cells, female athymic BALB/c nude mice	BRD4 :-: Ferritinophagy, Ferritinophagy :+: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Bromodomain-containing protein 4	060885 (BRD4_HUMAN)	####	_NA_
PRDX6	Peroxiredoxin 6	HGNC:16753	A negative regulator of ferroptotic cell death.	Western blot, flow cytometry, SRB assay, gene transfection, shRNA, LOOH quantification	Human	H1299 cells	PRDX6 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Peroxiredoxin-6	P30041 (PRDX6_HUMAN)	####	_NA_

MIR17	microRNA 17	HGNC:31547	Protects endothelial HUVEC cells from erastin-induced ferroptosis. Overexpression significantly reduced erastin-induced growth inhibition and ROS generation of HUVEC cells.	Lentivirus transduction, CCK-8 assay, DYE670 staining assay, ROS staining assay, RT-qPCR, western blot	Human	HUVEC cells	MIR17 :-: A20, A20 :+: ACSL4, ACSL4 :+: Lipid ROS, A20 :-: GPX4, GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	_NA_	_NA_	####	miR-17-92 in article
SCD	Stearoyl-CoA desaturase	HGNC:10571	Inhibition of SCD1 induces ferroptotic cell death. Expression of SCD1 protects cells	Cell viability, cell death, BODIPY staining, siRNA, RT-qPCR, western blot, gene overexpression,	Human, mice	OVCAR-4, COV362, FT-t cells, mouse orthotopic xenograft model	SCD :+: CoQ10, CoQ10 :-: Ferroptosis	Validated	_NA_	Acyl-CoA desaturase	000767 (ACOD_HUMAN)	####	SCD1 in article

			from ferroptosis.										
SESN2	Sestrin 2	HGNC:20746	Has cytoprotective effect against ferroptosis. In cells expressing Sesn2, erastin-induced cell death, ROS formation, and glutathione depletion were almost completely inhibited compared to that in contr	MTT assay, RT-PCR, luciferase assay, immunoblot, siRNA, Lipid peroxidation assay, GSH measurement	Human, mice	HepG2 and AML-12 cell lines, mouse embryonic fibroblasts cells, ICR mice	SESN2 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Sestrin-2	P58004 (SESN2_HUMAN)	####	Sesn2 in article

			ol cells.										
NF2	Neurofibromin 2	HGNC:7773	Genetic inactivation of NF2 rendered cancer cells more sensitive to ferroptosis. Mediates cell density-dependent inhibition of ferro	Cell death, cell viability, lipid peroxidation, immunoblotting, CRISPR/Cas9, ChIP assay, qRT-PCR	Human, mice	Mouse embryonic fibroblasts, NF639 cells, human epithelial tumour cells, human mesothelioma cells, xenograft mouse	NF2 :-: YAP, YAP :+: Ferroptosis	Validated	_NA_	Merlin	P35240 (MERL_HUMAN)	####	Also known as merlin

			ptosis.										
ARNTL	Aryl hydrocarbon receptor nuclear translocator like	HGNC:701	Degration of the protein is critical for ferroptosis. Blocking ARNTL degradation diminished ferroptotic tumor cell death.	Cytotoxicity assays, western blot, immunoprecipitation, RNA interference, gene transfection, qPCR, MDA assay	Human, mice	Calu-1, THP1, HT1080, and HL-60 cells, athymic nude mice	ARNTL :-: EGLN2, EGLN2 :-: HIF1A, HIF1A :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Aryl hydrocarbon receptor nuclear translocator-like protein 1	000327 (BMAL1_HUMAN)	####	_NA_

HIF1A	Hypoxia inducible factor 1 subunit alpha	HGNC:4910	Destabilizing HIF1A facilitated ferroptotic tumor cell death.	Cytotoxicity assays, western blot, immunoprecipitation, RNA interference, gene transfection, qPCR, MDA assay	Human, mice	Calu-1, THP1, HT1080, and HL-60 cells, athymic nude mice	HIF1A :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Hypoxia-inducible factor 1-alpha	Q16665 (HIF1A_HUMAN)	####	_NA_
JUN	Jun proto-oncogene, AP-1 transcription factor subunit	HGNC:6204	O-GlcNAcylated c-Jun represents an obstructive factor to ferroptosis.	Immunofluorescence, western blotting, immunohistochemistry, cell viability, colony formation, qPCR, lipid peroxidation assay, iron assay	Human, mice	Bel-7402, SMMC-7721 cells, athymic nude mice	JUN :+: GSH, GSH :-: Ferroptosis, JUN :+: PSAT1, PSAT1 :-: Ferroptosis, JUN :+: CBS, CBS :-: Ferroptosis	Deduced	_NA_	Transcription factor AP-1	P05412 (JUN_HUMAN)	####	c-Jun in article
CA9	Carbonic anhydrase 9	HGNC:1383	Inhibition induces ferroptosis.	qRT-PCR, western blot, cell viability assay, siRNA, ROS detection	Human	Mesothelioma cell lines ACC-Meso-1, NCI-H2373 and NCI-H2052, mesothelial cell line MeT-5A	CA9 :-: Ferroptosis	Validated	_NA_	Carbonic anhydrase 9	Q16790 (CAH9_HUMAN)	####	_NA_

HSPA5	Heat shock protein family A (Hsp70) member 5	HGNC:5238	Knockdown of GRP78 enhanced artesunate-induced ferroptosis of pancreatic cancer cells.	Fluorescent staining, CCK8, Western blot, shRNA, qRT-PCR	Human, mice	Pancreatic cancer cells AsPC-1 and PaTU 8988, BALB/c nude mice	GRP78 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Endoplasmic reticulum chaperone BiP	P11021 (BIP_HUMAN)	####	GRP78 in article
TMBIM4	Transmembrane BAX inhibitor motif containing 4	HGNC:24257	Protects against ferroptosis in HCC cells. Inhibition increased ferroptotic cel death.	Cell viability and clonogenic survival assay, immunofluorescence, western blot, RNAi, gene transfection, qRT-PCR, lipid peroxidation assay	Human, mice	Hep G2, Huh-7, SMMC-7721 and PLC/PRF/5 cells, nude mice	S1R :-: Ferroptosis	Validated	_NA_	Protein lifeguard 4	Q9HC24 (LFG4_HUMAN)	####	S1R in article

HSPA5	Heat shock protein family A (Hsp70) member 5	HGNC:5238	Serves as a negative regulator of DHA-induced ferroptosis.	Cell viability, colony formation, cell death, lipid ROS assay, GSH determination, siRNA, western blot, RT-PCR, xenograft tumor model	Human, mice	Glioma cell lines U251 and U373, mouse hippocampal neuronal cell line HT22, athymic nude BALB/c mice	HSPA5 :+: GPX4, GPX4 :-: Ferroptosis	Predicted	_NA_	Endoplasmic reticulum chaperone BiP	P11021 (BIP_HUMAN)	####	_NA_
PLIN2	Perilipin 2	HGNC:248	An indispensable gene and protein in the suppression of ferroptosis caused by abnormal lipometabolism in gastric carcinoma.	Cell proliferation and clonogenic assay, cell survival analysis, xenografts tumor, RNA-seq, RT-qPCR, ROS assay	Human, mice	SGC7901 and MGC803 cells, nude mice	PLIN2 :-: Ferroptosis	Screened	_NA_	Perilipin-2	Q99541 (PLIN2_HUMAN)	####	Also known as ADRP

MIR212	microRNA 212	HGNC:31589	Overexpression of miR-212-5p attenuated ferroptosis while downregulation of miR-212-5p promoted ferroptotic cell death.	Controlled cortical impact model, iron assay, MDA assay, RT-PCR, western blotting, cell death	Mice	HT22 and Neuro-2a cells, C57BL/6 J mice	(miR-212-5p/Ptgs2) :-: Ferroptosis	Validated	_NA_	_NA_	_NA_	####	miR-212-5p in article
Fer1HCH	Ferritin 1 Heavy Chain Homolog	_NA_	Reduced heavy chain levels caused severe mitochondrial defects and ferroptosis.	RT-qPCR, immunohistochemistry, EdU staining, TUNEL staining	Drosophila	Fly	Fer1HCH :-: ROS, ROS :+: Ferroptosis	Predicted	_NA_	Ferritin	H1UUD2 (H1UUD2_DROME)	####	_NA_

AIFM2	Apoptosis inducing factor mitochondria associated 2	HGNC: 21411	A glutathione-independent ferroptosis suppressor. Pharmacological targeting of FSP1 strongly synergizes with GPX4 inhibitors to trigger ferroptosis.	Expression cloning, cell death, cell viability, LDH assay, western blot, LC-MS, NADH consumption assay	Human, mice	MCF-7, HT1080, Pfa1 cells	FPS1 :+: CoQ10, CoQ10 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Apoptosis-inducing factor 2	Q9BRQ8 (AIFM2_HUMAN)	####	FSP1 in article

AIFM2	Apoptosis inducing factor mitochondria associated 2	HGNC:21411	A potent ferroptosis-resistance factor. Positively correlates with ferroptosis resistance.	Synthetic lethal CRISPR-Cas9 screen, cell death, western blotting, lipid droplet fractionation, glutathione measurement, tumour xenograft growth, CoQ measurement	Human, mice	U-2 OS cell line, NCI-H460, NCI-H2291, NCI-H1703 and NCIH446 cells, C.B17 SCID mice	FPS1 :+: CoQ10, CoQ10 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Apoptosis-inducing factor 2	Q9BRQ8 (AIFM2_HUMAN)	####	FSP1 in article
LAMP2	Lysosomal associated membrane protein 2	HGNC:6501	Knockdown promoted ferroptosis.	Cell viability, western blot, ROS induction, glutathione assay, lipid peroxidation assay	Human	ARPE-19, hfRPE cells	LAMP2 :+: Cysteine, Cysteine :+: GSH, GSH :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Lysosome-associated membrane glycoprotein 2	P13473 (LAMP2_HUMAN)	####	_NA_

ZFP36	ZFP36 ring finger protein	HGNC:12862	ZFP36 plasmid impaired FBXW7 plasmid-induced HSC ferroptosis. Overexpression of Zfp36 impaired erastin- or sorafenib-induced ferroptosis.	Cell viability, lipid peroxidation, iron, GSH and ROS assays, western blot, RT-PCR, RNA-seq	Human, mice	Hepatic stellate cells, C57BL/6 mice	ZFP36 :-: ATG16L1, ATG16L1 :+: Ferroptosis	Validated	_NA_	mRNA decay activator protein ZFP36	P26651 (TTP_HUMAN)	####	_NA_
GPX4	Glutathione peroxidase 4	HGNC:4556	Depletion or inhibition resulted in cell death by ferroptosis.	Quantitative proteomic analysis, siRNA, RNA-seq and qRT-PCR, cell viability, lipid peroxidation assay, GSH measurement, western blot	Human, mice, rat	H9c2 and C2C12 cells, rat ventricular myocytes, C57BL/6 mice	GPX4 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	####	_NA_

PROM2	Prominin 2	HGNC:20685	Induced by ferroptotic stress and promotes resistance to ferroptotic cell death. Facilitates ferroptosis resistance in mammary epithelial and breast carcinoma cells.	RNA-seq, western blot, qPCR, siRNA, cell count, cell death, iron assay	Human	MCF10A, Hs578t and MDA-MB-231 cells	Prominin2 :+: Ferritin-containing MVB, Ferritin-containing MVB :-: Ferroptosis	Validated	_NA_	Prominin-2	Q8N271 (PROM2_HUMAN)	####	Prominin 2 in article

CHMP5	Charged multivesicular body protein 5	HGNC:26942	Ferroptosis activators increase ESCRT-III subunits (e.g., CHMP5 and CHMP6). Knockdown of CHMP5 or CHMP6 sensitizes human cancer cells to ferroptosis.	RNAi, western blot, iron, malondialdehyde and cytotoxicity assays	Human, mice	PANC1 and HepG2 cells, athymic nude or B6 mice	CHMP5 :-: Ferroptosis	Validated	_NA_	Charged multivesicular body protein 5	Q9NZZ3 (CHMP5_HUMAN)	####	_NA_
CHMP6	Charged multivesicular body protein 6	HGNC:25675	Ferroptosis activators increase ESCRT-III subunits (e.g., CHMP5 and CHMP6). Knockdown of CHMP5 or CHMP6 sensitizes	RNAi, western blot, iron, malondialdehyde and cytotoxicity assays	Human, mice	PANC1 and HepG2 cells, athymic nude or B6 mice	CHMP6 :-: Ferroptosis	Validated	_NA_	Charged multivesicular body protein 6	Q96FZ7 (CHMP6_HUMAN)	####	_NA_

			human cancer cells to ferroptosis.										
AKR1C1	Aldo-keto reductase family 1 member C1	HGNC:384	Inhibition completely resensitizes resistant melanoma cells to ferroptosis execution.	RNAi, cell transfection, western blotting, qRT-PCR, cell viability, lipid peroxides evaluation	Human	MeWo, A2058, SK-Mel 5, SK-Mel 24, C8161, CHL-1, and A375 cells	AKR1C1 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Aldo-keto reductase family 1 member C1	Q04828 (AK1C1_HUMAN)	####	_NA_
AKR1C2	Aldo-keto reductase family 1 member C2	HGNC:385	Inhibition completely resensitizes resistant melanoma cells to ferro	RNAi, cell transfection, western blotting, qRT-PCR, cell viability, lipid peroxides evaluation	Human	MeWo, A2058, SK-Mel 5, SK-Mel 24, C8161, CHL-1, and	AKR1C2 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Aldo-keto reductase family 1 member C2	P52895 (AK1C2_HUMAN)	####	_NA_

			ptosis execution.			A375 cells							
AKR1C3	Aldo-keto reductase family 1 member C3	HGNC: 386	Inhibition completely resensitizes resistant melanoma cells to ferroptosis execution.	RNAi, cell transfection, western blotting, qRT-PCR, cell viability, lipid peroxides evaluation	Human	MeWo, A2058, SK-Mel 5, SK-Mel 24, C8161, CHL-1, and A375 cells	AKR1C3 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Aldo-keto reductase family 1 member C3	P42330 (AK1C3_HUMAN)	####	_NA_
CBS	Cystathionine beta-synthase	HGNC: 1550	Knockdown in erastin-resistant cells caused ferroptotic cell death, while overexpression conferred ferroptosis resis	RNAi, cell viability, ROS analysis, GSH, glutamate release and cystine uptake assays, western blotting, qRT-PCR	Human	SKOV3 and OVCA429 cells	CBS :+: Cystathionine, Cystathionine :+: Cysteine, Cysteine :+: GSH, GSH :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Cystathionine beta-synthase	P35520 (CBS_HUMAN)	####	_NA_

			tance.										
NFE2L2	Nuclear factor, erythroid 2 like 2	HGNC:7782	Genetically repression of NRF2 enhanced ferroptosis susceptibility.	RNAi, cell viability, ROS analysis, GSH, glutamate release and cystine uptake assays, western blotting, qRT-PCR	Human	SKOV3 and OVCA429 cells	NFE2L2 :+: CBS :+: Cystathionine, Cystathionine :+: Cysteine, Cysteine :+: GSH, GSH :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	Nuclear factor erythroid 2-related factor 2	Q16236 (NF2L2_HUMAN)	####	NRF2 in article

CAV1	Caveolin 1	HGNC:1527	Cav-1 deficiency aggravated ferroptosis. Short hairpin RNA of Cav-1 promoted ferroptosis, which was ameliorated by Cav-1 overexpression.	Immunofluorescence, western blot, ROS detection	Human, mice	LO2 cells, mice model	CAV-1 :+: xCT, xCT :+: GPX4, GPX4 :-: Ferroptosis, CAV-1 :-: RNS, RNS :+: Ferroptosis	Validated	_NA_	Caveolin-1	Q03135 (CAV1_HUMAN)	####	Cav-1 in article

GCH1	GTP cyclohydrolase 1	HGNC:4193	Gch1 overexpression and its downstream metabolites BH4/BH2 rescue from ferroptosis. Inhibition of GCH1 activity can sensitize resistant cancer cells to ferroptosis induction.	CRISPR activation screening, qRT-PCR, cell viability, cell counts, western blot	Human	HT-1080,786-O, A-498, Caki-1, AU565, DU4475, MCF-7 cells	GCH1 :+: Phospholipid, Phospholipid :-: Ferroptosis, GCH1 :+: COQ10, COQ10 :-: Lipid ROS, Lipid ROS :+: Ferroptosis	Validated	_NA_	GTP cyclohydrolase 1	P30793 (GCH1_HUMAN)	####	_NA_
Marker													
Symbol	Name	HGNC_ID	Evidence	Test method	Test in	Test setting	Confidence	Caution	Protein encoded	UniProtKB	PMID	Remark	_NA_

PTGS2	Prostaglandin-endoperoxide synthase 2	HGNC:9605	Simply a downstream marker of ferroptosis. The most upregulated gene in BJeLR cells upon treatment with either erastin or (1S, 3R)-RSL3, but ferroptotic cell death was not affected by inhibition of the enzyme.	RT-qPCR, cell viability	Human	BJeLR cells	Validated	_NA_	Prostaglandin G/H synthase 2	P35354 (PGH2_HUMAN)	###	May promote ferroptosis.	_NA_

DUSP1	Dual specificity phosphatase 1	HGNC:3064	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Dual specificity protein phosphatase 1	P28562 (DUS1_HUMAN)	###	May promote ferroptosis.	_NA_

NOS2	Nitric oxide synthase 2	HGNC:7873	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Nitric oxide synthase	P35228 (NOS2_HUMAN)	###	May promote ferroptosis.	_NA_

NCF2	Neutrophil cytosolic factor 2	HGNC:7661	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Neutrophil cytosol factor 2	P19878 (NCF2_HUMAN)	###	May promote ferroptosis.	_NA_

MT3	Metallothionein 3	HGNC:7408	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Metallothionein-3	P25713 (MT3_HUMAN)	###	May promote ferroptosis.	_NA_

UBC	Ubiquitin C	HGNC: 12468	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Polyubiquitin-C	P0CG48 (UBC_HUMAN)	###	May promote ferroptosis.	_NA_

ALB	Albumin	HGNC:399	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Serum albumin	P02768 (ALBU_HUMAN)	###	May promote ferroptosis.	_NA_

TXNRD1	Thioredoxin reductase 1	HGNC:12437	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Thioredoxin reductase 1	Q16881 (TRXR1_HUMAN)	###	May promote ferroptosis.	_NA_

SRXN1	Sulfiredoxin 1	HGNC:16132	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Sulfiredoxin-1	Q9BYN0 (SRXN1_HUMAN)	###	May promote ferroptosis.	_NA_

GPX2	Glutathione peroxidase 2	HGNC:4554	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Glutathione peroxidase 2	P18283 (GPX2_HUMAN)	###	May promote ferroptosis.	_NA_

BNIP3	BCL2 interacting protein 3	HGNC:1084	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3	Q12983 (BNIP3_HUMAN)	###	May promote ferroptosis.	_NA_

OXSR1	Oxidative stress responsive kinase 1	HGNC:8508	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Serine/threonine-protein kinase OSR1	O95747 (OXSR1_HUMAN)	###	May promote ferroptosis.	_NA_

SELENOS	Selenoprotein S	HGNC:30396	Expression was upregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Selenoprotein S	Q9BQE4 (SELS_HUMAN)	###	SELS in article. May promote ferroptosis.	_NA_

ANGPTL7	Angiopoietin like 7	HGNC:24078	Expression was downregulated during ferroptosis induced by erastin or RSL3.	RT-qPCR, cell viability	Human	BJeLR cells	Deduced	Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.	Angiopoietin-related protein 7	O43827 (ANGL7_HUMAN)	###	May promote ferroptosis.	_NA_

CHAC1	ChaC glutathione specific gamma-glutamylcyclotransferase 1	HGNC:28680	Up-regulated in erastin-treated samples. A useful pharmacodynamic marker of system Xc-inhibition.	RNA-seq, RT-qPCR	Human	HT-1080 and Calu-1 cells	Validated	Further study needed to confirm connection to ferroptosis.	Glutathione-specific gamma-glutamylcyclotransferase 1	Q9BUX1 (CHAC1_HUMAN)	###	_NA_	_NA_

SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Similar to erastin treatment, silencing of this gene inhibits glutamate release. Erastin specifically inhibits SLC7A11-dependent system Xc- function.	RNA silencing, RT-qPCR	Human	HT-1080 cells	Deduced	Further study needed to confirm connection to ferroptosis.	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	###	May inhibit ferroptosis.	_NA_
DDIT4	DNA damage inducible transcript 4	HGNC:24944	Up-regulated (>=2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	DNA damage-inducible transcript 4 protein	Q9NX09 (DDIT4_HUMAN)	###	May promote ferroptosis.	_NA_

LOC284561	_NA_	_NA_	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	_NA_	_NA_	###	Not found in HGNC. May promote ferroptosis.	_NA_
ASNS	Asparagine synthetase (glutamine-hydrolyzing)	HGNC:753	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Asparagine synthetase [glutamine-hydrolyzing]	P08243 (ASNS_HUMAN)	###	May promote ferroptosis.	_NA_

TSC22D3	TSC22 domain family member 3	HGNC:3051	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	TSC22 domain family protein 3	Q99576 (T22D3_HUMAN)	###	May promote ferroptosis.	_NA_
DDIT3	DNA damage inducible transcript 3	HGNC:2726	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	DDIT3 upstream open reading frame protein	P0DPQ6 (DT3UO_HUMAN)	###	May promote ferroptosis.	_NA_

JDP2	Jun dimerization protein 2	HGNC:17546	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Jun dimerization protein 2	Q8WYK2 (JDP2_HUMAN)	###	May promote ferroptosis.	_NA_
SESN2	Sestrin 2	HGNC:20746	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Sestrin-2	P58004 (SESN2_HUMAN)	###	May promote ferroptosis.	_NA_

SLC1A4	Solute carrier family 1 member 4	HGNC:10942	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Neutral amino acid transporter A	P43007 (SATT_HUMAN)	###	May promote ferroptosis.	_NA_
PCK2	Phosphoenolpyruvate carboxykinase 2, mitochondrial	HGNC:8725	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Phosphoenolpyruvate carboxykinase [GTP]	Q16822 (PCKGM_HUMAN)	###	May promote ferroptosis.	_NA_

TXNIP	Thioredoxin interacting protein	HGNC:16952	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Thioredoxin-interacting protein	Q9H3M7 (TXNIP_HUMAN)	###	May promote ferroptosis.	_NA_
VLDLR	Very low density lipoprotein receptor	HGNC:12698	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Very low-density lipoprotein receptor	P98155 (VLDLR_HUMAN)	###	May promote ferroptosis.	_NA_

GPT2	Glutamic--pyruvic transaminase 2	HGNC:18062	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Alanine aminotransferase 2	Q8TD30 (ALAT2_HUMAN)	###	May promote ferroptosis.	_NA_
PSAT1	Phosphoserine aminotransferase 1	HGNC:19129	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Phosphoserine aminotransferase	Q9Y617 (SERC_HUMAN)	###	May promote ferroptosis.	_NA_

LURAP1L	Leucine rich adaptor protein 1 like	HGNC:31452	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Leucine rich adaptor protein 1-like	Q8IV03 (LUR1L_HUMAN)	###	C9ORF150 in article. May promote ferroptosis.	_NA_
SLC7A5	Solute carrier family 7 member 5	HGNC:11063	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Large neutral amino acids transporter small subunit 1	Q01650 (LAT1_HUMAN)	###	May promote ferroptosis.	_NA_

HERPUD1	Homocysteine inducible ER protein with ubiquitin like domain 1	HGNC:13744	Up-regulated (>=2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein	Q15011 (HERP1_HUMAN)	###	May promote ferroptosis.	_NA_
XBP1	X-box binding protein 1	HGNC:12801	Up-regulated (>=2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	X-box-binding protein 1	P17861 (XBP1_HUMAN)	###	May promote ferroptosis.	_NA_

ATF3	Activating transcription factor 3	HGNC:785	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Cyclic AMP-dependent transcription factor ATF-3	P18847 (ATF3_HUMAN)	###	May promote ferroptosis.	_NA_
SLC3A2	Solute carrier family 3 member 2	HGNC:11026	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	4F2 cell-surface antigen heavy chain	P08195 (4F2_HUMAN)	###	May promote ferroptosis.	_NA_

CBS	Cystathionine beta-synthase	HGNC:1550	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Cystathionine beta-synthase	P35520 (CBS_HUMAN)	###	May promote ferroptosis.	_NA_
ATF4	Activating transcription factor 4	HGNC:786	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Cyclic AMP-dependent transcription factor ATF-4	P18848 (ATF4_HUMAN)	###	May promote ferroptosis.	_NA_

ZNF419	Zinc finger protein 419	HGNC:20648	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Zinc finger protein 419	Q96HQ0 (ZN419_HUMAN)	###	May promote ferroptosis.	_NA_
KLHL24	Kelch like family member 24	HGNC:25947	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Kelch-like protein 24	Q6TFL4 (KLH24_HUMAN)	###	May promote ferroptosis.	_NA_

TRIB3	Tribbles pseudokinase 3	HGNC:16228	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Tribbles homolog 3	Q96RU7 (TRIB3_HUMAN)	###	May promote ferroptosis.	_NA_
ZFP69B	ZFP69 zinc finger protein B	HGNC:28053	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Zinc finger protein 69 homolog B	Q9UJL9 (ZF69B_HUMAN)	###	ZNF643 in article. May promote ferroptosis.	_NA_

ATP6V1G2	ATPase H+ transporting V1 subunit G2	HGNC:862	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	V-type proton ATPase subunit G 2	O95670 (VATG2_HUMAN)	###	May promote ferroptosis.	_NA_
VEGFA	Vascular endothelial growth factor A	HGNC:12680	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Vascular endothelial growth factor A	P15692 (VEGFA_HUMAN)	###	May promote ferroptosis.	_NA_

GDF15	Growth differentiation factor 15	HGNC:30142	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Growth/differentiation factor 15	Q99988 (GDF15_HUMAN)	###	May promote ferroptosis.	_NA_
TUBE1	Tubulin epsilon 1	HGNC:20775	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Tubulin epsilon chain	Q9UJT0 (TBE_HUMAN)	###	May promote ferroptosis.	_NA_

ARRDC3	Arrestin domain containing 3	HGNC:29263	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Arrestin domain-containing protein 3	Q96B67 (ARRD3_HUMAN)	###	May promote ferroptosis.	_NA_
CEBPG	CCAAT enhancer binding protein gamma	HGNC:1837	Up-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	CCAAT/enhancer-binding protein gamma	P53567 (CEBPG_HUMAN)	###	May promote ferroptosis.	_NA_

SNORA16A	Small nucleolar RNA, H/ACA box 16A	HGNC:32605	Down-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	_NA_	_NA_	###	May inhibit ferroptosis.	_NA_
RGS4	Regulator of G protein signaling 4	HGNC:10000	Down-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	Regulator of G-protein signaling 4	P49798 (RGS4_HUMAN)	###	May inhibit ferroptosis.	_NA_

BLOC1S5-TXNDC5	BLOC1S5-TXNDC5 readthrough (NMD candidate)	HGNC:42001	Down-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	_NA_	_NA_	###	MUTED-TXNDC5 in article. May inhibit ferroptosis.	_NA_
LOC390705	_NA_	_NA_	Down-regulated (>= 2 fold) in erastin-treated samples.	RNA-seq	Human	HT-1080 cells	Screened	Further study needed to confirm connection to ferroptosis.	_NA_	_NA_	###	Not found in HGNC. May inhibit ferroptosis.	_NA_

EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	HGNC:3265	Phosphorylated in erastin-treated sample.	Western blot	Human	HT-1080 cells	Deduced	_NA_	Eukaryotic translation initiation factor 2 subunit 1	P05198 (IF2A_HUMAN)	###	eIF2alpha in article. May promote ferroptosis.	_NA_
KIM-1	Kidney injury molecule-1	_NA_	Down-regulated upon Fer-1 appearance	Real-time quantitative RT-PCR	Mice	Fer-1–treated CaOx model	Deduced	_NA_	_NA_	_NA_	###	Not found in HGNC. May promote ferroptosis.	_NA_
IL6	Interleukin 6	HGNC:6018	Down-regulated upon Fer-1 appearance	Real-time quantitative RT-PCR	Mice	Fer-1–treated CaOx model	Deduced	_NA_	Interleukin-6	P05231 (IL6_HUMAN)	###	IL-6 in article. May promote ferroptosis.	_NA_

CXCL2	C-X-C motif chemokine ligand 2	HGNC:4603	Down-regulated upon Fer-1 appearance	Real-time quantitative RT-PCR	Mice	Fer-1–treated CaOx model	Deduced	_NA_	C-X-C motif chemokine 2	P19875 (CXCL2_HUMAN)	###	May promote ferroptosis.	_NA_
RELA	RELA proto-oncogene, NF-kB subunit	HGNC:9955	Down-regulated upon Fer-1 appearance	Real-time quantitative RT-PCR	Mice	Fer-1–treated CaOx model	Deduced	_NA_	Transcription factor p65	Q04206 (TF65_HUMAN)	###	p65 in article. May promote ferroptosis.	_NA_

HSD17B11	Hydroxysteroid 17-beta dehydrogenase 11	HGNC:22960	Enriched in RSL3-resistant cells.	Gene trap insertion	Human	Chronic myeloid leukemia cell line KBM7	Screened	_NA_	Estradiol 17-beta-dehydrogenase 11	Q8NBQ5 (DHB11_HUMAN)	###	May promote ferroptosis.	_NA_
AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	HGNC:326	Enriched in RSL3-resistant cells.	Gene trap insertion	Human	Chronic myeloid leukemia cell line KBM7	Screened	_NA_	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	Q9NRZ7 (PLCC_HUMAN)	###	May promote ferroptosis.	_NA_

SETD1B	SET domain containing 1B, histone lysine methyltransferase	HGNC:29187	Enriched in GPX4 inhibitor ML162-resistant cells.	Gene trap insertion	Human	Chronic myeloid leukemia cell line KBM7	Screened	_NA_	Histone-lysine N-methyltransferase SETD1B	Q9UPS6 (SET1B_HUMAN)	###	May promote ferroptosis.	_NA_

HMOX1	Heme oxygenase 1	HGNC:5013	Its expression increased in response to artesunate-induced ferroptosis, indicating activation of ROS-mediated signaling pathways.	Western blotting	Human	Pancreatic adenocarcinoma cell line Panc-1 cells	Deduced	_NA_	Heme oxygenase 1	P09601 (HMOX1_HUMAN)	###	HO-1 in article. May promote ferroptosis.	_NA_
TF	Transferrin	HGNC:11740	Its expression is decreased in patients.	Gene expression analysis	Human	Patient PDAC tissues	Deduced	_NA_	Serotransferrin	P02787 (TRFE_HUMAN)	###	May promote ferroptosis.	_NA_

FTL	Ferritin light chain	HGNC:3999	Its expression is decreased in patients.	Gene expression analysis	Human	Patient PDAC tissues	Deduced	_NA_	Ferritin light chain	P02792 (FRIL_HUMAN)	###	May promote ferroptosis.	_NA_
RPL8	Ribosomal protein L8	HGNC:10368	Significantly reduced in tumor tissues	Gene expression analysis	Human	Patient PDAC tissues	Deduced	_NA_	60S ribosomal protein L8	P62917 (RL8_HUMAN)	###	May promote ferroptosis.	_NA_
ATP5MC3	ATP synthase membrane subunit c locus 3	HGNC:843	Significantly reduced in tumor tissues	Gene expression analysis	Human	Patient PDAC tissues	Deduced	_NA_	ATP synthase F(0) complex subunit C3	P48201 (AT5G3_HUMAN)	###	ATP5G3 in article. May promote ferroptosis.	_NA_

TFRC	Transferrin receptor	HGNC: 11763	Expression of this gene is increased in patients.	Gene expression analysis	Human	Patient PDAC tissues	Deduced	_NA_	Transferrin receptor protein 1	P02786 (TFR1_HUMAN)	###	May inhibit ferroptosis.	_NA_
MAFG	MAF bZIP transcription factor G	HGNC: 6781	The interaction between NRF2 and MafG was increased in response to erastin and sorafenib.	Western blot	Human, mice	HepG2, Hepa 1-6, Hep3B, and SNU-182 cells	Deduced	_NA_	Transcription factor MafG	O15525 (MAFG_HUMAN)	###	May inhibit ferroptosis.	_NA_

IL33	Interleukin 33	HGNC:16028	IL-33 upregulation is a feature of ferroptosis. Ferrostatin-1, an inhibitor of ferroptosis, prevented the upregulation of IL-33.	Western blot, quantitative PCR, ELISA	Mice	C57BL/6 mice	Deduced	_NA_	Interleukin-33	O95760 (IL33_HUMAN)	###	IL-33 in article. May promote ferroptosis.	_NA_

FTH1	Ferritin heavy chain 1	HGNC:3976	An increase of endogenous FTH1 level during ferroptosis. Degradation of FTH1 protein upon ferroptosis induction.	Immunoblotting, q-PCR	Human	HT1080 cells	Validated	An error may exist in the original article, where the authors wrote "ferritin light chain 1 (FTH1)". According to HGNC, FTH1 is the official symbol for "ferritin heavy chain 1".	Ferritin heavy chain	P02794 (FRIH_HUMAN)	###	_NA_	_NA_

SLC40A1	Solute carrier family 40 member 1	HGNC:10909	Erastin-induced mRNA expression is upregulated in FANCD2-deficient cells.	Q-PCR	Mice	Bone marrow stromal cells	Validated	Used as a marker in this study but has been proved to be a suppressor (PMID 27441659).	Solute carrier family 40 member 1	Q9NP59 (S40A1_HUMAN)	###	May promote ferroptosis.	_NA_

TF	Transferrin	HGNC:11740	Erastin-induced mRNA expression is upregulated in FANCD2-deficient cells.	Q-PCR	Mice	Bone marrow stromal cells	Validated	Used as a marker in this study but has been proved to be a driver (PMID 27441659).	Serotransferrin	P02787 (TRFE_HUMAN)	###	May promote ferroptosis.	_NA_

TFRC	Transferrin receptor	HGNC:11763	Erastin-induced mRNA expression is upregulated in FANCD2-deficient cells.	Q-PCR	Mice	Bone marrow stromal cells	Validated	Used as a marker in this study but has been proved to be a driver (PMID 27514700).	Transferrin receptor protein 1	P02786 (TFR1_HUMAN)	###	May promote ferroptosis.	_NA_

FTH1	Ferritin heavy chain 1	HGNC:3976	Erastin-induced mRNA expression is downregulated in FANCD2-deficient cells.	Q-PCR, western blot	Mice	Bone marrow stromal cells	Validated	Used as a marker in this study but has been proved to be a suppressor (PMID 26403645).	Ferritin heavy chain	P02794 (FRIH_HUMAN)	###	May inhibit ferroptosis.	_NA_

GPX4	Glutathione peroxidase 4	HGNC: 4556	Erastin-induced mRNA expression is downregulated in FANCD2-deficient cells.	Q-PCR, western blot	Mice	Bone marrow stromal cells	Validated	Used as a marker in this study but has been proved to be a suppressor (PMID 25824823).	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	###	May inhibit ferroptosis.	_NA_

HAMP	Hepcidin antimicrobial peptide	HGNC:15598	Erastin-induced mRNA expression is downregulated in FANCD2-deficient cells.	Q-PCR	Mice	Bone marrow stromal cells	Deduced	_NA_	Hepcidin	P81172 (HEPC_HUMAN)	###	May inhibit ferroptosis.	_NA_

HSPB1	Heat shock protein family B (small) member 1	HGNC:5246	Erastin-induced mRNA expression is downregulated in FANCD2-deficient cells.	Q-PCR	Mice	Bone marrow stromal cells	Validated	Used as a marker in this study but has been proved to be a suppressor (PMID 25728673).	Heat shock protein beta-1	P04792 (HSPB1_HUMAN)	###	May inhibit ferroptosis.	_NA_

NFE2L2	Nuclear factor, erythroid 2 like 2	HGNC:7782	Erastin-induced mRNA expression is downregulated in FANCD2-deficient cells.	Q-PCR	Mice	Bone marrow stromal cells	Validated	Used as a marker in this study but has been proved to be a suppressor (PMID 27015352).	Nuclear factor erythroid 2-related factor 2	Q16236 (NF2L2_HUMAN)	###	NRF2 in article. May inhibit ferroptosis.	_NA_

