Table S4 Significant differentially expressed genes between sirolimus (S) and vehicle (V) treatment listed by fold change.

Ensembl_Gene	Gene Symbol	Name	Mean S (n=4)	SEM S	Mean V (n=4)	SEM V	t-test	Fold change
ENSRNOG00000013552	Scd1	Stearoyl-Coenzyme A desaturase 1	6.74	0.34	8.88	0.42	0.007	0.227
ENSRNOG00000012404	Thrsp	Thyroid hormone responsive	7.30	0.42	9.41	0.33	0.007	0.232
ENSRNOG00000015308	Pbk	PDZ binding kinase	5.50	0.46	7.56	0.31	0.010	0.240
ENSRNOG00000001796	Dgkg	Diacylglycerol kinase, gamma	7.57	0.10	9.00	0.12	0.000	0.371
ENSRNOG00000015850	Rbp7	Retinol binding protein 7, cellular	5.30	0.14	6.69	0.32	0.008	0.381
ENSRNOG00000039103		Transcribed locus, moderately similar to XP_002725225.1 PREDICTED: mCG140493-like [Rattus norvegicus]	6.36	0.32	7.74	0.18	0.010	0.385
ENSRNOG00000037198	Usp18	Ubiquitin specific peptidase 18	5.29	0.10	6.63	0.09	0.000	0.394
ENSRNOG00000023272	Rrm2	Ribonucleotide reductase M2	6.33	0.17	7.60	0.13	0.001	0.417
ENSRNOG00000031211	Acsm5	Acyl-CoA synthetase medium-chain family member 5	6.61	0.31	7.87	0.16	0.012	0.418
ENSRNOG00000015550	Ptgds	prostaglandin D2 synthase 21kDa	7.76	0.10	9.01	0.22	0.002	0.421
ENSRNOG00000003202			4.89	0.16	6.12	0.26	0.007	0.427
ENSRNOG00000032404	Top2a	topoisomerase (DNA) II alpha 170kDa	7.14	0.28	8.35	0.25	0.018	0.433
ENSRNOG00000012640	Dpp7	Dipeptidylpeptidase 7	7.26	0.05	8.45	0.08	0.000	0.439
ENSRNOG00000037304	Casc5	cancer susceptibility candidate 5	4.88	0.08	6.05	0.16	0.001	0.446
ENSRNOG00000026440	RGD1559891		4.73	0.21	5.88	0.21	0.008	0.449
ENSRNOG00000019542	MGC108823;RGD1559715	Similar to interferon-inducible GTPase	4.99	0.19	6.13	0.14	0.003	0.453

Ensembl_Gene	Gene Symbol	Name	Mean S (n=4)	SEM S	Mean V (n=4)	SEM V	t-test	Fold change
ENSRNOG00000001821	Adipoq	Adiponectin, C1Q and collagen domain containing	6.69	0.17	7.82	0.31	0.019	0.456
ENSRNOG00000009086	Apcs	Amyloid P component, serum	9.41	0.11	10.53	0.11	0.000	0.460
ENSRNOG00000003959	Rgs18	regulator of G-protein signaling 18	5.86	0.16	6.97	0.11	0.001	0.463
ENSRNOG00000017539	Mmp9	Matrix metallopeptidase 9	6.24	0.12	7.35	0.14	0.001	0.465
ENSRNOG00000028137	RGD1566252		6.63	0.22	7.74	0.22	0.012	0.465
ENSRNOG00000015411	Apobec1	Apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	7.46	0.09	8.55	0.18	0.002	0.472
ENSRNOG00000000045	Cd244	Cd244 molecule, natural killer cell receptor 2B4	4.09	0.22	5.15	0.31	0.032	0.481
ENSRNOG00000034190	LOC678701	Transcribed locus, moderately similar to XP_002729795.1 PREDICTED: mCG129376-like [Rattus norvegicus]	7.34	0.13	8.39	0.39	0.042	0.483
ENSRNOG00000014938	Gabrb3	Gamma-aminobutyric acid (GABA) A receptor, beta 3	5.76	0.12	6.81	0.40	0.047	0.483
ENSRNOG00000018505	Cidea	Cell death-inducing DFFA-like effector a	7.32	0.25	8.35	0.31	0.041	0.490
ENSRNOG00000038738			7.35	0.25	8.38	0.09	0.008	0.490
ENSRNOG00000000168	Gatm	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	9.95	0.06	10.97	0.04	0.000	0.494
ENSRNOG00000002925	Tsx	Testis specific X-linked gene	7.07	0.05	8.08	0.18	0.001	0.495
ENSRNOG00000006731	Spc25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	6.35	0.19	7.36	0.23	0.015	0.495
ENSRNOG00000038960	RGD1309362	Similar to interferon-inducible GTPase	7.57	0.29	8.58	0.14	0.020	0.496

