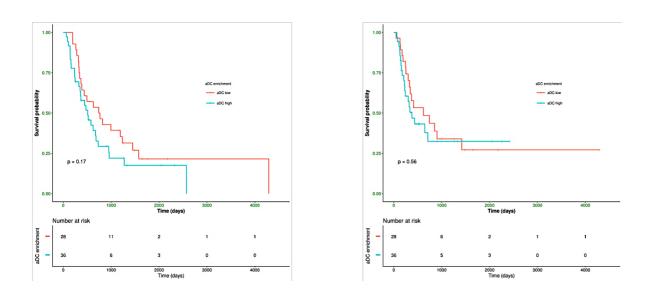
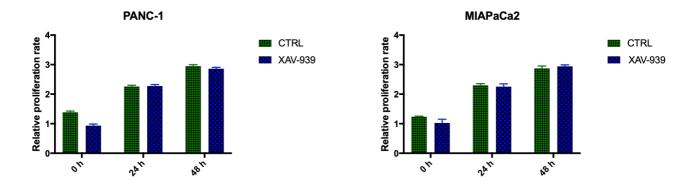
File S1: List of significant terms and the related genes involved in the KEGG, GO Biological Process, Reactome pathway and GO immune system process databases network enrichment showed in Figure 3 (a) and (b).

| | Ontology Source GOTerm | GOLevels | 60Groups | | | ted Genes Tenn Pivalue | Term Pilalue Corrected v | ith Bonferroni step down Group Pitalue | Group Ph'alue Corrected with Bonferroni step down | Associated Genes Found | All Associated Genes |
|--|--|---|--|---|---|--|---|---|---|---|--|
| G:00005759 (| GO_BiologicalProcess-681-UniProt-GOA_06.09.2018_00900 organ induction | [3,4,5,6,7,8,9] | [Groupi, Group?] | 2 | | | 6800764 0.007286236289360553 | (GroupS+R 79624307038887N-R, Group7+2 8509622753718204E-12) | (Group5+6.1503701492722096-7, Group7+2.56586604793463836-11) | [GDNF, WNT2] | [AKK181, AR, ARSG, BMP2, BMP4, DKK1, FGF1, FGF10, FGFR, FGFR1, FLG, FRS2, GATAS, GDNF |
| G:00005976 (| GO_BiologicalProcess-EBI-UniProt-GOA_06.09.2018_00h00 neurological system process involved in regulation of systemic arterial blood pressure | [4, 5, 7] | [Group6, Group7] | 2 | 1 | 11 111 111 0 0020495472 | 1283542 0.016393177834268337 | (Group6+4.9542074826216466-7, Group7+2.95096227537182046-12) | (Group6+2.9125244895729876-6, Group7+2.56586604783463836-11) | [ADRASA, CALCA] | [ACE2, ADRASA, ADRASD, AGT, AGTR2, AGNT, ANHXS, ASIC2, CALCA, DRD2, MECP2, NAV2, P2RX |
| G:0005978 (| GO BiologicalProcess-Bit-UniProt-GOA 06:09:2018 00:00 Impulation of systemic arterial blood pressure by carotid sinus baromorestor feedback | [5, 6, 7, 8, 9] | [Group6, Group7] | 2 | - 6 | 96,696,664 | 4.175+11 0.001125136275785625 | 1G10up6+4.8542074826216466-7, G10up7+2.85096227537182046-125 | (Grpup6+2.912524489572987K-6, Grpup7+2.56586604793465835-11) | (ADRA1A, CALCA) | (ADRAIA ADRAID CALCA) |
| C 5892000 C | GO, BiologicalProcess-EBI-UniProt-GOA, 06.09.3018, 00h00 barrowceptor response to increased systemic arterial blood pressure | [6, 7, 8, 9, 10] | 16 roupi, Group? | | - 6 | 56 666 664 | 4.175+11 0.001125136275785625 | Group6+4.9542074826216466-7, Group7+2.96096227637182046-12 | (Group6-2 9125244995729976-6, Group7-2 56596604793463936-11) | [ADRASA, CALCA] | (ADRAIA, ADRAID, CALCA) |
| | GO, BiologicalProcess-68: UniProt -GOA, 06.09.2018, 00h00 vegulation of the force of heart contraction | 13.6.71 | (Group) | - 4 | | 0 000 000 | 2.626+11 | 7,086+11 (Group2+2-02668112971876976-6) | (Group2+5.21229056485938496-4) | (ADRALA, MUCZ, MYLR, NOS1) | (ADM, ADRAIA, ADRAID, ADRRI, APLN, ATF7/P, ATPIAI, ATPIAI, ATPIAI, ATPIAI, ATPIAI, ATPIAI, ATPIAI, ATPIAI, ATPIAI |
| | GO, BiologicalProcess-Eit-UniProc GOA, 06.09.2018, 00h00 vigulation of cytoline secretion involved in immune response | [5, 6, 7, 8, 9, 10, 11] | [Groupk] | | | 6 coc cra la sessa varacce | 8223114 0.010042977519466933 | (Grouph/7.7981714752040946-11) | (Grouph 6.2385371801632756-10) | (APOA1, ILIO) | TAICS, ANGETT, APOAT, APOAT, ASP, ASPA, ASPM, ATGS, CR, FZRLT, HNRNPK, ILID, KARS, LILR |
