

Supplementary Table 8. 83 genes are common to ChIP-SEQ and microarray analyses

Name	Peak numbers	Expression (fold change RER/WT)	Full name	Process
Abcb10	739, 1367	1.69	ATP-binding cassette, sub-family B (MDR/TAP), member 10	transport
Adrb2	151, 2077, 2273, 2598	0.64	adrenergic, beta-2-, receptor, surface	signaling (G-protein)
Agrn	1656	0.35	agrin	signaling (receptor clustering)
Ap1m1	406, 2739	0.63	adaptor-related protein complex 1, mu 1 subunit	transport
Aqp11	2194	0.53	aquaporin 11	transport, water channel
Aqp9	38, 885, 2497	0.105	aquaporin 9	transport, water channel
Arl3	1080	0.58	ADP-ribosylation factor-like 3	signaling (GTPase), cell cycle
Atp6v0a1	279, 2274	0.63	ATPase, H+ transporting, lysosomal V0 subunit a1	transport (H+), ATPase
B3gnt7	2701	0.67	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	metabolic process (glycosylation)
Blvra	2973	0.63	biliverdin reductase A	heme catabolism
Bzrpl1	228	0.41	benzodiazapine receptor (peripheral)-like 1	signaling
Capn5	1700	0.35	calpain 5	metabolism, proteolysis
Cd47	146, 855, 2902	0.53	CD47 molecule	adhesion
Chd3	2249	1.61	chromodomain helicase DNA binding protein 3	transcription (chromatin modification)
Cldn10	603	2.04	claudin 10	adhesion
Cnnm2	1150, 1762	1.54	cyclin M2	transport
Dapp1	696, 1012, 1956	3.57	dual adaptor of phosphotyrosine and 3-phosphoinositides	signaling (dual adaptor)
Ddhd1	1554	0.53	DDHD domain containing 1	metabolism
Dusp1	1351, 2565	1.64	dual specificity phosphatase 1	signaling (MAP kinase)
E2f2	179	0.57	E2F transcription factor 2	transcription (regulation) cell cycle
Eapp	763, 1037, 1388, 1445, 2616	0.58	E2F-associated phosphoprotein	transcription (regulation) cell cycle
Egln3	1025, 2061, 2139	0.59	egl nine homolog 3 (C. elegans)	oxidation reduction, response to hypoxia
Emilin2	1049, 1907, 2543	2.22	elastin microfibril interfacer 2	adhesion
Epor	44	0.7	erythropoietin receptor	signaling (erythroid)
Etohd2	63, 1811	0.47	ethanol decreased 2	
F2rl2	1104	0.67	coagulation factor II (thrombin) receptor-like 2	signaling (G-protein) (coagulation)
Fhl1	2491	1.75	four and a half LIM domains 1	transcription (regulation)
Gadd45q	387, 749, 1412, 1689	0.69	growth arrest and DNA-damage-inducible, gamma	cell cycle arrest, DNA repair
Galnt10	846, 985	2.38	10 (GalNAc-T10)	metabolism (glycosylation)
Gda	1415	0.63	guanine deaminase	metabolism
Gfap	417	0.68	glial fibrillary acidic protein	cytoskeleton organisation (actin)
Glrp1	2365	0.7	glutamine repeat protein 1	
Gnq2	2447	2.22	guanine nucleotide binding protein (G protein), gamma 2	signaling (G-protein)
Gpr146	655, 1014, 1055	0.63	G protein-coupled receptor 146	signaling (G-protein)
Gtpbp2	531	0.48	GTP binding protein 2	signaling (G-protein)
Hbb-b2	327, 403, 977 (Mare)	20	hemoglobin, beta 2	transport
Hemgn	172, 325	0.37	hemogen	proliferation, hematopoiesis
Hmbs	109, 112	0.38	hydroxymethylbilane synthase	heme catabolism
Hs3st3a1	1641	0.54	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	metabolic process
Iqsf3	461	0.42	immunoglobulin superfamily, member 3	
Il10ra	316	0.53	interleukin 10 receptor, alpha	signaling (Jak-Stat)
Isg20	675	0.6	interferon stimulated exonuclease gene 20kDa	metabolism (DNA and RNA catabolism)
Itga2b	2001	0.64	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	adhesion, signaling, hematopoiesis (CD41)
Itga4	1665, 2311	0.52	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	adhesion, signaling, hematopoiesis (CD49d)
Klf5	1619	2.12	Kruppel-like factor 5 (intestinal)	transcription (regulation)
Klf7	2619	0.54	Kruppel-like factor 7 (ubiquitous)	transcription (regulation)
Lama5	2185	0.66	laminin, alpha 5	adhesion, migration
Lpin2	330, 2058	1.87	lipin 2	metabolism
Lpl	1885	0.04	lipoprotein lipase	metabolism
Ltbp1	1454	0.53	latent transforming growth factor beta binding protein 1	signaling (TGFbeta)
Mef2c	2188	0.71	myocyte enhancer factor 2C	transcription (regulation)

