Transcript II	Gene Symbol	Acession	Gene Name	FDR corrected p-value	FDR corrected p-value	Fold-Change in Expres	FDR corrected p-value	Fold-Change in Expres	FDR corrected p-value	Fold-Change in Expres	Log2 transform	Log2 transform	Log2 transformed Mean 9-
17324745	Bex6	NM_001033539	brain expressed gene 6	0.00158259	0.00186318	-7.33049	0.00187219	-4.59099	0.393685	1.59671	8.5491	5.67519	6.35029
17344126	Hspa1b	NM_010478	heat shock protein 1B	0.00208463	0.00228411	-3.85817	0.00265648	-2.78074	0.403457	1.38746	8.77829	6.83037	7.30282
17257593		---		0.0140458	0.0273696	-2.48142	0.00594557	-2.89427	0.815002	-1.16638	7.24871	5.93755	5.71551
17365098	Scd1	NM_009127	stearoyl-Coenzyme A desaturase 1	0.0114199	0.0105695	-2.19999	0.0129642	-1.83458	0.635346	1.19917	10.345	9.20749	9.46953
17311807	Sqle	NM_009270	squalene epoxidase	0.000316021	0.000943523	-2.09513	0.000112932	-2.44847	0.332478	-1.16865	11.0891	10.0221	9.79726
17445308	Cyp51	ENSMUST000000015(	cytochrome P450, family 51	0.00141668	0.0019657	-2.04547	0.00107132	-1.87648	0.718271	1.09005	9.8821	8.84968	8.97408
17234552	Lss	ENSMUST000000486`	lanosterol synthase	0.0026575	0.00325504	-2.00389	0.00218414	-1.81637	0.708404	1.10324	9.70831	8.7055	8.84725
17509629	Sc4mol	ENSMUST000000340`	sterol-C4-methyl oxidase-like	0.000572807	0.00125104	-2.00125	0.000280112	-2.08763	0.852846	-1.04316	9.9685	8.9676	8.90664
17349549	Mir1949	NR_035472	microRNA 1949	0.000114828	0.000698481	-1.98977	3.74E-05	-2.94092	0.0128809	-1.47802	9.97852	8.98592	8.42225
17280836	Gm889	BC147387	predicted gene 889	0.00470562	0.00804228	-1.94203	0.00223215	-2.03616	0.907509	-1.04847	8.73268	7.77512	7.70683
17307623	Blk	NM_007549	B lymphoid kinase	0.00305562	0.012607	-1.92455	0.00104165	-2.5523	0.317287	-1.32618	9.87388	8.92936	8.52209
17307588	Fdft1	NM_010191	farnesyl diphosphate farnesyl transferase 1	0.00148624	0.00272067	-1.91859	0.000726644	-1.97777	0.923597	-1.03084	11.4427	10.5027	10.4588
17406921		---		0.00213029	0.00255807	-1.88603	0.00198384	-1.68628	0.593687	1.11846	8.92631	8.01096	8.17247
17344122		---		0.0020357	0.0067063	-1.87296	0.00711367	-2.29642	0.395307	-1.22609	10.756	9.85072	9.55665
17456772	Fam40b	NM_177204	family with sequence similarity 40, member B	0.0169496	0.0215981	-1.84721	0.0104276	-1.80436	0.966032	1.02375	8.5691	7.68375	7.71761
17344120	Snord52	NR_028527	small nucleolar RNA, C/D box 52	0.00120916	0.00477817	-1.81659	0.000428456	-2.23537	0.293177	-1.23053	7.75241	6.89118	6.5919
17548102	Cycs	NM_007808	cytochrome c, somatic	0.00208463	0.0054864	-1.80698	0.000809107	-2.05337	0.586689	-1.13635	9.55414	8.70056	8.51614
17548541	Cycs	NM_007808	cytochrome c, somatic	0.00208463	0.0054864	-1.80698	0.000809107	-2.05337	0.586689	-1.13635	9.55414	8.70056	8.51614
17429632	Mfsd2a	NM_029662	major facilitator superfamily domain containing 2A	0.00292244	0.00756383	-1.79145	0.00115108	-2.03065	0.625737	-1.13352	8.44391	7.60278	7.42197
17515315	Ldlr	NM_010700	low density lipoprotein receptor	0.00214274	0.00554298	-1.78586	0.000843793	-2.01483	0.608755	-1.12821	10.665	9.8284	9.65436
17239755		---		0.00378979	0.0169631	-1.78358	0.00127242	-2.32985	0.316673	-1.30628	8.49588	7.6611	7.27564
17379871	1500012F01Rik	ENSMUST000001363`	RIKEN cDNA 1500012F01 gene	0.00952348	0.0291727	-1.78219	0.00338131	-2.19481	0.55179	-1.23153	8.98913	8.15548	7.85503