STEAP3	STEAP3 metalloreductase	HGNC:24592	Erastin-induced mRNA expression is downregulated in FANCD2-deficient cells.	Q-PCR	Mice	Bone marrow stromal cells	Deduced	_NA_	Metalloreductase STEAP3	Q658P3 (STEA3_HUMAN)	###	May inhibit ferroptosis.	_NA_
DRD5	Dopamine receptor D5	HGNC:3026	Ferroptotic erastin induces DRD5 gene expression in ferroptosis.	Western blot, Q-PCR	Human	PANC1 cells	Deduced	_NA_	D(1B) dopamine receptor	P21918 (DRD5_HUMAN)	###	May promote ferroptosis.	_NA_

GPX4	Glutathione peroxidase 4	HGNC: 4556	Erastin promoted GPX4 degradation. Antiferroptotic dopamine increased the protein stability of glutathione peroxidase 4.	Western blot, Q-PCR	Human	PANC1 cells	Deduced	Has been proved to be a suppressor (PMID 25824823).	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	###	May inhibit ferroptosis.	_NA_

DRD4	Dopamine receptor D4	HGNC:3025	Antiferroptotic dopamine suppressed dopamine receptor D4 protein degradation. Ferroptotic erastin promotes DRD4 protein degradation.	Western blot, Q-PCR	Human	PANC1 cells	Deduced	_NA_	D(4) dopamine receptor	P21917 (DRD4_HUMAN)	###	May inhibit ferroptosis.	_NA_

MAP3K5	Mitogen-activated protein kinase kinase kinase 5	HGNC:6857	Cold stress evokes ferroptosis, and the ASK1-p38 pathway is activated downstream of lipid peroxide, leading to the cell death. ASK1-p38 axis is also activated in the erastin-induced ferroptosis model.	LDH assay, immunoblot, RNAi, CCK-8	Human	A549 cells	Deduced	_NA_	Mitogen-activated protein kinase kinase kinase 5	Q99683 (M3K5_HUMAN)	###	ASK1 in article. May promote ferroptosis.	_NA_

MAPK14	Mitogen-activated protein kinase 14	HGNC: 6876	Cold stress evokes ferroptosis, and the ASK1-p38 pathway is activated downstream of lipid peroxide, leading to the cell death. ASK1-p38 axis is also activated in the erastin-induced ferroptosis model.	LDH assay, immunoblot, RNAi, CCK-8	Human	A549 cells	Deduced	_NA_	Mitogen-activated protein kinase 14	Q16539 (MK14_HUMAN)	###	p38 in article. May promote ferroptosis.	_NA_

SLC2A1	Solute carrier family 2 member 1	HGNC:11005	Increased at LSH overexpression. Decreased at LSH knockdown. LSH can inhibit ferroptosis.	ChIP analysis, RT-qPCR	Human	H358, A549 cells	Deduced	_NA_	Solute carrier family 2	P11166 (GTR1_HUMAN)	###	GLUT1 in article. May inhibit ferroptosis.	_NA_
SLC2A3	Solute carrier family 2 member 3	HGNC:11007	Decreased at LSH knockdown. LSH can inhibit ferroptosis.	RT-qPCR	Human	H358, A549 cells	Deduced	_NA_	Solute carrier family 2	P11169 (GTR3_HUMAN)	###	GLUT3 in article. May inhibit ferroptosis.	_NA_

SLC2A6	Solute carrier family 2 member 6	HGNC:11011	Increased at LSH overexpression. Decreased at LSH knockdown. LSH can inhibit ferroptosis.	RT-qPCR	Human	H358, A549 cells	Deduced	_NA_	Solute carrier family 2	Q9UGQ3 (GTR6_HUMAN)	###	GLUT6 in article. May inhibit ferroptosis.	_NA_
SLC2A8	Solute carrier family 2 member 8	HGNC:13812	Decreased at LSH knockdown. LSH can inhibit ferroptosis.	RT-qPCR	Human	H358, A549 cells	Deduced	_NA_	Solute carrier family 2	Q9NY64 (GTR8_HUMAN)	###	GLUT8 in article. May inhibit ferroptosis.	_NA_

SLC2A12	Solute carrier family 2 member 12	HGNC:18067	Increased at LSH overexpression. Decreased at LSH knockdown. LSH can inhibit ferroptosis.	RT-qPCR	Human	H358, A549 cells	Deduced	_NA_	Solute carrier family 2	Q8TD20 (GTR12_HUMAN)	###	GLUT12 in article. May inhibit ferroptosis.	_NA_

GLUT13	_NA_	_NA_	Increased at LSH overexpression. Decreased at LSH knockdown. LSH can inhibit ferroptosis.	RT-qPCR	Human	H358, A549 cells	Deduced	_NA_	_NA_	_NA_	###	Not found in HGNC. May inhibit ferroptosis.	_NA_
SLC2A14	Solute carrier family 2 member 14	HGNC:18301	Decreased at LSH knockdown. LSH can inhibit ferroptosis.	RT-qPCR	Human	H358, A549 cells	Deduced	_NA_	Solute carrier family 2	Q8TDB8 (GTR14_HUMAN)	###	GLUT14 in article. May inhibit ferroptosis.	_NA_

EIF2AK4	Eukaryotic translation initiation factor 2 alpha kinase 4	HGNC:19687	CHAC1 degradation of GSH enhances cystine-starvation-induced ferroptosis through the activated GCN2-eIF2 alpha-ATF4 pathway.	Western blot, real-time PCR, cell viability assay, siRNA, GSH assay kit	Human	MDA-MB-231, Hs 578T, and HCC1937 cells	Deduced	_NA_	eIF-2-alpha kinase GCN2	Q9P2K8 (E2AK4_HUMAN)	###	GCN2 in article. May promote ferroptosis.	_NA_

EIF2S1	Eukaryotic translation initiation factor 2 subunit alpha	HGNC:3265	CHAC1 degradation of GSH enhances cystine-starvation-induced ferroptosis through the activated GCN2-eIF2alpha-ATF4 pathway.	Western blot, real-time PCR, cell viability assay, siRNA, GSH assay kit	Human	MDA-MB-231, Hs 578T, and HCC 1937 cells	Deduced	_NA_	Eukaryotic translation initiation factor 2 subunit 1	P05198 (IF2A_HUMAN)	###	eIF2alpha in article. May promote ferroptosis.	_NA_

ATF4	Activating transcription factor 4	HGNC:786	CHAC1 degradation of GSH enhances cystine-starvation-induced ferroptosis through the activated GCN2-eIF2 alpha-ATF4 pathway.	Western blot, real-time PCR, cell viability assay, siRNA, GSH assay kit	Human	MDA-MB-231, Hs 578T, and HCC1937 cells	Deduced	_NA_	Cyclic AMP-dependent transcription factor ATF-4	P18848 (ATF4_HUMAN)	###	May promote ferroptosis.	_NA_
ALOX5	Arachidonate 5-lipoxygenase	HGNC:435	Overexpression sensitizes cells to ferroptosis.	Western blot, mass spectrometry, cell viability assay, gene overexpression	Human	HEK293 cells	Deduced	Not essential but may play a role in ferroptotis initiation.	Arachidonate 5-lipoxygenase	P09917 (LOX5_HUMAN)	###	5-LOX in article	_NA_

ALOX12	Arachidonate 12-lipoxygenase, 12S type	HGNC:429	Overexpression sensitizes cells to ferroptosis.	Western blot, mass spectrometry, cell viability assay, gene overexpression	Human	HEK 293 cells	Deduced	Not essential but may play a role in ferroptotis initiation.	Arachidonate 12-lipoxygenase	P18054 (LOX12_HUMAN)	###	p12-LOX in article	_NA_
ALOX15	Arachidonate 15-lipoxygenase	HGNC:433	Overexpression sensitizes cells to ferroptosis.	Western blot, mass spectrometry, cell viability assay, gene overexpression	Human	HEK 293 cells	Deduced	Not essential but may play a role in ferroptotis initiation.	Arachidonate 15-lipoxygenase	P16050 (LOX15_HUMAN)	###	15-LOX-1 in article	_NA_

ALOX5	Arachidonate 5-lipoxygenase	HGNC:435	Necessary for hemin-induced ferroptosis in vitro.	qRT-PCR, immunoblotting, MTT assay	Mice	C57BL/6 and pregnant CD1 mice, primary cortical neurons	Deduced	_NA_	Arachidonate 5-lipoxygenase	P09917 (LOX5_HUMAN)	###	May promote ferroptosis.	_NA_
ACSF2	Acyl-CoA synthetase family member 2	HGNC:26101	Increased in ferroptotic events. Decreased in DFO-induced resistance to ferroptosis.	Western blot, glutathione detection, RT-qPCR, immunofluorescence staining	Rat	Wistar rats	Deduced	_NA_	Medium-chain acyl-CoA ligase ACSF2	Q96CM8 (ACSF2_HUMAN)	###	There is a corrigendum for this article. May promote ferroptosis.	_NA_

IREB2	Iron responsive element binding protein 2	HGNC:6115	Increased in ferroptotic events. Decreased in DFO-induced resistance to ferroptosis.	Western blot, glutathione detection, RT-qPCR, immunofluorescence staining	Rat	Wistar rats	Deduced	_NA_	Iron-responsive element-binding protein 2	P48200 (IREB2_HUMAN)	###	There is a corrigendum for this article. May promote ferroptosis.	_NA_
GPX4	Glutathione peroxidase 4	HGNC:4556	Upregulated in DFO-induced resistance to ferroptosis.	Western blot, glutathione detection, RT-qPCR, immunofluorescence staining	Rat	Wistar rats	Validated	Inhibits ferroptosis but used as a marker in this study.	Phospholipid hydroperoxide glutathione peroxidase	P36969 (GPX4_HUMAN)	###	There is a corrigendum for this article.	_NA_

HMGB1	High mobility group box 1	HGNC:4983	Associated with ferroptotic cell death. Ferroptosis activators induce HMGB1 release.	ELISA, western blot, RNAi	Human, mice	HT1080 and PANC1 cells, mouse embryonic fibroblasts	Deduced	_NA_	High mobility group protein B1	P09429 (HMGB1_HUMAN)	###	May promote ferroptosis.	_NA_
HMOX1	Heme oxygenase 1	HGNC:5013	Required for DOX-induced ferroptosis.	RNA-seq, qRT-PCR, HIS	Mice	Mice	Deduced	_NA_	Heme oxygenase 1	P09601 (HMOX1_HUMAN)	###	May promote ferroptosis.	_NA_

NFE2L2	Nuclear factor, erythroid 2 like 2	HGNC:7782	DOX treatment induced ferroptosis. Protein and mRNA levels of Nrf2 were increased after DOX treatment.	RNA-seq, QuantiChrom Heme Assay Kit, iron staining, qRT-PCR, survival curve, HIS	Mice	Mice	Deduced	_NA_	Nuclear factor erythroid 2-related factor 2	Q16236 (NF2L2_HUMAN)	###	NRF2 in article.	_NA_

ELAVL1	ELAV like RNA binding protein 1	HGNC:3312	Binds to and increases the expression of the negative ferroptosis regulator LINC00336.	RNA pulldown, mass spectrometry, qRT-PCR, gene overexpression, gene knockdown, western blot	Human	H358, PC9, SPC-A-1, and A549 cells	Deduced	_NA_	ELAV-like protein 1	Q15717 (ELAV1_HUMAN)	###	May inhibit ferroptosis.	_NA_
SLC3A2	Solute carrier family 3 member 2	HGNC:11026	Strongly correlated with resistance to ferroptosis inducers.	Western blot, cell viability assay, cell viability assay, MDA assay, glutamate assay	Human	HT-1080 cells	Deduced	_NA_	4F2 cell-surface antigen heavy chain	P08195 (4F2_HUMAN)	###	May inhibit ferroptosis.	_NA_

SLC7A11	Solute carrier family 7 member 11	HGNC:11059	Strongly correlated with resistance to ferroptosis inducers.	Western blot, cell viability assay, cell viability assay, MDA assay, glutamate assay	Human	HT-1080 cells	Deduced	_NA_	Cystine/glutamate transporter	Q9UPY5 (XCT_HUMAN)	###	May inhibit ferroptosis.	_NA_

TFAP2C	Transcription factor AP-2 gamma	HGNC:11744	Activated by ferroptosis inhibitor selenium.	Behavioral analysis, infarct volume analysis, immunocytochemistry, TUNEL staining, fluoro-jade Staining, qRT-PCR, cell death assay, ChIP assay, siRNA, western blot, immunoblotting, RNA-seq, mass spectrometry	Mice	C57BL/6 mice, primary cortical neurons, HT22 murine hippocampal cells	Deduced	_NA_	Transcription factor AP-2 gamma	Q92754 (AP2C_HUMAN)	###	May inhibit ferroptosis.	_NA_

SP1	Sp1 transcription factor	HGNC:11205	Activated by ferroptosis inhibitor selenium.	Behavioral analysis, infarct volume analysis, immunocytochemistry, TUNEL staining, fluoro-jade Staining, qRT-PCR, cell death assay, ChIP assay, siRNA, western blot, immunoblotting, RNA-seq, mass spectrometry	Mice	C57BL/6 mice, primary cortical neurons, HT22 murine hippocampal cells	Deduced	_NA_	Transcription factor Sp1	P08047 (SP1_HUMAN)	###	May inhibit ferroptosis.	_NA_

HBA1	Hemoglobin subunit alpha 1	HGNC:4823	Upregulated in cells treated with ferroptosis inducer erastin. Stimulates ferroptosis possibly in a GSH-dependent manner.	Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC	Human	HepG2, Bel-7402 cells	Deduced	_NA_	Hemoglobin subunit alpha	P69905 (HBA_HUMAN)	###	May promote ferroptosis.	_NA_

NNMT	Nicotinamide N-methyltransferase	HGNC:7861	Upregulated in cells treated with ferroptosis inducer erastin. Stimulates ferroptosis possibly in a GSH-dependent manner.	Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC	Human	HepG2, Bel-7402 cells	Deduced	_NA_	Nicotinamide N-methyltransferase	P40261 (NNMT_HUMAN)	###	May promote ferroptosis.	_NA_

PLIN4	Perilipin 4	HGNC:29393	Upregulated in cells treated with ferroptosis inducer erastin. Stimulates ferroptosis possibly in a GSH-dependent manner.	Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC	Human	HepG2, Bel-7402 cells	Deduced	_NA_	Perilipin-4	Q96Q06 (PLIN4_HUMAN)	###	May promote ferroptosis.	_NA_

HIC1	HIC ZBTB transcriptional repressor 1	HGNC: 4909	Essential for stimulation of pro-ferroptotic gene transcription upon ferroptosis induction.	Immunohistochemistry, immunofluorescence, western blot, qPCR, metabolites examination, ChIP	Human	HepG2, Bel-7402 cells	Deduced	_NA_	Hypermethylated in cancer 1 protein	Q14526 (HIC1_HUMAN)	###	May promote ferroptosis.	_NA_

STMN1	Stathmin 1	HGNC:6510	Downregulated in cells treated with ferroptosis inducer erastin. Suppresses ferroptosis possibly in a GSH-dependent manner.	Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC	Human	HepG2, Bel-7402 cells	Deduced	_NA_	Stathmin	P16949 (STMN1_HUMAN)	###	May inhibit ferroptosis.	_NA_

RRM2	Ribonucleotide reductase regulatory subunit M2	HGNC:10452	Downregulated in cells treated with ferroptosis inducer erastin. Suppresses ferroptosis possibly in a GSH-dependent manner.	Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC	Human	HepG2, Bel-7402 cells	Deduced	_NA_	Ribonucleoside-diphosphate reductase subunit M2	P31350 (RIR2_HUMAN)	###	May inhibit ferroptosis.	_NA_

CAPG	Capping actin protein, gelsolin like	HGNC:1474	Downregulated in cells treated with ferroptosis inducer erastin. Suppresses ferroptosis possibly in a GSH-dependent manner.	Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC	Human	HepG2, Bel-7402 cells	Deduced	_NA_	Macrophage-capping protein	P40121 (CAPG_HUMAN)	###	May inhibit ferroptosis.	_NA_

HNF4A	Hepatocyte nuclear factor 4 alpha	HGNC:5024	Essential for stimulation of anti-ferroptotic gene transcription.	Immunohistochemistry, immunofluorescence, western blot, qPCR, metabolites examination, ChIP	Human	HepG2, Bel-7402 cells	Deduced	_NA_	Hepatocyte nuclear factor 4-alpha	P41235 (HNF4A_HUMAN)	###	May inhibit ferroptosis.	_NA_

NGB	Neuroglobin	HGNC:14077	Human neuroglobin (hNgb)-EGFP-expressing SH-SY5Y cells to be significantly more resistant to ferroptosis induction.	Cell death, cell viability, lipid peroxidation assay, RT-qPCR	Human	SH-SY5Y cells	Deduced	_NA_	Neuroglobin	Q9NPG2 (NGB_HUMAN)	###	May inhibit ferroptosis.	_NA_

YWHAE	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon	HGNC:12851	Required by RSL3 (a ferroptosis inducer) to inactivate GPX4 (a ferroptosis inhibitor).	Mass spectrometry, siRNA, western blot	Human	HEK 293T cells	Deduced	_NA_	14-3-3 protein epsilon	P62258 (1433E_HUMAN)	###	14-3-3epsilon in article. May promote ferroptosis.	_NA_

GABPB1	GA binding protein transcription factor subunit beta 1	HGNC:4074	Downregulated by lncRNA GABPB1-AS1 upon erastin treatment.	RT-qPCR, western blot, siRNA, cell viability, lipid peroxidation assay	Human	HepG2, Huh7, and Hep3B cells	Deduced	_NA_	GA-binding protein subunit beta-1	Q06547 (GABP1_HUMAN)	###	May inhibit ferroptosis.	_NA_

AURKA	Aurora kinase A	HGNC:11393	Inhibition of AURKA or reconstitution of miR-4715-3p inhibited GPX4 and induced cell death, suggesting a link between AURKA and ferroptosis.	qRT-PCR, western blot, lentiviral infection, CellTiter-Glo luminescence assay	Human	OE33, STKM2, MKN45 cells	Predicted	_NA_	Aurora kinase A	O14965 (AURKA_HUMAN)	###	May inhibit ferroptosis.	_NA_

MIR4715	microRNA 4715	HGNC:41666	Inhibition of AURKA or reconstitution of miR-4715-3p inhibited GPX4 and induced cell death, suggesting a link between AURKA and ferroptosis.	qRT-PCR, western blot, lentiviral infection, CellTiter-Glo luminescence assay	Human	OE33, STKM2, MKN45 cells	Predicted	_NA_	_NA_	_NA_	###	miR-4715-3p in article. May promote ferroptosis.	_NA_

RIPK1	Receptor interacting serine/threonine kinase 1	HGNC:10019	Reduced expression results in resistance to ferroptosis.	Cell viability, western blot, RNA-seq, GSH assay, qRT-PCR, immunofluorescence imaging	Human	Patient-derived fibroblasts	Deduced	_NA_	Receptor-interacting serine/threonine-protein kinase 1	Q13546 (RIPK1_HUMAN)	###	May promote ferroptosis.	_NA_
PRDX1	Peroxiredoxin 1	HGNC:9352	Necessary to ferroptosis-related lipid peroxidation.	Western blot, siRNA, flow cytometry, cell viability, RT-PCR	Human	Primary corneal endothelial cells, B4G12 and HT1080 cells	Deduced	_NA_	Peroxiredoxin-1	Q06830 (PRDX1_HUMAN)	###	May promote ferroptosis.	_NA_

MIR30B	microRNA 30b	HGNC:31625	Upregulation of miR-30b-5p in preeclampsia models plays a pivotal role in ferroptosis.	GSH assay, MDA measurement, western blot, immunohistochemistry, microarray, RT-qPCR, labile iron assay, cell viability, LDH assay	Human, rat	Trophoblasts, preeclampsia model, HTR-8/SVneo and TEV-1 cells	Deduced	_NA_	_NA_	_NA_	###	miR-30b-5p in article. May promote ferroptosis.	_NA_

Supplementary Table 3: Shows the primers sequences.

The primers sequences.	
Primer name	**Primer sequence**
β-ACTIN（Internal reference）	Forward：5‘-CATGTACGTTGCTATCCAGGC-3’;
	Reverse：5‘- CTCCTTAATGTCACGCACGAT-3’;
MIR4435-2HG	Forward：5‘- GACATTCCAGACAAGCGGTG-3’;
	Reverse：5‘- CCTTTGCTGATCCACTTTGCT-3’;
SNHG4	Forward：5′-GCCCTGTGTGACACCAAGATA-3′;
	Reverse：5′-TAAGTCCCCTACCCCCATCT-3′;
PTOV1-AS1	Forward：5′-AAGAACGAAGGCGACACCAA-3′;
	Reverse：5′-CCTGATGTATTTTGGCGCGG-3′
PRRT3-AS1	Forward：5′-TTCAGAAATGCCTTGCAGTG-3′;
	Reverse：5′-CACCTCTTTGCTCTGCTCCT-3′

Supplementary Table 4: Ferroptosis associated DEGs.

Ferroptosis associated DEGs					
gene	conMean	treatMean	logFC	pValue	fdr
SLC7A11	0.030108219	0.889909177	4.885428826	1.65E-19	8.94E-19
AKR1C1	27.5295606	64.19352837	1.221446277	0.000384398	0.000512531
AKR1C2	16.24967136	50.10020952	1.624406096	5.01E-06	7.68E-06
AKR1C3	17.68298576	83.41396337	2.237927015	1.18E-23	1.28E-22
HSPB1	71.3546348	339.0671749	2.248492077	7.65E-24	9.18E-23
HSF1	6.46639172	17.74508412	1.456386603	3.17E-25	6.23E-24
SQSTM1	29.986829	99.91756718	1.73640938	9.02E-17	3.54E-16
NQO1	1.459665414	57.95383069	5.311194409	6.82E-16	2.58E-15
FTH1	139.0992968	286.4863544	1.042351297	8.93E-17	3.54E-16
MT1G	1204.510548	315.6051655	-1.932254305	3.78E-23	3.41E-22
FANCD2	0.131554973	1.016427162	2.949769141	2.65E-25	5.72E-24
HSPA5	110.1952336	231.5746734	1.071415656	1.04E-19	5.89E-19
HELLS	0.093803492	0.861082317	3.198437622	3.84E-24	5.18E-23
FADS2	9.642111654	20.05759983	1.056727937	0.011186336	0.013276091
SRC	1.476430456	5.368635276	1.862441994	2.16E-10	4.71E-10
PML	1.502346692	3.136545956	1.061958923	9.29E-18	4.36E-17
TP63	0.032491359	0.121941676	1.908063267	0.002370479	0.00297688
ENPP2	4.152915006	9.060232331	1.1254237	9.16E-05	0.000128476
NF2	1.559213984	3.964333605	1.346259438	2.04E-24	2.94E-23
PLIN2	127.3620102	62.57489293	-1.025279189	1.68E-12	4.48E-12
AIFM2	3.50634928	9.472166484	1.433724723	4.82E-21	3.36E-20
ZFP36	164.713622	57.41977027	-1.520340409	8.00E-18	3.84E-17
CAV1	4.2223471	8.723696484	1.046894395	3.25E-09	6.50E-09
PTGS2	0.685695488	0.209820152	-1.708414783	5.31E-17	2.29E-16
DUSP1	210.2613598	101.3656724	-1.052614583	6.88E-14	2.07E-13
NOS2	0.097262382	0.402505335	2.049054083	5.21E-13	1.52E-12
NCF2	1.947159412	4.045334212	1.054887898	0.011789214	0.013915137
MT3	0.017154865	0.505603758	4.881317496	0.000988025	0.001277924
ALB	34010.3836	14088.94358	-1.271411838	6.53E-21	4.40E-20
TXNRD1	6.76314148	28.10662419	2.055144747	1.93E-17	8.71E-17
SRXN1	0.361866934	1.48891374	2.040728982	5.06E-15	1.73E-14
GPX2	106.9847132	267.7036539	1.323232162	0.010097916	0.012185195
DDIT4	14.47339472	30.41606729	1.071430285	6.49E-05	9.23E-05
ASNS	0.500573577	2.570302345	2.36028403	2.43E-09	4.90E-09
DDIT3	9.15750984	26.0192576	1.506552547	3.18E-17	1.40E-16
SLC1A4	1.912717952	5.006493795	1.388176442	6.03E-15	2.03E-14
SLC7A5	2.46271565	5.037566261	1.032476849	0.026349194	0.030599064
ATF3	20.57439198	9.029725136	-1.188095818	1.07E-11	2.62E-11
ZNF419	0.28562535	0.643774158	1.172430639	9.43E-13	2.58E-12
ZFP69B	0.135103686	0.407535666	1.592859284	8.39E-17	3.42E-16
TUBE1	3.046223142	1.329053445	-1.196622505	8.33E-21	5.45E-20

IL6	0.867031633	0.3207223	-1.434759961	3.10E-05	4.47E-05
FTL	6020.63136	12148.79179	1.012826153	7.28E-07	1.19E-06
RPL8	211.681118	704.8365225	1.735396096	4.54E-21	3.27E-20
TFRC	3.67960518	10.99097577	1.578696594	1.93E-16	7.46E-16
MAFG	1.056158954	4.158994522	1.977407805	7.43E-23	6.42E-22
HAMP	148.2531032	15.96737045	-3.214863653	6.51E-25	1.08E-23
STEAP3	47.6771802	21.83947636	-1.126360647	2.11E-19	1.11E-18
DRD4	0.155276041	1.075831994	2.792545653	1.06E-14	3.31E-14
SLC2A1	0.680046992	2.534008045	1.897714758	3.92E-05	5.61E-05
SLC2A6	0.92058238	3.1106768	1.756609772	9.57E-08	1.68E-07
SLC2A14	0.045282326	0.175219828	1.952146072	0.003583758	0.004423381
ALOX12	0.109011063	0.275266308	1.336353479	1.04E-12	2.81E-12
ALOX15	0.021905219	0.096188973	2.134596898	8.16E-06	1.23E-05
NNMT	469.3829578	140.666585	-1.738485801	1.15E-17	5.28E-17
STMN1	1.902557888	13.51991775	2.82907412	1.90E-27	1.03E-25
RRM2	0.469398657	6.378298565	3.764286013	3.18E-26	1.14E-24
CAPG	3.486875492	13.19529075	1.920016385	1.95E-11	4.53E-11
AURKA	0.655430176	6.892745036	3.394564649	4.06E-28	2.92E-26
CS	5.37878536	13.8183489	1.361232919	1.45E-22	1.21E-21
EMC2	4.26184004	9.932170316	1.220632556	4.52E-24	5.74E-23
NOX1	0.1464184	0.4156075	1.505124822	9.70E-15	3.17E-14
NOX4	0.021636554	0.242609902	3.487095782	1.94E-28	2.10E-26
NOX5	0.003047159	0.012757427	2.065800918	2.62E-05	3.84E-05
DUOX1	0.056932242	0.494105535	3.117501407	5.88E-20	3.53E-19
G6PD	1.311714874	13.58214647	3.372185434	6.03E-25	1.08E-23
ACSL4	7.321489016	46.1219159	2.65524345	3.57E-12	9.08E-12
NRAS	5.76945708	11.90251214	1.044758631	7.64E-17	3.17E-16
HRAS	4.5210733	13.56736589	1.585403435	7.59E-25	1.17E-23
SLC38A1	1.293731364	4.376645077	1.758287313	3.00E-05	4.35E-05
SLC1A5	2.72911939	8.7961468	1.688436173	0.004122994	0.005051029
GLS2	4.778706618	1.78680446	-1.419238437	1.24E-15	4.63E-15
ALOX15B	0.142066661	1.817887709	3.677623143	7.72E-07	1.25E-06
MAPK3	3.65701124	9.508187623	1.378505311	5.73E-26	1.77E-24
CDKN2A	0.162719125	4.097589759	4.654319821	1.87E-25	4.49E-24
MYB	0.046397883	0.133439792	1.524058057	7.29E-08	1.29E-07
PRKAA2	0.279371851	1.628445762	2.543237099	2.30E-10	4.97E-10
BAP1	7.2785839	15.18775534	1.061178967	1.68E-23	1.72E-22
ABCC1	0.707154126	2.380373825	1.751091565	3.82E-06	5.94E-06
YY1AP1	3.8363725	9.089088053	1.244392742	1.04E-23	1.19E-22
EGLN2	1.5968142	3.789287075	1.246729987	1.96E-20	1.21E-19
MIOX	0.025307544	0.730525513	4.851295268	1.25E-11	3.03E-11
TAZ	1.723546396	5.52082373	1.679503404	7.52E-29	1.62E-26
DNAJB6	1.465015098	3.293091859	1.168527223	2.68E-26	1.14E-24

Supplementary Table 5: GO and KEGG pathway anaysis.

GO and KEGG pathway anaysis									
ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:0062197	cellular response to chemical stress	25/83	347/18862	####	#####	####	SLC7A11/AKR1C3/HSPB1/HSF1/NQO1/FANCD2/SRC/PML/AIFM2/CAV1/NCF2/MT3/TXNRD1/SRXN1/GPX2/DDIT3/IL6/SLC2A1/NOX1/NOX4/NOX5/G6PD/MAPK3/MYB/PRKAA2	25

BP	GO:0006979	response to oxidative stress	25/83	444/18862	####	#####	####	SLC7A11/AKR1C3/HSPB1/HSF1/NQO1/FANCD2/SRC/PML/AIFM2/PTGS2/DUSP1/NCF2/MT3/TXNRD1/SRXN1/GPX2/IL6/NOX1/NOX4/NOX5/DUOX1/G6PD/MAPK3/MYB/PRKAA2	25

BP	GO:0034599	cellular response to oxidative stress	22/83	299/18862	####	#####	####	SLC7A11/AKR1C3/HSPB1/HSF1/NQO1/FANCD2/SRC/PML/AIFM2/NCF2/MT3/TXNRD1/SRXN1/GPX2/IL6/NOX1/NOX4/NOX5/G6PD/MAPK3/MYB/PRKAA2	22
BP	GO:0072593	reactive oxygen species metabolic process	15/83	281/18862	####	#####	####	AKR1C3/NQO1/CAV1/PTGS2/NOS2/NCF2/MT3/DDIT4/ALOX12/NOX1/NOX4/NOX5/DUOX1/G6PD/GLS2	15

BP	GO:0031667	response to nutrient levels	17/83	451/18862	####	#####	####	AKR1C3/HSF1/NQO1/HSPA5/SRC/ZFP36/MT3/ALB/ASNS/DDIT3/ATF3/HAMP/SLC2A1/G6PD/ACSL4/MAPK3/PRKAA2	17
BP	GO:0006801	superoxide metabolic process	9/83	70/18862	####	#####	####	NQO1/NOS2/NCF2/MT3/ALOX12/NOX1/NOX4/NOX5/DUOX1	9
BP	GO:0009991	response to extracellular stimulus	17/83	477/18862	####	#####	####	AKR1C3/HSF1/NQO1/HSPA5/SRC/ZFP36/MT3/ALB/ASNS/DDIT3/ATF3/HAMP/SLC2A1/G6PD/ACSL4/MAPK3/PRKAA2	17

BP	GO:0009636	response to toxic substance	12/83	239/18862	####	#####	####	SLC7A11/NQO1/MT1G/PTGS2/MT3/ALB/TXNRD1/SRXN1/GPX2/ASNS/DUOX1/MAPK3	12
BP	GO:0042594	response to starvation	11/83	196/18862	####	#####	####	AKR1C3/HSPA5/ZFP36/ALB/ASNS/DDIT3/ATF3/HAMP/SLC2A1/MAPK3/PRKAA2	11
BP	GO:0015849	organic acid transport	13/83	324/18862	####	#####	####	SLC7A11/AKR1C1/PLIN2/SLC1A4/SLC7A5/DRD4/SLC2A1/ACSL4/SLC38A1/SLC1A5/GLS2/PRKAA2/ABCC1	13

BP	GO:0033559	unsaturated fatty acid metabolic process	9/83	115/18862	####	#####	####	AKR1C1/AKR1C2/AKR1C3/FADS2/PTGS2/ALOX12/ALOX15/ALOX15B/MAPK3	9
BP	GO:0120254	olefinic compound metabolic process	9/83	119/18862	####	#####	####	AKR1C1/AKR1C2/AKR1C3/FADS2/PTGS2/ALOX12/ALOX15/ALOX15B/MAPK3	9
BP	GO:0006690	icosanoid metabolic process	9/83	123/18862	####	#####	####	AKR1C1/AKR1C2/AKR1C3/PTGS2/ALOX12/ALOX15/ALOX15B/MAPK3/ABCC1	9

BP	GO:0010038	response to metal ion	13/83	352/18862	####	#####	####	AKR1C3/HSF1/NQO1/MT1G/HSPA5/CAV1/DUSP1/MT3/HAMP/ALOX15/G6PD/MAPK3/PRKAA2	13
BP	GO:0042554	superoxide anion generation	6/83	35/18862	####	#####	####	NCF2/ALOX12/NOX1/NOX4/NOX5/DUOX1	6
BP	GO:0015711	organic anion transport	13/83	376/18862	####	#####	####	SLC7A11/AKR1C1/NOS2/SLC1A4/SLC7A5/DRD4/SLC2A1/SLC2A6/SLC2A14/SLC38A1/SLC1A5/GLS2/ABCC1	13
BP	GO:0098754	detoxification	9/83	138/18862	####	#####	####	NQO1/MT1G/PTGS2/MT3/ALB/TXNRD1/SRXN1/GPX2/DUOX1	9

BP	GO:0006869	lipid transport	14/83	461/18862	####	#####	####	SLC7A11/AKR1C1/PLIN2/CAV1/NOS2/SLC1A4/DRD4/SLC2A1/ACSL4/SLC1A5/GLS2/MYB/PRKAA2/ABCC1	14
BP	GO:0070482	response to oxygen levels	13/83	385/18862	####	#####	####	HSF1/SRC/PML/CAV1/PTGS2/NOS2/MT3/DDIT4/SLC2A1/NOX1/NOX4/MYB/EGLN2	13
BP	GO:0098869	cellular oxidant detoxification	8/83	102/18862	####	#####	####	NQO1/PTGS2/MT3/ALB/TXNRD1/SRXN1/GPX2/DUOX1	8

BP	GO:0070997	neuron death	12/83	342/18862	####	#####	####	SLC7A11/HSF1/NQO1/HSPA5/TP63/MT3/DDIT4/DDIT3/G6PD/HRAS/MYB/EGLN2	12
BP	GO:0045454	cell redox homeostasis	6/83	43/18862	####	#####	####	NQO1/NOS2/NCF2/TXNRD1/DDIT3/EGLN2	6
BP	GO:0001666	response to hypoxia	12/83	348/18862	####	#####	####	HSF1/SRC/PML/CAV1/PTGS2/NOS2/MT3/DDIT4/SLC2A1/NOX4/MYB/EGLN2	12
BP	GO:1990748	cellular detoxification	8/83	115/18862	####	#####	####	NQO1/PTGS2/MT3/ALB/TXNRD1/SRXN1/GPX2/DUOX1	8

BP	GO:0036293	response to decreased oxygen levels	12/83	360/18862	####	#####	####	HSF1/SRC/PML/CAV1/PTGS2/NOS2/MT3/DDIT4/SLC2A1/NOX4/MYB/EGLN2	12
BP	GO:0001676	long-chain fatty acid metabolic process	8/83	120/18862	####	#####	####	AKR1C3/FADS2/PTGS2/ALOX12/ALOX15/ACSL4/ALOX15B/MAPK3	8
BP	GO:0036003	positive regulation of transcription from RNA polymerase II promoter in response to stress	5/83	24/18862	####	#####	####	HSF1/HSPA5/MT3/DDIT3/ATF3	5
BP	GO:0097237	cellular response to toxic substance	8/83	122/18862	####	#####	####	NQO1/PTGS2/MT3/ALB/TXNRD1/SRXN1/GPX2/DUOX1	8

BP	GO:0006636	unsaturated fatty acid biosynthetic process	6/83	51/18862	####	#####	####	AKR1C3/FADS2/PTGS2/ALOX12/ALOX15/ALOX15B	6
BP	GO:0150104	transport across blood-brain barrier	7/83	87/18862	####	#####	####	SLC1A4/SLC7A5/TFRC/SLC2A1/SLC38A1/SLC1A5/ABCC1	7
BP	GO:0010332	response to gamma radiation	6/83	53/18862	####	#####	####	HSF1/FANCD2/HSPA5/PML/NOX4/HRAS	6
BP	GO:0010232	vascular transport	7/83	88/18862	####	#####	####	SLC1A4/SLC7A5/TFRC/SLC2A1/SLC38A1/SLC1A5/ABCC1	7
BP	GO:0006631	fatty acid metabolic process	12/83	392/18862	####	#####	####	AKR1C1/AKR1C2/AKR1C3/FADS2/CAV1/PTGS2/ALOX12/ALOX15/ACSL4/ALOX15B/MAPK3/PRKAA2	12