| | | [5, 6, 7, 8, 9, 10, 11, 12] | (Groupi) | | | 9 C21 A29 | 3 895 411 0 005 1997 16307 6322939 | (Grouph 7.7981714752040961-11) | 16mmalus 2005271011522755.415 | (ARCAT ILLO) | (ANGPT), APOAS, APOAS, ILSO LURBS, LPALS, TIM! |
| | GO_BiologicalProcess-EBI-UniProt-GOA_66.09.2018_00b00 negative regulation of cytokine secretion involved in immune response | | | | 40.0 | 28.5/1.428 | 1 395+13 0.006199796937627929 | Groups 7.74817187330098-11) Groups 4.8642074836216466-7, Group7+2.86096227517282046-12) | [Group6-2.9125244995729876-6.Group7-2.56586604793463935-11] | (ADRAIA, CALCA) | |
| 0.0000003 | GO_BiologicalProcess-EBI-UniProt-GOA_64.09.2018_00h00 regulation of systemic arterial blood pressure by baraneceptor feedback | [5,6,4] | (Groupé, Group?) | | 40.0 | | 1,884+13 (0.00000110%5488278578 5663155 (0.01599275682152251 | | | MORATA CALCAL | [ADRAIA, ADRAID, ASIC2, CALCA, NAV2] |
| | GO_BiologicalProcess-68n-uniProt-GOA_08.09.2018_00h00 negative regulation of systemic arterial blood pressure | [3, 7] | (Groups, Group?) | | | | ###2114 0.01149271##2112811 ############################# | (Group6-4.8542074826216466-7, Group7+2.86096227637182046-12) | [Group6-2 9125246995729876-6, Group7-2 56586608783463836-11] | DARKASA, CALCAL DARKASA, CALCAL | ADDRAI, ADRAIA, ADRAID, ADREI, ADREI, ADREI, AGTRI, ARHGAPEI, BESS, BAPS, BAPS, |
| | GO_BiologicalProcess-68t-UniProt-GOA_06.09.2018_00h00 cardiac chamber formation | [3,4,6,6,7,4,6] | (Groups) | 2 | | 16.666.666 | | (G10up6+4.8543074836216466-7) | (Group6+2-9135344895729876-4) | | |
| 0.0008211 0 | GO_BiologicalProcess-Bit-UniProt-GOA_08.09.2018_00h00 cardiac wentricle formation | [4, 5, 6, 7, 8, 9, 20] | [Group6] | 2 | 20.0 | | 6,156+11 0.009832262924133828 | (G10up6+4.8542074826216466-7) | (Group6+2-9125244895729876-4) | [HANDS, NOO2-6] | [HANDS, HANDS, MEF2C, MESPS, NOX2-5, NOTCHS, SMARCDR, SCHIS, SCHIS, SCHIS, TEXE] |
| 0.0000315 | GO_BiologicalProcess-681-UniProt-GOA_06.09.2018_00900 cardiac right westicle morphogenesis | [5, 6, 7, 8, 9, 10] | [Groupii] | 2 | | | 6800764 0.007286236289360553 | (Groupé-4.8542074826216466-7) | (Group6+2:9125244895729876-6) | [HANDS, NIXX2-5] | [BMPRIA, O407, FOIH1, GATA3, GATA4, GDF1, HAND1, HAND2, HERPUD1, HEY2, ISL1, JAG1, NI |
| G:0007512 (| GO BiologicalProcess-SBI-UniProt-GOA 06.09.2018 00h00 adult heart development | [5, 6, 7] | (Groupi) | 2 | 12.5 | 0.0016169996 | 6279084 0.016149946876279084 | (Groups-4.8542074826216466-7) | (Grpup6+2.9125244899729876-6) | [ADRALA, NIXX2-5] | TADRATA, ADRASD, APELA, APLINE, BMPSD, CHD7, GSAS, HANDZ, MEF2D, MNATS, MYH6, MYH7, |
