

Table S2. Probe level information of differentially expressed genes.

ProbeID	FC	logFC	P.Value	adj.P.Val	seqname	GeneName	GeneSymbol	GroupContrast
8113073	-2.69	-1.42638	0.03268	0.82043	chr5	arrestin domain containing 3	ARRDC3	1 (Norm v GDM)
8067288	2.58	1.36496	0.03638	0.82043	chr20	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit	ATP5E	1 (Norm v GDM)
8018288	-2.36	-1.24040	0.02840	0.82043	chr17	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit d	ATP5H	1 (Norm v GDM)
8142464	-2.20	-1.13860	0.04573	0.82043	chr7	capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2	1 (Norm v GDM)
8128714	-10.48	-3.38976	0.02408	0.82043	chr6	coiled-coil domain containing 162, pseudogene	CCDC162P	1 (Norm v GDM)
8086515	-2.61	-1.38550	0.04848	0.82043	chr3	C-type lectin domain family 3, member B	CLEC3B	1 (Norm v GDM)
8127629	3.90	1.96168	0.00415	0.82043	chr6	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	COX7A2	1 (Norm v GDM)
8149380	-4.97	-2.31217	0.04060	0.82043	chr8	defensin, beta 109, pseudogene 1B	DEFB109P1B	1 (Norm v GDM)
8144392	-5.15	-2.36397	0.02975	0.82043	chr8	defensin, beta 109, pseudogene 1B	DEFB109P1B	1 (Norm v GDM)
8149245	-5.15	-2.36397	0.02975	0.82043	chr8	defensin, beta 109, pseudogene 1B	DEFB109P1B	1 (Norm v GDM)
8126934	2.78	1.47507	0.03767	0.82043	chr6	defensin, beta 114	DEFB114	1 (Norm v GDM)
8110520	-2.89	-1.53050	0.00005	0.14822	chr5	high mobility group box 3 pseudogene 22	HMGB3P22	1 (Norm v GDM)
8043480	-6.85	-2.77673	0.00121	0.82043	chr2	immunoglobulin kappa variable 1/OR2-118 (pseudogene)	IGKV1OR2-118	1 (Norm v GDM)
8105523	-2.79	-1.47794	0.00705	0.82043	chr5	kinesin heavy chain member 2A	KIF2A	1 (Norm v GDM)
8125750	2.54	1.34634	0.04268	0.82043	chr6	kinesin family member C1	KIFC1	1 (Norm v GDM)
8082248	-2.23	-1.16027	0.01499	0.82043	chr3	MGC72080 pseudogene	MGC72080	1 (Norm v GDM)

8045887	-2.59	-1.37337	0.01414	0.82043	chr2	MGC72080 pseudogene	MGC72080	1 (Norm v GDM)
7968787	-2.59	-1.37362	0.01329	0.82043	chr13	MGC72080 pseudogene	MGC72080	1 (Norm v GDM)
8082244	-2.60	-1.37743	0.02730	0.82043	chr3	MGC72080 pseudogene	MGC72080	1 (Norm v GDM)
7971241	-2.60	-1.37798	0.01193	0.82043	chr13	MGC72080 pseudogene	MGC72080	1 (Norm v GDM)
7911566	-3.26	-1.70277	0.04176	0.82043	chr1	mitochondrial ribosomal protein L20	MRPL20	1 (Norm v GDM)
8039945	-3.26	-1.70277	0.04176	0.82043	chr1	mitochondrial ribosomal protein L20	MRPL20	1 (Norm v GDM)
8117714	-2.83	-1.49946	0.00695	0.82043	chr6	olfactory receptor, family 2, subfamily J, member 3	OR2J3	1 (Norm v GDM)
8177694	-2.93	-1.55331	0.00391	0.82043	chr6	olfactory receptor, family 2, subfamily J, member 3	OR2J3	1 (Norm v GDM)
