Supplementary Table 8. Molecular function analysis of differentially downregulated genes.

GO.ID	Term	Ontology	Count	Pop.Hits	List.Total	Pop.Total	Fold.Enrichment	Pvalue	FDR	Enrichment.Score	GENES
GO:0005488	binding	Molecular function	104	10871	169	23059	1.30532185136177	0.000112351631878832	0.100554710531555	3.94942061518233	D630042P16RIK//ATP7B//CIRBP//GALK1//KIF9//LATS1//LATS2//STK35//CPEB4//DYRK2//ITGB1BP3//RASL12//KATNAL2//ESRP2//MAGI3//TUBG2//ACVR1C//IP6K3//BFSP1//CACNB1//RUNX1T1//GRIN2B//MARCKS//PIAS2//NKX3-1//STMN2//SIX1//TERF2//ZBTB17//HEYL//CD200R1//RNF220//TEX19.2//WHRN//TNFRSF23//ANK2//EMID2//MKL1//ISLR2//KCP//A730011L01RIK//PDP1//C1RA//CD248//CAPN9//EFHD1//SCGN//SYNRG//EGFL7//CDA//ZFP2//ZFP62//SREK1IP1//ZFP618//ARPP21//HHEX//HOXB6//MBD4//PITX1//RFX2//TCF25//SMARCC2//CASZ1//HIST3H2A//FOXO6//LSM6//TCEAL8//TCEAL5//LIMA1//MIB2//GPRC5C//CCL24//IFNE//ALOX8//HEPH//B4GALT2//ZFP566//NT5DC3//TPH2//WDFY2//CACNA2D4//ENKUR//ECM2//NME5//BAIAP2L2//FAM109B//MGLL//GOLPH3//SEC14L2//HMGA1//LIPH//ADAM23//C1QTNF6//ABAT//PDE6H//ADRA2C//ACPP//CHRNB4//PCSK5//PROM1//GALR2//CTNNA2//CHDH//TTC5
GO:0043176	amine binding	Molecular function	5	145	169	23059	4.70495817180167	0.00435525456783478	0.902475224163372	2.36098645508232	GRIN2B//TPH2//ACPP//CHRNB4//ADRA2C
GO:0003785	actin monomer binding	Molecular function	2	14	169	23059	19.4919695688926	0.004585957150133	0.902475224163372	2.33857000751008	LIMA1//MKL1
GO:0043169	cation binding	Molecular function	38	3426	169	23059	1.51338701264607	0.00518972340324717	0.902475224163372	2.28485578813315	LATS1//DYRK2//A730011L01RIK//PDP1//C1RA//CD248//CAPN9//EFHD1//SCGN//SYNRG//EGFL7//ALOX8//ATP7B//RUNX1T1//GRIN2B//HEPH//PIAS2//ZBTB17//ZFP2//ZFP62//LATS2//B4GALT2//LIMA1//RNF220//SREK1IP1//ITGB1BP3//CASZ1//CDA//ZFP566//ZFP618//MIB2//NT5DC3//TPH2//WDFY2//ACVR1C//CACNA2D4//ADAM23//ACPP
GO:0043167	ion binding	Molecular function	38	3438	169	23059	1.5081046845042	0.00550069784323376	0.902475224163372	2.25958221046203	LATS1//DYRK2//A730011L01RIK//PDP1//C1RA//CD248//CAPN9//EFHD1//SCGN//SYNRG//EGFL7//ALOX8//ATP7B//RUNX1T1//GRIN2B//HEPH//PIAS2//ZBTB17//ZFP2//ZFP62//LATS2//B4GALT2//LIMA1//RNF220//SREK1IP1//ITGB1BP3//CASZ1//CDA//ZFP566//ZFP618//MIB2//NT5DC3//TPH2//WDFY2//ACVR1C//CACNA2D4//ADAM23//ACPP
GO:0042803	protein homodimerization activity	Molecular function	10	538	169	23059	2.53612986955852	0.00648057175405533	0.902475224163372	2.1883866764323	ADRA2C//RUNX1T1//HHEX//TERF2//MGLL//HEYL//ACPP//CDA//ABAT//FAM109B
GO:0046872	metal ion binding	Molecular function	37	3385	169	23059	1.49140919301128	0.00741123949254666	0.902475224163372	2.13010915237742	LATS1//DYRK2//A730011L01RIK//PDP1//C1RA//CD248//CAPN9//EFHD1//SCGN//SYNRG//EGFL7//ALOX8//TPH2//ATP7B//HEPH//RUNX1T1//GRIN2B//PIAS2//ZBTB17//ZFP2//ZFP62//ADAM23//LIMA1//RNF220//SREK1IP1//CASZ1//CDA//ZFP618//MIB2//LATS2//B4GALT2//ITGB1BP3//ZFP566//NT5DC3//WDFY2//ACVR1C//CACNA2D4

