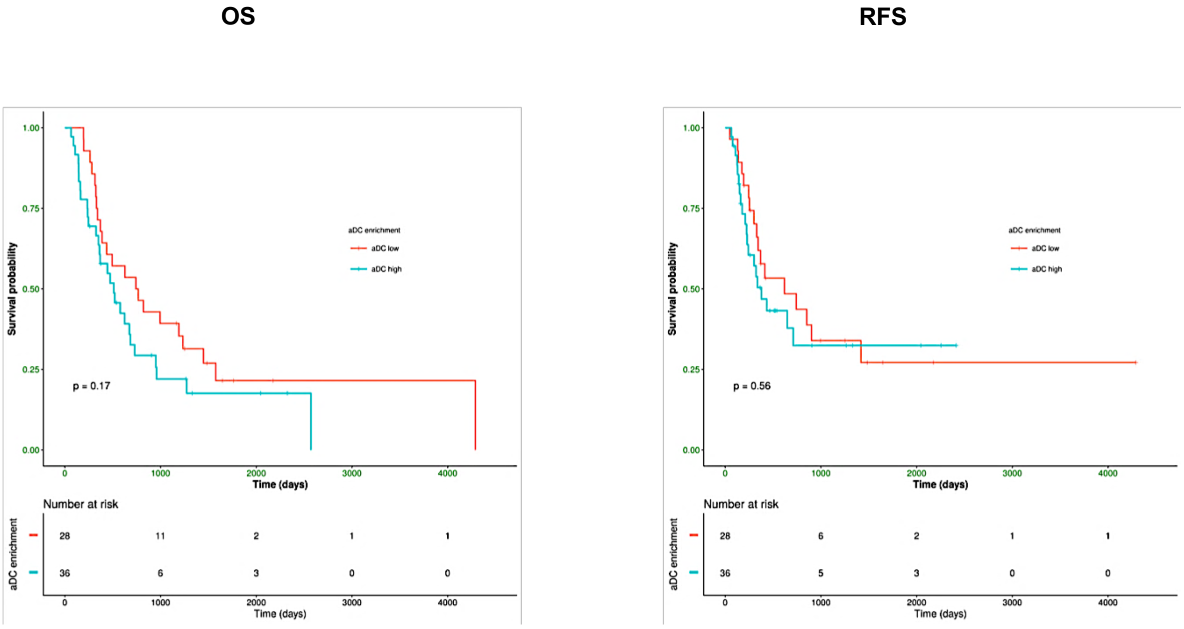
File S1: List of significant terms and the related genes involved in the KEGG, GO Biological Process, Reactome pathway and GO immune system process databases network enrichment showed in Figure 3 (a) and (b).

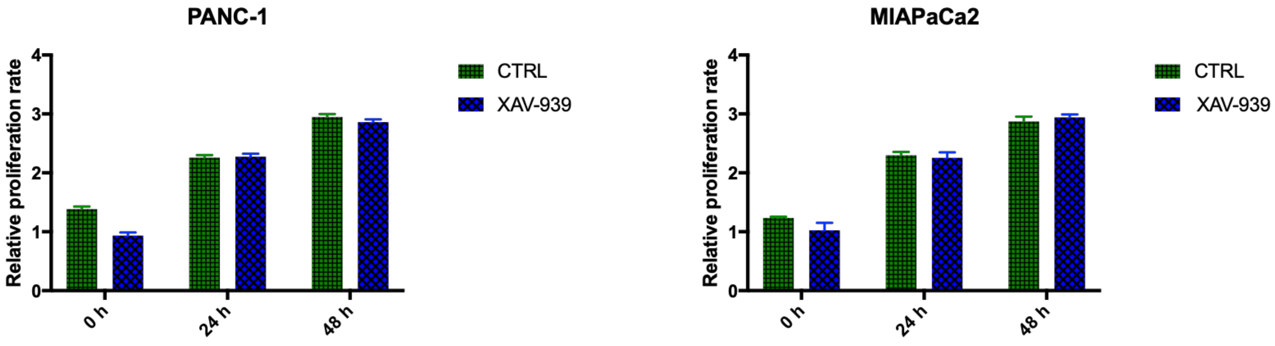
GOID	Ontology Source	GOTerm	GOLevels	GOGroups	Nr. Genes	% Associated Genes	Term PValue	Term PValue Corrected with Bonferroni step down	Group PValue	Group PValue Corrected with Bonferroni step down	Associated Genes Found	All Associated Genes	OverViewTerm
GO:0001759	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	organ induction	[3, 4, 5, 6, 7, 8, 9]	[Group5, Group7]	2	8.333.333	0.0036431181446800764	0.007286236289360153	{Group5=8.78624307038887E-8, Group7=2.8509622753718204E-12}	{Group5=6.150370149272209E-7, Group7=2.5658660478346383E-11}	[GDNF, WNT2]	[AKR1B1, AR, AREG, BMP2, BMP4, DKK1, FGF1, FGF10, FGF8, FGFR1, FLG, FRS2, GATA5, GDNF,	FALSE
GO:0001976	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	neurological system process involved in regulation of systemic arterial blood pressure	[4, 5, 7]	[Group6, Group7]	2	11.111.111	0.002049147229283542	0.016393177834268337	{Group6=4.854207482621646E-7, Group7=2.8509622753718204E-12}	{Group6=2.912524489572987E-6, Group7=2.5658660478346383E-11}	[ADRA1A, CALCA]	[ACE2, ADRA1A, ADRA1D, AGT, AGTR2, AGXT, ANKK1, ASIC2, CALCA, DRD2, MECP2, NAV2, P2RX2,	FALSE
GO:0001978	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of systemic arterial blood pressure by carotid sinus baroreceptor feedback	[5, 6, 7, 8, 9]	[Group6, Group7]	2	66.666.664	4,17E+11	0.0011251362757856253	{Group6=4.854207482621646E-7, Group7=2.8509622753718204E-12}	{Group6=2.912524489572987E-6, Group7=2.5658660478346383E-11}	[ADRA1A, CALCA]	[ADRA1A, ADRA1D, CALCA]	TRUE
GO:0001983	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	baroreceptor response to increased systemic arterial blood pressure	[6, 7, 8, 9, 10]	[Group6, Group7]	2	66.666.664	4,17E+11	0.0011251362757856253	{Group6=4.854207482621646E-7, Group7=2.8509622753718204E-12}	{Group6=2.912524489572987E-6, Group7=2.5658660478346383E-11}	[ADRA1A, CALCA]	[ADRA1A, ADRA1D, CALCA]	FALSE
GO:0002026	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of the force of heart contraction	[3, 6, 7]	[Group2]	4	8.888.889	2,42E+11	7,03E+11	{Group2=2.4245811297187697E-5}	{Group2=1.2122905648593849E-4}	[ADRA1A, MUC2, MYL3, NOS1]	[ADM, ADRA1A, ADRA1D, ADRB1, APLN, ATF7IP, ATP1A1, ATP1A2, ATP1A3, ATP1A4, ATP2A2, ATP	TRUE
GO:0002739	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of cytokine secretion involved in immune response	[5, 6, 7, 8, 9, 10, 11]	[Group8]	2	8.695.652	0.0033476258398223114	0.010042877519466933	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, IL10]	[A1CF, ANGPT1, APOA1, APOA2, ASIP, ASPA, ASPM, ATG5, C3, F2RL1, HNRNPK, IL10, KARS, LILRB1	FALSE
GO:0002740	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of cytokine secretion involved in immune response	[5, 6, 7, 8, 9, 10, 11, 12]	[Group8]	2	28.571.428	2,89E+11	0.005199746307637928	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, IL10]	[ANGPT1, APOA1, APOA2, IL10, LILRB1, LPAL2, TNF]	FALSE
