

Supplemental Table 5. GO-terms enriched in differentially expressed genes when comparing β -cell clusters *Beta1* versus *Beta2*, *Beta3*, or *Beta4*, and biological processes enriched in highly expressed genes of OB -CH or NZO -CH *Beta1* cells. Validated by Fisher's exact test (p-value). Related to Figure 2.

Category	Term	Count	Percentage	p-value	Genes	List.Total	Pop.Hits	Pop.Total	Fold.Enrichment	Bonferroni	Benjamini	FDR	Comparison
GOTERM_BP_DIRECT	GO:0006412-translation	17	28.33333333	8.6903E-14	Rpl9, Rps13, Rps18, Rpl23, Rps3, Rps2, Rpl17, Rpl7, Rpl35a, Rpl10, Rps5, Rpl26, Rpl32, Rpl21, Rpl29, Rpl30, Rps7	59	401	18082	12.99268777	3.09472E-11	3.09472E-11	1.19194E-10	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0042773-ATP synthesis coupled electron transport	5	8.333333333	1.42241E-09	Ndufa7, mt-Nd5, mt-Nd4l, mt-Nd4, mt-Co2	59	6	18082	255.3954802	5.06378E-07	2.53189E-07	1.95032E-06	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0002181-cytoplasmic translation	5	8.333333333	4.11299E-06	Rpl7, Rpl35a, Rpl9, Rpl26, Rpl29	59	34	18082	45.06979063	0.001463158	0.000487957	0.005639323	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0055114-oxidation-reduction process	11	18.33333333	5.13603E-05	mt-Nd1, Ndufa7, mt-Nd5, Ero1lb, mt-Nd3, mt-Co1, mt-Nd2, mt-Cytb, mt-Nd4l, mt-Nd4, mt-Co2	59	676	18082	4.987012336	0.018118585	0.004560752	0.070398903	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0006810-transport	17	28.33333333	0.000138603	Oaz1, Fxyd6, Naca, Slc2a2, mt-Nd3, mt-Co1, mt-Nd2, mt-Cytb, mt-Nd4l, mt-Nd4, mt-Co2, mt-Nd1, mt-Atp6, Ndufa7, mt-Nd5, Slc30a8, Ero1lb	59	1822	18082	2.85953227	0.04814834	0.009820674	0.189876007	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0032024-positive regulation of insulin secretion	4	6.666666667	0.000551533	Glpr1, Slc30a8, Isl1, Ucn3	59	50	18082	24.5179661	0.178316471	0.032203389	0.753581031	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0006120-mitochondrial electron transport, NADH to ubiquinone	3	5	0.000653747	Ndufa7, mt-Nd2, mt-Nd4	59	12	18082	76.61864407	0.207695918	0.032711588	0.892660127	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0006882-cellular zinc ion homeostasis	3	5	0.001496875	Slc30a8, Mt2, Mt1	59	18	18082	51.07909605	0.413326533	0.064487584	2.033005429	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0009749-response to glucose	4	6.666666667	0.002008971	Txnip, Glpr1, Slc30a8, Ucn3	59	78	18082	15.71664494	0.511254317	0.076464361	2.719672595	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0042273-ribosomal large subunit biogenesis	3	5	0.002667098	Rpl7, Rpl35a, Rpl26	59	24	18082	38.30932203	0.613550932	0.090695739	3.595601096	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0006364-rRNA processing	4	6.666666667	0.007712453	Rpl7, Rpl35a, Rpl26, Rps7	59	126	18082	9.729351628	0.936472077	0.221643413	10.07174587	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0006979-response to oxidative stress	4	6.666666667	0.008940125	Txnip, mt-Nd3, mt-Co1, Rps3	59	133	18082	9.217280489	0.959115196	0.233879953	11.58533979	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0010273-detoxification of copper ion	2	3.333333333	0.012769893	Mt2, Mt1	59	4	18082	153.2372881	0.989697388	0.296685135	16.15664827	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0042985-negative regulation of amyloid precursor protein biosynthetic process	2	3.333333333	0.019094605	Itm2b, Bace2	59	6	18082	102.1581921	0.998954664	0.38752311	23.22910801	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0007218-neuropeptide signaling pathway	3	5	0.024761966	Glpr1, Ucn3, Pyy	59	76	18082	12.09768064	0.999867143	0.448482923	29.09251491	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0002485-antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP-dependent	2	3.333333333	0.028507078	H2-D1, H2-K1	59	9	18082	68.10546139	0.999966231	0.474549254	32.73632889	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0010038-response to metal ion	2	3.333333333	0.037830774	Mt2, Mt1	59	12	18082	51.07909605	0.99999891	0.554070791	41.06748168	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0071294-cellular response to zinc ion	2	3.333333333	0.037830774	Mt2, Mt1	59	12	18082	51.07909605	0.99999891	0.554070791	41.06748168	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0045926-negative regulation of growth	2	3.333333333	0.037830774	Mt2, Mt1	59	12	18082	51.07909605	0.99999891	