Ensembl_Gene	Gene Symbol	Name	Mean S (n=4)	SEM S	Mean V (n=4)	SEM V	t-test	Fold change
ENSRNOG00000015945	Cd3g	CD3g molecule, gamma (CD3-TCR complex)	4.86	0.07	5.86	0.18	0.002	0.500
ENSRNOG00000028288	Clrn3	Clarin 3	6.51	0.19	7.51	0.09	0.003	0.501
ENSRNOG00000009785	Cdkn3	cyclin-dependent kinase inhibitor 3	6.02	0.31	7.01	0.11	0.023	0.502
ENSRNOG00000010149	Cmc1	COX assembly mitochondrial protein homolog (S. cerevisiae)	7.35	0.20	8.33	0.09	0.004	0.508
ENSRNOG00000014407		Transcribed locus, moderately similar to XP_224795.4 PREDICTED: similar to C28H8.3 [Rattus norvegicus]	5.28	0.09	6.25	0.18	0.003	0.512
ENSRNOG00000031078	RGD1566137		3.26	0.02	4.22	0.25	0.008	0.512
ENSRNOG00000004601	Hao1	Hydroxyacid oxidase (glycolate oxidase) 1	5.20	0.20	6.15	0.13	0.007	0.516
ENSRNOG00000036701	Actg1;LOC295810	Actin, gamma 1	3.85	0.23	4.80	0.31	0.050	0.518
ENSRNOG00000026501	Slc6a19	Solute carrier family 6 (neutral amino acid transporter), member 19	8.31	0.12	9.25	0.08	0.001	0.519
ENSRNOG00000028626			6.51	0.24	7.46	0.09	0.010	0.520
ENSRNOG00000028870	Acot1	acyl-CoA thioesterase 1	8.03	0.11	8.97	0.11	0.001	0.522
ENSRNOG00000014541	Ddx60;LOC684383	Transcribed locus	5.41	0.20	6.35	0.11	0.007	0.523
ENSRNOG00000015763	Cml3	Camello-like 3	8.40	0.03	9.34	0.12	0.000	0.523
ENSRNOG00000013727	Ndc80	Transcribed locus	5.54	0.15	6.46	0.26	0.023	0.526
ENSRNOG00000000632	Cdc2	Cell division cycle 2, G1 to S and G2 to M	4.95	0.11	5.87	0.19	0.005	0.526
ENSRNOG00000004921	Nusap1	Nucleolar and spindle associated protein 1	6.45	0.32	7.37	0.14	0.039	0.529

Ensembl_Gene	Gene Symbol	Name	Mean S (n=4)	SEM S	Mean V (n=4)	SEM V	t-test	Fold change
ENSRNOG00000003802	Pttg1	Pituitary tumor-transforming 1	6.50	0.12	7.41	0.15	0.003	0.533
ENSRNOG00000037267	Renbp	Renin binding protein	6.48	0.05	7.39	0.06	0.000	0.533
ENSRNOG00000026378	Casc5	cancer susceptibility candidate 5	6.20	0.25	7.10	0.23	0.038	0.535
ENSRNOG00000038035	Kif4	Kinesin family member 4	5.92	0.21	6.82	0.20	0.022	0.539
ENSRNOG00000032778	Bub1	Budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	5.46	0.17	6.34	0.26	0.029	0.542
ENSRNOG00000005348	Pamr1	peptidase domain containing associated with muscle regeneration 1	7.53	0.27	8.40	0.13	0.027	0.544
ENSRNOG00000018454	Apoe	Apolipoprotein E	8.02	0.07	8.90	0.08	0.000	0.545
ENSRNOG00000013794	Rbp1	Retinol binding protein 1, cellular	9.48	0.11	10.35	0.12	0.002	0.546
ENSRNOG00000008165	Tpx2	TPX2, microtubule-associated, homolog (Xenopus laevis)	6.73	0.15	7.60	0.07	0.002	0.550
ENSRNOG00000030689	Ms4a6b	Membrane-spanning 4-domains, subfamily A, member 6B	6.60	0.16	7.46	0.24	0.025	0.550
ENSRNOG00000001959	Mx1	Myxovirus (influenza virus) resistance 1	5.78	0.13	6.63	0.18	0.008	0.556
ENSRNOG00000000925	Psph	Phosphoserine phosphatase	7.75	0.10	8.59	0.12	0.002	0.561
ENSRNOG00000013057	Prc1	Protein regulator of cytokinesis 1	6.49	0.26	7.32	0.16	0.034	0.562
ENSRNOG00000018503	Bcl2l1;LOC293190;LOC684140		6.16	0.34	6.99	0.10	0.061	0.565
ENSRNOG00000000903	Asl		8.49	0.06	9.32	0.03	0.000	0.565
ENSRNOG00000009597	Cyp4a10;Cyp4a1	Cytochrome P450, family 4, subfamily a, polypeptide 1	8.61	0.15	9.43	0.31	0.052	0.566
ENSRNOG00000010252	Hexa	Hexosaminidase A	9.24	0.06	10.06	0.03	0.000	0.566

