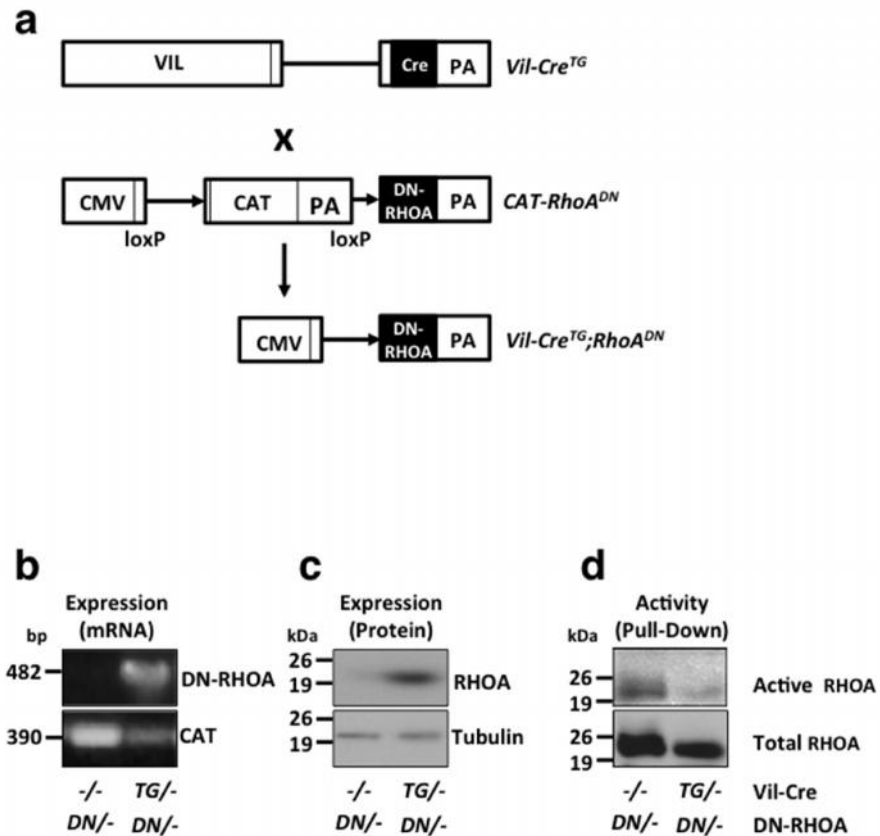


SUPPLEMENTARY INFORMATION

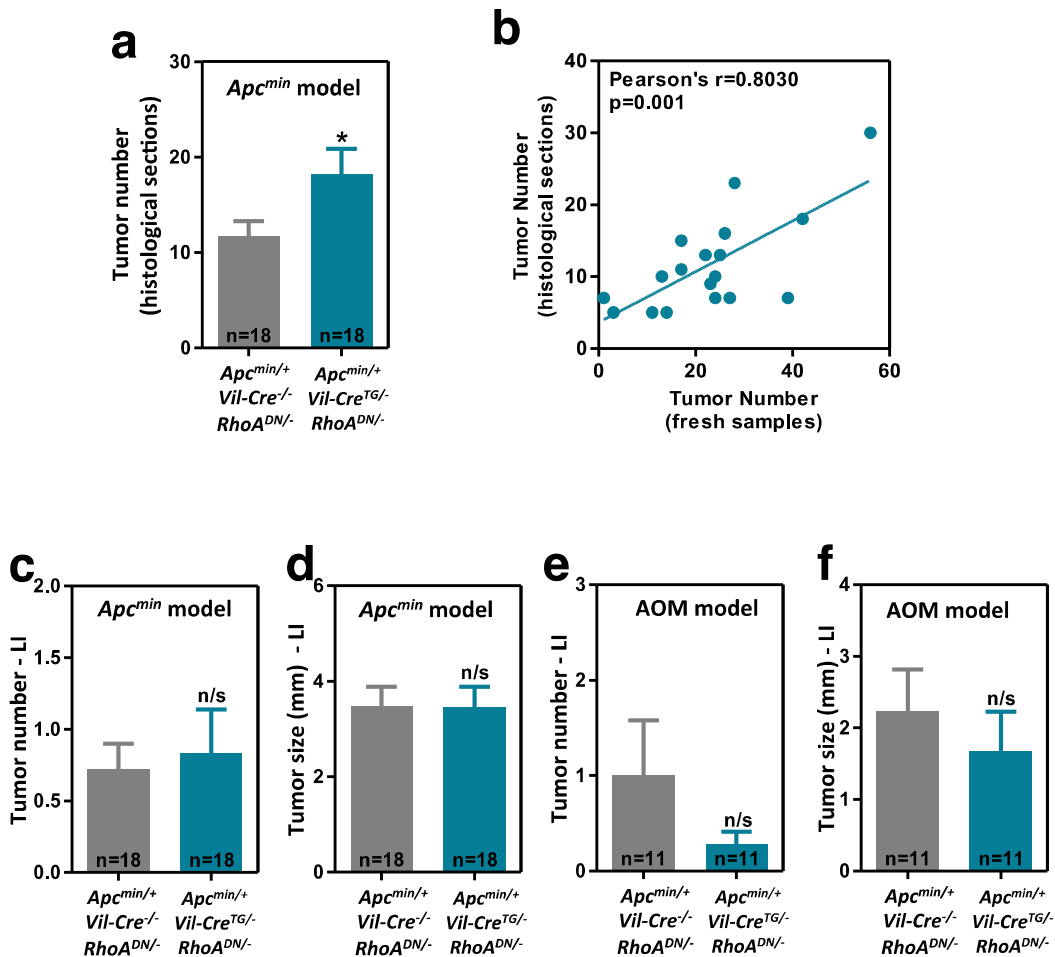
RHOA inactivation enhances Wnt signaling and promotes colorectal cancer

Paulo Rodrigues, Irati Macaya, Sarah Bazzocco, Rocco Mazzolini, Elena Andretta, Higinio Dopeso, Silvia Mateo-Lozano, Josipa Bilic, Fernando Cartón-García, Rocio Nieto, Lucia Suárez-López, Elsa Afonso, Stefania Landolfi, Javier Hernandez-Losa, Kazuto Kobayashi; Santiago Ramón y Cajal, Josep Taberner, Niall C. Tebbutt, John M. Mariadason, Simo Schwartz Jr, Diego Arango.

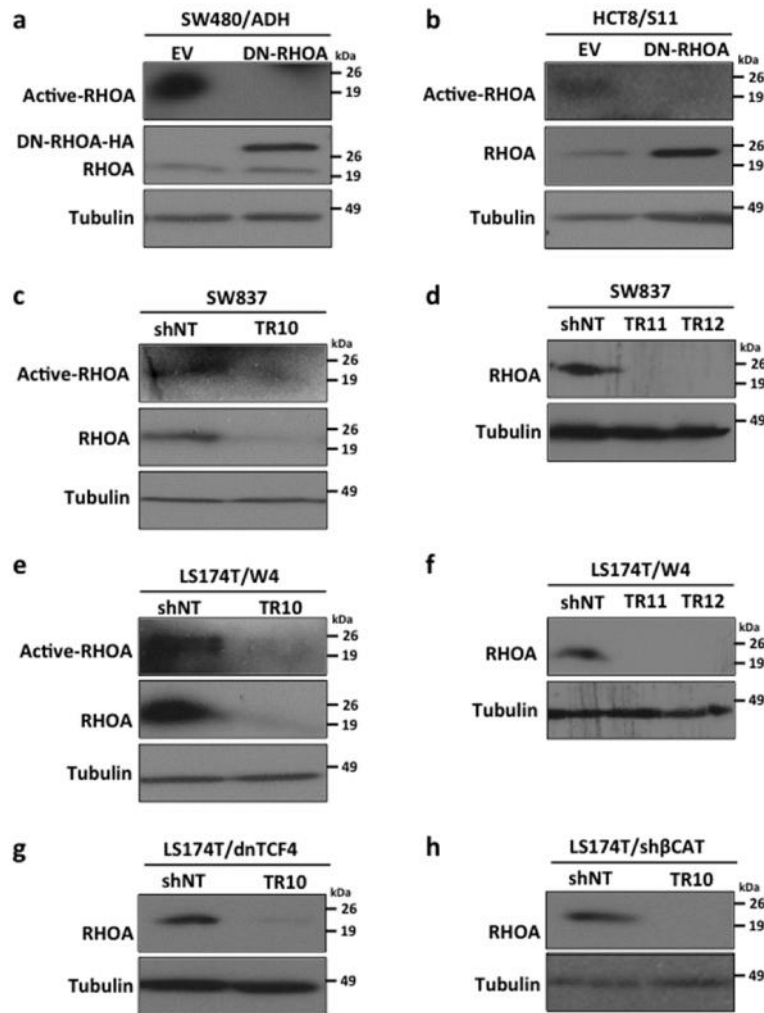
SI FIGURES AND LEGENDS



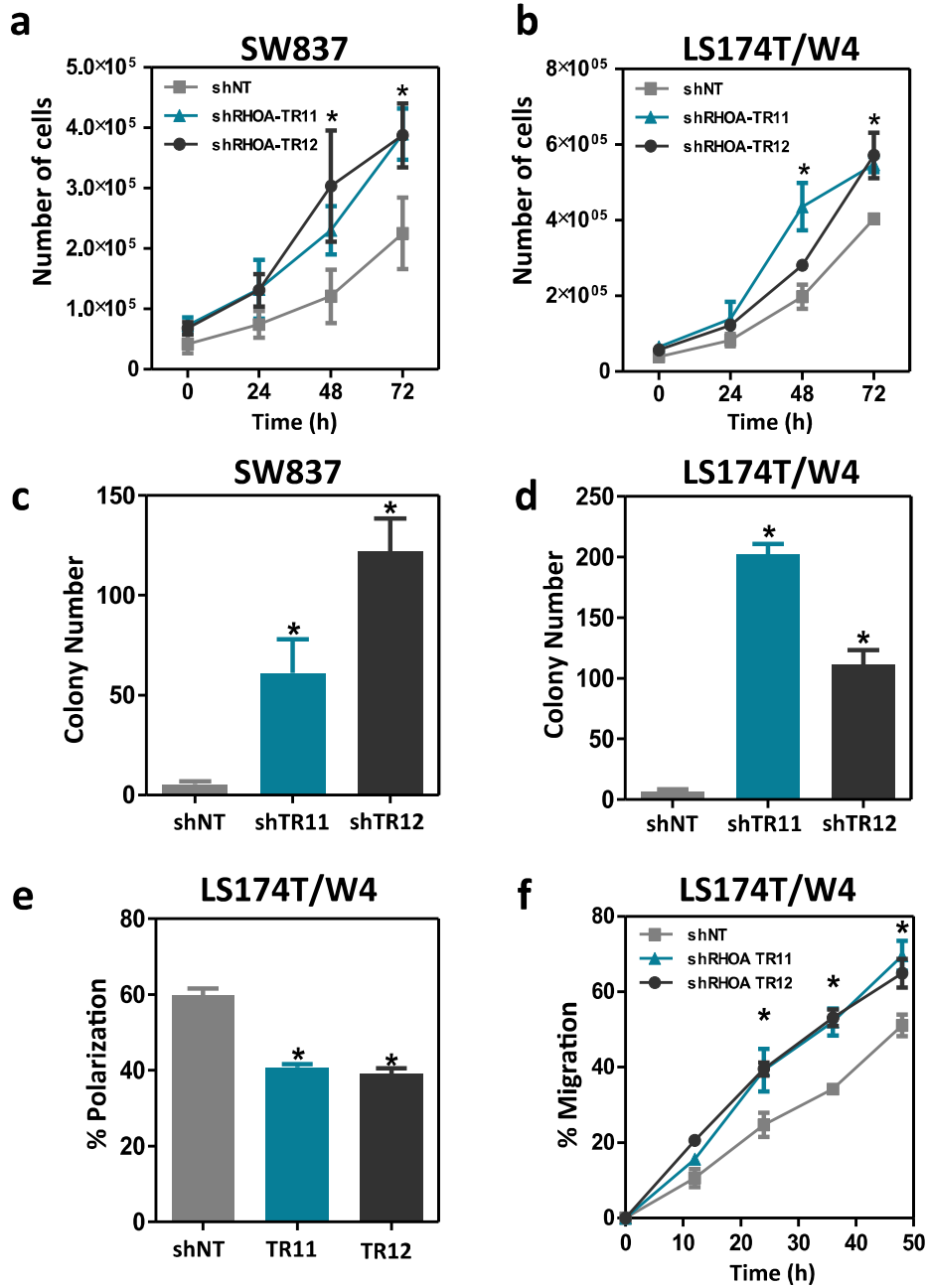
Supplementary Figure 1: Validation of a mouse model conditionally expressing dominant negative RHOA. (a) Mice expressing Cre recombinase under the control of the intestine-specific promoter of *Villin 1* (*Vil-Cre*) were crossed with *Cat-DN-RhoA* mice. In the double transgenic mice (*Vil-Cre*^{TG/-};*RhoA*^{DN/-}), Cre-loxP recombination deletes the *Cat* cassette in the epithelial cells of the intestine, and *DN-RhoA* is then expressed. (b) Total RNA prepared from epithelial cells of the small intestine of *Vil-Cre*^{-/-};*RhoA*^{DN/-} or *Vil-Cre*^{TG/-};*RhoA*^{DN/-} mice was reverse transcribed and the levels of *Cat* and *RhoA* expression in the resulting cDNA samples were assessed after PCR amplification. (c) *RhoA* protein levels were assessed by Western blotting in mucosal samples from *Vil-Cre*^{-/-};*RhoA*^{DN/-} or *Vil-Cre*^{TG/-};*RhoA*^{DN/-} mice. (d) *RhoA* activity in the small intestinal mucosa of *Vil-Cre*^{-/-};*RhoA*^{DN/-} or *Vil-Cre*^{TG/-};*RhoA*^{DN/-} mice was determined by a GST-Rhotekin pulldown assay.



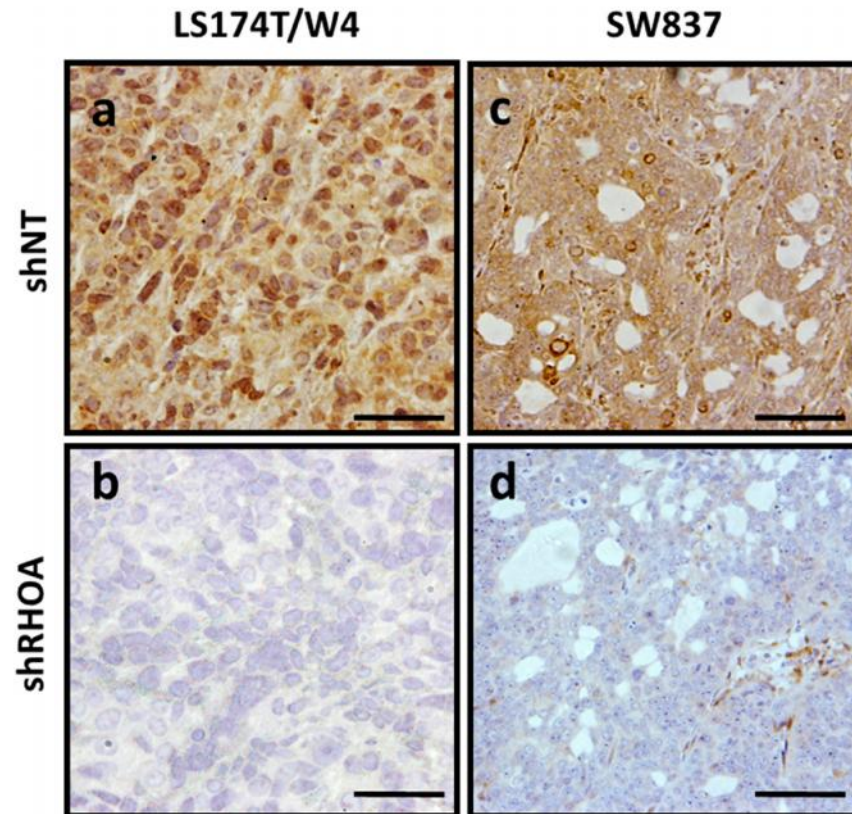
Supplementary Figure 2: Effects of RhoA inactivation on intestinal tumorigenesis in mouse models. (a) Number of tumors in histological sections from the small intestine of *Apc^{min/+}* mice with RhoA inactivation (*Apc^{min/+}; Vil-Cre^{TG/-}; RhoA^{DN/-}*) and control animals with no DN-RhoA expression (*Apc^{min/+}; Vil-Cre^{-/-}; RhoA^{DN/-}*). (b) Correlation between the number of intestinal tumors observed macroscopically and on histological sections. (c-f) The number (c and e) and size (d and f) of macroscopically visible tumors in the large intestine of mice with or without DN-RhoA expression after either genetic (*Apc^{min}* mutations; c and d) or carcinogen (AOM treatment; e and f) tumor initiation was quantified blinded from the animal identity. LI: large intestine. Mean \pm SEM is shown. *Student's t-test $p < 0.05$. N: number of animals. n/s: Student's t-test $p > 0.05$.



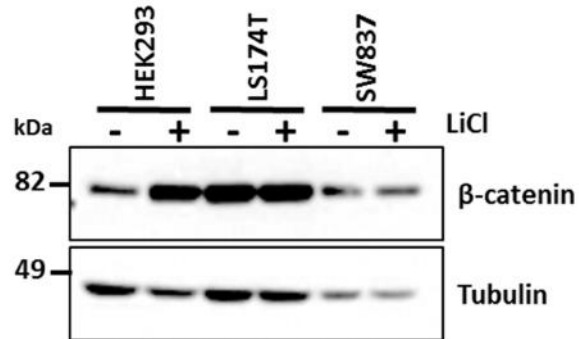
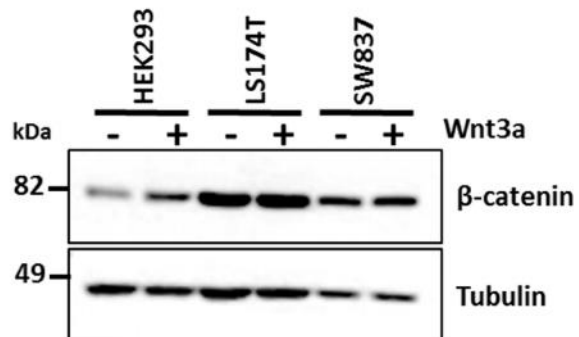
Supplementary Figure 3: Validation of *in vitro* models of RHOA inactivation in colon cancer cells. A dominant negative mutant of RHOA (T19N) was stably overexpressed in SW480/ADH (HA-tagged RHOA; **a**) and HCT8/S11 (un-tagged RHOA; **b**). EV: empty vector control. Stable RHOA knockdowns were generated by transduction with lentivirus expressing three different shRNAs against RHOA (TR10, TR11 and TR12) or a non-target shRNA (shNT) in the colon cancer cell lines SW837 (**c-d**), LS174T/W4 (**e-f**), LS174T/dnTCF4 (**g**) and LS174T/sh β CAT (**h**). The levels of total or active RHOA, as assessed by a GST-Rhotekin pulldown assay, are shown. Tubulin was used as a loading control.



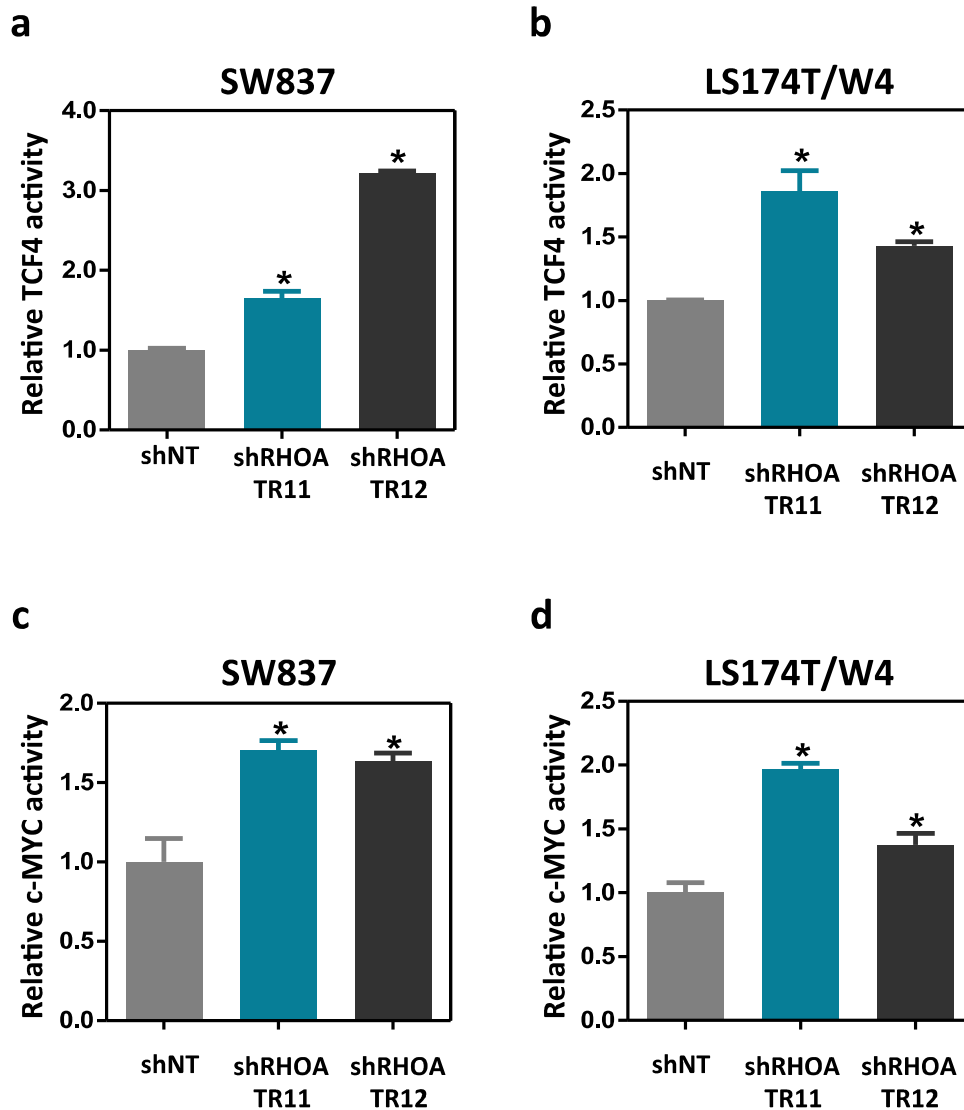
Supplementary Figure 4: Effects of RHOA knockdown on growth, polarization capacity and migration of colon cancer cells. To confirm on-target effects of the RHOA shRNAs used in the study, we assessed the effects of two additional shRNAs (TR11 and TR12) on cell proliferation (**a-b**), soft agar colony formation (**c-d**), polarization (**e**; LS174T/W4 cells after doxycycline-mediated LKB1 activation) and migration (**f**; percentage of wounded area closed after the indicated time) of the indicated colon cancer cells. The mean (\pm SEM) of three independent experiments carried out in triplicate is shown. *Student's t-test $p < 0.05$.