GO:0003025	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of systemic arterial blood pressure by baroreceptor feedback	[5, 6, 8]	[Group6, Group7]	2	40.0	1,38E+12	0.0030410765484795797	{Group6=4.854207482621646E-7, Group7=2.8509622753718204E-12}	{Group6=2.912524489572987E-6, Group7=2.5658660478346383E-11}	[ADRA1A, CALCA]	[ADRA1A, ADRA1D, ASIC2, CALCA, NAV2]	FALSE
GO:0003085	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of systemic arterial blood pressure	[5, 7]	[Group6, Group7]	2	10.526.316	0.0022846738316462155	0.01599271682152351	{Group6=4.854207482621646E-7, Group7=2.8509622753718204E-12}	{Group6=2.912524489572987E-6, Group7=2.5658660478346383E-11}	[ADRA1A, CALCA]	[ADORA1, ADRA1A, ADRA1D, ADRB1, ADRB2, ADRB3, AGTR2, ARHGAP42, BBS4, BMP1, BMPR2, C	FALSE
GO:0003207	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	cardiac chamber formation	[3, 4, 5, 6, 7, 8, 9]	[Group6]	2	16.666.666	8,97E+11	0.012556871568513055	{Group6=4.854207482621646E-7}	{Group6=2.912524489572987E-6}	[HAND1, NKX2-5]	[HAND1, HAND2, MEF2C, MESP1, NKX2-5, NOTCH1, SMARCD3, SOX11, SOX4, TBX2, TBX20, TBX5]	FALSE
GO:0003211	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	cardiac ventricle formation	[4, 5, 6, 7, 8, 9, 10]	[Group6]	2	20.0	6,15E+11	0.009832262924133828	{Group6=4.854207482621646E-7}	{Group6=2.912524489572987E-6}	[HAND1, NKX2-5]	[HAND1, HAND2, MEF2C, MESP1, NKX2-5, NOTCH1, SMARCD3, SOX11, SOX4, TBX5]	FALSE
GO:0003215	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	cardiac right ventricle morphogenesis	[5, 6, 7, 8, 9, 10]	[Group6]	2	8.333.333	0.0036431181446800764	0.007286236289360153	{Group6=4.854207482621646E-7}	{Group6=2.912524489572987E-6}	[HAND1, NKX2-5]	[BMPR1A, CHD7, FOXH1, GATA3, GATA4, GDF1, HAND1, HAND2, HERPUD1, HEY2, ISL1, JAG1, NKX	FALSE
GO:0007512	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	adult heart development	[5, 6, 7]	[Group6]	2	12.5	0.0016149946876273084	0.016149946876273084	{Group6=4.854207482621646E-7}	{Group6=2.912524489572987E-6}	[ADRA1A, NKX2-5]	[ADRA1A, ADRA1D, APELA, APLNR, BMP10, CHD7, GJA1, HAND2, MEF2D, MNAT1, MYH6, MYH7, N	FALSE
GO:0010523	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of calcium ion transport into cytosol	[3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14]	[Group0]	3	11.111.111	1,39E+11	0.0029264419913142097	{Group0=1.393543805387719E-4}	{Group0=4.1806314161631566E-4}	[CALCA, CASQ2, NOS1]	[BCL2, CALCA, CALM1, CALM2, CALM3, CAMK2B, CASQ2, CLIC2, EPO, EPX, FKBP1B, FKBP9, GSTM2,	TRUE
GO:0010832	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of myotube differentiation	[6, 7, 8]	[Group6]	2	9.090.909	0.003063944337310526	0.012255777349242105	{Group6=4.854207482621646E-7}	{Group6=2.912524489572987E-6}	[NKX2-5, PLPP7]	[ANKRD2, BDNF, BDNF-AS, BHLHA15, BHLHE41, CEACAM3, CEACAM5, CFLAR, CXCL10, HDAC4, HDA	FALSE
GO:0010838	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	positive regulation of keratinocyte proliferation	[4, 5, 6, 7]	[Group7]	2	9.090.909	0.003063944337310526	0.012255777349242105	{Group7=2.8509622753718204E-12}	{Group7=2.5658660478346383E-11}	[REG3G, TP63]	[ASAP1, ASAP2, CDH15, CDH3, FGF10, FGF7, HAS2, HHIP, LPIN1, METTL9, MRPS30, PAPOLA, PDAP	FALSE