8179003	-2.93	-1.55331	0.00391	0.82043	chr6	olfactory receptor, family 2, subfamily J, member 3	OR2J3	1 (Norm v GDM)
8117718	-16.82	-4.07244	0.00001	0.04509	chr6	olfactory receptor, family 2, subfamily J, member 3	OR2J3	1 (Norm v GDM)
7945873	-2.49	-1.31828	0.03203	0.82043	chr11	olfactory receptor, family 7, subfamily E, member 12 pseudogene	OR7E12P	1 (Norm v GDM)
7938683	-2.57	-1.36176	0.02068	0.82043	chr11	olfactory receptor, family 7, subfamily E, member 14 pseudogene	OR7E14P	1 (Norm v GDM)
7907572	-2.06	-1.03950	0.02215	0.82043	chr1	pappalysin 2	PAPPA2	1 (Norm v GDM)
8027330	-2.79	-1.48245	0.03516	0.82043	chr19	polycomb group ring finger 7 pseudogene	PCGF7P	1 (Norm v GDM)
8140258	-2.06	-1.04015	0.02022	0.82043	chr7	postmeiotic segregation increased 2 pseudogene 10	PMS2P10	1 (Norm v GDM)
8133309	-3.25	-1.70182	0.00432	0.82043	chr7	postmeiotic segregation increased 2 pseudogene 10	PMS2P10	1 (Norm v GDM)
8161024	2.44	1.28537	0.02693	0.82043	chr9	RNA component of mitochondrial RNA processing endoribonuclease	RMRP	1 (Norm v GDM)
8107857	2.49	1.31505	0.03881	0.82043	chr5	RNA, 5S ribosomal pseudogene 191	RNA5SP191	1 (Norm v

8135943	3.33	1.73416	0.01934	0.82043	chr7	RNA, 5S ribosomal pseudogene 242	RNA5SP242	GDM) 1 (Norm v GDM)
7951131	-2.71	-1.43781	0.01570	0.82043	chr11	RNA, 5S ribosomal pseudogene 345	RNA5SP345	1 (Norm v GDM)
8033460	-2.89	-1.53177	0.03257	0.82043	chr19	RNA, 5S ribosomal pseudogene 463	RNA5SP463	1 (Norm v GDM)
8168079	2.36	1.23952	0.04318	0.82043	chrX	RNA, 5S ribosomal pseudogene 506	RNA5SP506	1 (Norm v GDM)
8009006	-6.06	-2.59975	0.04537	0.82043	chr17	RNA, U7 small nuclear 52 pseudogene	RNU7-52P	1 (Norm v GDM)
7970567	-2.36	-1.24106	0.04550	0.82043	chr13	RNA, Ro-associated Y3 pseudogene 4	RNY3P4	1 (Norm v GDM)
8126450	4.19	2.06677	0.00002	0.07642	chr6	ribosomal protein L24	RPL24	1 (Norm v GDM)
8089249	3.32	1.73299	0.00003	0.09438	chr3	ribosomal protein L24	RPL24	1 (Norm v GDM)
7937476	2.17	1.11683	0.02762	0.82043	chr11	ribosomal protein, large, P2	RPLP2	1 (Norm v GDM)
7946812	9.57	3.25925	0.02417	0.82043	chr11	ribosomal protein S13	RPS13	1 (Norm v GDM)
8012891	2.15	1.10657	0.02920	0.82043	chr17	ribosomal protein S18 pseudogene 12	RPS18P12	1 (Norm v GDM)
8095488	-2.55	-1.34880	0.00451	0.82043	chr4	submaxillary gland androgen regulated protein 3A	SMR3A	1 (Norm v GDM)
7899480	6.39	2.67648	0.02338	0.82043	chr1	small nucleolar RNA host gene 3 (non-protein coding)	SNHG3	1 (Norm v GDM)
8059708	5.75	2.52480	0.04003	0.82043	chr2	small nucleolar RNA, H/ACA box 75	SNORA75	1 (Norm v GDM)