BP	GO:0071248	cellular response to metal ion	9/83	189/18862	####	#####	####	AKR1C3/HSF1/NQO1/MT1G/HSPA5/MT3/ALOX15/MAPK3/PRKAA2	9
BP	GO:1901654	response to ketone	9/83	193/18862	####	#####	####	AKR1C2/AKR1C3/HSF1/NQO1/SRC/CAV1/DUSP1/DDIT4/PRKAA2	9
BP	GO:0055076	transition metal ion homeostasis	8/83	139/18862	####	#####	####	FTH1/MT1G/MT3/FTL/TFRC/HAMP/STEAP3/NOX5	8
BP	GO:0019369	arachidonic acid metabolic process	6/83	59/18862	####	#####	####	AKR1C3/PTGS2/ALOX12/ALOX15/ALOX15B/MAPK3	6
BP	GO:1905039	carboxylic acid transmembrane transport	8/83	154/18862	####	#####	####	SLC7A11/SLC1A4/SLC7A5/SLC2A1/SLC38A1/SLC1A5/PRKAA2/ABCC1	8

BP	GO:1903825	organic acid transmembrane transport	8/83	155/18862	####	#####	####	SLC7A11/SLC1A4/SLC7A5/SLC2A1/SLC38A1/SLC1A5/PRKAA2/ABCC1	8
BP	GO:0009267	cellular response to starvation	8/83	157/18862	####	#####	####	AKR1C3/HSPA5/ALB/ASNS/ATF3/SLC2A1/MAPK3/PRKAA2	8
BP	GO:0071241	cellular response to inorganic substance	9/83	216/18862	####	#####	####	AKR1C3/HSF1/NQO1/MT1G/HSPA5/MT3/ALOX15/MAPK3/PRKAA2	9
BP	GO:0046942	carboxylic acid transport	10/83	284/18862	####	#####	####	SLC7A11/AKR1C1/NOS2/SLC1A4/SLC7A5/DRD4/SLC38A1/SLC1A5/GLS2/ABCC1	10

BP	GO:0034614	cellular response to reactive oxygen species	8/83	159/18862	####	#####	####	AKR1C3/HSF1/NQO1/SRC/MT3/IL6/MAPK3/MYB	8
BP	GO:0019372	lipoxygenase pathway	4/83	16/18862	####	#####	####	PTGS2/ALOX12/ALOX15/ALOX15B	4
BP	GO:0000302	response to reactive oxygen species	9/83	224/18862	####	#####	####	AKR1C3/HSF1/NQO1/SRC/DUSP1/MT3/IL6/MAPK3/MYB	9
BP	GO:0071276	cellular response to cadmium ion	5/83	38/18862	####	#####	####	AKR1C3/HSF1/MT1G/MT3/MAPK3	5
BP	GO:0051402	neuron apoptotic process	9/83	230/18862	####	#####	####	NQO1/HSPA5/TP63/MT3/DDIT3/G6PD/HRAS/MYB/EGLN2	9
BP	GO:1901214	regulation of neuron death	10/83	302/18862	####	#####	####	SLC7A11/HSF1/NQO1/MT3/DDIT4/DDIT3/G6PD/HRAS/MYB/EGLN2	10

BP	GO:0071216	cellular response to biotic stimulus	9/83	233/18862	####	#####	####	HSF1/HSPA5/SRC/ZFP36/NOS2/DDIT3/IL6/HAMP/MAPK3	9
BP	GO:0046916	cellular transition metal ion homeostasis	7/83	118/18862	####	#####	####	FTH1/MT1G/MT3/FTL/TFRC/HAMP/NOX5	7
BP	GO:0003018	vascular process in circulatory system	9/83	245/18862	####	#####	####	SRC/CAV1/SLC1A4/SLC7A5/TFRC/SLC2A1/SLC38A1/SLC1A5/ABCC1	9
BP	GO:0006826	iron ion transport	6/83	79/18862	####	#####	####	FTH1/FTL/TFRC/HAMP/STEAP3/NOX5	6
BP	GO:0000041	transition metal ion transport	7/83	127/18862	####	#####	####	FTH1/MT3/FTL/TFRC/HAMP/STEAP3/NOX5	7

BP	GO:0042180	cellular ketone metabolic process	9/83	254/18862	####	#####	####	SLC7A11/AKR1C1/AKR1C2/AKR1C3/NQO1/AIFM2/CAV1/PTGS2/PRKAA2	9
BP	GO:0048732	gland development	11/83	413/18862	####	#####	####	SRC/PML/TP63/CAV1/ASNS/IL6/HAMP/AURKA/HRAS/ALOX15B/MAPK3	11
BP	GO:0043651	linoleic acid metabolic process	4/83	21/18862	####	#####	####	FADS2/ALOX12/ALOX15/ALOX15B	4
BP	GO:0055072	iron ion homeostasis	6/83	86/18862	####	1E-04	####	FTH1/FTL/TFRC/HAMP/STEAP3/NOX5	6
BP	GO:0036499	PERK-mediated unfolded protein response	4/83	23/18862	####	1E-04	####	HSPA5/ASNS/DDIT3/ATF3	4
BP	GO:0010212	response to ionizing radiation	7/83	142/18862	####	1E-04	####	HSF1/FANCD2/HSPA5/PML/HAMP/NOX4/HRAS	7

BP	GO:0042493	response to drug	10/83	359/18862	####	2E-04	0	HSF1/NQO1/HSPA5/SRC/PLIN2/NOS2/TFRC/NNMT/PRKAA2/ABCC1	10
BP	GO:0031669	cellular response to nutrient levels	8/83	210/18862	####	2E-04	0	AKR1C3/HSPA5/ALB/ASNS/ATF3/SLC2A1/MAPK3/PRKAA2	8
BP	GO:0097193	intrinsic apoptotic signaling pathway	9/83	283/18862	####	2E-04	0	HSPB1/SRC/PML/TP63/CAV1/DDIT4/DDIT3/NOX1/HRAS	9
BP	GO:0015908	fatty acid transport	7/83	150/18862	####	2E-04	0	SLC7A11/PLIN2/DRD4/SLC2A1/ACSL4/GLS2/PRKAA2	7
BP	GO:0140467	integrated stress response signaling	4/83	27/18862	####	2E-04	0	HSPA5/ASNS/DDIT3/ATF3	4
BP	GO:0071480	cellular response to gamma radiation	4/83	28/18862	####	3E-04	0	HSF1/HSPA5/NOX4/HRAS	4

BP	GO:0046686	response to cadmium ion	5/83	61/18862	####	3E-04	0	AKR1C3/HSF1/MT1G/MT3/MAPK3	5
BP	GO:0007568	aging	9/83	304/18862	####	3E-04	0	NQO1/PML/TP63/HAMP/ALOX12/NOX4/HRAS/MAPK3/CDKN2A	9
BP	GO:0098657	import into cell	8/83	230/18862	####	3E-04	0	SLC7A11/SLC1A4/SLC7A5/DRD4/SLC2A1/NOX5/SLC38A1/SLC1A5	8
BP	GO:0035690	cellular response to drug	5/83	63/18862	####	3E-04	0	HSF1/HSPA5/NOS2/TFRC/PRKAA2	5
BP	GO:1902475	L-alpha-amino acid transmembrane transport	5/83	63/18862	####	3E-04	0	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5	5
BP	GO:0043618	regulation of transcription from RNA polymerase II promoter in respons	6/83	109/18862	####	3E-04	0	HSF1/HSPA5/MT3/DDIT3/ATF3/EGLN2	6

		e to stress							
BP	GO:0031668	cellular response to extracellular stimulus	8/83	235/18862	####	4E-04	0	AKR1C3/HSPA5/ALB/ASNS/ATF3/SLC2A1/MAPK3/PRKAA2	8
BP	GO:0006633	fatty acid biosynthetic process	7/83	168/18862	####	4E-04	0	AKR1C3/FADS2/PTGS2/ALOX12/ALOX15/ALOX15B/PRKAA2	7
BP	GO:0030647	aminoglycoside antibiotic metabolic process	3/83	10/18862	####	4E-04	0	AKR1C1/AKR1C2/AKR1C3	3
BP	GO:0071479	cellular response to ionizing radiation	5/83	65/18862	####	4E-04	0	HSF1/HSPA5/HAMP/NOX4/HRAS	5
BP	GO:0015807	L-amino acid transport	5/83	66/18862	####	4E-04	0	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5	5

BP	GO:0051235	maintenance of location	9/83	319/18862	####	4E-04	0	FTH1/HSPA5/PML/PLIN2/CAV1/ALB/DDIT3/IL6/FTL	9
BP	GO:0043620	regulation of DNA-templated transcription in response to stress	6/83	115/18862	####	4E-04	0	HSF1/HSPA5/MT3/DDIT3/ATF3/EGLN2	6
BP	GO:0042759	long-chain fatty acid biosynthetic process	4/83	33/18862	####	5E-04	0	PTGS2/ALOX12/ALOX15/ALOX15B	4
BP	GO:1990440	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	3/83	11/18862	####	5E-04	0	HSPA5/DDIT3/ATF3	3
BP	GO:0015718	monocarboxylic acid transport	7/83	178/18862	####	5E-04	0	SLC7A11/AKR1C1/NOS2/SLC1A4/DRD4/SLC1A5/GLS2	7

BP	GO:0046394	carboxylic acid biosynthetic process	9/83	327/18862	####	5E-04	0	AKR1C3/FADS2/PTGS2/ASNS/ALOX12/ALOX15/GLS2/ALOX15B/PRKAA2	9
BP	GO:0006879	cellular iron ion homeostasis	5/83	70/18862	####	5E-04	0	FTH1/FTL/TFRC/HAMP/NOX5	5
BP	GO:0048545	response to steroid hormone	9/83	330/18862	####	5E-04	0	AKR1C3/SRC/TP63/ZFP36/CAV1/DUSP1/DDIT4/IL6/EGLN2	9
BP	GO:0140354	lipid import into cell	4/83	34/18862	####	5E-04	0	SLC7A11/SLC1A4/SLC2A1/SLC1A5	4
BP	GO:1901661	quinone metabolic process	4/83	34/18862	####	5E-04	0	AKR1C1/AKR1C2/AKR1C3/AIFM2	4
BP	GO:0016053	organic acid biosynthetic process	9/83	335/18862	####	5E-04	0	AKR1C3/FADS2/PTGS2/ASNS/ALOX12/ALOX15/GLS2/ALOX15B/PRKAA2	9

BP	GO:1903409	reactive oxygen species biosynthetic process	6/83	123/18862	####	5E-04	0	NQO1/CAV1/PTGS2/NOS2/NOX4/DUOX1	6
BP	GO:0072584	caveolin-mediated endocytosis	3/83	12/18862	####	5E-04	0	SRC/CAV1/MAPK3	3
BP	GO:2001235	positive regulation of apoptotic signaling pathway	6/83	126/18862	####	6E-04	0	PML/TP63/CAV1/DDIT3/ATF3/NOX1	6
BP	GO:0062012	regulation of small molecule metabolic process	10/83	437/18862	####	7E-04	0	SLC7A11/AKR1C3/NQO1/SRC/CAV1/PTGS2/NOS2/DDIT4/SLC2A6/PRKAA2	10
BP	GO:0071398	cellular response to fatty acid	4/83	38/18862	####	7E-04	0	AKR1C1/AKR1C2/AKR1C3/SRC	4
BP	GO:0043523	regulation of neuron apoptotic process	7/83	197/18862	####	8E-04	0	NQO1/MT3/DDIT3/G6PD/HRAS/MYB/EGLN2	7
BP	GO:0071222	cellular response to lipopolysaccharide	7/83	197/18862	####	8E-04	0	HSF1/SRC/ZFP36/NOS2/IL6/HAMP/MAPK3	7

BP	GO:0009314	response to radiation	10/83	447/18862	####	8E-04	0	SLC7A11/HSF1/FANCD2/HSPA5/PML/DUSP1/ASNS/HAMP/NOX4/HRAS	10
BP	GO:0042542	response to hydrogen peroxide	6/83	135/18862	####	8E-04	0	HSF1/NQO1/SRC/DUSP1/IL6/MYB	6
BP	GO:0051180	vitamin transport	4/83	41/18862	####	9E-04	0	SLC2A1/SLC2A6/SLC2A14/ABCC1	4
BP	GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	7/83	205/18862	####	9E-04	0	HSF1/SRC/PML/TP63/MT3/ALOX12/DNAJB6	7
BP	GO:0089718	amino acid import across plasma membrane	4/83	42/18862	####	1E-03	0	SLC7A11/SLC1A4/SLC7A5/SLC1A5	4
BP	GO:0042448	progesterone metabolic process	3/83	15/18862	####	0.001	0	AKR1C1/AKR1C2/AKR1C3	3
BP	GO:0051651	maintenance of location in cell	7/83	209/18862	####	0.001	0	FTH1/HSPA5/PML/CAV1/ALB/DDIT3/FTL	7

BP	GO:0071219	cellular response to molecule of bacterial origin	7/83	209/18862	####	0.001	0	HSF1/SRC/ZFP36/NOS2/IL6/HAMP/MAPK3	7
BP	GO:0015804	neutral amino acid transport	4/83	44/18862	####	0.001	0	SLC1A4/SLC7A5/SLC38A1/SLC1A5	4
BP	GO:0045124	regulation of bone resorption	4/83	44/18862	####	0.001	0	SRC/IL6/TFRC/HAMP	4
BP	GO:0002262	myeloid cell homeostasis	6/83	145/18862	####	0.001	0	SLC7A11/ZFP36/IL6/HAMP/G6PD/BAP1	6
BP	GO:0051592	response to calcium ion	6/83	145/18862	####	0.001	0	AKR1C3/HSPA5/CAV1/DUSP1/ALOX15/PRKAA2	6
BP	GO:0070301	cellular response to hydrogen peroxide	5/83	90/18862	####	0.001	0	HSF1/NQO1/SRC/IL6/MYB	5
BP	GO:1901655	cellular response to ketone	5/83	92/18862	####	0.001	0	AKR1C2/AKR1C3/SRC/DDIT4/PRKAA2	5

BP	GO:0071496	cellular response to external stimulus	8/83	303/18862	####	0.001	0	AKR1C3/HSPA5/ALB/ASNS/ATF3/SLC2A1/MAPK3/PRKAA2	8
BP	GO:0006865	amino acid transport	6/83	152/18862	####	0.001	0	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5/GLS2	6
BP	GO:0031960	response to corticosteroid	6/83	152/18862	####	0.001	0	AKR1C3/SRC/ZFP36/DUSP1/DDIT4/IL6	6
BP	GO:0006692	prostanoid metabolic process	4/83	48/18862	####	0.001	0	AKR1C1/AKR1C2/AKR1C3/PTGS2	4
BP	GO:0006693	prostaglandin metabolic process	4/83	48/18862	####	0.001	0	AKR1C1/AKR1C2/AKR1C3/PTGS2	4
BP	GO:0042149	cellular response to glucose starvation	4/83	48/18862	####	0.001	0	HSPA5/ASNS/SLC2A1/PRKAA2	4
BP	GO:0043090	amino acid import	4/83	48/18862	####	0.001	0	SLC7A11/SLC1A4/SLC7A5/SLC1A5	4

BP	GO:0072330	monocarboxylic acid biosynthetic process	7/83	224/18862	####	0.001	0	AKR1C3/FADS2/PTGS2/ALOX12/ALOX15/ALOX15B/PRKAA2	7
BP	GO:0097501	stress response to metal ion	3/83	18/18862	####	0.002	0	MT1G/HSPA5/MT3	3
BP	GO:0003333	amino acid transmembrane transport	5/83	96/18862	####	0.002	0	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5	5
BP	GO:0018105	peptidyl-serine phosphorylation	8/83	310/18862	####	0.002	0	SRC/CAV1/DDIT4/IL6/TFRC/AURKA/MAPK3/PRKAA2	8
BP	GO:0030168	platelet activation	6/83	157/18862	####	0.002	0	SLC7A11/HSPB1/SRC/IL6/ALOX12/MAPK3	6
BP	GO:2000116	regulation of cysteine-type endopeptidase activity	7/83	230/18862	####	0.002	0	HSF1/SRC/PML/TP63/MT3/ALOX12/DNAJB6	7
BP	GO:0046850	regulation of bone remodeling	4/83	51/18862	####	0.002	0	SRC/IL6/TFRC/HAMP	4

BP	GO:0097305	response to alcohol	7/83	233/18862	####	0.002	0	AKR1C2/AKR1C3/NQO1/HAMP/DRD4/G6PD/PRKAA2	7
BP	GO:0007050	cell cycle arrest	7/83	235/18862	####	0.002	0	PML/DUSP1/DDIT3/AURKA/HRAS/CDKN2A/PRKAA2	7
BP	GO:0006984	ER-nucleus signaling pathway	4/83	53/18862	####	0.002	0	HSPA5/ASNS/DDIT3/ATF3	4
BP	GO:0006925	inflammatory cell apoptotic process	3/83	20/18862	####	0.002	0	SLC7A11/IL6/CDKN2A	3
BP	GO:0071379	cellular response to prostaglandin stimulus	3/83	20/18862	####	0.002	0	AKR1C2/AKR1C3/PRKAA2	3
BP	GO:1902644	tertiary alcohol metabolic process	3/83	20/18862	####	0.002	0	AKR1C1/AKR1C2/AKR1C3	3
BP	GO:0071214	cellular response to abiotic stimulus	8/83	330/18862	0	0.002	0	HSF1/HSPA5/HAMP/SLC2A1/NOX1/NOX4/HRAS/MAPK3	8

BP	GO:0104004	cellular response to environmental stimulus	8/83	330/18862	0	0.002	0	HSF1/HSPA5/HAMP/SLC2A1/NOX1/NOX4/HRAS/MAPK3	8
BP	GO:0016137	glycoside metabolic process	3/83	21/18862	0	0.002	0	AKR1C1/AKR1C2/AKR1C3	3
BP	GO:0019748	secondary metabolic process	4/83	56/18862	0	0.002	0	SLC7A11/AKR1C1/AKR1C2/AKR1C3	4
BP	GO:0018209	peptidyl-serine modification	8/83	333/18862	0	0.002	0	SRC/CAV1/DDIT4/IL6/TFRC/AURKA/MAPK3/PRKAA2	8
BP	GO:1901617	organic hydroxy compound biosynthetic process	7/83	251/18862	0	0.002	0	SLC7A11/AKR1C3/ALOX12/ALOX15/G6PD/ALOX15B/PRKAA2	7
BP	GO:0001819	positive regulation of cytokine production	9/83	437/18862	0	0.003	0	HSPB1/PTGS2/DDIT3/SLC7A5/IL6/NOX1/HRAS/ALOX15B/MYB	9
BP	GO:0022612	gland morphogenesis	5/83	111/18862	0	0.003	0	SRC/PML/TP63/CAV1/IL6	5

BP	GO:0007596	blood coagulation	8/83	342/18862	0	0.003	0	SLC7A11/HSPB1/SRC/CAV1/IL6/MAFG/ALOX12/MAPK3	8
BP	GO:1904385	cellular response to angiotensin	3/83	23/18862	0	0.003	0	HSF1/SRC/CAV1	3
BP	GO:0007599	hemostasis	8/83	346/18862	0	0.003	0	SLC7A11/HSPB1/SRC/CAV1/IL6/MAFG/ALOX12/MAPK3	8
BP	GO:0050817	coagulation	8/83	347/18862	0	0.003	0	SLC7A11/HSPB1/SRC/CAV1/IL6/MAFG/ALOX12/MAPK3	8
BP	GO:2001233	regulation of apoptotic signaling pathway	8/83	348/18862	0	0.003	0	HSPB1/SRC/PML/TP63/CAV1/DDIT3/ATF3/NOX1	8
BP	GO:0001894	tissue homeostasis	7/83	260/18862	0	0.003	0	HSPB1/SRC/ALB/IL6/TFRC/HAMP/SLC2A1	7
BP	GO:0070542	response to fatty acid	4/83	61/18862	0	0.003	0	AKR1C1/AKR1C2/AKR1C3/SRC	4

BP	GO:0007569	cell aging	5/83	115/18862	0	0.003	0	PML/TP63/NOX4/HRAS/CDKN2A	5
BP	GO:0061436	establishment of skin barrier	3/83	24/18862	0	0.003	0	TP63/ALOX12/STMN1	3
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	7/83	262/18862	0	0.003	0	HSF1/SRC/ENPP2/NF2/CAV1/IL6/NOX4	7
BP	GO:0009896	positive regulation of catabolic process	9/83	450/18862	0	0.003	0	HSF1/ZFP36/CAV1/IL6/HAMP/AURKA/MAPK3/PRKAA2/EGLN2	9
BP	GO:0045453	bone resorption	4/83	62/18862	0	0.003	0	SRC/IL6/TFRC/HAMP	4
BP	GO:0045604	regulation of epidermal cell differentiation	4/83	62/18862	0	0.003	0	TP63/ZFP36/MAFG/ALOX15B	4
BP	GO:1901570	fatty acid derivative biosynthetic process	4/83	62/18862	0	0.003	0	ALOX12/ALOX15/ACSL4/ALOX15B	4
BP	GO:0006986	response to unfolded protein	6/83	185/18862	0	0.003	0	HSPB1/HSF1/HSPA5/ASNS/DDIT3/ATF3	6

BP	GO:0010565	regulation of cellular ketone metabolic process	6/83	185/18862	0	0.003	0	SLC7A11/AKR1C3/NQO1/CAV1/PTGS2/PRKAA2	6
BP	GO:1990776	response to angiotensin	3/83	25/18862	0	0.003	0	HSF1/SRC/CAV1	3
BP	GO:0033561	regulation of water loss via skin	3/83	26/18862	0	0.004	0	TP63/ALOX12/STMN1	3
BP	GO:2000377	regulation of reactive oxygen species metabolic process	6/83	192/18862	0	0.004	0	AKR1C3/CAV1/PTGS2/MT3/NOX4/G6PD	6
BP	GO:0030522	intracellular receptor signaling pathway	7/83	274/18862	0	0.004	0	AKR1C3/SRC/PML/TP63/ALOX15/ALOX15B/EGLN2	7
BP	GO:0060249	anatomical structure homeostasis	9/83	466/18862	0	0.004	0	HSPB1/SRC/PML/ALB/IL6/TFRC/HAMP/SLC2A1/MAPK3	9
BP	GO:0018108	peptidyl-tyrosine phosphorylation	8/83	369/18862	0	0.004	0	HSF1/SRC/ENPP2/NF2/CAV1/IL6/NOX4/MAPK3	8

BP	GO:0018212	peptidyl-tyrosine modification	8/83	372/18862	0	0.004	0	HSF1/SRC/ENPP2/NF2/CAV1/IL6/NOX4/MAPK3	8
BP	GO:0051054	positive regulation of DNA metabolic process	6/83	198/18862	0	0.004	0	HSF1/SRC/PML/IL6/TFRC/MAPK3	6
BP	GO:0045682	regulation of epidermis development	4/83	69/18862	0	0.004	0	TP63/ZFP36/MAFG/ALOX15B	4
BP	GO:0010575	positive regulation of vascular endothelial growth factor production	3/83	28/18862	0	0.004	0	PTGS2/IL6/NOX1	3
BP	GO:0033028	myeloid cell apoptotic process	3/83	28/18862	0	0.004	0	SLC7A11/IL6/CDKN2A	3
BP	GO:0071280	cellular response to copper ion	3/83	28/18862	0	0.004	0	HSF1/MT1G/MT3	3
BP	GO:0071383	cellular response to steroid hormone stimulus	6/83	201/18862	0	0.004	0	AKR1C3/SRC/TP63/ZFP36/DDIT4/EGLN2	6
BP	GO:0046683	response to organophosphorus	5/83	130/18862	0	0.005	0	AKR1C1/HSPA5/DUSP1/NOX4/DUOX1	5

BP	GO:0072337	modified amino acid transport	3/83	29/18862	0	0.005	0	SLC7A11/SLC1A4/ABCC1	3
BP	GO:0015909	long-chain fatty acid transport	4/83	72/18862	0	0.005	0	PLIN2/DRD4/SLC2A1/PRKAA2	4
BP	GO:0031331	positive regulation of cellular catabolic process	8/83	384/18862	0	0.005	0	HSF1/ZFP36/CAV1/IL6/HAMP/AURKA/MAPK3/PRKAA2	8
BP	GO:0035966	response to topologically incorrect protein	6/83	206/18862	0	0.005	0	HSPB1/HSF1/HSPA5/ASNS/DDIT3/ATF3	6
BP	GO:0006809	nitric oxide biosynthetic process	4/83	73/18862	0	0.005	0	NQO1/CAV1/PTGS2/NOS2	4
BP	GO:0031100	animal organ regeneration	4/83	73/18862	0	0.005	0	IL6/HAMP/NNMT/AURKA	4
BP	GO:0034694	response to prostaglandin	3/83	30/18862	0	0.005	0	AKR1C2/AKR1C3/PRKAA2	3
BP	GO:1903829	positive regulation of cellular protein localization	7/83	295/18862	0	0.005	0	SQSTM1/SRC/TP63/TFRC/HRAS/PRKAA2/BAP1	7

BP	GO:0034976	response to endoplasmic reticulum stress	7/83	296/18862	0	0.005	0	HSPA5/PML/CAV1/ASNS/DDIT3/ATF3/ALOX15	7
BP	GO:0051348	negative regulation of transferase activity	7/83	296/18862	0	0.005	0	HSPB1/SRC/NF2/ZFP36/CAV1/DUSP1/CDKN2A	7
BP	GO:0009064	glutamine family amino acid metabolic process	4/83	75/18862	0	0.005	0	SLC7A11/NOS2/ASNS/GLS2	4
BP	GO:0097421	liver regeneration	3/83	31/18862	0	0.005	0	IL6/HAMP/AURKA	3
BP	GO:0001889	liver development	5/83	138/18862	0	0.006	0	ASNS/IL6/HAMP/AURKA/HRAS	5
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	7/83	301/18862	0	0.006	0	SRC/DUSP1/MT3/ATF3/ALOX15/HRAS/MAPK3	7
BP	GO:0046209	nitric oxide metabolic process	4/83	77/18862	0	0.006	0	NQO1/CAV1/PTGS2/NOS2	4
BP	GO:0031333	negative regulation of protein-containing comple	5/83	139/18862	0	0.006	0	HSF1/HSPA5/SRC/STMN1/CAPG	5

		x assembly							
BP	GO:0061008	hepatic obiliary system development	5/83	140/18862	0	0.006	0	ASNS/IL6/HAMP/AURKA/HRAS	5
BP	GO:2001057	reactive nitrogen species metabolic process	4/83	78/18862	0	0.006	0	NQO1/CAV1/PTGS2/NOS2	4
BP	GO:0071277	cellular response to calcium ion	4/83	82/18862	0	0.007	0	AKR1C3/HSPA5/ALOX15/PRKAA2	4
BP	GO:1901568	fatty acid derivative metabolic process	4/83	82/18862	0	0.007	0	ALOX12/ALOX15/ACSL4/ALOX15B	4
BP	GO:0006739	NADP metabolic process	3/83	35/18862	0	0.007	0	NQO1/NOX1/G6PD	3
BP	GO:0034620	cellular response to unfolded protein	5/83	149/18862	0	0.008	0.01	HSF1/HSPA5/ASNS/DDIT3/ATF3	5
BP	GO:1900407	regulation of cellular response to oxidative stress	4/83	84/18862	0	0.008	0.01	SLC7A11/HSPB1/AIFM2/NOX1	4

BP	GO:0070371	ERK1 and ERK2 cascade	7/83	320/18862	0	0.008	0.01	SRC/DUSP1/MT3/ATF3/ALOX15/HRAS/MAPK3	7
BP	GO:0006691	leukotriene metabolic process	3/83	36/18862	0	0.008	0.01	ALOX12/ALOX15/ABCC1	3
BP	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	4/83	85/18862	0	0.008	0.01	HSF1/NF2/CAV1/IL6	4
BP	GO:0071453	cellular response to oxygen levels	6/83	231/18862	0	0.008	0.01	SRC/CAV1/PTGS2/MT3/NOX1/EGLN2	6
BP	GO:0034103	regulation of tissue remodeling	4/83	86/18862	0	0.008	0.01	SRC/IL6/TFRC/HAMP	4
BP	GO:0032496	response to lipopolysaccharide	7/83	326/18862	0	0.008	0.01	HSF1/SRC/ZFP36/NOS2/IL6/HAMP/MAPK3	7
BP	GO:0007260	tyrosine phosphorylation of STAT protein	4/83	88/18862	0	0.009	0.01	HSF1/NF2/CAV1/IL6	4
BP	GO:0030856	regulation of epithelial cell differentiation	5/83	156/18862	0	0.009	0.01	TP63/ZFP36/CAV1/MAFG/ALOX15B	5

BP	GO:0036473	cell death in response to oxidative stress	4/83	89/18862	0	0.009	0.01	SLC7A11/HSPB1/PML/NOX1	4
BP	GO:0046849	bone remodeling	4/83	89/18862	0	0.009	0.01	SRC/IL6/TFRC/HAMP	4
BP	GO:0016572	histone phosphorylation	3/83	39/18862	0	0.009	0.01	AURKA/MAPK3/PRKAA2	3
BP	GO:0032660	regulation of interleukin-17 production	3/83	39/18862	0	0.009	0.01	DDIT3/SLC7A5/IL6	3
BP	GO:0022407	regulation of cell-cell adhesion	8/83	437/18862	0	0.009	0.01	SRC/NF2/CAV1/IL6/TFRC/ALOX12/ALOX15/MYB	8
BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	5/83	160/18862	0	0.01	0.01	HSPB1/SRC/CAV1/DDIT3/NOX1	5
BP	GO:0008207	C21-steroid hormone metabolic process	3/83	40/18862	0	0.01	0.01	AKR1C1/AKR1C2/AKR1C3	3
BP	GO:0042908	xenobiotic transport	3/83	40/18862	0	0.01	0.01	SLC7A5/SLC2A1/ABCC1	3
BP	GO:0060443	mammary gland morphogenesis	3/83	40/18862	0	0.01	0.01	SRC/PML/CAV1	3

BP	GO:0098739	import across plasma membrane	5/83	161/18862	0	0.01	0.01	SLC7A11/SLC1A4/SLC7A5/SLC2A1/SLC1A5	5
BP	GO:1901216	positive regulation of neuron death	4/83	92/18862	0	0.01	0.01	NQO1/DDIT4/DDIT3/MYB	4
BP	GO:0045926	negative regulation of growth	6/83	245/18862	0	0.01	0.01	MT1G/PML/MT3/G6PD/ALOX15B/CDKN2A	6
BP	GO:0006835	dicarboxylic acid transport	4/83	93/18862	0	0.01	0.01	SLC7A11/SLC1A4/SLC1A5/GLS2	4
BP	GO:0051591	response to cAMP	4/83	93/18862	0	0.01	0.01	HSPA5/DUSP1/NOX4/DUOX1	4
BP	GO:1902882	regulation of response to oxidative stress	4/83	93/18862	0	0.01	0.01	SLC7A11/HSPB1/AIFM2/NOX1	4
BP	GO:0001953	negative regulation of cell-matrix adhesion	3/83	41/18862	0	0.01	0.01	SRC/NF2/CDKN2A	3
BP	GO:0033574	response to testosterone	3/83	41/18862	0	0.01	0.01	HSF1/NQO1/DUSP1	3

BP	GO:0048872	homeostasis of number of cells	6/83	249/18862	0	0.01	0.01	SLC7A11/ZFP36/IL6/HAMP/G6PD/BAP1	6
BP	GO:0007584	response to nutrient	5/83	165/18862	0	0.01	0.01	AKR1C3/HSF1/NQO1/HAMP/ACSL4	5
BP	GO:0002237	response to molecule of bacterial origin	7/83	346/18862	0	0.01	0.01	HSF1/SRC/ZFP36/NOS2/IL6/HAMP/MAPK3	7
BP	GO:0007259	receptor signaling pathway via JAK-STAT	5/83	166/18862	0	0.01	0.01	HSF1/NF2/CAV1/IL6/HAMP	5
BP	GO:0045616	regulation of keratinocyte differentiation	3/83	42/18862	0	0.01	0.01	TP63/ZFP36/ALOX15B	3
BP	GO:0046688	response to copper ion	3/83	42/18862	0	0.01	0.01	HSF1/MT1G/MT3	3
BP	GO:0032329	serine transport	2/83	10/18862	0	0.01	0.01	SLC1A4/SLC1A5	2
BP	GO:0036500	ATF6-mediated unfolded protein response	2/83	10/18862	0	0.01	0.01	HSPA5/DDIT3	2

BP	GO:1902510	regulation of apoptotic DNA fragmentation	2/83	10/18862	0	0.01	0.01	HSF1/IL6	2
BP	GO:0048010	vascular endothelial growth factor receptor signaling pathway	4/83	96/18862	0	0.011	0.01	HSPB1/SRC/NCF2/MT3	4
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	4/83	96/18862	0	0.011	0.01	IL6/ALOX12/NOX1/MYB	4
BP	GO:0052547	regulation of peptidase activity	8/83	455/18862	0	0.011	0.01	HSF1/SRC/PML/TP63/CAV1/MT3/ALOX12/DNAJB6	8
BP	GO:0035967	cellular response to topologically incorrect protein	5/83	168/18862	0	0.011	0.01	HSF1/HSPA5/ASNS/DDIT3/ATF3	5
BP	GO:0032620	interleukin-17 production	3/83	43/18862	0	0.011	0.01	DDIT3/SLC7A5/IL6	3
BP	GO:0051052	regulation of DNA metabolic process	7/83	353/18862	0	0.011	0.01	HSF1/SRC/PML/DUSP1/IL6/TFRC/MAPK3	7

BP	GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	3/83	44/18862	0	0.012	0.01	HSPB1/PML/NOX1	3
BP	GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	3/83	44/18862	0	0.012	0.01	PML/TP63/DDIT4	3
BP	GO:0051098	regulation of binding	7/83	357/18862	0	0.012	0.01	HSF1/SRC/CAV1/DDIT3/STMN1/AURKA/MAPK3	7
BP	GO:0019371	cyclooxygenase pathway	2/83	11/18862	0	0.012	0.01	AKR1C3/PTGS2	2
BP	GO:0035404	histone-serine phosphorylation	2/83	11/18862	0	0.012	0.01	AURKA/PRKAA2	2
BP	GO:0070778	L-aspartate transmembrane transport	2/83	11/18862	0	0.012	0.01	SLC1A4/SLC1A5	2
BP	GO:0090084	negative regulation of inclusion body	2/83	11/18862	0	0.012	0.01	HSF1/DNAJB6	2

		assembly							
BP	GO:2000392	regulation of lamellipodium morphogenesis	2/83	11/18862	0	0.012	0.01	SRC/ENPP2	2
BP	GO:0010634	positive regulation of epithelial cell migration	5/83	175/18862	0	0.012	0.01	HSPB1/SRC/ENPP2/PTGS2/ALOX12	5
BP	GO:0048771	tissue remodeling	5/83	175/18862	0	0.012	0.01	SRC/CAV1/IL6/TFRC/HAMP	5
BP	GO:0052126	movement in host environment	5/83	175/18862	0	0.012	0.01	SRC/PML/CAV1/TFRC/SLC1A5	5
BP	GO:0097696	receptor signaling pathway via STAT	5/83	175/18862	0	0.012	0.01	HSF1/NF2/CAV1/IL6/HAMP	5
BP	GO:0031349	positive regulation of defense response	7/83	361/18862	0	0.012	0.01	SRC/PTGS2/IL6/NRAS/HRAS/MAPK3/ABCC1	7
BP	GO:0016049	cell growth	8/83	470/18862	0	0.012	0.01	PML/MT3/HAMP/AURKA/G6PD/CDKN2A/BAP1/EGLN2	8
BP	GO:0006	acute-phase response	3/83	46/18862	0	0.012	0.01	PTGS2/IL6/HAMP	3