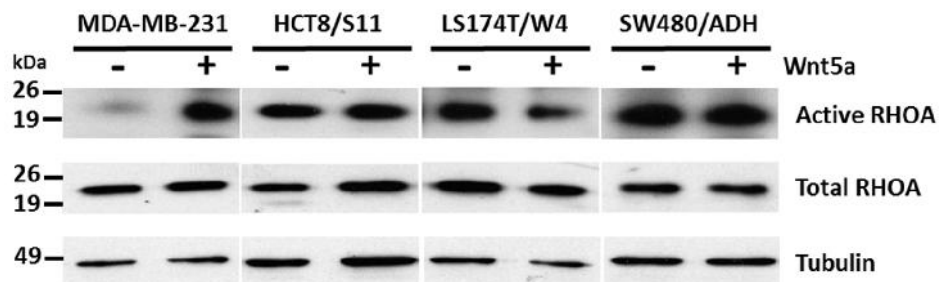
Supplementary Figure 5: Stable shRNA-mediated knockdown of RHOA on colon cancer cells and confirmation of the specificity of the anti-RHOA antibody used. RHOA protein levels were assessed by immunohistochemical staining with a mouse monoclonal anti-RHOA antibody (Santa Cruz; SC-418) on formalin-fixed, paraffin-embedded (FFPE) samples from subcutaneous xenografts of control (shNT) LS174T/W4 (**a**) and SW837 (**c**) cells, or the derivative cell lines with targeted inactivation of RHOA (shRHOA-TR10; **b** and **d**). The reduced levels of RHOA observed in the shRHOA xenografts compared to xenografts of control cells confirms both the knockdown of RHOA and the specificity of this antibody for immunostaining of RHOA on FFPE samples. Scale bars, 50 μ m.

a**b**

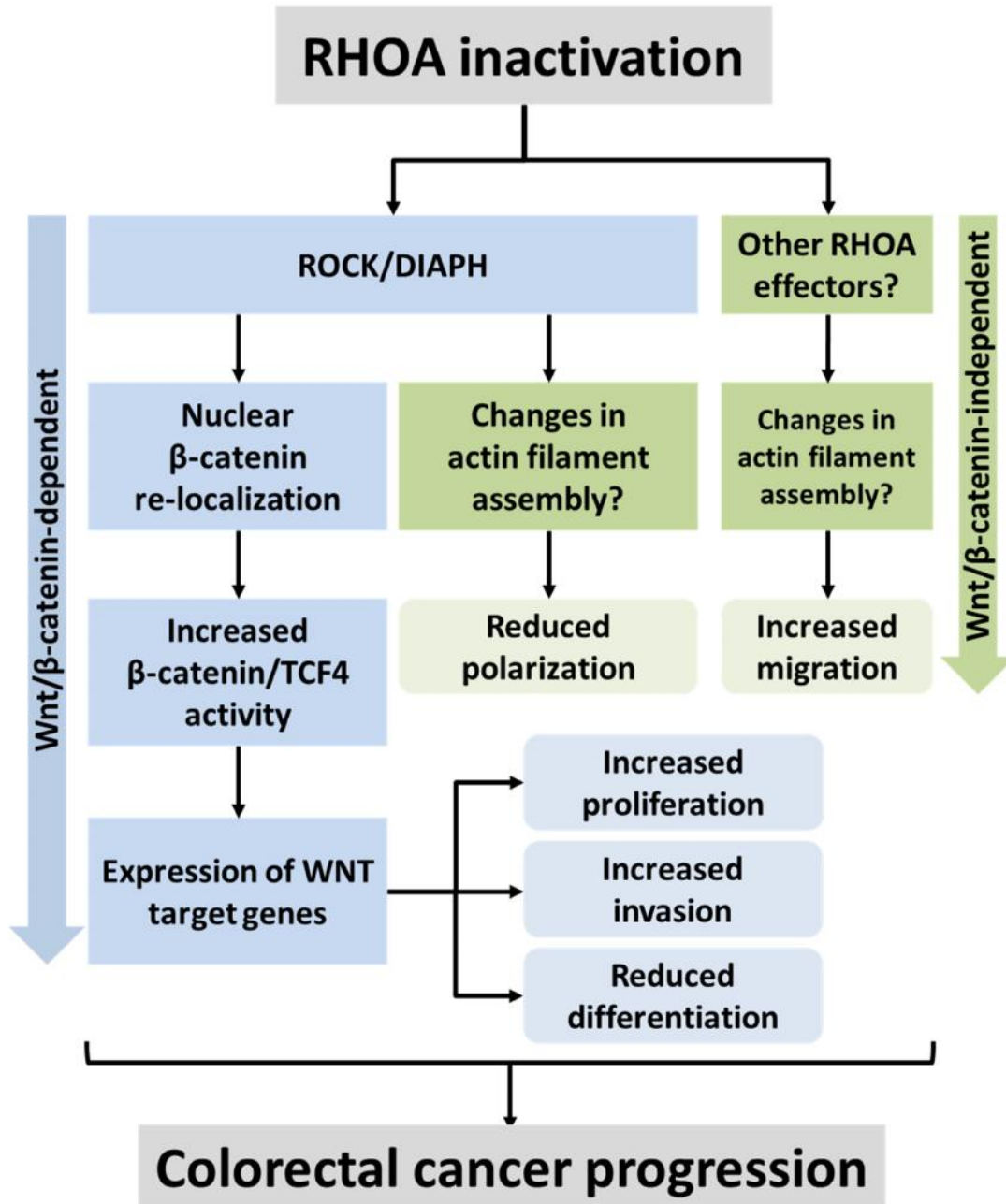
Supplementary Figure 6: β -catenin destruction complex in colon cancer cells. The β -catenin destruction complex was inhibited by either the GSK3 β inhibitor LiCl (**a**) or the physiological canonical Wnt ligand Wnt3a (**b**). Western blotting of total cellular lysates showed elevated β -catenin levels in response to LiCl or Wnt3a in human kidney embryonic HEK293 cells, while no changes in total β -catenin were observed in the colon cancer cell lines tested (LS174T and SW837 cells). Tubulin was used as a loading control.



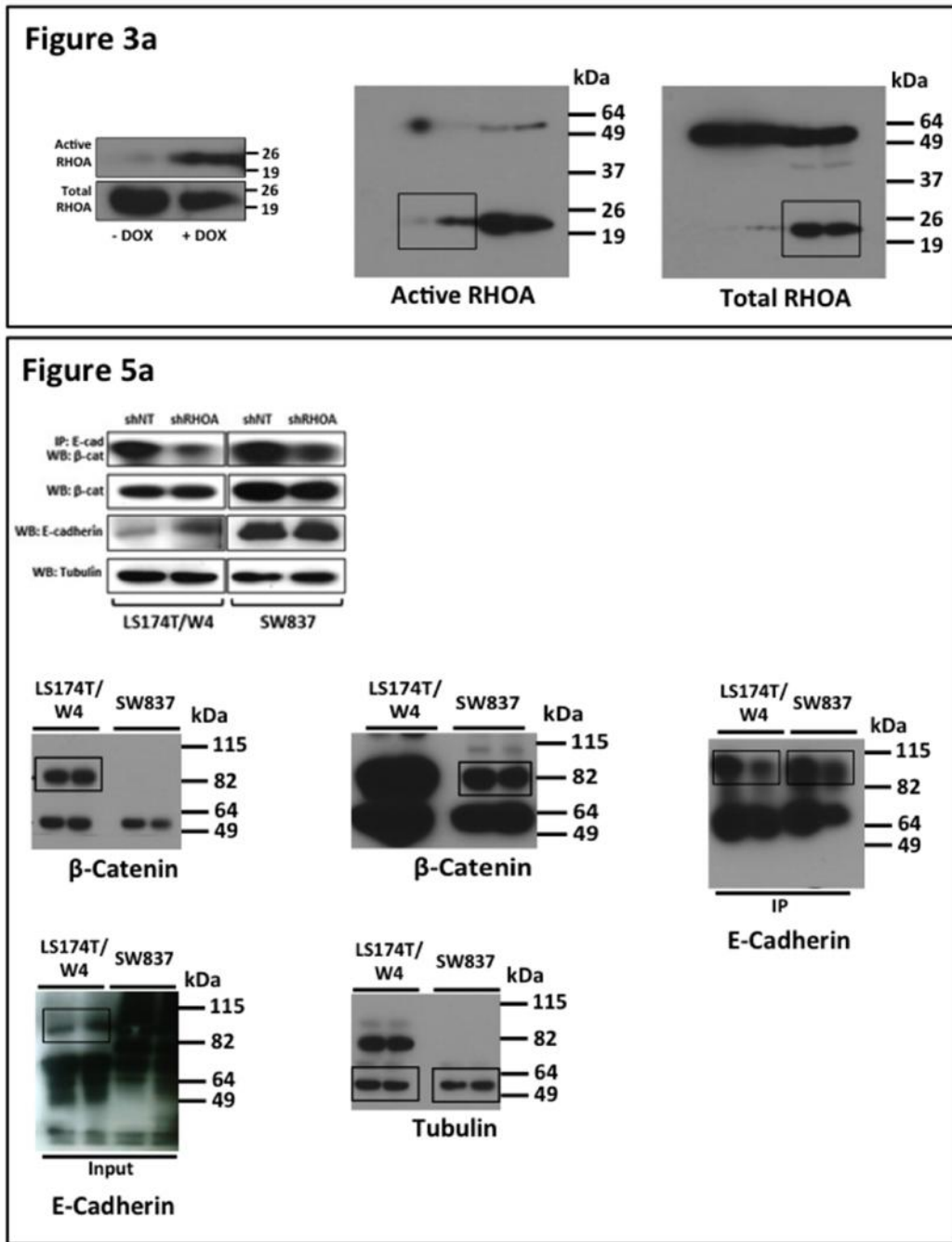
Supplementary Figure 7: Effects of RHOA knockdown on TCF4/ β -catenin and c-MYC activity. To confirm on-target effects of the RHOA shRNA-TR10 used, we assessed the effects of two additional RHOA shRNAs (TR11 and TR12) on the transactivation activity of TCF4/ β -catenin (**a** and **b**) and c-MYC (**c** and **d**) in SW837 (**a** and **c**) and LS174T/W4 (**b** and **d**) colon cancer cells. The mean (\pm SEM) of three independent experiments carried out in triplicate is shown. *Student's t-test $p < 0.05$.



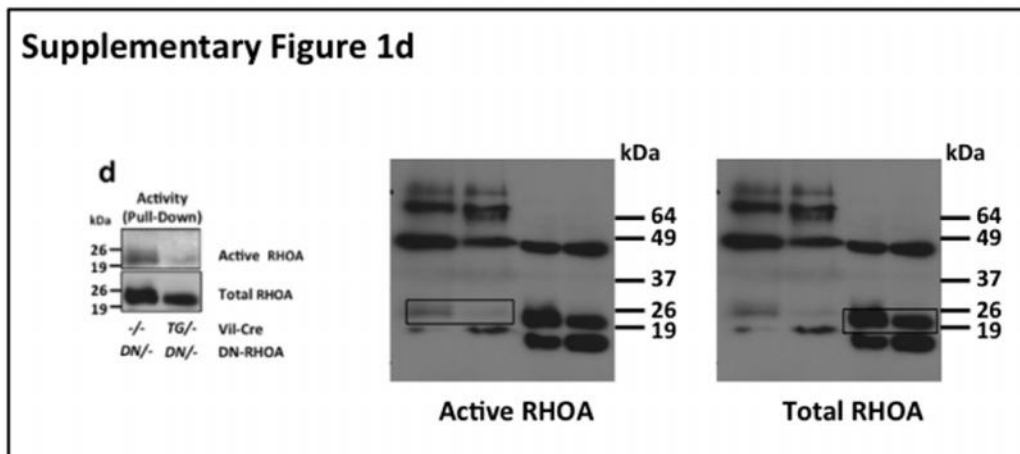
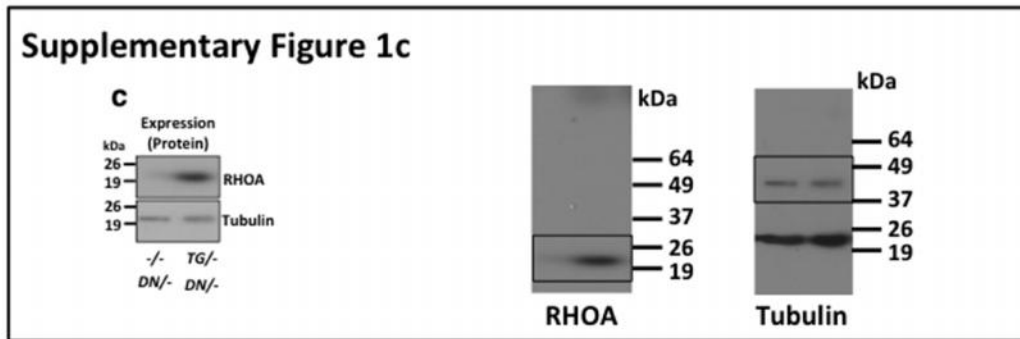
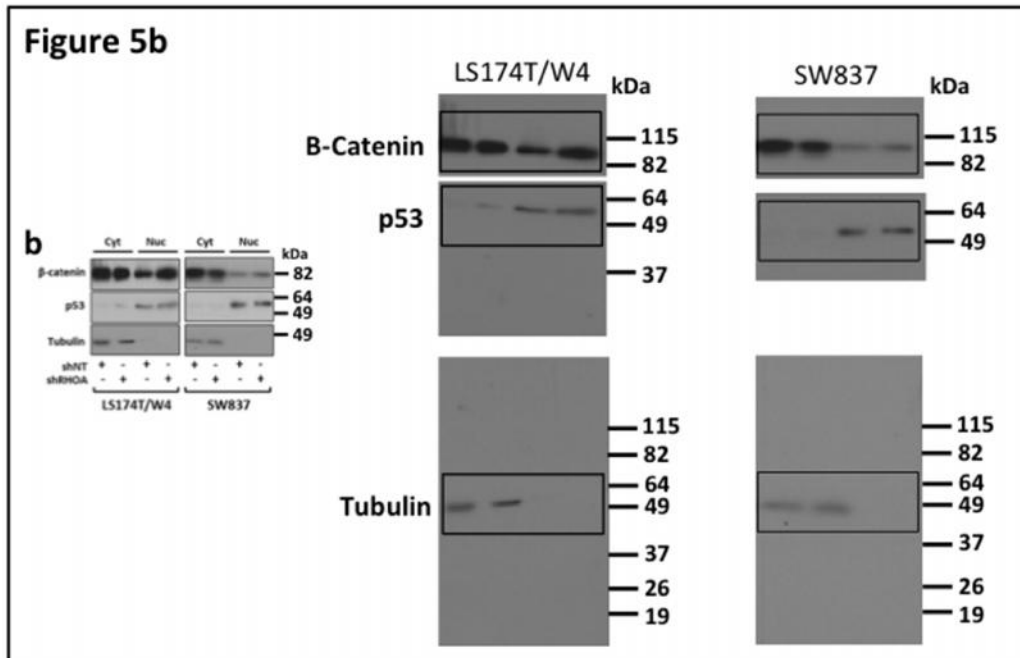
Supplementary Figure 8: non-canonical Wnt signaling and RHOA activity in colon cancer cells. MDA-MB-231 breast cancer cells and HCT8/S11, LS174T/W4 and SW480/ADH colon cancer cells were treated with the non-canonical Wnt ligand Wnt5a. The levels of active GTP-bound RHOA were determined using a GST-Rhotekin-RBD pull-down assay. Although as previously reported (Ref 42) Wnt5a treatment resulted in elevated active RHOA in MDA-MB-231 breast cancer cells, no significant changes were observed in colon cancer cells after Wnt5a treatment. Total RHOA levels are also shown. Tubulin was used as a loading control.



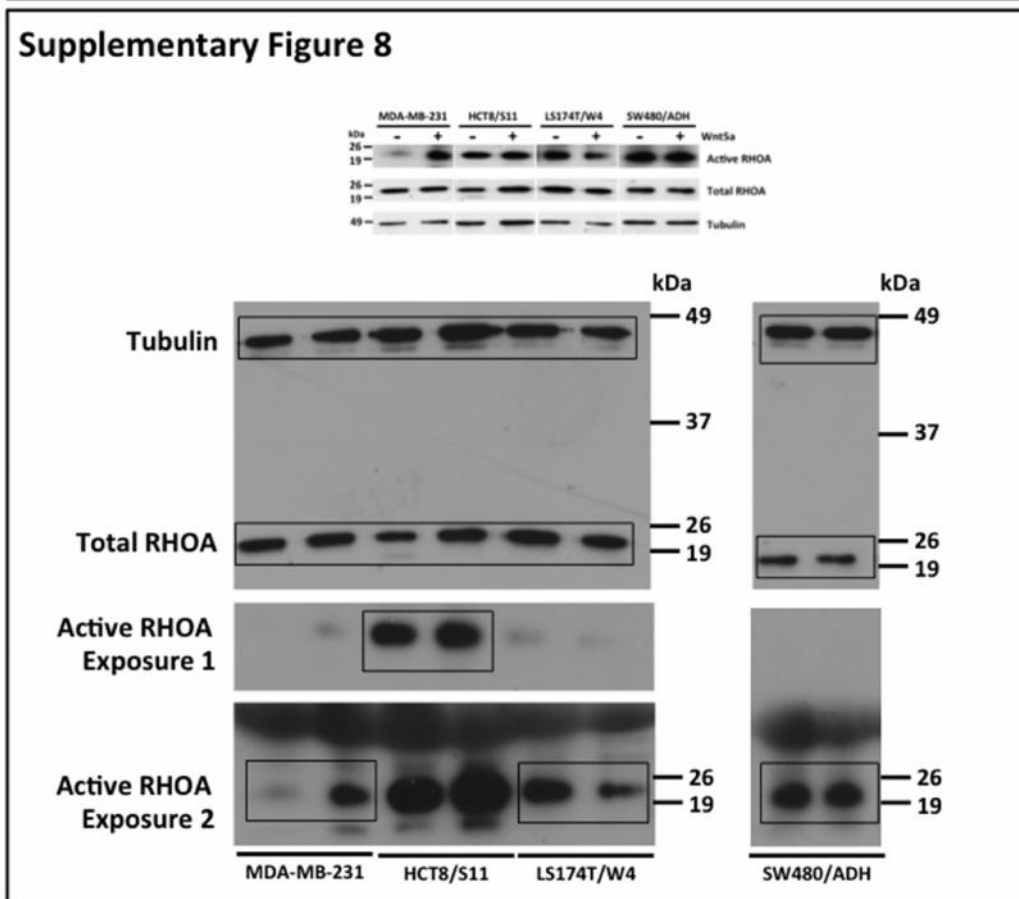
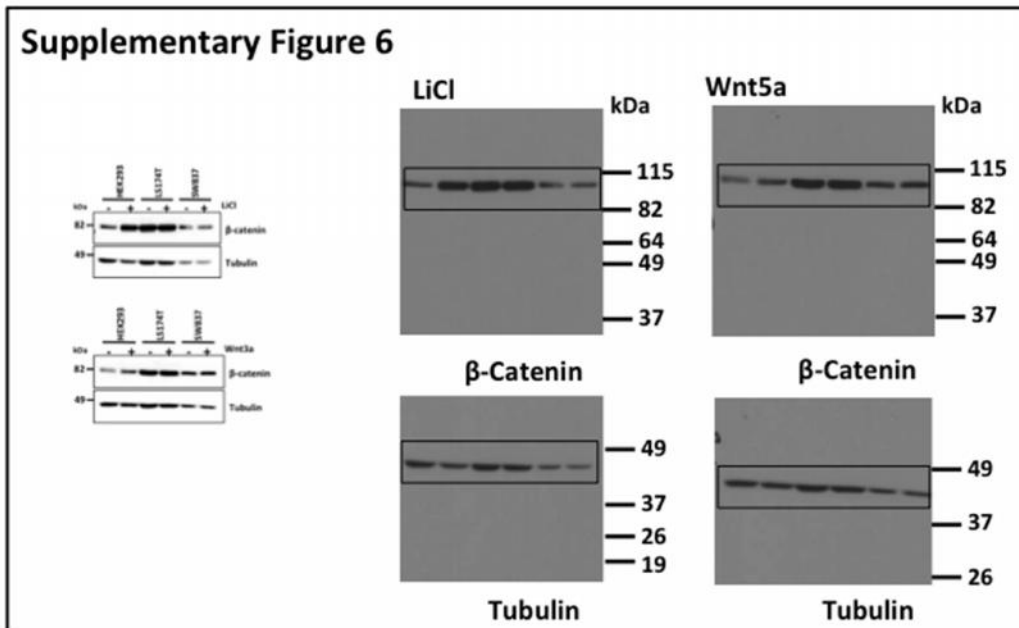
Supplementary Figure 9: schematic representation of the main findings of the study. RHOA inactivation in colon cancer cells results in the translocation of β -catenin from the membrane E-cadherin-bound pool to the nucleus and the ROCK/DIAPH1-dependent activation of β -catenin/TCF4 signaling, resulting in increased proliferation/invasion and reduced differentiation. In addition, the loss of RHOA leads to reduced polarization that is ROCK/DIAPH1-dependent and increased migration through alternative RHOA effector molecules. In blue and green are effects of RHOA inactivation that are Wnt/ β -catenin-dependent and -independent, respectively.



Supplementary Figure 10: Full-scan images of representative western blot.



Supplementary Figure 10: continued



Supplementary Figure 10: continued

Supplmentary Table 1

Supplementary Table 1: Gene expression changes after Wnt signaling inhibition in LS174T cells and in tumors from control *Apc^{min}* mice and *ApcMin* mice with forced expression of DN-RhoA.

