Supplementary Fig.1. Complete list of Hand2-regulated genes.

Gene Symbol	Fold Change	Gene Name	Functional Class	P-value	Affymatrix ID
Lepr	-30.40	leptin receptor	receptor	0.0017	1425644_at
Gja5	-23.87	gap junction membrane channel protein alpha 5; connexin 40	channels/transporters	0.0150	1429101_at
Insm1	-20.70	insulinoma-associated 1; IA-1	transcription factors	0.0039	1455865_at
Ctsl	-20.58	cathepsin L	enzymes	0.0050	1457724_at
8030497I03Rik	-18.9	RIKEN cDNA 8030497I03 gene	unknown	0.0269	1442824_at
Amph	-18.8	amphiphysin	cytoskeleton	0.0021	1427044_a_at
2810417H13Rik	-16.53	RIKEN cDNA 2810417H13 gene	unknown	0.0001	1419152_at
9030411K21Rik	-15.77	RIKEN cDNA 9030411K21 gene	unknown	0.0334	1429846_at
Ifnz	-14.86	interferon zeta	ligands	0.0140	1427216_at
Cdc42bpa	-14.43	Cdc42 binding protein kinase alpha	kinases/phosphatases	0.0079	1442260_at
Nav2	-12.87	neuron navigator 2	enzymes	0.0226	1441353_at
Prdx2	-12.02	peroxiredoxin 2	enzymes	0.0019	1430979_a_at
2700078E11Rik	-11.38	RIKEN cDNA 2700078E11 gene	enzymes	0.0481	1438748_at
Arhgap26	-10.09	Rho GTPase activating protein 26	GTPases/G protein adaptors/regulators	0.0043	1444128_at
5730409L17Rik	-9.71	RIKEN cDNA 5730409L17 gene	unknown	0.0017	1431380_at
Khdrbs1	-8.85	KH domain containing, RNA binding, signal transduction associated 1	nucleotide binding	0.0082	1438462_x_at
1110030E23Rik	-8.4	RIKEN cDNA 1110030E23 gene	unknown	0.0344	1455219_at
Mid1	-8.26	midline 1	cytoskeleton	0.0272	1438239_at
Efhd1	-8.2	EF hand domain containing 1	adaptors/regulators	0.0437	1448507_at
Mtmr7	-6.41	myotubularin related protein 7	kinases/phosphatases	0.0028	1447831_s_at
Prph	-6.41	peripherin	receptors	0.0195	1422530_at
E030030I06Rik	-6.29	RIKEN cDNA E030030I06 gene	unknown	0.0288	1442156_at
Rgs5	*-6.13*	*regulator of G-protein signaling 5*	*GTPases/G protein adaptors/regulators*	*0.0127*	*1420940_x_at, 1417466_at*
3110045C21Rik	-6.1	RIKEN cDNA 3110045C21 gene	unknown	0.0138	1430401_at
5730508B09Rik	-5.35	RIKEN cDNA 5730508B09 gene	unknown	0.0212	1447100_s_at
Abcc10	-5.00	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	channels/transporters	0.0252	1447476_at
Rpl17	-5	ribosomal protein L17	adaptors/regulators	0.0005	1453752_at
Rif1	-4.98	Rap1 interacting factor 1 homolog (yeast)	adaptors/regulators	0.0196	1429490_at
Il15	-4.83	interleukin 15	ligands	0.0352	1418219_at
Ank3	-4.81	ankyrin 3, epithelial	cytoskeleton	0.0413	1447259_at
Serpinb6b	-4.74	serine (or cysteine) peptidase inhibitor, clade B, member 6b	adaptors/regulators	0.0064	1422804_at
Mybpc1	-4.67	myosin binding protein C, slow-type	cell adhesion	0.0357	1455645_at
Rab6b	-4.67	RAB6B, member RAS oncogene family	GTPases/G protein adaptors/regulators	0.0071	1434914_at
Efhd2	-4.57	EF hand domain containing 2	adaptors/regulators	0.0014	1437478_s_at
C80913	-4.52	expressed sequence C80913	unknown	0.0005	1433913_at
BC005512 /// EG641366 /// LOC215866 /// LOC629242	-4.52	cDNA sequence BC005512 /// hypothetical protein LOC215866 /// hypothetical protein LOC629242 /// predicted gene, EG641366	unknown	0.0426	1435628_x_at
Ang	-4.50	angiogenin, ribonuclease, RNase A family, 5	enzymes	0.0182	1438936_s_at
Fam132a	-4.48	family with sequence similarity 132, member A	unknown	0.0007	1439422_a_at
LOC553091	-4.39	hypothetical LOC553091	unknown	0.0009	1456130_at

Epcam	-4.27	epithelial cell adhesion molecule	cell adhesion	0.0303	1447899_x_at