8005547	4.93	2.30093	0.02216	0.82043	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	1 (Norm v GDM)
8005553	4.93	2.30093	0.02216	0.82043	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	1 (Norm v GDM)
8013323	4.93	2.30093	0.02216	0.82043	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	1 (Norm v GDM)

8013325	4.93	2.30093	0.02216	0.82043	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	1 (Norm v GDM)
8013329	4.93	2.30093	0.02216	0.82043	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	1 (Norm v GDM)
7982020	-2.47	-1.30396	0.04178	0.82043	chr15	small nuclear ribonucleoprotein polypeptide N	SNRPN	1 (Norm v GDM)
7987449	2.92	1.54393	0.00771	0.82043	chr15	signal recognition particle 14kDa (homologous Alu RNA binding protein)	SRP14	1 (Norm v GDM)
8079630	-3.05	-1.61114	0.02890	0.82043	chr3	translation machinery associated 7 homolog (S. cerevisiae)	TMA7	1 (Norm v GDM)
7899346	-5.66	-2.50082	0.01756	0.82043	chr1	translation machinery associated 7 homolog (S. cerevisiae)	TMA7	1 (Norm v GDM)
7971124	-3.24	-1.69569	0.00389	0.82043	chr13	ubiquitin-fold modifier 1	UFM1	1 (Norm v GDM)
8055261	-4.21	-2.07390	0.00433	0.82043	chr2	RAB6C-like	WTH3DI	1 (Norm v GDM)
8029435	-2.08	-1.05554	0.00110	0.82043	chr19	zinc finger protein 285B, pseudogene	ZNF285B	1 (Norm v GDM)
8030980	-4.17	-2.06067	0.00834	0.82043	chr19	zinc finger protein 600	ZNF600	1 (Norm v GDM)
8030978	-2.04	-1.02841	0.00866	0.82043	chr19	zinc finger protein 845	ZNF845	1 (Norm v GDM)
8132209	2.02	1.01437	0.03094	0.82043	chr7	zinc and ring finger 2 pseudogene 1	ZNRF2P1	1 (Norm v GDM)
8067288	2.78	1.47507	0.02589	0.99994	chr20	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit	ATP5E	2 (Norm v Ob)
8000692	2.04	1.02679	0.00844	0.99994	chr16	bolA family member 2	BOLA2	2 (Norm v Ob)
8127629	3.34	1.74078	0.00847	0.99994	chr6	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	COX7A2	2 (Norm v Ob)
7904414	2.74	1.45571	0.04181	0.99994	chr1	hydroxy-delta-5-steroid dehydrogenase, 3 beta, pseudogene 2	HSD3BP2	2 (Norm v Ob)
7958130	2.32	1.21452	0.03542	0.99994	chr12	heat shock protein 90kDa beta (Grp94), member 1	HSP90B1	2 (Norm v Ob)
8007976	2.06	1.04577	0.03296	0.99994	chr17	aminopeptidase puromycin sensitive	NPEPPS	2 (Norm v Ob)
8078603	-2.59	-1.37150	0.03391	0.99994	chr3	RNA, 5S ribosomal pseudogene 129	RNA5SP129	2 (Norm v Ob)

8121670	-2.33	-1.21989	0.02905	0.99994	chr6	RNA, 5S ribosomal pseudogene 214	RNA5SP214	2 (Norm v Ob)
7951131	-3.38	-1.75607	0.00513	0.99994	chr11	RNA, 5S ribosomal pseudogene 345	RNA5SP345	2 (Norm v Ob)