Row Labels	Name	Fold exp difference in LS174T cells (Control/DN-TCF4) ¹	Fold exp difference in mice tumors (Control/DN-RhoA) ²
Ascl2	achaete-scute complex homolog 2 (Drosophila)	0.03	0.83
C2cd4a	C2 calcium-dependent domain containing 4A	0.07	1.19
Asb4	ankyrin repeat and SOCS box-containing 4	0.12	0.97
Pnma3	paraneoplastic antigen MA3	0.18	0.96
Ephb3	Eph receptor B3	0.18	0.93
Smoc2	SPARC related modular calcium binding 2	0.19	0.82
Lgr5	leucine rich repeat containing G protein coupled receptor 5	0.20	0.98
Cldn2	claudin 2	0.21	1.00
Axin2	axin2	0.22	1.09
Znrf3	zinc and ring finger 3	0.24	1.20
Lrp4	low density lipoprotein receptor-related protein 4	0.25	0.98
Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	0.28	1.07
Ets2	E26 avian leukemia oncogene 2, 3' domain	0.28	0.93
Srek1	splicing regulatory glutamine/lysine-rich protein 1	0.30	1.03
Slc12a2	solute carrier family 12, member 2	0.30	0.95
Rgmb	RGM domain family, member B	0.31	1.01
Hes6	hairy and enhancer of split 6 (Drosophila)	0.31	1.10
Epha4	Eph receptor A4	0.31	1.05
Myh4	myosin, heavy polypeptide 4, skeletal muscle	0.32	1.14
Chrnb1	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	0.33	1.12
Hexdc	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	0.33	1.02
Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	0.34	1.02
Id4	inhibitor of DNA binding 4	0.34	0.88
Lox13	lysyl oxidase-like 3	0.34	1.10
Il17rb	interleukin 17 receptor B	0.34	1.09
Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	0.34	1.01
Ephb2	Eph receptor B2	0.34	1.03
Cytip	cytohesin 1 interacting protein	0.35	1.09
Rab15	RAB15, member RAS oncogene family	0.35	0.99
Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	0.35	0.83

Supplementary Table 1

Row Labels	Name	Fold exp difference in LS174T cells (Control/DN-TCF4) ¹	Fold exp difference in mice tumors (Control/DN-RhoA) ²
Id3	inhibitor of DNA binding 3	0.36	0.92
Tmem80	transmembrane protein 80	0.36	1.13
Cdca7	cell division cycle associated 7	0.36	0.89
Brip1	BRCA1 interacting protein C-terminal helicase 1	0.37	0.85
Rnf43	ring finger protein 43	0.37	1.10
Cdc25a	cell division cycle 25 homolog A (S. pombe)	0.37	0.92
Smad9	MAD homolog 9 (Drosophila)	0.38	1.00
Tmem201	transmembrane protein 201	0.39	1.04
Ccnf	cyclin F	0.40	1.00
Khk	ketoheokinase	0.40	0.94
Wdr76	WD repeat domain 76	0.40	0.88
Slc19a1	solute carrier family 19 (folate transporter), member 1	0.40	0.92
Stxbp6	syntaxin binding protein 6 (amisyn)	0.40	0.95
Rad1	RAD1 homolog (S. pombe)	0.40	1.06
Tspan5	tetraspanin 5	0.40	0.95
Nmt1	N-myristoyltransferase 1	0.41	0.87
Cntnap2	contactin associated protein-like 2	0.41	0.96
Snhg9	small nucleolar RNA host gene (non-protein coding) 9	0.41	1.03
Nsmf	NMDA receptor synaptonuclear signaling and neuronal migration facto	0.42	0.88
Nrtn	neurturin	0.42	1.05
Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	0.42	1.04
Bgn	biglycan	0.43	0.87
Pold1	polymerase (DNA directed), delta 1, catalytic subunit	0.43	0.91
Sh3rf3	SH3 domain containing ring finger 3	0.43	1.08
Slc3a2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	0.43	0.93
Pald1	phosphatase domain containing, paladin 1	0.43	1.10
Arhgef26	Rho guanine nucleotide exchange factor (GEF) 26	0.43	1.06
Ppan	peter pan homolog (Drosophila)	0.43	1.15
Dhrs2	dehydrogenase/reductase member 2	0.43	1.07
Cdt1	chromatin licensing and DNA replication factor 1	0.44	0.95
Rad54l	RAD54 like (S. cerevisiae)	0.44	0.94
Bcl11a	B cell CLL/lymphoma 11A (zinc finger protein)	0.44	0.87
Pdzd2	PDZ domain containing 2	0.44	0.99

Supplementary Table 1

Row Labels	Name	Fold exp difference in LS174T cells (Control/DN-TCF4) ¹	Fold exp difference in mice tumors (Control/DN-RhoA) ²
Haus7	HAUS augmin-like complex, subunit 7	0.44	0.74
Mcm2	minichromosome maintenance deficient 2 mitotin (<i>S. cerevisiae</i>)	0.45	0.91
Pdzd8	PDZ domain containing 8	0.45	0.90
Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (<i>S. cerevisiae</i>)	0.45	0.97
Dtl	denticleless homolog (<i>Drosophila</i>)	0.45	0.95
Lyar	Lyl antibody reactive clone	0.45	0.86
Klhdc4	kelch domain containing 4	0.46	0.89
Pold3	polymerase (DNA-directed), delta 3, accessory subunit	0.46	0.98
Tcf7	transcription factor 7, T cell specific	0.46	1.12
Telo2	TEL2, telomere maintenance 2, homolog (<i>S. cerevisiae</i>)	0.46	0.96
Cbx2	chromobox homolog 2 (<i>Drosophila</i> Pc class)	0.46	1.10
Them6	thioesterase superfamily member 6	0.46	1.13
Exo1	exonuclease 1	0.46	1.08
Mcm7	minichromosome maintenance deficient 7 (<i>S. cerevisiae</i>)	0.46	1.00
Samd1	sterile alpha motif domain containing 1	0.47	1.05
Dclrelb	DNA cross-link repair 1B, PS02 homolog (<i>S. cerevisiae</i>)	0.47	1.02
Aldh1b1	aldehyde dehydrogenase 1 family, member B1	0.47	0.84
Eril	exoribonuclease 1	0.47	0.98
Haus8	4HAUS augmin-like complex, subunit 8	0.47	1.02
Hells	helicase, lymphoid specific	0.47	0.95
Fkbp4	FK506 binding protein 4	0.48	0.85
Tmem97	transmembrane protein 97	0.48	0.93
Mcm3	minichromosome maintenance deficient 3 (<i>S. cerevisiae</i>)	0.48	0.87
Slca4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	0.48	1.03
Plekha2	pleckstrin homology domain-containing, family A (phosphoinositide binding	0.48	0.92
Myo19	myosin XIX	0.48	1.02
Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	0.48	0.83
Edar	ectodysplasin-A receptor	0.48	1.25
Gins2	GINS complex subunit 2 (Psf2 homolog)	0.48	0.86
G3bp1	Ras-GTPase-activating protein SH3-domain binding protein 1	0.48	0.94
Msh6	mutS homolog 6 (<i>E. coli</i>)	0.48	0.80
Rfc4	replication factor C (activator 1) 4	0.49	1.00
Nasp	nuclear autoantigenic sperm protein (histone-binding)	0.49	1.05

Supplementary Table 1

Row Labels	Name	Fold exp difference in LS174T cells (Control/DN-TCF4) ¹	Fold exp difference in mice tumors (Control/DN-RhoA) ²
Gpatch4	G patch domain containing 4	0.49	0.92
Maneal	mannosidase, endo-alpha-like	0.49	1.00
Tyms	thymidylate synthase	0.49	0.99
Slc25a19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	0.49	0.97
Slc39a3	solute carrier family 39 (zinc transporter), member 3	0.49	0.95
Timeless	timeless homolog (Drosophila)	0.50	1.04
Ccpg1	cell cycle progression 1	2.00	0.94
Actn4	actinin alpha 4	2.01	0.92
Nucb2	nucleobindin 2	2.01	0.84
Enpp5	ectonucleotide pyrophosphatase/phosphodiesterase 5	2.01	1.22
Elmod2	ELMO domain containing 2	2.02	0.92
Rab4b	RAB4B, member RAS oncogene family	2.02	0.93
S100a11	S100 calcium binding protein A11 (calgizzarin)	2.03	0.95
Ncoa3	nuclear receptor coactivator 3	2.03	1.02
Anxa3	annexin A3	2.06	0.68
Il1r2	interleukin 1 receptor, type II	2.10	0.97
Ccn11	cyclin Y-like 1	2.10	0.78
Klf9	Kruppel-like factor 9	2.10	0.93
Nr3c2	nuclear receptor subfamily 3, group C, member 2	2.10	1.04
Gramd1b	GRAM domain containing 1B	2.11	1.08
Wdfy3	WD repeat and FYVE domain containing 3	2.12	1.12
Lig4	ligase IV, DNA, ATP-dependent	2.13	1.04
Mical2	microtubule associated monooxygenase, calponin and LIM domain containing 2	2.13	0.96
Slc37a1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	2.14	0.97
Irs1	insulin receptor substrate 1	2.15	1.00
Edem1	ER degradation enhancer, mannosidase alpha-like 1	2.15	0.83
Ceacam5	carcinoembryonic antigen-related cell adhesion molecule 5	2.18	1.02
Antxr2	anthrax toxin receptor 2	2.18	0.95
Spink4	serine peptidase inhibitor, Kazal type 4	2.20	0.85
Tmc4	transmembrane channel-like gene family 4	2.21	1.02
Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	2.25	0.93
Plat	plasminogen activator, tissue	2.26	1.13
Myof	myoferlin	2.28	0.93

Supplementary Table 1

Row Labels	Name	Fold exp difference in LS174T cells (Control/DN-TCF4) ¹	Fold exp difference in mice tumors (Control/DN-RhoA) ²
Ehd1	EH-domain containing 1	2.28	0.88
Cpeb3	cytoplasmic polyadenylation element binding protein 3	2.28	0.98
Kcnk5	potassium channel, subfamily K, member 5	2.29	0.74
Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	2.30	0.92
Xdh	xanthine dehydrogenase	2.30	1.00
Sqstm1	sequestosome 1	2.32	0.90
Ptpr	protein tyrosine phosphatase, receptor type, R	2.33	1.05
Tmem198b	transmembrane protein 198b	2.34	1.11
Acbd4	acyl-Coenzyme A binding domain containing 4	2.34	1.03
Efnb2	ephrin B2	2.36	1.05
Kifap3	kinesin-associated protein 3	2.36	1.06
Glrx	glutaredoxin	2.37	0.80
Agr3	anterior gradient homolog 3 (<i>Xenopus laevis</i>)	2.38	1.19
Krcc1	lysine-rich coiled-coil 1	2.39	0.96
Gjb1	gap junction protein, beta 1	2.42	0.83
Prr15l	proline rich 15-like	2.42	1.00
Pagl	phosphoprotein associated with glycosphingolipid microdomains 1	2.43	1.09
Mtm1	X-linked myotubular myopathy gene 1	2.44	0.98
Galnt5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosam	2.44	0.88
Arfgap3	ADP-ribosylation factor GTPase activating protein 3	2.44	0.94
Fam214a	family with sequence similarity 214, member A	2.45	0.94
Trnp1	TMF1-regulated nuclear protein 1	2.45	0.98
Best2	bestrophin 2	2.46	0.98
Capg	capping protein (actin filament), gelsolin-like	2.46	0.78
Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	2.50	1.10
Odf2l	outer dense fiber of sperm tails 2-like	2.52	0.76
Smim14	small integral membrane protein 14	2.52	0.91
Gskip	GSK3B interacting protein	2.54	0.74
Opn3	opsin 3	2.54	0.94
Ddx60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	2.57	0.88
Neat1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	2.61	0.96
Casp1	caspase 1	2.61	0.86
Dusp4	dual specificity phosphatase 4	2.67	1.01

Supplmentary Table 1

Row Labels	Name	Fold exp difference in LS174T cells (Control/DN-TCF4) ¹	Fold exp difference in mice tumors (Control/DN-RhoA) ²
Irf9	interferon regulatory factor 9	2.69	1.09
Nt5e	5' nucleotidase, ecto	2.72	0.97
Garem	GRB2 associated, regulator of MAPK1	2.76	0.96
Asph	aspartate-beta-hydroxylase	2.76	1.02
Pbx1	pre B cell leukemia homeobox 1	2.76	0.98
Tmem139	transmembrane protein 139	2.76	0.95
At11	atlastin GTPase 1	2.77	0.95
Shroom3	shroom family member 3	2.82	0.92
Tob1	transducer of ErbB-2.1	2.83	0.97
Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	2.83	0.86
Cda	cytidine deaminase	2.84	0.82
Bhlhe41	basic helix-loop-helix family, member e41	2.87	1.02
Higd1a	HIG1 domain family, member 1A	2.87	0.95
Flnb	filamin, beta	2.89	0.87
Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	2.90	0.94
Reg4	regenerating islet-derived family, member 4	2.91	0.97
Rab27b	RAB27b, member RAS oncogene family	2.93	0.90
Agr2	anterior gradient 2 (<i>Xenopus laevis</i>)	2.94	0.90
Bcl3	B cell leukemia/lymphoma 3	2.94	1.05
Mlph	melanophilin	2.97	0.93
Ifit2	interferon-induced protein with tetratricopeptide repeats 2	2.98	1.06
Flrt3	fibronectin leucine rich transmembrane protein 3	2.98	0.90
Krt19	keratin 19	2.99	0.84
Pdzklp1	PDZK1 interacting protein 1	2.99	1.02
Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	3.00	1.07
Tff3	trefoil factor 3, intestinal	3.01	0.81
Abat	4-aminobutyrate aminotransferase	3.06	0.90
Fam114a1	family with sequence similarity 114, member A1	3.06	0.97
Mvp	major vault protein	3.08	0.78
Ifit1	interferon-induced protein with tetratricopeptide repeats 1	3.09	1.14
Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	3.09	1.07
Plaur	plasminogen activator, urokinase receptor	3.11	0.72
Acsf2	acyl-CoA synthetase family member 2	3.14	0.88

Supplementary Table 1

Row Labels	Name	Fold exp difference in LS174T cells (Control/DN-TCF4) ¹	Fold exp difference in mice tumors (Control/DN-RhoA) ²
Lama3	laminin, alpha 3	3.14	0.75
Gprc5a	G protein-coupled receptor, family C, group 5, member A	3.14	0.77
Hbegf	heparin-binding EGF-like growth factor	3.15	1.01
Pdlim2	PDZ and LIM domain 2	3.15	0.82
Mob3b	MOB kinase activator 3B	3.16	0.98
Zfp36	zinc finger protein 36	3.22	1.16
Ras	Harvey rat sarcoma oncogene, subgroup R	3.24	0.99
Dhrs3	dehydrogenase/reductase (SDR family) member 3	3.26	1.04
Prrg1	proline rich Gla (G-carboxyglutamic acid) 1	3.29	1.02
Styk1	serine/threonine/tyrosine kinase 1	3.32	0.98
Mical1	microtubule associated monooxygenase, calponin and LIM domain containing 1	3.36	1.02
Abpl	amiloride binding protein 1 (amine oxidase, copper-containing)	3.40	1.04
Fndc3b	fibronectin type III domain containing 3B	3.41	0.91
Pla2g10	phospholipase A2, group X	3.44	0.94
Bcar3	breast cancer anti-estrogen resistance 3	3.45	1.02
Gjb5	gap junction protein, beta 5	3.49	1.17
Rnf19a	ring finger protein 19A	3.53	0.92
Trim31	tripartite motif-containing 31	3.55	0.89
Sult1c2	sulfotransferase family, cytosolic, 1C, member 2	3.56	1.09
Rin2	Ras and Rab interactor 2	3.63	1.09
Rab37	RAB37, member of RAS oncogene family	3.67	0.97
Selm	selenoprotein M	3.71	0.79
Itgb6	integrin beta 6	3.71	0.89
Fabp1	fatty acid binding protein 1, liver	3.81	1.30
Akrlb10	aldo-keto reductase family 1, member B10 (aldose reductase)	3.85	1.03
Sfta2	surfactant associated 2	3.87	1.00
Slc22a18	solute carrier family 22 (organic cation transporter), member 18	3.89	0.98
Frm4b	FERM domain containing 4B	3.90	1.02
Klf6	Kruppel-like factor 6	3.94	0.99
Pkib	protein kinase inhibitor beta, cAMP dependent, testis specific	4.04	1.09
Ahnak	AHNAK nucleoprotein (desmoyokin)	4.07	0.91
Atp9b	ATPase, class II, type 9B	4.11	0.80
Spdef	SAM pointed domain containing ets transcription factor	4.20	0.86

Supplementary Table 1

Row Labels	Name	Fold exp difference in LS174T cells (Control/DN-TCF4) ¹	Fold exp difference in mice tumors (Control/DN-RhoA) ²
Fos	FBJ osteosarcoma oncogene	4.21	1.09
Slc44a4	solute carrier family 44, member 4	4.22	0.91
Optn	optineurin	4.23	1.03
B3galt4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	4.26	0.87
Bdkrb1	bradykinin receptor, beta 1	4.27	1.06
Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	4.30	1.01
Klf2	Kruppel-like factor 2 (lung)	4.33	0.84
Muc2	mucin 2	4.38	0.80
Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	4.38	1.04
Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	4.39	0.83
Plscr4	phospholipid scramblase 4	4.42	1.01
Slpi	secretory leukocyte peptidase inhibitor	4.44	0.81
Cd200r1	CD200 receptor 1	4.44	1.11
Pold4	polymerase (DNA-directed), delta 4	4.45	0.95
Fxyd3	FXD domain-containing ion transport regulator 3	4.45	1.12
Clic3	chloride intracellular channel 3	4.49	0.89
Ptk6	PTK6 protein tyrosine kinase 6	4.52	0.70
Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	4.84	0.89
Mir22hg	Mir22 host gene (non-protein coding)	4.91	0.85
Lgals4	lectin, galactose binding, soluble 4	4.92	0.87
Tnnc1	troponin C, cardiac/slow skeletal	4.93	1.10
Mpl	myeloproliferative leukemia virus oncogene	4.95	0.95
Coro2a	coronin, actin binding protein 2A	4.97	0.90
Capn8	calpain 8	5.31	0.79
Klf4	Kruppel-like factor 4 (gut)	5.35	0.81
Ifit3	interferon-induced protein with tetratricopeptide repeats 3	5.36	0.93
Rgs2	regulator of G-protein signaling 2	5.38	0.90
Lamb3	laminin, beta 3	5.59	0.75
Cldn4	claudin 4	5.61	0.85
Ceacam1	carcinoembryonic antigen-related cell adhesion molecule 1	5.86	0.75
Myo7b	myosin VIIb	5.98	0.85
Ankle2	ankyrin repeat and LEM domain containing 2	6.02	0.81
Ldhd	lactate dehydrogenase D	6.11	0.99

Supplementary Table 1

Row Labels	Name	Fold exp difference in LS174T cells (Control/DN-TCF4) ¹	Fold exp difference in mice tumors (Control/DN-RhoA) ²
Aldh3b1	aldehyde dehydrogenase 3 family, member B1	6.36	0.88
Hyal1	hyaluronoglucosaminidase 1	6.51	0.79
Vill	villin-like	6.84	1.07
Capn5	calpain 5	6.84	0.98
Dpcr1	diffuse panbronchiolitis critical region 1 (human)	6.86	0.89
Rarres1	retinoic acid receptor responder (tazarotene induced) 1	7.12	0.92
Arl14	ADP-ribosylation factor-like 14	7.15	0.88
Sema3b	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (se	7.20	1.14
Plac8	placenta-specific 8	7.24	1.02
Liph	lipase, member H	7.32	0.87
Elf3	E74-like factor 3	7.35	1.00
Krt7	keratin 7	7.50	0.98
Tspan1	tetraspanin 1	7.74	0.74
Erp27	endoplasmic reticulum protein 27	7.77	1.03
Frmd3	FERM domain containing 3	7.86	1.07
Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	7.97	0.88
S100a1	S100 calcium binding protein A1	8.44	0.86
Lbh	limb-bud and heart	8.99	1.10
Slc25a45	solute carrier family 25, member 45	9.46	0.91
Dhrs9	dehydrogenase/reductase (SDR family) member 9	9.54	0.83

¹Fold expression differences between untreated and Doxycycline-treated LS174T-dnTCF4 cells for the 281 genes with >2-fold difference in exp p<0.05 (GEO ID: GDS4386)

²Fold expression differences in tumors from *Apc^{min}* mice and *Apc^{min}* mice with DN-RhoA expression for the set of 281 genes regulated by Wnt in LS

Supplementary Table 2

Supplementary Table 2: List of 1,268 showing significant expression difference in the tumors from control and DN-RhoA mice.