GO:0030299	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	intestinal cholesterol absorption	[4, 6, 7, 8]	[Group8]	3	15.0	5,53E+10	0.001438998178919702	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, CEL, LEP]	[ABCG5, ABCG8, ACAT2, AKR1C1, APOA1, APOA2, APOA4, APOA5, CD36, CDH11, CEL, LDLR, LEP, LI	FALSE
GO:0030300	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of intestinal cholesterol absorption	[5, 6, 7, 8, 9]	[Group7, Group8]	2	22.222.221	4,93E+11	0.008377772913190525	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[APOA1, LEP]	[ABCG5, ABCG8, APOA1, APOA2, APOA4, APOA5, CDH11, LEP, LPAL2]	FALSE
GO:0030889	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of B cell proliferation	[6, 7, 8, 9]	[Group8]	2	8.0	0.003950331078647926	0.003950331078647926	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[IL10, PROK1]	[ATM, BTK, CASP3, CD300A, CDK2, CDKN2A, CMM, CTLA4, F2RL3, FCGR2A, FCGR2B, FCGR2C, IL10,	FALSE
GO:0031034	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	myosin filament assembly	[5, 6, 7]	[Group4]	2	14.285.714	0.0012306668278873928	0.014768001934648714	{Group4=0.0012306668278873928}	{Group4=0.0024613336557747856}	[MYBPC2, MYBPH]	[IGSF22, MYBPC1, MYBPC2, MYBPC3, MYBPH, MYBPHL, MYH11, MYOM1, MYOM2, MYOM3, OBSL	FALSE
GO:0032095	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of response to food	[4, 6, 7]	[Group7, Group8]	2	9.523.809	0.002792164306308243	0.013960821531541214	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[CARTPT, LEP]	[BBS2, BBS4, CARTPT, CCK, CDH11, GHRL, GHSR, LEP, MDH2, MKKS, MT3, MTOR, NENF, NPFF, NP	FALSE
GO:0032096	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of response to food	[4, 5, 6, 7, 8]	[Group7, Group8]	2	14.285.714	0.0012306668278873928	0.014768001934648714	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[CARTPT, LEP]	[BBS2, BBS4, CARTPT, CCK, CDH11, GHSR, LEP, MKKS, NENF, NPFF, PPARA, RIPK2, SPX, UCN]	FALSE
GO:0032099	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of appetite	[4, 5, 6, 7, 8, 9]	[Group7, Group8]	2	14.285.714	0.0012306668278873928	0.014768001934648714	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[CARTPT, LEP]	[BBS2, BBS4, CARTPT, CCK, CDH11, GHSR, LEP, MKKS, NENF, NPFF, PPARA, RIPK2, SPX, UCN]	FALSE
GO:0032108	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of response to nutrient levels	[5, 6, 7]	[Group7, Group8]	2	10.0	0.0025323769147974373	0.015194261488784624	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[CARTPT, LEP]	[BBS2, BBS4, CACYBP, CARTPT, CCK, CDH11, GHSR, KANK2, LEP, MKKS, NENF, NPFF, PPARA, RBM1	FALSE
GO:0032488	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	Cdc42 protein signal transduction	[7, 8, 9]	[Group7, Group8]	2	11.111.111	0.002049147229283542	0.016393177834268337	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[APOA1, MTTP]	[ABCA1, ABL1, APOA1, APOC3, APOE, CDC42, HEATR6, MTTP, NAP1L1, NELL1, NRP1, NTN1, OPTN,	FALSE
GO:0032489	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of Cdc42 protein signal transduction	[8, 9, 10]	[Group7, Group8]	2	15.384.615	0.0010574230020981433	0.013746499027275863	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[APOA1, MTTP]	[ABCA1, ABL1, APOA1, APOC3, APOE, HEATR6, MTTP, NAP1L1, NELL1, NRP1, OPTN, RIT2, RNF7]	FALSE