8126450	2.46	1.29884	0.00088	0.99994	chr6	ribosomal protein L24	RPL24	2 (Norm v Ob)
8089249	2.43	1.27848	0.00034	0.99994	chr3	ribosomal protein L24	RPL24	2 (Norm v Ob)
7986765	6.91	2.78942	0.01136	0.99994	chr15	ribosomal protein L5	RPL5	2 (Norm v Ob)
8076511	4.19	2.06752	0.03530	0.99994	chr22	ribosomal protein L5	RPL5	2 (Norm v Ob)
8065325	2.78	1.47368	0.02863	0.99994	chr20	ribosomal protein S15a pseudogene 1	RPS15AP1	2 (Norm v Ob)
8042052	2.93	1.55300	0.00815	0.99994	chr2	ribosomal protein S27a	RPS27A	2 (Norm v Ob)
7994006	4.13	2.04584	0.02154	0.99994	chr16	SMG1 pseudogene 1	SMG1P1	2 (Norm v Ob)
7899480	10.03	3.32616	0.00751	0.99994	chr1	small nucleolar RNA host gene 3 (non-protein coding)	SNHG3	2 (Norm v Ob)
8059708	6.83	2.77147	0.02678	0.99994	chr2	small nucleolar RNA, H/ACA box 75	SNORA75	2 (Norm v Ob)
7968232	3.58	1.83965	0.01693	0.99994	chr13	small nucleolar RNA, C/D box 102	SNORD102	2 (Norm v Ob)
7981964	-4.94	-2.30489	0.04854	0.99994	chr15	small nucleolar RNA, C/D box 116-8	SNORD116-8	2 (Norm v Ob)
8005547	4.10	2.03656	0.03809	0.99994	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	2 (Norm v Ob)
8005553	4.10	2.03656	0.03809	0.99994	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	2 (Norm v Ob)
8013323	4.10	2.03656	0.03809	0.99994	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	2 (Norm v Ob)
8013325	4.10	2.03656	0.03809	0.99994	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	2 (Norm v Ob)
8013329	4.10	2.03656	0.03809	0.99994	chr17	small nucleolar RNA, C/D box 3B-1	SNORD3B-1	2 (Norm v Ob)
8127989	-2.11	-1.07489	0.03127	0.99994	chr6	small nucleolar RNA, C/D box 50B	SNORD50B	2 (Norm v Ob)
7987449	2.19	1.13413	0.03578	0.99994	chr15	signal recognition particle 14kDa (homologous Alu RNA binding protein)	SRP14	2 (Norm v Ob)
7935002	2.01	1.00868	0.03563	0.99994	chr10	signal recognition particle 9kDa	SRP9	2 (Norm v Ob)
8063011	-2.14	-1.10086	0.04853	0.99994	chr20	WAP four-disulfide core domain 10A	WFDC10A	2 (Norm v Ob)
8113073	2.55	1.35187	0.04092	0.61369	chr5	arrestin domain containing 3	ARRDC3	3 (GDM v Ob)
8000692	2.10	1.07333	0.00653	0.61369	chr16	bolA family member 2	BOLA2	3 (GDM v Ob)
8142464	2.24	1.16408	0.04187	0.61369	chr7	capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2	3 (GDM v Ob)
8128714	14.61	3.86926	0.01246	0.61369	chr6	coiled-coil domain containing 162, pseudogene	CCDC162P	3 (GDM v Ob)

8088844	2.43	1.28065	0.03981	0.61369	chr3	coiled-coil domain containing 75 pseudogene 1	CCDC75P1	3 (GDM v Ob)
7984188	2.15	1.10521	0.04716	0.61369	chr15	casein kinase 1, gamma 1	CSNK1G1	3 (GDM v Ob)