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17403864	Mir186	microRNA 186	8.96	7.54	16.50	43.34	3.63
17372970	Olfir1265	olfactory receptor 1265	12.54	7.40	12.87	44.02	2.85
17410828			24.33	12.70	78.15	20.39	2.66
17505740			11.70	14.90	35.38	26.50	2.33
17379104			37.37	22.00	70.74	65.05	2.29
17384657	Mir5128	microRNA 5128	13.52	16.47	27.66	39.95	2.25
17449710	Cxc19	chemokine (C-X-C motif) ligand 9	19.50	20.16	30.01	57.57	2.21
17406454			20.56	22.23	45.96	47.42	2.18
17410773			9.77	16.78	26.62	29.76	2.12
17530501			8.47	10.28	27.81	11.81	2.11
17466936			6.44	7.28	22.28	6.57	2.10
17233226	Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4	12.53	10.99	16.69	32.33	2.08
17507306			16.82	13.35	32.58	29.28	2.05
17526657			9.78	6.67	8.22	25.28	2.04
17424088	Mir5123	microRNA 5123	104.45	140.24	263.95	221.59	1.98
17238860			37.32	28.26	78.14	51.00	1.97
17470829	Grccl0	gene rich cluster, C10 gene	13.11	9.86	18.41	25.52	1.91
17397331			44.82	52.38	79.60	105.62	1.91
17548808	Gpc3	glypican 3	50.85	83.01	206.70	47.61	1.90
17412121			5.11	5.48	6.01	13.97	1.89
17312686	Apo19b	apolipoprotein L 9b	23.31	21.24	26.72	57.35	1.89
17379126			54.25	24.36	70.53	76.40	1.87
17366151			15.20	10.45	37.34	10.33	1.86
17293704			6.16	5.70	9.77	12.25	1.85
17472233			9.05	9.16	11.73	22.02	1.85
17313037	n-R5s40	nuclear encoded rRNA 5S 40	19.01	26.02	40.43	42.92	1.85
17326700	Mir99a	microRNA 99a	7.82	7.58	8.52	19.69	1.83
17451943	Gml6065	predicted gene 16065	28.79	23.17	71.98	22.87	1.83
17370483	Mir181a-2	microRNA 181a-2	106.32	73.31	187.73	138.90	1.82
17238858			31.55	34.61	48.18	71.51	1.81
17527164			13.68	26.76	29.24	42.83	1.78
17491014			7.31	7.10	9.05	16.44	1.77
17300145	Traj54	T cell receptor alpha joining 54	323.10	140.92	467.22	352.38	1.77
17288105	Mir23b	microRNA 23b	14.87	12.90	28.31	20.63	1.76
17502421			4.61	6.93	7.22	13.04	1.76
17221371			19.39	11.60	15.69	38.71	1.75
17300153	Traj50	T cell receptor alpha joining 50	281.19	185.41	412.44	405.57	1.75
17503118	Mir27a	microRNA 27a	80.56	55.61	140.18	98.14	1.75
17459377			12.82	27.09	10.42	59.26	1.75
17457773	Tcrb-J	T cell receptor beta, joining region	15.45	12.50	26.00	22.67	1.74
17248890	Gnb211	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	94.53	96.03	193.06	138.72	1.74
17470623	Gm5316	predicted gene 5316	11.02	10.59	21.76	15.55	1.73
17372742			615.12	350.45	879.87	773.58	1.71
17547732	Exoc2	exocyst complex component 2	23.70	15.76	34.46	32.92	1.71
17291193			16.51	12.22	28.09	20.80	1.70
17306360			68.51	32.14	79.67	91.26	1.70
17309262			153.77	157.52	251.57	276.53	1.70
17490090	Vmn2r62	vomer nasal 2, receptor 62	7.46	7.69	12.20	13.43	1.69
17410433			8.47	7.38	11.72	15.01	1.69
17395189	Gml4393	predicted gene 14393	14.61	16.73	35.59	17.11	1.68
17530033	Esyt3	extended synaptotagmin-like protein 3	50.97	40.08	82.88	69.74	1.68
17266901			18.08	6.07	9.19	31.15	1.67
17540092	Ssxb2	synovial sarcoma, X member B, breakpoint 2	9.60	11.69	12.30	23.06	1.66
17317799			9.62	6.77	14.24	12.76	1.65
17378168	Bpifb5	BPI fold containing family B, member 5	226.86	141.42	344.26	261.60	1.65
17352573			21.68	18.01	43.47	21.55	1.64
17221286			982.76	546.38	1323.00	1177.08	1.63
17287294			49.83	25.90	58.97	64.35	1.63
17408088	Rpl21-ps11	ribosomal protein L21, pseudogene 11	11.93	12.73	19.78	20.33	1.63
17309366			8.65	7.73	13.98	12.64	1.63
17334302	2610019E17Rik	RIKEN cDNA 2610019E17 gene	13.18	18.41	23.00	28.31	1.62
17523190	Snora62	small nucleolar RNA, H/ACA box 62	40.07	41.92	57.56	75.64	1.62
17394063	Ada	adenosine deaminase	58.12	56.83	67.15	119.44	1.62
17546232	Zf12	Zf12 pseudogene	32.60	30.80	42.40	60.47	1.62
17424452	Gm2023	predicted gene 2023	11.01	11.29	13.93	22.19	1.62
17248894	Gnb211	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	76.07	43.59	95.91	97.55	1.62
17289584	Cenpk	centromere protein K	11.44	11.50	15.34	21.70	1.61
17239872			7.60	6.11	11.37	10.67	1.61
17277756			22.68	16.88	30.81	32.75	1.61
17342595	Nme4	NME/NM23 nucleoside diphosphate kinase 4	50.38	46.69	100.78	54.22	1.60
17406323	Mnd1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	10.49	7.86	20.99	8.30	1.60
17291057	Hist1h2ag	histone cluster 1, H2ag	38.31	80.70	92.06	97.68	1.59
17266617			6.31	6.21	11.61	8.28	1.59
17232189	Taar7d	trace amine-associated receptor 7D	14.49	13.76	29.58	15.18	1.58
17224682			18.78	15.66	35.29	19.19	1.58
17516030	Tmem218	transmembrane protein 218	34.23	26.79	49.63	46.89	1.58
17424090			106.05	141.08	193.56	196.65	1.58
17439813			18.66	58.90	78.65	43.75	1.58
17465156			14.50	15.51	23.61	23.60	1.57
17320811			520.70	249.99	606.69	602.27	1.57
17326640	Rbm11	RNA binding motif protein 11	26.92	21.04	35.64	39.44	1.57
17243523			13.47	11.55	19.36	19.74	1.56
17513769			32.83	14.26	34.37	39.17	1.56
17446524	Speer4b	spermatogenesis associated glutamate (E)-rich protein 4b	7.91	8.11	17.42	7.59	1.56
17437801			35.97	19.96	29.96	57.34	1.56

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17366892			12.77	7.84	20.53	11.57	1.56
17398266	Mir16-2	microRNA 16-2	25.26	11.76	29.29	28.28	1.56
17249700	3230401D17Rik	RIKEN cDNA 3230401D17 gene	34.87	52.32	70.87	64.63	1.55
17492327			17.98	19.23	33.13	24.70	1.55
17337614	Olf1r127	olfactory receptor 127	7.20	8.46	13.61	10.71	1.55
17504372	1700047G07Rik	RIKEN cDNA 1700047G07 gene	27.96	20.72	31.98	43.58	1.55
17214907	Gml6025	predicted gene 16025	16.21	12.80	25.01	20.00	1.55
17517346	Gml6124	predicted gene 16124	12.28	13.19	17.59	21.84	1.55
17411319	Rabggtb	RAB geranylgeranyl transferase, b subunit	13.38	8.13	16.36	16.93	1.55
17268846	Gml2356	predicted gene 12356	14.42	14.54	26.77	18.01	1.55
17223828	Cryge	crystallin, gamma E	4.95	5.73	10.18	6.33	1.55
17221071	Sox17	SRY-box containing gene 17	110.32	131.03	244.02	128.54	1.54
17273280	Stra13	stimulated by retinoic acid 13	87.55	80.77	169.08	89.94	1.54
17334126	D930048G16Rik	RIKEN cDNA D930048G16 gene	20.97	17.83	31.34	28.32	1.54
17421222	Gml3083	predicted gene 13083	16.92	11.06	21.15	21.87	1.54
17219895			5.46	5.44	6.65	10.06	1.53
17499111			89.98	67.41	96.39	144.53	1.53
17217169	Mir135b	microRNA 135b	10.32	13.76	17.47	19.30	1.53
17261169			6.83	6.84	8.95	11.92	1.53
17349174	Polr2d	polymerase (RNA) II (DNA directed) polypeptide D	36.07	42.66	60.02	59.99	1.52
17518933	9530091C08Rik	RIKEN cDNA 9530091C08 gene	16.58	19.20	26.89	27.53	1.52
17491315	Mrgpra9	MAS-related GPR, member A9	14.91	7.64	19.76	14.51	1.52
17294682	Mef2c	myocyte enhancer factor 2C	21.77	20.30	24.51	39.37	1.52
17294803			32.79	18.47	31.13	46.69	1.52
17486505			12.46	12.58	14.10	23.90	1.52
17318734	Zfp647	zinc finger protein 647	19.57	16.07	30.74	23.33	1.52
17236525	Mir1931	microRNA 1931	13.78	10.96	15.64	21.86	1.52
17330963			5.37	6.01	6.66	10.56	1.51
17399876	Sprr2f	small proline-rich protein 2F	10.13	8.99	18.24	10.69	1.51
17369717	Prrc2b	proline-rich coiled-coil 2B	53.20	64.02	96.50	80.60	1.51
17369719			53.20	64.02	96.50	80.60	1.51
17290913	Gpx5	glutathione peroxidase 5	22.35	27.27	54.84	20.10	1.51
17532623	mt-Tr	mitochondrially encoded tRNA arginine	10.54	9.27	13.93	15.89	1.51
17378896			57.20	80.87	112.48	95.31	1.50
17540127			24.77	21.34	31.88	37.49	1.50
17487572	Vmn1r127	vomeronal 1 receptor 127	13.64	10.72	20.23	16.37	1.50
17545756	Gml5241	predicted gene 15241	13.25	10.32	23.67	11.58	1.49
17512691	Pdf	peptide deformylase (mitochondrial)	8.15	8.69	12.20	12.98	1.49
17331880	Krtap19-9a	keratin associated protein 19-9A	5.02	5.57	6.59	9.20	1.49
17364187			24.26	36.58	31.42	59.37	1.49
17403106	Adh6b	alcohol dehydrogenase 6B (class V)	9.27	8.07	11.68	14.19	1.49
17270615			39.68	45.18	67.64	58.91	1.49
17489705			16.46	9.38	25.57	12.92	1.49
17249034			779.86	395.05	848.41	900.99	1.49
17294130	A530095107Rik	RIKEN cDNA A530095107 gene	13.18	14.71	14.84	26.61	1.49
17216127			9.94	9.80	17.75	11.56	1.49
17503942	Mt1	metallothionein 1	310.46	397.65	576.46	472.78	1.48
17519345			22.42	21.33	40.44	24.32	1.48
17309372			6.23	6.13	9.31	8.99	1.48
17420011	Gml3008	predicted gene 13008	21.95	19.90	13.57	48.33	1.48
17495027			16.84	16.19	23.19	25.61	1.48
17547020	Gm20770	predicted gene, 20770	9.77	8.44	15.86	11.04	1.48
17455787	Gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1	6.10	6.18	10.29	8.30	1.48
17523186			37.51	18.98	40.51	42.88	1.48
17306753	Ipo4	importin 4	46.43	30.45	51.49	61.97	1.48
17300027			29.50	29.63	45.10	42.12	1.48
17317391			8.03	7.33	9.08	13.55	1.47
17290601	Gm2444	predicted gene 2444	9.42	6.93	14.03	10.04	1.47
17407489	Lce3a	late cornified envelope 3A	117.95	87.14	137.20	164.71	1.47
17366884			53.24	49.28	79.04	71.64	1.47
17422659	B930041F14Rik	RIKEN cDNA B930041F14 gene	26.36	26.80	45.91	32.21	1.47
17280191	Gm20535	predicted gene 20535	30.24	32.61	49.26	43.07	1.47
17474744	Vmn1r116	vomeronal 1 receptor 116	9.25	8.76	10.78	15.66	1.47
17411489	Vmn1r2	vomeronal 1 receptor 2	136.24	100.69	179.82	168.07	1.47
17300221	Traj15	T cell receptor alpha joining 15	10.49	15.23	24.81	12.95	1.47
17476902			6.35	6.95	12.84	6.66	1.47
17507904			151.09	111.48	210.53	174.32	1.47
17504138	Ccl17	chemokine (C-C motif) ligand 17	14.27	12.45	14.89	24.22	1.46
17416743	3110021N24Rik	RIKEN cDNA 3110021N24 gene	42.36	30.73	62.31	44.53	1.46
17335129	Hmgal	high mobility group AT-hook 1	38.42	44.98	51.65	70.18	1.46
17518310			7.43	6.94	9.03	11.94	1.46
17417654			39.47	35.09	60.47	48.34	1.46
17517244	4933407105Rik	RIKEN cDNA 4933407105 gene	8.88	9.45	13.21	13.52	1.46
17509125			6.31	5.82	9.47	8.21	1.46
17423490	Ripk2	receptor (INFRSF)-interacting serine-threonine kinase 2	19.16	15.34	27.43	22.83	1.46
17307801	Gulo	gulonolactone (L-) oxidase	31.43	25.81	50.17	33.14	1.46
17383816	Gml3609	predicted gene 13609	80.60	61.47	112.78	93.62	1.45
17353574			12.45	13.03	12.85	24.10	1.45
17535274	1110012L19Rik	RIKEN cDNA 1110012L19 gene	36.22	30.44	43.06	53.52	1.45
17297299	B230110C06Rik	RIKEN cDNA B230110C06 gene	9.85	8.40	14.02	12.42	1.45
17409500			12.07	13.05	22.06	14.28	1.45
17238760			21.29	17.91	22.83	33.85	1.45
17433973	Mir200a	microRNA 200a	11.21	13.19	12.43	22.85	1.45
17416009	Gml2794	predicted gene 12794	5.58	6.61	7.52	10.10	1.45
17470794	Mir200c	microRNA 200c	24.66	12.87	27.56	26.68	1.45
17332891	n-R5s26	nuclear encoded rRNA 5S 26	7.65	10.61	10.24	16.14	1.44
17263140			15.86	11.74	26.24	13.60	1.44

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17221932			53.60	27.94	51.15	66.54	1.44
17424199			85.81	50.49	67.95	128.69	1.44
17267482			13.73	16.83	14.93	29.13	1.44
17527982	Glce	glucuronyl C5-epimerase	27.24	23.80	30.13	43.44	1.44
17511211	Mast1	microtubule associated serine/threonine kinase 1	39.77	33.96	47.38	58.88	1.44
17369948	Mir1954	microRNA 1954	113.23	104.63	155.33	158.54	1.44
17237004			8.25	10.87	15.07	12.46	1.44
17428799	Rps8	ribosomal protein S8	82.51	73.69	112.05	112.69	1.44
17542090	Mir465b-1	microRNA 465b-1	7.45	6.82	9.32	11.21	1.44
17542094	Mir465b-1	microRNA 465b-1	7.45	6.82	9.32	11.21	1.44
17504958	Nutf2	nuclear transport factor 2	33.37	27.66	45.39	42.25	1.44
17345122			8.27	10.57	19.23	7.79	1.43
17418154	Oxct2b	3-oxoacid CoA transferase 2B	10.81	12.02	21.72	11.01	1.43
17289794	Plk2	polo-like kinase 2 (Drosophila)	92.63	110.95	154.71	137.07	1.43
17339497	Snord92	small nucleolar RNA, C/D box 92	59.26	46.19	82.77	68.36	1.43
17274412			12.62	13.00	23.43	13.27	1.43
17511112	Ccdc130	coiled-coil domain containing 130	24.64	21.27	34.55	31.15	1.43
17467193	Vmn1r25	vomeronal 1 receptor 25	9.27	7.28	12.57	11.10	1.43
17544149	Hmgn5	high-mobility group nucleosome binding domain 5	32.08	51.36	55.62	63.70	1.43
17341283	Gm7535	predicted gene 7535	28.33	26.84	51.24	27.64	1.43
17493398			6.72	5.84	7.31	10.64	1.43
17507790			72.19	50.83	84.86	90.73	1.43
17313645			75.77	92.73	105.86	134.58	1.43
17353030			11.25	9.63	12.28	17.49	1.43
17419371	Gm13063	predicted gene 13063	15.85	17.35	26.12	21.18	1.42
17494813	Olf1r516	olfactory receptor 516	7.51	6.61	11.87	8.24	1.42
17446507	Gm10220	predicted gene 10220	7.77	9.55	13.97	10.68	1.42
17284447			47.65	38.24	55.35	66.83	1.42
17331272	Olf1r205	olfactory receptor 205	6.86	6.68	11.78	7.48	1.42
17544158			5.46	5.51	9.55	6.04	1.42
17478745	Atp10a	ATPase, class V, type 10A	34.15	40.01	59.26	46.11	1.42
17493681	Rps3	ribosomal protein S3	50.40	29.92	38.30	75.81	1.42
17314575			57.00	38.35	63.59	71.83	1.42
17424243	AI464131	expressed sequence AI464131	36.91	34.81	59.08	42.74	1.42
17405612	Vmn2r3	vomeronal 2, receptor 3	77.83	49.93	94.69	86.55	1.42
17229257			55.05	55.05	84.47	71.61	1.42
17256314	Krtap9-1	keratin associated protein 9-1	68.51	64.46	94.20	94.26	1.42
17430004			7.49	5.21	10.96	7.04	1.42
17393998			9.20	8.77	12.08	13.33	1.41
17390806			16.22	13.87	25.20	17.36	1.41
17254614			74.24	78.49	120.55	95.47	1.41
17528214			9.83	7.75	9.31	15.52	1.41
17358092			60.68	28.16	60.85	64.61	1.41
17300608	Rec8	RECS homolog (yeast)	21.83	23.34	34.56	29.20	1.41
17471598	Klrl1	killer cell lectin-like receptor subfamily C, member 1	10.03	10.80	15.61	13.79	1.41
17337110	H2-Q5	histocompatibility 2, Q region locus 5	14.10	11.95	21.78	14.98	1.41
17331987	Mis18a	MIS18 kinetochore protein homolog A (S. pombe)	25.93	28.55	31.99	44.82	1.41
17303599	Oxsm	3-oxoacyl-ACP synthase, mitochondrial	16.46	13.79	22.03	20.62	1.41
17318312	Nrbp2	nuclear receptor binding protein 2	43.70	37.28	61.44	52.72	1.41
17265524			46.56	38.22	67.92	51.57	1.41
17324473			10.80	12.28	14.22	18.29	1.41
17426695	Gm11261	predicted gene 11261	12.87	11.79	14.92	19.83	1.41
17263416	Zfp867	zinc finger protein 867	13.56	11.37	19.50	15.60	1.41
17457969	Olf1r38	olfactory receptor 38	41.44	26.44	42.94	52.60	1.41
17240663			6.69	6.25	6.36	11.85	1.41
17287866	1700066J03Rik	RIKEN cDNA 1700066J03 gene	17.93	13.66	28.27	16.18	1.41
17541719	Mir450-2	microRNA 450-2	14.74	16.25	22.76	20.82	1.41
17416811	Mir761	microRNA 761	1559.97	739.15	1659.58	1572.02	1.41
17535710			62.29	42.60	74.87	72.56	1.41
17467401			22.01	15.06	26.70	25.39	1.41
17366912			10.44	5.68	13.38	9.27	1.41
17271531	Gm11677	predicted gene 11677	19.92	16.68	24.21	27.21	1.41
17300086	Trav3-4	T cell receptor alpha variable 3-4	14.34	11.64	18.52	17.97	1.40
17302709			30.20	27.51	49.06	31.96	1.40
17533774			5.89	5.02	8.55	6.76	1.40
17506270	Gm10614	predicted gene 10614	12.06	13.21	24.05	11.39	1.40
17465856	Ptn	pleiotrophin	26.53	30.01	46.62	32.66	1.40
17287033			25.49	45.19	26.85	72.22	1.40
17481167	Olf1r582	olfactory receptor 582	6.45	5.44	6.54	10.12	1.40
17529367	Ube2cbp	ubiquitin-conjugating enzyme E2C binding protein	10.23	11.40	11.66	18.64	1.40
17272743			13.01	7.21	7.23	21.04	1.40
17337945	Gm17080	predicted gene 17080	8.66	7.51	9.79	12.82	1.40
17288583			29.21	25.94	44.90	32.19	1.40
17339852	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	33.35	14.70	19.74	47.38	1.40
17495318			417.19	249.13	488.11	442.56	1.40
17439365			27.05	21.77	32.30	35.90	1.40
17547713	Gm19929	predicted gene, 19929	38.09	26.54	42.88	47.34	1.40
17487507	n-R5s152	nuclear encoded rRNA 5S 152	15.03	12.72	22.97	15.75	1.40
17344692	Gm10499	predicted gene 10499	19.84	16.21	30.46	19.83	1.40
17462985			66.32	41.33	54.02	96.12	1.39
17237681	9230105E05Rik	RIKEN cDNA 9230105E05 gene	33.31	30.21	55.34	33.19	1.39
17512084			11.19	11.08	14.16	16.87	1.39
17486543	Vmn2r54	vomeronal 2, receptor 54	15.92	21.34	25.67	26.24	1.39
17463837	LOC627096	uncharacterized LOC627096	25.32	21.37	33.41	31.64	1.39
17364988	Cpn1	carboxypeptidase N, polypeptide 1	23.51	27.33	28.13	42.58	1.39
17387674	Olf1r1061	olfactory receptor 1061	5.83	5.27	6.72	8.72	1.39
17499818	Defb2	defensin beta 2	25.42	20.31	28.73	34.83	1.39