GO:0033278	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	cell proliferation in midbrain	[3, 4, 6, 7, 8, 9]	[Group5]	2	18.181.818	7,49E+11	0.011238776685893749	{Group5=8.78624307038887E-8}	{Group5=6.150370149272209E-7}	[WNT1, WNT2]	[FZD3, FZD6, FZD9, INTS1, PITX3, PTX3, RYK, WNT1, WNT2, WNT3A, WNT5A]	FALSE
GO:0033605	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	positive regulation of catecholamine secretion	[4, 5, 6, 7, 8, 9]	[Group5, Group7]	2	16.666.666	8,97E+11	0.012556871568513055	{Group5=8.78624307038887E-8, Group7=2.8509622753718204E-12}	{Group5=6.150370149272209E-7, Group7=2.5658660478346383E-11}	[CARTPT, GDNF]	[CARTPT, CHRNB2, CXCL12, GDNF, GRK2, KCNB1, NPY2R, OPRK1, OXT, OXTR, PINK1, STX1A]	FALSE
GO:0034115	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of heterotypic cell-cell adhesion	[5, 6, 7, 8, 9]	[Group8]	2	14.285.714	0.0012306668278873928	0.014768001934648714	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, IL10]	[ADIPOQ, APOA1, IL10, IL1R1, IL1RN, KLF4, MAP2K5, MAPK7, MBL2, MBP, MYADM, PRG2, WNK1,	FALSE
GO:0034370	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	triglyceride-rich lipoprotein particle remodeling	[4, 5, 6, 7]	[Group8]	2	11.764.706	0.0018258897858015452	0.016433008072213907	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB]	[ANAPC2, APC2, APOA1, APOA2, APOA4, APOA5, APOB, APOC2, APOC3, APOE, CETP, LCAT, LCP1, L	FALSE
GO:0034371	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	chylomicron remodeling	[5, 6, 7, 8]	[Group8]	2	15.384.615	0.0010574230020981433	0.013746499027275863	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB]	[ANAPC2, APC2, APOA1, APOA2, APOA4, APOB, APOC2, APOC3, APOE, LCP1, LPAL2, LPL, SLC25A23	FALSE
GO:0034375	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	high-density lipoprotein particle remodeling	[4, 5, 6, 7]	[Group8]	2	9.090.909	0.003063944337310526	0.012255777349242105	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[ALB, APOA1]	[ABCA5, ABCG1, ALB, ANAPC2, APC2, APOA1, APOA2, APOA4, APOC1, APOC2, APOC3, APOE, APOM	FALSE
GO:0034378	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	chylomicron assembly	[4, 5, 6, 7]	[Group8]	3	16.666.666	3,98E+11	0.0011152466646060803	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB, MTTP]	[ANAPC2, APC2, APOA1, APOA2, APOA4, APOB, APOC2, APOC3, APOE, LPAL2, MT1B, MTTP, P4HB,	FALSE
GO:0034379	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	very-low-density lipoprotein particle assembly	[4, 5, 6, 7]	[Group7, Group8]	2	9.090.909	0.003063944337310526	0.012255777349242105	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[APOB, MTTP]	[ACAT1, ACAT2, ACSL3, APOB, APOC1, APOC3, APOC4, ARF1, ARF1P1, CASD1, CES1, DGAT1, MT1B	FALSE
GO:0042953	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	lipoprotein transport	[5, 6, 7, 8]	[Group7, Group8]	2	8.695.652	0.0033476258398223114	0.010042877519466933	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[APOB, MTTP]	[ANAPC2, APC2, APOB, APOBEC1, APOC2, ARNT, C1D, CD36, CUBN, HIP1R, LRP1, LRP2, MIA3, MSR	FALSE
GO:0045617	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of keratinocyte differentiation	[3, 4, 5, 6, 7, 8, 9]	[Group7]	2	10.0	0.0025323769147974373	0.015194261488784624	{Group7=2.8509622753718204E-12}	{Group7=2.5658660478346383E-11}	[REG3G, TP63]	[ASAP1, ASAP2, CDSN, GRHL2, HHIP, HOXA7, LPIN1, METTL9, MRPS30, MSX2, PAPOLA, PDAP1, RE	FALSE