Upk1b	-4.15	uroplakin 1B	receptors	0.0319	1435831_at
Pcdh9	-4.07	protocadherin 9	cell adhesion	0.0200	1429861_at
Gins1	-4.00	GINS complex subunit 1 (Psf1 homolog)	nucleotide binding	0.0212	1457981_x_at
Eme2	-3.97	essential meiotic endonuclease 1 homolog 2 (S. pombe)	enzymes	0.0102	1460628_at
Pdgfd	-3.89	platelet-derived growth factor, D polypeptide	ligands	0.0118	1456532_at
Pcdh21	-3.82	protocadherin 21	cell adhesion	0.0116	1418304_at
C79461	-3.75	expressed sequence C79461	unknown	0.0095	1445973_at
Foxc1	-3.73	forkhead box C1	transcription factors	0.0248	1419485_at
Akr1e1	-3.68	aldo-keto reductase family 1, member E1	enzymes	0.0158	1417826_at
AU044157	-3.65	expressed sequence AU044157	unknown	0.0424	1441151_at
Trim34	-3.57	tripartite motif-containing 34	adaptors/regulators	0.0116	1424857_a_at
ENSMUSG00000073738	-3.55	predicted gene, ENSMUSG00000073738	unknown	0.0058	1439816_at
OTTMUSG00000010657	-3.45	predicted gene, OTTMUSG00000010657	unknown	0.0006	1424784_at
Meox1	-3.44	mesenchyme homeobox 1	transcription factors	0.0317	1417595_at
Galc	-3.36	galactosylceramidase	enzymes	0.0115	1452907_at
Snx6	-3.32	sorting nexin 6	channels/transporters	0.0066	1451602_at
Sox11	*-3.31*	*SRY-box containing gene 11*	*transcription factors*		*1431225_at, 1453002_at*
Pcp4	-3.3	Purkinje cell protein 4	adaptors/regulators	0.0217	1460214_at
Cenpa	-3.27	Centromere protein A	nucleotide binding	0.0209	1444416_at
0610007P08Rik	-3.27	RIKEN cDNA 0610007P08 gene	nucleotide binding	0.0195	1453985_at
A730017C20Rik	-3.27	RIKEN cDNA A730017C20 gene	unknown	0.0234	1437528_x_at
Rala	-3.19	v-ral simian leukemia viral oncogene homolog A (ras related)	GTPases/G protein adaptors/regulators	0.0059	1450870_at
Adamts18	-3.17	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 18	enzymes	0.0434	1437574_at
Wfdc2	-3.11	WAP four-disulfide core domain 2	adaptors/regulators	0.0303	1424351_at
Mdfi	-3.1	MyoD family inhibitor	transcription factors	0.0043	1420713_a_at
BC053393	-3.1	cDNA sequence BC053393	unknown	0.0230	1447604_at
Garnl3	-3.09	GTPase activating RANGAP domain-like 3	GTPases/G protein adaptors/regulators	0.0107	1433553_at
Tns3	-3.08	tensin 3	kinases/phosphatases	0.0289	1446636_at
Stk25	-3.06	serine/threonine kinase 25 (yeast)	kinases/phosphatases	0.0454	1416770_at
Lgals7 /// Samd4	-3.01	lectin, galactose binding, soluble 7 /// sterile alpha motif domain containing 4	cell adhesion	0.0101	1436356_at
Bach2	-3.00	BTB and CNC homology 2	transcription factors	0.0027	1437667_a_at
Mxra7	-3	matrix-remodelling associated 7	unknown	0.0374	1440975_at
Tmeff2	-2.99	transmembrane protein with EGF-like and two follistatin-like domains 2	unknown	0.0081	1419073_at
2610035D17Rik	-2.98	RIKEN cDNA 2610035D17 gene	unknown	0.0332	1453261_at
Usp43	-2.97	ubiquitin specific peptidase 43	enzymes	0.0096	1424866_at
5430405H02Rik	-2.97	RIKEN cDNA 5430405H02 gene	unknown	0.0232	1430366_at
Unc13c	-2.96	unc-13 homolog C (C. elegans)	receptors	0.0051	1455304_at
Dlc1	*-2.93*	*deleted in liver cancer 1*	*GTPases/G protein adaptors/regulators*	*0.0202*	*1436173_at, 1450206_at*
G730007D18Rik	-2.92	RIKEN cDNA G730007D18 gene	unknown	0.0059	1442120_at
LOC552908	-2.89	hypothetical LOC552908	unknown	0.0269	1442213_at
Dsp	-2.86	desmoplakin	cytoskeleton	0.0100	1435493_at
Kcnj11	-2.80	potassium inwardly rectifying channel, subfamily J, member 11	channels/transporters	0.0241	1455417_at