	953								
BP	GO:0071354	cellular response to interleukin-6	3/83	46/18862	0	0.012	0.01	SRC/IL6/HAMP	3
BP	GO:0050727	regulation of inflammatory response	7/83	366/18862	0	0.013	0.01	FANCD2/PTGS2/IL6/HAMP/ALOX15/BAP1/ABCC1	7
BP	GO:0030038	contractile actin filament bundle assembly	4/83	104/18862	0	0.013	0.01	SRC/NF2/STMN1/NOX4	4
BP	GO:0043149	stress fiber assembly	4/83	104/18862	0	0.013	0.01	SRC/NF2/STMN1/NOX4	4
BP	GO:1903793	positive regulation of anion transport	8/83	478/18862	0	0.013	0.01	SRC/TP63/CAV1/DRD4/ACSL4/HRAS/MYB/BAP1	8
BP	GO:0006983	ER overload response	2/83	12/18862	0	0.013	0.01	HSPA5/DDIT3	2
BP	GO:0035672	oligopeptide transmembrane transport	2/83	12/18862	0	0.013	0.01	SLC7A11/ABCC1	2
BP	GO:1903624	regulation of DNA catabolic process	2/83	12/18862	0	0.013	0.01	HSF1/IL6	2

BP	GO:0014009	glial cell proliferation	3/83	48/18862	0	0.013	0.01	NF2/IL6/MYB	3
BP	GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	3/83	48/18862	0	0.013	0.01	PML/CAV1/ATF3	3
BP	GO:0006066	alcohol metabolic process	7/83	373/18862	0	0.014	0.01	AKR1C1/AKR1C2/AKR1C3/MT3/G6PD/PRKAA2/MIOX	7
BP	GO:0072348	sulfur compound transport	3/83	49/18862	0	0.014	0.01	SLC7A11/SLC1A4/ABCC1	3
BP	GO:0022409	positive regulation of cell-cell adhesion	6/83	276/18862	0	0.015	0.01	SRC/CAV1/IL6/TFRC/ALOX15/MYB	6
BP	GO:0002931	response to ischemia	3/83	50/18862	0	0.015	0.01	SQSTM1/NQO1/CAV1	3
BP	GO:0070741	response to interleukin-6	3/83	50/18862	0	0.015	0.01	SRC/IL6/HAMP	3
BP	GO:1902001	fatty acid transmembrane transport	3/83	50/18862	0	0.015	0.01	SLC7A11/SLC2A1/PRKAA2	3

BP	GO:0071900	regulation of protein serine/threonine kinase activity	8/83	492/18862	0	0.015	0.01	HSPB1/SRC/CAV1/DUSP1/DRD4/HRAS/MAPK3/CDKN2A	8
BP	GO:0006857	oligopeptide transport	2/83	13/18862	0	0.015	0.01	SLC7A11/ABCC1	2
BP	GO:0071715	icosanoid transport	3/83	51/18862	0	0.016	0.01	NOS2/DRD4/ABCC1	3
BP	GO:0071478	cellular response to radiation	5/83	191/18862	0	0.016	0.01	HSF1/HSPA5/HAMP/NOX4/HRAS	5
BP	GO:1901605	alpha-amino acid metabolic process	5/83	191/18862	0	0.016	0.01	SLC7A11/NOS2/ASNS/NOX4/GLS2	5
BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	5/83	193/18862	0	0.017	0.01	HSF1/SRC/ENPP2/IL6/NOX4	5
BP	GO:0032970	regulation of actin filament-based process	7/83	389/18862	0	0.017	0.01	NF2/CAV1/ALOX15/STMN1/CAPG/NOX4/HRAS	7
BP	GO:0001780	neutrophil homeostasis	2/83	14/18862	0	0.017	0.01	SLC7A11/IL6	2

BP	GO:0034356	NAD biosynthesis via nicotinamide riboside salvage pathway	2/83	14/18862	0	0.017	0.01	PTGS2/NNMT	2
BP	GO:0035358	regulation of peroxisome proliferator activated receptor signaling pathway	2/83	14/18862	0	0.017	0.01	ALOX15/ALOX15B	2
BP	GO:0036295	cellular response to increased oxygen levels	2/83	14/18862	0	0.017	0.01	CAV1/NOX1	2
BP	GO:0038166	angiotensin-activated signaling pathway	2/83	14/18862	0	0.017	0.01	SRC/CAV1	2
BP	GO:0086103	G protein-coupled receptor signaling pathway involved in heart process	2/83	14/18862	0	0.017	0.01	SRC/CAV1	2
BP	GO:0043525	positive regulation of neuron apoptotic process	3/83	54/18862	0	0.018	0.01	NQO1/DDIT3/MYB	3

BP	GO:0043393	regulation of protein binding	5/83	196/18862	0	0.018	0.01	HSF1/SRC/CAV1/AURKA/MAPK3	5
BP	GO:0046164	alcohol catabolic process	3/83	55/18862	0	0.018	0.01	AKR1C3/MT3/MIOX	3
BP	GO:0048511	rhythmic process	6/83	294/18862	0	0.019	0.01	HSPA5/SRC/PML/NOS2/DRD4/PRKAA2	6
BP	GO:0010273	detoxification of copper ion	2/83	15/18862	0	0.019	0.01	MT1G/MT3	2
BP	GO:0035635	entry of bacterium into host cell	2/83	15/18862	0	0.019	0.01	SRC/CAV1	2
BP	GO:0042574	retinal metabolic process	2/83	15/18862	0	0.019	0.01	AKR1C1/AKR1C3	2
BP	GO:1990169	stress response to copper ion	2/83	15/18862	0	0.019	0.01	MT1G/MT3	2
BP	GO:1900542	regulation of purine nucleotide metabolic process	4/83	120/18862	0	0.019	0.01	NOS2/DDIT4/SLC2A6/PRKAA2	4
BP	GO:0019216	regulation of lipid metabolic process	7/83	402/18862	0	0.019	0.01	AKR1C3/SRC/PLIN2/CAV1/PTGS2/TXNRD1/PRKAA2	7
BP	GO:0010	response to zinc ion	3/83	57/18862	0	0.02	0.01	MT1G/MT3/HAMP	3

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BP	GO:0030520	intracellular estrogen receptor signaling pathway	3/83	57/18862	0	0.02	0.01	SRC/TP63/EGLN2	3
BP	GO:0006140	regulation of nucleotide metabolic process	4/83	122/18862	0	0.02	0.01	NOS2/DDIT4/SLC2A6/PRKAA2	4
BP	GO:0001558	regulation of cell growth	7/83	406/18862	0	0.02	0.01	PML/MT3/HAMP/G6PD/CDKN2A/BAP1/EGLN2	7
BP	GO:0010574	regulation of vascular endothelial growth factor production	3/83	58/18862	0	0.021	0.01	PTGS2/IL6/NOX1	3
BP	GO:0045779	negative regulation of bone resorption	2/83	16/18862	0	0.021	0.01	IL6/HAMP	2
BP	GO:0051238	sequestering of metal ion	2/83	16/18862	0	0.021	0.01	FTH1/FTL	2
BP	GO:0072673	lamellipodium morphogenesis	2/83	16/18862	0	0.021	0.01	SRC/ENPP2	2

BP	GO:0090083	regulation of inclusion body assembly	2/83	16/18862	0	0.021	0.01	HSF1/DNAJB6	2
BP	GO:1902074	response to salt	2/83	16/18862	0	0.021	0.01	HSF1/HSPA5	2
BP	GO:0045471	response to ethanol	4/83	126/18862	0	0.022	0.02	NQO1/HAMP/DRD4/G6PD	4
BP	GO:0043405	regulation of MAP kinase activity	6/83	307/18862	0	0.022	0.02	SRC/CAV1/DUSP1/DRD4/HRAS/MAPK3	6
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	5/83	210/18862	0	0.022	0.02	SRC/MT3/ALOX15/HRAS/MAPK3	5
BP	GO:0071384	cellular response to corticosteroid stimulus	3/83	60/18862	0	0.022	0.02	AKR1C3/ZFP36/DDIT4	3
BP	GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	3/83	60/18862	0	0.022	0.02	CAV1/DDIT3/NOX1	3
BP	GO:0030968	endoplasmic reticulum unfolded protein response	4/83	127/18862	0	0.022	0.02	HSPA5/ASNS/DDIT3/ATF3	4

BP	GO:0050870	positive regulation of T cell activation	5/83	212/18862	0	0.023	0.02	SRC/CAV1/IL6/TFRC/MYB	5
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STAT protein	2/83	17/18862	0	0.023	0.02	NF2/CAV1	2
BP	GO:0061687	detoxification of inorganic compound	2/83	17/18862	0	0.023	0.02	MT1G/MT3	2
BP	GO:2000811	negative regulation of anoikis	2/83	17/18862	0	0.023	0.02	SRC/CAV1	2
BP	GO:0009914	hormone transport	6/83	312/18862	0	0.023	0.02	NOS2/SLC7A5/IL6/SLC2A1/ACSL4/MYB	6
BP	GO:0010573	vascular endothelial growth factor production	3/83	62/18862	0	0.023	0.02	PTGS2/IL6/NOX1	3
BP	GO:0070527	platelet aggregation	3/83	62/18862	0	0.023	0.02	SLC7A11/HSPB1/ALOX12	3
BP	GO:0061041	regulation of wound healing	4/83	131/18862	0	0.024	0.02	CAV1/ALOX12/DUOX1/HRAS	4

BP	GO:2000378	negative regulation of reactive oxygen species metabolic process	3/83	63/18862	0	0.024	0.02	CAV1/MT3/G6PD	3
BP	GO:0052548	regulation of endopeptidase activity	7/83	426/18862	0	0.024	0.02	HSF1/SRC/PML/TP63/MT3/ALOX12/DNAJB6	7
BP	GO:0050673	epithelial cell proliferation	7/83	428/18862	0	0.025	0.02	TP63/ZFP36/CAV1/IL6/NOX5/NRAS/HRAS	7
BP	GO:0032740	positive regulation of interleukin-17 production	2/83	18/18862	0	0.025	0.02	SLC7A5/IL6	2
BP	GO:0046851	negative regulation of bone remodeling	2/83	18/18862	0	0.025	0.02	IL6/HAMP	2
BP	GO:0060252	positive regulation of glial cell proliferation	2/83	18/18862	0	0.025	0.02	IL6/MYB	2
BP	GO:0071243	cellular response to arsenic-containing substance	2/83	18/18862	0	0.025	0.02	HSF1/ATF3	2

BP	GO:2000641	regulation of early endosome to late endosome transport	2/83	18/18862	0	0.025	0.02	SRC/MAPK3	2
BP	GO:0002699	positive regulation of immune effector process	5/83	219/18862	0	0.025	0.02	NOS2/SLC7A5/IL6/TFRC/MYB	5
BP	GO:0051701	biological process involved in interaction with host	5/83	219/18862	0	0.025	0.02	SRC/PML/CAV1/TFRC/SLC1A5	5
BP	GO:0032507	maintenance of protein location in cell	3/83	64/18862	0	0.025	0.02	HSPA5/PML/CAV1	3
BP	GO:0051384	response to glucocorticoid	4/83	135/18862	0	0.026	0.02	ZFP36/DUSP1/DDIT4/IL6	4
BP	GO:0045598	regulation of fat cell differentiation	4/83	136/18862	0	0.027	0.02	ZFP36/PTGS2/DDIT3/IL6	4
BP	GO:0051900	regulation of mitochondrial depolarization	2/83	19/18862	0	0.027	0.02	SRC/ALOX12	2
BP	GO:0050863	regulation of T cell activation	6/83	327/18862	0	0.028	0.02	FANCD2/SRC/CAV1/IL6/TFRC/MYB	6
BP	GO:0010812	negative regulation of cell-substrate	3/83	67/18862	0	0.028	0.02	SRC/NF2/CDKN2A	3

		adhesion							
BP	GO:0008202	steroid metabolic process	6/83	329/18862	0	0.028	0.02	AKR1C1/AKR1C2/AKR1C3/MT3/G6PD/PRKAA2	6
BP	GO:1900015	regulation of cytokine production involved in inflammatory response	3/83	68/18862	0	0.029	0.02	NOS2/IL6/BAP1	3
BP	GO:1903201	regulation of oxidative stress-induced cell death	3/83	68/18862	0	0.029	0.02	SLC7A11/HSPB1/NOX1	3
BP	GO:0006520	cellular amino acid metabolic process	6/83	331/18862	0	0.029	0.02	SLC7A11/NQO1/NOS2/ASNS/NOX4/GLS2	6
BP	GO:0051090	regulation of DNA-binding transcription factor activity	7/83	444/18862	0	0.029	0.02	FANCD2/CAV1/DDIT3/IL6/TFRC/MAPK3/CDKN2A	7
BP	GO:0034104	negative regulation of tissue remodeling	2/83	20/18862	0	0.029	0.02	IL6/HAMP	2

BP	GO:0060444	branching involved in mammary gland duct morphogenesis	2/83	20/18862	0	0.029	0.02	SRC/PML	2
BP	GO:0062013	positive regulation of small molecule metabolic process	4/83	141/18862	0	0.029	0.02	SRC/PTGS2/NOS2/PRKAA2	4
BP	GO:0002534	cytokine production involved in inflammatory response	3/83	69/18862	0	0.029	0.02	NOS2/IL6/BAP1	3
BP	GO:0014823	response to activity	3/83	69/18862	0	0.029	0.02	HSF1/IL6/PRKAA2	3
BP	GO:0043254	regulation of protein-containing complex assembly	7/83	446/18862	0	0.029	0.02	HSF1/HSPA5/SRC/TFRC/ALOX15/STMN1/CAPG	7
BP	GO:0033135	regulation of peptidyl-serine phosphorylation	4/83	143/18862	0	0.03	0.02	CAV1/DDIT4/IL6/TFRC	4
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	5/83	234/18862	0	0.031	0.02	SRC/CAV1/IL6/TFRC/MYB	5

BP	GO:0014074	response to purine-containing compound	4/83	144/18862	0	0.031	0.02	HSPA5/DUSP1/NOX4/DUOX1	4
BP	GO:0035357	peroxisome proliferator activated receptor signaling pathway	2/83	21/18862	0	0.031	0.02	ALOX15/ALOX15B	2
BP	GO:0038083	peptidyl-tyrosine autophosphorylation	2/83	21/18862	0	0.031	0.02	CAV1/MAPK3	2
BP	GO:0071636	positive regulation of transforming growth factor beta production	2/83	21/18862	0	0.031	0.02	PTGS2/MYB	2
BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	4/83	145/18862	0	0.031	0.02	HSPB1/CAV1/DUSP1/CDKN2A	4
BP	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	3/83	72/18862	0	0.032	0.02	SRC/MT3/DNAJB6	3

BP	GO:0048708	astrocyte differentiation	3/83	72/18862	0	0.032	0.02	MT3/IL6/MAPK3	3
BP	GO:0050891	multicellular organismal water homeostasis	3/83	72/18862	0	0.032	0.02	TP63/ALOX12/STMN1	3
BP	GO:0031281	positive regulation of cyclase activity	2/83	22/18862	0	0.033	0.02	NOS2/MAPK3	2
BP	GO:0051882	mitochondrial depolarization	2/83	22/18862	0	0.033	0.02	SRC/ALOX12	2
BP	GO:0055093	response to hyperoxia	2/83	22/18862	0	0.033	0.02	CAV1/NOX1	2
BP	GO:0016569	covalent chromatin modification	7/83	461/18862	0	0.033	0.02	HELLS/MT3/AURKA/MAPK3/MYB/PRKAA2/BAP1	7
BP	GO:0006469	negative regulation of protein kinase activity	5/83	243/18862	0	0.035	0.02	HSPB1/NF2/CAV1/DUSP1/CDKN2A	5
BP	GO:0043536	positive regulation of blood vessel endothelial cell migration	3/83	75/18862	0	0.035	0.02	HSPB1/PTGS2/ALOX12	3
BP	GO:0072332	intrinsic apoptotic signaling pathway by	3/83	75/18862	0	0.035	0.02	PML/TP63/DDIT4	3

		p53 class mediator							
BP	GO:0006541	glutamine metabolic process	2/83	23/18862	0	0.036	0.02	ASNS/GLS2	2
BP	GO:0019430	removal of superoxide radicals	2/83	23/18862	0	0.036	0.02	NQO1/MT3	2
BP	GO:0033032	regulation of myeloid cell apoptotic process	2/83	23/18862	0	0.036	0.02	SLC7A11/CDKN2A	2
BP	GO:0060547	negative regulation of necrotic cell death	2/83	23/18862	0	0.036	0.02	CAV1/MT3	2
BP	GO:0061050	regulation of cell growth involved in cardiac muscle cell development	2/83	23/18862	0	0.036	0.02	HAMP/G6PD	2
BP	GO:0070841	inclusion body assembly	2/83	23/18862	0	0.036	0.02	HSF1/DNAJB6	2
BP	GO:0032956	regulation of actin cytoskeleton organization	6/83	352/18862	0	0.036	0.02	NF2/ALOX15/STMN1/CAPG/NOX4/HRAS	6
BP	GO:0044409	entry into host	4/83	153/18862	0	0.036	0.02	SRC/CAV1/TFRC/SLC1A5	4

BP	GO:0033238	regulation of cellular amine metabolic process	3/83	77/18862	0	0.037	0.03	SLC7A11/NQO1/DRD4	3
BP	GO:1901616	organic hydroxy compound catabolic process	3/83	77/18862	0	0.037	0.03	AKR1C3/MT3/MIOX	3
BP	GO:0051017	actin filament bundle assembly	4/83	154/18862	0	0.037	0.03	SRC/NF2/STMN1/NOX4	4
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	4/83	154/18862	0	0.037	0.03	SRC/PML/CAV1/ATF3	4
BP	GO:0006309	apoptotic DNA fragmentation	2/83	24/18862	0	0.038	0.03	HSF1/IL6	2
BP	GO:0015740	C4-dicarboxylate transport	2/83	24/18862	0	0.038	0.03	SLC1A4/SLC1A5	2
BP	GO:0071294	cellular response to zinc ion	2/83	24/18862	0	0.038	0.03	MT1G/MT3	2
BP	GO:2000209	regulation of anoikis	2/83	24/18862	0	0.038	0.03	SRC/CAV1	2
BP	GO:0071560	cellular response to transforming growth factor beta stimulus	5/83	251/18862	0.01	0.038	0.03	HSPA5/SRC/PML/CAV1/NOX4	5

BP	GO:0009615	response to virus	6/83	359/18862	0.01	0.038	0.03	HSPB1/SRC/PML/DDIT4/IL6/STMN1	6
BP	GO:0001776	leukocyte homeostasis	3/83	79/18862	0.01	0.038	0.03	SLC7A11/IL6/BAP1	3
BP	GO:0006110	regulation of glycolytic process	3/83	79/18862	0.01	0.038	0.03	DDIT4/SLC2A6/PRKAA2	3
BP	GO:0030104	water homeostasis	3/83	79/18862	0.01	0.038	0.03	TP63/ALOX12/STMN1	3
BP	GO:0032204	regulation of telomere maintenance	3/83	79/18862	0.01	0.038	0.03	SRC/PML/MAPK3	3
BP	GO:0048145	regulation of fibroblast proliferation	3/83	79/18862	0.01	0.038	0.03	FTH1/PML/MYB	3
BP	GO:0090398	cellular senescence	3/83	79/18862	0.01	0.038	0.03	PML/HRAS/CDKN2A	3
BP	GO:1900034	regulation of cellular response to heat	3/83	79/18862	0.01	0.038	0.03	HSF1/MAPK3/DNAJB6	3
BP	GO:0061572	actin filament bundle organization	4/83	158/18862	0.01	0.038	0.03	SRC/NF2/STMN1/NOX4	4
BP	GO:0001933	negative regulation of protein phosphorylation	6/83	362/18862	0.01	0.039	0.03	HSPB1/NF2/CAV1/DUSP1/DDIT4/CDKN2A	6

BP	GO:0001895	retina homeostasis	3/83	80/18862	0.01	0.039	0.03	HSPB1/ALB/SLC2A1	3
BP	GO:0010660	regulation of muscle cell apoptotic process	3/83	80/18862	0.01	0.039	0.03	HSF1/ALOX12/CDKN2A	3
BP	GO:0048144	fibroblast proliferation	3/83	80/18862	0.01	0.039	0.03	FTH1/PML/MYB	3
BP	GO:2000117	negative regulation of cysteine-type endopeptidase activity	3/83	80/18862	0.01	0.039	0.03	SRC/MT3/DNAJB6	3
BP	GO:0007093	mitotic cell cycle checkpoint	4/83	159/18862	0.01	0.039	0.03	FANCD2/PML/DUSP1/AURKA	4
BP	GO:0051100	negative regulation of binding	4/83	159/18862	0.01	0.039	0.03	CAV1/DDIT3/AURKA/MAPK3	4
BP	GO:2000241	regulation of reproductive process	4/83	159/18862	0.01	0.039	0.03	SRC/DUSP1/AURKA/NOX5	4
BP	GO:0010447	response to acidic pH	2/83	25/18862	0.01	0.039	0.03	SRC/NOX1	2
BP	GO:0071450	cellular response to oxygen radical	2/83	25/18862	0.01	0.039	0.03	NQO1/MT3	2
BP	GO:0071451	cellular response to superoxide	2/83	25/18862	0.01	0.039	0.03	NQO1/MT3	2

BP	GO:0043467	regulation of generation of precursor metabolites and energy	4/83	160/18862	0.01	0.039	0.03	NOS2/DDIT4/SLC2A6/PRKAA2	4
BP	GO:0048660	regulation of smooth muscle cell proliferation	4/83	160/18862	0.01	0.039	0.03	IL6/ALOX12/NOX1/MYB	4
BP	GO:0140353	lipid export from cell	3/83	81/18862	0.01	0.039	0.03	NOS2/GLS2/MYB	3
BP	GO:1905897	regulation of response to endoplasmic reticulum stress	3/83	81/18862	0.01	0.039	0.03	HSPA5/CAV1/DDIT3	3
BP	GO:0071559	response to transforming growth factor beta	5/83	257/18862	0.01	0.039	0.03	HSPA5/SRC/PML/CAV1/NOX4	5
BP	GO:0009306	protein secretion	6/83	367/18862	0.01	0.039	0.03	NOS2/IL6/STEAP3/DRD4/SLC2A1/ACSL4	6
BP	GO:0045862	positive regulation of proteolysis	6/83	367/18862	0.01	0.039	0.03	HSF1/SRC/PML/CAV1/ALOX12/AURKA	6

BP	GO:0035592	establishment of protein localization to extracellular region	6/83	368/18862	0.01	0.04	0.03	NOS2/IL6/STEAP3/DRD4/SLC2A1/ACSL4	6
BP	GO:0048659	smooth muscle cell proliferation	4/83	162/18862	0.01	0.04	0.03	IL6/ALOX12/NOX1/MYB	4
BP	GO:0000188	inactivation of MAPK activity	2/83	26/18862	0.01	0.04	0.03	CAV1/DUSP1	2
BP	GO:0046883	regulation of hormone secretion	5/83	260/18862	0.01	0.04	0.03	NOS2/IL6/SLC2A1/ACSL4/MYB	5
BP	GO:0051403	stress-activated MAPK cascade	5/83	261/18862	0.01	0.041	0.03	ZFP36/DUSP1/NOX1/HRAS/MAPK3	5
BP	GO:1903034	regulation of response to wounding	4/83	164/18862	0.01	0.041	0.03	CAV1/ALOX12/DUOX1/HRAS	4
BP	GO:0010657	muscle cell apoptotic process	3/83	84/18862	0.01	0.042	0.03	HSF1/ALOX12/CDKN2A	3
BP	GO:0072331	signal transduction by p53 class mediator	5/83	263/18862	0.01	0.042	0.03	PML/TP63/DDIT4/AURKA/PRKAA2	5
BP	GO:0009165	nucleotide biosynthetic process	5/83	264/18862	0.01	0.042	0.03	PTGS2/NOS2/NNMT/RRM2/ACSL4	5

BP	GO:0071692	protein localization to extracellular region	6/83	375/18862	0.01	0.042	0.03	NOS2/IL6/STEAP3/DRD4/SLC2A1/ACSL4	6
BP	GO:0002675	positive regulation of acute inflammatory response	2/83	27/18862	0.01	0.042	0.03	PTGS2/IL6	2
BP	GO:0009065	glutamine family amino acid catabolic process	2/83	27/18862	0.01	0.042	0.03	NOS2/GLS2	2
BP	GO:0015949	nucleobase-containing small molecule interconversion	2/83	27/18862	0.01	0.042	0.03	TXNRD1/RRM2	2
BP	GO:1903649	regulation of cytoplasmic transport	2/83	27/18862	0.01	0.042	0.03	SRC/MAPK3	2
BP	GO:0019915	lipid storage	3/83	85/18862	0.01	0.042	0.03	PLIN2/CAV1/IL6	3
BP	GO:0034109	homotypic cell-cell adhesion	3/83	85/18862	0.01	0.042	0.03	SLC7A11/HSPB1/ALOX12	3
BP	GO:0033673	negative regulation of kinase activity	5/83	267/18862	0.01	0.044	0.03	HSPB1/NF2/CAV1/DUSP1/CDKN2A	5

BP	GO:1901293	nucleoside phosphate biosynthetic process	5/83	267/18862	0.01	0.044	0.03	PTGS2/NOS2/NNMT/RRM2/ACSL4	5
BP	GO:0051899	membrane depolarization	3/83	87/18862	0.01	0.044	0.03	SRC/CAV1/ALOX12	3
BP	GO:1904063	negative regulation of cation transmembrane transport	3/83	87/18862	0.01	0.044	0.03	CAV1/HAMP/DRD4	3
BP	GO:0000303	response to superoxide	2/83	28/18862	0.01	0.044	0.03	NQO1/MT3	2
BP	GO:0010039	response to iron ion	2/83	28/18862	0.01	0.044	0.03	HAMP/G6PD	2
BP	GO:0046426	negative regulation of receptor signaling pathway via JAK-STAT	2/83	28/18862	0.01	0.044	0.03	NF2/CAV1	2
BP	GO:0060603	mammary gland duct morphogenesis	2/83	28/18862	0.01	0.044	0.03	SRC/PML	2
BP	GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling	2/83	28/18862	0.01	0.044	0.03	HSPB1/NOX1	2

		pathway							
BP	GO:0042176	regulation of protein catabolic process	6/83	383/18862	0.01	0.045	0.03	PML/CAV1/NOS2/HAMP/AURKA/EGLN2	6
BP	GO:0001659	temperature homeostasis	4/83	171/18862	0.01	0.045	0.03	HSF1/CAV1/PTGS2/DDIT3	4
BP	GO:0002532	production of molecular mediator involved in inflammatory response	3/83	88/18862	0.01	0.045	0.03	NOS2/IL6/BAP1	3
BP	GO:0033044	regulation of chromosome organization	5/83	273/18862	0.01	0.046	0.03	SRC/PML/DUSP1/MAPK3/MYB	5
BP	GO:0043491	protein kinase B signaling	5/83	273/18862	0.01	0.046	0.03	AKR1C2/AKR1C3/SRC/MT3/DDIT3	5
BP	GO:0110053	regulation of actin filament organization	5/83	273/18862	0.01	0.046	0.03	NF2/ALOX15/STMN1/CAPG/NOX4	5
BP	GO:0051492	regulation of stress fiber assembly	3/83	89/18862	0.01	0.046	0.03	NF2/STMN1/NOX4	3

BP	GO:0097306	cellular response to alcohol	3/83	89/18862	0.01	0.046	0.03	AKR1C2/AKR1C3/PRKAA2	3
BP	GO:0000305	response to oxygen radical	2/83	29/18862	0.01	0.046	0.03	NQO1/MT3	2
BP	GO:0009435	NAD biosynthetic process	2/83	29/18862	0.01	0.046	0.03	PTGS2/NNMT	2
BP	GO:0036296	response to increased oxygen levels	2/83	29/18862	0.01	0.046	0.03	CAV1/NOX1	2
BP	GO:1900027	regulation of ruffle assembly	2/83	29/18862	0.01	0.046	0.03	CAV1/HRAS	2
BP	GO:2000637	positive regulation of gene silencing by miRNA	2/83	29/18862	0.01	0.046	0.03	ZFP36/IL6	2
BP	GO:0043470	regulation of carbohydrate catabolic process	3/83	90/18862	0.01	0.047	0.03	DDIT4/SLC2A6/PRKAA2	3
BP	GO:0031098	stress-activated protein kinase signaling cascade	5/83	276/18862	0.01	0.047	0.03	ZFP36/DUSP1/NOX1/HRAS/MAPK3	5
BP	GO:0033137	negative regulation of peptidyl-serine phosphorylation	2/83	30/18862	0.01	0.049	0.03	CAV1/DDIT4	2

BP	GO:0046685	response to arsenic-containing substance	2/83	30/18862	0.01	0.049	0.03	HSF1/ATF3	2
BP	GO:0060148	positive regulation of posttranscriptional gene silencing	2/83	30/18862	0.01	0.049	0.03	ZFP36/IL6	2
BP	GO:0070102	interleukin-6-mediated signaling pathway	2/83	30/18862	0.01	0.049	0.03	SRC/IL6	2
BP	GO:1901796	regulation of signal transduction by p53 class mediator	4/83	177/18862	0.01	0.049	0.03	PML/TP63/AURKA/PRKAA2	4
BP	GO:0050708	regulation of protein secretion	5/83	279/18862	0.01	0.049	0.03	NOS2/IL6/DRD4/SLC2A1/ACSL4	5
BP	GO:0045185	maintenance of protein location	3/83	92/18862	0.01	0.049	0.03	HSPA5/PML/CAV1	3
BP	GO:0022900	electron transport chain	4/83	178/18862	0.01	0.049	0.03	AIFM2/NCF2/GPX2/NOX4	4
BP	GO:0050796	regulation of insulin secretion	4/83	178/18862	0.01	0.049	0.03	NOS2/IL6/SLC2A1/ACSL4	4
BP	GO:0014013	regulation of gliogenesis	3/83	93/18862	0.01	0.05	0.03	NF2/IL6/MYB	3

BP	GO:0000737	DNA catabolic process, endonucleolytic	2/83	31/18862	0.01	0.051	0.03	HSF1/IL6	2
BP	GO:0001516	prostaglandin biosynthetic process	2/83	31/18862	0.01	0.051	0.03	AKR1C3/PTGS2	2
BP	GO:0046457	prostanoid biosynthetic process	2/83	31/18862	0.01	0.051	0.03	AKR1C3/PTGS2	2
BP	GO:0070306	lens fiber cell differentiation	2/83	31/18862	0.01	0.051	0.03	SLC7A11/NF2	2
BP	GO:0042063	gliogenesis	5/83	283/18862	0.01	0.051	0.03	NF2/MT3/IL6/MAPK3/MYB	5
BP	GO:0034308	primary alcohol metabolic process	3/83	94/18862	0.01	0.051	0.03	AKR1C1/AKR1C2/AKR1C3	3
BP	GO:0061097	regulation of protein tyrosine kinase activity	3/83	94/18862	0.01	0.051	0.03	SRC/CAV1/NOX4	3
BP	GO:1904035	regulation of epithelial cell apoptotic process	3/83	94/18862	0.01	0.051	0.03	AKR1C3/ZFP36/IL6	3
BP	GO:0032872	regulation of stress-activated MAPK cascade	4/83	181/18862	0.01	0.051	0.04	DUSP1/NOX1/HRAS/MAPK3	4
BP	GO:0043409	negative regulation of MAPK cascade	4/83	181/18862	0.01	0.051	0.04	NF2/CAV1/DUSP1/ATF3	4

BP	GO:0002696	positive regulation of leukocyte activation	6/83	401/18862	0.01	0.052	0.04	SRC/CAV1/IL6/TFRC/HAMP/MYB	6
BP	GO:0002790	peptide secretion	6/83	401/18862	0.01	0.052	0.04	NOS2/IL6/STEAP3/DRD4/SLC2A1/ACSL4	6
BP	GO:0030641	regulation of cellular pH	3/83	95/18862	0.01	0.052	0.04	MAFG/NOX1/MAPK3	3
BP	GO:0019359	nicotinamide nucleotide biosynthetic process	2/83	32/18862	0.01	0.052	0.04	PTGS2/NNMT	2
BP	GO:0019363	pyridine nucleotide biosynthetic process	2/83	32/18862	0.01	0.052	0.04	PTGS2/NNMT	2
BP	GO:0032673	regulation of interleukin-4 production	2/83	32/18862	0.01	0.052	0.04	DDIT3/SLC7A5	2
BP	GO:0048011	neurotrophin TRK receptor signaling pathway	2/83	32/18862	0.01	0.052	0.04	SRC/DDIT4	2
BP	GO:0048384	retinoic acid receptor signaling pathway	2/83	32/18862	0.01	0.052	0.04	AKR1C3/PML	2
BP	GO:0071	cellular response to	2/83	32/18862	0.01	0.052	0.04	HSPA5/PML	2

	353	interleukin-4							
BP	GO:0032091	negative regulation of protein binding	3/83	96/18862	0.01	0.052	0.04	CAV1/AURKA/MAPK3	3
BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	4/83	184/18862	0.01	0.053	0.04	DUSP1/NOX1/HRAS/MAPK3	4
BP	GO:0048608	reproductive structure development	6/83	405/18862	0.01	0.053	0.04	AKR1C3/HSPA5/SRC/TP63/ALOX15B/MAPK3	6
BP	GO:0030308	negative regulation of cell growth	4/83	185/18862	0.01	0.054	0.04	PML/MT3/G6PD/CDKN2A	4
BP	GO:0042326	negative regulation of phosphorylation	6/83	407/18862	0.01	0.054	0.04	HSPB1/NF2/CAV1/DUSP1/DDIT4/CDKN2A	6
BP	GO:0061458	reproductive system development	6/83	408/18862	0.01	0.054	0.04	AKR1C3/HSPA5/SRC/TP63/ALOX15B/MAPK3	6
BP	GO:0003298	physiological muscle hypertrophy	2/83	33/18862	0.01	0.054	0.04	HAMP/G6PD	2

BP	GO:0003301	physiological cardiac muscle hypertrophy	2/83	33/18862	0.01	0.054	0.04	HAMP/G6PD	2
BP	GO:0006536	glutamate metabolic process	2/83	33/18862	0.01	0.054	0.04	SLC7A11/GLS2	2
BP	GO:0030262	apoptotic nuclear changes	2/83	33/18862	0.01	0.054	0.04	HSF1/IL6	2
BP	GO:0032633	interleukin-4 production	2/83	33/18862	0.01	0.054	0.04	DDIT3/SLC7A5	2
BP	GO:0060251	regulation of glial cell proliferation	2/83	33/18862	0.01	0.054	0.04	IL6/MYB	2
BP	GO:0061049	cell growth involved in cardiac muscle cell development	2/83	33/18862	0.01	0.054	0.04	HAMP/G6PD	2
BP	GO:1904893	negative regulation of receptor signaling pathway via STAT	2/83	33/18862	0.01	0.054	0.04	NF2/CAV1	2
BP	GO:0019217	regulation of fatty acid metabolic process	3/83	98/18862	0.01	0.054	0.04	CAV1/PTGS2/PRKAA2	3
BP	GO:0110020	regulation of actomyosin structure	3/83	98/18862	0.01	0.054	0.04	NF2/STMN1/NOX4	3

		organization							
BP	GO:0010632	regulation of epithelial cell migration	5/83	293/18862	0.01	0.055	0.04	HSPB1/SRC/ENPP2/PTGS2/ALOX12	5
BP	GO:0002702	positive regulation of production of molecular mediator of immune response	3/83	99/18862	0.01	0.055	0.04	SLC7A5/IL6/TFRC	3
BP	GO:0043279	response to alkaloid	3/83	99/18862	0.01	0.055	0.04	NQO1/HSPA5/DRD4	3
BP	GO:0050867	positive regulation of cell activation	6/83	412/18862	0.01	0.055	0.04	SRC/CAV1/IL6/TFRC/HAMP/MYB	6
BP	GO:1905952	regulation of lipid localization	4/83	189/18862	0.01	0.056	0.04	PLIN2/CAV1/IL6/MYB	4
BP	GO:0007162	negative regulation of cell adhesion	5/83	295/18862	0.01	0.056	0.04	SRC/NF2/DUSP1/ALOX12/CDKN2A	5
BP	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	3/83	100/18862	0.01	0.056	0.04	PML/TP63/DDIT4	3

BP	GO:0043276	anoikis	2/83	34/18862	0.01	0.056	0.04	SRC/CAV1	2
BP	GO:2000758	positive regulation of peptidyl-lysine acetylation	2/83	34/18862	0.01	0.056	0.04	MAPK3/PRKAA2	2
BP	GO:0043588	skin development	6/83	415/18862	0.01	0.056	0.04	AKR1C3/TP63/ZFP36/ALOX12/STMN1/ALOX15B	6
BP	GO:0046425	regulation of receptor signaling pathway via JAK-STAT	3/83	101/18862	0.01	0.057	0.04	NF2/CAV1/IL6	3
BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	3/83	101/18862	0.01	0.057	0.04	AKR1C3/PTGS2/NOX4	3
BP	GO:0031032	actomyosin structure organization	4/83	191/18862	0.01	0.057	0.04	SRC/NF2/STMN1/NOX4	4
BP	GO:0031099	regeneration	4/83	192/18862	0.01	0.057	0.04	IL6/HAMP/NNMT/AURKA	4
BP	GO:0032231	regulation of actin filament bundle assembly	3/83	102/18862	0.01	0.057	0.04	NF2/STMN1/NOX4	3