GO:0045671	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of osteoclast differentiation	[6, 7, 8, 9, 10, 11, 12]	[Group7]	4	12.5	6,07E+09	1,94E+12	{Group7=2.8509622753718204E-12}	{Group7=2.5658660478346383E-11}	[CALCA, CARTPT, GPR55, SFRP1]	[ATR, CALCA, CARTPT, CCL3, CLDN18, FBN1, FBXO44, FBXW7, FSTL1, FSTL3, GPR55, IL4, INHBA, IN	TRUE
GO:0045779	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of bone resorption	[4, 5, 6, 7, 8]	[Group6, Group7]	2	14.285.714	0.0012306668278873928	0.014768001934648714	{Group6=4.854207482621646E-7, Group7=2.8509622753718204E-12}	{Group6=2.912524489572987E-6, Group7=2.5658660478346383E-11}	[CALCA, CARTPT]	[BTF3P11, CALCA, CARTPT, CD38, CLDN18, CSK, FSHR, IAPP, IL6, INPP5D, P2RX7, TNFAIP3, TNFRSF	FALSE
GO:0050908	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	detection of light stimulus involved in visual perception	[5, 6, 7]	[Group1]	2	11.111.111	0.002049147229283542	0.016393177834268337	{Group1=0.002049147229283542}	{Group1=0.002049147229283542}	[GRM6, RGS9BP]	[ATP8A2, BEST1, CACNA1F, CACNA2D4, CCDC66, CNGB1, EYS, GJA10, GJA9, GNAT1, GNAT2, GRM	TRUE
GO:0055003	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	cardiac myofibril assembly	[5, 6, 7, 8, 9, 10]	[Group6]	2	8.333.333	0.0036431181446800764	0.007286236289360153	{Group6=4.854207482621646E-7}	{Group6=2.912524489572987E-6}	[MUC2, NKX2-5]	[ACTC1, CALML3, COTL1, CSRP3, FHOD3, FMNL3, MARCKSL1, MEF2A, MUC2, MYL2, MYL9, MYLK,	FALSE
GO:0060431	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	primary lung bud formation	[4, 5, 6, 7, 8, 9, 10]	[Group5]	2	40.0	1,38E+12	0.0030410765484795797	{Group5=8.78624307038887E-8}	{Group5=6.150370149272209E-7}	[PRLH, WNT2]	[HHEX, PRLH, RDH10, WNT2, WNT2B]	FALSE
GO:0060525	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	prostate glandular acinus development	[4, 5, 6, 7, 8]	[Group7]	2	14.285.714	0.0012306668278873928	0.014768001934648714	{Group7=2.8509622753718204E-12}	{Group7=2.5658660478346383E-11}	[SFRP1, TP63]	[ATR, ESR1, FGFR2, FOXA1, FRS2, FSTL1, HOXB13, HOXD13, INHBA, NOTCH1, RXRA, SFRP1, TP63,	FALSE
GO:0060572	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	morphogenesis of an epithelial bud	[6, 7]	[Group5]	3	15.0	5,53E+10	0.001438998178919702	{Group5=8.78624307038887E-8}	{Group5=6.150370149272209E-7}	[PRLH, TP63, WNT2]	[AKR1B1, AR, AREG, BMP4, BMP7, FGF10, FGFR2, GLI2, HHEX, NOG, PRLH, RDH10, SHH, SOSTDC1	TRUE
GO:0070091	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	glucagon secretion	[6, 7, 8, 9]	[Group7, Group8]	2	14.285.714	0.0012306668278873928	0.014768001934648714	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[CARTPT, LEP]	[AIMP1, C1QTNF1, CARTPT, CDH11, CRH, EML2, FAM3D, GIP, GNAI2, IL6, LEP, PASK, STK39, SYT7]	FALSE
GO:0070092	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of glucagon secretion	[5, 6, 7, 8, 9, 10]	[Group7, Group8]	2	15.384.615	0.0010574230020981433	0.013746499027275863	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[CARTPT, LEP]	[AIMP1, C1QTNF1, CARTPT, CDH11, CRH, EML2, FAM3D, GIP, GNAI2, LEP, PASK, STK39, SYT7]	FALSE
