

**Table S3.** Gene Ontology term enrichment analysis.

High confidence GO terms were considered as those with at least 3 associated genes identified from our input list (bolded entries). Based on this criterion, significantly enriched GO terms for Contrast 1 and Contrast 2 were virtually identical and related to a wide range of processes including protein metabolic process, RNA processing, gene expression and translational processes with the exception of GO:0022904 (respiratory electron transport chain) which was associated with Contrast 1 but not Contrast 2. In contrast, significantly enriched GO terms for Contrast 3 are distinct from those of Contrast 1 and 2; enriched GO terms annotated to RNA splicing processes, intracellular transport of proteins to Golgi.

Items	Items_Details	Support	List size	F. Enrich.	Hyp	Hyp_c	Genes	GroupContrast
<b>GO:0006412</b>	<b>translation (BP)</b>	<b>4</b>	<b>26</b>	<b>21.8</b>	<b>3.18E-05</b>	<b>0.00184436</b>	<b>MRPL20,RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0010467</b>	<b>gene expression (BP)</b>	<b>3</b>	<b>26</b>	<b>9.7</b>	<b>0.00357177</b>	<b>0.00986489</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0006414</b>	<b>translational elongation (BP)</b>	<b>3</b>	<b>26</b>	<b>42.4</b>	<b>4.83E-05</b>	<b>0.000467207</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0007596</b>	<b>blood coagulation (BP)</b>	<b>3</b>	<b>26</b>	<b>8.6</b>	<b>0.00490134</b>	<b>0.0113711</b>	<b>KIF2A,KIFC1,CAPZA2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0031018</b>	<b>endocrine pancreas development (BP)</b>	<b>3</b>	<b>26</b>	<b>32.6</b>	<b>0.000105756</b>	<b>0.000876268</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0044267</b>	<b>cellular protein metabolic process (BP)</b>	<b>3</b>	<b>26</b>	<b>13.9</b>	<b>0.00127796</b>	<b>0.00673831</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0016070</b>	<b>RNA metabolic process (BP)</b>	<b>3</b>	<b>26</b>	<b>15.4</b>	<b>0.000958899</b>	<b>0.00556161</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0016032</b>	<b>viral reproduction (BP)</b>	<b>3</b>	<b>26</b>	<b>12.0</b>	<b>0.00194516</b>	<b>0.00805851</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0016071</b>	<b>mRNA metabolic process (BP)</b>	<b>3</b>	<b>26</b>	<b>17.7</b>	<b>0.000636119</b>	<b>0.00461187</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0006415</b>	<b>translational termination (BP)</b>	<b>3</b>	<b>26</b>	<b>45.4</b>	<b>3.96E-05</b>	<b>0.000765557</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0019058</b>	<b>viral infectious cycle (BP)</b>	<b>3</b>	<b>26</b>	<b>43.4</b>	<b>4.53E-05</b>	<b>0.0005254</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
<b>GO:0019083</b>	<b>viral transcription (BP)</b>	<b>3</b>	<b>26</b>	<b>48.1</b>	<b>3.32E-05</b>	<b>0.000961868</b>	<b>RPS13,RPL24,RPLP2</b>	<b>Contrast 1 (Norm v GDM)</b>
GO:0007018	microtubule-based movement (BP)	2	26	29.2	0.00213511	0.00773979	KIF2A,KIFC1	Contrast 1 (Norm v GDM)
GO:0051301	cell division (BP)	2	26	9.2	0.0198359	0.0319579	KIF2A,KIFC1	Contrast 1 (Norm v GDM)
GO:0022904	respiratory electron transport chain (BP)	2	26	30.6	0.00195216	0.00754837	ATP5H,ATP5E	Contrast 1 (Norm v GDM)

