

Figure 3-Source Data 4. Biological Process and pathways overrepresented in β -cells

GO identified by WebGestalt using the list of DE genes overexpressed in CTL β cells (versus 20dpt bihormonal cells) (DESeq FC>2x, Padj<0.05)

GO Padj (FDR) <0.25

Biological Process (non redundant)

geneSet	description	enrichmentRatio	pValue	FDR	userid
GO:0032879	regulation of localization	2,58036999	3,56E-08	1,01E-05	dpysl3;stxbp5a;rnd1b;plxna3;srp1a;mmp14b;rab3c;panx1b;rhbdf1b;cacna1ba;klf6a;nexmifb; cacng2a;plxnb3;sulf1;arhgap4a;cxcr4b;anxa3b;kcj8;kcj11;sema4e;pparab;ccdc125;jph1a; bin1b;rims4;stim1a;ripor2;cplx2;pm20d1.2;kcj19b;pllp;sema4ba;cacng3b;rnd3a;si:dkey-183c2.4; mcu;parietopsin;vegfaa
GO:0051674	localization of cell	2,113862421	1,02E-04	0,01061422	dpysl3;esr1;rnd1b;fmln3;plxna3;srp1a;mmp14b;arpc5b;tnc;klf6a;nexmifb;plxnb3;cebpa;sulf1; arhgap4a;cxcr4b;anxa3b;sema4e;pld1a;ccdc125;alcamb;ripor2;met;sema4ba;cxcl20;pik3cb; rnd3a;si:dkey-183c2.4;vegfaa
GO:0098657	import into cell	2,709388489	1,12E-04	0,01061422	gulp1a;vldlr;cacng2a;slc7a2;lgals3bpb;anxa3b;kcj8;kcj11;zgc:91818;slc6a4b;bin1b;slc12a9; hhipl1;kcj19b;pllp;met;cacng3b;scarb2a
GO:1901264	carbohydrate derivative transport	6,947149972	1,67E-04	0,011870554	slc25a24;slc25a25a;slc25a4;mfsd2aa;slc25a25b;slc29a4
GO:0022610	biological adhesion	2,342748369	3,41E-04	0,019346833	plxna3;cntn5;tnc;ctnna2;nexmifb;itga9;plxnb3;itga3a;lamb4;lgals3bpb;parvaa;anxa3b;clstn2; ripor2;dchs1a;si:ch211-74m13.3;tbs3a;si:dkey-183c2.4;epd;vegfaa
GO:0040011	locomotion	1,87396348	5,08E-04	0,024025397	dpysl3;esr1;rnd1b;fmln3;plxna3;srp1a;mmp14b;arpc5b;tnc;klf6a;nexmifb;plxnb3;cebpa;sulf1; arhgap4a;cxcr4b;anxa3b;cyfip1;sema4e;pld1a;ccdc125;alcamb;ripor2;met;sema4ba;cxcl20; pik3cb;kif5c;rnd3a;si:dkey-183c2.4;vegfaa
GO:0006812	cation transport	1,833049719	0,001981178	0,080379225	si:ch211-247n2.1;atp2b1b;micu2;panx1b;cax2;abcc9;cacna1ba;cacng2a;slc7a2;anxa3b;kcj8; kcj11;zgc:91818;slc6a4b;jph1a;slc25a47a;slc12a9;stim1a;pm20d1.2;kcj19b;slc6a15;slc31a2; cacng3b;cox8b;mcu;ndufa4l2a
GO:0015748	organophosphate ester transport	3,763039568	0,00238089	0,084521592	slc25a24;slc25a25a;slc25a4;mfsd2aa;slc25a25b;slc25a33;prelid3a
GO:0051336	regulation of hydrolase activity	1,89278637	0,003656415	0,09310942	stxbp5a;plxna3;srp1a;arhgap12a;agt;rcan2;cst14a.1;rasa4;plxnb3;rasgef1ba;tfpia;arhgap4a; rap1gap2a;ppp1r15a;tnfrsf1b;myo9aa;ppp1r14c;si:dkey-183c2.4;gchfr;vegfaa;cst14b.1
GO:0071526	semaphorin-plexin signaling pathway	4,70379946	0,003762361	0,09310942	plxna3;plxnb3;sema4e;sema4ba;si:dkey-183c2.4
GO:0071875	adrenergic receptor signaling pathway	6,020863309	0,00379002	0,09310942	adrb1;hrh3;gpr101;adra2b
GO:0009611	response to wounding	2,424508715	0,003934201	0,09310942	dpysl3;fgf20a;dysf;gucy1a1;tnc;socs3a;tfpia;cxcr4b;ctsba;pik3cb;hcar1-4;lmo2
GO:0022603	regulation of anatomical structure morphogenesis	2,022819689	0,004477354	0,097812966	rnd1b;lypd6;fmln3;plxna3;palm1b;ism1;tnc;plxnb3;sulf1;cxcr4b;cyfip1;sema4e;ripor2;sema4ba; rnd3a;si:dkey-183c2.4;vegfaa
GO:0032989	cellular component morphogenesis	1,688778733	0,009459357	0,191889809	dpysl3;tmem59l;rnd1b;fmln3;plxna3;palm1b;dnajb6b;tnc;ctnna2;plxnb3;mnx1;cxcr4b;elp3; parvaa;cyfip1;sema4e;alcamb;sema4ba;kif5c;myo9aa;rnd3a;si:dkey-183c2.4;vegfaa
GO:0098660	inorganic ion transmembrane transport	1,730133135	0,011797485	0,223365721	si:ch211-247n2.1;atp2b1b;micu2;ttyh2l;cax2;abcc9;cacna1ba;cacng2a;kcj8;kcj11;jph1a; slc12a9;stim1a;pm20d1.2;kcj19b;slc31a2;cacng3b;cox8b;mcu;ndufa4l2a
GO:0033993	response to lipid	2,263482447	0,012949478	0,225550479	esr1;rorcb;nr1i2;esr2b;cxcr4b;jun;anxa3b;pparab;cxcl20;vdra
GO:0030522	intracellular receptor signaling pathway	3,010431655	0,014184152	0,225550479	esr1;rorcb;nr1i2;esr2b;pparab;vdra
GO:0032409	regulation of transporter activity	3,420945062	0,014697831	0,225550479	cacng2a;anxa3b;stim1a;pm20d1.2;cacng3b
GO:0040007	growth	1,858291145	0,015338373	0,225550479	tmem59l;plxna3;fgf20a;mmp14b;tnc;klf6a;cxcr4b;cyfip1;sema4e;ctsba;mpzl1;sema4ba; myo9aa;lmo2;ndrg4
GO:0007264	small GTPase mediated signal transduction	1,843121421	0,016414535	0,225550479	rnd1b;cyth3a;arhgef18a;rab3c;rasa4;rasgef1ba;eps8l2;rap1gap2a;ripor2;kalrn;rnd3a;iqsec2b; rapgef3;ngfra;ksr2
GO:1901700	response to oxygen-containing compound	2,006954436	0,016678028	0,225550479	esr1;sesn3;sesn1;socs3a;ins;cxcr4b;jun;entpd1;cxcl20;vdra;vegfaa;gcgra