Tgif2	-2.80	TGFB-induced factor 2	transcription factors	0.0494	1431115_at
Pmaip1	-2.8	phorbol-12-myristate-13-acetate-induced protein 1	unknown	0.0071	1418203_at
Zfp593	-2.79	zinc finger protein 593	nucleotide binding	0.0055	1447703_x_at
Zkscan3	-2.79	zinc finger with KRAB and SCAN domains 3	transcription factors	0.0499	1437892_at
BC002163 /// Ndufs5	-2.75	cDNA sequence BC002163 /// NADH dehydrogenase (ubiquinone) Fe-S protein 5	enzymes	0.0107	1416494_at
Coro2b	-2.74	coronin, actin binding protein, 2B	cytoskeleton	0.0087	1434326_x_at
Asah3l	-2.74	N-acylsphingosine amidohydrolase 3-like	enzymes	0.0345	1421496_at
9030425E11Rik	*-2.67*	*RIKEN cDNA 9030425E11 gene*	*cell adhesion*		*1448250_at, 1448251_at*
Hist2h2be	-2.67	histone cluster 2, H2be	nucleotide binding	0.0064	1447854_s_at
Pclo	-2.65	piccolo (presynaptic cytomatrix protein)	cytoskeleton	0.0001	1419392_at
Rfxank	-2.65	regulatory factor X-associated ankyrin-containing protein	transcription factors	0.0060	1455371_at
Spata5l1	-2.63	spermatogenesis associated 5-like 1	unknown	0.0216	1455863_at
2610528B01Rik	-2.62	RIKEN cDNA 2610528B01 gene	unknown	0.0012	1429232_at
Anxa6	-2.6	annexin A6	cytoskeleton	0.0184	1429247_at
D5Ertd255e	-2.57	DNA segment, Chr 5, ERATO Doi 255, expressed	unknown	0.0371	1447526_at
Atp1a2	*-2.56*	*ATPase, Na+/K+ transporting, alpha 2 polypeptide*	*channels/transporters*		*1434893_at, 1427465_at*
1110018J18Rik	-2.56	RIKEN cDNA 1110018J18 gene	unknown	0.0039	1434441_at
Sostdc1	-2.55	sclerostin domain containing 1	ligands	0.0139	1460250_at
H3f3b	-2.55	H3 histone, family 3B	nucleotide binding	0.0178	1430357_at
Gli3	-2.54	GLI-Kruppel family member GLI3	transcription factors	0.0312	1456067_at
Stox2	-2.54	storkhead box 2	unknown	0.0319	1436166_at
Tmem18	-2.54	transmembrane protein 18	unknown	0.0032	1454836_at
Unc84b	-2.53	unc-84 homolog B (C. elegans)	cytoskeleton	0.0483	1439238_at
3110007F17Rik	-2.53	RIKEN cDNA 3110007F17 gene	unknown	0.0219	1439279_at
6720475J19Rik	*-2.49*	*RIKEN cDNA 6720475J19 gene*	*unknown*		*1423071_x_at, 1423072_at*
2210020M01Rik	-2.49	RIKEN cDNA 2210020M01 gene	unknown	0.0007	1435378_at
Eps8	-2.48	epidermal growth factor receptor pathway substrate 8	adaptors/regulators	0.0385	1422824_s_at
Foxp2	-2.45	forkhead box P2	transcription factors	0.0368	1438231_at
Cbln1	-2.44	cerebellin 1 precursor protein	cell adhesion	0.0281	1423286_at
Etaa1	-2.44	Ewing's tumor-associated antigen 1	unknown	0.0064	1457882_at
2700079J08Rik /// Ccrn4l /// LOC100043775	-2.44	CCR4 carbon catabolite repression 4-like (S. cerevisiae) /// RIKEN cDNA 2700079J08 gene /// hypothetical protein LOC100043775	unknown	0.0099	1436362_x_at
Nav1	-2.43	Neuron navigator 1	cytoskeleton	0.0036	1455849_at
Cox6a2	-2.43	cytochrome c oxidase, subunit VI a, polypeptide 2	enzymes	0.0443	1457633_x_at
Ptprg	-2.43	protein tyrosine phosphatase, receptor type, G	receptors	0.0026	1429691_at
1500015A07Rik	-2.42	RIKEN cDNA 1500015A07 gene	unknown	0.0089	1429162_at
LOC100040515	-2.42	Hypothetical protein LOC100040515	unknown	0.0258	1446812_at
Nrxn1	-2.41	neurexin I	cell adhesion	0.0496	1454691_at
Stk38l	-2.38	serine/threonine kinase 38 like	kinases/phosphatases	0.0194	1435878_at
Efha2	-2.38	EF-hand domain family, member A2	unknown	0.0121	1435400_at
Sulf1	-2.35	sulfatase 1	enzymes	0.0260	1436319_at