Ensembl_Gene	Gene Symbol	Name	Mean S (n=4)	SEM S	Mean V (n=4)	SEM V	t-test	Fold change
ENSRNOG00000021735	Akr1cl1	Aldo-keto reductase family 1, member C-like 1	5.54	0.18	6.36	0.14	0.012	0.568
ENSRNOG00000016561	Ns5atp9	NS5A (hepatitis C virus) transactivated protein 9	6.72	0.15	7.53	0.10	0.004	0.571
ENSRNOG00000007314	Slc26a4	Solute carrier family 26, member 4	8.49	0.18	9.30	0.07	0.006	0.572
ENSRNOG00000039098	Vom2r64	Vomeronasal 2 receptor, 64	4.84	0.19	5.64	0.15	0.015	0.574
ENSRNOG00000020480	Fads1	Fatty acid desaturase 1	8.52	0.16	9.31	0.14	0.010	0.578
ENSRNOG00000005556	Snrpf	Small nuclear ribonucleoprotein polypeptide F	7.05	0.16	7.83	0.24	0.035	0.581
ENSRNOG00000029369	Olr1673	Olfactory receptor 1673	3.64	0.12	4.42	0.12	0.003	0.583
ENSRNOG00000031335	Ankrd37	Ankyrin repeat domain 37	7.77	0.13	8.54	0.12	0.005	0.585
ENSRNOG00000026605	Ifi27l2b		7.51	0.09	8.28	0.06	0.000	0.586
ENSRNOG00000037626			6.23	0.22	6.99	0.13	0.023	0.587
ENSRNOG00000038407			3.01	0.05	3.78	0.19	0.008	0.588
ENSRNOG00000010721	Dlgap5	discs, large (Drosophila) homolog-associated protein 5	6.19	0.17	6.96	0.10	0.009	0.589
ENSRNOG00000002711	Nuf2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	5.74	0.06	6.50	0.12	0.001	0.591
ENSRNOG00000009513	Akr1b1;Akr1b1-ps2	Aldo-keto reductase family 1, member B1 (aldose reductase)	9.92	0.09	10.68	0.20	0.013	0.593
ENSRNOG00000007139	Ttpa	Tocopherol (alpha) transfer protein	6.49	0.10	7.24	0.12	0.003	0.596
ENSRNOG00000038686	Ap1s2	Adaptor-related protein complex 1, sigma 2 subunit	6.17	0.19	6.92	0.09	0.013	0.598
ENSRNOG00000032417	Gabrp	gamma-aminobutyric acid	8.45	0.07	9.19	0.27	0.037	0.598

Ensembl_Gene	Gene Symbol	Name	Mean S (n=4)	SEM S	Mean V (n=4)	SEM V	t-test	Fold change
		(GABA) A receptor, pi						
ENSRNOG00000011598	Slc15a1	Solute carrier family 15 (oligopeptide transporter), member 1	7.14	0.22	7.88	0.13	0.027	0.598
ENSRNOG00000003927	Cd55	Transcribed locus	6.86	0.16	7.60	0.07	0.006	0.600
ENSRNOG00000005037	Kif18a	Kinesin family member 18A	6.62	0.19	7.36	0.17	0.028	0.600
ENSRNOG00000038792	Olr1662;LOC682056	Olfactory receptor 1662	4.03	0.16	4.76	0.12	0.010	0.602
ENSRNOG00000028185	LOC500420	Similar to CG12279-PA	7.41	0.18	8.14	0.10	0.012	0.602
ENSRNOG00000005180			6.02	0.12	6.75	0.11	0.004	0.605
ENSRNOG00000021357	Slfn3	Schlafen 3	6.75	0.15	7.47	0.20	0.026	0.607
ENSRNOG00000010283	Cd28	Cd28 molecule	5.68	0.08	6.40	0.23	0.025	0.608
ENSRNOG00000001926	Cldn1	Claudin 1	8.59	0.09	9.31	0.06	0.000	0.609
ENSRNOG00000015857	Ctsa	Cathepsin A	11.03	0.05	11.74	0.08	0.000	0.611
ENSRNOG00000022505	Slc17a4;LOC684568	Solute carrier family 17 (urate transporter), member 4	7.96	0.08	8.66	0.19	0.015	0.614
ENSRNOG00000006395	RGD1561343	Similar to C20orf118	6.16	0.12	6.87	0.06	0.002	0.614
ENSRNOG00000039801	RGD1563091		6.72	0.15	7.42	0.08	0.006	0.615
ENSRNOG00000030250			3.92	0.15	4.62	0.09	0.007	0.617
ENSRNOG00000004405	Pigr	Polymeric immunoglobulin receptor	8.56	0.17	9.25	0.12	0.017	0.622
ENSRNOG00000001333	Azgp1	alpha-2-glycoprotein 1, zinc-binding	8.25	0.26	8.94	0.08	0.048	0.622
ENSRNOG00000001295	S100b	Transcribed locus	5.93	0.05	6.61	0.12	0.002	0.622
ENSRNOG00000012804	C1qc	Complement component 1, q subcomponent, C	7.27	0.08	7.95	0.11	0.002	0.624