BP	GO:0043200	response to amino acid	3/83	102/18862	0.01	0.057	0.04	HSF1/NQO1/ASNS	3
BP	GO:0044773	mitotic DNA damage checkpoint	3/83	102/18862	0.01	0.057	0.04	FANCD2/PML/AURKA	3
BP	GO:0071887	leukocyte apoptotic process	3/83	102/18862	0.01	0.057	0.04	SLC7A11/IL6/CDKN2A	3
BP	GO:0006921	cellular component disassembly involved in execution phase of apoptosis	2/83	35/18862	0.01	0.057	0.04	HSF1/IL6	2
BP	GO:0019362	pyridine nucleotide metabolic process	2/83	35/18862	0.01	0.057	0.04	PTGS2/NNMT	2
BP	GO:0032148	activation of protein kinase B activity	2/83	35/18862	0.01	0.057	0.04	SRC/MT3	2
BP	GO:0046496	nicotinamide nucleotide metabolic process	2/83	35/18862	0.01	0.057	0.04	PTGS2/NNMT	2
BP	GO:0051354	negative regulation of oxidoreductase activity	2/83	35/18862	0.01	0.057	0.04	CAV1/MT3	2
BP	GO:0070670	response to interleukin-4	2/83	35/18862	0.01	0.057	0.04	HSPA5/PML	2

BP	GO:0072525	pyridine-containing compound biosynthetic process	2/83	35/18862	0.01	0.057	0.04	PTGS2/NNMT	2
BP	GO:1905898	positive regulation of response to endoplasmic reticulum stress	2/83	35/18862	0.01	0.057	0.04	CAV1/DDIT3	2
BP	GO:0030099	myeloid cell differentiation	6/83	419/18862	0.01	0.057	0.04	MT1G/SRC/PML/ZFP36/TFRC/G6PD	6
BP	GO:0006885	regulation of pH	3/83	103/18862	0.01	0.058	0.04	MAFG/NOX1/MAPK3	3
BP	GO:0032637	interleukin-8 production	3/83	103/18862	0.01	0.058	0.04	NOS2/DDIT3/IL6	3
BP	GO:0032651	regulation of interleukin-1 beta production	3/83	103/18862	0.01	0.058	0.04	HSPB1/PML/IL6	3
BP	GO:0070498	interleukin-1-mediated signaling pathway	3/83	103/18862	0.01	0.058	0.04	SQSTM1/IL6/MAPK3	3
BP	GO:1905475	regulation of protein localization to membrane	4/83	194/18862	0.01	0.058	0.04	SLC7A11/SQSTM1/TP63/HRAS	4

BP	GO:0046879	hormone secretion	5/83	302/18862	0.01	0.058	0.04	NOS2/IL6/SLC2A1/ACSL4/MYB	5
BP	GO:1901215	negative regulation of neuron death	4/83	195/18862	0.01	0.058	0.04	SLC7A11/HSF1/MT3/HRAS	4
BP	GO:0033572	transferrin transport	2/83	36/18862	0.01	0.059	0.04	TFRC/STEAP3	2
BP	GO:0045730	respiratory burst	2/83	36/18862	0.01	0.059	0.04	NCF2/NOX1	2
BP	GO:0045785	positive regulation of cell adhesion	6/83	425/18862	0.01	0.06	0.04	SRC/CAV1/IL6/TFRC/ALOX15/MYB	6
BP	GO:0016052	carbohydrate catabolic process	4/83	197/18862	0.01	0.06	0.04	DDIT4/SLC2A6/PRKAA2/MIOX	4
BP	GO:0060326	cell chemotaxis	5/83	306/18862	0.01	0.06	0.04	HSPB1/DUSP1/IL6/MAPK3/ABCC1	5
BP	GO:0018958	phenol-containing compound metabolic process	3/83	106/18862	0.01	0.061	0.04	SLC7A11/DRD4/DUOX1	3
BP	GO:0044774	mitotic DNA integrity checkpoint	3/83	106/18862	0.01	0.061	0.04	FANCD2/PML/AURKA	3
BP	GO:0000096	sulfur amino acid metabo	2/83	37/18862	0.01	0.061	0.04	SLC7A11/NOX4	2

		lic process							
BP	GO:0010837	regulation of keratinocyte proliferation	2/83	37/18862	0.01	0.061	0.04	TP63/ZFP36	2
BP	GO:1902745	positive regulation of lamellipodium organization	2/83	37/18862	0.01	0.061	0.04	SRC/ENPP2	2
BP	GO:0002791	regulation of peptide secretion	5/83	308/18862	0.01	0.061	0.04	NOS2/IL6/DRD4/SLC2A1/ACSL4	5
BP	GO:0002526	acute inflammatory response	3/83	107/18862	0.01	0.062	0.04	PTGS2/IL6/HAMP	3
BP	GO:0032649	regulation of interferon-gamma production	3/83	107/18862	0.01	0.062	0.04	DDIT3/SLC7A5/HRAS	3
BP	GO:0033138	positive regulation of peptidyl-serine phosphorylation	3/83	107/18862	0.01	0.062	0.04	CAV1/IL6/TFRC	3
BP	GO:2000278	regulation of DNA biosynthetic process	3/83	107/18862	0.01	0.062	0.04	SRC/DUSP1/MAPK3	3
BP	GO:0010952	positive regulation of peptidase activity	4/83	200/18862	0.01	0.062	0.04	HSF1/PML/CAV1/ALOX12	4
BP	GO:0032611	interleukin-1 beta production	3/83	108/18862	0.01	0.063	0.04	HSPB1/PML/IL6	3

BP	GO:0001504	neurotransmitter uptake	2/83	38/18862	0.01	0.063	0.04	DRD4/SLC38A1	2
BP	GO:0006882	cellular zinc ion homeostasis	2/83	38/18862	0.01	0.063	0.04	MT1G/MT3	2
BP	GO:0032094	response to food	2/83	38/18862	0.01	0.063	0.04	MT3/G6PD	2
BP	GO:0038179	neurotrophin signaling pathway	2/83	38/18862	0.01	0.063	0.04	SRC/DDIT4	2
BP	GO:0007179	transforming growth factor beta receptor signaling pathway	4/83	202/18862	0.01	0.063	0.04	HSPA5/SRC/PML/CAV1	4
BP	GO:0009612	response to mechanical stimulus	4/83	202/18862	0.01	0.063	0.04	SRC/ASNS/SLC2A1/MAPK3	4
BP	GO:0009895	negative regulation of catabolic process	5/83	312/18862	0.01	0.063	0.04	PML/ZFP36/NOS2/MT3/DDIT4	5
BP	GO:0051222	positive regulation of protein transport	5/83	312/18862	0.01	0.063	0.04	SRC/TP63/ACSL4/HRAS/BAP1	5
BP	GO:0007015	actin filament organization	6/83	435/18862	0.01	0.063	0.04	SRC/NF2/ALOX15/STMN1/CAPG/NOX4	6

BP	GO:1904659	glucose transmembrane transport	3/83	109/18862	0.01	0.063	0.04	SLC2A1/SLC2A6/SLC2A14	3
BP	GO:0034440	lipid oxidation	3/83	110/18862	0.01	0.065	0.04	ALOX12/ALOX15/ALOX15B	3
BP	GO:1904892	regulation of receptor signaling pathway via STAT	3/83	110/18862	0.01	0.065	0.04	NF2/CAV1/IL6	3
BP	GO:0033146	regulation of intracellular estrogen receptor signaling pathway	2/83	39/18862	0.01	0.065	0.04	SRC/TP63	2
BP	GO:0050892	intestinal absorption	2/83	39/18862	0.01	0.065	0.04	AKR1C1/HAMP	2
BP	GO:2000279	negative regulation of DNA biosynthetic process	2/83	39/18862	0.01	0.065	0.04	SRC/DUSP1	2
BP	GO:0031623	receptor internalization	3/83	111/18862	0.01	0.065	0.04	CAV1/TFRC/DRD4	3
BP	GO:0046660	female sex differentiation	3/83	111/18862	0.01	0.065	0.04	HSPA5/SRC/TP63	3
BP	GO:1905954	positive regulation of lipid	3/83	111/18862	0.01	0.065	0.04	PLIN2/CAV1/MYB	3

		localization							
BP	GO:0006109	regulation of carbohydrate metabolic process	4/83	206/18862	0.01	0.065	0.04	SRC/DDIT4/SLC2A6/PRKAA2	4
BP	GO:0030100	regulation of endocytosis	4/83	206/18862	0.01	0.065	0.04	SRC/CAV1/DRD4/ALOX15	4
BP	GO:0070555	response to interleukin-1	4/83	206/18862	0.01	0.065	0.04	SQSTM1/SRC/IL6/MAPK3	4
BP	GO:0071456	cellular response to hypoxia	4/83	206/18862	0.01	0.065	0.04	SRC/PTGS2/MT3/EGLN2	4
BP	GO:0030073	insulin secretion	4/83	207/18862	0.01	0.066	0.05	NOS2/IL6/SLC2A1/ACSL4	4
BP	GO:0008645	hexose transmembrane transport	3/83	112/18862	0.01	0.066	0.05	SLC2A1/SLC2A6/SLC2A14	3
BP	GO:0032609	interferon-gamma production	3/83	112/18862	0.01	0.066	0.05	DDIT3/SLC7A5/HRAS	3
BP	GO:0006308	DNA catabolic process	2/83	40/18862	0.01	0.066	0.05	HSF1/IL6	2
BP	GO:0045022	early endosome to late endosome transport	2/83	40/18862	0.01	0.066	0.05	SRC/MAPK3	2
BP	GO:0055069	zinc ion homeostasis	2/83	40/18862	0.01	0.066	0.05	MT1G/MT3	2

BP	GO:0071634	regulation of transforming growth factor beta production	2/83	40/18862	0.01	0.066	0.05	PTGS2/MYB	2
BP	GO:0150077	regulation of neuroinflammatory response	2/83	40/18862	0.01	0.066	0.05	PTGS2/IL6	2
BP	GO:1904037	positive regulation of epithelial cell apoptotic process	2/83	40/18862	0.01	0.066	0.05	AKR1C3/IL6	2
BP	GO:0030518	intracellular steroid hormone receptor signaling pathway	3/83	113/18862	0.01	0.067	0.05	SRC/TP63/EGLN2	3
BP	GO:0000075	cell cycle checkpoint	4/83	209/18862	0.01	0.067	0.05	FANCD2/PML/DUSP1/AURKA	4
BP	GO:0006338	chromatin remodeling	4/83	209/18862	0.01	0.067	0.05	HELLS/TP63/CDKN2A/MYB	4
BP	GO:0090276	regulation of peptide hormone secretion	4/83	209/18862	0.01	0.067	0.05	NOS2/IL6/SLC2A1/ACSL4	4
BP	GO:0045930	negative regulation of mitotic cell cycle	5/83	321/18862	0.01	0.067	0.05	FANCD2/PML/DUSP1/AURKA/CDKN2A	5

BP	GO:0002223	stimulatory C-type lectin receptor signaling pathway	3/83	114/18862	0.01	0.068	0.05	SRC/NRAS/HRAS	3
BP	GO:0006096	glycolytic process	3/83	114/18862	0.01	0.068	0.05	DDIT4/SLC2A6/PRKAA2	3
BP	GO:0015749	monosaccharide transmembrane transport	3/83	114/18862	0.01	0.068	0.05	SLC2A1/SLC2A6/SLC2A14	3
BP	GO:0002251	organ or tissue specific immune response	2/83	41/18862	0.01	0.068	0.05	NOS2/IL6	2
BP	GO:0009268	response to pH	2/83	41/18862	0.01	0.068	0.05	SRC/NOX1	2
BP	GO:0010939	regulation of necrotic cell death	2/83	41/18862	0.01	0.068	0.05	CAV1/MT3	2
BP	GO:0030850	prostate gland development	2/83	41/18862	0.01	0.068	0.05	TP63/ALOX15B	2
BP	GO:0051602	response to electrical stimulus	2/83	41/18862	0.01	0.068	0.05	NQO1/SRC	2
BP	GO:0072524	pyridine-containing compound metabolic process	2/83	41/18862	0.01	0.068	0.05	PTGS2/NNMT	2

BP	GO:0016570	histone modification	6/83	448/18862	0.01	0.068	0.05	MT3/AURKA/MAPK3/MYB/PRKAA2/BAP1	6
BP	GO:0001704	formation of primary germ layer	3/83	115/18862	0.01	0.068	0.05	NF2/DUSP1/TXNRD1	3
BP	GO:0006757	ATP generation from ADP	3/83	115/18862	0.01	0.068	0.05	DDIT4/SLC2A6/PRKAA2	3
BP	GO:0030004	cellular monovalent inorganic cation homeostasis	3/83	115/18862	0.01	0.068	0.05	MAFG/NOX1/MAPK3	3
BP	GO:0007623	circadian rhythm	4/83	212/18862	0.01	0.068	0.05	PML/NOS2/DRD4/PRKAA2	4
BP	GO:0034219	carbohydrate transmembrane transport	3/83	116/18862	0.01	0.07	0.05	SLC2A1/SLC2A6/SLC2A14	3
BP	GO:1904019	epithelial cell apoptotic process	3/83	116/18862	0.01	0.07	0.05	AKR1C3/ZFP36/IL6	3
BP	GO:0014002	astrocyte development	2/83	42/18862	0.01	0.07	0.05	MT3/IL6	2
BP	GO:0014075	response to amine	2/83	42/18862	0.01	0.07	0.05	NQO1/DRD4	2
BP	GO:0032965	regulation of collagen biosynthetic process	2/83	42/18862	0.01	0.07	0.05	IL6/MYB	2

BP	GO:0071604	transforming growth factor beta production	2/83	42/18862	0.01	0.07	0.05	PTGS2/MYB	2
BP	GO:0072595	maintenance of protein localization in organelle	2/83	42/18862	0.01	0.07	0.05	HSPA5/PML	2
BP	GO:0036294	cellular response to decreased oxygen levels	4/83	214/18862	0.01	0.07	0.05	SRC/PTGS2/MT3/EGLN2	4
BP	GO:0010506	regulation of autophagy	5/83	328/18862	0.01	0.07	0.05	HSPB1/MT3/DDIT3/MAPK3/PRKAA2	5
BP	GO:1904951	positive regulation of establishment of protein localization	5/83	328/18862	0.01	0.07	0.05	SRC/TP63/ACSL4/HRAS/BAP1	5
BP	GO:0030534	adult behavior	3/83	117/18862	0.01	0.07	0.05	SLC7A11/MAFG/DRD4	3
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	5/83	330/18862	0.02	0.071	0.05	SRC/CAV1/IL6/TFRC/MYB	5
BP	GO:0002220	innate immune response activating cell surface receptor signalin	3/83	118/18862	0.02	0.071	0.05	SRC/NRAS/HRAS	3

		g pathway							
BP	GO:0042752	regulation of circadian rhythm	3/83	118/18862	0.02	0.071	0.05	PML/DRD4/PRKAA2	3
BP	GO:0021762	substantia nigra development	2/83	43/18862	0.02	0.071	0.05	HSPA5/G6PD	2
BP	GO:0022602	ovulation cycle process	2/83	43/18862	0.02	0.071	0.05	HSPA5/SRC	2
BP	GO:0032309	icosanoid secretion	2/83	43/18862	0.02	0.071	0.05	NOS2/DRD4	2
BP	GO:0042220	response to cocaine	2/83	43/18862	0.02	0.071	0.05	HSPA5/DRD4	2
BP	GO:0097178	ruffle assembly	2/83	43/18862	0.02	0.071	0.05	CAV1/HRAS	2
BP	GO:0098927	vesicle-mediated transport between endosomal compartments	2/83	43/18862	0.02	0.071	0.05	SRC/MAPK3	2
BP	GO:0097191	extrinsic apoptotic signaling pathway	4/83	217/18862	0.02	0.071	0.05	SRC/PML/CAV1/ATF3	4

BP	GO:0001101	response to acid chemical	3/83	119/18862	0.02	0.071	0.05	HSF1/NQO1/ASNS	3
BP	GO:0002688	regulation of leukocyte chemotaxis	3/83	119/18862	0.02	0.071	0.05	DUSP1/IL6/MAPK3	3
BP	GO:0002758	innate immune response-activating signal transduction	3/83	119/18862	0.02	0.071	0.05	SRC/NRAS/HRAS	3
BP	GO:0032652	regulation of interleukin-1 production	3/83	119/18862	0.02	0.071	0.05	HSPB1/PML/IL6	3
BP	GO:0034766	negative regulation of ion transmembrane transport	3/83	119/18862	0.02	0.071	0.05	CAV1/HAMP/DRD4	3
BP	GO:1903578	regulation of ATP metabolic process	3/83	119/18862	0.02	0.071	0.05	DDIT4/SLC2A6/PRKAA2	3
BP	GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	3/83	119/18862	0.02	0.071	0.05	PML/AURKA/CDKN2A	3
BP	GO:0010810	regulation of cell-substrate adhesion	4/83	218/18862	0.02	0.071	0.05	SRC/NF2/ALOX15/CDKN2A	4

BP	GO:0042445	hormone metabolic process	4/83	218/18862	0.02	0.071	0.05	AKR1C1/AKR1C2/AKR1C3/DUOX1	4
BP	GO:0034605	cellular response to heat	3/83	120/18862	0.02	0.072	0.05	HSF1/MAPK3/DNAJB6	3
BP	GO:0034763	negative regulation of transmembrane transport	3/83	120/18862	0.02	0.072	0.05	CAV1/HAMP/DRD4	3
BP	GO:0002639	positive regulation of immunoglobulin production	2/83	44/18862	0.02	0.072	0.05	IL6/TFRC	2
BP	GO:0003254	regulation of membrane depolarization	2/83	44/18862	0.02	0.072	0.05	SRC/ALOX12	2
BP	GO:0150076	neuroinflammatory response	2/83	44/18862	0.02	0.072	0.05	PTGS2/IL6	2
CC	GO:0043020	NADPH oxidase complex	4/83	12/19520	####	#####	####	NCF2/NOX1/NOX4/DUOX1	4
CC	GO:0005767	secondary lysosome	4/83	16/19520	####	#####	####	SQSTM1/FTH1/NCF2/FTL	4
CC	GO:0042470	melanosome	6/83	106/19520	####	3E-04	0	HSPA5/SLC1A4/TFRC/SLC2A1/CAPG/SLC1A5	6

CC	GO:0048770	pigment granule	6/83	106/19520	####	3E-04	0	HSPA5/SLC1A4/TFRC/SLC2A1/CAPG/SLC1A5	6
CC	GO:0044754	autolysosome	3/83	10/19520	####	4E-04	0	SQSTM1/FTH1/FTL	3
CC	GO:0005811	lipid droplet	5/83	95/19520	####	0.002	0	PLIN2/AIFM2/CAV1/ALOX15/ACSL4	5
CC	GO:0045177	apical part of cell	9/83	414/19520	####	0.002	0	SLC7A11/NF2/SLC7A5/HAMP/SLC2A1/NOX4/DUOX1/SLC38A1/ABCC1	9
CC	GO:0000792	heterochromatin	4/83	72/19520	0	0.007	0.01	HSF1/HELLS/PML/CDKN2A	4
CC	GO:0005901	caveola	4/83	80/19520	0	0.008	0.01	SRC/CAV1/SLC2A1/MAPK3	4
CC	GO:0005925	focal adhesion	8/83	416/19520	0	0.008	0.01	HSPB1/HSPA5/SRC/CAV1/RPL8/NOX4/ALOX15B/MAPK3	8

CC	GO:0030055	cell-substrate junction	8/83	423/19520	0	0.008	0.01	HSPB1/HSPA5/SRC/CAV1/RPL8/NOX4/ALOX15B/MAPK3	8
CC	GO:0009925	basal plasma membrane	6/83	240/19520	0	0.01	0.01	SLC7A5/TFRC/SLC2A1/SLC38A1/SLC1A5/ABCC1	6
CC	GO:0045178	basal part of cell	6/83	258/19520	0	0.013	0.01	SLC7A5/TFRC/SLC2A1/SLC38A1/SLC1A5/ABCC1	6
CC	GO:0045120	pronucleus	2/83	12/19520	0	0.017	0.01	SLC2A1/AURKA	2
CC	GO:0044853	plasma membrane raft	4/83	111/19520	0	0.017	0.01	SRC/CAV1/SLC2A1/MAPK3	4
CC	GO:1990204	oxidoreductase complex	4/83	111/19520	0	0.017	0.01	NCF2/NOX1/NOX4/DUOX1	4
CC	GO:0016323	basolateral plasma membrane	5/83	211/19520	0	0.026	0.02	SLC7A5/TFRC/SLC2A1/SLC38A1/ABCC1	5

CC	GO:0016324	apical plasma membrane	6/83	351/19520	0	0.044	0.04	SLC7A5/SLC2A1/NOX4/DUOX1/SLC38A1/ABCC1	6
CC	GO:0016234	inclusion body	3/83	74/19520	0	0.044	0.04	SQSTM1/MT3/MIOX	3
CC	GO:0005769	early endosome	6/83	378/19520	0.01	0.059	0.05	PML/NF2/CAV1/TFRC/NOX1/MAPK3	6
MF	GO:0016651	oxidoreductase activity, acting on NAD(P)H	12/83	102/18337	####	#####	####	AKR1C1/AKR1C2/AKR1C3/NQO1/AIFM2/NCF2/TXNRD1/NOX1/NOX4/NOX5/DUOX1/MIOX	12
MF	GO:0016175	superoxide-generating NAD(P)H oxidase activity	5/83	11/18337	####	#####	####	NCF2/NOX1/NOX4/NOX5/DUOX1	5
MF	GO:0016209	antioxidant activity	8/83	86/18337	####	#####	####	NQO1/PTGS2/MT3/ALB/TXNRD1/SRXN1/GPX2/DUOX1	8

MF	GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	5/83	16/18337	####	#####	####	NCF2/NOX1/NOX4/NOX5/DUOX1	5
MF	GO:0008514	organic anion transmembrane transporter activity	9/83	177/18337	####	#####	####	SLC7A11/SLC1A4/SLC7A5/SLC2A1/SLC2A6/SLC2A14/SLC38A1/SLC1A5/ABCC1	9
MF	GO:0015175	neutral amino acid transmembrane transporter activity	5/83	34/18337	####	#####	####	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5	5
MF	GO:0050661	NADP binding	5/83	53/18337	####	2E-04	0	NOS2/NOX1/NOX5/DUOX1/G6PD	5
MF	GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	4/83	25/18337	####	2E-04	0	ALOX12/ALOX15/ALOX15B/MIOX	4

MF	GO:0005506	iron ion binding	7/83	150/18337	####	2E-04	0	FTH1/FTL/ALOX12/ALOX15/ALOX15B/EGLN2/MIOX	7
MF	GO:0004033	aldo-keto reductase (NADP) activity	4/83	27/18337	####	2E-04	0	AKR1C1/AKR1C2/AKR1C3/MIOX	4
MF	GO:0015179	L-amino acid transmembrane transporter activity	5/83	59/18337	####	2E-04	0	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5	5
MF	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	5/83	60/18337	####	2E-04	0	AKR1C1/AKR1C2/AKR1C3/NQO1/AIFM2	5
MF	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	7/83	160/18337	####	2E-04	0	AKR1C1/AKR1C2/AKR1C3/FADS2/PTGS2/NOS2/EGLN2	7

MF	GO:0090482	vitamin transmembrane transporter activity	4/83	29/18337	####	2E-04	0	SLC2A1/SLC2A6/SLC2A14/ABCC1	4
MF	GO:0008199	ferric iron binding	3/83	10/18337	####	2E-04	0	FTH1/FTL/MIOX	3
MF	GO:0032052	bile acid binding	3/83	11/18337	####	3E-04	0	AKR1C1/AKR1C2/AKR1C3	3
MF	GO:0004032	alditol: NADP+ 1-oxidoreductase activity	3/83	12/18337	####	4E-04	0	AKR1C1/AKR1C2/AKR1C3	3
MF	GO:0015171	amino acid transmembrane transporter activity	5/83	81/18337	####	6E-04	0	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5	5
MF	GO:0050660	flavin adenine dinucleotide binding	5/83	81/18337	####	6E-04	0	AIFM2/NOS2/TXNRD1/NOX4/NOX5	5
MF	GO:0020037	heme binding	6/83	140/18337	####	7E-04	0	SRC/PTGS2/NOS2/NOX4/NOX5/DUOX1	6
MF	GO:0015172	acidic amino acid transmembrane transporter activity	3/83	16/18337	####	8E-04	0	SLC7A11/SLC1A4/SLC1A5	3

MF	GO:0051213	dioxygenase activity	5/83	89/18337	####	8E-04	0	PTGS2/ALOX12/ALOX15/ALOX15B/EGLN2	5
MF	GO:0046906	tetrapyrrole binding	6/83	150/18337	####	9E-04	0	SRC/PTGS2/NOS2/NOX4/NOX5/DUOX1	6
MF	GO:0016709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	4/83	48/18337	####	9E-04	0	AKR1C1/AKR1C2/AKR1C3/NOS2	4
MF	GO:0004303	estradiol 17-beta-dehydrogenase activity	3/83	18/18337	####	9E-04	0	AKR1C1/AKR1C2/AKR1C3	3
MF	GO:0046943	carboxylic acid transmembrane transporter activity	6/83	157/18337	####	1E-03	0	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5/ABCC1	6

MF	GO:0005342	organic acid transmembrane transporter activity	6/83	158/18337	####	1E-03	0	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5/ABCC1	6
MF	GO:0016722	oxidoreductase activity, acting on metal ions	3/83	19/18337	####	1E-03	0	FTH1/STEAP3/NOX5	3
MF	GO:0005355	glucose transmembrane transporter activity	3/83	21/18337	0	0.001	0	SLC2A1/SLC2A6/SLC2A14	3
MF	GO:0008106	alcohol dehydrogenase (NADP+) activity	3/83	21/18337	0	0.001	0	AKR1C1/AKR1C2/AKR1C3	3
MF	GO:0015149	hexose transmembrane transporter activity	3/83	21/18337	0	0.001	0	SLC2A1/SLC2A6/SLC2A14	3
MF	GO:0072349	modified amino acid transmembrane transporter activity	3/83	21/18337	0	0.001	0	SLC7A11/SLC1A4/ABCC1	3
MF	GO:0015145	monosaccharide transmembrane transporter activity	3/83	23/18337	0	0.002	0	SLC2A1/SLC2A6/SLC2A14	3

MF	GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	3/83	24/18337	0	0.002	0	ALOX12/ALOX15/ALOX15B	3
MF	GO:0031406	carboxylic acid binding	6/83	184/18337	0	0.002	0	AKR1C1/AKR1C2/AKR1C3/NOS2/ALB/EGLN2	6
MF	GO:0051119	sugar transmembrane transporter activity	3/83	25/18337	0	0.002	0	SLC2A1/SLC2A6/SLC2A14	3
MF	GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	5/83	120/18337	0	0.002	0	AKR1C1/AKR1C2/AKR1C3/G6PD/MIOX	5
MF	GO:0008198	ferrous iron binding	3/83	26/18337	0	0.002	0	FTH1/FTL/EGLN2	3

MF	GO:0016628	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	3/83	26/18337	0	0.002	0	AKR1C1/AKR1C2/AKR1C3	3
MF	GO:0008509	anion transmembrane transporter activity	9/83	459/18337	0	0.002	0	SLC7A11/SLC1A4/SLC7A5/SLC2A1/SLC2A6/SLC2A14/SLC38A1/SLC1A5/ABCC1	9
MF	GO:0033293	monocarboxylic acid binding	4/83	71/18337	0	0.002	0	AKR1C1/AKR1C2/AKR1C3/ALB	4
MF	GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	5/83	130/18337	0	0.003	0	AKR1C1/AKR1C2/AKR1C3/G6PD/MIOX	5
MF	GO:0033764	steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	3/83	30/18337	0	0.003	0	AKR1C1/AKR1C2/AKR1C3	3

MF	GO:0016229	steroid dehydrogenase activity	3/83	34/18337	0	0.004	0	AKR1C1/AKR1C2/AKR1C3	3
MF	GO:0015144	carbohydrate transmembrane transporter activity	3/83	37/18337	0	0.005	0	SLC2A1/SLC2A6/SLC2A14	3
MF	GO:0019825	oxygen binding	3/83	39/18337	0	0.005	0	ALB/NOX4/EGLN2	3
MF	GO:0005319	lipid transporter activity	5/83	162/18337	0	0.006	0	SLC7A11/SLC1A4/SLC2A1/SLC1A5/ABCC1	5
MF	GO:0016803	ether hydrolase activity	2/83	10/18337	0	0.006	0	ALOX12/ALOX15	2
MF	GO:0030283	testosterone dehydrogenase [NAD(P)] activity	2/83	10/18337	0	0.006	0	AKR1C1/AKR1C3	2
MF	GO:0004712	protein serine/threonine/tyrosine kinase activity	3/83	44/18337	0	0.007	0.01	AURKA/MAPK3/PRKAA2	3
MF	GO:0016801	hydrolase activity, acting on ether bonds	2/83	11/18337	0	0.007	0.01	ALOX12/ALOX15	2
MF	GO:0140299	small molecule sensor activity	2/83	11/18337	0	0.007	0.01	NOX4/EGLN2	2

MF	GO:0004497	monooxygenase activity	4/83	101/18337	0	0.007	0.01	AKR1C1/AKR1C2/AKR1C3/NOS2	4
MF	GO:1901682	sulfur compound transmembrane transporter activity	3/83	48/18337	0	0.008	0.01	SLC7A11/SLC1A4/ABCC1	3
MF	GO:0004601	peroxidase activity	3/83	53/18337	0	0.011	0.01	PTGS2/GPX2/DUOX1	3
MF	GO:0005080	protein kinase C binding	3/83	54/18337	0	0.011	0.01	HSPB1/SQSTM1/SRC	3
MF	GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	3/83	57/18337	0	0.013	0.01	PTGS2/GPX2/DUOX1	3
MF	GO:0015556	C4-dicarboxylate transmembrane transporter activity	2/83	16/18337	0	0.013	0.01	SLC1A4/SLC1A5	2
MF	GO:0035173	histone kinase activity	2/83	16/18337	0	0.013	0.01	AURKA/PRKAA2	2
MF	GO:0031072	heat shock protein binding	4/83	123/18337	0	0.013	0.01	HSF1/HSPA5/ZFP36/DNAJB6	4
MF	GO:0016627	oxidoreductase activity, acting on the CH-CH group	3/83	59/18337	0	0.013	0.01	AKR1C1/AKR1C2/AKR1C3	3

		of donors							
MF	GO:0022804	active transmembrane transporter activity	6/83	301/18337	0	0.013	0.01	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5/ABCC1	6
MF	GO:0005507	copper ion binding	3/83	60/18337	0	0.014	0.01	MT3/ALB/HAMP	3
MF	GO:0046982	protein heterodimerization activity	6/83	324/18337	0	0.019	0.01	HSF1/CAV1/DDIT3/ATF3/MAFG/AURKA	6
MF	GO:0009055	electron transfer activity	4/83	138/18337	0	0.019	0.01	AIFM2/NCF2/GPX2/NOX4	4
MF	GO:0015291	secondary active transmembrane transporter activity	5/83	239/18337	0	0.024	0.02	SLC7A11/SLC1A4/SLC7A5/SLC38A1/SLC1A5	5
MF	GO:0140272	exogenous protein binding	3/83	77/18337	0.01	0.026	0.02	ALB/TFRC/SLC1A5	3
MF	GO:0005310	dicarboxylic acid transmembrane transporter activity	2/83	30/18337	0.01	0.04	0.03	SLC1A4/SLC1A5	2

MF	GO:0042910	xenobiotic transmembrane transporter activity	2/83	30/18337	0.01	0.04	0.03	SLC2A1/ABCC1	2
MF	GO:0071889	14-3-3 protein binding	2/83	31/18337	0.01	0.042	0.03	ZFP36/DDIT4	2
MF	GO:0030291	protein serine/threonine kinase inhibitor activity	2/83	32/18337	0.01	0.044	0.03	HSPB1/CDKN2A	2
MF	GO:0031625	ubiquitin protein ligase binding	5/83	293/18337	0.01	0.05	0.04	SQSTM1/HSPA5/SRC/PML/AURKA	5
MF	GO:0032182	ubiquitin-like protein binding	3/83	101/18337	0.01	0.05	0.04	HSPB1/SQSTM1/PML	3
MF	GO:0051087	chaperone binding	3/83	101/18337	0.01	0.05	0.04	HSPA5/ALB/DNAJB6	3
MF	GO:0044183	protein folding chaperone	2/83	36/18337	0.01	0.052	0.04	HSPB1/HSPA5	2
MF	GO:0042169	SH2 domain binding	2/83	38/18337	0.01	0.057	0.04	SQSTM1/SRC	2
MF	GO:0044389	ubiquitin-like protein ligase binding	5/83	312/18337	0.01	0.06	0.04	SQSTM1/HSPA5/SRC/PML/AURKA	5

KEGG	hsa04216	Ferroptosis	7/68	41/8101	####	#####	####	SLC7A11/FTH1/FTL/TFRC/STEAP3/ALOX15/ACSL4	7
KEGG	hsa05230	Central carbon metabolism in cancer	8/68	70/8101	####	#####	####	SLC7A5/SLC2A1/G6PD/NRAS/HRAS/SLC1A5/GLS2/MAPK3	8
KEGG	hsa05208	Chemical carcinogenesis - reactive oxygen species	11/68	223/8101	####	2E-04	0	AKR1C1/AKR1C2/AKR1C3/NQO1/SRC/NCF2/NOX1/NOX4/NRAS/HRAS/MAPK3	11
KEGG	hsa04726	Serotonergic synapse	8/68	115/8101	####	3E-04	0	PTGS2/DUSP1/ALOX12/ALOX15/NRAS/HRAS/ALOX15B/MAPK3	8
KEGG	hsa04370	VEGF signaling pathway	6/68	59/8101	####	4E-04	0	HSPB1/SRC/PTGS2/NRAS/HRAS/MAPK3	6

KEGG	hsa00590	Arachidonic acid metabolism	6/68	61/8101	####	4E-04	0	AKR1C3/PTGS2/GPX2/ALOX12/ALOX15/ALOX15B	6
KEGG	hsa05418	Fluid shear stress and atherosclerosis	8/68	139/8101	####	6E-04	0	SQSTM1/NQO1/SRC/CAV1/DUSP1/NCF2/NOX1/PRKAA2	8
KEGG	hsa05219	Bladder cancer	5/68	41/8101	####	6E-04	0	SRC/NRAS/HRAS/MAPK3/CDKN2A	5
KEGG	hsa05417	Lipid and atherosclerosis	9/68	215/8101	####	0.002	0	HSPA5/SRC/NCF2/DDIT3/IL6/NOX1/NRAS/HRAS/MAPK3	9
KEGG	hsa04933	AGE-RAGE signaling pathway in diabetic complications	6/68	100/8101	0	0.004	0	IL6/NOX1/NOX4/NRAS/HRAS/MAPK3	6
KEGG	hsa04625	C-type lectin receptor signaling pathway	6/68	104/8101	0	0.004	0	SRC/PTGS2/IL6/NRAS/HRAS/MAPK3	6

KEGG	hsa05206	MicroRNAs in cancer	10/68	310/8101	0	0.004	0	TP63/PTGS2/DDIT4/STMN1/NRAS/HRAS/GLS2/MAPK3/CDKN2A/ABCC1	10
KEGG	hsa05211	Renal cell carcinoma	5/68	69/8101	0	0.005	0	SLC2A1/NRAS/HRAS/MAPK3/EGLN2	5
KEGG	hsa04066	HIF-1 signaling pathway	6/68	109/8101	0	0.005	0	NOS2/IL6/TFRC/SLC2A1/MAPK3/EGLN2	6
KEGG	hsa01521	EGFR tyrosine kinase inhibitor resistance	5/68	79/8101	0	0.007	0	SRC/IL6/NRAS/HRAS/MAPK3	5
KEGG	hsa05022	Pathways of neurodegeneration - multiple diseases	12/68	476/8101	0	0.007	0	SQSTM1/HSPA5/PTGS2/NOS2/GPX2/DDIT3/IL6/NOX1/NOX4/NRAS/HRAS/MAPK3	12
KEGG	hsa04140	Autophagy - animal	6/68	141/8101	0	0.014	0.01	SQSTM1/DDIT4/NRAS/HRAS/MAPK3/PRKAA2	6