Pdpn	-2.34	podoplanin	cell adhesion	0.0164	1419309_at
Cadps	-2.34	Ca2+-dependent secretion activator	adaptors/regulators	0.0042	1448955_s_at
Pcdhb3	-2.32	protocadherin beta 3	cell adhesion	0.0425	1420429_at

Rgnef	-2.32	Rho-guanine nucleotide exchange factor	GTPases/G protein adaptors/regulators	0.0331	1419457_at
Sept2	-2.31	septin 2	cytoskeleton	0.0341	1423473_at
4933436C20Rik	-2.31	RIKEN cDNA 4933436C20 gene	unknown	0.0340	1431297_a_at
1700013G23Rik	-2.31	RIKEN cDNA 1700013G23 gene	unknown	0.0064	1438378_at
Sbk1	-2.30	SH3-binding kinase 1	kinases/phosphatases	0.0053	1423978_at
Rabl4	-2.29	RAB, member of RAS oncogene family-like 4	GTPases/G protein adaptors/regulators	0.0023	1434299_x_at
Tgfbi	*-2.29*	*transforming growth factor, beta induced*	*ligands*	*0.0014*	*3_s_at, 1415871_at, 14562*
Nfatc2	-2.29	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	transcription factors	0.0370	1439205_at
Cenpk	-2.28	centromere protein K	adaptors/regulators	0.0183	1457001_at
Sost	-2.27	sclerostin	ligands	0.0471	1450179_at
H2afv	*-2.27*	*H2A histone family, member V*	*nucleotide binding*		*1428029_a_at, 1436596_at*
Fam115a	-2.26	family with sequence similarity 115, member A	unknown	0.0189	1428541_at
1700086O06Rik	-2.26	RIKEN cDNA 1700086O06 gene	unknown	0.0466	1443633_at
Nudt7	-2.25	nudix (nucleoside diphosphate linked moiety X)-type motif 7		0.0036	1430896_s_at
6230424C14Rik	-2.25	RIKEN cDNA 6230424C14 gene	enzymes	0.0413	1429543_at
Fgd6	-2.25	FYVE, RhoGEF and PH domain containing 6	GTPases/G protein adaptors/regulators	0.0058	1435467_at
Thap4	-2.25	THAP domain containing 4	nucleotide binding	0.0275	1447754_x_at
Zfr	-2.25	zinc finger RNA binding protein	nucleotide binding	0.0311	1449552_at
Zfp617	-2.25	zinc finger protein 617	transcription factors	0.0375	1449546_a_at
Cbln4	-2.24	cerebellin 4 precursor protein		0.0342	1433607_at
Txnl4a	-2.23	thioredoxin-like 4A	nucleotide binding	0.0009	1419179_at
Hspa1b	*-2.23*	*heat shock protein 1B*	adaptors/regulators		*1452318_a_at, 1427126_at, 14271*
Tial1	-2.22	Tia1 cytotoxic granule-associated RNA binding protein-like 1	nucleotide binding	0.0125	1426352_s_at
Lca5l /// LOC100044994	-2.21	Leber congenital amaurosis 5-like /// hypothetical protein LOC100044994	unknown	0.0203	1436086_at
1600012F09Rik	-2.21	RIKEN cDNA 1600012F09 gene	unknown	0.0275	1449557_at
EG546524	-2.2	predicted gene, EG546524	unknown	0.0114	1448012_at
Ankrd6	-2.19	ankyrin repeat domain 6	cytoskeleton	0.0363	1437217_at
Vamp3	-2.19	vesicle-associated membrane protein 3	adaptors/regulators	0.0191	1437708_x_at
Slain1	-2.19	SLAIN motif family, member 1	unknown	0.0344	1424824_at
Rhpn2	-2.18	rhophilin, Rho GTPase binding protein 2	cytoskeleton	0.0046	1431805_a_at
Car8 /// LOC676792	-2.18	carbonic anhydrase 8 /// similar to Carbonic anhydrase-related protein (CARP) (CA-VIII)	enzymes	0.0119	1427482_a_at
Ccnjl	-2.18	cyclin J-like	kinases/phosphatases	0.0433	1456168_at
Cxcl12	*-2.18*	*chemokine (C-X-C motif) ligand 12*	*ligands*	*0.0061*	*1448823_at, 1417574_at*
Stau1	-2.18	staufen (RNA binding protein) homolog 1 (Drosophila)	nucleotide binding	0.0002	1435347_at
Arap3	-2.17	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	GTPases/G protein adaptors/regulators	0.0145	1419833_s_at
Camk2a	-2.17	calcium/calmodulin-dependent protein kinase II alpha	kinases/phosphatases	0.0388	1457311_at