0.554070791	41.06748168	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0007263-nitric oxide mediated signal transduction	2	3.333333333	0.047066516	Mt2, Mt1	59	15	18082	40.86327684	0.999999965	0.614606391	48.36788879	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0046688-response to copper ion	2	3.333333333	0.056215119	mt-Co1, mt-Cytb	59	18	18082	34.0527307	0.999999999	0.661779705	54.76493548	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0055093-response to hyperoxia	2	3.333333333	0.056215119	mt-Atp6, mt-Cytb	59	18	18082	34.0527307	0.999999999	0.661779705	54.76493548	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0001916-positive regulation of T cell mediated cytotoxicity	2	3.333333333	0.059245429	H2-D1, H2-K1	59	19	18082	32.26048171	1	0.662806807	56.71625123	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0022904-respiratory electron transport chain	2	3.333333333	0.059245429	mt-Co3, mt-Cytb	59	19	18082	32.26048171	1	0.662806807	56.71625123	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0031116-positive regulation of microtubule polymerization	2	3.333333333	0.059245429	Rgs2, Rps3	59	19	18082	32.26048171	1	0.662806807	56.71625123	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0000028-ribosomal small subunit assembly	2	3.333333333	0.065277392	Rps5, Rps2	59	21	18082	29.18805488	1	0.681578224	60.37028138	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0042593-glucose homeostasis	3	5	0.067974034	Slc30a8, G6pc2, Ero1lb	59	133	18082	6.912960367	1	0.67989707	61.90948171	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0071385-cellular response to glucocorticoid stimulus	2	3.333333333	0.068279103	Isl1, mt-Nd3	59	22	18082	27.86132512	1	0.665344354	62.08007618	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0097421-liver regeneration	2	3.333333333	0.089027455	Rpl32, Rpl30	59	29	18082	21.13617767	1	0.749199474	72.15398978	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0046686-response to cadmium ion	2	3.333333333	0.089027455	mt-Cytb, Mt1	59	29	18082	21.13617767	1	0.749199474	72.15398978	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0002479-antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	2	3.333333333	0.091954194	H2-D1, H2-K1	59	30	18082	20.43163842	1	0.746805387	73.35590679	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0043524-negative regulation of neuron apoptotic process	3	5	0.093324049	Glpr1, Isl1, Mt1	59	160	18082	5.746398305	1	0.738530515	73.90177611	<i>Beta1</i> -OB vs <i>Beta1</i> -NZO (higher in OB)
GOTERM_BP_DIRECT	GO:0006412-translation	16	23.1884058	1.13978E-11	Rpl38, Rpl4, Rps29, Rpl6, Rps17, Rpl35, Rpsa, Rps15a, Rpl31, Rps27, Rps28, Rrbp1, Rpl24, Rps19, Rpl8, Rps23	67	401	18082	10.76830312	4.5819E-09	4.5819E-09	1.59092E-08	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)

GOTERM_BP_DIRECT	GO:0006457~protein folding	8	11.5942029	4.1577E-07	Canx, Hsp90aa1, Calr, Fkbp2, P4hb, Hsp90ab1, Fkbp11, Dnaja1	67	128	18082	16.86753731	0.000167126	8.35663E-05	0.000580338	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0000028~ribosomal small subunit assembly	5	7.246376812	9.24543E-07	Rps28, Rps27, Rps19, Rps17, Rpsa	67	21	18082	64.257285	0.000371597	0.000123881	0.001290486	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0030433~ER-associated ubiquitin-dependent protein catabolic process	6	8.695652174	2.00795E-06	Vcp, Ubxn4, Edem2, Selenos, Dnajb9, Sec61b	67	57	18082	28.4084839	0.00080687	0.000201778	0.002802692	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0061077~chaperone-mediated protein folding	4	5.797101449	0.000213576	Canx, Calr, Fkbp2, Fkbp11	67	32	18082	33.73507463	0.082283596	0.017026751	0.297701595	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0002181~cytoplasmic translation	4	5.797101449	0.00025633	Rplp1, Rpl131, Rpl6, Rpl8	67	34	18082	31.75065847	0.097925118	0.017029619	0.357196051	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0030970~retrograde protein transport, ER to cytosol	3	4.347826087	0.00152345	Vcp, Selenos, Sec61b	67	16	18082	50.60261194	0.458219197	0.083832668	2.10559653	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0042274~ribosomal small subunit biogenesis	3	4.347826087	0.002155641	Rps28, Rps19, Rps17	67	19	18082	42.61272584	0.580001118	0.102765392	2.967218803	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0015986~ATP synthesis coupled proton transport	3	4.347826087	0.003159483	Atp5l, Atp5e, Atp5g1	