KEGG	hsa05167	Kaposi sarcoma-associated herpesvirus infection	7/68	194/8101	0	0.014	0.01	SRC/ZFP36/PTGS2/IL6/NRAS/HRAS/MAPK3	7
KEGG	hsa01522	Endocrine resistance	5/68	98/8101	0	0.016	0.01	SRC/NRAS/HRAS/MAPK3/CDKN2A	5
KEGG	hsa04921	Oxytocin signaling pathway	6/68	154/8101	0	0.019	0.01	SRC/PTGS2/NRAS/HRAS/MAPK3/PRKAA2	6
KEGG	hsa04150	mTOR signaling pathway	6/68	155/8101	0	0.019	0.01	DDIT4/SLC7A5/NRAS/HRAS/MAPK3/PRKAA2	6
KEGG	hsa04218	Cellular senescence	6/68	156/8101	0	0.019	0.01	SQSTM1/IL6/NRAS/HRAS/MAPK3/CDKN2A	6
KEGG	hsa01523	Antifolate resistance	3/68	31/8101	0	0.021	0.01	IL6/ALOX12/ABCC1	3
KEGG	hsa05221	Acute myeloid leukemia	4/68	67/8101	0	0.022	0.01	PML/NRAS/HRAS/MAPK3	4
KEGG	hsa05166	Human T-cell leukemia virus 1 infection	7/68	222/8101	0	0.022	0.01	ZFP36/IL6/SLC2A1/NRAS/HRAS/MAPK3/CDKN2A	7

KEGG	hsa05163	Human cytomegalovirus infection	7/68	225/8101	0	0.022	0.01	SRC/PTGS2/IL6/NRAS/HRAS/MAPK3/CDKN2A	7
KEGG	hsa04917	Prolactin signaling pathway	4/68	70/8101	0	0.022	0.01	SRC/NRAS/HRAS/MAPK3	4
KEGG	hsa05225	Hepatocellular carcinoma	6/68	168/8101	0	0.022	0.01	NQO1/TXNRD1/NRAS/HRAS/MAPK3/CDKN2A	6
KEGG	hsa04137	Mitophagy - animal	4/68	72/8101	0	0.022	0.01	SQSTM1/SRC/NRAS/HRAS	4
KEGG	hsa05218	Melanoma	4/68	72/8101	0	0.022	0.01	NRAS/HRAS/MAPK3/CDKN2A	4
KEGG	hsa05223	Non-small cell lung cancer	4/68	72/8101	0	0.022	0.01	NRAS/HRAS/MAPK3/CDKN2A	4
KEGG	hsa04115	p53 signaling pathway	4/68	73/8101	0	0.022	0.01	AIFM2/STEAP3/RRM2/CDKN2A	4
KEGG	hsa04919	Thyroid hormone signaling pathway	5/68	121/8101	0	0.022	0.01	SRC/SLC2A1/NRAS/HRAS/MAPK3	5
KEGG	hsa04918	Thyroid hormone synthesis	4/68	75/8101	0	0.022	0.01	HSPA5/ALB/GPX2/DUOX1	4

KEGG	hsa05214	Glioma	4/68	75/8101	0	0.022	0.01	NRAS/HRAS/MAPK3/CDKN2A	4
KEGG	hsa05216	Thyroid cancer	3/68	37/8101	0	0.022	0.01	NRAS/HRAS/MAPK3	3
KEGG	hsa05220	Chronic myeloid leukemia	4/68	76/8101	0	0.022	0.01	NRAS/HRAS/MAPK3/CDKN2A	4
KEGG	hsa05140	Leishmaniasis	4/68	77/8101	0	0.023	0.02	PTGS2/NOS2/NCF2/MAPK3	4
KEGG	hsa04926	Relaxin signaling pathway	5/68	129/8101	0	0.025	0.02	SRC/NOS2/NRAS/HRAS/MAPK3	5
KEGG	hsa05010	Alzheimer disease	9/68	384/8101	0	0.025	0.02	PTGS2/NOS2/DDIT3/IL6/NOX1/NOX4/NRAS/HRAS/MAPK3	9
KEGG	hsa04068	FoxO signaling pathway	5/68	131/8101	0	0.025	0.02	IL6/NRAS/HRAS/MAPK3/PRKAA2	5
KEGG	hsa04012	ErbB signaling pathway	4/68	85/8101	0.01	0.029	0.02	SRC/NRAS/HRAS/MAPK3	4
KEGG	hsa04371	Apelin signaling pathway	5/68	139/8101	0.01	0.031	0.02	NOS2/NRAS/HRAS/MAPK3/PRKAA2	5

KEGG	hsa04540	Gap junction	4/68	88/8101	0.01	0.031	0.02	SRC/NRAS/HRAS/MAPK3	4
KEGG	hsa04912	GnRH signaling pathway	4/68	93/8101	0.01	0.037	0.03	SRC/NRAS/HRAS/MAPK3	4
KEGG	hsa04010	MAPK signaling pathway	7/68	294/8101	0.01	0.054	0.04	HSPB1/DUSP1/DDIT3/STMN1/NRAS/HRAS/MAPK3	7
KEGG	hsa05161	Hepatitis B	5/68	162/8101	0.01	0.054	0.04	SRC/IL6/NRAS/HRAS/MAPK3	5
KEGG	hsa00480	Glutathione metabolism	3/68	58/8101	0.01	0.057	0.04	GPX2/RRM2/G6PD	3
KEGG	hsa05213	Endometrial cancer	3/68	58/8101	0.01	0.057	0.04	NRAS/HRAS/MAPK3	3
KEGG	hsa04730	Long-term depression	3/68	60/8101	0.01	0.06	0.04	NRAS/HRAS/MAPK3	3
KEGG	hsa04978	Mineral absorption	3/68	60/8101	0.01	0.06	0.04	FTH1/MT1G/FTL	3
KEGG	hsa00220	Arginine biosynthesis	2/68	22/8101	0.01	0.06	0.04	NOS2/GLS2	2
KEGG	hsa00140	Steroid hormone biosynthesis	3/68	61/8101	0.01	0.06	0.04	AKR1C1/AKR1C2/AKR1C3	3
KEGG	hsa04213	Longevity regulating pathway - multiple species	3/68	62/8101	0.02	0.062	0.04	NRAS/HRAS/PRKAA2	3

KEGG	hsa04929	GnRH secretion	3/68	64/8101	0.02	0.066	0.04	NRAS/HRAS/MAPK3	3
KEGG	hsa04071	Sphingolipid signaling pathway	4/68	119/8101	0.02	0.069	0.05	NRAS/HRAS/MAPK3/ABCC1	4
KEGG	hsa04720	Long-term potentiation	3/68	67/8101	0.02	0.072	0.05	NRAS/HRAS/MAPK3	3
KEGG	hsa04664	Fc epsilon RI signaling pathway	3/68	68/8101	0.02	0.073	0.05	NRAS/HRAS/MAPK3	3

Supplementary Table 6: Ferroptosis associated lncRNAs.

Ferroptosis associated lncRNAs				
ferrGene	lncRNA	cor	pvalue	Regulation
BECN1	ABALON	0.52906	2.31E-28	postive
CS	ABALON	0.59677	1.88E-37	postive
SLC38A1	ABALON	0.56645	4.02E-33	postive
SP1	ABALON	0.58957	2.21E-36	postive
DNAJB6	AC000123.1	0.52344	1.07E-27	postive
FANCD2	AC002116.2	0.55063	4.91E-31	postive
STMN1	AC002116.2	0.52665	4.48E-28	postive
EGLN2	AC002398.1	0.54417	3.26E-30	postive
OTUB1	AC002398.1	0.5371	2.46E-29	postive
HBA1	AC002398.2	0.72638	1.49E-62	postive
PLIN4	AC002398.2	0.8438	1.37E-102	postive
MUC1	AC003070.1	0.57837	9.05E-35	postive
PTGS2	AC003070.1	0.67439	6.10E-51	postive
PLIN4	AC004130.2	0.57801	1.01E-34	postive
ALOX5	AC004540.1	0.53782	2.01E-29	postive

CA9	AC004540.1	0.52408	9.01E-28	postive
CS	AC004540.1	0.55658	8.31E-32	postive
CYBB	AC004585.1	0.65245	1.00E-46	postive
IFNG	AC004585.1	0.58332	1.78E-35	postive
KRAS	AC004803.1	0.50083	3.85E-25	postive
ABCC1	AC004812.2	0.50867	5.25E-26	postive
OTUB1	AC004812.2	0.51907	3.46E-27	postive
FANCD2	AC004816.1	0.56008	2.87E-32	postive
STMN1	AC004816.1	0.59127	1.24E-36	postive
PCK2	AC004832.5	0.51465	1.11E-26	postive
SCP2	AC004832.5	0.58974	2.09E-36	postive
ATM	AC004908.1	0.58755	4.37E-36	postive
CYBB	AC004921.1	0.61331	5.15E-40	postive
FANCD2	AC004943.2	0.53973	1.17E-29	postive
NRAS	AC004943.2	0.50199	2.88E-25	postive
PIK3CA	AC004943.2	0.5125	1.95E-26	postive
ANO6	AC005034.5	0.54445	3.00E-30	postive
IREB2	AC005034.5	0.54454	2.92E-30	postive
KLHL24	AC005034.5	0.5098	3.93E-26	postive
PIK3CA	AC005034.5	0.53309	7.57E-29	postive
ZEB1	AC005034.5	0.50547	1.19E-25	postive
PLIN4	AC005046.1	0.58305	1.95E-35	postive
HSPB1	AC005076.1	0.52377	9.80E-28	postive
ATG16L1	AC005104.1	0.50262	2.46E-25	postive
ATM	AC005104.1	0.55138	3.94E-31	postive
SETD1B	AC005104.1	0.52081	2.17E-27	postive
ATM	AC005253.1	0.5377	2.08E-29	postive
SETD1B	AC005253.1	0.52516	6.73E-28	postive
SP1	AC005253.1	0.56262	1.32E-32	postive
NF2	AC005261.1	0.52065	2.27E-27	postive

ZNF419	AC005261.1	0.64276	5.67E-45	postive
EGLN2	AC005261.3	0.52106	2.03E-27	postive
ALOX12	AC005288.1	0.52123	1.94E-27	postive
ATG16L1	AC005288.1	0.59963	6.95E-38	postive
ATM	AC005288.1	0.6472	9.08E-46	postive
BACH1	AC005288.1	0.55607	9.68E-32	postive
BECN1	AC005288.1	0.72539	2.61E-62	postive
CHMP5	AC005288.1	0.5451	2.48E-30	postive
CS	AC005288.1	0.53009	1.74E-28	postive
HIF1A	AC005288.1	0.55226	3.03E-31	postive
IREB2	AC005288.1	0.6858	2.79E-53	postive
MAPK1	AC005288.1	0.68514	3.84E-53	postive
MAPK8	AC005288.1	0.57206	6.87E-34	postive
MAPK9	AC005288.1	0.53792	1.95E-29	postive
NRAS	AC005288.1	0.60346	1.80E-38	postive
OXSR1	AC005288.1	0.6207	3.29E-41	postive
PIK3CA	AC005288.1	0.68643	2.06E-53	postive
PRKAA1	AC005288.1	0.52399	9.23E-28	postive
RB1	AC005288.1	0.53321	7.32E-29	postive
SETD1B	AC005288.1	0.64516	2.12E-45	postive
SIRT1	AC005288.1	0.53436	5.32E-29	postive
SNX4	AC005288.1	0.55929	3.65E-32	postive
SP1	AC005288.1	0.74009	4.46E-66	postive
ZEB1	AC005288.1	0.57629	1.77E-34	postive
ZFP69B	AC005288.1	0.53961	1.21E-29	postive
WIPI1	AC005332.6	0.51355	1.48E-26	postive
EGLN2	AC005393.1	0.5097	4.03E-26	postive
BECN1	AC005670.3	0.54141	7.20E-30	postive
ALOX12	AC005696.1	0.52671	4.40E-28	postive
CS	AC005696.1	0.57533	2.42E-34	postive

HBA1	AC005785.1	0.56646	4.01E-33	postive
PLIN4	AC005785.1	0.68341	8.81E-53	postive
ACO1	AC005920.4	0.50947	4.28E-26	postive
GLS2	AC005920.4	0.5066	8.94E-26	postive
EGLN2	AC006213.3	0.57424	3.42E-34	postive
ZNF419	AC006213.4	0.55282	2.56E-31	postive
HELLS	AC006213.5	0.55714	7.02E-32	postive
HSPB1	AC006273.1	0.58796	3.80E-36	postive
ALOX12	AC006435.2	0.50141	3.33E-25	postive
ZNF419	AC007066.2	0.56301	1.17E-32	postive
SOCS1	AC007220.1	0.5154	9.14E-27	postive
ALOX12	AC007406.4	0.52835	2.82E-28	postive
ATG16L1	AC007406.4	0.56596	4.68E-33	postive
ATM	AC007406.4	0.63381	2.08E-43	postive
IREB2	AC007406.4	0.61989	4.47E-41	postive
MAPK1	AC007406.4	0.61261	6.66E-40	postive
MAPK8	AC007406.4	0.50498	1.35E-25	postive
OXSR1	AC007406.4	0.50537	1.22E-25	postive
PIK3CA	AC007406.4	0.55091	4.53E-31	postive
RB1	AC007406.4	0.51266	1.87E-26	postive
SETD1B	AC007406.4	0.58247	2.36E-35	postive
SIRT1	AC007406.4	0.54222	5.72E-30	postive
SP1	AC007406.4	0.66956	5.54E-50	postive
ZEB1	AC007406.4	0.53033	1.63E-28	postive
IREB2	AC007637.1	0.55491	1.37E-31	postive
HRAS	AC007773.1	0.59364	5.54E-37	postive
HSPB1	AC007773.1	0.59254	8.06E-37	postive
ABCC1	AC008074.2	0.50798	6.28E-26	postive
CYBB	AC008105.2	0.55833	4.90E-32	postive
ALOX12	AC008124.1	0.50302	2.22E-25	postive

ATM	AC008124.1	0.50709	7.89E-26	postive
GABPB1	AC008124.1	0.58029	4.83E-35	postive
SP1	AC008124.1	0.55506	1.31E-31	postive
HRAS	AC008443.4	0.53395	5.96E-29	postive
HSPB1	AC008443.4	0.57848	8.71E-35	postive
DPP4	AC008549.1	0.53428	5.43E-29	postive
PANX1	AC008549.1	0.58801	3.74E-36	postive
PEBP1	AC008549.1	0.53272	8.39E-29	postive
HRAS	AC008608.2	0.53479	4.71E-29	postive
HSPB1	AC008608.2	0.55883	4.21E-32	postive
RPL8	AC008608.2	0.51461	1.12E-26	postive
HRAS	AC008610.1	0.61003	1.71E-39	postive
HSPB1	AC008610.1	0.66542	3.57E-49	postive
NOS2	AC008708.1	0.57717	1.33E-34	postive
ZNF419	AC008735.2	0.51707	5.88E-27	postive
SETD1B	AC008735.4	0.51575	8.32E-27	postive
DUOX2	AC008736.1	0.86698	1.44E-114	postive
MUC1	AC008736.1	0.64536	1.95E-45	postive
IREB2	AC008764.2	0.52463	7.77E-28	postive
MAPK1	AC008764.2	0.50908	4.73E-26	postive
ATM	AC008770.3	0.53258	8.73E-29	postive
IREB2	AC008770.3	0.52636	4.85E-28	postive
EGLN2	AC008915.2	0.55933	3.61E-32	postive
HRAS	AC008915.2	0.52564	5.89E-28	postive
SLC40A1	AC008966.1	0.50753	7.03E-26	postive
CYBB	AC008972.2	0.50731	7.46E-26	postive
EGLN2	AC009065.4	0.52286	1.25E-27	postive
HRAS	AC009065.4	0.62825	1.84E-42	postive
HSPB1	AC009065.4	0.59141	1.19E-36	postive
ABCC1	AC009120.2	0.5007	3.98E-25	postive

ABCC1	AC009133.1	0.50497	1.35E-25	postive
HRAS	AC009275.1	0.52372	9.94E-28	postive
HSPB1	AC009275.1	0.54035	9.76E-30	postive
KRAS	AC009318.2	0.50943	4.32E-26	postive
HRAS	AC009686.2	0.54023	1.01E-29	postive
HSPB1	AC009686.2	0.61578	2.07E-40	postive
ATM	AC010186.3	0.53349	6.79E-29	postive
PCK2	AC010205.1	0.54238	5.46E-30	postive
ZNF419	AC010326.3	0.60006	5.97E-38	postive
PCK2	AC010336.2	0.59258	7.95E-37	postive
ATG4D	AC010503.4	0.53699	2.53E-29	postive
DPP4	AC010531.5	0.58194	2.81E-35	postive
HRAS	AC010531.6	0.54206	5.98E-30	postive
HSPB1	AC010531.6	0.61488	2.89E-40	postive
RGS4	AC010547.2	0.5577	5.93E-32	postive
HRAS	AC010618.3	0.53364	6.50E-29	postive
ALOX12	AC010834.3	0.51908	3.45E-27	postive
ATM	AC010834.3	0.61861	7.22E-41	postive
IREB2	AC010834.3	0.54908	7.78E-31	postive
MAPK1	AC010834.3	0.51021	3.53E-26	postive
MAPK8	AC010834.3	0.50154	3.22E-25	postive
PIK3CA	AC010834.3	0.53134	1.23E-28	postive
SETD1B	AC010834.3	0.58973	2.09E-36	postive
SP1	AC010834.3	0.62407	9.15E-42	postive
EGLN2	AC010969.2	0.50789	6.42E-26	postive
EGLN2	AC011445.1	0.61355	4.71E-40	postive
ABCC1	AC011462.4	0.51502	1.01E-26	postive
EGLN2	AC011468.1	0.57506	2.64E-34	postive
ZNF419	AC011468.1	0.59244	8.34E-37	postive
HBA1	AC011472.4	0.52151	1.80E-27	postive

DUOX1	AC011477.1	0.51201	2.21E-26	postive
SLC2A1	AC012615.1	0.55965	3.28E-32	postive
ALOX12	AC012615.6	0.52479	7.43E-28	postive
SETD1B	AC012615.6	0.50487	1.39E-25	postive
HSF1	AC012676.1	0.54683	1.50E-30	postive
RPL8	AC012676.1	0.51927	3.28E-27	postive
CYBB	AC015819.1	0.55461	1.50E-31	postive
ATM	AC015849.3	0.53781	2.01E-29	postive
SETD1B	AC015849.3	0.575	2.68E-34	postive
GABPB1	AC015871.3	0.51861	3.91E-27	postive
HRAS	AC015912.3	0.62917	1.28E-42	postive
HSPB1	AC015912.3	0.67763	1.35E-51	postive
PTGS2	AC015922.2	0.57361	4.20E-34	postive
GABPB1	AC016355.1	0.5816	3.14E-35	postive
HSPB1	AC016405.3	0.53295	7.89E-29	postive
RPL8	AC016405.3	0.60644	6.22E-39	postive
PROM2	AC016590.3	0.52131	1.90E-27	postive
RGS4	AC016735.1	0.64147	9.59E-45	postive
DRD4	AC018638.7	0.74099	2.57E-66	postive
FANCD2	AC018690.1	0.50442	1.56E-25	postive
OXSR1	AC018690.1	0.51022	3.52E-26	postive
ATF4	AC018904.1	0.50089	3.79E-25	postive
PLIN4	AC019197.1	0.5107	3.11E-26	postive
DUOX1	AC020907.4	0.51146	2.56E-26	postive
GLS2	AC020978.4	0.60354	1.75E-38	postive
PROM2	AC021016.1	0.5191	3.43E-27	postive
FANCD2	AC022007.1	0.55393	1.85E-31	postive
SP1	AC022150.2	0.51953	3.06E-27	postive
ZNF419	AC022150.2	0.54776	1.14E-30	postive
KRAS	AC022364.1	0.61822	8.35E-41	postive

ATF4	AC024060.2	0.53034	1.63E-28	postive
ATM	AC024075.1	0.51256	1.92E-26	postive
IREB2	AC024075.1	0.5815	3.25E-35	postive
MAPK1	AC024075.1	0.548	1.07E-30	postive
SETD1B	AC024075.1	0.52642	4.77E-28	postive
SP1	AC024075.1	0.51543	9.07E-27	postive
HRAS	AC025048.4	0.6505	2.29E-46	postive
HSPB1	AC025048.4	0.56465	7.03E-33	postive
HIF1A	AC026356.1	0.56214	1.53E-32	postive
SLC38A1	AC026356.1	0.55378	1.93E-31	postive
CDKN2A	AC026401.3	0.61101	1.19E-39	postive
FANCD2	AC026401.3	0.58273	2.17E-35	postive
G6PD	AC026401.3	0.53328	7.18E-29	postive
MAPK3	AC026401.3	0.60905	2.44E-39	postive
PHKG2	AC026401.3	0.55034	5.36E-31	postive
SLC1A5	AC026401.3	0.59242	8.39E-37	postive
STMN1	AC026401.3	0.64747	8.13E-46	postive
MT1G	AC026461.2	0.80386	6.07E-86	postive
EGLN2	AC026803.1	0.55259	2.75E-31	postive
HRAS	AC026803.1	0.51733	5.49E-27	postive
HRAS	AC026979.2	0.58362	1.62E-35	postive
HSPB1	AC026979.2	0.62806	1.97E-42	postive
ATM	AC027097.1	0.50668	8.76E-26	postive
EGLN2	AC027644.3	0.6068	5.47E-39	postive
HRAS	AC027644.3	0.62464	7.36E-42	postive
HSPB1	AC027644.3	0.56635	4.15E-33	postive
GABPB1	AC034236.2	0.50839	5.65E-26	postive
PEBP1	AC036176.1	0.50146	3.28E-25	postive
ATM	AC037459.2	0.59719	1.63E-37	postive
PIK3CA	AC037459.2	0.50822	5.91E-26	postive

SP1	AC037459.2	0.53073	1.46E-28	postive
EGLN2	AC046143.2	0.59922	8.01E-38	postive
HRAS	AC046143.2	0.5743	3.36E-34	postive
GCLC	AC055720.2	0.50399	1.74E-25	postive
ATF4	AC055822.1	0.50091	3.77E-25	postive
SP1	AC055855.1	0.51489	1.04E-26	postive
ABCC1	AC060766.3	0.52154	1.79E-27	postive
CAV1	AC060766.3	0.53333	7.08E-29	postive
ABCC1	AC060766.6	0.57982	5.63E-35	postive
CAV1	AC060766.6	0.55602	9.83E-32	postive
PML	AC060766.6	0.51908	3.45E-27	postive
DUOX1	AC061975.6	0.51292	1.75E-26	postive
ASNS	AC061992.2	0.53754	2.17E-29	postive
BECN1	AC067852.2	0.67885	7.65E-52	postive
FANCD2	AC068756.1	0.51627	7.27E-27	postive
HRAS	AC069281.2	0.56093	2.21E-32	postive
HSPB1	AC069281.2	0.60437	1.30E-38	postive
ANO6	AC073046.1	0.50255	2.50E-25	postive
ATM	AC073046.1	0.6218	2.17E-41	postive
BACH1	AC073046.1	0.50901	4.81E-26	postive
IREB2	AC073046.1	0.64447	2.81E-45	postive
MAPK1	AC073046.1	0.61606	1.87E-40	postive
PIK3CA	AC073046.1	0.58572	8.03E-36	postive
PRKAA1	AC073046.1	0.50502	1.34E-25	postive
SETD1B	AC073046.1	0.5983	1.10E-37	postive
SP1	AC073046.1	0.61699	1.32E-40	postive
ZEB1	AC073046.1	0.51945	3.13E-27	postive
SETD1B	AC073575.2	0.5053	1.24E-25	postive
EGLN2	AC073896.4	0.54227	5.64E-30	postive
HRAS	AC073896.4	0.65339	6.73E-47	postive

HSPB1	AC073896.4	0.60132	3.84E-38	postive
EGLN2	AC074212.1	0.58985	2.01E-36	postive
RPL8	AC074212.1	0.52159	1.76E-27	postive
HSPB1	AC078846.1	0.52034	2.47E-27	postive
DRD4	AC078909.2	0.54586	1.99E-30	postive
DPP4	AC078993.1	0.52838	2.79E-28	postive
PANX1	AC078993.1	0.55542	1.18E-31	postive
CYBB	AC079015.1	0.64377	3.76E-45	postive
PML	AC079015.1	0.51392	1.35E-26	postive
IL33	AC079305.1	0.50241	2.59E-25	postive
SCP2	AC079848.1	0.51076	3.07E-26	postive
ATM	AC084018.1	0.51463	1.12E-26	postive
SETD1B	AC084018.1	0.61281	6.20E-40	postive
SP1	AC084018.1	0.51342	1.54E-26	postive
ULK1	AC084018.1	0.55328	2.24E-31	postive
SLC1A5	AC087501.4	0.56348	1.01E-32	postive
CHMP6	AC087741.2	0.55983	3.10E-32	postive
HRAS	AC087741.2	0.5163	7.21E-27	postive
PANX1	AC090150.1	0.50015	4.56E-25	postive
GABPB1	AC090517.2	0.57653	1.64E-34	postive
ATG7	AC090559.1	0.50981	3.92E-26	postive
CYBB	AC090559.1	0.82545	2.04E-94	postive
HIF1A	AC090559.1	0.58643	6.35E-36	postive
JDP2	AC090559.1	0.52982	1.88E-28	postive
PML	AC090559.1	0.56932	1.64E-33	postive
RB1	AC090559.1	0.51851	4.01E-27	postive
TLR4	AC090559.1	0.62506	6.28E-42	postive
YWHAE	AC090617.5	0.53894	1.46E-29	postive
ATM	AC091057.1	0.5134	1.54E-26	postive
ELAVL1	AC091057.1	0.50707	7.92E-26	postive

FANCD2	AC091057.1	0.76357	1.18E-72	postive
HELLS	AC091057.1	0.6887	6.82E-54	postive
HMGB1	AC091057.1	0.5581	5.24E-32	postive
MAPK1	AC091057.1	0.52123	1.94E-27	postive
MAPK8	AC091057.1	0.50619	9.91E-26	postive
OXSR1	AC091057.1	0.52476	7.50E-28	postive
RRM2	AC091057.1	0.5908	1.46E-36	postive
SETD1B	AC091057.1	0.54959	6.69E-31	postive
SP1	AC091057.1	0.60494	1.07E-38	postive
STMN1	AC091057.1	0.63241	3.62E-43	postive
VEGFA	AC091057.1	0.52581	5.64E-28	postive
YY1AP1	AC091057.1	0.51252	1.94E-26	postive
HSPB1	AC091488.1	0.50995	3.78E-26	postive
NQO1	AC092115.3	0.70426	2.64E-57	postive
ABCC1	AC092118.1	0.544	3.42E-30	postive
NF2	AC092171.2	0.53923	1.34E-29	postive
LPCAT3	AC092941.1	0.53671	2.75E-29	postive
DUOX2	AC093001.1	0.55818	5.12E-32	postive
PROM2	AC093010.2	0.53348	6.80E-29	postive
ATM	AC093227.1	0.52927	2.18E-28	postive
MAPK1	AC093227.1	0.51239	2.01E-26	postive
MAPK8	AC093227.1	0.58043	4.61E-35	postive
SIRT1	AC093227.1	0.52673	4.39E-28	postive
SP1	AC093227.1	0.55771	5.92E-32	postive
ZNF419	AC093227.1	0.51112	2.79E-26	postive
EPAS1	AC093278.2	0.55176	3.52E-31	postive
ZEB1	AC093278.2	0.51483	1.06E-26	postive
IREB2	AC093752.2	0.55697	7.39E-32	postive
NRAS	AC098484.1	0.55466	1.48E-31	postive
SCP2	AC099508.2	0.52984	1.87E-28	postive

ATG3	AC099850.3	0.53013	1.72E-28	postive
ATG5	AC099850.3	0.50103	3.66E-25	postive
AURKA	AC099850.3	0.51376	1.40E-26	postive
ELAVL1	AC099850.3	0.54417	3.26E-30	postive
FANCD2	AC099850.3	0.73169	6.82E-64	postive
HELLS	AC099850.3	0.63885	2.77E-44	postive
HMGB1	AC099850.3	0.50816	5.99E-26	postive
MAPK1	AC099850.3	0.51511	9.84E-27	postive
NRAS	AC099850.3	0.61429	3.59E-40	postive
OXSR1	AC099850.3	0.54092	8.30E-30	postive
PIK3CA	AC099850.3	0.5439	3.52E-30	postive
RRM2	AC099850.3	0.71951	7.17E-61	postive
SLC1A5	AC099850.3	0.52483	7.36E-28	postive
SP1	AC099850.3	0.54085	8.46E-30	postive
STMN1	AC099850.3	0.64402	3.39E-45	postive
ZFP69B	AC099850.3	0.5782	9.54E-35	postive
HBA1	AC100793.4	0.65826	8.30E-48	postive
PLIN4	AC100793.4	0.79653	2.62E-83	postive
HBA1	AC104463.2	0.54148	7.07E-30	postive
PLIN4	AC104463.2	0.59676	1.89E-37	postive
ATM	AC104532.2	0.5378	2.01E-29	postive
SIRT1	AC104532.2	0.50509	1.31E-25	postive
SP1	AC104532.2	0.50274	2.38E-25	postive
MT3	AC105118.1	0.60852	2.95E-39	postive
PHKG2	AC106820.3	0.50731	7.46E-26	postive
PLIN4	AC106897.1	0.52468	7.66E-28	postive
MAPK1	AC107027.3	0.52528	6.50E-28	postive
SNX4	AC107027.3	0.50186	2.97E-25	postive
SP1	AC107027.3	0.53905	1.42E-29	postive
SLC38A1	AC107959.3	0.57992	5.46E-35	postive

ATM	AC108010.1	0.57129	8.79E-34	postive
IREB2	AC108010.1	0.62464	7.37E-42	postive
PIK3CA	AC108010.1	0.5488	8.45E-31	postive
SETD1B	AC108010.1	0.52307	1.18E-27	postive
SP1	AC108010.1	0.53726	2.35E-29	postive
ZEB1	AC108010.1	0.52342	1.08E-27	postive
EGLN2	AC108047.1	0.5216	1.76E-27	postive
HRAS	AC108047.1	0.55151	3.79E-31	postive
HSPB1	AC108047.1	0.55564	1.10E-31	postive
CYBB	AC108134.3	0.61385	4.22E-40	postive
ATM	AC108449.2	0.55891	4.10E-32	postive
IREB2	AC108449.2	0.60294	2.17E-38	postive
MAPK1	AC108449.2	0.53321	7.33E-29	postive
PIK3CA	AC108449.2	0.60324	1.95E-38	postive
RB1	AC108449.2	0.52305	1.19E-27	postive
SP1	AC108449.2	0.53559	3.76E-29	postive
ZEB1	AC108449.2	0.54695	1.45E-30	postive
IL6	AC108451.2	0.54134	7.35E-30	postive
KRAS	AC108451.2	0.54812	1.03E-30	postive
ABCC1	AC108463.2	0.52951	2.05E-28	postive
VLDLR	AC108463.2	0.51933	3.23E-27	postive
EGLN2	AC108673.3	0.52388	9.51E-28	postive
HRAS	AC109322.1	0.62026	3.88E-41	postive
HSF1	AC109322.1	0.55663	8.18E-32	postive
HSPB1	AC109322.1	0.63779	4.25E-44	postive
RPL8	AC109322.1	0.74472	2.57E-67	postive
ATM	AC109460.2	0.60407	1.45E-38	postive
IREB2	AC109460.2	0.51523	9.54E-27	postive
PIK3CA	AC109460.2	0.53848	1.66E-29	postive
PRKAA1	AC109460.2	0.55828	4.96E-32	postive

SETD1B	AC109460.2	0.58114	3.66E-35	postive
SP1	AC109460.2	0.56894	1.84E-33	postive
CYBB	AC110995.1	0.5596	3.32E-32	postive
OXSR1	AC112220.2	0.52612	5.18E-28	postive
EGLN2	AC112491.1	0.59673	1.91E-37	postive
WIPI2	AC113145.1	0.55936	3.58E-32	postive
ABCC1	AC116351.1	0.69181	1.47E-54	postive
SLC38A1	AC116351.1	0.56806	2.43E-33	postive
TP53	AC116914.2	0.50028	4.42E-25	postive
HRAS	AC117386.2	0.50664	8.83E-26	postive
HSPB1	AC117386.2	0.50028	4.41E-25	postive
ZNF419	AC120053.1	0.54466	2.83E-30	postive
ELAVL1	AC124045.1	0.51968	2.94E-27	postive
DDIT3	AC124798.1	0.50175	3.05E-25	postive
SLC38A1	AC124798.1	0.52833	2.83E-28	postive
SP1	AC125257.1	0.50473	1.44E-25	postive
HELLS	AC127024.4	0.5489	8.19E-31	postive
SETD1B	AC127024.4	0.55511	1.30E-31	postive
SP1	AC127024.4	0.50912	4.68E-26	postive
ATF4	AC127024.5	0.50169	3.10E-25	postive
FANCD2	AC127024.5	0.5109	2.95E-26	postive
ZNF419	AC127024.5	0.52576	5.71E-28	postive
CS	AC127521.1	0.51293	1.74E-26	postive
PROM2	AC127521.1	0.50076	3.92E-25	postive
RGS4	AC127521.1	0.56282	1.24E-32	postive
SLC38A1	AC129510.1	0.50651	9.14E-26	postive
SP1	AC129510.1	0.55899	4.01E-32	postive
HRAS	AC131009.3	0.56408	8.40E-33	postive
HSPB1	AC131009.3	0.62876	1.50E-42	postive
FANCD2	AC132807.2	0.50794	6.33E-26	postive

HELLS	AC132938.1	0.50734	7.40E-26	postive
ALOX5	AC133644.1	0.52133	1.89E-27	postive
IREB2	AC135050.5	0.53287	8.05E-29	postive
PLIN4	AC135507.1	0.54932	7.24E-31	postive
SCP2	AC137056.1	0.5089	4.96E-26	postive
ATM	AC138028.4	0.55312	2.35E-31	postive
EGLN2	AC138207.2	0.51184	2.31E-26	postive
HRAS	AC138207.2	0.56594	4.71E-33	postive
CAV1	AC138207.4	0.51903	3.50E-27	postive
CYBB	AC138207.4	0.55847	4.69E-32	postive
PML	AC138207.4	0.58374	1.55E-35	postive
CYBB	AC138207.5	0.70111	1.35E-56	postive
PML	AC138207.5	0.60056	5.02E-38	postive
GPX4	AC138696.2	0.56595	4.71E-33	postive
HSPB1	AC138696.2	0.53537	4.00E-29	postive
CHMP6	AC139530.1	0.58514	9.76E-36	postive
HRAS	AC139530.1	0.55539	1.19E-31	postive
ATM	AC145098.1	0.56335	1.05E-32	postive
CAPG	AC145098.1	0.56327	1.08E-32	postive
CYBB	AC145098.1	0.78164	2.89E-78	postive
PML	AC145098.1	0.54132	7.40E-30	postive
TLR4	AC145098.1	0.52758	3.47E-28	postive
HELLS	AC145207.5	0.50895	4.89E-26	postive
SRXN1	AC145207.8	0.59598	2.47E-37	postive
TXNRD1	AC145207.8	0.56178	1.71E-32	postive
PLIN4	AC145423.1	0.57336	4.54E-34	postive
DPP4	AC231981.1	0.51473	1.09E-26	postive
ALOX12	AC232271.1	0.5026	2.47E-25	postive
ATM	AC232271.1	0.50754	7.02E-26	postive
SP1	AC232271.1	0.51633	7.15E-27	postive