Mreg	-2.17	melanoregulin	unknown	0.0246	1437250_at
Zfp503	-2.17	zinc finger protein 503	unknown	0.0195	1423836_at
Adam19 /// LOC100045780	-2.16	a disintegrin and metallopeptidase domain 19 (meltrin beta) /// similar to metalloprotease-disintegrin meltrin beta	enzymes	0.0079	1418402_at
Ube2j2	-2.16	ubiquitin-conjugating enzyme E2, J2 homolog (yeast)	enzymes	0.0450	1430317_at
Usp38	-2.16	ubiquitin specific peptidase 38	enzymes	0.0060	1428592_s_at
Hoxa3	-2.15	homeo box A3	transcription factors	0.0206	1427433_s_at

Cacna2d1	-2.14	calcium channel, voltage-dependent, alpha2/delta subunit 1	channels/transporters	0.0430	1440397_at
Serhl	-2.14	serine hydrolase-like	enzymes	0.0437	1434145_s_at
Ltbp1	-2.13	latent transforming growth factor beta binding protein 1	cell adhesion	0.0371	1447547_at
Scn2b	-2.13	sodium channel, voltage-gated, type II, beta	channels/transporters	0.0138	1430648_at
Tulp4	-2.13	tubby like protein 4	unknown	0.0196	1434585_at
Syt11	-2.12	synaptotagmin XI	receptors	0.0071	1455176_a_at
Rtn1	-2.12	reticulon 1	adaptors/regulators	0.0209	1429761_at
Pard3	-2.11	par-3 (partitioning defective 3) homolog (C. elegans)	cell adhesion	0.0304	1420391_at
B3galnt1	-2.11	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1	enzymes	0.0051	1418736_at
Rnf216	-2.11	Ring finger protein 216	enzymes	0.0162	1458507_at
Ctdspl	-2.11	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	kinases/phosphatases	0.0117	1422510_at
Nr4a2	-2.11	nuclear receptor subfamily 4, group A, member 2	transcription factors	0.0258	1455034_at
Vps41	-2.11	vacuolar protein sorting 41 (yeast)	adaptors/regulators	0.0035	1437901_a_at
1110005A03Rik	*-2.11*	*RIKEN cDNA 1110005A03 gene*	unknown		*1453485_s_at, 1451448_a_at*
Diras2	-2.1	DIRAS family, GTP-binding RAS-like 2	GTPases/G protein adaptors/regulators	0.0104	1455436_at
Bub1	-2.10	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	kinases/phosphatases	0.0221	1438571_at
Hist1h2bb /// Hist1h2bc /// Hist1h2be /// Hist1h2bg /// LOC665622 /// RP23-38E20.1	-2.10	histone cluster 1, H2bc /// histone cluster 1, H2bb /// histone cluster 1, H2be /// histone cluster 1, H2bg /// H2b histone family, member A /// H2b histone family member	nucleotide binding	0.0240	1418072_at
Slc35a5	-2.09	solute carrier family 35, member A5; nucleotide-sugar transporter family	channels/transporters	0.0019	1419971_s_at
Dctn4	-2.09	dynactin 4	cytoskeleton	0.0146	1458541_at
Cask	-2.09	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	kinases/phosphatases	0.0028	1422518_at
Fam89a	-2.09	family with sequence similarity 89, member A	unknown	0.0410	1427356_at
Col11a1	*-2.08*	*collagen, type XI, alpha 1*	*cell adhesion*	*0.0132*	*1418599_at, 1449154_at*
Rerg	-2.08	RAS-like, estrogen-regulated, growth-inhibitor	GTPases/G protein adaptors/regulators	0.0403	1451236_at
Rgs2	-2.08	regulator of G-protein signaling 2	GTPases/G protein adaptors/regulators	0.0111	1447830_s_at
Ssr1	-2.08	signal sequence receptor, alpha; translocon-associated protein (TRAP), alpha	adaptors/regulators	0.0196	1441327_a_at
Tmem66	-2.08	transmembrane protein 66	unknown	0.0081	1424039_at
LOC100047339	-2.07	similar to lysyl oxidase-like 2	cell adhesion	0.0158	1431004_at
Pcmt1	-2.07	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	enzymes	0.0492	1431086_s_at
Mthfd2l	-2.07	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	enzymes	0.0311	1429600_at