17347448	Cyp1b1	NM_009994	cytochrome P450, family 1, subfamily b, polypeptide 1	0.000851483	0.00136491	-1.74606	0.000489049	-1.67507	0.818192	1.04238	6.65278	5.84868	5.90856
17550454		---		0.00104124	0.006552	-1.7441	0.000336768	-2.40136	0.108702	-1.37685	9.56971	8.76722	8.30585
17406908	Fdps	NM_001253751	farnesyl diphosphate synthetase	0.00281772	0.00361661	-1.71251	0.00210697	-1.61226	0.788722	1.06218	12.0528	11.2767	11.3638
17416325	Dhcr24	NM_053272	24-dehydrocholesterol reductase	0.000460707	0.00125104	-1.69904	0.000172322	-1.84433	0.548419	-1.08551	11.4682	10.7035	10.5851
17290173	Hmgcs1	NM_145942	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	0.0194626	0.0231986	-1.66754	0.0125167	-1.61855	0.946117	1.03027	11.7602	11.0225	11.0655
17218653	Gas5	NR_002840	growth arrest specific 5	0.00284469	0.00531841	-1.6535	0.00136641	-1.71731	0.885995	-1.03859	8.66999	7.94447	7.88984
17291854	Rpp40	ENSMUST000001716(	ribonuclease P 40 subunit (human)	0.00159662	0.00408016	-1.6511	0.000625627	-1.81983	0.60762	-1.1022	7.89614	7.17271	7.03233
17523158	Ccr8	NM_007720	chemokine (C-C motif) receptor 8	0.0105598	0.0184646	-1.64633	0.00469506	-1.74329	0.871242	-1.0589	9.95839	9.23914	9.15657
17535434	Nsdhl	NM_010941	NAD(P) dependent steroid dehydrogenase-like	0.0210565	0.041892	-1.62866	0.00861701	-1.8	0.79588	-1.1052	11.5338	10.8301	10.6858
17440812	Ung	ENSMUST000001025(	uracil DNA glycosylase	0.00141668	0.00508196	-1.62221	0.000513471	-1.89276	0.35639	-1.16677	8.70893	8.01096	7.78844
17222800	Slc39a10	ENSMUST000002715(	solute carrier family 39 (zinc transporter), member 10	0.00548836	0.017769	-1.61642	0.00187219	-1.91869	0.48185	-1.187	9.19221	8.4994	8.25208
17295233	Hmgcr	NM_008255	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0.00037293	0.000885942	-1.61557	0.000167255	-1.65871	0.854342	-1.02671	12.0097	11.3177	11.2797
17285056	Idi1	NM_145360	isopentenyl-diphosphate delta isomerase	0.000316021	0.00119214	-1.61548	0.000110368	-1.83259	0.228051	-1.13439	11.0878	10.3958	10.2139
17229466	Hsd17b7	NM_010476	hydroxysteroid (17-beta) dehydrogenase 7	0.00180875	0.00477206	-1.6134	0.000715979	-1.77216	0.614584	-1.0984	9.24596	8.55585	8.42044
17223863	Idh1	NM_001111320	isocitrate dehydrogenase 1 (NADP+), soluble	0.00654201	0.00819822	-1.60528	0.00416562	-1.55718	0.919469	1.03088	10.4366	9.75373	9.79761
17435584	Insig1	NM_153526	insulin induced gene 1	0.00596369	0.00560964	-1.60416	0.00912804	-1.39698	0.425645	1.14831	11.48	10.7982	10.9977
17364725	Rrp12	NM_199447	ribosomal RNA processing 12 homolog (S. cerevisiae)	0.00367186	0.0118273	-1.59873	0.00129347	-1.87371	0.456839	-1.172	8.99982	8.32289	8.09392
17421694	Srm	NM_009272	spermidine synthase	0.000354355	0.00166949	-1.5965	0.000110368	-1.96059	0.0824874	-1.22806	11.6227	10.9478	10.6514
17305980	Ccnb1ip1	NM_001111119	cyclin B1 interacting protein 1	0.000851483	0.00205744	-1.59228	0.000305368	-1.75214	0.49083	-1.1004	7.51664	6.84555	6.70752
17518314		---		0.00216582	0.0114178	-1.58966	0.00071241	-2.02006	0.203596	-1.27075	8.26164	7.59293	7.24724
17362050	Rps6ka4	NM_019924	ribosomal protein S6 kinase, polypeptide 4	0.0095345	0.0102085	-1.57325	0.0076907	-1.47591	0.798321	1.06595	8.40317	7.74943	7.84157
17345696	Bysl	NM_016859	bystin-like	0.00423671	0.00854955	-1.57092	0.00177112	-1.67243	0.789358	-1.06462	9.27701	8.6254	8.53506
