Transcript Cluster ID	MET Bi-weight Avg Signal (log2)	SAL Bi-weight Avg Signal (log2)	Fold Change (linear) (MET vs. SAL)	ANOVA p-value (MET vs. SAL)	Gene Symbol	Description
10458560	8.23	7.12	2.17	0.04005	Fgf1	fibroblast growth factor 1
10508719	7.33	6.45	1.84	0.045515	Snora16a	small nucleolar RNA, H/ACA box 16A
10410362	7.52	6.68	1.78	0.015996	Zfp738	zinc finger protein 738
10516906	8.96	8.39	1.49	0.025634	Snora73b	small nucleolar RNA, H/ACA box 73b
10580077	7.29	6.74	1.46	0.044445	Rln3	relaxin 3
10398338	6.57	6.03	1.45	0.041128	Mir665	microRNA 665
10411454	6.57	6.04	1.44	0.004069	Sec61b	Sec61 beta subunit
10608699	8.29	7.77	1.44	0.02862	Noc2l	nucleolar complex associated 2 homolog (S. cerevisiae)
10398426	7.28	6.78	1.41	0.006827	Mir485	microRNA 485; miRNA containing gene
10470768	7.46	6.97	1.41	0.040507	Urm1	ubiquitin related modifier 1 homolog (S. cerevisiae)
10598203	5.94	5.45	1.4	0.035818	Ccl28	chemokine (C-C motif) ligand 28
10608689	9.28	8.8	1.39	0.022267		
10375127	6.11	5.65	1.37	0.031856	1700072H12Rik	RIKEN cDNA 1700072H12 gene
10465831	7.22	6.78	1.36	0.007574	5730408K05Rik	RIKEN cDNA 5730408K05 gene
10596190	5.9	5.45	1.36	0.013023	Bfsp2	beaded filament structural protein 2, phakinin
10376885	9.42	8.97	1.36	0.021461	Snord49b	small nucleolar RNA, C/D box 49B
10398727	10.26	9.82	1.35	0.042803	Klc1	kinesin light chain 1
10487645	6.04	5.62	1.34	0.014879	Cpxm1	carboxypeptidase X 1 (M14 family)
10563961	6.99	6.6	1.31	0.008838		
10560311	5.74	5.34	1.31	0.019417		
10350742	5.39	5.01	1.31	0.025608	Rnasel	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)
10563919	8.64	8.26	1.3	0.000502		
10424860	8.42	8.05	1.3	0.014228	Heatr7a	HEAT repeat containing 7A
10505917	5.71	5.34	1.3	0.047962		
10526838	6.64	6.27	1.29	0.017813	Got2	glutamate oxaloacetate transaminase 2, mitochondrial
10445741	5.42	5.08	1.26	0.002836		
10470816	8.32	7.98	1.26	0.035061	Gle1	GLE1 RNA export mediator (yeast)
10491695	4.84	4.51	1.26	0.04403	Bbs12	Bardet-Biedl syndrome 12 (human)
10411167	5.22	4.89	1.26	0.049527		
10435305	8.78	8.46	1.25	0.000582	Itgb5	integrin beta 5
10427718	7.85	7.54	1.25	0.026473	Brix1	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)
10488912	7.33	7.01	1.25	0.039039	Edem2	ER degradation enhancer, mannosidase alpha-like 2

10364402	7.78	7.46	1.25	0.047364	Slc1a6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6
10359917	7.52	7.21	1.24	0.001646	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7
10347335	6.26	5.95	1.24	0.008124	Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
10553475	7.62	7.31	1.24	0.01694	Rps27a	ribosomal protein S27A
10479217	9.04	8.72	1.24	0.038827	Gm14420	predicted gene 14420
10414990	4.94	4.62	1.24	0.0452		
10537406	9.08	8.77	1.24	0.048642	Clec2l	C-type lectin domain family, member L
10597309	5.22	4.92	1.23	0.002467	Stac	src homology three (SH3) and cysteine rich domain
10577219	4.19	3.89	1.23	0.003426	AF366264	cDNA sequence AF366264
10489204	6.6	6.3	1.23	0.02806	Tgm2	transglutaminase 2, C polypeptide
10424853	7.19	6.9	1.23	0.036385	Fam203a	family with sequence similarity 203, member A
10582562	10.97	10.69	1.22	0.013583		
10460735	4.88	4.6	1.22	0.014254	BC048609	cDNA sequence BC048609
10569069	9.87	9.59	1.22	0.015903		
10444685	8.59	8.3	1.22	0.031102	Abhd16a	abhydrolase domain containing 16A
10563101	10.82	10.55	1.21	0.006816	Rpl13a	ribosomal protein L13A
10510034	7.15	6.87	1.21	0.007333	Casp9	caspase 9
10551319	7.19	6.92	1.21	0.008999	Adck4	aarF domain containing kinase 4
10406541	8.79	8.52	1.21	0.013597	Rps23	ribosomal protein S23; predicted gene 5148
10457020	7.28	7.01	1.21	0.014711		
10473551	3.76	3.49	1.21	0.018223	Olfr153	olfactory receptor 153
10605143	6.07	5.8	1.21	0.026364	Arhgap4	Rho GTPase activating protein 4
10601848	8.21	7.93	1.21	0.036126	Arxes1	adipocyte-related X-chromosome expressed sequence 1; adipocyte-related X-chromosome expressed sequence 2
10396936	7.66	7.39	1.21	0.039558	Smoc1	SPARC related modular calcium binding 1