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17351224			6.04	5.87	7.06	9.49	1.39
17337576	Olf1r110	olfactory receptor 110	6.89	6.50	9.73	8.87	1.39
17234798	n-R5s77	nuclear encoded rRNA 5S 77	10.85	13.79	23.33	10.89	1.39
1741452	Klrb1c	killer cell lectin-like receptor subfamily B member 1C	10.94	13.50	18.26	15.66	1.39
17399233			71.73	52.79	92.61	80.19	1.39
17361600	Ccdc85b	coiled-coil domain containing 85B	16.80	17.38	25.98	21.45	1.39
17473166	Cacng6	calcium channel, voltage-dependent, gamma subunit 6	9.80	9.77	13.92	13.20	1.39
17548944	Slamf6	SLAM family member 6	28.28	26.05	39.69	35.53	1.38
17545899	S100g	S100 calcium binding protein G	439.97	762.53	1037.79	626.82	1.38
17231491	Gm3213	predicted gene 3213	7.21	5.73	10.24	7.66	1.38
17238528			16.48	14.84	25.63	17.67	1.38
17321939	Krt6b	keratin 6B	7.93	6.00	11.29	7.97	1.38
17354297			7.07	10.31	14.45	9.57	1.38
17322075	Krt4	keratin 4	32.14	34.01	48.01	43.39	1.38
17269333	Krt36	keratin 36	11.05	15.00	15.27	20.71	1.38
17293517	6720489N17Rik	RIKEN cDNA 6720489N17 gene	20.31	18.40	23.81	29.65	1.38
17346932	5031415H12Rik	RIKEN cDNA 5031415H12 gene	12.63	11.83	17.72	16.06	1.38
17372771	Olf1r1022	olfactory receptor 1022	4.83	4.66	7.15	5.94	1.38
17457874	Tas2r144	taste receptor, type 2, member 144	8.88	10.24	16.45	9.91	1.38
17342338			53.54	51.33	74.32	70.09	1.38
17467554			44.53	80.68	58.80	113.54	1.38
17278820	Mir494	microRNA 494	57.50	47.36	76.49	67.81	1.38
17467298	Vmn1r34	vomeranosal 1 receptor 34	13.38	12.55	13.72	21.96	1.38
17533939	Gmcl11	germ cell-less homolog 1 (Drosophila)-like	12.44	14.66	17.63	19.65	1.38
17512529	Cenpt	centromere protein T	40.83	33.00	53.82	47.66	1.37
17327426			11.19	12.79	16.00	16.95	1.37
17333344	Snora20	small nucleolar RNA, H/ACA box 20	15.40	7.94	13.73	18.34	1.37
17473736	Vmn1r80	vomeranosal 1 receptor 80	7.96	8.61	13.91	8.85	1.37
17484261	Mir1962	microRNA 1962	34.30	38.84	50.08	50.38	1.37
17513278	Gm16117	predicted gene 16117	7.86	7.41	9.80	11.17	1.37
17384175			12.20	16.11	24.05	14.84	1.37
17507940	Defb9	defensin beta 9	7.42	7.15	7.66	12.35	1.37
17298895	Mir346	microRNA 346	55.04	34.85	71.69	51.75	1.37
17348280			30.55	38.65	55.67	39.30	1.37
17211984	4930556123Rik	RIKEN cDNA 4930556123 gene	21.89	25.12	36.39	28.14	1.37
17372779	Olf1r1028	olfactory receptor 1028	6.77	5.65	9.36	7.69	1.37
17255874			5.50	5.69	6.29	9.06	1.37
17494473	Olf1r686	olfactory receptor 686	18.35	18.66	23.32	27.45	1.37
17392828	Gm14167	predicted gene 14167	15.06	12.28	23.17	14.31	1.37
17459312			21.49	20.83	27.38	30.62	1.37
17342483	Fam195a	family with sequence similarity 195, member A	26.55	42.44	30.52	64.04	1.37
17416891			22.91	24.13	31.12	33.33	1.37
17518268			9.05	8.66	8.72	15.53	1.37
17256323	Krtap31-1	keratin associated protein 31-1	11.63	10.63	15.17	15.32	1.37
17545761	Gm15243	predicted gene 15243	28.44	30.42	41.06	39.50	1.37
17305854			7.15	6.50	8.64	10.03	1.37
17460634	Gata2	GATA binding protein 2	26.05	19.65	30.91	31.61	1.37
17488735	Spred3	sprouty-related, EVH1 domain containing 3	40.74	36.52	55.12	50.56	1.37
17230327			107.53	86.56	133.72	131.58	1.37
17321511			6.07	6.29	6.95	9.94	1.37
17434869	Gm21083	predicted gene, 21083	4.78	5.58	7.11	7.06	1.37
17366886	Mir467e	microRNA 467e	293.97	136.51	253.54	334.50	1.37
17547980	Olf1r175-ps1	olfactory receptor 175, pseudogene 1	6.75	6.30	8.40	9.42	1.37
17284650			15.94	11.58	20.95	16.63	1.37
17288302	Rsl1	regulator of sex limited protein 1	7.18	7.23	9.64	10.05	1.37
17299860	Trav12-2	T cell receptor alpha variable 12-2	18.17	19.95	28.23	23.80	1.36
17299937	Trav12-2	T cell receptor alpha variable 12-2	18.17	19.95	28.23	23.80	1.36
17300733			36.92	17.41	31.25	42.87	1.36
17497709	Ifitm5	interferon induced transmembrane protein 5	32.93	40.92	57.54	43.23	1.36
17325232			28.44	27.29	41.47	34.54	1.36
17475295	4732471J01Rik	RIKEN cDNA 4732471J01 gene	26.72	26.72	37.09	35.75	1.36
17515715	Zbtb44	zinc finger and BTB domain containing 44	28.37	25.86	40.37	33.55	1.36
17333672	Rio2	RIO kinase 2 (yeast)	17.02	17.89	23.64	23.94	1.36
17486058	Vmn1r61	vomeranosal 1 receptor 61	4.64	5.54	5.82	8.05	1.36
17369368	Nesl	neuronal calcium sensor 1	17.93	17.73	26.02	22.57	1.36
17481330	Olf1r661	olfactory receptor 661	11.43	11.81	12.82	18.84	1.36
17421364	Gm13212	predicted gene 13212	6.12	5.81	8.40	7.84	1.36
17250744	2410006H16Rik	RIKEN cDNA 2410006H16 gene	45.91	71.24	76.56	82.86	1.36
17500375	4933433F19Rik	RIKEN cDNA 4933433F19 gene	9.85	8.76	12.30	13.01	1.36
17412717			25.02	21.15	36.39	26.41	1.36
17495404	Rps13	ribosomal protein S13	92.12	71.61	144.67	78.05	1.36
17515238	AB124611	cDNA sequence AB124611	29.73	23.48	38.28	34.10	1.36
17288836			60.66	75.74	74.64	110.89	1.36
17495692	Dcun1d3	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	37.23	41.02	60.60	45.83	1.36
17507128	Fcor	Foxo1 corepressor	19.73	20.39	21.43	33.13	1.36
17280270	Gm9292	predicted gene 9292	28.79	21.37	36.15	32.06	1.36
17307799			42.54	24.99	42.93	48.88	1.36
17391054			8.77	8.31	12.60	10.62	1.36
17252329	4930563E22Rik	RIKEN cDNA 4930563E22 gene	16.41	13.02	18.02	21.97	1.36
17515813	Kcnj1	potassium inwardly-rectifying channel, subfamily J, member 1	10.56	13.36	14.89	17.58	1.36
17518543			26.71	24.82	38.03	31.92	1.36
17405627	Vmn2r5	vomeranosal 2, receptor 5	8.50	7.10	12.51	8.65	1.36
17535296	n-R5s8	nuclear encoded rRNA 5S 8	12.24	10.19	19.35	11.08	1.36
17479929	Vmn2r71	vomeranosal 2, receptor 71	6.33	5.58	9.04	7.13	1.36
17274735	Tmem18	transmembrane protein 18	31.73	35.77	50.52	41.06	1.36
17269905			38.39	42.59	52.43	57.45	1.36
17539271	Gpr64	G protein-coupled receptor 64	24.60	21.63	30.90	31.79	1.36

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17539824	Mir188	microRNA 188	21.89	29.96	32.80	37.52	1.36
17225630	Kif1a	kinesin family member 1A	15.50	17.71	23.88	21.14	1.36
17439797	Dspp	dentin sialophosphoprotein	10.62	9.29	13.12	13.83	1.35
17248621	Ccnj1	cyclin J-like	29.27	32.08	44.26	38.79	1.35
17424771	Spag8	sperm associated antigen 8	40.71	27.60	50.39	42.06	1.35
17369487	Ass1	argininosuccinate synthetase 1	22.03	19.67	29.06	27.37	1.35
17348589	Mir1948	microRNA 1948	8.89	9.15	10.40	14.00	1.35
17390614	Mfap1b	microfibrillar-associated protein 1B	37.83	27.38	42.61	45.62	1.35
17246449	Olfir818	olfactory receptor 818	7.01	7.00	10.94	8.01	1.35
17312095			23.74	25.78	23.60	43.36	1.35
17262598	Olfir1371	olfactory receptor 1371	58.90	47.09	78.45	64.84	1.35
17359304	Cyp2c39	cytochrome P450, family 2, subfamily c, polypeptide 39	23.19	22.79	32.38	29.77	1.35
17323707	Gm15764	predicted gene 15764	20.66	17.66	28.81	22.98	1.35
17543850	Mir672	microRNA 672	11.15	7.41	12.62	12.46	1.35
17431811	Pla2g2f	phospholipase A2, group IIF	149.13	160.45	183.47	234.79	1.35
17285065			10.14	9.26	15.46	10.73	1.35
17240431	Smpd2	sphingomyelin phosphodiesterase 2, neutral	39.62	39.26	47.74	58.76	1.35
17277970	D130020L05Rik	RIKEN cDNA D130020L05 gene	15.41	15.71	23.84	18.14	1.35
17505475	Gm16349	predicted gene 16349	12.08	11.21	15.82	15.60	1.35
17397552	C820005J03Rik	RIKEN cDNA C820005J03 gene	7.86	7.50	10.76	9.95	1.35
17233037			7.74	7.66	9.17	11.61	1.35
17216554			143.31	62.59	143.59	134.08	1.35
17326794	LOC100653389	uncharacterized LOC100653389	27.77	24.79	39.02	31.81	1.35
17356622	Cdca5	cell division cycle associated 5	49.31	55.62	60.29	81.11	1.35
17532653	mt-Tp	mitochondrially encoded tRNA proline	107.46	69.68	125.39	113.18	1.35
17300119			157.91	118.97	183.20	189.49	1.35
17225811			54.90	25.27	54.83	53.09	1.35
17439326	Gm3286	predicted gene 3286	10.68	9.45	12.65	14.44	1.35
17233663	Mir466j	microRNA 466j	355.57	200.41	393.60	354.43	1.35
17232547	Stfal	stefin A1	10.09	8.95	16.75	8.87	1.35
17293475	Gm19792	predicted gene, 19792	7.93	7.35	10.98	9.57	1.34
17467382			11.19	9.29	14.90	12.64	1.34
17260175			7.53	7.07	8.48	11.16	1.34
17273159	Ppp1r27	protein phosphatase 1, regulatory subunit 27	18.84	17.94	23.55	25.90	1.34
17239182			24.65	48.27	45.37	52.64	1.34
17324742	Gm15729	predicted gene 15729	8.54	8.34	11.09	11.61	1.34
17483061	Ccdc101	coiled-coil domain containing 101	30.45	25.92	38.68	37.07	1.34
17544826			5.72	6.01	9.62	6.14	1.34
17352203	Zfp516	zinc finger protein 516	30.20	31.76	42.32	40.93	1.34
17392801			33.30	26.54	38.91	41.48	1.34
17396876			11.61	14.40	16.76	18.17	1.34
17507915			64.93	67.18	94.25	83.12	1.34
17339572			13.73	14.76	20.02	18.22	1.34
17313953			21.36	28.71	26.13	41.11	1.34
17353333	A830052D11Rik	RIKEN cDNA A830052D11 gene	13.76	13.67	17.39	19.44	1.34
17339460	Lpin2	lipin 2	7.33	7.13	10.15	9.26	1.34
17435636	9530036011Rik	RIKEN cDNA 9530036011Rik	11.53	10.97	17.77	12.43	1.34
17220898			4.69	4.57	6.43	5.99	1.34
17216745	Gpr39	G protein-coupled receptor 39	47.94	46.31	68.03	58.39	1.34
17418059	Col9a2	collagen, type IX, alpha 2	64.87	75.44	94.00	94.19	1.34
17418304	Mir697	microRNA 697	14.98	21.22	26.08	22.46	1.34
17476528	Sbsn	suprabasin	28.78	41.32	47.92	46.06	1.34
17420895			92.52	81.46	128.28	104.98	1.34
17459151			9.59	9.83	15.17	10.88	1.34
17524139			16.49	13.90	19.98	20.73	1.34
17447610	Msx1	homeobox, msh-like 1	62.01	67.51	114.73	58.72	1.34
17532577	2010315B03Rik	RIKEN cDNA 2010315B03 gene	18.53	18.42	26.77	22.70	1.34
17507825	Defb40	defensin beta 40	6.45	6.16	8.14	8.75	1.34
17287790	H2afy	H2A histone family, member Y	54.85	75.16	116.30	57.75	1.34
17284362	Ighj1	immunoglobulin heavy joining 1	60.08	35.99	84.47	44.12	1.34
17284426	Ighm	immunoglobulin heavy constant mu	125.78	87.01	152.58	132.23	1.34
17324332	Fetub	fetuin beta	36.92	23.05	31.99	48.26	1.34
17486299	Vmn2r45	vomer nasal 2, receptor 45	17.95	14.38	24.36	18.90	1.34
17299991	Trav7-4	T cell receptor alpha variable 7-4	6.64	6.28	9.88	7.40	1.34
17334404	Gm8842	predicted gene 8842	12.87	14.11	18.42	17.68	1.34
17271201			12.26	24.93	40.69	9.07	1.34
17407706			89.73	57.61	103.49	93.63	1.34
17270724	5330430P22Rik	RIKEN cDNA 5330430P22 gene	12.02	15.28	16.58	19.93	1.34
17356924	Nrxn2	neuroligin II	15.25	16.46	21.23	21.18	1.34
17281607			11.17	12.28	17.95	13.42	1.34
17494168	Olfir601	olfactory receptor 601	14.56	12.41	17.30	18.77	1.34
17218565	Scarna3a	small Cajal body-specific RNA 3A	45.61	43.30	57.16	61.72	1.34
17215832	Mir149	microRNA 149	71.31	59.83	100.95	74.39	1.34
17305381	Gm8020	predicted gene 8020	7.04	6.25	9.47	8.30	1.34
17328040			19.73	24.87	31.88	27.74	1.34
17303821	Mss51	MSS51 mitochondrial translational activator	9.95	8.77	12.43	12.59	1.34
17277900	Kcnk13	potassium channel, subfamily K, member 13	13.56	13.97	19.05	17.74	1.34
17249301	Col23a1	collagen, type XXIII, alpha 1	28.01	29.23	44.96	31.50	1.34
17533469	Cypt1	cysteine-rich perinuclear theca 1	6.55	5.87	8.32	8.27	1.34
17324637	Fam43a	family with sequence similarity 43, member A	70.71	82.46	111.81	92.77	1.34
17218321	Rgs16	regulator of G-protein signaling 16	26.72	23.11	22.10	44.42	1.33
17285922	Slc17a1	solute carrier family 17 (sodium phosphate), member 1	23.86	16.27	27.19	26.36	1.33
17536496	Tmem28	transmembrane protein 28	21.16	21.01	28.39	27.88	1.33
17235821	Gm10778	predicted gene 10778	18.82	22.62	31.24	24.05	1.33
17548530	Ldhd	lactate dehydrogenase B	24.84	25.25	36.74	30.07	1.33
17309065	Mzt1	mitotic spindle organizing protein 1	60.55	79.21	78.92	107.52	1.33
17396369	Nceh1	arylacetamide deacetylase-like 1	16.31	15.26	19.72	22.38	1.33

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17261031			48.69	40.66	62.48	56.63	1.33
17401725			7.10	7.14	11.08	7.89	1.33
17531705	Ccr12	chemokine (C-C motif) receptor-like 2	11.25	9.25	12.99	14.34	1.33
17464713			8.99	9.00	14.52	9.45	1.33
17334666	Tpsb2	tryptase beta 2	46.27	14.92	35.87	45.64	1.33
17438233	Gsx2	GS homeobox 2	15.07	15.75	17.27	23.77	1.33
17455673	LOC100862180	PRAME family member 12-like	373.28	167.64	307.44	412.91	1.33
17490104	Vmn2r63	vomeronasal 2, receptor 63	5.20	5.30	7.58	6.40	1.33
17302928	AA536875	expressed sequence AA536875	8.23	8.69	12.29	10.24	1.33
17474858			5.05	5.05	7.47	5.97	1.33
17311341			43.30	32.75	47.12	54.07	1.33
17284910	Calm5	calmodulin 5	41.49	39.78	57.68	50.41	1.33
17516280	Olf1r150	olfactory receptor 150	6.90	7.95	11.02	8.73	1.33
17218607	Mrps14	mitochondrial ribosomal protein S14	12.30	11.34	15.38	16.05	1.33
17367947			15.42	16.87	14.21	28.72	1.33
17290394			27.15	22.29	27.74	37.98	1.33
17290396			27.15	22.29	27.74	37.98	1.33
17503360			21.25	15.66	30.59	18.47	1.33
17324402			43.89	36.59	52.80	54.15	1.33
17221999			6.52	4.91	6.95	8.24	1.33
17382841	C330006A16Rik	RIKEN cDNA C330006A16 gene	36.88	67.68	41.89	96.94	1.33
17282557	Syndig11	synapse differentiation inducing 1 like	17.33	14.35	25.41	16.65	1.33
17240661			8.19	9.15	12.72	10.29	1.33
17332117	Gml15966	predicted gene 15966	8.39	7.36	10.08	10.82	1.33
17313246			6.16	4.68	7.47	6.92	1.33
17501299			25.65	19.45	22.28	37.54	1.33
17543560			7.20	7.25	9.94	9.22	1.33
17541681	Gpc3	glypican 3	15.62	20.28	29.58	18.00	1.33
17344309	Tnf	tumor necrosis factor	51.22	43.47	63.07	62.42	1.33
17522647			11.92	8.93	14.34	13.28	1.33
17396878	Sox2	SRY-box containing gene 2	6.57	7.55	9.00	9.70	1.33
17296084	Zswim6	zinc finger, SWIM domain containing 6	42.86	46.93	46.18	72.78	1.32
17367004	Ill15ra	interleukin 15 receptor, alpha chain	32.70	34.18	40.79	47.81	1.32
17475101	Dmrtc2	doublesex and mab-3 related transcription factor like family C2	37.78	32.30	49.16	43.69	1.32
17454326	1700123K08Rik	RIKEN cDNA 1700123K08 gene	13.76	13.64	21.14	15.16	1.32
17523985	4930568E12Rik	RIKEN cDNA 4930568E12 gene	13.61	11.84	16.51	17.21	1.32
17421764			172.77	142.94	250.18	167.99	1.32
17241234			32.14	24.48	45.97	29.01	1.32
17305683			28.14	42.38	60.23	33.15	1.32
17330544	Sid1l	SID1 transmembrane family, member 1	90.52	80.99	115.22	111.89	1.32
17446058			279.17	205.19	284.69	356.65	1.32
17210996			24.07	18.51	22.63	33.73	1.32
17411274	2510003D18Rik	RIKEN cDNA 2510003D18 gene	11.83	13.15	16.24	16.81	1.32
17233303			16.10	15.67	19.96	22.07	1.32
17342403	Rhot2	ras homolog gene family, member T2	13.53	15.72	21.83	16.84	1.32
17480924			64.91	55.60	53.23	106.00	1.32
17281479	n-R5s60	nuclear encoded rRNA 5S 60	6.90	5.93	6.73	10.23	1.32
17217625	Tnni1	troponin I, skeletal, slow 1	29.56	32.89	48.62	33.88	1.32
17548551	4631423B10Rik	RIKEN cDNA 4631423B10 gene	74.23	69.03	87.34	101.90	1.32
17408052	Terc	telomerase RNA component	83.94	71.65	107.75	97.77	1.32
17429331	4930538K18Rik	RIKEN cDNA 4930538K18 gene	14.21	12.49	19.03	16.23	1.32
17302234	Zbtbd6	kelch repeat and BTB (POZ) domain containing 6	20.19	19.42	24.16	28.13	1.32
17306477	Slc7a8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	61.20	52.77	60.86	89.61	1.32
17352913	Dsc3	desmocollin 3	10.18	12.63	17.37	12.74	1.32
17533124	Ssx9	synovial sarcoma, X member B, breakpoint 9	6.36	5.88	9.45	6.70	1.32
17312899	Galr3	galanin receptor 3	18.64	22.92	28.98	25.86	1.32
17486474	Zscan4b	zinc finger and SCAN domain containing 4B	6.40	6.78	9.20	8.19	1.32
17421452			6.33	5.59	7.22	8.50	1.32
17423105			8.65	8.80	13.13	9.88	1.32
17445751			11.01	7.81	13.98	10.83	1.32
17221430			10.46	8.39	9.45	15.40	1.32
17473514	Gm5065	predicted gene 5065	15.62	11.19	16.77	18.57	1.32
17233767	Mir5108	microRNA 5108	20.43	21.73	22.81	32.73	1.32
17356517	Kcnk7	potassium channel, subfamily K, member 7	18.03	17.12	18.52	27.77	1.32
17317622	Tmem71	transmembrane protein 71	10.10	10.51	14.17	12.97	1.32
17352016			120.11	114.53	130.47	178.42	1.32
17429414	Ppcs	phosphopantothenoylcysteine synthetase	50.19	60.96	63.70	82.60	1.32
17331842	Krtap26-1	keratin associated protein 26-1	10.27	9.99	14.52	12.14	1.32
17250530			14.43	14.57	20.18	17.99	1.32
17354359			4.66	8.00	8.10	8.57	1.32
17357416			108.89	56.66	113.05	104.78	1.32
17370485	Mir181b-2	microRNA 181b-2	20.39	17.16	35.49	13.91	1.32
17510254	Snora68	small nucleolar RNA, H/ACA box 68	50.23	57.89	65.16	77.09	1.32
17489917	Gm6818	predicted gene 6818	20.55	15.74	25.07	22.67	1.32
17450748	Mfsd7a	major facilitator superfamily domain containing 7A	25.34	28.34	40.80	29.81	1.32
17374188	Olf1r1285	olfactory receptor 1285	8.98	7.81	15.07	7.02	1.32
17402357	1810037117Rik	RIKEN cDNA 1810037117 gene	350.97	389.13	425.28	546.83	1.31
17250089	Olf1r322	olfactory receptor 322	16.35	13.44	19.12	20.00	1.31
17507938			444.11	321.01	526.96	477.66	1.31
17353597			7.60	7.26	9.18	10.33	1.31
17457745	Gm5771	predicted gene 5771	20.57	21.71	25.42	30.07	1.31
17434508			42.07	32.03	47.91	49.36	1.31
17214220	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase	59.81	81.89	77.23	108.10	1.31
17459353			33.37	17.07	38.01	28.18	1.31
17398285			6.67	6.36	9.24	7.86	1.31
17443901	Fam20c	family with sequence similarity 20, member C	24.60	28.87	29.47	40.68	1.31
17402408			88.25	40.99	97.66	71.85	1.31