Ensembl_Gene	Gene Symbol	Name	Mean S (n=4)	SEM S	Mean V (n=4)	SEM V	t-test	Fold change
		chain						
ENSRNOG00000023093	LOC689296	Similar to expressed sequence C79407	5.34	0.09	6.02	0.12	0.004	0.627
ENSRNOG00000018812	Rpp25	Ribonuclease P 25 subunit (human)	7.66	0.13	8.33	0.10	0.006	0.628
ENSRNOG00000011622	Echdc1	Enoyl Coenzyme A hydratase domain containing 1	6.63	0.14	7.30	0.17	0.024	0.629
ENSRNOG00000014224	LOC684509;Ndufa3		8.61	0.20	9.28	0.06	0.017	0.629
ENSRNOG00000038572	RGD1562646	Similar to chromosome condensation protein G	5.51	0.05	6.17	0.11	0.001	0.631
ENSRNOG00000029924	Klk1l	Kallikrein 1-like peptidase	10.77	0.11	11.43	0.20	0.026	0.632
ENSRNOG00000003388	Cenpf	centromere protein F, 350/400kDa (mitosin)	6.78	0.20	7.44	0.15	0.038	0.632
ENSRNOG00000033996	RGD1565900	Transcribed locus, strongly similar to NP_990668.1 60S ribosomal protein L27 [Gallus gallus]	9.71	0.20	10.37	0.14	0.037	0.634
ENSRNOG00000004280	Tcn2	Transcobalamin 2	8.91	0.05	9.56	0.07	0.000	0.635
ENSRNOG00000029778	Maob	Monoamine oxidase B	6.32	0.04	6.97	0.13	0.003	0.635
ENSRNOG00000022657	Tmem97	Transmembrane protein 97	7.23	0.12	7.89	0.11	0.007	0.637
ENSRNOG00000019716	Ntf3	Transcribed locus	7.19	0.04	7.84	0.13	0.004	0.640
ENSRNOG00000029370	Abhd3		7.39	0.20	8.04	0.13	0.037	0.641
ENSRNOG00000039696	Olr1547	Olfactory receptor 1547	2.70	0.13	3.34	0.17	0.024	0.642
ENSRNOG00000002382	Mfap4	Microfibrillar-associated protein 4	7.16	0.20	7.80	0.14	0.043	0.643
ENSRNOG00000029055	Ttk	Ttk protein kinase	4.92	0.10	5.56	0.10	0.004	0.643
ENSRNOG00000024159	Fcer1g	Fc fragment of IgE, high affinity I, receptor for;	9.97	0.18	10.61	0.12	0.024	0.644