8111772	2.02	1.01431	0.03579	0.61369	chr5	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	DAB2	3 (GDM v Ob)
7912852	5.23	2.38600	0.03560	0.61369	chr1	eukaryotic translation initiation factor 1A, X-linked pseudogene 1	EIF1AXP1	3 (GDM v Ob)
8055978	4.81	2.26466	0.03892	0.61369	chr2	family with sequence similarity 133, member B	FAM133B	3 (GDM v Ob)
8170326	2.31	1.20592	0.00714	0.61369	chrX	fragile X mental retardation 1	FMR1	3 (GDM v Ob)
7991762	-2.73	-1.44779	0.02693	0.61369	chr16	hemoglobin, alpha 1	HBA1	3 (GDM v Ob)
7991766	-2.73	-1.44779	0.02693	0.61369	chr16	hemoglobin, alpha 1	HBA1	3 (GDM v Ob)
8034313	4.58	2.19562	0.01976	0.61369	chr19	heterogeneous nuclear ribonucleoprotein A1 pseudogene 10	HNRNPA1P10	3 (GDM v Ob)
7995574	3.19	1.67526	0.02456	0.61369	chr16	heterogeneous nuclear ribonucleoprotein A1 pseudogene 33	HNRNPA1P33	3 (GDM v Ob)
8022814	4.95	2.30677	0.01651	0.61369	chr18	heterogeneous nuclear ribonucleoprotein A1 pseudogene 7	HNRNPA1P7	3 (GDM v Ob)
8046590	2.48	1.30866	0.00099	0.61369	chr2	heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	3 (GDM v Ob)
7977657	2.09	1.06215	0.04618	0.61369	chr14	heterogeneous nuclear ribonucleoprotein C (C1/C2)	HNRNPC	3 (GDM v Ob)
7904414	3.37	1.75391	0.01812	0.61369	chr1	hydroxy-delta-5-steroid dehydrogenase, 3 beta, pseudogene 2	HSD3BP2	3 (GDM v Ob)
8043480	5.87	2.55300	0.00218	0.61369	chr2	immunoglobulin kappa variable 1/OR2-118 (pseudogene)	IGKV1OR2-118	3 (GDM v Ob)
8112139	3.12	1.64201	0.01462	0.61369	chr5	interleukin 6 signal transducer	IL6ST	3 (GDM v Ob)
8105523	2.23	1.16013	0.02494	0.61369	chr5	kinesin heavy chain member 2A	KIF2A	3 (GDM v Ob)
8048703	3.17	1.66277	0.03836	0.61369	chr2	LLP homolog, long-term synaptic facilitation (Aplysia)	LLPH	3 (GDM v Ob)
7986323	-2.06	-1.04028	0.02251	0.61369	chr15	glioma tumor suppressor candidate region gene 2 pseudogene	LOC440311	3 (GDM v Ob)
8014650	2.32	1.21446	0.02727	0.61369	chr17	aminopeptidase puromycin sensitive pseudogene	LOC440434	3 (GDM v Ob)
7911566	3.55	1.82642	0.03109	0.61369	chr1	mitochondrial ribosomal protein L20	MRPL20	3 (GDM v Ob)
8039945	3.55	1.82642	0.03109	0.61369	chr1	mitochondrial ribosomal protein L20	MRPL20	3 (GDM v Ob)

8047161	2.20	1.13523	0.02676	0.61369	chr2	nucleic acid binding protein 1	NABP1	3 (GDM v Ob)
8006112	2.02	1.01440	0.03738	0.61369	chr17	nuclear speckle splicing regulatory protein 1	NSRP1	3 (GDM v Ob)
8117718	15.78	3.98018	0.00001	0.06702	chr6	olfactory receptor, family 2, subfamily J, member 3	OR2J3	3 (GDM v Ob)
8177694	3.12	1.64110	0.00274	0.61369	chr6	olfactory receptor, family 2, subfamily J, member 3	OR2J3	3 (GDM v Ob)