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17517716	Gm5121	predicted gene 5121	151.53	142.92	204.13	182.04	1.31
17251001	Myh2	myosin, heavy polypeptide 2, skeletal muscle, adult	8.57	10.03	10.22	14.17	1.31
17437049	Mxslas	homeobox, msh-like 1 antisense	41.17	55.10	79.19	47.05	1.31
17366940			77.58	59.85	83.47	96.73	1.31
17537906	Kir3d11	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail	5.50	6.13	7.91	7.34	1.31
17240665			23.35	11.57	23.18	22.58	1.31
17333879	Gm6811	predicted gene 6811	17.49	16.05	23.80	20.14	1.31
17462224			8.92	15.14	17.66	13.86	1.31
17503784	Fto	fat mass and obesity associated	46.48	43.25	64.10	53.41	1.31
17427886	Gm12786	predicted gene 12786	8.95	7.73	11.82	10.02	1.31
17238646	Olfrr774	olfactory receptor 774	7.07	5.33	5.85	10.38	1.31
17473910			17.94	7.96	20.80	13.12	1.31
17267011	Gm11437	predicted gene 11437	38.60	40.06	46.71	56.23	1.31
17535342			85.97	69.63	97.92	105.64	1.31
17401058	Gm16160	predicted gene 16160	13.58	14.95	20.52	16.79	1.31
17499610	Defb5	defensin beta 5	6.58	5.30	8.01	7.52	1.31
17344334	Gm20527	predicted gene 20527	7.44	7.13	8.41	10.64	1.31
17397492	n-R5s196	nuclear encoded rRNA 5S 196	6.03	8.41	8.83	10.05	1.31
17542836	4933407K13Rik	RIKEN cDNA 4933407K13 gene	17.35	16.08	20.56	23.14	1.31
17264634			79.50	132.57	131.46	145.82	1.31
17335177	Uhrflbp1	UHRF1 (ICBP90) binding protein 1	27.71	28.78	40.34	33.50	1.31
17365508	Gm16068	predicted gene 16068	47.56	30.42	47.16	54.80	1.31
17300201	Traj25	T cell receptor alpha joining 25	9.18	8.27	10.21	12.61	1.31
17388033	Olfrr142	olfactory receptor 142	7.66	6.97	10.12	8.99	1.31
17513603	Zcchc14	zinc finger, CCHC domain containing 14	65.38	68.64	98.22	76.90	1.31
17433234			30.33	28.82	39.10	38.17	1.31
17290447	Chrm3	cholinergic receptor, muscarinic 3, cardiac	11.23	10.98	15.08	13.94	1.31
17535096			128.68	68.10	101.75	155.26	1.31
17458514	Npy	neuropeptide Y	131.42	73.72	155.10	112.81	1.31
17491352	Mrgprb4	MAS-related GPR, member B4	9.23	7.80	12.74	9.49	1.31
17442780	Glt1dl	glycosyltransferase 1 domain containing 1	16.45	22.33	25.04	25.61	1.31
17331583			6.85	6.39	8.50	8.79	1.31
17424042	Aptx	aprataxin	20.27	18.20	25.86	24.37	1.31
17232731	Rnu3a	U3A small nuclear RNA	291.72	248.62	329.18	376.11	1.31
17500170			18.88	18.48	21.91	26.85	1.31
17255352	Dlx3	distal-less homeobox 3	38.40	35.32	55.85	40.36	1.31
17330183	Stfa3	stefin A3	6.20	6.42	6.97	9.49	1.30
17322827			256.32	200.40	309.87	285.92	1.30
17303609	Rarb	retinoic acid receptor, beta	35.73	34.39	48.45	43.01	1.30
17243866			12.94	18.72	19.47	21.80	1.30
17493382	Gm15412	predicted gene 15412	36.26	29.91	46.45	39.80	1.30
17539534			5.70	5.30	7.50	6.84	1.30
17211294	Gdap1	ganglioside-induced differentiation-associated-protein 1	8.34	7.53	10.88	9.79	1.30
17359583	Cnml1	cyclin M1	16.98	16.13	23.48	19.66	1.30
17395193			9.24	8.96	11.91	11.81	1.30
17538318			9.79	9.43	11.33	13.70	1.30
17459455	Fabp1	fatty acid binding protein 1, liver	902.62	696.07	847.56	1234.92	1.30
17291076	Vmn1r202	vomeranase 1 receptor 202	5.18	5.92	8.23	6.23	1.30
17251328	Pik3r6	phosphoinositide-3-kinase, regulatory subunit 6	21.86	19.71	27.46	26.66	1.30
17324616			11.90	9.79	18.44	9.80	1.30
17284539			18.76	22.81	28.65	25.46	1.30
17355058			50.62	48.99	81.76	47.86	1.30
17479967	Vmn2r79	vomeranase 2, receptor 79	72.17	64.78	100.47	77.73	1.30
17286958	Gm9817	predicted gene 9817	22.96	23.63	32.54	28.02	1.30
17227532			25.96	17.05	28.94	26.98	1.30
17430654			42.04	49.94	58.93	60.63	1.30
17490695	Dkk1	dickkopf-like 1	9.30	10.15	11.83	13.43	1.30
17514340	Gm10718	predicted gene 10718	44.69	32.42	54.60	45.58	1.30
17269218	Gm14188	predicted gene 14188	32.76	25.69	38.27	37.66	1.30
17337574	Olfrr109	olfactory receptor 109	9.67	8.65	13.16	10.64	1.30
17543870	Zdhc15	zinc finger, DHHC domain containing 15	69.20	52.83	74.29	84.22	1.30
17239773	Gm15270	predicted gene 15270	12.36	13.82	17.33	16.67	1.30
17543623			5.60	5.14	6.66	7.29	1.30
17548577			28.40	26.83	33.80	37.92	1.30
17531799	Mir128-2	microRNA 128-2	11.80	8.73	9.75	16.90	1.30
17296007			14.13	11.84	17.72	15.98	1.30
17235941	Chst11	carbohydrate sulfotransferase 11	52.48	66.05	68.98	84.84	1.30
17362521	5730408K05Rik	RIKEN cDNA 5730408K05 gene	109.50	119.60	146.96	150.38	1.30
17548786			11.02	9.18	9.93	16.29	1.30
17531256			6.00	8.36	8.04	10.59	1.30
17462131	Olfrr211	olfactory receptor 211	27.93	20.38	36.68	26.00	1.30
17214368	Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	53.75	60.41	78.48	69.60	1.30
17546429			14.09	20.67	31.91	13.18	1.30
17383173	Surf1	surfeit gene 1	49.20	48.45	57.58	69.03	1.30
17214757	Gm19537	predicted gene, 19537	16.99	16.36	19.56	23.68	1.30
17284435	Igh-VJ558	immunoglobulin heavy chain (J558 family)	14.71	8.12	12.16	17.41	1.30
17373937	Renl	reticulocalbin 1	104.64	82.48	136.98	105.43	1.30
17398565	Gm6525	predicted pseudogene 6525	154.11	84.30	137.62	171.22	1.30
17325608	Cd80	CD80 antigen	13.20	11.29	15.63	16.08	1.30
17248664	Ublcpl	ubiquitin-like domain containing CTD phosphatase 1	56.78	53.31	47.87	94.72	1.30
17349514	Egr1	early growth response 1	67.13	59.34	79.66	84.14	1.30
17330080	Dir2	disrupted in renal carcinoma 2 (human)	48.42	44.82	60.14	60.60	1.30
17291085	Vmn1r206	vomeranase 1 receptor 206	49.38	42.17	56.49	62.05	1.29
17547265			8.05	9.20	10.59	11.75	1.29
17382154			68.82	47.61	75.39	75.35	1.29
17380119	Cass4	Cas scaffolding protein family member 4	12.15	13.72	15.65	17.84	1.29
17250511	Smcr8	Smith-Magenis syndrome chromosome region, candidate 8 homolog (human)	54.62	57.11	68.09	76.53	1.29

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17233329	Gm5423	predicted gene 5423	17.69	18.28	28.17	18.38	1.29
17409621	S1pr1	sphingosine-1-phosphate receptor 1	12.85	14.13	14.10	20.83	1.29
17327655	Gm15879	predicted gene 15879	9.48	9.32	11.63	12.69	1.29
17361878	Slc22a20	solute carrier family 22 (organic anion transporter), member 20	18.69	17.23	21.00	25.48	1.29
17239817	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	29.74	27.66	33.82	40.45	1.29
17259311	0610009L18Rik	RIKEN cDNA 0610009L18 gene	39.32	28.10	40.39	46.82	1.29
17245751	Arhgef25	Rho guanine nucleotide exchange factor (GEF) 25	15.36	13.42	17.63	19.60	1.29
17355437			288.02	352.07	421.04	406.90	1.29
17347896			27.60	27.34	36.01	35.05	1.29
17393910	Chd6	chromodomain helicase DNA binding protein 6	37.80	42.68	54.58	49.51	1.29
17525471	Gm3434	predicted gene 3434	8.79	9.73	10.84	13.12	1.29
17544814			60.30	25.23	54.82	55.77	1.29
17358503	Rc11	RNA terminal phosphate cyclase-like 1	31.83	43.06	43.28	53.55	1.29
17513270	4933408N05Rik	RIKEN cDNA 4933408N05 gene	16.84	16.17	22.79	19.90	1.29
17397875	Gpr171	G protein-coupled receptor 171	26.19	18.04	31.56	25.62	1.29
17272077	Gm11721	predicted gene 11721	7.95	8.08	8.51	12.21	1.29
17475695	Gm10046	predicted gene 10046	25.93	23.02	33.32	29.96	1.29
17522812	Mir467h	microRNA 467h	23.20	19.50	30.16	25.05	1.29
17379480			8.88	6.38	8.69	11.04	1.29
17380911	9230112E08Rik	RIKEN cDNA 9230112E08 gene	18.04	17.33	19.09	26.62	1.29
17537630	Mir3112	microRNA 3112	19.87	16.50	25.44	21.57	1.29
17337693	Gm20580	predicted gene, 20580	6.24	5.39	5.97	9.05	1.29
17255485			43.41	49.64	73.92	46.27	1.29
17249140	3010026009Rik	RIKEN cDNA 3010026009 gene	30.83	28.04	32.31	43.68	1.29
17247921	Gm6899	predicted gene 6899	19.86	26.13	26.10	33.27	1.29
17402319			15.99	16.19	17.19	24.34	1.29
17438361	Cep135	centrosomal protein 135	13.47	15.18	17.05	19.92	1.29
17389571	Zfp770	zinc finger protein 770	17.07	18.31	27.70	17.96	1.29
17399173	Gm17146	predicted gene 17146	17.00	16.32	17.00	25.99	1.29
17548965	LOC100503923	uncharacterized LOC100503923	14.39	12.30	17.64	16.80	1.29
17427181	Gm12669	predicted gene 12669	17.20	11.86	21.00	16.50	1.29
17367858	Fam166a	family with sequence similarity 166, member A	23.07	22.31	25.88	32.67	1.29
17332595	Prdm15	PR domain containing 15	20.64	22.75	31.93	24.04	1.29
17494228	Hbb-bs	hemoglobin, beta adult s chain	19.39	15.63	23.75	21.42	1.29
17496547	Prrt2	proline-rich transmembrane protein 2	20.43	24.43	25.81	32.02	1.29
17540460	BC049702	cDNA sequence BC049702	9.87	10.25	13.32	12.61	1.29
17494795	Olf488	olfactory receptor 488	8.63	7.18	9.90	10.48	1.29
17349974	2010320007Rik	RIKEN cDNA 2010320007 gene	29.49	22.32	33.64	33.14	1.29
17530920	Gm16343	predicted gene 16343	10.09	10.80	16.82	10.10	1.29
17362839	Msa10	membrane-spanning 4-domains, subfamily A, member 10	150.41	151.80	203.69	185.73	1.29
17473695	Gm6909	predicted gene 6909	13.55	15.00	20.78	16.00	1.29
17543691	Phka1	phosphorylase kinase alpha 1	28.62	22.88	28.96	37.40	1.29
17528615			10.66	8.86	17.70	7.45	1.29
17412296	Epha7	Eph receptor A7	16.96	17.85	20.46	24.39	1.29
17451400	1700069L16Rik	RIKEN cDNA 1700069L16 gene	8.74	9.92	13.78	10.25	1.29
17408442			26.62	23.75	30.93	33.94	1.29
17514355			82.97	52.17	100.95	73.08	1.29
17451867	Rfc5	replication factor C (activator 1) 5	46.35	49.40	55.97	67.30	1.29
17500744	B430010123Rik	RIKEN cDNA B430010123 gene	33.11	31.34	42.49	40.47	1.29
17274480			6.65	6.64	9.14	7.98	1.29
17390261	n-R5s205	nuclear encoded rRNA 5S 205	13.61	12.20	21.55	11.65	1.29
17395695	Gm14342	predicted gene 14342	13.90	13.14	15.87	18.91	1.29
17541067	Rhox2g	reproductive homeobox 2G	7.02	8.48	9.44	10.49	1.29
17290904	Olf1370	olfactory receptor 1370	13.95	13.47	16.56	18.70	1.29
17503503			9.26	8.37	10.49	12.19	1.29
17465447			10.66	12.15	10.81	18.53	1.29
17533806	Gm4907	predicted gene 4907	13.82	8.17	10.58	17.70	1.29
17265545	Gm12324	predicted gene 12324	8.30	9.04	11.25	11.03	1.29
17234873	Vmn2r81	vomer nasal 2, receptor 81	8.96	8.28	13.74	8.42	1.29
17238091	1700012D01Rik	RIKEN cDNA 1700012D01 gene	13.74	12.68	17.63	16.33	1.29
17218594	Gm10530	predicted gene 10530	15.66	15.32	19.07	20.74	1.29
17484952	Tspan4	tetraspanin 4	55.34	61.06	77.67	71.89	1.28
17214904	Gm16028	predicted gene 16028	28.17	25.91	34.81	34.68	1.28
17539123			4.82	4.80	6.32	6.04	1.28
17286551	Gm19865	predicted gene, 19865	6.69	6.81	9.32	8.02	1.28
17230960	Prox1	prospero-related homeobox 1	293.45	193.14	319.63	305.44	1.28
17508848			14.30	15.19	18.22	19.66	1.28
17255479	Gm11534	predicted gene 11534	14.24	15.36	20.02	17.99	1.28
17545618	Ptchd1	patched domain containing 1	20.27	21.67	28.84	25.02	1.28
17257798	Gm11669	predicted gene 11669	17.55	15.06	25.89	15.98	1.28
17235352			99.45	191.38	240.38	133.05	1.28
17416347	Pars2	prolyl-tRNA synthetase (mitochondrial) (putative)	13.66	14.66	16.31	20.05	1.28
17307738	Fzd3	frizzled homolog 3 (Drosophila)	14.06	14.48	17.91	18.73	1.28
17312209	Ly6e	lymphocyte antigen 6 complex, locus E	353.53	263.65	367.54	424.64	1.28
17529981	Foxl2os	forkhead box L2 opposite strand transcript	9.27	10.46	12.85	12.47	1.28
17443062	4930563F08Rik	RIKEN cDNA 4930563F08 gene	7.76	7.48	11.27	8.29	1.28
17535644	P1xn3	plexin B3	15.11	14.39	16.98	20.88	1.28
17246404	Olf1771	olfactory receptor 771	8.67	8.78	11.29	11.10	1.28
17490084	Gm17768	predicted gene, 17768	6.58	5.90	9.02	6.98	1.28
17545245	Gm8334	predicted gene 8334	25.56	30.94	37.15	35.33	1.28
17407494			5.89	5.49	7.58	7.02	1.28
17487489	Pvr	poliovirus receptor	28.90	28.98	39.35	34.89	1.28
17442940			41.20	27.28	36.68	51.14	1.28
17360766	1810018F18Rik	RIKEN cDNA 1810018F18 gene	19.58	18.72	20.37	28.73	1.28
17407531	Gm10697	predicted gene 10697	7.65	7.52	9.29	10.16	1.28
17366283	LOC100041877	nuclear body protein SP140-like	8.81	13.29	13.75	14.57	1.28
17504391			6.58	8.42	8.67	10.56	1.28

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17486481	Gm7789	predicted pseudogene 7789	16.67	17.40	16.27	27.37	1.28
17234936	Hen2	hyperpolarization-activated, cyclic nucleotide-gated K ⁺ 2	26.39	28.32	35.28	34.82	1.28
17299500	Olfir743	olfactory receptor 743	9.36	8.32	13.38	9.27	1.28
17393962	Ptprt	protein tyrosine phosphatase, receptor type, T	18.16	17.95	24.47	21.79	1.28
17515058	Ppan	peter pan homolog (Drosophila)	124.16	127.13	174.20	147.58	1.28
17474785	Vmnlr148	vomeranosal 1 receptor 148	5.83	6.42	8.05	7.63	1.28
17246038	Gpr182	G protein-coupled receptor 182	39.39	39.89	55.69	45.81	1.28
17317013	Gm10020	predicted pseudogene 10020	62.43	60.59	92.24	65.28	1.28
17342991			13.78	23.45	25.99	21.67	1.28
17521483			6.76	6.81	6.62	10.75	1.28
17382848	Gm13553	predicted gene 13553	6.77	7.40	9.39	8.75	1.28
17242957			54.37	33.28	55.06	57.09	1.28
17280624			12.79	11.35	15.07	15.81	1.28
17406395	Arfip1	ADP-ribosylation factor interacting protein 1	54.94	65.00	70.67	82.79	1.28
17383785	Gm13425	predicted gene 13425	9.30	10.38	14.72	10.46	1.28
17315198	Mir1941	microRNA 1941	17.94	14.22	17.82	23.31	1.28
17307736			31.32	29.46	45.67	32.08	1.28
17311138	Gm15942	predicted gene 15942	8.06	8.07	11.32	9.29	1.28
17262594	Olfir1373	olfactory receptor 1373	29.95	30.33	44.13	32.93	1.28
17216436	Serpinb11	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11	10.70	11.34	14.54	13.63	1.28
17414651	Zfp618	zinc finger protein 618	32.90	43.70	53.58	44.29	1.28
17435180	Lhfp13	lipoma HMGIC fusion partner-like 3	9.52	9.40	13.79	10.38	1.28
17513666	Thrh2	thyrotropin releasing hormone receptor 2	16.48	15.39	22.44	18.27	1.28
17370350	Olfir350	olfactory receptor 350	4.64	6.18	6.39	7.43	1.28
17459355			25.68	21.57	31.55	28.79	1.28
17309412	Sox21	SRY-box containing gene 21	75.15	100.01	133.63	90.01	1.28
17219684	Olfir429	olfactory receptor 429	6.61	8.13	9.34	9.49	1.28
17300155	Traj49	T cell receptor alpha joining 49	7.53	7.08	9.95	8.71	1.28
17462143			6.00	5.82	6.56	8.52	1.28
17533492			6.45	6.18	9.80	6.33	1.28
17221914	Gm20172	predicted gene, 20172	8.40	7.23	7.61	12.33	1.28
17300015	A430107P09Rik	RIKEN cDNA A430107P09 gene	62.18	47.64	72.44	67.71	1.28
17446474	Speer4a	spermatogenesis associated glutamate (E)-rich protein 4a	74.94	63.80	101.88	75.18	1.28
17220595			43.58	36.02	42.79	58.79	1.28
17267954	Epn3	epsin 3	39.76	39.89	54.66	46.97	1.28
17366800	Mir669g	microRNA 669g	10.31	8.94	11.68	12.88	1.28
17366836	Mir669g	microRNA 669g	10.31	8.94	11.68	12.88	1.28
17511806	4930488L21Rik	RIKEN cDNA 4930488L21 gene	32.33	33.22	34.93	48.71	1.28
17395057	Gm20490	predicted gene 20490	47.14	71.93	83.75	68.17	1.28
17223813	Akr1c1	aldo-keto reductase family 1, member C-like	5.93	7.48	8.80	8.29	1.28
17494408	Trim30d	tripartite motif-containing 30D	29.85	25.81	40.44	30.56	1.28
17290288	Akr1c20	aldo-keto reductase family 1, member C20	6.69	7.49	10.47	7.61	1.28
17354585			4.82	4.74	6.33	5.88	1.28
17222179	Lman2l	lectin, mannose-binding 2-like	36.18	31.53	42.48	43.85	1.27
17387174	Olfir1096-ps1	olfactory receptor 1096, pseudogene 1	6.08	5.19	7.16	7.21	1.27
17514375			4.96	4.57	7.18	4.97	1.27
17219639	Olfir418-ps1	olfactory receptor 418, pseudogene 1	14.73	13.57	19.46	16.62	1.27
17340502	Seracl1	serine active site containing 1	21.93	27.94	32.95	30.62	1.27
17400244	Lysmd1	LysM, putative peptidoglycan-binding, domain containing 1	106.21	88.65	113.28	135.05	1.27
17387131	Ccdc141	coiled-coil domain containing 141	70.10	58.29	87.70	75.91	1.27
17548844			7.37	5.49	8.34	8.03	1.27
17448168			5.92	5.46	6.65	7.85	1.27
17525163	Acad8	acyl-Coenzyme A dehydrogenase family, member 8	23.77	31.92	38.35	32.61	1.27
17321918	Gm5476	predicted gene 5476	11.93	11.53	17.96	11.93	1.27
17394765			151.74	111.82	158.78	177.01	1.27
17456836	Zc3hc1	zinc finger, C3HC type 1	32.75	28.71	35.38	42.91	1.27
17548662	Gm5606	predicted gene 5606	12.25	14.18	13.76	19.91	1.27
17487513	Vmnlr94	vomeranosal 1 receptor 94	15.64	13.53	19.42	17.73	1.27
17524393	Zfp426	zinc finger protein 426	21.34	21.15	26.45	27.67	1.27
17435725	I16	interleukin 6	6.22	5.86	7.03	8.35	1.27
17289279			11.22	10.64	12.79	15.06	1.27
17516434	D630033011Rik	RIKEN cDNA D630033011 gene	21.68	20.97	30.48	23.83	1.27
17335900			17.20	14.59	20.67	19.80	1.27
17406264	Gm10710	predicted gene 10710	12.03	13.22	13.82	18.33	1.27
17415711	A730085A09Rik	RIKEN cDNA A730085A09 gene	25.51	19.88	27.23	30.53	1.27
17261517	Efcab9	EF-hand calcium binding domain 9	8.38	9.20	11.53	10.84	1.27
17341350	Vmnlr232	vomeranosal 1 receptor 232	6.05	6.41	8.25	7.60	1.27
17322453	Olfir161	olfactory receptor 161	9.99	8.60	12.06	11.60	1.27
17359419	A130015J22Rik	RIKEN cDNA A130015J22 gene	12.28	12.69	15.95	15.81	1.27
17302565	4930449E01Rik	RIKEN cDNA 4930449E01 gene	12.24	12.04	16.73	14.15	1.27
17399081	Gm6821	predicted gene 6821	17.15	15.80	19.93	21.98	1.27
17278261	Serpina3b	serine (or cysteine) peptidase inhibitor, clade A, member 3B /	8.10	8.46	9.68	11.38	1.27
17252845	Snord91a	small nucleolar RNA, C/D box 91A	7.47	6.56	9.17	8.69	1.27
17476239	LOC101056654	uncharacterized LOC101056654	17.62	19.12	24.78	21.95	1.27
17546259	Ubaly	ubiquitin-activating enzyme, Chr Y	8.55	8.39	8.89	12.65	1.27
17274310	Hpcal1	hippocalcin-like 1	25.67	41.47	32.08	53.30	1.27
17472676			16.33	12.54	18.09	18.63	1.27
17284654			36.29	49.34	62.21	46.68	1.27
17369838	Gm13412	predicted gene 13412	10.18	8.39	11.71	11.91	1.27
17435053	A630072M18Rik	RIKEN cDNA A630072M18 gene	19.28	18.63	24.50	23.69	1.27
17245890	Inhbe	inhibin beta E	7.72	9.33	13.01	8.66	1.27
17260806			11.14	8.05	9.65	14.74	1.27
17281402			35.69	28.55	44.64	36.98	1.27
17381071	Gm16119	predicted gene 16119	21.65	24.70	35.30	23.57	1.27
17249355	D930048N14Rik	RIKEN cDNA D930048N14 gene	37.98	46.24	50.16	56.79	1.27
17422066	Plekhhg5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	36.58	44.58	57.04	46.01	1.27
17387697	Olfir1084	olfactory receptor 1084	7.97	6.71	10.51	8.13	1.27