17550390		---		0.0022426	0.00500392	-1.57007	0.000974125	-1.67173	0.743137	-1.06475	10.3401	9.68932	9.5988
17353358	Stard4	ENSMUST000000252`	StAR-related lipid transfer (START) domain containing 4	0.0122649	0.0128042	-1.56525	0.00992187	-1.47024	0.815074	1.06463	9.06512	8.41872	8.50907
17344132	Hspa1a	ENSMUST000000873`	heat shock protein 1A	0.0493048	0.0396626	-1.56121	0.0944021	-1.32975	0.58646	1.17406	7.19895	6.55629	6.78779
17442719	Aacs	ENSMUST000000314(	acetoacetyl-CoA synthetase	0.00082026	0.00179125	-1.5585	0.000294249	-1.67379	0.58646	-1.07397	9.66272	9.02256	8.9196
17301247	Pinx1	NM_028228	PIN2/TERF1 interacting, telomerase inhibitor 1	0.0023485	0.00629712	-1.55258	0.000922604	-1.71709	0.582929	-1.10596	9.89938	9.26471	9.11941
17472903	Pthlh	ENSMUST000000522(	parathyroid hormone-like peptide	0.000851483	0.00584547	-1.5512	0.000282063	-2.04757	0.0750468	-1.31999	8.42268	7.78929	7.38877
17376096	Polr1b	NM_009086	polymerase (RNA) I polypeptide B	0.00195718	0.00610308	-1.54927	0.000703384	-1.76023	0.441034	-1.13616	10.0298	9.39819	9.21402
17490599	Rps11	NM_013725	ribosomal protein S11	0.00931748	0.0258573	-1.54753	0.00335969	-1.78074	0.586842	-1.1507	10.1095	9.47957	9.27705
17480636	Lipt2	ENSMUST000000329(	lipoyl(octanoyl) transferase 2 (putative)	0.000759223	0.0014064	-1.54596	0.000309033	-1.58125	0.888423	-1.02283	9.5527	8.9242	8.89164
17279190	Trmt61a	NM_177374	tRNA methyltransferase 61 homolog A (S. cerevisiae)	0.0095652	0.0218782	-1.54222	0.00376106	-1.70026	0.713839	-1.10248	9.14301	8.518	8.37726
17437072	Lyar	NM_025281	Ly1 antibody reactive clone	0.000460707	0.00136491	-1.53944	0.000163223	-1.68586	0.391975	-1.09511	10.1465	9.52404	9.39297
17319405	Snord43	NR_028281	small nucleolar RNA, C/D box 43	0.0010542	0.00587896	-1.51936	0.000350967	-1.87934	0.136867	-1.23693	7.60326	6.9998	6.69304
17394063	Ada	ENSMUST000000178(	adenosine deaminase	0.0050235	0.0164881	-1.51748	0.00174762	-1.75846	0.476416	-1.1588	9.2401	8.63843	8.42579
17276520	Mthfd1	NM_138745	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate c	0.000446191	0.00253144	-1.51489	0.000130101	-1.89582	0.0607019	-1.25146	11.0016	10.4024	10.0788
17263673	Shmt1	ENSMUST000000187(	serine hydroxymethyltransferase 1 (soluble)	0.000851483	0.00387421	-1.51387	0.000282063	-1.8391	0.128258	-1.21484	10.4406	9.84234	9.56158
17435978	Cad	ENSMUST000000137(	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	0.00011807	0.000596212	-1.51309	4.10E-05	-1.71437	0.0789267	-1.13302	10.6548	10.0573	9.87713
17530669	Acy1	NM_025371	aminoacylase 1	0.00732517	0.0142035	-1.50854	0.00302632	-1.61375	0.778775	-1.06974	8.67384	8.08069	7.98343
17463108	Nop2	NM_138747	NOP2 nucleolar protein homolog (yeast)	0.000468005	0.00148523	-1.50599	0.000162508	-1.67526	0.282889	-1.11239	11.2424	10.6517	10.4981
17408483	Ptgfrn	ENSMUST000001026(	prostaglandin F2 receptor negative regulator	0.0014939	0.0105447	-1.50166	0.000489049	-1.93036	0.123495	-1.28548	7.74038	7.15382	6.79151
17526929	1110032A03Rik	NM_023483	RIKEN cDNA 1110032A03 gene	0.000721408	0.00186318	1.50259	0.00026789	1.65712	0.375133	1.10285	8.97571	9.56316	9.70439
17285834	Hist1h2bg	NM_178196	histone cluster 1, H2bg	0.0186052	0.0329841	1.51234	0.00830266	1.60026	0.8679	1.05814	9.4851	10.0819	10.1634