67	23	18082	35.201817	0.71976391	0.131811988	4.320914581	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0006810~transport	15	21.73913043	0.005391391	Ndufs2, Ndufb11, Atp5l, Atp5e, Atp5g1, Sec61b, Lman1, Vcp, Uqcrcq, Rrbp1, Sec61a1, Kdelr2, Hdldb, Ndufv3, Scg5	67	1822	18082	2.221849042	0.886187491	0.195327796	7.268096664	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0045787~positive regulation of cell cycle	3	4.347826087	0.009360018	Rps15a, BC004004, Calr	67	40	18082	20.24104478	0.977187517	0.290842077	12.30138811	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0046034~ATP metabolic process	3	4.347826087	0.009360018	Vcp, Atp5l, Atp5g1	67	40	18082	20.24104478	0.977187517	0.290842077	12.30138811	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	7	10.14492754	0.017041342	Ccnd2, Atf5, Gcg, Hsp90ab1, Hyou1, Dnaja1, Hspa5	67	566	18082	3.337745899	0.999001906	0.43774807	21.33062645	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0015992~proton transport	3	4.347826087	0.019019875	Atp5l, Atp5e, Atp5g1	67	58	18082	13.95934122	0.999555979	0.447785273	23.51228813	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0006898~receptor-mediated endocytosis	3	4.347826087	0.020271506	Ftl1, Calr, Hyou1	67	60	18082	13.49402985	0.999734229	0.444597735	24.86327135	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0034976~response to endoplasmic reticulum stress	3	4.347826087	0.031449993	P4hb, Hyou1, Hspa5	67	76	18082	10.65318146	0.999997363	0.575311103	35.9839274	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0006888~ER to Golgi vesicle-mediated transport	3	4.347826087	0.032985178	Lman1, Vcp, Hyou1	67	78	18082	10.38002296	0.999998606	0.56946604	37.38577853	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0006983~ER overload response	2	2.898550725	0.035915453	Selenos, Hspa5	67	10	18082	53.9761194	0.999999589	0.578915408	39.98276637	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0060736~prostate gland growth	2	2.898550725	0.035915453	Psap, Prlr	67	10	18082	53.9761194	0.999999589	0.578915408	39.98276637	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0005975~carbohydrate metabolic process	4	5.797101449	0.039501682	Gfpt1, Ppp1r1a, Mlec, Gapdh	67	206	18082	5.240399942	0.999999908	0.593471567	43.0249819	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0009651~response to salt stress	2	2.898550725	0.049923218	Hsp90aa1, Hsp90ab1	67	14	18082	38.554371	0.999999999	0.661607275	51.0726216	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0033160~positive regulation of protein import into nucleus, translocation	2	2.898550725	0.049923218	Hsp90aa1, Hsp90ab1	67	14	18082	38.554371	0.999999999	0.661607275	51.0726216	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0031396~regulation of protein ubiquitination	2	2.898550725	0.056851741	Hsp90aa1, Hsp90ab1	67	16	18082	33.73507463	1	0.691640488	55.82439021	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0045793~positive regulation of cell size	2	2.898550725	0.056851741	Hsp90aa1, Hsp90ab1	67	16	18082	33.73507463	1	0.691640488	55.82439021	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0021680~cerebellar Purkinje cell layer development	2	2.898550725	0.056851741	Uqcrcq, Hspa5	67	16	18082	33.73507463	1	0.691640488	55.82439021	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0030490~maturation of SSU-rRNA	2	2.898550725	0.056851741	Rps28, Rps19	67	16	18082	33.73507463	1	0.691640488	55.82439021	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0006364~rRNA processing	3	4.347826087	0.077456188	Rps28, Rps19, Rps17	67	126	18082	6.4257285	1	0.786326265	67.54495905	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0006754~ATP biosynthetic process	2	2.898550725	0.080711959	Atp5l, Atp5e	67	23	18082	23.467878	1	0.785137192	69.10765213	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0000027~ribosomal large subunit assembly	2	2.898550725	0.090754853	Rpl6, Rpl24	67	26	18082	20.76004592	1	0.810409926	73.49903126	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0007029~endoplasmic reticulum organization	2	2.898550725	0.094078412	Lman1, Sec61a1	67	27	18082	19.99115533	1	0.808896913	74.81958417	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)
GOTERM_BP_DIRECT	GO:0071353~cellular response to interleukin-4	2	2.898550725	0.094078412	Hsp90ab1, Hspa5	67	27	18082	19.99115533	1	0.808896913	74.81958417	<i>Beta1</i> -NZO vs <i>Beta1</i> -OB (higher in NZO)