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17354428			28.60	17.75	42.87	15.97	1.27
17335788			8.56	8.24	10.51	10.81	1.27
17366778			5.92	6.53	8.77	7.04	1.27
17389281	Olfir1297	olfactory receptor 1297	12.18	11.31	16.65	13.17	1.27
17326391			19.23	16.82	21.49	24.25	1.27
17499579	Spag11b	sperm associated antigen 11B	12.04	10.27	14.59	13.71	1.27
17214126	Rufy4	RUN and FYVE domain containing 4	22.92	27.09	33.02	30.41	1.27
17376119	Chchd5	coiled-coil-helix-coiled-coil-helix domain containing 5	44.12	47.86	46.67	69.97	1.27
17316348	Snord123	small nucleolar RNA, C/D box 123	54.03	66.61	94.50	58.49	1.27
17475081	Ceacam10	carcinoembryonic antigen-related cell adhesion molecule 10	18.69	16.35	25.16	19.27	1.27
17471324	Itfg2	integrin alpha FG-GAP repeat containing 2	40.43	33.29	43.90	49.56	1.27
17311142			29.34	20.40	24.42	38.63	1.27
17344694	Gm10499	predicted gene 10499	17.30	12.18	20.47	16.91	1.27
17351196	Apcddl	adenomatosis polyposis coli down-regulated 1	28.08	30.78	45.92	28.69	1.27
17514836	Tafld	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, D	731.61	839.86	969.99	1021.67	1.27
17288059			731.61	839.86	969.99	1021.67	1.27
17415391	Gm12609	predicted gene 12609	6.83	6.03	7.90	8.41	1.27
17211256			45.61	28.42	36.32	57.49	1.27
17288246	LOC100861707	zinc finger protein 709-like	6.37	7.40	8.45	9.00	1.27
17412202	Faxe	failed axon connections homolog (Drosophila)	12.78	17.73	21.31	17.35	1.27
17469634			5.61	5.32	7.80	6.06	1.27
17465270			16.73	13.63	15.06	23.40	1.27
17440971	Gm13790	predicted gene 13790	18.07	19.21	27.02	20.21	1.27
17458003	Olfir437	olfactory receptor 437	18.73	16.10	19.92	24.21	1.27
17472111	Gm6728	predicted gene 6728	12.16	14.79	13.97	20.16	1.27
17353215	Rpl29-ps5	ribosomal protein L29, pseudogene 5	42.28	50.52	51.80	65.73	1.27
17287336			195.21	235.15	242.00	302.92	1.27
17387678	Olfir1065	olfactory receptor 1065	5.84	5.27	8.20	5.87	1.27
17511069	Nanos3	nanos homolog 3 (Drosophila)	69.68	55.47	98.06	60.31	1.27
17317708	Mir30d	microRNA 30d	33.58	31.84	43.70	39.09	1.27
17382098	Gm13335	predicted gene 13335	7.20	7.37	7.83	10.60	1.27
17293813			12.68	11.32	16.38	13.99	1.27
17500494			32.72	44.33	47.99	49.47	1.26
17287957	Spata31d1b	spermatogenesis associated 31 subfamily D, member 1B	8.41	7.78	9.11	11.37	1.26
17535915	Gm5936	predicted gene 5936	146.98	84.68	161.89	131.05	1.26
17516908	Apoa4	apolipoprotein A-IV	510.21	559.98	723.59	629.70	1.26
17387694	Olfir1082	olfactory receptor 1082	5.97	6.04	7.00	8.17	1.26
17361285	Syt12	synaptotagmin XII	77.07	98.49	125.98	95.98	1.26
17448170			37.64	27.83	42.43	40.35	1.26
17244864	Nav3	neuron navigator 3	16.55	15.40	18.72	21.66	1.26
17437490	Rbpj	recombination signal binding protein for immunoglobulin kappa J region	11.85	10.99	13.03	15.85	1.26
17536950	1700018605Rik	RIKEN cDNA 1700018605 gene	8.20	8.05	12.48	8.05	1.26
17360305	AA387883	expressed sequence AA387883	10.94	10.54	12.93	14.20	1.26
17491695			21.19	17.96	27.81	21.66	1.26
17252875	1700016P03Rik	RIKEN cDNA 1700016P03 gene	14.63	13.98	17.05	19.09	1.26
17548973	Pten	phosphatase and tensin homolog	18.91	13.40	15.47	25.34	1.26
17363156			192.11	59.22	173.42	144.00	1.26
17363158			192.11	59.22	173.42	144.00	1.26
17247627	Tmem17	transmembrane protein 17	10.86	10.97	14.39	13.17	1.26
17357715			6.72	7.88	8.75	9.69	1.26
17440457			78.20	60.49	81.66	93.41	1.26
17443166	Stx1a	syntaxin 1A (brain)	47.16	43.03	59.20	54.64	1.26
17526633	LOC100502818	uncharacterized LOC100502818	494.59	596.16	746.38	630.24	1.26
17273191	Alyref	Aly/REF export factor	14.38	15.14	18.87	18.39	1.26
17437565			11.04	14.64	15.35	17.05	1.26
17337557	H2-M3	histocompatibility 2, M region locus 3	14.76	17.20	20.77	19.56	1.26
17342999	Cpne5	copine V	14.85	14.07	21.64	14.85	1.26
17487270			18.86	28.57	29.61	30.22	1.26
17268817			222.04	269.61	306.50	313.61	1.26
17222070	Mir5103	microRNA 5103	8.33	11.90	14.96	10.55	1.26
17469797	Ghrl	ghrelin	46.47	35.78	51.11	52.61	1.26
17337381	Gm19684	predicted gene, 19684	18.92	16.51	22.43	22.24	1.26
17387742	Olfir259	olfactory receptor 259	13.80	15.73	19.48	17.74	1.26
17377065	Zfp133-ps	zinc finger protein 133, pseudogene	15.91	14.78	22.42	16.26	1.26
17481332	Olfir663	olfactory receptor 663	8.77	5.93	9.23	9.29	1.26
17264090	Gm12284	predicted gene 12284	14.52	13.88	20.56	15.22	1.26
17476604	Scgb2b2	secretoglobin, family 2B, member 2	6.21	5.40	7.65	6.97	1.26
17487102			16.96	14.12	22.55	16.59	1.26
17333505	Gm3435	predicted gene 3435	25.30	29.91	31.36	38.17	1.26
17240577	Gm15199	predicted gene 15199	33.15	37.92	39.21	50.29	1.26
17363817	A930007119Rik	RIKEN cDNA A930007119 gene	11.22	11.43	13.59	14.94	1.26
17366728	Mir669d	microRNA 669d	83.61	51.14	86.22	83.46	1.26
17439159	Gm20500	predicted gene 20500	14.88	17.68	20.65	20.35	1.26
17363129	Olfir1447	olfactory receptor 1447	6.84	6.48	9.27	7.50	1.26
17324772			9.28	10.45	14.27	10.56	1.26
17421437	LOC101056605	zinc finger protein 708-like	8.02	7.29	11.65	7.62	1.26
17285821	Hist1h3g	histone cluster 1, H3g	8.86	6.50	9.55	9.80	1.26
17325721			43.46	19.37	32.74	46.36	1.26
17214899	Gm7609	predicted pseudogene 7609	31.52	43.87	42.15	52.76	1.26
17426926	Gm12414	predicted gene 12414	15.07	14.61	20.30	17.06	1.26
17281071	Gpr33	G protein-coupled receptor 33	8.59	8.29	9.40	11.85	1.26
17540521	Cfp	complement factor properdin	41.03	38.68	50.92	49.40	1.26
17335312	Fance	Fanconi anemia, complementation group E	45.13	41.64	50.81	58.41	1.26
17311789	Rnf139	ring finger protein 139	27.86	21.36	30.50	31.45	1.26
17516960	Cadml	cell adhesion molecule 1	52.07	40.05	52.51	63.41	1.26
17367740	Zmynd19	zinc finger, MYND domain containing 19	26.32	22.51	31.64	29.79	1.26
17305520	Earl	eosinophil-associated, ribonuclease A family, member 1	6.77	7.15	9.68	7.83	1.26

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17367738			36.95	26.79	39.24	40.95	1.26
17531286	Gm7628	predicted gene 7628	22.83	26.76	29.68	32.71	1.26
17464776	Rpa3	replication protein A3	55.29	86.29	74.29	103.82	1.26
17535191			231.55	168.55	251.26	252.05	1.26
17492890	n-R5s154	nuclear encoded rRNA 5S 154	16.23	22.46	15.83	32.84	1.26
17384689	Gm13584	predicted gene 13584	7.64	8.55	11.40	8.96	1.26
17545567	Magea2	melanoma antigen, family A, 2	6.31	6.45	9.40	6.64	1.26
17515729	Prdm10	PR domain containing 10	23.28	33.34	37.50	33.70	1.26
17463806	Gm8994	predicted gene 8994	49.94	52.04	56.49	71.73	1.26
17387778	Olfir1141	olfactory receptor 1141	11.51	11.19	14.99	13.54	1.26
17505197	Cirh1a	cirrrosis, autosomal recessive 1A (human)	71.82	74.08	82.66	100.70	1.26
17368546	Gm13421	predicted gene 13421	11.20	10.77	11.23	16.38	1.26
17535532	Gm5639	predicted pseudogene 5639	18.22	22.63	25.04	26.28	1.26
17481190	Olfir597	olfactory receptor 597	4.64	4.80	6.50	5.36	1.26
17316153	Acot10	acyl-CoA thioesterase 10	49.29	37.59	48.89	60.25	1.26
17404230	Gm5150	predicted gene 5150	8.82	7.39	11.33	9.03	1.26
17548338	Tmeff1	transmembrane protein with EGF-like and two follistatin-like doma	21.72	17.54	25.17	24.14	1.26
17503703	Rps6-ps2	ribosomal protein S6, pseudogene 2	17.66	23.29	20.03	31.40	1.26
17402400	Gm9372	predicted gene 9372	25.73	22.75	34.43	26.46	1.26
17415432			148.23	120.53	166.81	170.70	1.26
17379887			69.54	39.84	72.53	64.81	1.26
17378149	Bpifb1	BPI fold containing family B, member 1	217.55	113.63	152.84	262.97	1.26
17240089	Tpd5211	tumor protein D52-like 1	36.01	52.36	52.99	57.96	1.26
17343176	Tff1	trefoil factor 1	80.33	71.56	91.51	99.17	1.26
17310528			7.67	7.14	9.27	9.32	1.26
17283641	Serpina1e	serine (or cysteine) peptidase inhibitor, clade A, member 1E	40.13	47.52	46.75	63.28	1.26
17427488	IOCO044D17Rik	RIKEN cDNA IOCO044D17 gene	7.65	8.98	12.01	8.85	1.26
17272969	Mir338	microRNA 338	17.94	13.40	20.21	19.12	1.26
17307280	Phf11b	PHD finger protein 11B	39.36	25.79	46.23	35.54	1.26
17321336	Wnt10b	wingless related MMTV integration site 10b	11.36	12.99	15.12	15.44	1.25
17232786	Wasf1	WAS protein family, member 1	17.85	13.88	21.08	18.74	1.25
17506065			6.62	5.31	7.44	7.53	1.25
17494822	Nlrp10	NLR family, pyrin domain containing 10	13.60	12.38	17.50	15.09	1.25
17319339	Cbx6	chromobox homolog 6	27.99	28.41	38.23	32.53	1.25
17313911	Trnu	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	16.72	16.02	21.48	19.58	1.25
17303333	Gm3476	predicted gene 3476	7.04	7.04	9.28	8.37	1.25
17294544	Atp5c1-ps	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma	7.53	7.68	9.82	9.26	1.25
17344892	Olfir113	olfactory receptor 113	10.33	8.83	14.04	9.97	1.25
17299268	Cdkn3	cyclin-dependent kinase inhibitor 3	79.65	75.24	83.03	111.16	1.25
17283475	Mir1936	microRNA 1936	9.61	9.40	13.03	10.80	1.25
17350581	1700034E13Rik	RIKEN cDNA 1700034E13 gene	9.94	11.63	13.71	13.34	1.25
17239985			131.28	97.62	149.30	137.62	1.25
17300181	Trav9d-3	T cell receptor alpha variable 9D-3	7.02	7.47	9.75	8.42	1.25
17534982	Gpr112	G protein-coupled receptor 112	9.15	9.14	12.00	10.93	1.25
17389820	Dnajc17	DnaJ (Hsp40) homolog, subfamily C, member 17	25.66	26.38	30.12	35.11	1.25
17300030			7.86	8.62	11.25	9.39	1.25
17387624	Olfir1019	olfactory receptor 1019	6.85	6.35	8.45	8.09	1.25
17457052	9430029A11Rik	RIKEN cDNA 9430029A11 gene	29.22	27.08	34.11	36.45	1.25
17458924	Vmn1r4	vomer nasal 1 receptor 4	25.99	16.73	20.68	32.86	1.25
17307096	Zym5	zinc finger, MYM-type 5	24.93	21.96	27.98	30.78	1.25
17336031			16.41	15.14	23.61	15.92	1.25
17390530	Stre	stereocilin	12.59	11.34	17.30	12.68	1.25
17299621	Gm5622	predicted gene 5622	20.73	21.82	30.13	23.17	1.25
17541125	Rhox9	reproductive homeobox 9	22.04	22.35	30.01	25.60	1.25
17547692			8.82	6.99	8.77	11.04	1.25
17473810	Zfp324	zinc finger protein 324	18.76	20.43	22.16	26.93	1.25
17467522			7.83	9.01	9.35	11.74	1.25
17480489			8.19	8.14	8.74	11.71	1.25
17310827	Fam173b	family with sequence similarity 173, member B	30.76	30.87	35.65	41.54	1.25
17371616	Sp5	trans-acting transcription factor 5	44.07	51.77	64.55	55.48	1.25
17416596	4930407G08Rik	RIKEN cDNA 4930407G08 gene	22.80	21.37	31.00	24.31	1.25
17480028			6.77	6.08	8.65	7.45	1.25
17330850			153.43	151.05	191.03	190.09	1.25
17256910	BC030867	cDNA sequence BC030867	24.22	21.15	34.95	21.85	1.25
17299910	Trav12-2	T cell receptor alpha variable 12-2	173.99	129.39	194.72	184.99	1.25
17278848	Mir539	microRNA 539	197.50	139.24	222.44	199.01	1.25
17387846	Olfir1196	olfactory receptor 1196	6.65	8.09	8.31	10.13	1.25
17481960	Arnt1	aryl hydrocarbon receptor nuclear translocator-like	32.00	37.53	46.46	40.56	1.25
17310882	Cpq	carboxypeptidase Q	21.85	18.99	24.32	26.80	1.25
17240971	Edar	ectodysplasin-A receptor	15.72	18.03	22.66	19.57	1.25
17525418	Hyls1	hydrolethalus syndrome 1	30.39	22.21	18.14	18.50	0.70
17424461	Ccl21a	chemokine (C-C motif) ligand 21A (serine)	45.66	79.08	43.50	43.34	0.70
17224771	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	71.10	68.19	30.28	66.58	0.70
17337122	H2-Q6	histocompatibility 2, Q region locus 6	48.13	54.85	39.34	32.24	0.70
17467474			12.94	12.30	9.04	8.50	0.70
17371053	Gm13572	predicted gene 13572	20.76	15.28	11.27	13.78	0.69
17467534			8.26	10.46	6.29	6.72	0.69
17432496			12.90	7.65	7.35	6.93	0.69
17284913	Tuba13	tubulin, alpha-like 3	23.34	27.78	17.81	17.72	0.69
17282435	Numb	numb gene homolog (Drosophila)	63.22	70.56	43.02	49.90	0.69
17288014			24.64	12.43	14.46	11.28	0.69
17214729	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	985.40	1303.97	535.47	1054.25	0.69
17298775	Anxa8	annexin A8	61.44	65.05	39.91	47.90	0.69
17473061	Dennd5b	DENN/MADD domain containing 5B	21.86	26.39	17.93	15.56	0.69
17492466	2610034B18Rik	RIKEN cDNA 2610034B18 gene	76.73	81.14	47.57	61.99	0.69
17365098	Scd1	stearoyl-Coenzyme A desaturase 1	95.05	73.88	58.65	58.59	0.69
17481274	Trim34a	tripartite motif-containing 34A	11.05	10.43	7.16	7.75	0.69

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17541008	Snora69	small nucleolar RNA, H/ACA box 69	10.73	12.41	7.21	8.85	0.69
17313581			52.81	47.03	36.17	33.05	0.69
17316390	Rpl30	ribosomal protein L30	16.43	21.48	12.27	13.99	0.69
17326814			23.48	12.67	12.20	12.83	0.69
17548675	4930412F12Rik	RIKEN cDNA 4930412F12 gene	33.68	38.82	23.83	26.36	0.69
17459412			5.54	10.92	5.72	5.66	0.69
17272939	A430071A18Rik	RIKEN cDNA A430071A18 gene	197.36	253.17	134.15	176.74	0.69
17212968			23.17	13.15	11.37	13.68	0.69
17286882	Nol7	nucleolar protein 7	74.16	94.08	57.74	58.20	0.69
17506510	Rpl13	ribosomal protein L13	29.79	11.64	12.76	15.74	0.69
17527661	Islr	immunoglobulin superfamily containing leucine-rich repeat	38.48	60.02	30.67	37.08	0.69
17388599	Ttc17	tetratricopeptide repeat domain 17	39.93	36.14	24.29	28.00	0.69
17317203	Derl1	Derl-like domain family, member 1	34.87	24.91	17.86	23.23	0.69
17253858	Atad5	ATPase family, AAA domain containing 5	16.01	12.68	8.98	10.72	0.69
17519673	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	493.38	657.91	338.11	452.15	0.69
17300205	Traj23	T cell receptor alpha joining 23	9.17	11.60	6.64	7.59	0.69
17525731	Olfir955	olfactory receptor 955	21.54	25.06	16.66	15.28	0.69
17415302	Ifnz	interferon zeta	29.78	36.84	23.79	21.86	0.69
17520820			8.91	14.11	7.43	8.34	0.68
17353948	Gnpdal	glucosamine-6-phosphate deaminase 1	22.87	23.88	16.69	15.32	0.68
17518328	Uch13	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	37.91	54.22	25.53	37.48	0.68
17499788	Defa26	defensin, alpha, 26	96.97	153.07	87.31	83.40	0.68
17529590	9430037G07Rik	RIKEN cDNA 9430037G07 gene	60.07	39.45	31.05	36.85	0.68
17529557			60.07	39.45	31.05	36.85	0.68
17212874	E330011M16Rik	RIKEN cDNA E330011M16 gene	133.22	125.72	80.74	95.85	0.68
17439464	Anxa3	annexin A3	72.40	89.34	50.64	59.34	0.68
17339079			45.13	38.62	32.32	24.63	0.68
17485952	Isoc2b	isochorismatase domain containing 2b	23.73	26.24	16.69	17.29	0.68
17344593	H2-T22	histocompatibility 2, T region locus 22	27.91	42.62	23.38	24.57	0.68
17336314			15.04	9.70	10.35	6.46	0.68
17232438			21.54	41.97	19.02	24.12	0.68
17459421	Igk	immunoglobulin kappa chain complex	590.29	1130.39	514.22	654.19	0.68
17366734	mmu-mir-297a-2	mmu-mir-297a-2	13.34	16.67	10.33	10.03	0.68
17467449			37.61	70.51	34.26	39.09	0.68
17409540	Amy2a1	amylase 2a1	9.67	16.37	8.60	9.06	0.68
17284450	Igh-VJ558	immunoglobulin heavy chain (J558 family)	6.88	12.93	5.98	7.46	0.68
17317349	E430025E21Rik	RIKEN cDNA E430025E21 gene	83.75	102.90	58.61	67.98	0.68
17280528			5.64	14.15	7.18	6.24	0.68
17308783	Gm3362	predicted pseudogene 3362	37.98	29.81	24.07	21.88	0.68
17434285	Ccl21a	chemokine (C-C motif) ligand 21A (serine)	53.63	82.65	50.94	41.42	0.68
17333493	9030025P20Rik	RIKEN cDNA 9030025P20 gene	15.98	14.23	8.62	11.85	0.68
17412965	Ccl21a	chemokine (C-C motif) ligand 21A (serine)	45.14	83.07	44.66	42.16	0.68
17413025	Ccl21a	chemokine (C-C motif) ligand 21A (serine)	45.14	83.07	44.66	42.16	0.68
17413123	Ccl21a	chemokine (C-C motif) ligand 21A (serine)	45.14	83.07	44.66	42.16	0.68
17434150	Ccl21a	chemokine (C-C motif) ligand 21A (serine)	45.14	83.07	44.66	42.16	0.68
17447504			86.24	67.04	61.76	42.02	0.68
17463617			59.07	64.16	42.39	40.90	0.68
17363505	Smc5	structural maintenance of chromosomes 5	46.94	39.59	30.19	28.24	0.68
17518312	Snord16a	small nucleolar RNA, C/D box 16A	85.89	80.17	55.43	56.69	0.68
17414264			65.96	79.95	45.52	52.79	0.67
17231086			23.46	23.10	12.77	18.59	0.67
17436481	Fgfr3	fibroblast growth factor receptor 3	23.33	29.05	14.67	20.55	0.67
17311058			41.96	40.94	28.67	27.03	0.67
17314691	Gm8973	predicted gene 8973	23.33	48.76	24.44	23.97	0.67
17374053	Kcna4	potassium voltage-gated channel, shaker-related subfamily, member 4	21.65	33.73	18.18	18.99	0.67
17372354	Ssfa2	sperm specific antigen 2	102.96	130.83	78.38	78.50	0.67
17322829	Nubp1	nucleotide binding protein 1	95.03	114.09	69.26	71.04	0.67
17244070	Nrlh4	nuclear receptor subfamily 1, group H, member 4	42.46	50.77	30.99	31.40	0.67
17532627	mt-Th	mitochondrially encoded tRNA histidine	103.60	89.10	35.03	93.81	0.67
17254300	1100001G20Rik	RIKEN cDNA 1100001G20 gene	81.16	43.84	40.05	43.46	0.67
17469463	Rybp	RING1 and YY1 binding protein	68.73	100.93	52.10	61.24	0.67
17467471			46.67	55.78	30.89	37.52	0.67
17483770			16.29	10.41	8.44	9.39	0.67
1744486	Bri3	brain protein I3	52.34	60.18	40.86	34.25	0.67
17375997	Mertk	c-mer proto-oncogene tyrosine kinase	72.20	86.55	49.33	56.55	0.67
17480102	Syt12	synaptotagmin-like 2	51.56	42.20	28.58	33.95	0.67
17284482			57.17	61.89	37.02	42.35	0.67
17397240	Hspa41	heat shock protein 4 like	33.84	40.06	22.34	26.91	0.67
17368515	Gml7071	predicted gene 17071	27.59	29.09	19.37	18.39	0.67
17491205	Saal	serum amyloid A 1	21.61	14.60	16.12	7.98	0.67
17467469			82.32	19.58	17.60	50.19	0.67
17422697	Ankrd65	ankyrin repeat domain 65	85.20	88.22	57.30	58.04	0.67
17346528	C3	complement component 3	128.43	72.86	56.07	77.75	0.66
17467461			55.62	118.34	46.65	68.98	0.66
17463781	Emp1	epithelial membrane protein 1	442.20	483.53	317.24	297.15	0.66
17363407	Anxa1	annexin A1	234.80	210.59	130.12	165.17	0.66
17365030	Chuk	conserved helix-loop-helix ubiquitous kinase	72.41	61.05	47.24	41.21	0.66
17401331			11.90	29.54	15.51	11.94	0.66
17547969	Gml5798	predicted gene 15798	69.88	72.40	55.65	38.58	0.66
17410939	Clica3	chloride channel calcium activated 3	202.11	131.08	85.92	134.60	0.66
17375641	Dut	deoxyuridine triphosphatase	69.12	84.55	48.00	53.68	0.66
17507308	Slc10a2	solute carrier family 10, member 2	56.92	83.29	49.44	43.11	0.66
17267418	A130040M12Rik	RIKEN cDNA A130040M12 gene	136.62	172.59	93.71	110.32	0.66
17268905			50.53	93.09	37.90	56.82	0.66
17514482	Mmp13	matrix metalloproteinase 13	59.42	51.18	25.37	47.57	0.66
17234707	Gml10272	predicted gene 10272	16.01	20.54	13.67	10.43	0.66
17519658	Gm3776	predicted gene 3776	186.54	191.37	90.25	158.67	0.66