ATM	AC243960.1	0.56948	1.55E-33	postive
CYBB	AC243960.1	0.52612	5.17E-28	postive
IFNG	AC243960.1	0.5842	1.33E-35	postive
ATG4D	AC245041.1	0.50949	4.26E-26	postive
DUOX2	AC245041.1	0.60043	5.25E-38	postive
MUC1	AC245041.1	0.50088	3.80E-25	postive
ABCC1	AC245041.2	0.63704	5.75E-44	postive
PROM2	AC245041.2	0.73985	5.15E-66	postive
ABCC1	AF131215.6	0.59627	2.23E-37	postive
PROM2	AF131215.6	0.53083	1.42E-28	postive
CAV1	AGAP2-AS1	0.52163	1.74E-27	postive
HIC1	AGAP2-AS1	0.52543	6.24E-28	postive
PLIN4	AGAP2-AS1	0.64472	2.53E-45	postive
ATM	AL031600.1	0.51378	1.40E-26	postive
SETD1B	AL031600.1	0.56008	2.87E-32	postive
ATM	AL031714.1	0.58216	2.61E-35	postive
FBXW7	AL031714.1	0.50412	1.68E-25	postive
SETD1B	AL031714.1	0.56262	1.32E-32	postive
SP1	AL031714.1	0.54927	7.36E-31	postive
NRAS	AL031985.3	0.53828	1.76E-29	postive
ZFP69B	AL031985.3	0.84786	1.54E-104	postive
AKR1C2	AL033397.1	0.50114	3.56E-25	postive
SRXN1	AL033397.1	0.50646	9.25E-26	postive
TXNRD1	AL033397.1	0.5462	1.80E-30	postive
ATF4	AL035071.1	0.51579	8.24E-27	postive
OTUB1	AL035071.1	0.52049	2.37E-27	postive
SLC1A5	AL035446.1	0.51084	3.00E-26	postive
VLDLR	AL035446.1	0.64855	5.17E-46	postive
EGLN2	AL035461.2	0.53252	8.89E-29	postive
FANCD2	AL035461.2	0.54009	1.05E-29	postive

NF2	AL035461.2	0.52546	6.20E-28	postive
SLC1A5	AL035461.2	0.53832	1.74E-29	postive
STMN1	AL035461.2	0.58375	1.55E-35	postive
PROM2	AL049555.1	0.6162	1.77E-40	postive
PROM2	AL049629.1	0.55574	1.07E-31	postive
ATM	AL049840.2	0.56877	1.94E-33	postive
FBXW7	AL049840.2	0.51971	2.92E-27	postive
SETD1B	AL049840.2	0.50535	1.23E-25	postive
ATG16L1	AL049840.3	0.51045	3.32E-26	postive
MAPK1	AL049840.3	0.55042	5.23E-31	postive
ATG16L1	AL049840.4	0.50653	9.09E-26	postive
ATM	AL049840.4	0.51438	1.19E-26	postive
MAPK1	AL049840.4	0.54306	4.49E-30	postive
SETD1B	AL049840.4	0.56626	4.27E-33	postive
FANCD2	AL050341.2	0.51293	1.74E-26	postive
GABPB1	AL050341.2	0.58897	2.70E-36	postive
STMN1	AL050341.2	0.52796	3.13E-28	postive
DRD4	AL109615.3	0.61869	7.01E-41	postive
ALOX12	AL118506.1	0.51359	1.47E-26	postive
IREB2	AL118506.1	0.54363	3.81E-30	postive
PIK3CA	AL118506.1	0.53224	9.61E-29	postive
SP1	AL118506.1	0.50475	1.43E-25	postive
PLIN4	AL118558.3	0.62818	1.88E-42	postive
PLIN4	AL118558.4	0.51479	1.07E-26	postive
EGLN2	AL121832.2	0.55757	6.17E-32	postive
RPL8	AL121832.2	0.5652	5.94E-33	postive
DUOX2	AL122035.1	0.51612	7.54E-27	postive
HIF1A	AL122035.1	0.67391	7.61E-51	postive
IREB2	AL132639.2	0.52598	5.38E-28	postive
ATM	AL132989.1	0.56574	5.02E-33	postive

IREB2	AL132989.1	0.50774	6.68E-26	postive
SETD1B	AL132989.1	0.53182	1.08E-28	postive
SP1	AL132989.1	0.57652	1.64E-34	postive
ALOX12	AL133355.1	0.53156	1.16E-28	postive
ATG4D	AL133355.1	0.51419	1.25E-26	postive
CS	AL133355.1	0.59318	6.48E-37	postive
SP1	AL133355.1	0.54659	1.61E-30	postive
CYBB	AL133371.2	0.7208	3.50E-61	postive
PML	AL133371.2	0.52076	2.20E-27	postive
TLR4	AL133371.2	0.50235	2.63E-25	postive
SOCS1	AL137186.2	0.51451	1.15E-26	postive
PLIN4	AL139260.1	0.67986	4.74E-52	postive
ZNF419	AL139287.1	0.51427	1.23E-26	postive
DUOX1	AL139288.1	0.56458	7.20E-33	postive
ALOX12	AL139349.1	0.55751	6.28E-32	postive
ATM	AL157392.3	0.51111	2.80E-26	postive
SETD1B	AL157392.3	0.56098	2.18E-32	postive
SP1	AL157392.3	0.60322	1.96E-38	postive
YY1AP1	AL157392.3	0.5252	6.66E-28	postive
ZNF419	AL157392.3	0.51417	1.26E-26	postive
VLDLR	AL157394.1	0.57297	5.14E-34	postive
PCK2	AL161668.4	0.60476	1.14E-38	postive
SCP2	AL161668.4	0.53755	2.16E-29	postive
EGLN2	AL161729.3	0.53983	1.13E-29	postive
PRKAA2	AL163953.1	0.51591	7.99E-27	postive
IREB2	AL353804.1	0.50498	1.35E-25	postive
PIK3CA	AL353804.1	0.51191	2.27E-26	postive
SIRT1	AL353804.1	0.54839	9.50E-31	postive
SP1	AL353804.1	0.55332	2.21E-31	postive
IREB2	AL354733.3	0.51057	3.22E-26	postive

SETD1B	AL354733.3	0.50103	3.66E-25	postive
SIRT1	AL354733.3	0.51846	4.06E-27	postive
ABCC1	AL354836.1	0.537	2.53E-29	postive
PROM2	AL354836.1	0.51755	5.17E-27	postive
FANCD2	AL355488.1	0.54533	2.32E-30	postive
HELLS	AL355488.1	0.50658	8.97E-26	postive
HRAS	AL357079.1	0.51068	3.13E-26	postive
VLDLR	AL359076.1	0.52205	1.56E-27	postive
HNF4A	AL359915.1	0.51869	3.83E-27	postive
ALOX12	AL360181.2	0.51835	4.19E-27	postive
SETD1B	AL360181.2	0.5533	2.22E-31	postive
SIRT1	AL360181.2	0.5208	2.18E-27	postive
SP1	AL360181.2	0.50124	3.47E-25	postive
KRAS	AL365226.1	0.56975	1.43E-33	postive
ATM	AL365361.1	0.62345	1.16E-41	postive
PROM2	AL390719.2	0.53339	6.98E-29	postive
HSPB1	AL391056.1	0.55074	4.77E-31	postive
RPL8	AL391056.1	0.57612	1.87E-34	postive
GOT1	AL391684.1	0.667	1.76E-49	postive
HRAS	AL441992.1	0.50164	3.14E-25	postive
IREB2	AL450326.1	0.51805	4.54E-27	postive
SNX4	AL450326.1	0.51134	2.64E-26	postive
TXNRD1	AL512353.1	0.51782	4.82E-27	postive
NOX1	AL591686.1	0.81151	8.05E-89	postive
DRD4	AL596223.2	0.61098	1.21E-39	postive
SLC2A6	AL596223.2	0.50683	8.42E-26	postive
VLDLR	AL596244.1	0.50889	4.96E-26	postive
HBA1	AL596442.2	0.59361	5.59E-37	postive
PLIN4	AL596442.2	0.63257	3.38E-43	postive
FANCD2	AL606489.1	0.57292	5.23E-34	postive

SP1	AL606489.1	0.52591	5.48E-28	postive
STMN1	AL606489.1	0.50753	7.04E-26	postive
YY1AP1	AL606489.1	0.57534	2.40E-34	postive
ABCC1	AL607028.1	0.52984	1.87E-28	postive
PROM2	AL607028.1	0.52004	2.67E-27	postive
ATG4D	AL645608.7	0.51192	2.27E-26	postive
PROM2	AL645608.7	0.52328	1.12E-27	postive
GABPB1	AL662844.4	0.51268	1.86E-26	postive
ATF4	AL671710.1	0.55811	5.23E-32	postive
MUC1	AL691482.3	0.53746	2.22E-29	postive
PTGS2	AL691482.3	0.65631	1.93E-47	postive
IREB2	AL731577.2	0.55861	4.50E-32	postive
KLHL24	AL731577.2	0.50118	3.52E-25	postive
SIRT1	AL731577.2	0.53459	4.98E-29	postive
SNX4	AL731577.2	0.52183	1.65E-27	postive
ATM	ANKRD10-IT1	0.58012	5.12E-35	postive
SETD1B	ANKRD10-IT1	0.52637	4.84E-28	postive
SP1	ANKRD10-IT1	0.57892	7.56E-35	postive
ATG4D	AP000757.1	0.51478	1.08E-26	postive
CS	AP000757.1	0.57505	2.64E-34	postive
ABCC1	AP000759.1	0.5103	3.46E-26	postive
OTUB1	AP000873.1	0.51101	2.87E-26	postive
EGLN2	AP000892.3	0.57234	6.28E-34	postive
RPL8	AP000892.3	0.57461	3.04E-34	postive
EPAS1	AP001189.3	0.54923	7.43E-31	postive
ZEB1	AP001189.3	0.54209	5.92E-30	postive
PLIN4	AP001437.1	0.5639	8.89E-33	postive
ABCC1	AP001453.2	0.53496	4.49E-29	postive
OTUB1	AP001453.2	0.50137	3.36E-25	postive
PROM2	AP001453.2	0.5174	5.38E-27	postive

SLC38A1	AP001453.2	0.5311	1.32E-28	postive
EGLN2	AP001505.1	0.58212	2.65E-35	postive
HRAS	AP001505.1	0.56066	2.41E-32	postive
VLDLR	AP002336.2	0.53055	1.54E-28	postive
EGLN2	AP002360.1	0.51069	3.12E-26	postive
HRAS	AP002360.1	0.60222	2.80E-38	postive
HSPB1	AP002360.1	0.50733	7.42E-26	postive
CHMP6	AP002748.4	0.50674	8.62E-26	postive
CYBB	AP002954.1	0.74975	1.07E-68	postive
IFNG	AP002954.1	0.53851	1.65E-29	postive
HRAS	AP003068.1	0.59766	1.38E-37	postive
HSPB1	AP003068.1	0.64727	8.84E-46	postive
RPL8	AP003068.1	0.5349	4.57E-29	postive
TXNRD1	AP003119.1	0.51974	2.89E-27	postive
DDIT3	AP003171.1	0.52404	9.11E-28	postive
RPL8	AP003352.1	0.53311	7.55E-29	postive
ATM	AP003392.1	0.59867	9.70E-38	postive
DUOX2	AP003392.1	0.52863	2.60E-28	postive
PIK3CA	AP003392.1	0.54102	8.06E-30	postive
SETD1B	AP003392.1	0.54495	2.60E-30	postive
SP1	AP003392.1	0.54367	3.76E-30	postive
HRAS	AP003419.3	0.50421	1.64E-25	postive
EGLN2	AP004609.3	0.56943	1.58E-33	postive
SP1	AP005899.1	0.56932	1.63E-33	postive
ACVR1B	AP006621.4	0.50088	3.80E-25	postive
DUOX2	AP006621.4	0.61093	1.23E-39	postive
MUC1	AP006621.4	0.5195	3.09E-27	postive
HRAS	ARF4-AS1	0.55678	7.83E-32	postive
HSPB1	ARF4-AS1	0.58123	3.56E-35	postive
RPL8	ARF4-AS1	0.53719	2.40E-29	postive

OTUB1	ARRDC1-AS1	0.51728	5.56E-27	postive
NRAS	ATP1A1-AS1	0.55147	3.83E-31	postive
PLIN4	ATP6V0E2-AS1	0.50227	2.68E-25	postive
NF2	BACE1-AS	0.54105	7.99E-30	postive
OTUB1	BACE1-AS	0.54512	2.47E-30	postive
HELLS	C1orf220	0.56767	2.74E-33	postive
ATG16L1	C2orf49-DT	0.5005	4.18E-25	postive
ATG16L1	CAPN10-DT	0.50171	3.08E-25	postive
SOCS1	CCR5AS	0.59525	3.18E-37	postive
ABCC1	CD27-AS1	0.55177	3.51E-31	postive
CS	CD27-AS1	0.50685	8.38E-26	postive
ISCU	CD27-AS1	0.50063	4.05E-25	postive
HRAS	CH17-340M24.3	0.57157	8.02E-34	postive
PML	CHROMR	0.53763	2.12E-29	postive
ATM	CR936218.1	0.62354	1.12E-41	postive
IREB2	CR936218.1	0.50667	8.77E-26	postive
MAPK1	CR936218.1	0.51702	5.96E-27	postive
PIK3CA	CR936218.1	0.52779	3.28E-28	postive
PRKAA1	CR936218.1	0.5092	4.59E-26	postive
SETD1B	CR936218.1	0.59726	1.59E-37	postive
SP1	CR936218.1	0.59394	4.99E-37	postive
ISCU	CRIM1-DT	0.53047	1.57E-28	postive
CS	CTBP1-DT	0.51657	6.70E-27	postive
MAPK1	CTBP1-DT	0.51962	2.99E-27	postive
SP1	CTBP1-DT	0.55536	1.20E-31	postive
HRAS	CYTOR	0.58667	5.86E-36	postive
HSPB1	CYTOR	0.54505	2.52E-30	postive
SCP2	DHRS4-AS1	0.55299	2.44E-31	postive
FANCD2	DLEU2	0.52661	4.53E-28	postive
HELLS	DLEU2	0.53175	1.10E-28	postive

HMGB1	DLEU2	0.50118	3.52E-25	postive
EGLN2	DM1-AS	0.51006	3.67E-26	postive
OTUB1	DNAJC9-AS1	0.51232	2.05E-26	postive
ANO6	EBLN3P	0.51562	8.61E-27	postive
ATM	EBLN3P	0.64393	3.51E-45	postive
CHMP5	EBLN3P	0.67211	1.74E-50	postive
IREB2	EBLN3P	0.63019	8.63E-43	postive
KLHL24	EBLN3P	0.56992	1.35E-33	postive
MAPK1	EBLN3P	0.5837	1.58E-35	postive
MAPK8	EBLN3P	0.51698	6.02E-27	postive
NFE2L2	EBLN3P	0.50633	9.57E-26	postive
OXSR1	EBLN3P	0.50379	1.83E-25	postive
PIK3CA	EBLN3P	0.67965	5.24E-52	postive
PRKAA1	EBLN3P	0.56095	2.20E-32	postive
SETD1B	EBLN3P	0.57128	8.79E-34	postive
SIRT1	EBLN3P	0.53831	1.74E-29	postive
SNX4	EBLN3P	0.54295	4.63E-30	postive
SP1	EBLN3P	0.65117	1.72E-46	postive
ZEB1	EBLN3P	0.60002	6.06E-38	postive
CS	EIF3J-DT	0.5167	6.48E-27	postive
GABPB1	EIF3J-DT	0.52384	9.61E-28	postive
SP1	EIF3J-DT	0.52179	1.67E-27	postive
HSPB1	ELFN1-AS1	0.55903	3.96E-32	postive
CAV1	EPB41L4A-DT	0.51088	2.97E-26	postive
ABCC1	FAM111A-DT	0.6282	1.87E-42	postive
ATM	FAM111A-DT	0.53933	1.31E-29	postive
PIK3CA	FAM111A-DT	0.50623	9.83E-26	postive
SLC38A1	FAM111A-DT	0.54619	1.81E-30	postive
SP1	FAM111A-DT	0.60054	5.05E-38	postive
ATG4D	FAM201A	0.51	3.73E-26	postive

CS	FAM201A	0.50019	4.52E-25	postive
SLC38A1	FAM201A	0.52419	8.75E-28	postive
ACVR1B	FBXL19-AS1	0.50543	1.21E-25	postive
CS	FBXL19-AS1	0.53973	1.16E-29	postive
DUOX2	FBXL19-AS1	0.58129	3.48E-35	postive
SLC38A1	FBXL19-AS1	0.51189	2.29E-26	postive
SP1	FBXL19-AS1	0.55316	2.32E-31	postive
ANO6	FGD5-AS1	0.5624	1.41E-32	postive
ATG16L1	FGD5-AS1	0.51595	7.89E-27	postive
ATM	FGD5-AS1	0.56831	2.24E-33	postive
BACH1	FGD5-AS1	0.52109	2.01E-27	postive
BECN1	FGD5-AS1	0.59774	1.34E-37	postive
IREB2	FGD5-AS1	0.69201	1.33E-54	postive
KLHL24	FGD5-AS1	0.56365	9.61E-33	postive
MAPK1	FGD5-AS1	0.68848	7.58E-54	postive
MAPK8	FGD5-AS1	0.59089	1.41E-36	postive
NFE2L2	FGD5-AS1	0.50081	3.87E-25	postive
NRAS	FGD5-AS1	0.56367	9.54E-33	postive
OXSR1	FGD5-AS1	0.68783	1.04E-53	postive
PIK3CA	FGD5-AS1	0.68572	2.89E-53	postive
SETD1B	FGD5-AS1	0.58201	2.74E-35	postive
SIRT1	FGD5-AS1	0.55719	6.91E-32	postive
SNX4	FGD5-AS1	0.65211	1.16E-46	postive
SP1	FGD5-AS1	0.69317	7.50E-55	postive
ZEB1	FGD5-AS1	0.51916	3.37E-27	postive
HBA1	FLJ20021	0.54736	1.29E-30	postive
PLIN4	FLJ20021	0.62355	1.12E-41	postive
GABPB1	FLJ37453	0.50599	1.04E-25	postive
RPL8	FOXP4-AS1	0.64815	6.12E-46	postive
ATF4	GAS5	0.54888	8.23E-31	postive

RPL8	GAS5	0.65518	3.13E-47	postive
DPP4	GCC2-AS1	0.56593	4.73E-33	postive
PANX1	GCC2-AS1	0.61078	1.30E-39	postive
STMN1	GIHCG	0.51619	7.42E-27	postive
OTUB1	GPRC5D-AS1	0.52574	5.74E-28	postive
AKR1C3	GSEC	0.54309	4.45E-30	postive
G6PD	GSEC	0.5685	2.12E-33	postive
MAFG	GSEC	0.50099	3.70E-25	postive
NQO1	GSEC	0.50175	3.06E-25	postive
PGD	GSEC	0.5261	5.20E-28	postive
PTGS2	HCG11	0.76219	3.00E-72	postive
ATG16L1	HCG18	0.52016	2.59E-27	postive
CS	HCG18	0.54543	2.26E-30	postive
MAPK1	HCG18	0.50291	2.28E-25	postive
MAPK14	HCG18	0.59009	1.85E-36	postive
SP1	HCG18	0.5813	3.47E-35	postive
IFNG	HLA-DQB1-AS1	0.53349	6.78E-29	postive
HSPB1	HMGA1P4	0.54023	1.01E-29	postive
ABCC1	HMGN3-AS1	0.5457	2.09E-30	postive
HNF4A	HNF4A-AS1	0.55234	2.96E-31	postive
PCK2	HNF4A-AS1	0.52821	2.92E-28	postive
SCP2	HNF4A-AS1	0.52108	2.02E-27	postive
CAV1	HOTAIRM1	0.50019	4.51E-25	postive
HBA1	HOTAIRM1	0.58428	1.30E-35	postive
HIC1	HOTAIRM1	0.68291	1.12E-52	postive
PLIN4	HOTAIRM1	0.73764	1.97E-65	postive
HBA1	HOXB-AS1	0.56275	1.27E-32	postive
HIC1	HOXB-AS1	0.53069	1.48E-28	postive
PLIN4	HOXB-AS1	0.80339	9.01E-86	postive
ATM	INE1	0.51662	6.61E-27	postive

SETD1B	INE1	0.50162	3.15E-25	postive
CA9	ITGB1-DT	0.63783	4.18E-44	postive
CS	ITGB1-DT	0.5011	3.59E-25	postive
CYBB	ITGB2-AS1	0.6172	1.22E-40	postive
IFNG	ITGB2-AS1	0.56076	2.33E-32	postive
FANCD2	KDM4A-AS1	0.54118	7.70E-30	postive
HSPB1	KMT2E-AS1	0.51904	3.48E-27	postive
PROM2	KRT7-AS	0.51783	4.81E-27	postive
HNF4A	LBX2-AS1	0.5183	4.24E-27	postive
ATM	LENG8-AS1	0.50688	8.32E-26	postive
SP1	LENG8-AS1	0.51207	2.18E-26	postive
ZNF419	LENG8-AS1	0.51885	3.66E-27	postive
FANCD2	LINC00205	0.5072	7.67E-26	postive
STMN1	LINC00205	0.52673	4.39E-28	postive
ZNF419	LINC00205	0.50339	2.02E-25	postive
ATM	LINC00265	0.61233	7.37E-40	postive
PML	LINC00265	0.53101	1.35E-28	postive
PTGS2	LINC00265	0.51123	2.71E-26	postive
SETD1B	LINC00265	0.51169	2.40E-26	postive
SLC38A1	LINC00265	0.5538	1.91E-31	postive
SP1	LINC00265	0.5287	2.56E-28	postive
ABCC1	LINC00342	0.55132	4.01E-31	postive
PROM2	LINC00342	0.58716	4.96E-36	postive
PLIN4	LINC00622	0.57578	2.09E-34	postive
CAV1	LINC00839	0.50276	2.37E-25	postive
HIC1	LINC00839	0.53574	3.61E-29	postive
PML	LINC00839	0.52862	2.61E-28	postive
SLC1A5	LINC00839	0.51713	5.78E-27	postive
ATM	LINC00909	0.50485	1.39E-25	postive
SP1	LINC00909	0.55547	1.16E-31	postive

EPAS1	LINC00924	0.50131	3.41E-25	postive
ATM	LINC00926	0.57189	7.24E-34	postive
NQO1	LINC00942	0.58249	2.35E-35	postive
TXNRD1	LINC00942	0.53215	9.84E-29	postive
ATG4D	LINC00992	0.52842	2.76E-28	postive
CS	LINC00992	0.50129	3.43E-25	postive
ABCC1	LINC01011	0.52271	1.31E-27	postive
SCP2	LINC01018	0.67689	1.92E-51	postive
GPX4	LINC01023	0.50047	4.21E-25	postive
CD44	LINC01116	0.51926	3.29E-27	postive
SLC1A5	LINC01116	0.64248	6.36E-45	postive
VLDLR	LINC01116	0.62674	3.28E-42	postive
DPP4	LINC01124	0.58827	3.43E-36	postive
PANX1	LINC01124	0.57684	1.48E-34	postive
STMN1	LINC01194	0.50449	1.53E-25	postive
FANCD2	LINC01224	0.5259	5.49E-28	postive
HELLS	LINC01224	0.5034	2.02E-25	postive
STMN1	LINC01224	0.54562	2.14E-30	postive
SLC40A1	LINC01269	0.53856	1.63E-29	postive
PIK3CA	LINC01278	0.53227	9.53E-29	postive
SP1	LINC01278	0.50422	1.64E-25	postive
WIPI2	LINC01474	0.53408	5.76E-29	postive
SOCS1	LINC01503	0.50702	8.03E-26	postive
ALOX12	LINC01521	0.52474	7.53E-28	postive
BECN1	LINC01521	0.52305	1.19E-27	postive
CS	LINC01521	0.54215	5.82E-30	postive
IREB2	LINC01521	0.52672	4.39E-28	postive
MAPK1	LINC01521	0.55352	2.08E-31	postive
PIK3CA	LINC01521	0.52383	9.65E-28	postive
SP1	LINC01521	0.54168	6.67E-30	postive

CA9	LINC01559	0.55454	1.54E-31	postive
ATM	LINC01560	0.5162	7.39E-27	postive
GABPB1	LINC01560	0.50661	8.90E-26	postive
IREB2	LINC01560	0.50549	1.18E-25	postive
PIK3CA	LINC01560	0.55847	4.69E-32	postive
SP1	LINC01560	0.57347	4.39E-34	postive
GPX2	LINC01770	0.50342	2.00E-25	postive
SLC38A1	LINC01836	0.50926	4.51E-26	postive
ATM	LINC01857	0.50357	1.93E-25	postive
CYBB	LINC01857	0.59434	4.35E-37	postive
IFNG	LINC01871	0.67077	3.21E-50	postive
CYBB	LINC01943	0.59131	1.22E-36	postive
IFNG	LINC01943	0.63881	2.82E-44	postive
PCK2	LINC02028	0.52735	3.70E-28	postive
ABCC1	LINC02035	0.65529	2.99E-47	postive
ALOX12	LINC02035	0.53361	6.56E-29	postive
CAV1	LINC02035	0.51557	8.74E-27	postive
PIK3CA	LINC02035	0.51947	3.11E-27	postive
PROM2	LINC02035	0.5654	5.59E-33	postive
SP1	LINC02035	0.52747	3.58E-28	postive
DUOX2	LINC02041	0.57802	1.01E-34	postive
CYBB	LINC02084	0.61538	2.40E-40	postive
IFNG	LINC02084	0.69479	3.35E-55	postive
PML	LINC02084	0.50129	3.43E-25	postive
HSPB1	LINC02313	0.55244	2.87E-31	postive
ABCC1	LINC02331	0.52915	2.26E-28	postive
DUOX2	LINC02331	0.50748	7.14E-26	postive
IFNG	LINC02446	0.81165	7.13E-89	postive
TXNRD1	LINC02561	0.53995	1.09E-29	postive
DPP4	LINC02637	0.51208	2.18E-26	postive

IL33	LINC02889	0.58056	4.42E-35	postive
DRD4	LMNTD2-AS1	0.81492	3.79E-90	postive
HBA1	LNCTAM34A	0.67346	9.35E-51	postive
PLIN4	LNCTAM34A	0.80053	9.85E-85	postive
AKR1C1	LUCAT1	0.66671	2.00E-49	postive
AKR1C2	LUCAT1	0.50528	1.25E-25	postive
AKR1C3	LUCAT1	0.54599	1.92E-30	postive
PGD	LUCAT1	0.57395	3.76E-34	postive
SQSTM1	LUCAT1	0.52552	6.10E-28	postive
SRXN1	LUCAT1	0.62259	1.61E-41	postive
TXNRD1	LUCAT1	0.65766	1.08E-47	postive
SLC1A5	MACORIS	0.54774	1.15E-30	postive
MT3	MAFA-AS1	0.53835	1.73E-29	postive
ATF4	MAPKAPK5-AS1	0.50363	1.90E-25	postive
DDIT3	MAPKAPK5-AS1	0.51031	3.44E-26	postive
EGLN2	MAPKAPK5-AS1	0.52669	4.43E-28	postive
HRAS	MAPKAPK5-AS1	0.68353	8.31E-53	postive
HSPB1	MAPKAPK5-AS1	0.56126	2.00E-32	postive
OTUB1	MAPKAPK5-AS1	0.60309	2.06E-38	postive
ALOX12	MCCC1-AS1	0.50128	3.44E-25	postive
RPL8	MHENCR	0.51932	3.23E-27	postive
HRAS	MINCR	0.52961	1.99E-28	postive
HSPB1	MINCR	0.60829	3.20E-39	postive
RPL8	MINCR	0.67127	2.55E-50	postive
CYBB	MIR155HG	0.76251	2.43E-72	postive
IFNG	MIR155HG	0.74837	2.58E-68	postive
SLC1A5	MIR181A2HG	0.52084	2.15E-27	postive
ZNF419	MIR181A2HG	0.5072	7.67E-26	postive
DRD4	MIR200CHG	0.6143	3.58E-40	postive
VEGFA	MIR210HG	0.53235	9.31E-29	postive

TP53	MIR222HG	0.52032	2.48E-27	postive
ABCC1	MIR23AHG	0.53494	4.52E-29	postive
SLC40A1	MIR325HG	0.50971	4.03E-26	postive
HRAS	MIR4435-2HG	0.53874	1.54E-29	postive
HSPB1	MIR4435-2HG	0.52804	3.07E-28	postive
ATM	MIR4453HG	0.55977	3.16E-32	postive
FBXW7	MIR4453HG	0.53528	4.11E-29	postive
GABPB1	MIR4453HG	0.5064	9.41E-26	postive
HBA1	MIR497HG	0.58495	1.04E-35	postive
PLIN4	MIR497HG	0.7492	1.53E-68	postive
PLIN4	MIR503HG	0.58158	3.16E-35	postive
SOCS1	MIR583HG	0.50417	1.66E-25	postive
PLIN4	MIR99AHG	0.5059	1.07E-25	postive
BECN1	MKLN1-AS	0.50978	3.95E-26	postive
MAFG	MKLN1-AS	0.61987	4.50E-41	postive
TXNRD1	MKLN1-AS	0.50954	4.21E-26	postive
TXNRD1	MSC-AS1	0.52373	9.92E-28	postive
HSPB1	MUC12-AS1	0.57684	1.48E-34	postive
EGLN2	MYLK-AS1	0.5189	3.62E-27	postive
SIRT1	NADK2-AS1	0.50055	4.13E-25	postive
ATG3	NCK1-DT	0.50092	3.76E-25	postive
ATG7	NCK1-DT	0.51288	1.77E-26	postive
FANCD2	NCK1-DT	0.50968	4.05E-26	postive
ALOX12	NFYC-AS1	0.52862	2.61E-28	postive
ATM	NFYC-AS1	0.51568	8.47E-27	postive
IREB2	NFYC-AS1	0.50505	1.33E-25	postive
PIK3CA	NFYC-AS1	0.50223	2.71E-25	postive
SP1	NFYC-AS1	0.51914	3.40E-27	postive
GABPB1	NIFK-AS1	0.52962	1.98E-28	postive
SP1	NNT-AS1	0.51128	2.68E-26	postive

ATM	NORAD	0.53718	2.40E-29	postive
IREB2	NORAD	0.55479	1.43E-31	postive
KLHL24	NORAD	0.50906	4.76E-26	postive
MAPK1	NORAD	0.5795	6.25E-35	postive
PIK3CA	NORAD	0.53585	3.50E-29	postive
SETD1B	NORAD	0.56021	2.76E-32	postive
SP1	NORAD	0.63463	1.50E-43	postive
ABCC1	NRAV	0.65101	1.85E-46	postive
CS	NRAV	0.56824	2.30E-33	postive
OTUB1	NRAV	0.51162	2.45E-26	postive
SLC38A1	NRAV	0.60528	9.43E-39	postive
SP1	NRAV	0.512	2.22E-26	postive
ABCC1	NRSN2-AS1	0.54926	7.38E-31	postive
CS	NRSN2-AS1	0.53325	7.25E-29	postive
SLC38A1	NRSN2-AS1	0.50657	9.00E-26	postive
VDAC2	NRSN2-AS1	0.52981	1.88E-28	postive
VDAC2	NUTM2A-AS1	0.5157	8.43E-27	postive
VDAC2	NUTM2B-AS1	0.52337	1.09E-27	postive
ANO6	OIP5-AS1	0.50501	1.34E-25	postive
EIF2AK4	OIP5-AS1	0.54577	2.04E-30	postive
IREB2	OIP5-AS1	0.67617	2.67E-51	postive
KLHL24	OIP5-AS1	0.50084	3.84E-25	postive
MAPK1	OIP5-AS1	0.52375	9.84E-28	postive
PIK3CA	OIP5-AS1	0.52488	7.25E-28	postive
SIRT1	OIP5-AS1	0.52712	3.94E-28	postive
SP1	OIP5-AS1	0.57946	6.33E-35	postive
EMC2	OTUD6B-AS1	0.66746	1.43E-49	postive
HSF1	OTUD6B-AS1	0.53045	1.58E-28	postive
MTDH	OTUD6B-AS1	0.58402	1.42E-35	postive
ANO6	PAXIP1-AS2	0.57254	5.91E-34	postive

IREB2	PAXIP1-AS2	0.55457	1.52E-31	postive
PIK3CA	PAXIP1-AS2	0.55548	1.16E-31	postive
CYBB	PCED1B-AS1	0.70044	1.90E-56	postive
IFNG	PCED1B-AS1	0.63838	3.35E-44	postive
HBA1	PDCD4-AS1	0.66079	2.75E-48	postive
PLIN4	PDCD4-AS1	0.81226	4.13E-89	postive
CAPG	PELATON	0.5349	4.57E-29	postive
CYBB	PELATON	0.52969	1.95E-28	postive
YWHAE	PITPNA-AS1	0.55602	9.84E-32	postive
HRAS	PPP1R14B-AS1	0.52676	4.34E-28	postive
HSPB1	PPP1R35-AS1	0.50175	3.06E-25	postive
HSPB1	PRKAR1B-AS1	0.50096	3.73E-25	postive
ABCC1	PRKAR1B-AS2	0.52184	1.65E-27	postive
CS	PRKAR1B-AS2	0.50548	1.19E-25	postive
BAP1	PRKAR2A-AS1	0.56425	7.97E-33	postive
HRAS	PRR34-AS1	0.55238	2.93E-31	postive
HSPB1	PRR34-AS1	0.50989	3.84E-26	postive
RPL8	PRRT3-AS1	0.5424	5.43E-30	postive
SP1	PSMA3-AS1	0.56271	1.28E-32	postive
IFNG	PSMB8-AS1	0.51275	1.83E-26	postive
FANCD2	PTOV1-AS1	0.5183	4.25E-27	postive
STMN1	PTOV1-AS1	0.51994	2.74E-27	postive
ZNF419	PTOV1-AS1	0.60782	3.79E-39	postive
HELLS	PTOV1-AS2	0.5197	2.93E-27	postive
ZNF419	PTOV1-AS2	0.50948	4.26E-26	postive
CAPG	PTPRN2-AS1	0.50846	5.55E-26	postive
CYBB	PTPRN2-AS1	0.68676	1.75E-53	postive
CHMP6	PXN-AS1	0.52256	1.36E-27	postive
HRAS	PXN-AS1	0.58493	1.05E-35	postive
HSPB1	PXN-AS1	0.52222	1.49E-27	postive

OTUB1	PXN-AS1	0.50341	2.01E-25	postive
RPL8	PXN-AS1	0.55393	1.84E-31	postive
ATM	RAD51-AS1	0.51345	1.52E-26	postive
GABPB1	RAD51-AS1	0.52256	1.36E-27	postive
SP1	RAD51-AS1	0.53623	3.14E-29	postive
HRAS	RASSF1-AS1	0.52285	1.26E-27	postive
HSPB1	RASSF1-AS1	0.5434	4.07E-30	postive
KRAS	RASSF8-AS1	0.70526	1.57E-57	postive
CA9	RBPMS-AS1	0.52204	1.56E-27	postive
MAPK1	REPIN1-AS1	0.53673	2.73E-29	postive
HBA1	RFX5-AS1	0.61135	1.05E-39	postive
PLIN4	RFX5-AS1	0.77859	2.79E-77	postive
HSF1	RHPN1-AS1	0.52024	2.53E-27	postive
CS	SBF2-AS1	0.51159	2.47E-26	postive
FANCD2	SCAT2	0.51211	2.16E-26	postive
HELLS	SCAT2	0.50109	3.61E-25	postive
HBA1	SCGB1B2P	0.58409	1.38E-35	postive
PLIN4	SCGB1B2P	0.62405	9.22E-42	postive
DPP4	SIAH2-AS1	0.52879	2.49E-28	postive
HRAS	SLC12A9-AS1	0.50531	1.24E-25	postive
HSPB1	SLC12A9-AS1	0.58461	1.16E-35	postive
RPL8	SLC12A9-AS1	0.68361	7.98E-53	postive
HSPB1	SLCO4A1-AS1	0.54471	2.79E-30	postive
ATF4	SNHG1	0.52674	4.37E-28	postive
OTUB1	SNHG1	0.60537	9.13E-39	postive
OTUB1	SNHG12	0.51552	8.84E-27	postive
ATF4	SNHG17	0.53507	4.36E-29	postive
RPL8	SNHG17	0.59625	2.25E-37	postive
HRAS	SNHG19	0.52338	1.09E-27	postive
HSPB1	SNHG19	0.55456	1.53E-31	postive