8179003	3.12	1.64110	0.00274	0.61369	chr6	olfactory receptor, family 2, subfamily J, member 3	OR2J3	3 (GDM v Ob)
8117714	2.81	1.48872	0.00724	0.61369	chr6	olfactory receptor, family 2, subfamily J, member 3	OR2J3	3 (GDM v Ob)
7938683	2.27	1.18245	0.03883	0.61369	chr11	olfactory receptor, family 7, subfamily E, member 14 pseudogene	OR7E14P	3 (GDM v Ob)
8066402	2.56	1.35628	0.00419	0.61369	chr20	oxidative stress responsive serine-rich 1	OSER1	3 (GDM v Ob)
8060736	3.00	1.58475	0.03655	0.61369	chr20	pantothenate kinase 2	PANK2	3 (GDM v Ob)
8027330	2.84	1.50468	0.03299	0.61369	chr19	polycomb group ring finger 7 pseudogene	PCGF7P	3 (GDM v Ob)
7999766	2.15	1.10484	0.02829	0.61369	chr16	polycystic kidney disease 1 (autosomal dominant) pseudogene 1	PKD1P1	3 (GDM v Ob)
8133309	4.97	2.31316	0.00050	0.61369	chr7	postmeiotic segregation increased 2 pseudogene 10	PMS2P10	3 (GDM v Ob)
8140258	2.66	1.41239	0.00364	0.61369	chr7	postmeiotic segregation increased 2 pseudogene 10	PMS2P10	3 (GDM v Ob)
8139896	3.53	1.82170	0.03200	0.61369	chr7	postmeiotic segregation increased 2 pseudogene 4	PMS2P4	3 (GDM v Ob)
8037246	2.05	1.03744	0.00791	0.61369	chr19	pregnancy specific beta-1-glycoprotein 6	PSG6	3 (GDM v Ob)
8106784	2.24	1.16655	0.01601	0.61369	chr5	RAS p21 protein activator (GTPase activating protein) 1	RASA1	3 (GDM v Ob)
8054414	3.43	1.77753	0.01298	0.61369	chr2	RANBP2-like and GRIP domain containing 4	RGPD4	3 (GDM v Ob)
8054532	3.93	1.97492	0.01801	0.61369	chr2	RANBP2-like and GRIP domain containing 5	RGPD5	3 (GDM v Ob)
8054676	4.24	2.08565	0.01328	0.61369	chr2	RANBP2-like and GRIP domain containing 8	RGPD8	3 (GDM v Ob)
8161024	-2.23	-1.15963	0.04186	0.61369	chr9	RNA component of mitochondrial RNA processing endoribonuclease	RMRP	3 (GDM v Ob)
8121670	-2.28	-1.19109	0.03226	0.61369	chr6	RNA, 5S ribosomal pseudogene 214	RNA5SP214	3 (GDM v Ob)
8135943	-3.13	-1.64638	0.02475	0.61369	chr7	RNA, 5S ribosomal pseudogene 242	RNA5SP242	3 (GDM v Ob)
8022279	6.49	2.69779	0.04620	0.61369	chr18	RNA, 5S ribosomal pseudogene 449	RNA5SP449	3 (GDM v Ob)
7970567	2.74	1.45299	0.02304	0.61369	chr13	RNA, Ro-associated Y3 pseudogene 4	RNY3P4	3 (GDM v Ob)

8000192	2.53	1.33950	0.01893	0.61369	chr16	RNA polymerase I transcription factor homolog (<i>S. cerevisiae</i>) pseudogene 1	RRN3P1	3 (GDM v Ob)
7967304	2.41	1.26870	0.00815	0.61369	chr12	arginine/serine-rich coiled-coil 2	RSRC2	3 (GDM v Ob)
8091778	4.31	2.10635	0.04011	0.61369	chr3	small Cajal body-specific RNA 7	SCARNA7	3 (GDM v Ob)
8077528	2.07	1.05037	0.01685	0.61369	chr3	SET domain containing 5	SETD5	3 (GDM v Ob)