Mrpl9	2917	0.72	mitochondrial ribosomal protein L9	translation
Nars	411, 1876	0.62	asparaginyl-tRNA synthetase	translation
Nfia	2223, 2672	1.69	nuclear factor I/A	transcription (regulation)
P2ry1	190	1.45	purinergic receptor P2Y, G-protein coupled, 1	signaling and transport
P4ha2	2204	0.57	prolyl 4-hydroxylase, alpha polypeptide II	oxidation reduction, metabolism
Pacs1	783	0.61	phosphofurin acidic cluster sorting protein 1	metabolic process (protein)
Pcsk9	1081, 1301	0.55	proprotein convertase subtilisin/kexin type 9	metabolism
Pcx	337	0.67	pyruvate carboxylase	metabolism (lipid biosynthetic process)
Pdk1	1686	0.44	pyruvate dehydrogenase kinase, isozyme 1	signaling
Ppm1e	1023, 1510	0.61	protein phosphatase 1E (PP2C domain containing)	cell cycle
Ppox	30	0.6	protoporphyrinogen oxidase	metabolic process, heme catabolic process
Prdx2	158	0.11	peroxiredoxin 2	oxidation reduction, apoptosis
Prkar2b	93, 99, 195, 1755	0.37	protein kinase, cAMP-dependent, regulatory, type II, beta	signaling
Ptdss2	556, 1230, 1916, 2911	0.7	phosphatidylserine synthase 2	metabolic process
Rad23a	750	0.56	RAD23 homolog A (S. cerevisiae)	DNA repair
Rgs10	1083, 1272	0.45	regulator of G-protein signaling 10	signaling (G-protein)
Ryk	1778	1.47	RYK receptor-like tyrosine kinase	signaling
Scoc	277	0.36	short coiled-coil protein	
Sds1	1097	2.13	serine dehydratase-like	metabolism
Slc2a3	1040	1.43	solute carrier family 2 (facilitated glucose transporter), member 3	transport (solute carrier)
Slc4a1	505, 585	0.2	band 3, Diego blood group)	transport (solute carrier), erythroid, band3
Slc6a9	308, 450	0.54	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	transport (solute carrier)
Sphk1	392, 593, 903, 2591	0.34	sphingosine kinase 1	signaling (VEGF), apoptosis, migration, cell cycle, sphingolipid metabolism
Spna1	22, 1197	0.47	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	cytoskeleton organisation (actin), spectrin 1, erythroid
Tbxas1	85	1.72	thromboxane A synthase 1 (platelet)	oxidation reduction, metabolism
Tgfb3	1654	0.48	transforming growth factor, beta receptor III	signaling (TGFbeta, BMP)
Tnfaip8	131, 2089	1.51	tumor necrosis factor, alpha-induced protein 8	apoptosis (TNF-induced)
Trib2	1737	2.94	tribbles homolog 2 (Drosophila)	apoptosis, hematopoiesis, signaling (MAP kinase)
Trib3	2803	0.6	tribbles homolog 3 (Drosophila)	apoptosis, hematopoiesis
Txn1l	809	0.1	thioredoxin-like 1	oxidation reduction, electron transport chain
Ubash3a	2323, 2818	0.63	ubiquitin associated and SH3 domain containing, A	ubiquitination
Uros	364, 488, 2426	0.67	uroporphyrinogen III synthase	heme catabolism