RPL8	SNHG19	0.61356	4.70E-40	postive
ATF4	SNHG20	0.50936	4.40E-26	postive
EGLN2	SNHG25	0.66311	9.94E-49	postive
HRAS	SNHG25	0.51302	1.70E-26	postive
TP53	SNHG29	0.5074	7.29E-26	postive
ABCC1	SNHG4	0.54767	1.18E-30	postive
RPL8	SNHG5	0.60841	3.07E-39	postive
HRAS	SNHG6	0.60401	1.48E-38	postive
HSF1	SNHG6	0.5523	3.00E-31	postive
HSPB1	SNHG6	0.61251	6.90E-40	postive
RPL8	SNHG6	0.8395	1.39E-100	postive
OTUB1	SNHG7	0.51792	4.69E-27	postive
RPL8	SNHG7	0.60479	1.12E-38	postive
RPL8	SNHG8	0.59841	1.06E-37	postive
EGLN2	SNHG9	0.55757	6.16E-32	postive
HRAS	SNHG9	0.57555	2.25E-34	postive
HSPB1	SNHG9	0.5345	5.11E-29	postive
ATG4D	SPINT1-AS1	0.50866	5.26E-26	postive
PROM2	SPINT1-AS1	0.55996	2.98E-32	postive
ATF4	SREBF2-AS1	0.5263	4.93E-28	postive
NF2	SREBF2-AS1	0.64613	1.42E-45	postive
ATM	STARD4-AS1	0.51868	3.84E-27	postive
IREB2	STARD4-AS1	0.53596	3.39E-29	postive
SP1	STARD4-AS1	0.51861	3.90E-27	postive
ATG13	STARD7-AS1	0.51171	2.39E-26	postive
SP1	TAPT1-AS1	0.55002	5.89E-31	postive
ABCC1	TGFB2-AS1	0.52476	7.49E-28	postive
PROM2	TGFB2-AS1	0.61954	5.09E-41	postive
ABCC1	THAP9-AS1	0.5051	1.31E-25	postive
ALOX12	THAP9-AS1	0.50381	1.81E-25	postive

FANCD2	THUMPD3-AS1	0.53838	1.71E-29	postive
G6PD	TMCC1-AS1	0.50179	3.02E-25	postive
FANCD2	TMPO-AS1	0.56102	2.16E-32	postive
HELLS	TMPO-AS1	0.55127	4.07E-31	postive
STMN1	TMPO-AS1	0.6356	1.02E-43	postive
GABPB1	TOLLIP-AS1	0.52828	2.87E-28	postive
EGLN2	TP53TG1	0.50535	1.23E-25	postive
DPP4	TPRG1-AS1	0.61422	3.68E-40	postive
HNF4A	TPRG1-AS1	0.53519	4.21E-29	postive
PANX1	TPRG1-AS1	0.59286	7.23E-37	postive
GCLC	TRAM2-AS1	0.51827	4.28E-27	postive
MUC1	TRAPPC12-AS1	0.52393	9.39E-28	postive
SP1	TRAPPC12-AS1	0.56921	1.69E-33	postive
EGLN2	TRIM52-AS1	0.50539	1.21E-25	postive
HRAS	TRIM52-AS1	0.54199	6.11E-30	postive
HSPB1	TRIM52-AS1	0.51341	1.54E-26	postive
RPL8	TRIM52-AS1	0.5562	9.33E-32	postive
MAPK14	U91328.1	0.54626	1.78E-30	postive
RIPK1	U91328.1	0.60338	1.85E-38	postive
ABCC1	UBA6-AS1	0.55801	5.40E-32	postive
IREB2	UBL7-AS1	0.54106	7.97E-30	postive
EMC2	UBR5-AS1	0.58285	2.08E-35	postive
ABCC1	VIM-AS1	0.6124	7.18E-40	postive
PROM2	VIM-AS1	0.59652	2.05E-37	postive
HSF1	VPS13B-DT	0.53675	2.72E-29	postive
RPL8	VPS13B-DT	0.54044	9.52E-30	postive
CS	WAC-AS1	0.53176	1.10E-28	postive
ABCC1	WARS2-AS1	0.57118	9.09E-34	postive
ALOX12	WARS2-AS1	0.51247	1.97E-26	postive
NRAS	WARS2-AS1	0.50848	5.52E-26	postive

SLC38A1	WARS2-AS1	0.54176	6.52E-30	postive
SP1	WARS2-AS1	0.58093	3.92E-35	postive
GABPB1	WASL-DT	0.50528	1.25E-25	postive
RPL8	YTHDF3-AS1	0.59615	2.33E-37	postive
HRAS	Z69706.1	0.50294	2.26E-25	postive
ATM	Z83843.1	0.5128	1.81E-26	postive
SETD1B	Z83843.1	0.50884	5.04E-26	postive
GABPB1	Z95115.1	0.50395	1.75E-25	postive
SOCS1	Z98257.1	0.56906	1.78E-33	postive
CHMP5	ZEB1-AS1	0.5269	4.19E-28	postive
SP1	ZEB1-AS1	0.50275	2.37E-25	postive
HSF1	ZFAS1	0.52011	2.62E-27	postive
OTUB1	ZFAS1	0.58845	3.22E-36	postive
RPL8	ZFAS1	0.68349	8.45E-53	postive
G6PD	ZFPM2-AS1	0.54714	1.37E-30	postive
PGD	ZFPM2-AS1	0.53444	5.19E-29	postive
SQSTM1	ZFPM2-AS1	0.55663	8.19E-32	postive
PHKG2	ZNF213-AS1	0.50493	1.37E-25	postive
HRAS	ZNF232-AS1	0.55125	4.10E-31	postive
HSPB1	ZNF232-AS1	0.51617	7.46E-27	postive
ATM	ZNF32-AS2	0.56405	8.49E-33	postive
HELLS	ZNF32-AS2	0.50424	1.63E-25	postive
MAPK8	ZNF32-AS2	0.54283	4.80E-30	postive
PIK3CA	ZNF32-AS2	0.51687	6.19E-27	postive
SETD1B	ZNF32-AS2	0.53767	2.09E-29	postive
SP1	ZNF32-AS2	0.59495	3.53E-37	postive
HBA1	ZNF426-DT	0.65738	1.22E-47	postive
PLIN4	ZNF426-DT	0.7923	7.87E-82	postive
ZNF419	ZNF528-AS1	0.59872	9.54E-38	postive
EGLN2	ZNF529-AS1	0.5456	2.15E-30	postive

OTUB1	ZNF529-AS1	0.51156	2.49E-26	postive
ZNF419	ZNF529-AS1	0.52098	2.08E-27	postive
ZNF419	ZNF582-AS1	0.5406	9.09E-30	postive
ZNF419	ZNF667-AS1	0.53386	6.11E-29	postive
ZNF419	ZNF790-AS1	0.59622	2.27E-37	postive
HSF1	ZNNT1	0.51715	5.75E-27	postive
EGLN2	ZSCAN16-AS1	0.50795	6.32E-26	postive

Supplementary Table 7: Univariate cox analysis and multivarite cox analysis.

Univariate Cox analysis				
gene	HR	HR.95L	HR.95H	pvalue
AC091057.1	2.42443	1.29013	4.55602	0.005934
AL357079.1	1.76063	1.22539	2.52965	0.002219
SNHG4	1.48215	1.28392	1.71099	7.81E-08
SNHG1	1.04177	1.01464	1.06962	0.002369
AC010969.2	1.3211	1.07883	1.61778	0.007059
CYTOR	1.0349	1.01142	1.05893	0.003395
NIFK-AS1	1.28443	1.07904	1.52892	0.004868
AL671710.1	2.69436	1.35926	5.34084	0.004523
AC004816.1	1.20591	1.07723	1.34997	0.001146
KDM4A-AS1	2.85183	1.89762	4.28586	4.60E-07
AC087741.2	1.13517	1.04211	1.23654	0.003671
BACE1-AS	1.21334	1.09954	1.33892	0.000119
PTOV1-AS1	1.26132	1.06896	1.48829	0.005963
ARRDC1-AS1	1.10517	1.02561	1.1909	0.00871
AC022007.1	1.56619	1.12677	2.17699	0.007577
RHPN1-AS1	1.68093	1.25526	2.25094	0.00049
AC026356.1	4.25643	2.29654	7.88889	4.21E-06
MKLN1-AS	3.37753	2.28509	4.99223	1.03E-09
AC099850.3	1.14451	1.09263	1.19885	1.18E-08
Z95115.1	1.21825	1.06085	1.39899	0.005159
PRRT3-AS1	1.09534	1.0419	1.15153	0.00036
AP003119.1	1.16161	1.03855	1.29927	0.008744
SNHG12	1.13375	1.03629	1.24037	0.006195
AC002116.2	1.55871	1.12176	2.16586	0.00818
ZEB1-AS1	1.46189	1.1794	1.81203	0.000528
LINC01011	1.99652	1.32599	3.00614	0.000929
GSEC	1.71455	1.3278	2.21396	3.57E-05
AC145207.8	1.17867	1.08355	1.28215	0.000129
AC018690.1	2.10374	1.43468	3.08482	0.00014
AL031985.3	1.87921	1.54689	2.28294	2.10E-10
LINC01224	1.86891	1.411	2.47542	1.29E-05
AP000873.1	2.5085	1.31963	4.76844	0.005012

LINC00942	1.03677	1.02071	1.05307	5.77E-06
SREBF2-AS1	1.45836	1.16984	1.81804	0.000795
THUMPD3-AS1	1.38138	1.18187	1.61457	4.92E-05
AC026401.3	1.08611	1.03843	1.13599	0.000311
LINC00205	1.23451	1.1011	1.38407	0.000305
DNAJC9-AS1	2.56497	1.58604	4.14808	0.000123
AC004943.2	2.14332	1.23677	3.71438	0.006579
TMCC1-AS1	2.64072	1.8462	3.77717	1.05E-07
AL512353.1	1.36667	1.0942	1.70698	0.005896
NRAV	1.2347	1.1296	1.34959	3.41E-06
C2orf49-DT	2.45316	1.32538	4.54058	0.00428
HMGN3-AS1	2.14799	1.43587	3.2133	0.000199
AC145207.5	1.77077	1.36827	2.29169	1.41E-05
NCK1-DT	1.53111	1.22695	1.91068	0.000163
MIR4435-2HG	1.12057	1.04079	1.20646	0.002519
AC124798.1	1.21642	1.09001	1.35748	0.000466
MIR210HG	1.14075	1.0677	1.21879	9.61E-05
SCAT2	1.36258	1.08464	1.71174	0.00786
ZFPM2-AS1	1.09609	1.05617	1.13752	1.25E-06
AC107959.3	1.34887	1.13808	1.59871	0.000557
AP001453.2	1.595	1.13148	2.24839	0.007696
AL050341.2	1.14033	1.04254	1.2473	0.004097
LINC02561	1.42312	1.16734	1.73494	0.000482
LUCAT1	1.1787	1.0945	1.26938	1.37E-05
AL049840.3	1.8456	1.23985	2.74729	0.002535
SBF2-AS1	1.43478	1.14462	1.79848	0.001738

Multivarite Cox analysis					
LncRNA	coef	HR	HR.95L	HR.95H	pvalue
AC091057.1	-1.84842	0.15749	0.04187	0.5923	0.00624
AL357079.1	-0.642	0.52624	0.26899	1.0295	0.06078
SNHG4	0.613	1.84596	1.23696	2.75479	0.00269
AL671710.1	-1.13956	0.31996	0.07761	1.31902	0.11484
KDM4A-AS1	0.98901	2.68857	1.36348	5.30142	0.0043
PTOV1-AS1	-0.7203	0.48661	0.32625	0.72578	0.00041
AC022007.1	-0.40949	0.66399	0.38344	1.1498	0.14383
MKLN1-AS	0.78579	2.19414	1.25511	3.83573	0.00583
AC099850.3	0.07054	1.07309	0.98259	1.17192	0.11659
Z95115.1	-0.45454	0.63474	0.48211	0.83568	0.0012
PRRT3-AS1	0.07394	1.07674	0.98294	1.1795	0.11184
SNHG12	-0.13897	0.87025	0.72605	1.04309	0.13271
LINC01224	0.33356	1.39594	0.93753	2.07848	0.10052
SREBF2-AS1	0.461	1.58567	1.07256	2.34423	0.02082
LINC00205	0.19848	1.21955	1.00113	1.48562	0.0487

NRAV	0.29424	1.3421	1.12608	1.59957	0.00102
AC145207.5	0.49438	1.63949	1.06224	2.53041	0.02557
MIR4435-2HG	0.10234	1.10776	0.98762	1.2425	0.08059
MIR210HG	0.08987	1.09404	0.99321	1.2051	0.06847
ZFPM2-AS1	0.06627	1.06851	1.00321	1.13806	0.03943
AL050341.2	0.22187	1.24841	1.01813	1.53078	0.03295
LUCAT1	-0.10611	0.89933	0.78159	1.03481	0.13833

Supplementary Table 8: GSEA enrichment analysis.

GSEA enrichment analysis										
NAME	**GS follow link to MSigDB**	**GS DETAILS**	**SIZE**	**ES**	**NES**	**NOM p-val**	**FDR q-val**	**FWER p-val**	**RANK AT MAX**	**LEADING EDGE**
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	Details ...	##	1	2	0	0	0	###	tags=70%, list=17%, signal=84%
KEGG_OOCYTE_MEIOSIS	KEGG_OOCYTE_MEIOSIS	Details ...	##	1	2	0	0	0	###	tags=58%, list=17%, signal=70%
KEGG_SPLICEOSOME	KEGG_SPLICEOSOME	Details ...	##	1	2	0	0	0	###	tags=80%, list=14%, signal=93%
KEGG_PYRIMIDINE_METABOLISM	KEGG_PYRIMIDINE_METABOLISM	Details ...	98	1	2	0	0	0	###	tags=53%, list=14%, signal=61%

KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	Details ...	68	1	2	0	0	0	###	tags=59%, list=18%, signal=72%
KEGG_RNA_DEGRADATION	KEGG_RNA_DEGRADATION	Details ...	59	1	2	0	0	0	###	tags=78%, list=18%, signal=95%
KEGG_PURINE_METABOLISM	KEGG_PURINE_METABOLISM	Details ...	##	1	2	0	0	0	###	tags=57%, list=25%, signal=75%
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	Details ...	41	1	2	0	0	0	###	tags=83%, list=17%, signal=100%
KEGG_CELL_CYCLE	KEGG_CELL_CYCLE	Details ...	##	1	2	0	0	0	###	tags=76%, list=16%, signal=91%
KEGG_HOMOLOGOUS_RECOMBINATION	KEGG_HOMOLOGOUS_RECOMBINATION	Details ...	28	1	2	0	0	0	###	tags=71%, list=8%, signal=77%

KEGG_N_GLYCAN_BIOSYNTHESIS	KEGG_N_GLYCAN_BIOSYNTHESIS	Details ...	46	1	2	0	0	0	###	tags=65%, list=19%, signal=80%
KEGG_LYSOSOME	KEGG_LYSOSOME	Details ...	##	1	2	0	0	0	###	tags=54%, list=19%, signal=66%
KEGG_WNT_SIGNALING_PATHWAY	KEGG_WNT_SIGNALING_PATHWAY	Details ...	##	1	2	0	0	0	###	tags=50%, list=21%, signal=63%
KEGG_BASE_EXCISION_REPAIR	KEGG_BASE_EXCISION_REPAIR	Details ...	35	1	2	0	0	0	###	tags=60%, list=12%, signal=68%
KEGG_VIBRIO_CHOLERAE_INFECTION	KEGG_VIBRIO_CHOLERAE_INFECTION	Details ...	54	1	2	0	0	0	###	tags=56%, list=17%, signal=67%
KEGG_BASAL_TRANSCRIPTION_FACTORS	KEGG_BASAL_TRANSCRIPTION_FACTORS	Details ...	35	1	2	0	0	0	###	tags=69%, list=16%, signal=82%
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	Details ...	85	1	2	0	0	0	###	tags=51%, list=17%, signal=61%

KEGG_ENDOCYTOSIS	KEGG_ENDOCYTOSIS	Details ...	##	1	2	0	0.01	0	###	tags=57%, list=25%, signal=76%
KEGG_OTHER_GLYCAN_DEGRADATION	KEGG_OTHER_GLYCAN_DEGRADATION	Details ...	16	1	2	0	0.01	0	###	tags=69%, list=18%, signal=83%
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	Details ...	25	1	2	0	0.01	0	###	tags=68%, list=15%, signal=80%
KEGG_THYROID_CANCER	KEGG_THYROID_CANCER	Details ...	29	1	2	0	0.01	0.1	###	tags=52%, list=13%, signal=59%
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	Details ...	##	1	2	0	0.01	0.1	###	tags=54%, list=19%, signal=66%
KEGG_ADHERENS_JUNCTION	KEGG_ADHERENS_JUNCTION	Details ...	73	1	2	0	0.01	0.1	###	tags=63%, list=24%, signal=83%

KEGG_PATHWAYS_IN_CANCER	KEGG_PATHWAYS_IN_CANCER	Details ...	##	1	2	0	0.01	0.1	###	tags=46%, list=21%, signal=59%
KEGG_MISMATCH_REPAIR	KEGG_MISMATCH_REPAIR	Details ...	23	1	2	0	0.01	0.1	###	tags=70%, list=10%, signal=77%
KEGG_SMALL_CELL_LUNG_CANCER	KEGG_SMALL_CELL_LUNG_CANCER	Details ...	84	1	2	0	0.01	0.1	###	tags=48%, list=14%, signal=56%
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	Details ...	38	1	2	0	0.01	0.1	###	tags=58%, list=22%, signal=74%
KEGG_RNA_POLYMERASE	KEGG_RNA_POLYMERASE	Details ...	29	1	2	0	0.01	0.1	###	tags=52%, list=10%, signal=58%
KEGG_BLADDER_CANCER	KEGG_BLADDER_CANCER	Details ...	42	1	2	0	0.02	0.2	###	tags=40%, list=13%, signal=46%
KEGG_ENDOMETRIAL_CANCER	KEGG_ENDOMETRIAL_CANCER	Details ...	52	1	2	0	0.02	0.2	###	tags=44%, list=14%, signal=52%

KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	Details ...	56	1	2	0	0.02	0.2	###	tags=70%, list=26%, signal=94%
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	Details ...	62	1	2	0	0.02	0.2	###	tags=61%, list=24%, signal=81%
KEGG_MTOR_SIGNALING_PATHWAY	KEGG_MTOR_SIGNALING_PATHWAY	Details ...	52	1	2	0	0.02	0.2	###	tags=46%, list=16%, signal=55%
KEGG_PANCREATIC_CANCER	KEGG_PANCREATIC_CANCER	Details ...	70	1	2	0	0.02	0.2	###	tags=53%, list=21%, signal=67%
KEGG_MAPK_SIGNALING_PATHWAY	KEGG_MAPK_SIGNALING_PATHWAY	Details ...	##	0	2	0	0.03	0.4	###	tags=55%, list=31%, signal=79%
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	Details ...	44	1	2	0	0.02	0.2	###	tags=59%, list=18%, signal=72%

KEGG_TIGHT_JUNCTION	KEGG_TIGHT_JUNCTION	Details ...	##	1	2	0	0.03	0.3	###	tags=41%, list=23%, signal=53%
KEGG_DNA_REPLICATION	KEGG_DNA_REPLICATION	Details ...	36	1	2	0	0.01	0.1	###	tags=78%, list=10%, signal=87%
KEGG_BASAL_CELL_CARCINOMA	KEGG_BASAL_CELL_CARCINOMA	Details ...	55	1	2	0	0.03	0.4	###	tags=53%, list=28%, signal=74%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	Details ...	15	1	2	0	0.03	0.4	###	tags=87%, list=31%, signal=126%
KEGG_NUCLEOTIDE_EXCISION_REPAIR	KEGG_NUCLEOTIDE_EXCISION_REPAIR	Details ...	44	1	2	0	0.01	0	###	tags=61%, list=13%, signal=71%
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	Details ...	21	1	2	0	0.03	0.3	###	tags=48%, list=18%, signal=58%

KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	Details ...	77	0	2	0	0.05	0.5	###	tags=53%, list=29%, signal=75%
KEGG_PROTEIN_EXPORT	KEGG_PROTEIN_EXPORT	Details ...	24	1	2	0	0.03	0.3	###	tags=67%, list=24%, signal=87%
KEGG_ERBB_SIGNALING_PATHWAY	KEGG_ERBB_SIGNALING_PATHWAY	Details ...	87	1	2	0	0.03	0.3	###	tags=47%, list=19%, signal=58%
KEGG_CHRONIC_MYELOID_LEUKEMIA	KEGG_CHRONIC_MYELOID_LEUKEMIA	Details ...	73	1	2	0	0.03	0.3	###	tags=56%, list=21%, signal=71%
KEGG_GLIOMA	KEGG_GLIOMA	Details ...	65	1	2	0	0.03	0.4	###	tags=42%, list=19%, signal=51%
KEGG_P53_SIGNALING_PATHWAY	KEGG_P53_SIGNALING_PATHWAY	Details ...	68	1	2	0	0.03	0.4	###	tags=41%, list=16%, signal=49%
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	Details ...	71	1	2	0	0.04	0.5	###	tags=42%, list=20%, signal=53%

KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	Details ...	15	1	2	0	0.03	0.4	###	tags=60%, list=19%, signal=74%
KEGG_NON_SMALL_CELL_LUNG_CANCER	KEGG_NON_SMALL_CELL_LUNG_CANCER	Details ...	54	1	2	0	0.03	0.3	###	tags=39%, list=13%, signal=45%
KEGG_MELANOGENESIS	KEGG_MELANOGENESIS	Details ...	##	0	2	0	0.03	0.4	###	tags=41%, list=20%, signal=51%
KEGG_LONG_TERM_POTENTIATION	KEGG_LONG_TERM_POTENTIATION	Details ...	70	1	2	0	0.03	0.3	###	tags=44%, list=19%, signal=55%
KEGG_COLORECTAL_CANCER	KEGG_COLORECTAL_CANCER	Details ...	62	1	2	0	0.03	0.3	###	tags=44%, list=14%, signal=51%
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	Details ...	55	1	2	0	0.03	0.4	###	tags=33%, list=15%, signal=38%

KEGG_INSULIN_SIGNALING_PATHWAY	KEGG_INSULIN_SIGNALING_PATHWAY	Details ...	##	0	2	0	0.03	0.3	###	tags=45%, list=21%, signal=56%
KEGG_SELENOAMINO_ACID_METABOLISM	KEGG_SELENOAMINO_ACID_METABOLISM	Details ...	26	1	2	0	0.03	0.4	###	tags=54%, list=17%, signal=65%
KEGG_AXON_GUIDANCE	KEGG_AXON_GUIDANCE	Details ...	##	1	2	0	0.03	0.3	###	tags=47%, list=21%, signal=60%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	KEGG_HEDGEHOG_SIGNALING_PATHWAY	Details ...	56	0	2	0	0.06	0.7	###	tags=48%, list=28%, signal=67%
KEGG_VEGF_SIGNALING_PATHWAY	KEGG_VEGF_SIGNALING_PATHWAY	Details ...	76	0	2	0	0.05	0.6	###	tags=47%, list=29%, signal=67%
KEGG_RENAL_CELL_CARCINOMA	KEGG_RENAL_CELL_CARCINOMA	Details ...	70	1	2	0	0.03	0.4	###	tags=47%, list=17%, signal=57%
KEGG_LONG_TERM_DEPRESSION	KEGG_LONG_TERM_DEPRESSION	Details ...	70	0	2	0	0.04	0.5	###	tags=44%, list=24%, signal=59%

KEGG_PROSTATE_CANCER	KEGG_PROSTATE_CANCER	Details ...	89	1	2	0	0.03	0.4	###	tags=43%, list=17%, signal=51%
KEGG_INOSITOL_PHOSPHATE_METABOLISM	KEGG_INOSITOL_PHOSPHATE_METABOLISM	Details ...	54	1	2	0	0.03	0.4	###	tags=56%, list=21%, signal=71%
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	Details ...	44	1	2	0	0.02	0.2	###	tags=48%, list=15%, signal=56%
KEGG_APOPTOSIS	KEGG_APOPTOSIS	Details ...	87	1	2	0	0.03	0.3	###	tags=47%, list=17%, signal=57%
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	Details ...	##	0	2	0	0.04	0.5	###	tags=45%, list=21%, signal=57%
KEGG_RIBOFLAVIN_METABOLISM	KEGG_RIBOFLAVIN_METABOLISM	Details ...	16	1	2	0	0.05	0.6	###	tags=50%, list=16%, signal=60%

KEGG_GNRH_SIGNALING_PATHWAY	KEGG_GNRH_SIGNALING_PATHWAY	Details ...	##	0	2	0	0.05	0.6	###	tags=38%, list=19%, signal=46%
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	Details ...	96	1	2	0	0.03	0.4	###	tags=51%, list=21%, signal=65%
KEGG_TGF_BETA_SIGNALING_PATHWAY	KEGG_TGF_BETA_SIGNALING_PATHWAY	Details ...	86	1	2	0	0.05	0.6	###	tags=58%, list=30%, signal=83%
KEGG_SPHINGOLIPID_METABOLISM	KEGG_SPHINGOLIPID_METABOLISM	Details ...	39	1	2	0	0.05	0.6	###	tags=54%, list=26%, signal=73%
KEGG_GLUTATHIONE_METABOLISM	KEGG_GLUTATHIONE_METABOLISM	Details ...	49	0	2	0	0.05	0.6	###	tags=39%, list=20%, signal=48%
KEGG_PROTEASOME	KEGG_PROTEASOME	Details ...	46	1	2	0	0.03	0.4	###	tags=61%, list=21%, signal=77%

KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	Details ...	41	1	2	0	0.05	0.6	###	tags=44%, list=14%, signal=51%
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	Details ...	76	1	2	0	0.05	0.6	###	tags=54%, list=27%, signal=74%
KEGG_GAP_JUNCTION	KEGG_GAP_JUNCTION	Details ...	90	1	2	0	0.06	0.6	###	tags=49%, list=26%, signal=66%
KEGG_REGULATION_OF_AUTOPHAGY	KEGG_REGULATION_OF_AUTOPHAGY	Details ...	35	0	2	0	0.07	0.7	###	tags=37%, list=23%, signal=48%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	Details ...	26	1	2	0	0.09	0.8	###	tags=73%, list=35%, signal=112%

KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	Details ...	34	0	2	0	0.07	0.7	###	tags=41%, list=12%, signal=47%
KEGG_PENTOSE_PHOSPHATE_PATHWAY	KEGG_PENTOSE_PHOSPHATE_PATHWAY	Details ...	27	0	2	0	0.08	0.7	###	tags=33%, list=12%, signal=38%
KEGG_NOTCH_SIGNALING_PATHWAY	KEGG_NOTCH_SIGNALING_PATHWAY	Details ...	47	1	2	0	0.07	0.7	###	tags=55%, list=26%, signal=75%
KEGG_ACUTE_MYELOID_LEUKEMIA	KEGG_ACUTE_MYELOID_LEUKEMIA	Details ...	57	0	2	0.1	0.09	0.8	###	tags=49%, list=24%, signal=65%
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	Details ...	34	0	2	0.1	0.09	0.8	###	tags=41%, list=11%, signal=46%
KEGG_HUNTINGTONS_DISEASE	KEGG_HUNTINGTONS_DISEASE	Details ...	##	0	2	0.1	0.09	0.8	###	tags=36%, list=18%, signal=44%

KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	Details ...	##	0	1	0.1	0.1	0.8	###	tags=39%, list=21%, signal=49%
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	Details ...	##	1	1	0.1	0.1	0.8	###	tags=39%, list=17%, signal=47%
KEGG_FOCAL_ADHESION	KEGG_FOCAL_ADHESION	Details ...	##	0	1	0.1	0.12	0.8	###	tags=38%, list=20%, signal=48%
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	Details ...	74	0	1	0.1	0.15	0.9	###	tags=38%, list=21%, signal=48%
KEGG_MELANOMA	KEGG_MELANOMA	Details ...	71	0	1	0.1	0.17	0.9	###	tags=42%, list=28%, signal=59%

KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	Details ...	22	1	1	0.1	0.15	0.9	###	tags=50%, list=20%, signal=63%
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	Details ...	53	0	1	0.1	0.23	1	###	tags=47%, list=33%, signal=70%
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	Details ...	##	0	1	0.1	0.16	0.9	###	tags=57%, list=38%, signal=92%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	Details ...	26	0	1	0.1	0.22	1	###	tags=50%, list=31%, signal=72%

KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	Details ...	81	1	1	0.1	0.11	0.8	###	tags=42%, list=26%, signal=57%
KEGG_ONE_CARBON_POOL_BY_FOLATE	KEGG_ONE_CARBON_POOL_BY_FOLATE	Details ...	17	0	1	0.1	0.19	0.9	###	tags=41%, list=12%, signal=47%
KEGG_LYSINE_DEGRADATION	KEGG_LYSINE_DEGRADATION	Details ...	44	0	1	0.1	0.16	0.9	###	tags=45%, list=15%, signal=53%
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	Details ...	79	0	1	0.1	0.19	0.9	###	tags=59%, list=42%, signal=102%
KEGG_CHEMOKINE_SIGNALING_PATHWAY	KEGG_CHEMOKINE_SIGNALING_PATHWAY	Details ...	##	0	1	0.1	0.19	0.9	###	tags=46%, list=28%, signal=64%
KEGG_ETHER_LIPID_METABOLISM	KEGG_ETHER_LIPID_METABOLISM		33	0	1	0.2	0.27	1	###	tags=27%, list=18%, signal=33%

KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION		42	0	1	0.2	0.28	1	###	tags=24%, list=13%, signal=27%
KEGG_DORSO_VENTRAL_AXIS_FORMATION	KEGG_DORSO_VENTRAL_AXIS_FORMATION	Details ...	24	0	1	0.2	0.23	1	###	tags=50%, list=25%, signal=67%
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION		##	0	1	0.2	0.25	1	###	tags=28%, list=17%, signal=34%
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM		83	0	1	0.2	0.29	1	###	tags=42%, list=32%, signal=62%
KEGG_LEISHMANIA_INFECTION	KEGG_LEISHMANIA_INFECTION		70	0	1	0.2	0.23	1	###	tags=61%, list=32%, signal=91%

KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS		28	0	1	0.2	0.28	1	###	tags=43%, list=16%, signal=51%
KEGG_GALACTOSE_METABOLISM	KEGG_GALACTOSE_METABOLISM		26	0	1	0.2	0.33	1	###	tags=42%, list=27%, signal=58%
KEGG_ABC_TRANSPORTERS	KEGG_ABC_TRANSPORTERS		44	0	1	0.2	0.34	1	###	tags=36%, list=23%, signal=47%
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY		75	0	1	0.2	0.26	1	###	tags=32%, list=15%, signal=38%
KEGG_JAK_STAT_SIGNALING_PATHWAY	KEGG_JAK_STAT_SIGNALING_PATHWAY		##	0	1	0.2	0.31	1	###	tags=36%, list=28%, signal=50%
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	KEGG_DRUG_METABOLISM_OTHER_ENZYMES		51	0	1	0.3	0.34	1	###	tags=31%, list=14%, signal=36%

KEGG_VIRAL_MYOCARDITIS	KEGG_VIRAL_MYOCARDITIS		68	0	1	0.3	0.31	1	###	tags=37%, list=26%, signal=49%
KEGG_O_GLYCAN_BIOSYNTHESIS	KEGG_O_GLYCAN_BIOSYNTHESIS		30	0	1	0.3	0.31	1	###	tags=37%, list=16%, signal=44%
KEGG_GLYCEROLIPID_METABOLISM	KEGG_GLYCEROLIPID_METABOLISM		49	0	1	0.3	0.4	1	###	tags=39%, list=27%, signal=53%
KEGG_TASTE_TRANSDUCTION	KEGG_TASTE_TRANSDUCTION		51	0	1	0.3	0.38	1	###	tags=51%, list=40%, signal=85%
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION		##	0	1	0.3	0.36	1	###	tags=30%, list=19%, signal=36%
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY		67	0	1	0.3	0.42	1	###	tags=27%, list=18%, signal=33%

KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM		24	0	1	0.3	0.39	1	###	tags=63%, list=38%, signal=101%
KEGG_CALCIUM_SIGNALING_PATHWAY	KEGG_CALCIUM_SIGNALING_PATHWAY		##	0	1	0.3	0.41	1	###	tags=25%, list=20%, signal=32%
KEGG_ALZHEIMERS_DISEASE	KEGG_ALZHEIMERS_DISEASE		##	0	1	0.3	0.39	1	###	tags=25%, list=18%, signal=31%
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM		25	0	1	0.4	0.47	1	###	tags=36%, list=13%, signal=42%
KEGG_DILATED_CARDIOMYOPATHY	KEGG_DILATED_CARDIOMYOPATHY		90	0	1	0.4	0.47	1	###	tags=41%, list=32%, signal=61%
KEGG_TYPE_I_DIABETES_MELLITUS	KEGG_TYPE_I_DIABETES_MELLITUS		41	0	1	0.5	0.48	1	###	tags=46%, list=34%, signal=71%

KEGG_PRIMARY_IMMUNODEFICIENCY	KEGG_PRIMARY_IMMUNODEFICIENCY		35	0	1	0.5	0.45	1	###	tags=29%, list=18%, signal=35%
KEGG_ECM_RECEPTOR_INTERACTION	KEGG_ECM_RECEPTOR_INTERACTION		84	0	1	0.5	0.54	1	###	tags=44%, list=35%, signal=68%
KEGG_GRAFT_VERSUS_HOST_DISEASE	KEGG_GRAFT_VERSUS_HOST_DISEASE		37	0	1	0.5	0.52	1	###	tags=65%, list=44%, signal=115%
KEGG_STEROID_BIOSYNTHESIS	KEGG_STEROID_BIOSYNTHESIS		17	0	1	0.5	0.56	1	###	tags=41%, list=30%, signal=58%
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS		16	0	1	0.5	0.56	1	###	tags=31%, list=15%, signal=37%
KEGG_TYPE_II_DIABETES_MELLITUS	KEGG_TYPE_II_DIABETES_MELLITUS		47	0	1	0.6	0.57	1	###	tags=30%, list=23%, signal=39%

KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION		##	0	1	0.6	0.57	1	###	tags=38%, list=35%, signal=58%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS		##	0	1	0.6	0.61	1	###	tags=42%, list=34%, signal=64%
KEGG_ASTHMA	KEGG_ASTHMA		28	0	1	0.6	0.65	1	###	tags=64%, list=45%, signal=118%
KEGG_CARDIAC_MUSCLE_CONTRACTION	KEGG_CARDIAC_MUSCLE_CONTRACTION		79	0	1	0.6	0.61	1	###	tags=20%, list=18%, signal=25%
KEGG_RIBOSOME	KEGG_RIBOSOME		88	0	1	0.6	0.56	1	###	tags=77%, list=45%, signal=141%
KEGG_CELL_ADHESION_MOLECULES_CAMS	KEGG_CELL_ADHESION_MOLECULES_CAMS		##	0	1	0.6	0.68	1	###	tags=31%, list=31%, signal=46%
KEGG_ALLOGRAFT_REJECTION	KEGG_ALLOGRAFT_REJECTION		35	0	1	0.6	0.67	1	###	tags=60%, list=44%, signa

									l=107%
KEGG_OXIDATIVE_PHOSPHORYLATION	KEGG_OXIDATIVE_PHOSPHORYLATION		##	0	1	0.7	0.68	1	###	tags=23%, list=18%, signal=29%
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS		15	0	1	0.7	0.67	1	###	tags=20%, list=7%, signal=22%
KEGG_HEMATOPOIETIC_CELL_LINEAGE	KEGG_HEMATOPOIETIC_CELL_LINEAGE		85	0	1	0.7	0.69	1	###	tags=35%, list=34%, signal=54%
KEGG_PARKINSONS_DISEASE	KEGG_PARKINSONS_DISEASE		##	0	1	0.7	0.73	1	###	tags=22%, list=18%, signal=26%
KEGG_NITROGEN_METABOLISM	KEGG_NITROGEN_METABOLISM		23	0	1	0.7	0.68	1	###	tags=39%, list=29%, signal=55%
KEGG_AUTOIMMUNE_THYROID_DISEASE	KEGG_AUTOIMMUNE_THYROID_DISEASE		50	0	1	0.7	0.78	1	###	tags=44%, list=44%, signal=78%

KEGG_CITRATE_CYCLE_TCA_CYCLE	KEGG_CITRATE_CYCLE_TCA_CYCLE		31	0	1	0.7	0.75	1	###	tags=45%, list=29%, signal=64%
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION		46	0	1	0.8	0.81	1	###	tags=52%, list=43%, signal=92%
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG		25	0	1	0.8	0.73	1	###	tags=48%, list=39%, signal=78%
KEGG_OLFACTORY_TRANSDUCTION	KEGG_OLFACTORY_TRANSDUCTION		##	0	1	0.9	0.69	1	###	tags=26%, list=45%, signal=47%