GO:0070093	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	negative regulation of glucagon secretion	[5, 6, 7, 8, 9, 10, 11]	[Group7, Group8]	2	40.0	1,38E+12	0.0030410765484795797	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[CARTPT, LEP]	[CARTPT, CDH11, CRH, FAM3D, LEP]	FALSE
GO:0070365	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	hepatocyte differentiation	[5, 6, 7, 8]	[Group5]	3	13.043.478	8,53E+10	0.0019616368911192	{Group5=8.78624307038887E-8}	{Group5=6.150370149272209E-7}	[PRLH, SFRP1, WNT1]	[ANXA1, CPS1, CYP1A1, CYP21A2, E2F7, E2F8, FRZB, FSTL1, HHEX, HNF1A, HNF1B, HNF4A, INHBA,	FALSE
GO:0070586	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	cell-cell adhesion involved in gastrulation	[5, 6, 7]	[Group8]	2	13.333.333	0.001416555631598434	0.015582111947582775	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, IL10]	[ADIPOQ, APOA1, IL10, IL1R1, IL1RN, KLF4, MAP2K5, MAPK7, MBL2, MBP, MYADM, PRG2, RIC8A,	FALSE
GO:0070587	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of cell-cell adhesion involved in gastrulation	[4, 5, 6, 7, 8]	[Group8]	2	14.285.714	0.0012306668278873928	0.014768001934648714	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, IL10]	[ADIPOQ, APOA1, IL10, IL1R1, IL1RN, KLF4, MAP2K5, MAPK7, MBL2, MBP, MYADM, PRG2, WNK1,	FALSE
GO:0071688	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	striated muscle myosin thick filament assembly	[4, 5, 6, 7, 8]	[Group4]	2	15.384.615	0.0010574230020981433	0.013746499027275863	{Group4=0.0012306668278873928}	{Group4=0.0024613336557747856}	[MYBPC2, MYBPH]	[IGSF22, MYBPC1, MYBPC2, MYBPC3, MYBPH, MYBPHL, MYH11, MYOM1, MYOM2, MYOM3, OBSL	TRUE
GO:1904729	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of intestinal lipid absorption	[5, 6, 7]	[Group7, Group8]	2	22.222.221	4,93E+11	0.008377772913190525	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[APOA1, LEP]	[ABCG5, ABCG8, APOA1, APOA2, APOA4, APOA5, CDH11, LEP, LPAL2]	FALSE
GO:1904948	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	midbrain dopaminergic neuron differentiation	[4, 6, 7, 8, 9, 10]	[Group5]	3	13.636.364	7,44E+10	0.0018590999095197205	{Group5=8.78624307038887E-8}	{Group5=6.150370149272209E-7}	[SFRP1, WNT1, WNT2]	[ATR, CSNK1D, CSNK1E, CTNNB1, DKK1, FSTL1, FZD1, INHBA, INTS1, INTS4, LMX1A, LRP6, NR4A2,	FALSE
GO:1904953	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation	[5, 6, 7, 8, 9, 10, 11]	[Group5]	2	14.285.714	0.0012306668278873928	0.014768001934648714	{Group5=8.78624307038887E-8}	{Group5=6.150370149272209E-7}	[WNT1, WNT2]	[CSNK1D, CSNK1E, CTNNB1, FZD1, INTS1, INTS4, LRP6, RYK, WNT1, WNT2, WNT3, WNT3A, WNT5	FALSE
GO:1904954	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	canonical Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation	[6, 7, 8, 9, 10, 11, 12]	[Group5]	2	33.333.332	2,07E+12	0.003929997129045433	{Group5=8.78624307038887E-8}	{Group5=6.150370149272209E-7}	[WNT1, WNT2]	[CTNNB1, INTS1, INTS4, WNT1, WNT2, WNT3]	FALSE
GO:1905276	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of epithelial tube formation	[4, 5, 6, 7, 8]	[Group5, Group7]	2	9.090.909	0.003063944337310526	0.012255777349242105	{Group5=8.78624307038887E-8, Group7=2.8509622753718204E-12}	{Group5=6.150370149272209E-7, Group7=2.5658660478346383E-11}	[GDNF, SFRP1]	[ATR, CELSR1, DVL1, DVL1P1, DVL2, DVL3, FSTL1, FZD1, FZD2, GATA3, GDNF, GRHL3, INHBA, NPH	FALSE