GO:0006200	ATP catabolic process (BP)	2	26	32.1	0.00177708	0.00792853	ATP5H,ATP5E	Contrast 1 (Norm v GDM)
GO:0042776	mitochondrial ATP synthesis coupled proton transport (BP)	2	26	202.4	4.31E-05	0.000625027	ATP5H,ATP5E	Contrast 1 (Norm v GDM)
GO:0071560	cellular response to transforming growth factor beta stimulus (BP)	1	26	54.8	0.0180888	0.0308574	CLEC3B	Contrast 1 (Norm v GDM)
GO:0031290	retinal ganglion cell axon guidance (BP)	1	26	87.7	0.0113427	0.0212218	RPL24	Contrast 1 (Norm v GDM)
GO:0031575	mitotic cell cycle G1/S transition checkpoint (BP)	1	26	119.6	0.00833013	0.0172553	RPL24	Contrast 1 (Norm v GDM)
GO:0000070	mitotic sister chromatid segregation (BP)	1	26	87.7	0.0113427	0.0212218	KIFC1	Contrast 1 (Norm v GDM)
GO:0071310	cellular response to organic substance (BP)	1	26	164.5	0.00606492	0.0135294	CLEC3B	Contrast 1 (Norm v GDM)
GO:0045047	protein targeting to ER (BP)	1	26	328.9	0.00303689	0.00880699	SRP14	Contrast 1 (Norm v GDM)
GO:0051693	actin filament capping (BP)	1	26	77.4	0.0128457	0.0225772	CAPZA2	Contrast 1 (Norm v GDM)
GO:0030282	bone mineralization (BP)	1	26	50.6	0.0195819	0.0324501	CLEC3B	Contrast 1 (Norm v GDM)
GO:0010458	exit from mitosis (BP)	1	26	263.1	0.00379473	0.00956932	RPL24	Contrast 1 (Norm v GDM)
GO:0006613	cotranslational protein targeting to membrane (BP)	1	26	146.2	0.00682054	0.0146515	SRP14	Contrast 1 (Norm v GDM)
GO:0007052	mitotic spindle organization (BP)	1	26	82.2	0.0120945	0.0219212	KIF2A	Contrast 1 (Norm v GDM)
GO:0015986	ATP synthesis coupled proton transport (BP)	1	26	101.2	0.00983751	0.019675	ATP5H	Contrast 1 (Norm v GDM)
GO:0006614	SRP-dependent cotranslational protein targeting to membrane (BP)	1	26	219.3	0.00455201	0.0110007	SRP14	Contrast 1 (Norm v GDM)
GO:0021554	optic nerve development (BP)	1	26	328.9	0.00303689	0.00880699	RPL24	Contrast 1 (Norm v GDM)
GO:0071569	protein ufmylation (BP)	1	26	328.9	0.00303689	0.00880699	UFM1	Contrast 1 (Norm v GDM)
GO:0000027	ribosomal large subunit assembly (BP)	1	26	1315.7	0.000760056	0.00489814	RPL24	Contrast 1 (Norm v GDM)