8141133	10.15	3.34366	0.03004	0.61369	chr7	split hand/foot malformation (ectrodactyly) type 1	SHFM1	3 (GDM v Ob)
7962516	2.07	1.05173	0.01632	0.61369	chr12	solute carrier family 38, member 1	SLC38A1	3 (GDM v Ob)
8105991	2.05	1.03573	0.00734	0.61369	chr5	glucuronidase, beta pseudogene	SMA4	3 (GDM v Ob)
7994006	6.73	2.75152	0.00420	0.61369	chr16	SMG1 pseudogene 1	SMG1P1	3 (GDM v Ob)
7948902	2.42	1.27747	0.03264	0.61369	chr11	small nucleolar RNA host gene 1 (non-protein coding)	SNHG1	3 (GDM v Ob)
7982054	2.57	1.35985	0.03075	0.61369	chr15	small nucleolar RNA, C/D box 115-24	SNORD115-24	3 (GDM v Ob)
7981953	-4.30	-2.10458	0.03394	0.61369	chr15	small nucleolar RNA, C/D box 116-3	SNORD116-3	3 (GDM v Ob)
7981966	-4.30	-2.10458	0.03394	0.61369	chr15	small nucleolar RNA, C/D box 116-3	SNORD116-3	3 (GDM v Ob)
7981958	-2.19	-1.13236	0.03577	0.61369	chr15	small nucleolar RNA, C/D box 116-5	SNORD116-5	3 (GDM v Ob)
7981962	-2.19	-1.13236	0.03577	0.61369	chr15	small nucleolar RNA, C/D box 116-5	SNORD116-5	3 (GDM v Ob)
7981964	-5.60	-2.48482	0.03582	0.61369	chr15	small nucleolar RNA, C/D box 116-8	SNORD116-8	3 (GDM v Ob)
8145793	6.64	2.73207	0.01474	0.61369	chr8	small nucleolar RNA, C/D box 13	SNORD13	3 (GDM v Ob)
8086752	7.41	2.88863	0.01517	0.61369	chr3	small nucleolar RNA, C/D box 13 pseudogene 3	SNORD13P3	3 (GDM v Ob)
8076223	-3.09	-1.62941	0.04101	0.61369	chr22	small nucleolar RNA, C/D box 43	SNORD43	3 (GDM v Ob)
7982084	13.85	3.79140	0.04774	0.61369	chr15	small nuclear ribonucleoprotein polypeptide N	SNRPN	3 (GDM v Ob)
7982020	2.49	1.31392	0.04050	0.61369	chr15	small nuclear ribonucleoprotein polypeptide N	SNRPN	3 (GDM v Ob)
8096301	2.16	1.10884	0.02614	0.61369	chr4	secreted phosphoprotein 1	SPP1	3 (GDM v Ob)
7899346	6.64	2.73116	0.01111	0.61369	chr1	translation machinery associated 7 homolog (<i>S. cerevisiae</i>)	TMA7	3 (GDM v Ob)
8079630	3.34	1.74131	0.02015	0.61369	chr3	translation machinery associated 7 homolog (<i>S. cerevisiae</i>)	TMA7	3 (GDM v Ob)
8138581	2.16	1.10831	0.01687	0.61369	chr7	transformer 2 alpha homolog (<i>Drosophila</i>)	TRA2A	3 (GDM v Ob)

7971124	2.86	1.51836	0.00759	0.61369	chr13	ubiquitin-fold modifier 1	UFM1	3 (GDM v Ob)
8063011	-2.22	-1.15352	0.04030	0.61369	chr20	WAP four-disulfide core domain 10A	WFDC10A	3 (GDM v Ob)
8055261	3.74	1.90474	0.00724	0.61369	chr2	RAB6C-like	WTH3DI	3 (GDM v Ob)
8030980	7.73	2.94991	0.00079	0.61369	chr19	zinc finger protein 600	ZNF600	3 (GDM v Ob)
8030978	2.90	1.53554	0.00060	0.61369	chr19	zinc finger protein 845	ZNF845	3 (GDM v Ob)
8035842	3.30	1.72237	0.03285	0.61369	chr19	zinc finger protein 91	ZNF91	3 (GDM v Ob)