GO:1990051	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	activation of protein kinase C activity	[9, 10, 11, 12]	[Group7, Group8]	2	50.0	8,31E+10	0.001995375988682884	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[LEP, MTTP]	[ABL1, CDH11, LEP, MTTP]	FALSE
GO:2000052	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	positive regulation of non-canonical Wnt signaling pathway	[5, 6, 7, 8, 9, 10]	[Group7, Group8]	2	12.5	0.0016149946876273084	0.016149946876273084	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[MTTP, SFRP1]	[ABL1, ANKRD6, ATR, CSNK1D, CSNK1E, DAB2, DKK1, FSTL1, GPC3, INHBA, MLLT3, MTTP, NKD1, R	FALSE
GO:2000095	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of Wnt signaling pathway, planar cell polarity pathway	[6, 7, 8, 9, 10]	[Group7, Group8]	2	11.111.111	0.002049147229283542	0.016393177834268337	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[MTTP, SFRP1]	[ABL1, ANKRD6, ATR, DAB2, DACT1, DKK1, FSTL1, GPC3, INHBA, MKS1, MLLT3, MTTP, NKD1, NPHP	FALSE
GO:2000269	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	regulation of fibroblast apoptotic process	[6, 7]	[Group7]	2	11.111.111	0.002049147229283542	0.016393177834268337	{Group7=2.8509622753718204E-12}	{Group7=2.5658660478346383E-11}	[SFRP1, TP63]	[API5, ATR, BCL2L11, BID, BTG1, CFDP1, FSTL1, GAS6, IER3IP1, INHBA, PIK3CA, PIK3CG, PRDM11,	FALSE
GO:2000271	GO_BiologicalProcess-EBI-UniProt-GOA_04.09.2018_00h00	positive regulation of fibroblast apoptotic process	[6, 7, 8]	[Group7]	2	18.181.818	7,49E+11	0.011238776685893749	{Group7=2.8509622753718204E-12}	{Group7=2.5658660478346383E-11}	[SFRP1, TP63]	[ATR, BCL2L11, BID, BTG1, FSTL1, INHBA, PRDM11, SFRP1, STK17A, STK17B, TP63]	FALSE
KEGG:04975	KEGG_04.09.2018	Fat digestion and absorption	[-1]	[Group8]	6	14.634.147	9,16E+06	3,11E+08	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB, CEL, FABP1, MTTP, PLA2G2F]	[ABCA1, ABCG5, ABCG8, ACAT2, AGPAT1, AGPAT2, APOA1, APOA4, APOB, CD36, CEL, CLPS, DGAT	TRUE
KEGG:04977	KEGG_04.09.2018	Vitamin digestion and absorption	[-1]	[Group8]	2	8.333.333	0.0036431181446800764	0.007286236289360153	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB]	[ABCC1, APOA1, APOA4, APOB, AWAT2, BTD, CUBN, FOLH1, GIF, LMBRD1, LRAT, MMACHC, PLB1,	FALSE
R-HSA:2168880	REACTOME_Pathways_04.09.2018	Scavenging of heme from plasma	[-1]	[Group8]	3	23.076.923	1,41E+11	4,39E+12	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[ALB, APOA1, JCHAIN]	[ALB, AMBP, APOA1, APOL1, CD163, HBA1, HBA2, HBB, HP, HPR, HPX, JCHAIN, LRP1]	FALSE
R-HSA:2173782	REACTOME_Pathways_04.09.2018	Binding and Uptake of Ligands by Scavenger Receptors	[-1]	[Group8]	4	9.523.809	1,84E+10	5,51E+11	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[ALB, APOA1, APOB, JCHAIN]	[ALB, AMBP, APOA1, APOB, APOE, APOL1, CALR, CD163, CD36, COL1A1, COL1A2, COL3A1, COL4A1,	FALSE
R-HSA:2453902	REACTOME_Pathways_04.09.2018	The canonical retinoid cycle in rods (twilight vision)	[-1]	[Group3]	3	13.043.478	8,53E+10	0.0019616368911192	{Group3=8.528856048344347E-5}	{Group3=3.411542419337739E-4}	[ABCA4, RDH8, SDR9C7]	[ABCA4, CYP4V2, DHRS9, HSD17B1, HSD17B6, LRAT, MYO7A, NAPEPLD, RBP1, RBP3, RBP4, RDH10	TRUE