GO:0045900	negative regulation of translational elongation (BP)	1	26	657.8	0.00151956	0.00734452	SRP14	Contrast 1 (Norm v GDM)
GO:0033119	negative regulation of RNA splicing (BP)	1	26	263.1	0.00379473	0.00956932	RPS13	Contrast 1 (Norm v GDM)
GO:0010756	positive regulation of plasminogen activation (BP)	1	26	328.9	0.00303689	0.00880699	CLEC3B	Contrast 1 (Norm v GDM)
<b>GO:0010467</b>	<b>gene expression (BP)</b>	<b>3</b>	<b>16</b>	<b>15.7</b>	<b>0.000840309</b>	<b>0.00486179</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0006414</b>	<b>translational elongation (BP)</b>	<b>3</b>	<b>16</b>	<b>69.0</b>	<b>1.06E-05</b>	<b>0.000143332</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0031018</b>	<b>endocrine pancreas development (BP)</b>	<b>3</b>	<b>16</b>	<b>53.0</b>	<b>2.34E-05</b>	<b>0.000270477</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0044267</b>	<b>cellular protein metabolic process (BP)</b>	<b>3</b>	<b>16</b>	<b>22.6</b>	<b>0.000292675</b>	<b>0.00215515</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0006412</b>	<b>translation (BP)</b>	<b>3</b>	<b>16</b>	<b>26.6</b>	<b>0.000180712</b>	<b>0.00162641</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0016070</b>	<b>RNA metabolic process (BP)</b>	<b>3</b>	<b>16</b>	<b>25.0</b>	<b>0.000218319</b>	<b>0.00176838</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0016032</b>	<b>viral reproduction (BP)</b>	<b>3</b>	<b>16</b>	<b>19.5</b>	<b>0.000449853</b>	<b>0.00303651</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0016071</b>	<b>mRNA metabolic process (BP)</b>	<b>3</b>	<b>16</b>	<b>28.8</b>	<b>0.000143761</b>	<b>0.00145558</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0006415</b>	<b>translational termination (BP)</b>	<b>3</b>	<b>16</b>	<b>73.7</b>	<b>8.69E-06</b>	<b>0.000175915</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0019058</b>	<b>viral infectious cycle (BP)</b>	<b>3</b>	<b>16</b>	<b>70.5</b>	<b>9.95E-06</b>	<b>0.000161114</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
<b>GO:0019083</b>	<b>viral transcription (BP)</b>	<b>3</b>	<b>16</b>	<b>78.2</b>	<b>7.27E-06</b>	<b>0.000196251</b>	<b>RPL5,RPL24,RPS27A</b>	<b>Contrast 2 (Norm v Ob)</b>
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I (BP)	2	16	45.5	0.000874283	0.00472113	RPS27A,NPEPPS	Contrast 2 (Norm v Ob)
GO:0000209	protein polyubiquitination (BP)	2	16	40.0	0.0011303	0.00538553	RPS27A,NPEPPS	Contrast 2 (Norm v Ob)
GO:0006916	anti-apoptosis (BP)	2	16	21.4	0.00386709	0.0130514	RPS27A,HSP90B1	Contrast 2 (Norm v Ob)
GO:0006614	SRP-dependent cotranslational protein targeting to membrane (BP)	2	16	712.7	3.07E-06	0.000124463	SRP9,SRP14	Contrast 2 (Norm v Ob)

GO:0045900	negative regulation of translational elongation (BP)	2	16	2138.0	2.05E-07	1.66E-05	SRP9,SRP14	Contrast 2 (Norm v Ob)
GO:0030433	ER-associated protein catabolic process (BP)	1	16	66.8	0.0148659	0.0376294	HSP90B1	Contrast 2 (Norm v Ob)
GO:0051403	stress-activated MAPK cascade (BP)	1	16	40.3	0.0245089	0.0484199	RPS27A	Contrast 2 (Norm v Ob)
GO:0015992	proton transport (BP)	1	16	42.8	0.0231367	0.0493178	ATP5E	Contrast 2 (Norm v Ob)
GO:0007249	I-kappaB kinase/NF-kappaB cascade (BP)	1	16	56.3	0.0176301	0.0408012	RPS27A	Contrast 2 (Norm v Ob)
GO:0042776	mitochondrial ATP synthesis coupled proton transport (BP)	1	16	164.5	0.00606448	0.0175437	ATP5E	Contrast 2 (Norm v Ob)
GO:0060041	retina development in camera-type eye (BP)	1	16	41.9	0.0235943	0.0477785	RPL24	Contrast 2 (Norm v Ob)
GO:0042059	negative regulation of epidermal growth factor receptor signaling pathway (BP)	1	16	64.8	0.0153271	0.0376212	RPS27A	Contrast 2 (Norm v Ob)
GO:0031290	retinal ganglion cell axon guidance (BP)	1	16	142.5	0.00699441	0.0195361	RPL24	Contrast 2 (Norm v Ob)
GO:0032480	negative regulation of type I interferon production (BP)	1	16	71.3	0.0139429	0.0364315	RPS27A	Contrast 2 (Norm v Ob)
GO:0007254	JNK cascade (BP)	1	16	41.9	0.0235943	0.0477785	RPS27A	Contrast 2 (Norm v Ob)
GO:0031575	mitotic cell cycle G1/S transition checkpoint (BP)	1	16	194.4	0.00513373	0.0154012	RPL24	Contrast 2 (Norm v Ob)
GO:0016197	endosome transport (BP)	1	16	45.5	0.0217628	0.0476429	RPS27A	Contrast 2 (Norm v Ob)
GO:0071318	cellular response to ATP (BP)	1	16	534.5	0.00186968	0.00721161	HSP90B1	Contrast 2 (Norm v Ob)
GO:0051208	sequestering of calcium ion (BP)	1	16	712.7	0.00140257	0.00631154	HSP90B1	Contrast 2 (Norm v Ob)
GO:0031247	actin rod assembly (BP)	1	16	1069.0	0.000935249	0.0047347	HSP90B1	Contrast 2 (Norm v Ob)
GO:0043666	regulation of phosphoprotein phosphatase activity (BP)	1	16	267.3	0.00373608	0.0131575	HSP90B1	Contrast 2 (Norm v Ob)