Ensembl_Gene	Gene Symbol	Name	Mean S (n=4)	SEM S	Mean V (n=4)	SEM V	t-test	Fold change
		gamma polypeptide						
ENSRNOG00000017332	Dapk2	Death-associated kinase 2	6.72	0.02	7.35	0.25	0.043	0.645
ENSRNOG00000007089	Lgmn	Legumain	10.90	0.12	11.53	0.05	0.003	0.646
ENSRNOG00000028746	Gsto1	Glutathione S-transferase omega 1	9.08	0.08	9.71	0.11	0.004	0.646
ENSRNOG00000029057	Olr898	Olfactory receptor 898	4.28	0.16	4.91	0.17	0.039	0.647
ENSRNOG00000004667	Gen1	Gen homolog 1, endonuclease (Drosophila)	5.23	0.14	5.85	0.17	0.026	0.647
ENSRNOG00000019662	Tm6sf1	Transmembrane 6 superfamily member 1	8.31	0.05	8.94	0.05	0.000	0.648
ENSRNOG00000013215	Dctd	dCMP deaminase	7.11	0.19	7.73	0.08	0.025	0.651
ENSRNOG00000000137	Ly86	Lymphocyte antigen 86	7.50	0.11	8.12	0.17	0.022	0.651
ENSRNOG00000002253	Wdr5b	WD repeat domain 5B	5.91	0.13	6.53	0.12	0.014	0.651
ENSRNOG00000017259	Tacc3	Transforming, acidic coiled-coil containing protein 3	6.15	0.13	6.77	0.08	0.006	0.652
ENSRNOG00000018815	Plk1	Polo-like kinase 1 (Drosophila)	6.28	0.13	6.90	0.13	0.015	0.653
ENSRNOG00000000853	Aif1	Allograft inflammatory factor 1	8.36	0.08	8.97	0.06	0.001	0.653
ENSRNOG00000018899	C5	Complement component 5	8.74	0.09	9.35	0.09	0.003	0.655
ENSRNOG00000019189	Acat2;RGD1561787	Transcribed locus	9.78	0.14	10.38	0.08	0.010	0.656
ENSRNOG00000014064	Ctsh	Cathepsin H	11.50	0.10	12.11	0.03	0.001	0.656
ENSRNOG00000036674	Cd7	Cd7 molecule	6.76	0.14	7.36	0.14	0.024	0.660
ENSRNOG00000037940			4.83	0.08	5.43	0.18	0.025	0.660
ENSRNOG00000016717	Gas2	Growth arrest-specific 2	7.38	0.09	7.97	0.16	0.016	0.662
ENSRNOG00000006859	Insig1	insulin induced gene 1	9.09	0.12	9.68	0.13	0.014	0.663

Ensembl_Gene	Gene Symbol	Name	Mean S (n=4)	SEM S	Mean V (n=4)	SEM V	t-test	Fold change
ENSRNOG00000036402			5.03	0.03	5.62	0.17	0.015	0.664
ENSRNOG00000028623	Agpat5	Transcribed locus	5.88	0.11	6.47	0.11	0.008	0.665
ENSRNOG00000013001			6.42	0.12	7.01	0.12	0.013	0.666
ENSRNOG00000033056			6.17	0.09	6.76	0.13	0.010	0.666
ENSRNOG00000038319	Akr1c19	Transcribed locus	9.70	0.06	9.10	0.09	0.002	1.512
ENSRNOG00000001809	Hrg;LOC681544	Histidine-rich glycoprotein	9.17	0.10	8.40	0.12	0.003	1.701
ENSRNOG00000007923	Cgref1	Cell growth regulator with EF hand domain 1	8.75	0.14	7.99	0.07	0.002	1.701
ENSRNOG00000033527	Pappa		7.95	0.04	7.16	0.11	0.001	1.721
ENSRNOG00000011184	Slc13a4	Solute carrier family 13 (sodium/sulfate symporters), member 4	7.15	0.14	6.32	0.10	0.003	1.780
ENSRNOG00000023465	LOC500300	Similar to hypothetical protein MGC6835	7.10	0.13	6.26	0.14	0.004	1.785
ENSRNOG00000018693	Asgr1	Asialoglycoprotein receptor 1	7.44	0.15	6.57	0.09	0.002	1.835
ENSRNOG00000017944	Tbx10	Transcribed locus	7.35	0.06	6.45	0.05	0.000	1.876
ENSRNOG00000019260	Ceacam20		8.30	0.20	7.35	0.07	0.004	1.930
ENSRNOG00000036754			9.59	0.04	8.63	0.14	0.001	1.939
ENSRNOG00000028616	Pck1	Phosphoenolpyruvate carboxykinase 1 (soluble)	11.53	0.02	10.53	0.22	0.004	2.009
ENSRNOG00000015992	Ccl20	Chemokine (C-C motif) ligand 20	8.03	0.16	7.01	0.11	0.002	2.026
ENSRNOG00000029066			7.30	0.18	6.27	0.19	0.008	2.035
ENSRNOG00000006367	Slc5a8	Solute carrier family 5 (iodide transporter), member 8	9.46	0.11	8.40	0.21	0.004	2.086
ENSRNOG00000031231	Kng1;Kng2	Kininogen 1	7.27	0.28	5.85	0.17	0.005	2.681