GO:0120036	plasma membrane bounded cell projection organization	1,551768894	0,018726031	0,238246687	dpysl3;tmem59l;fmnl3;plxna3;ak5;tnc;ctnna2;socs3a;plxnb3;mnx1;cxcr4b;elp3;cyfip1;sema4e; dtnbp1a;eps8l2;alcamb;ripor2;map4l;sema4ba;kif5c;myo9aa;si:dkey-183c2.4;vegfaa;sept9b
GO:0010035	response to inorganic substance	2,778859989	0,020414727	0,238246687	si:ch211-247n2.1;slc25a24;rasa4;jun;entpd1;pcxb
GO:0051240	positive regulation of multicellular organismal process	2,019191964	0,020582906	0,238246687	plxna3;panx1b;tnc;plxnb3;ins;sulf1;anxa3b;clstn2;tnfrsf1b;si:dkey-183c2.4;vegfaa
GO:0051128	regulation of cellular component organization	1,535934518	0,02097242	0,238246687	dpysl3;rnd1b;fmnl3;plxna3;palml1b;mmp14b;arpc5b;tnc;ctnna2;socs3a;plxnb3;vil1;cxcr4b; cyfip1;sema4e;eps8l2;bin1b;clstn2;ripor2;pllp;sema4ba;rnd3a;si:dkey-183c2.4;rassf7a;vegfaa
GO:0008283	cell proliferation	1,77084215	0,022691697	0,244356751	btg2;ism1;tnc;tp53inp1;klf6a;sulf1;cdk6;plcd3b;lmo2;btc;vdra;parietopsin;si:ch211-260e23.9; vegfaa;ndrg4
GO:2000026	regulation of multicellular organismal development	1,565709135	0,024315188	0,244356751	dpysl3;lypd6;fam49a;plxna3;ism1;tnc;socs3a;maff;klf6a;nexmifb;plxnb3;ins;sulf1;cxcr4b; sema4e;clstn2;tnfrsf1b;sema4ba;twist1b;si:dkey-183c2.4;rflnb;vegfaa
GO:0014070	response to organic cyclic compound	2,27202389	0,024457375	0,244356751	esr1;rorcb;nr1i2;esr2b;jun;anxa3b;pparab;vdra
GO:0051094	positive regulation of developmental process	2,020423929	0,026487893	0,244356751	plxna3;tnc;plxnb3;ins;jun;clstn2;ripor2;tnfrsf1b;si:dkey-183c2.4;vegfaa
GO:0016192	vesicle-mediated transport	1,5178647	0,026556855	0,244356751	gulf1a;stxbp5a;vldlr;rab3c;mfsd2aa;cacng2a;arl4cb;lgals3bpb;cnih2;anxa3b;dtbnp1a; zgc:91818;bin1b;rims4;kif1aa;cplx2;hhpl1;pllp;met;kif5c;cacng3b;si:ch211-284f22.3;scarb2a;arl4aa
GO:0031016	pancreas development	2,394661543	0,026672744	0,244356751	klf6a;ins;mnx1;kcnj11;insm1b;met;nkx6.2

KEGG pathways

geneSet	description	enrichmentRatio	pValue	FDR	userId
dre04142	Lysosome	3,090536124	8,97E-05	0,0145294	ctsla;cd164;hexb;asah1a;lgmn;ctsh;ctsz;galns;si:ch211-122f10.4;ctsba;ctsd;nagpa;cln5; scarb2a;naga
dre04510	Focal adhesion	2,104447369	0,002804914	0,227197998	egfra;vaspb;tnr;tnc;itga9;itga3a;lamb4;jun;parvaa;ccnd2a;met;pik3cb;thbs3a;hrasa;pdgfab; lamb1a;vegfaa