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17501204			21.73	36.32	20.71	17.49	0.66
17305163	2610528A11Rik	RIKEN cDNA 2610528A11 gene	332.29	402.67	272.60	210.88	0.66
17457794	Tcrb-J	T cell receptor beta, joining region	33.91	26.09	14.83	24.64	0.66
17383381	Cel	carboxyl ester lipase	13.51	25.22	14.15	11.32	0.66
17542021	Mir505	microRNA 505	150.73	59.41	66.79	71.21	0.66
17548690	Gm6625	predicted gene 6625	358.91	308.80	206.12	231.73	0.66
17467447			12.62	8.80	7.30	6.73	0.65
17396260	Cp	ceruloplasmin	38.34	27.60	23.14	20.03	0.65
17236747	4732465J04Rik	RIKEN cDNA 4732465J04 gene	18.37	32.46	16.39	16.86	0.65
17413078	Cc121a	chemokine (C-C motif) ligand 21A (serine)	49.66	81.17	45.26	40.28	0.65
17434230	Cc121a	chemokine (C-C motif) ligand 21A (serine)	49.66	81.17	45.26	40.28	0.65
17341652	Gm15947	predicted gene 15947	53.83	48.18	37.55	29.14	0.65
17419268			30.00	32.27	21.41	19.23	0.65
17419270			30.00	32.27	21.41	19.23	0.65
17488470	Samd4b	sterile alpha motif domain containing 4B	88.59	122.32	67.80	69.56	0.65
17465170	Slc13a1	solute carrier family 13 (sodium/sulfate symporters), member 1	35.78	43.63	25.46	26.20	0.65
17274405			29.86	14.35	14.57	14.18	0.65
17548178	Snrpd1	small nuclear ribonucleoprotein D1	21.81	14.37	11.71	11.81	0.65
17314476	Tmem117	transmembrane protein 117	25.10	32.85	17.76	19.90	0.65
17526576	Tagln	transgelin	46.15	62.00	32.03	38.24	0.65
17219242	Nr1i3	nuclear receptor subfamily 1, group I, member 3	54.48	22.48	23.47	26.52	0.65
17478956	Gm7551	predicted gene 7551	101.76	92.62	73.32	52.68	0.65
17221662	Tram2	translocating chain-associating membrane protein 2	41.16	52.38	22.83	37.72	0.65
17489464	Scn1b	sodium channel, voltage-gated, type I, beta	31.53	30.97	21.44	19.02	0.65
17329023			26.49	39.75	17.01	25.85	0.65
17473779	Zfp128	zinc finger protein 128	26.68	22.11	16.71	14.80	0.65
17315519	Hoxc6	homeobox C6	19.99	25.08	15.05	14.05	0.65
17344120	Snord52	small nucleolar RNA, C/D box 52	15.29	16.52	11.21	9.32	0.65
17284652			7.10	12.93	7.06	5.85	0.64
17340197	Epas1	endothelial PAS domain protein 1	95.17	153.05	78.90	81.03	0.64
17357148	Shng1	small nucleolar RNA host gene (non-protein coding) 1	19.17	17.73	11.75	12.02	0.64
17293571	Mir3074-1	microRNA 3074-1	34.01	13.98	16.42	14.49	0.64
17521441	Nat6	N-acetyltransferase 6	80.50	118.02	62.00	65.85	0.64
17366235			13.14	12.50	8.07	8.44	0.64
17395302	Gm14402	predicted gene 14402	23.02	15.18	12.59	12.01	0.64
17238834			32.96	19.00	17.10	16.31	0.64
17442185	Gm6444	predicted gene 6444	59.26	43.10	28.31	37.49	0.64
17374827	1700020114Rik	RIKEN cDNA 1700020114 gene	80.34	103.10	65.62	52.28	0.64
17330323	Nr1i2	nuclear receptor subfamily 1, group I, member 2	50.00	84.59	34.82	51.56	0.64
17502369	Olfir372	olfactory receptor 372	12.11	17.35	9.83	9.05	0.64
17476364	Tyrobp	TYRO protein tyrosine kinase binding protein	86.89	74.70	52.87	50.64	0.64
17459361			35.59	40.61	24.80	23.98	0.64
17248127			29.48	38.30	20.55	22.84	0.64
17459769	Reg1	regenerating islet-derived 1	103.94	177.81	60.16	119.73	0.64
17298956	Matla	methionine adenosyltransferase I, alpha	33.81	14.56	17.44	13.44	0.64
17284607			104.10	136.58	70.53	82.68	0.64
17284631			104.10	136.58	70.53	82.68	0.64
17399574	1700094D03Rik	RIKEN cDNA 1700094D03 gene	16.12	25.61	13.65	12.81	0.63
17252032	Med11	mediator of RNA polymerase II transcription, subunit 11 homolog (S. cerevisiae)	55.07	61.14	37.81	35.82	0.63
17236096	Gm8394	predicted gene 8394	105.69	56.02	59.83	42.55	0.63
17318875	Myh9	myosin, heavy polypeptide 9, non-muscle	242.85	278.55	147.27	182.77	0.63
17284533			14.91	50.13	14.32	26.81	0.63
17311802	Gm5045	predicted gene 5045	92.13	79.53	50.15	58.41	0.63
17455534	Gm5566	predicted pseudogene 5566	64.05	74.39	39.99	47.45	0.63
17467389			82.81	103.34	51.50	65.72	0.63
17284460			12.96	47.42	8.52	29.50	0.63
17224180	Igfbp5	insulin-like growth factor binding protein 5	334.65	376.66	142.08	305.73	0.63
17548559	Empl1	epithelial membrane protein 1	291.78	266.79	169.80	181.85	0.63
17284993			58.48	76.65	46.14	38.64	0.63
17360695	Atrn11	attractin like 1	116.75	124.76	72.86	78.57	0.63
17213591			45.98	37.37	15.98	36.21	0.63
17482922			15.47	30.47	16.62	12.09	0.62
17343856	Btn15	butyrophilin-like 5	96.80	140.64	54.16	94.21	0.62
17501211			15.70	16.30	11.56	8.43	0.62
17226622	Cd55	CD55 antigen	83.21	71.19	43.55	52.81	0.62
17448738			29.01	13.14	17.55	8.76	0.62
17501041	Casp3	caspase 3	31.15	31.06	15.16	23.65	0.62
17284519			68.01	105.47	57.86	50.23	0.62
17513978			122.97	92.94	67.70	66.20	0.62
17513980			122.97	92.94	67.70	66.20	0.62
17406421	Arfip1	ADP-ribosylation factor interacting protein 1	32.83	35.99	13.60	29.07	0.62
17424928	Tomm5	translocase of outer mitochondrial membrane 5 homolog (yeast)	11.81	21.70	10.58	10.19	0.62
17459347	Igk	immunoglobulin kappa chain complex	66.70	137.29	46.55	79.74	0.62
17284445			25.88	35.74	13.17	24.96	0.62
17288043			17.26	12.88	8.69	9.93	0.62
17222777	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	38.79	60.42	27.59	33.61	0.62
17440132			37.27	21.03	20.24	15.56	0.61
17471357	Pzp	pregnancy zone protein	36.53	16.32	17.82	14.62	0.61
17249513			78.61	79.54	51.79	45.20	0.61
17459403			26.09	22.02	16.30	13.10	0.61
17324394	Snord2	small nucleolar RNA, C/D box 2	30.02	27.59	14.41	20.74	0.61
17371708	Cybrd1	cytochrome b reductase 1	31.08	68.31	26.55	34.01	0.61
17329009	Iglv1	immunoglobulin lambda variable 1	43.67	59.55	28.79	34.06	0.61
17321683	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	69.57	137.94	57.65	68.70	0.61
17398499	Fga	fibrinogen alpha chain	20.74	6.96	8.27	8.55	0.61
17284667			8.59	23.14	8.58	10.68	0.61
17279167	Eif5	eukaryotic translation initiation factor 5	32.21	20.21	15.26	16.49	0.61

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17352777			34.69	37.45	20.78	22.78	0.60
17232729			12.85	6.63	5.96	5.74	0.60
17423289			10.75	15.37	7.19	8.46	0.60
17507933	AY761184	cDNA sequence AY761184	254.12	435.20	217.18	195.47	0.60
17357486	Syt7	synaptotagmin VII	21.45	42.62	19.33	18.83	0.60
17316066			14.28	19.41	9.14	10.90	0.60
17402181	F3	coagulation factor III	197.85	282.22	137.28	147.82	0.59
17495368	Nup35	nucleoporin 35	29.60	25.62	21.14	11.57	0.59
17467404			10.13	28.45	10.75	12.01	0.59
17467466	Igkv4-55	immunoglobulin kappa variable 4-55	74.73	135.79	70.62	53.03	0.59
17476565	Gm17077	predicted gene 17077	21.07	28.78	14.28	14.95	0.59
17302360			46.93	18.76	22.05	16.46	0.59
17333938	Zfp52	zinc finger protein 52	14.20	16.08	9.17	8.58	0.59
17368521			11.19	17.67	6.29	10.63	0.59
17238900			24.18	28.83	14.56	16.49	0.59
17505478	Tat	tyrosine aminotransferase	68.41	86.69	56.32	34.42	0.59
17465731			74.65	78.59	27.72	61.84	0.58
17461153			32.33	21.89	16.32	15.29	0.58
17284602			12.16	14.96	6.33	9.47	0.58
17449473	Gc	group specific component	36.26	11.82	13.83	14.18	0.58
17425900	Gm2083	major urinary protein LOC100048885	19.88	7.11	7.80	7.92	0.58
17251299			22.71	22.62	11.20	15.15	0.58
17284527			11.34	20.20	10.26	8.02	0.58
17532629	mt-Ts2	mitochondrially encoded tRNA serine 2	34.63	30.59	10.18	27.60	0.58
17305826	Gm6055	predicted gene 6055	14.59	22.48	12.15	9.31	0.58
17246262	Rps26	ribosomal protein S26	51.66	28.57	23.18	23.19	0.58
17547897	Oxct1	3-oxoacid CoA transferase 1	189.62	170.33	62.25	145.38	0.58
17302617	Mirl7hg	MIR17 host gene 1 (non-protein coding)	138.05	157.33	80.42	89.78	0.58
17462057	Gm8203	predicted pseudogene 8203	153.82	274.35	88.67	157.98	0.58
17467392	Igkv19-93	immunoglobulin kappa chain variable 19-93	46.45	52.74	19.01	38.05	0.58
17318794	Apol17c	apolipoprotein L 7c	80.97	36.69	33.91	33.66	0.57
17275750			69.52	93.94	57.98	35.48	0.57
17400510	Sf3b4	splicing factor 3b, subunit 4	27.06	20.37	13.84	13.25	0.57
17284354	Igh-VX24	immunoglobulin heavy chain (X24 family)	640.95	931.73	388.25	509.46	0.57
17333658	Gm6712	predicted gene 6712	21.21	16.37	9.25	12.18	0.57
17245231	Lyz1	lysozyme 1	496.97	616.19	278.63	355.65	0.57
17462366			24.95	57.13	25.03	21.65	0.57
17406921			108.76	90.02	40.89	72.09	0.57
17253181	Tmigd1	transmembrane and immunoglobulin domain containing 1	49.01	102.95	43.33	42.44	0.56
17284554			49.11	132.53	48.79	53.63	0.56
17426000	Gm2083	major urinary protein LOC100048885	20.61	7.26	7.56	8.13	0.56
17449447	Igj	immunoglobulin joining chain	330.85	611.26	254.86	270.99	0.56
17513149	Ctrb1	chymotrypsinogen B1	20.86	50.94	20.50	19.52	0.56
17513974			19.45	17.73	10.16	10.55	0.56
17313583	Cyp2d9	cytochrome P450, family 2, subfamily d, polypeptide 9	15.76	6.10	6.78	5.31	0.55
17284633	Ighm	immunoglobulin heavy constant mu	115.50	281.99	95.02	124.69	0.55
17386477	Gm11084	predicted gene 11084	21.57	8.64	10.55	6.11	0.55
17284648			78.47	182.60	89.62	54.42	0.55
17284562			42.69	66.85	32.30	28.00	0.55
17308999	Gm10119	predicted gene 10119	61.38	74.30	38.72	35.49	0.55
17467499			15.94	6.81	7.33	5.06	0.54
17325661			13.55	14.71	7.66	7.64	0.54
17467483	Igkv5-43	immunoglobulin kappa chain variable 5-43	24.82	50.45	23.74	16.78	0.54
17425888	Gm2083	major urinary protein LOC100048885	23.36	7.27	8.09	8.23	0.53
17426097	Mup3	major urinary protein 3	22.74	8.94	8.71	8.15	0.53
17302279	Olfm4	olfactomedin 4	70.86	162.76	61.07	62.53	0.53
17266960	Ccl6	chemokine (C-C motif) ligand 6	116.89	200.18	70.09	96.95	0.53
17457765	Prss2	protease, serine, 2	10.24	27.19	11.20	8.38	0.52
17329013	Iglv1	immunoglobulin lambda variable 1	171.30	320.96	133.82	123.50	0.52
17238840			32.12	41.63	17.30	21.24	0.52
17426043	Gm2083	major urinary protein LOC100048885	32.18	8.19	10.40	10.62	0.52
17426032	Gm2083	major urinary protein LOC100048885	25.79	7.44	9.18	8.07	0.52
17290674	Gm7040	predicted gene 7040	59.72	62.62	23.97	38.89	0.51
17459409			15.99	49.38	24.64	8.89	0.51
17284536			21.16	45.92	22.77	11.58	0.51
17426011	Gm2083	major urinary protein LOC100048885	25.43	7.00	8.73	7.84	0.51
17459324	Igkv1-117	immunoglobulin kappa variable 1-117	96.21	182.67	75.47	66.71	0.51
17409526	Amy2a1	amylase 2a1	10.74	29.76	10.10	10.48	0.51
17417699	Gm12840	predicted gene 12840	41.95	61.07	25.22	27.10	0.51
17284560			12.75	23.12	5.82	12.25	0.50
17352366			14.03	14.88	6.37	8.14	0.50
17239755	Rps12	ribosomal protein S12	65.33	77.09	51.86	19.47	0.50
17240969			18.37	14.17	7.46	8.82	0.50
17467398	Igkv4-91	immunoglobulin kappa chain variable 4-91	73.18	54.81	22.43	41.49	0.50
17398485	Fgg	fibrinogen gamma chain	23.88	7.57	7.87	7.83	0.50
17506882			62.59	18.03	16.03	23.91	0.50
17425915	Gm2083	major urinary protein LOC100048885	25.50	7.13	8.37	7.74	0.49
17284609			25.91	75.77	18.80	31.00	0.49
17459417	Igkj3	immunoglobulin kappa joining 3	30.47	65.98	24.41	22.82	0.49
17290666	Gm7040	predicted gene 7040	46.49	44.41	17.97	26.16	0.49
17284437			56.01	29.13	17.14	24.14	0.48
17426062	Gm2083	major urinary protein LOC100048885	26.32	7.15	7.99	8.24	0.48
17467486			74.77	143.59	39.42	66.24	0.48
17467410	Igkv19-93	immunoglobulin kappa chain variable 19-93	22.72	34.51	14.78	12.76	0.48
17284571			12.92	47.50	10.33	18.50	0.48
17366183			242.26	515.28	151.61	208.98	0.48
17284379	Igh-VX24	immunoglobulin heavy chain (X24 family)	44.71	66.07	15.40	37.31	0.48

Supplementary Table 2

ID	Gene Symbol	Name	Control 1	Control 2	DN-RhoA 1	DN-RhoA 2	Fold exp difference (Control/DN-RhoA)
17280184	Zfp125	zinc finger protein 125	17.20	23.03	10.86	8.26	0.48
17426237	Ambp	alpha 1 microglobulin/bikunin	32.69	10.66	12.10	8.39	0.47
17284605	Igh-VJ558	immunoglobulin heavy chain (J558 family)	133.30	333.43	92.58	126.99	0.47
17438886	Alb	albumin	347.25	59.05	85.64	103.71	0.47
17467489			99.43	158.79	76.42	43.45	0.46
17425941	Gm2083	major urinary protein LOC100048885	32.47	8.35	9.20	9.70	0.46
17407412	Sprrla	small proline-rich protein 1A	155.30	203.32	65.91	99.60	0.46
17425990	Gm2083	major urinary protein LOC100048885	28.48	7.57	8.41	8.21	0.46
17459291			22.40	78.72	22.44	23.94	0.46
17284593			36.26	30.15	14.71	15.56	0.46
17462529	Mugl	murinoglobulin 1	27.60	7.34	8.39	7.38	0.45
17374848	Nusapl	nucleolar and spindle associated protein 1	69.90	98.52	41.68	34.23	0.45
17398509			47.56	13.45	15.22	12.25	0.45
17543785	Xist	inactive X specific transcripts	19.83	115.27	41.91	18.23	0.45
17338231			20.16	55.61	18.62	14.85	0.44
17355951			39.95	57.02	20.42	21.79	0.44
17459338	Igk	immunoglobulin kappa chain complex	95.38	429.67	154.28	70.78	0.43
17284334	Ighg	Immunoglobulin heavy chain (gamma polypeptide)	9.73	37.33	10.22	9.80	0.43
17297591			25.87	34.98	10.96	14.66	0.42
17484587	Cyp2e1	cytochrome P450, family 2, subfamily e, polypeptide 1	72.44	20.20	20.79	18.14	0.42
17284546			26.97	5.65	6.62	7.08	0.42
17284402	Ighm	immunoglobulin heavy constant mu	17.74	458.59	100.69	98.98	0.42
17284617			29.34	79.68	16.26	28.77	0.41
17284657			8.04	30.04	9.33	6.25	0.41
17532313	1700012L04Rik	RIKEN cDNA 1700012L04 gene	51.01	36.58	18.06	17.59	0.41
17281893			17.08	66.33	19.67	13.27	0.39
17284548			43.45	140.52	25.25	46.52	0.39
17409513	Amy2a1	amylase 2a1	10.74	44.44	9.98	11.14	0.38
17284628			13.48	37.56	9.19	9.99	0.38
17472581	Gm766	predicted gene 766	36.42	51.93	11.51	20.82	0.37
17284339	Ighm	immunoglobulin heavy constant mu	41.80	116.16	21.75	35.94	0.37
17284574	Igh-VJ558	immunoglobulin heavy chain (J558 family)	100.76	76.88	23.14	40.10	0.36
17487374	Apoc1	apolipoprotein C-I	76.59	16.58	15.95	17.15	0.36
17459309			8.24	38.65	9.58	6.81	0.35
17284530			25.25	73.26	16.00	17.39	0.34
17426022	Mup8	major urinary protein 8	46.26	9.14	9.12	9.59	0.34
17284660			17.16	45.57	12.27	8.51	0.33
17406252	Fgb	fibrinogen beta chain	57.67	10.80	10.06	11.42	0.31
17324322	Ahsg	alpha-2-HS-glycoprotein	83.54	16.10	16.85	12.87	0.30
17284662			48.22	251.38	62.07	25.33	0.29
17467384			116.46	417.80	89.27	61.29	0.28
17284432			48.93	187.60	36.89	26.03	0.27
17467537			22.87	83.94	15.11	12.49	0.26
17505769	Ctrb1	chymotrypsinogen B1	11.94	102.65	13.71	15.89	0.26
17401890	Amy2a5	amylase 2a5	7.90	61.80	8.61	8.44	0.24
17401893	Amy2a5	amylase 2a5	7.90	61.80	8.61	8.44	0.24
17401896	Amy2a5	amylase 2a5	7.90	61.80	8.61	8.44	0.24
17401899	Amy2a5	amylase 2a5	7.90	61.80	8.61	8.44	0.24
17284498			40.04	163.34	12.01	26.05	0.19
17284512			60.13	41.02	7.50	7.14	0.14
17283634	Serpinalc	serine (or cysteine) peptidase inhibitor, clade A, member 1C	116.21	9.89	7.89	6.94	0.12
17215166	Akp3	alkaline phosphatase 3, intestine, not Mn requiring	32.55	367.74	23.00	20.10	0.11

Supplementary Table 3

Supplementary Table 3: Functional group enrichment analysis using Gene Ontology categories. Only significantly enriched categories are shown (Benjamini-Hochberg-corrected p<0.05)

Category ¹	Term ²	Count ³	Percentage ⁴	PValue ⁵	List Total ⁶	Pop Hits ⁷	Pop Total ⁸	Fold Enrichment	Benjamini ⁹
GOTERM_CC_ALL	GO:0005615~extracellular space	38	5.8	1.17E-08	417	487	15531	2.91	3.29E-06
GOTERM_CC_ALL	GO:0044421~extracellular region part	45	6.9	8.47E-07	417	749	15531	2.24	1.19E-04
GOTERM_CC_ALL	GO:0005576~extracellular region	72	11.0	3.51E-05	417	1649	15531	1.63	3.28E-03
GOTERM_MF_ALL	GO:0060089~molecular transducer activity	101	15.4	9.72E-05	381	2777	14977	1.43	2.52E-02
GOTERM_MF_ALL	GO:0004871~signal transducer activity	101	15.4	9.72E-05	381	2777	14977	1.43	2.52E-02
GOTERM_MF_ALL	GO:0004872~receptor activity	95	14.5	5.51E-05	381	2533	14977	1.47	2.85E-02
GOTERM_MF_ALL	GO:0003823~antigen binding	7	1.1	2.62E-04	381	36	14977	7.64	3.39E-02
GOTERM_MF_ALL	GO:0003735~structural constituent of ribosome	3	2.0	3.93E-04	381	148	14977	3.45	4.06E-02
GOTERM_MF_ALL	GO:0004930~G-protein coupled receptor activity	67	10.1	2.49E-04	381	1663	14977	1.56	4.28E-02
GOTERM_BP_ALL	GO:0009605~response to external stimulus	34	5.2	1.00E-04	363	623	13799	2.07	4.77E-02

¹Category: Gene Ontology categories: biological process (BP), cellular compartment (CC) and molecular function (MF).

²Term: Gene set name

³Count: number of genes associated with this gene set

⁴Percentage: gene associated with this gene set/total number of query genes

⁵P-value: modified Fisher Exact P-value

⁶List Total: number of genes in the query list mapped to any gene set in this ontology

⁷Pop Hits: number of genes annotated to this gene set on the background list

⁸Pop Total: number of genes on the background list mapped to any gene set in this ontology.

⁹Benjamini: Benjamini-Hochberg-corrected p-value