Spag1	-2.07	sperm associated antigen 1	adaptors/regulators	0.0453	1419588_at
2900054J07Rik	-2.07	RIKEN cDNA 2900054J07 gene	unknown	0.0208	1439869_at
2610021K21Rik	-2.06	RIKEN cDNA 2610021K21 gene	adaptors/regulators	0.0231	1430339_at
Rpl21	-2.06	ribosomal protein L21	adaptors/regulators	0.0380	1423070_at
Lipa	-2.05	lysosomal acid lipase A	enzymes	0.0431	1423140_at
Zfp697	-2.05	zinc finger protein 697	transcription factors	0.0077	1440999_at

Tanc2	-2.04	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	cytoskeleton	0.0288	1436513_at
Igf2r	-2.04	insulin-like growth factor 2 receptor	receptors	0.0465	1424111_at
Aph1b	-2.04	anterior pharynx defective 1b homolog (C. elegans)	adaptors/regulators	0.0291	1435793_at
Rabif	-2.03	RAB interacting factor	GTPases/G protein adaptors/regulators	0.0389	1457969_at
Gpr116	-2.03	G protein-coupled receptor 116	receptors	0.0233	1440830_at
Rps6	-2.03	ribosomal protein S6	adaptors/regulators	0.0289	1416142_at
Cdh5	-2.02	cadherin 5	cell adhesion	0.0202	1433956_at
Col23a1	-2.02	collagen, type XXIII, alpha 1	cell adhesion	0.0429	1429210_at
Rims1	-2.02	regulating synaptic membrane exocytosis 1	cytoskeleton	0.0243	1438305_at
Mmp14	-2.02	matrix metallopeptidase 14 (membrane-inserted)	enzymes	0.0041	1448383_at
Olfml3	-2.02	olfactomedin-like 3	unknown	0.0108	1448475_at
2410002O22Rik	-2.02	RIKEN cDNA 2410002O22 gene	unknown	0.0040	1418667_at
Fry	-2.00	furry homolog (Drosophila)	cytoskeleton	0.0190	1456480_at
Trmt1	-2.00	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	enzymes	0.0032	1436494_x_at
Purg	-2.00	purine-rich element binding protein G	nucleotide binding	0.0035	1452029_a_at
Heyl	-2.00	hairy/enhancer-of-split related with YRPW motif-like	transcription factors	0.0184	1419302_at
Gm1673	-2	gene model 1673, (NCBI)	unknown	0.0468	1434498_at
Mapk8	2.00	mitogen-activated protein kinase 8	enzymes	0.0390	1457936_at
Elovl3	2.01	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	enzymes	0.0157	1420722_at
Metap2	2.01	methionine aminopeptidase 2	enzymes	0.0220	1451048_at
Rbm8a	2.01	RNA binding motif protein 8a	nucleotide binding	0.0488	1418120_at
Map3k10	2.02	mitogen-activated protein kinase kinase kinase 10	kinases/phosphatases	0.0220	1436373_at
4933403F05Rik	2.02	RIKEN cDNA 4933403F05 gene	unknown	0.0334	1443873_at
2210404J11Rik /// 9030025P20Rik /// LOC100041621	2.03	RIKEN cDNA 2210404J11 gene /// RIKEN cDNA 9030025P20 gene /// hypothetical protein LOC100041621	unknown	0.0068	1431007_at
2310035C23Rik	2.04	RIKEN cDNA 2310035C23 gene	adaptors/regulators	0.0331	1430126_at
Mtm1	2.05	X-linked myotubular myopathy gene 1	kinases/phosphatases	0.0426	1454904_at
Stat5b	2.05	signal transducer and activator of transcription 5B	transcription factors	0.0471	1422102_a_at
Tceb3	2.05	transcription elongation factor B (SIII), polypeptide 3	adaptors/regulators	0.0178	1450676_at
Lpin2	2.06	lipin 2	enzymes	0.0091	1460290_at
Pttg1	*2.06*	*pituitary tumor-transforming 1; securin*	*transcription factors*		*1438390_s_at, 1424105_a_a*
4930535I16Rik	2.06	RIKEN cDNA 4930535I16 gene	unknown	0.0267	1430608_at
Tmem37	2.09	transmembrane protein 37	channels/transporters	0.0340	1417611_at
Ppp1cb	2.09	protein phosphatase 1, catalytic subunit, beta isoform	kinases/phosphatases	0.0301	1431328_at
Hdhd3	2.1	haloacid dehalogenase-like hydrolase domain containing 3	kinases/phosphatases	0.0131	1425343_at