R-HSA:3000471	REACTOME_Pathways_04.09.2018	Scavenging by Class B Receptors	[-1]	[Group8]	2	33.333.332	2,07E+12	0.003929997129045433	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB]	[APOA1, APOB, CD36, SAA1, SCARB1, SSC5D]	FALSE
R-HSA:3000480	REACTOME_Pathways_04.09.2018	Scavenging by Class A Receptors	[-1]	[Group8]	2	10.526.316	0.0022846738316462155	0.01599271682152351	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB]	[APOA1, APOB, APOE, CALR, COL1A1, COL1A2, COL3A1, COL4A1, COL4A2, COLEC11, COLEC12, FTH	FALSE
R-HSA:3772470	REACTOME_Pathways_04.09.2018	Negative regulation of TCF-dependent signaling by WNT ligand antagonists	[-1]	[Group7]	2	13.333.333	0.001416555631598434	0.015582111947582775	{Group7=2.8509622753718204E-12}	{Group7=2.5658660478346383E-11}	[DKK2, SFRP1]	[DKK1, DKK2, DKK4, KREMEN1, KREMEN2, LRP5, LRP6, SFRP1, SFRP2, SOST, WIF1, WNT3A, WNT4	FALSE
R-HSA:8866423	REACTOME_Pathways_04.09.2018	VLDL assembly	[-1]	[Group7, Group8]	2	40.0	1,38E+12	0.0030410765484795797	{Group7=2.8509622753718204E-12, Group8=7.798171475204094E-11}	{Group7=2.5658660478346383E-11, Group8=6.238537180163275E-10}	[APOB, MTTP]	[APOB, APOC1, APOC4, MTTP, P4HB]	FALSE
R-HSA:8963888	REACTOME_Pathways_04.09.2018	Chylomicron assembly	[-1]	[Group8]	3	33.333.332	4,20E+09	1,39E+12	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB, MTTP]	[APOA1, APOA2, APOB, APOC2, APOC3, APOE, MTTP, P4HB, SAR1B]	FALSE
R-HSA:8963898	REACTOME_Pathways_04.09.2018	Plasma lipoprotein assembly	[-1]	[Group8]	3	16.666.666	3,98E+11	0.0011152466646060803	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB, MTTP]	[A2M, ABCA1, APOA1, APOA2, APOB, APOC1, APOC2, APOC3, APOC4, APOE, BMP1, MTTP, P4HB,	FALSE
R-HSA:8963899	REACTOME_Pathways_04.09.2018	Plasma lipoprotein remodeling	[-1]	[Group8]	3	10.0	1,92E+12	0.003837464836709233	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[ALB, APOA1, APOB]	[ABCG1, ALB, ANGPTL3, ANGPTL4, ANGPTL8, APOA1, APOA2, APOA5, APOB, APOC2, APOC3, APO	FALSE
R-HSA:8963901	REACTOME_Pathways_04.09.2018	Chylomicron remodeling	[-1]	[Group8]	2	22.222.221	4,93E+11	0.008377772913190525	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[APOA1, APOB]	[APOA1, APOA2, APOA5, APOB, APOC2, APOC3, APOE, GPIHBP1, LPL]	FALSE
R-HSA:8964058	REACTOME_Pathways_04.09.2018	HDL remodeling	[-1]	[Group8]	2	20.0	6,15E+11	0.009832262924133828	{Group8=7.798171475204094E-11}	{Group8=6.238537180163275E-10}	[ALB, APOA1]	[ABCG1, ALB, APOA1, APOC2, APOC3, APOE, CETP, LCAT, LIPG, PLTP]	FALSE



OS

RFS

Supplementary Figure 1. Survival curves for OS and RFS comparing N^{pos} patients stratified according to aDC enrichments.



Supplementary Figure 2. The proliferation of PANC-1 and MIAPaca-2 after XAV-939 treatment was evaluated by MTT assay at 0, 24, 48 h. Bars represent the mean ± SD, n = 5.

Supplementary Table 1. Gene Expression profile summary comparison between survival characteristics from 176 patients divided in high- and low-expressers from TCGA dataset [62-64].

	Total cohort patients (n=176)	
Gene	***P* score**	**5-years survival high vs low**
WNT-2	**0.014**	10% vs 36% (n=133 vs 43)
ANGPTL4	**0.0097**	20% vs 53% (n=137 vs 39)
Dkk-1	**0.00013**	19% vs 57% (n=135 vs 41)
FGF basic	**0.00098**	9% vs 36% (n=48 vs 128)
MST1	**0.00071**	53% vs 12% (n=49 vs 127)