GO:0045047	protein targeting to ER (BP)	1	16	534.5	0.00186968	0.00721161	SRP14	Contrast 2 (Norm v Ob)
GO:0071456	cellular response to hypoxia (BP)	1	16	57.8	0.0171699	0.0409049	NPEPPS	Contrast 2 (Norm v Ob)
GO:0010458	exit from mitosis (BP)	1	16	427.6	0.00233658	0.00860288	RPL24	Contrast 2 (Norm v Ob)
GO:0002218	activation of innate immune response (BP)	1	16	47.5	0.0208458	0.0469031	RPS27A	Contrast 2 (Norm v Ob)
GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway (BP)	1	16	85.5	0.0116318	0.031406	RPS27A	Contrast 2 (Norm v Ob)
GO:0006613	cotranslational protein targeting to membrane (BP)	1	16	237.6	0.00420217	0.013615	SRP14	Contrast 2 (Norm v Ob)
GO:0042273	ribosomal large subunit biogenesis (BP)	1	16	213.8	0.00466805	0.0145428	RPL5	Contrast 2 (Norm v Ob)
GO:0021554	optic nerve development (BP)	1	16	534.5	0.00186968	0.00721161	RPL24	Contrast 2 (Norm v Ob)
GO:0000027	ribosomal large subunit assembly (BP)	1	16	2138.0	0.000467727	0.0029143	RPL24	Contrast 2 (Norm v Ob)
<b>GO:0008380</b>	<b>RNA splicing (BP)</b>	<b>4</b>	<b>44</b>	<b>11.6</b>	<b>0.000385355</b>	<b>0.0146435</b>	<b>NSRP1,HNRNPC,TRA2A,HNRNPA3</b>	<b>Contrast 3 (GDM v Ob)</b>
<b>GO:0000398</b>	<b>nuclear mRNA splicing, via spliceosome (BP)</b>	<b>3</b>	<b>44</b>	<b>14.0</b>	<b>0.00130653</b>	<b>0.0165494</b>	<b>HNRNPC,TRA2A,HNRNPA3</b>	<b>Contrast 3 (GDM v Ob)</b>
<b>GO:0046907</b>	<b>intracellular transport (BP)</b>	<b>3</b>	<b>44</b>	<b>106.0</b>	<b>3.01E-06</b>	<b>0.000171318</b>	<b>RGPD8,RGPD4,RGPD5</b>	<b>Contrast 3 (GDM v Ob)</b>
<b>GO:0000042</b>	<b>protein targeting to Golgi (BP)</b>	<b>3</b>	<b>44</b>	<b>166.6</b>	<b>7.16E-07</b>	<b>8.16E-05</b>	<b>RGPD8,RGPD4,RGPD5</b>	<b>Contrast 3 (GDM v Ob)</b>
GO:0051028	mRNA transport (BP)	2	44	30.5	0.0019806	0.0225788	HNRNPA3,FMR1	Contrast 3 (GDM v Ob)
GO:0045768	positive regulation of anti-apoptosis (BP)	2	44	37.9	0.00128423	0.0366006	RASA1,IL6ST	Contrast 3 (GDM v Ob)
GO:0006907	pinocytosis (BP)	1	44	155.5	0.0064151	0.0406289	DAB2	Contrast 3 (GDM v Ob)
GO:0051481	reduction of cytosolic calcium ion concentration (BP)	1	44	129.6	0.00769328	0.0398652	IL6ST	Contrast 3 (GDM v Ob)
GO:0015807	L-amino acid transport (BP)	1	44	70.7	0.0140601	0.0485714	SLC38A1	Contrast 3 (GDM v Ob)