Cytl1	2.10	cytokine like 1	ligands	0.0053	1456793_at
Ywhag	2.1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	adaptors/regulators	0.0249	1420816_at
Nol9	2.1	nucleolar protein 9	unknown	0.0071	1432218_a_at
Atic /// LOC100046995	2.11	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase /// similar to 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	enzymes	0.0096	1452811_at
Pi4k2b	2.11	phosphatidylinositol 4-kinase type 2 beta	kinases/phosphatases	0.0168	1420411_a_at

Ssu72	2.11	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	kinases/phosphatases	0.0193	1441282_at
Pabpc4l	2.11	poly(A) binding protein, cytoplasmic 4-like	unknown	0.0386	1431353_at
Arhgef11	2.13	Rho guanine nucleotide exchange factor (GEF) 11	GTPases/G protein adaptors/regulators	0.0267	1443539_at
Cyp2d22	2.14	cytochrome P450, family 2, subfamily d, polypeptide 22	enzymes	0.0206	1419039_at
Nup160	2.15	nucleoporin 160	unknown	0.0308	1444892_at
Eif2ak1	2.16	eukaryotic translation initiation factor 2 alpha kinase 1	kinases/phosphatases	0.0281	1436006_at
Brcc3	2.16	BRCA1/BRCA2-containing complex, subunit 3	adaptors/regulators	0.0476	1426605_at
A930005H10Rik	2.16	RIKEN cDNA A930005H10 gene	unknown	0.0020	1441263_a_at
Lonrf3	2.17	LON peptidase N-terminal domain and ring finger 3	unknown	0.0490	1429863_at
Zfp64	2.21	zinc finger protein 64	adaptors/regulators	0.0042	1430117_a_at
Clock	2.22	circadian locomoter output cycles kaput	transcription factors	0.0102	1439314_at
Trim8	2.24	Tripartite motif protein 8	adaptors/regulators	0.0426	1438679_at
Isoc1	2.26	isochorismatase domain containing 1	enzymes	0.0010	1425050_at
Heatr1	2.27	HEAT repeat containing 1	adaptors/regulators	0.0047	1452419_at
Hddc3	2.28	HD domain containing 3	enzymes	0.0456	1428692_at
C130021I20Rik	2.29	Riken cDNA C130021I20 gene	unknown	0.0239	1455416_at
Kras	2.35	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	GTPases/G protein adaptors/regulators	0.0010	1426229_s_at
Cdyl2	2.42	chromodomain protein, Y chromosome-like 2	unknown	0.0027	1431139_at
Gosr1	2.44	golgi SNAP receptor complex member 1	channels/transporters	0.0087	1448256_at
Fv1	2.44	Friend virus susceptibility 1	adaptors/regulators	0.0360	1422279_at
Fv1	2.44	Friend virus susceptibility 1	unknown	0.0360	1422279_at
Cwc22	2.48	CWC22 spliceosome-associated protein homolog (S. cerevisiae)	adaptors/regulators	0.0403	1438278_a_at
Clasp2	*2.51*	*CLIP associating protein 2*	*cytoskeleton*		*1427328_a_at, 1456911_at*
Cdk6	2.53	cyclin-dependent kinase 6	kinases/phosphatases	0.0088	1460291_at
Rps19	2.55	ribosomal protein S19	adaptors/regulators	0.0326	1460442_at
Acbd4	2.56	acyl-Coenzyme A binding domain containing 4	adaptors/regulators	0.0472	1449626_s_at
Tfrc	*2.57*	*transferrin receptor*	*receptors*	*0.0360*	*X57349_3_at, AFFX-TransR*
Efcab7	2.61	EF-hand calcium binding domain 7	unknown	0.0007	1451349_at
Lsm12	2.67	LSM12 homolog (S. cerevisiae)	unknown	0.0225	1429509_at
Gda	2.69	guanine deaminase	enzymes	0.0319	1435748_at
Cps1	2.82	carbamoyl-phosphate synthetase 1	enzymes	0.0117	1455540_at
Rbm39	*2.91*	*RNA binding motif protein 39*	nucleotide binding		*1446147_at, 1446148_x_at*
Abhd1	2.92	abhydrolase domain containing 1	enzymes	0.0044	1418148_at
Itga9	2.94	integrin alpha 9	receptors	0.0030	1460285_at
Ms4a8a	2.98	membrane-spanning 4-domains, subfamily A, member 8A	receptors	0.0486	1418797_at
