

Table S5. GO and KEGG enrichment analysis of 73 FerRGs

ID	Description	Count	p-value	FDR	mRNAs
BP terms					
GO:0010038	response to metal ion	14	2.06E-10	7.69E-08	ATF4, CDH1, NQO1, G6PD, MTF1, NEDD4, NFE2L2, C11A2, MAPK3, MAPK8, TFR2, TXNIP, NEDD4L, SLC40A1
GO:0034599	cellular response to oxidative stress	14	1.73E-11	1.84E-08	ATF4, NQO1, FANCD2, G6PD, MYB, NCF2, NFE2L2, PRDX1, MAPK3, MAPK8, TSC1, ATG7, SIRT1, SRXN1
GO:0031668	cellular response to extracellular stimulus	13	5.60E-11	2.93E-08	ATF4, CDKN1A, LAMP2, NFE2L2, MAPK3, MAPK8, TSC1, VDR, ATG7, SIRT1, GABARAPL1, WIPI1, EIF2AK4
GO:0072593	reactive oxygen species metabolic process	9	4.59E-06	4.29E-04	NQO1, MYB, NFE2L2, PRDX1, MAPK3, MAPK8, TXNIP, SIRT1
GO:0030099	myeloid cell differentiation	8	2.85E-04	7.04E-03	ACVR1B, G6PD, SLC11A2, PRKCA, STAT3, TFRC, PIR, SIRT1
GO:1901568	fatty acid derivative metabolic process	6	6.10E-05	2.75E-03	ALOX12, AKR1C2, MAPK3, SCD, SIRT1, FAR1
GO:0000302	response to reactive oxygen species	8	4.59E-06	4.29E-04	NQO1, MYB, NFE2L2, PRDX1, MAPK3, MAPK8, TXNIP, SIRT1
GO:0071248	cellular response to metal ion	8	1.04E-06	1.36E-04	ATF4, CDH1, NQO1, NFE2L2, MAPK3, MAPK8, TFR2, SLC40A1
GO:0002262	myeloid cell homeostasis	6	2.99E-05	1.63E-03	ACVR1B, G6PD, HMGB1, SLC11A2, PRDX1, STAT3
GO:0006826	iron ion transport	6	2.31E-07	3.78E-05	FTL, SLC11A2, TFR2, TFRC, SLC39A14, SLC40A1
CC terms					
GO:0031252	cell leading edge	7	9.95E-04	2.64E-02	ATF4, CAPG, CD44, CDH1, TSC1, SLC39A14, GABARAPL1
GO:0005770	late endosome	5	3.28E-03	7.67E-02	LAMP2, SLC11A2, MAPK3, SQSTM1, NEDD4L

GO:0030027	lamellipodium	5	9.53E-04	2.64E-02	CAPG, CD44, CDH1, TSC1, SLC39A14
GO:0101002	ficolin-1-rich granule	5	7.88E-04	2.64E-02	CTSB, HMGB1, LAMP2, SLC2A3, ATG7
GO:0048770	pigment granule	5	5.93E-05	3.55E-03	CAPG, CTSB, PRDX1, SLC3A2, TFRC
GO:0042470	melanosome	5	5.93E-05	3.55E-03	CAPG, CTSB, PRDX1, SLC3A2, TFRC
GO:0005776	autophagosome	5	3.17E-05	3.55E-03	FTL, LAMP2, SQSTM1, GABARAPL1, WIPI1
GO:0005767	secondary lysosome	4	2.09E-07	4.99E-05	FTL, LAMP2, NCF2, SQSTM1
GO:0000421	autophagosome membrane	3	3.73E-04	1.48E-02	LAMP2, GABARAPL1, WIPI1
GO:0000407	phagophore assembly site	3	2.62E-04	1.25E-02	SQSTM1, ATG7, WIPI1
MF terms					
GO:0004674	protein serine/threonine kinase activity	9	1.19E-04	6.43E-03	ACVR1B, GSK3B, MAP3K11, PRKCA, MAPK3, MAPK8, AURKA, SQSTM1, EIF2AK4
GO:0031625	ubiquitin protein ligase binding	9	4.58E-06	1.21E-03	ACVR1B, BID, CDKN1A, GSK3B, AURKA, SQSTM1, TXNIP, GABARAPL1, TRIB3
GO:0050662	coenzyme binding	7	2.72E-04	8.84E-03	DECR1, G6PD, PGD, POR, NFS1, SIRT1, CYB5R1
GO:0051427	hormone receptor binding	5	1.27E-03	2.58E-02	STAT3, VDR, NCOA3, SIRT1, WIPI1
GO:0035257	nuclear hormone receptor binding	5	5.26E-04	1.42E-02	STAT3, VDR, NCOA3, SIRT1, WIPI1
GO:0005506	iron ion binding	4	4.36E-03	5.06E-02	ALOX12, FTL, RRM2, SCD
GO:0050661	NADP binding	4	7.65E-05	6.22E-03	DECR1, G6PD, PGD, POR
GO:0016209	antioxidant activity	3	6.26E-03	5.81E-02	NQO1, PRDX1, SRXN1
GO:0046915	transition metal ion transmembrane	3	5.10E-04	1.42E-02	SLC11A2, SLC39A14, SLC40A1

GO:0008199	transporter activity				
	ferric iron binding	2	1.00E-03	2.33E-02	FTL, RRM2
KEGG					
hsa04216	Ferroptosis	8	3.41E-10	6.93E-08	FTL, SLC11A2, SAT1, SLC3A2, TFRC, ATG7, SLC39A14, SLC40A1
hsa04218	Cellular senescence	6	8.34E-04	9.03E-03	CDKN1A, CDKN2A, MAPK3, TSC1, SQSTM1, SIRT1
hsa04068	FoxO signaling pathway	6	3.29E-04	5.74E-03	CDKN1A, MAPK3, MAPK8, STAT3, SIRT1, GABARAPL1
hsa04150	mTOR signaling pathway	5	4.93E-03	2.38E-02	GSK3B, PRKCA, MAPK3, SLC3A2, TSC1
hsa04066	HIF-1 signaling pathway	5	1.06E-03	9.78E-03	CDKN1A, PRKCA, MAPK3, STAT3, TFRC
hsa04012	ErbB signaling pathway	5	3.39E-04	5.74E-03	CDKN1A, GSK3B, PRKCA, MAPK3, MAPK8
hsa04115	p53 signaling pathway	5	1.66E-04	4.07E-03	BID, CDKN1A, CDKN2A, CD82, RRM2
hsa04912	GnRH signaling pathway	4	4.35E-03	2.21E-02	ATF4, PRKCA, MAPK3, MAPK8
hsa04978	Mineral absorption	4	8.12E-04	9.03E-03	FTL, SLC11A2, VDR, SLC40A1
hsa00480	Glutathione metabolism	3	7.82E-03	3.31E-02	G6PD, PGD, RRM2