17391521	Al847159	NR_045264	expressed sequence Al847159	0.0107837	0.0171616	1.5188	0.00520815	1.56051	0.93428	1.02746	7.29423	7.89716	7.93625
17241660	Arid5b	NM_023598	AT rich interactive domain 5B (MRF1-like)	0.00796933	0.0233029	1.53632	0.00287102	1.77653	0.555983	1.15635	9.16196	9.78144	9.99102
17307354	Atp8a2	ENSMUST000000803(	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	0.0156396	0.0338678	1.54025	0.00631577	1.69427	0.754984	1.1	7.41813	8.04129	8.17879
17225413	Col6a3	NM_001243008	collagen, type VI, alpha 3	0.000199369	0.000825701	1.54863	6.28E-05	1.79992	0.088538	1.16227	9.48915	10.1201	10.3371
17288876	Arrdc3	NM_001042591	arrestin domain containing 3	0.00017328	0.00486764	1.5539	5.14E-05	2.7608	0.00861345	1.77669	9.92697	10.5629	11.3921
17289602	Adamts6	NM_001081020	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 6	0.0392261	0.0463525	1.56898	0.0231934	1.5612	0.994042	-1.00498	7.79703	8.44686	8.4397
17408940	2010016I18Rik	NR_033207	RIKEN cDNA 2010016I18 gene	0.00547947	0.0266523	1.56985	0.00176613	1.99763	0.303755	1.2725	10.514	11.1646	11.5123
17537118	P2ry10	NM_172435	purinergic receptor P2Y, G-protein coupled 10	0.00267586	0.0118617	1.57185	0.000901261	1.931	0.280571	1.22849	8.20823	8.86069	9.15758
17295295	5330416C01Rik	AK045624	RIKEN cDNA 5330416C01 gene	0.00547947	0.033736	1.57232	0.00174192	2.09707	0.235498	1.33375	7.19156	7.84445	8.25994
17288859	A830082K12Rik	NR_045195	RIKEN cDNA A830082K12 gene	0.00109846	0.005136	1.58813	0.000381072	1.93409	0.196374	1.21784	7.17311	7.84044	8.12477
17303754	Gm20140	XR_105608	predicted gene, 20140	0.00715448	0.010493	1.59205	0.00353465	1.61842	0.96341	1.01657	7.60147	8.27236	8.29606
17294547	Nr2f1	ENSMUST000000914(	nuclear receptor subfamily 2, group F, member 1	0.000851483	0.00205744	1.63396	0.000294196	1.83083	0.415644	1.12048	8.08714	8.79552	8.95964
17547877	Deptor	ENSMUST000000964(	DEP domain containing MTOR-interacting protein	0.00277628	0.00815354	1.64108	0.00102747	1.88287	0.521648	1.14733	9.38897	10.1036	10.3019
17335770	Abcg1	NM_009593	ATP-binding cassette, sub-family G (WHITE), member 1	0.000603849	0.00092888	1.64666	0.000402256	1.53691	0.565449	-1.07141	8.83517	9.55471	9.45521
17478301	Nav2	NM_175272	neuron navigator 2	0.00215804	0.0103936	1.65932	0.00071241	2.11262	0.229796	1.27318	9.34286	10.0735	10.4219
17450461	Gbp4	NM_001256005	guanylate binding protein 4	0.00383816	0.0144638	1.7043	0.00133466	2.10835	0.39118	1.23707	7.59927	8.36845	8.67538
17336052	Zfp563	NM_001024950	zinc finger protein 563	0.000153365	0.000943523	1.72516	4.61E-05	2.34173	0.0221282	1.3574	8.96718	9.75391	10.1948
17445525	Rundc3b	NM_198620	RUN domain containing 3B	0.000108158	0.000698481	1.73525	3.24E-05	2.49975	0.00861345	1.44057	10.3853	11.1805	11.7071
17405458	Gpr171	NM_173398	G protein-coupled receptor 171	0.000169931	0.00136491	1.77936	4.72E-05	2.57798	0.0170007	1.44883	8.54731	9.37867	9.91355
17550428		---		0.00102227	0.00670063	1.88884	0.000327944	2.75584	0.0994207	1.45902	6.72659	7.64409	8.18908
17434555	Abcb1b	NM_011075	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	0.000120667	0.00163978	2.14534	4.10E-05	4.36667	0.00861345	2.03542	8.38039	9.4816	10.5069
17537936	Tceal1	ENSMUST000000551(	transcription elongation factor A (SII)-like 1	8.87E-06	2.45E-05	3.80708	3.04E-06	6.02176	0.00862317	1.58173	7.63373	9.56242	10.2239