---	3.04	(unknown) Transcribed locus, strongly similar to NP_033000.1 protein tyrosine phosphatase 4a2 [Mus musculus]	kinases/phosphatases	0.0135	1435129_at
Rrm1	3.06	ribonucleotide reductase M1	enzymes	0.0158	1440073_at
Ncl	3.14	nucleolin	transcription factors	0.0177	1442404_at
2410076I21Rik	*3.14*	*RIKEN cDNA 2410076I21 gene*	unknown		*1429203_at, 1441957_x_at*
4921537I17Rik	3.31	RIKEN cDNA 4921537I17 gene	unknown	0.0361	1431259_at
Insr	3.47	insulin receptor	receptors	0.0277	1421380_at
Atp10d	3.59	ATPase, class V, type 10D	channels/transporters	0.0150	1436544_at
Masp2	3.60	mannan-binding lectin serine peptidase 2	enzymes	0.0244	1420524_a_at
Pldn	3.63	pallidin	adaptors/regulators	0.0023	1457088_at

2410018L13Rik /// EG245297 /// EG668553 /// EG668645 /// EG668662 /// EG668701 /// EG668710 /// LOC100043377 /// LOC546752	3.72	RIKEN cDNA 2410018L13 gene /// predicted gene, EG245297 /// similar to neural visinin-like Ca2+-binding protein type 3 /// predicted gene, EG668553 /// predicted gene, EG668645 /// predicted gene, EG668662 /// predicted gene, EG668701 /// predicted gene, EG668710 /// similar to development and differentiation enhancing factor 2	unknown	0.0032	1439113_at
	3.83	integrin alpha 4 /// ceramide kinase-like	receptors	0.0311	1456498_at
Wdfy1	*3.93*	*WD repeat and FYVE domain containing 1*	adaptors/regulators		*1435588_at, 1437358_at*
OTTMUSG00000010173	3.95	Predicted gene, OTTMUSG00000010173	unknown	0.0220	1439065_x_at
Ddx39	4.46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	enzymes	0.0070	1438287_x_at
Tmem184a	4.57	transmembrane protein 184a	unknown	0.0131	1424477_at
Ap1s3	5.10	adaptor-related protein complex AP-1, sigma 3	channels/transporters	0.0015	1455735_at
Cyct	5.26	cytochrome c, testis	adaptors/regulators	0.0462	1450752_at
Calml3	5.57	calmodulin-like 3	adaptors/regulators	0.0148	1418608_at
Tmem87a	6.85	transmembrane protein 87A	unknown	0.0044	1424454_at
Cap1	*7.21*	*CAP, adenylate cyclase-associated protein 1 (yeast)*	*cytoskeleton*		*1417461_at, 1417462_at*
Defb10	8.19	defensin beta 10	adaptors/regulators	0.0090	1427775_at
Ttll4	8.95	tubulin tyrosine ligase-like family, member 4	enzymes	0.0001	1459031_at
Npvf	10.18	neuropeptide VF precursor	ligands	0.0459	1421686_at
Hba-a1 /// Hba-a2	10.59	hemoglobin alpha, adult chain 1 /// hemoglobin alpha, adult chain 2	channels/transporters	0.0096	1417714_x_at
BC023969	11.18	cDNA sequence BC023969	unknown	0.0002	1445226_at
Tcte3	12.18	t-complex-associated testis expressed 3	adaptors/regulators	0.0342	1421682_a_at
H2-D1	13.27	histocompatibility 2, D region locus 1	receptors	0.0136	1450170_x_at
Pabpc5	13.79	poly A binding protein, cytoplasmic 5	nucleotide binding	0.0236	1446162_at
OTTMUSG00000005148	14.13	predicted gene, OTTMUSG00000005148	unknown	0.0081	1455973_at
LOC100044383 /// Pnpt1	19.57	polyribonucleotide nucleotidyltransferase 1 /// similar to polynucleotide phosphorylase-like protein	enzymes	0.0392	1452677_at
AI506816	32.28	expressed sequence AI506816	unknown	0.0271	1439483_at
Ccnb1ip1	32.47	cyclin B1 interacting protein 1	enzymes	0.0363	1435998_at

Supplementary Fig. 1. **Complete Gene List**. This table contains all of the transcripts regulated downstream of Hand2. . Genes listed in *italics* were detected by multiple probe sets. The reported fold change for these genes is the average value.