GO:0015804	neutral amino acid transport (BP)	1	44	86.4	0.0115182	0.0452784	SLC38A1	Contrast 3 (GDM v Ob)
GO:0001504	neurotransmitter uptake (BP)	1	44	155.5	0.0064151	0.0406289	SLC38A1	Contrast 3 (GDM v Ob)
GO:0045947	negative regulation of translational initiation (BP)	1	44	70.7	0.0140601	0.0485714	FMR1	Contrast 3 (GDM v Ob)
GO:0015939	pantothenate metabolic process (BP)	1	44	70.7	0.0140601	0.0485714	PANK2	Contrast 3 (GDM v Ob)
GO:0009108	coenzyme biosynthetic process (BP)	1	44	129.6	0.00769328	0.0398652	PANK2	Contrast 3 (GDM v Ob)
GO:0015937	coenzyme A biosynthetic process (BP)	1	44	111.1	0.00896986	0.0409025	PANK2	Contrast 3 (GDM v Ob)
GO:0010613	positive regulation of cardiac muscle hypertrophy (BP)	1	44	111.1	0.00896986	0.0409025	IL6ST	Contrast 3 (GDM v Ob)
GO:0000904	cell morphogenesis involved in differentiation (BP)	1	44	111.1	0.00896986	0.0409025	DAB2	Contrast 3 (GDM v Ob)
GO:0045780	positive regulation of bone resorption (BP)	1	44	77.7	0.01279	0.0486019	SPP1	Contrast 3 (GDM v Ob)
GO:0002675	positive regulation of acute inflammatory response (BP)	1	44	97.2	0.0102448	0.0432559	IL6ST	Contrast 3 (GDM v Ob)
GO:0070102	interleukin-6-mediated signaling pathway (BP)	1	44	129.6	0.00769328	0.0398652	IL6ST	Contrast 3 (GDM v Ob)
GO:0032502	developmental process (BP)	1	44	155.5	0.0064151	0.0406289	NSRP1	Contrast 3 (GDM v Ob)
GO:0001953	negative regulation of cell-matrix adhesion (BP)	1	44	86.4	0.0115182	0.0452784	RASA1	Contrast 3 (GDM v Ob)
GO:0006642	triglyceride mobilization (BP)	1	44	129.6	0.00769328	0.0398652	IL6ST	Contrast 3 (GDM v Ob)
GO:0042511	positive regulation of tyrosine phosphorylation of Stat1 protein (BP)	1	44	97.2	0.0102448	0.0432559	IL6ST	Contrast 3 (GDM v Ob)
GO:0070104	negative regulation of interleukin-6-mediated signaling pathway (BP)	1	44	777.5	0.00128625	0.018329	IL6ST	Contrast 3 (GDM v Ob)
GO:0070106	interleukin-27-mediated signaling pathway (BP)	1	44	777.5	0.00128625	0.018329	IL6ST	Contrast 3 (GDM v Ob)

GO:0002821	positive regulation of adaptive immune response (BP)	1	44	259.2	0.0038539	0.036612	IL6ST	Contrast 3 (GDM v Ob)
GO:0070120	ciliary neurotrophic factor-mediated signaling pathway (BP)	1	44	155.5	0.0064151	0.0406289	IL6ST	Contrast 3 (GDM v Ob)
GO:0048861	leukemia inhibitory factor signaling pathway (BP)	1	44	194.4	0.0051353	0.041816	IL6ST	Contrast 3 (GDM v Ob)
GO:2000096	positive regulation of Wnt receptor signaling pathway, planar cell polarity pathway (BP)	1	44	388.7	0.00257088	0.0266437	DAB2	Contrast 3 (GDM v Ob)
GO:0071569	protein ufmylation (BP)	1	44	194.4	0.0051353	0.041816	UFM1	Contrast 3 (GDM v Ob)
GO:0048685	negative regulation of collateral sprouting of intact axon in response to injury (BP)	1	44	777.5	0.00128625	0.018329	SPP1	Contrast 3 (GDM v Ob)
GO:0051252	regulation of RNA metabolic process (BP)	1	44	777.5	0.00128625	0.018329	RASA1	Contrast 3 (GDM v Ob)