GO:0050839	cell adhesion molecule binding	Molecular function	3	56	169	23059	7.30948858833474	0.00806681764615305	0.902475224163372	2.09329776035772	CTNNA2//PROM1//GRIN2B
GO:0042165	neurotransmitter binding	Molecular function	2	22	169	23059	12.4039806347499	0.0112030151762681	1	1.95066507570628	CHRNB4//GRIN2B
GO:0045296	cadherin binding	Molecular function	2	22	169	23059	12.4039806347499	0.0112030151762681	1	1.95066507570628	CTNNA2//PROM1
GO:0003746	translation elongation factor activity	Molecular function	2	24	169	23059	11.370315581854	0.0132579979736347	1	1.87752205169647	TCEAL8//TCEAL5
GO:0046983	protein dimerization activity	Molecular function	12	799	169	23059	2.04921832764328	0.0149294962107943	1	1.82595484710174	ADRA2C//RUNX1T1//HHEX//TERF2//MGLL//HEYL//ACPP//CDA//ABAT//FAM109B//GRIN2B//LSM6
GO:0016776	phosphotransferase activity, phosphate group as acceptor	Molecular function	2	28	169	23059	9.74598478444632	0.0178142437407997	1	1.74923260980856	IP6K3//NME5
GO:0030331	estrogen receptor binding	Molecular function	2	28	169	23059	9.74598478444632	0.0178142437407997	1	1.74923260980856	PIAS2//NKX3-1
GO:0005262	calcium channel activity	Molecular function	3	76	169	23059	5.3859389598256	0.0184011334874324	1	1.73515542415485	CACNB1//GRIN2B//CACNA2D4
GO:0003676	nucleic acid binding	Molecular function	28	2565	169	23059	1.4894448481493	0.0204093433889738	1	1.69017096721595	NKX3-1//HEYL//HHEX//HOXB6//MBD4//PIAS2//PITX1//RFX2//SIX1//TERF2//ZBTB17//ZFP2//TCF25//SMARCC2//CASZ1//ZFP618//HIST3H2A//FOXO6//CIRBP//CPEB4//ESRP2//LSM6//TCEAL8//TCEAL5//ZFP62//SREK1IP1//ARPP21//MKL1
GO:0003700	sequence-specific DNA binding transcription factor activity	Molecular function	11	743	169	23059	2.02002914778564	0.0213039945678316	1	1.67153895730705	NKX3-1//HEYL//HMGA1//FOXO6//RUNX1T1//HHEX//HOXB6//PITX1//SIX1//ZBTB17//TCF25
GO:0001071	nucleic acid binding transcription factor activity	Molecular function	11	745	169	23059	2.01460625074461	0.0216779889405665	1	1.66398100961177	NKX3-1//HEYL//HMGA1//RUNX1T1//HHEX//HOXB6//PITX1//SIX1//ZBTB17//TCF25//FOXO6
GO:0046914	transition metal ion binding	Molecular function	19	1591	169	23059	1.62943554535683	0.0243455955748602	1	1.6135795966896	ALOX8//TPH2//ATP7B//HEPH//RUNX1T1//GRIN2B//PIAS2//ZBTB17//ZFP2//ZFP62//ADAM23//LIMA1//RNF220//SREK1IP1//CASZ1//CDA//ZFP618//MIB2//DYRK2
GO:0004252	serine-type endopeptidase activity	Molecular function	4	152	169	23059	3.59062597321707	0.0257989106806746	1	1.58839863106621	PCSK5//C1RA//PRSS23//PRSS48
GO:0016298	lipase activity	Molecular function	3	88	169	23059	4.6514927380312	0.026964375708401	1	1.56920963024454	LIPH//PRDX6//MGLL
GO:0016787	hydrolase activity	Molecular function	24	2171	169	23059	1.50836061150344	0.0274221727587433	1	1.56189813744772	RASL12//TUBG2//CAPN9//KIF9//PCSK5//C1RA//PRSS23//PRSS48//NAGPA//ACPP//ATP7B//KATNAL2//MGLL//PDE6H//CDA//BC051665//ADAM23//TRFR2//A730011L01RIK//LIPH//PRDX6//PDP1//MBD4//NT5DC3
GO:0000287	magnesium ion binding	Molecular function	4	159	169	23059	3.43254810018235	0.0297669740460767	1	1.52626531120091	LATS1//DYRK2//A730011L01RIK//PDP1
GO:0003824	catalytic activity	Molecular function	48	5078	169	23059	1.28974040471602	0.0303024020547532	1	1.5185229438483	RASL12//TUBG2//IP6K3//CAPN9//CHST2//KIF9//PCSK5//C1RA//PRSS23//PRSS48//B4GALT2//AGPAT1//ABAT//HMGA1//NAGPA//ACPP//ATP7B//KATNAL2//MGLL//PDE6H//CDA//BC051665//ADAM23//TRFR2//GALK1//TPH2//A730011L01RIK//NME5//PRDX6//LIPH//LATS1//LATS2//STK35//DYRK2//ACVR1C//PDP1//RNF220//MIB2//ALOX8//HEPH//CHDH//CHST1//ITGB1BP3//MAGI3//SEC14L2//MBD4//NT5DC3//PIAS2
GO:0035257	nuclear hormone receptor binding	Molecular function	3	94	169	23059	4.35458894624197	0.0319162244938063	1	1.49598848882773	PIAS2//NKX3-1//HMGA1
GO:0042802	identical protein binding	Molecular function	11	798	169	23059	1.88080408120894	0.0334480399400255	1	1.47562932686991	ADRA2C//RUNX1T1//HHEX//TERF2//MGLL//HEYL//ACPP//CDA//ABAT//FAM109B//C1QTNF6
GO:0005509	calcium ion binding	Molecular function	8	508	169	23059	2.14872105483856	0.0340493208420982	1	1.46789154623198	C1RA//CD248//CAPN9//EFHD1//SCGN//SYNRG//EGFL7//PDP1

GO:0043178	alcohol binding	Molecular function	2	42	169	23059	6.49732318963088	0.0379672961016392	1	1.42059033069668	ACPP//ADRA2C
GO:0005231	excitatory extracellular ligand-gated ion channel activity	Molecular function	2	45	169	23059	6.06416831032216	0.0430415177722582	1	1.36611242255323	CHRNB4//GRIN2B
GO:0001047	core promoter binding	Molecular function	2	46	169	23059	5.93233856444559	0.0447861662198357	1	1.34885611238968	HEYL//NKX3-1
GO:0008146	sulfotransferase activity	Molecular function	2	48	169	23059	5.68515779092702	0.04835248014889	1	1.31558124469675	CHST2//CHST1