| G:00010523 0 | GO, BiologicalProcess-EBI-UniProt-GOA, 06.09.3018, 00h00 registive regulation of calcium ion transport into cytosol | [3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 18, 14] | (Group)) | - 3 | - 1 | 11.111.111 | 1.395+11 0.002926441991314209 | (Group):1.2995439052877196-6) | (Grouptive 180681416168115666-4) | TONICA, CASOD, NOSSI | TBCLZ, CALCA, CALMS, CALMS, CALMS, CAMAGR, CASGO, CLICZ, EPO, EPX, FEBPSR, FEBPS, GSTM |
| | GO, BiologicalProcess-EBI-UniProt-GOA, 06.09.3018, 00h00 regative regulation of reyonable differentiation | [6, 7, 8] | (Groupi) | | | e non eng 'n mancaskea: | 1300526 0.012255777349242105 | (Group6-4.8542074826216466-7) | 16/pup6+2.9125244895729876-62 | DIOQ-5, PLPFT | (ANKROZ, BONF, BONF-AS, BHLHA1S, BHLHEEL, CEACAMS, CEACAMS, CFLAR, CYCLIO, HOACE, H |
| | GO, BiologicalProcess-Eill-UniProt-GOA, 06.09.2018, 00h00 positive regulation of Nertalinocyte proliferation | [4, 5, 6, 7] | [Group?] | | | | 300526 0.012255777349242105 | (Group?v2.850962275)7182095-121 | (Graup7+2 56586604788463836-11) | (REGIS, TREE) | TASAPI, ASAP2, CONES, CONES, FGF10, FGF7, HAS2, HMP, LPINE, METTER, MRPSR0, PAPOLA, POR |
| | GO_BiologicalProcess-681-uniProt-GOA_08.09.2018_00h00 intentival cholesterol absorption | [4, 6, 7, 8] | [Groupk] | | 15.0 | T.000.007 C.0030039045 | 5.535+10 0.005438998178919702 | (Grouple? 7981714752040945-11) | (Grouph 6.2385871801682756-10) | [APOA1, CEL, LEP] | (ABCGS, ABCGR, ACAT2, ARRIC1, APOA1, APOA2, APOA4, APOA5, CD45, CD411, CEL, LDLR, LEP, |
| | | | (Group?, Group#) | | | 22 222 224 | 4 935 411 0 009277779913199535 | (Janachas v. sant variancement et) | (Group?+2.56596604790463905-11. Group8+6.2395371901632756-10) | pron, or, or | TABLES ABOSE ABOSE ABOAT ABOAT ABOAT ABOAT MUST LED IDALT! |
| | GO_BiologicalProcess-68t-UniProt-GOA_08.09.3018_00h00 regulation of interctinal challesterol absorption | [5, 6, 7, 8, 9] | | | | | | | | | |
| 0030889 | GO_BiologicalProcess-GBI-UniProt-GOA_08.09.3018_00h00 negative regulation of B cell proliferation | [6,7,8,9] | (Groupk) | 2 | 8.0 | | 647926 0.009950331079647926 | (Groupkr7.7981714752040946-11) | {Group8=6.2385971801692756-10} | [ILSO, PROKS] | (ATM, BTK, CASPR, CD900A, CDK2, CDKN2A, CMM, CTLA4, F2RL3, F0GR2A, F0GR2B, F0GR2C, ILS |
| | GO_BiologicalProcess-Sitr-UniProt-GOA_08.09.2018_00h00 myosin filament assembly | [5, 6, 7] | (Groupt) | 2 | | | 9872928 0.014768001934648714 | (G10upti-0.0012306668278873928) | (Group4 d 0024613336557747856) | [MWRC, MWRH] | [IGSF22, MYRPC1, MYRPC2, MYRPC3, MYRPH, MYRPH, MYR11, MYOM1, MYOM2, MYOM3, OR |
| 0032095 | GO_BiologicalProcess-Bit-UniProt-GOA_06.09.2018_00900 regulation of response to food | [4,6,7] | [Group?, Groupii] | 2 | | | 308243 0.013960821531541214 | | {Group3+2.56586604783463836-11, Group8+6.2385371801632756-10} | | [BBS2, BBS4, CARTPT, COX, COH11, GHR1, GHSR, LEP, MDH2, MHS5, MTX, MTDR, NENF, NPFF, N |
| 0032096 0 | GO_BiologicalProcess-681-UniProt-GOA_06.09.2018_00900 negative regulation of response to food | [4, 6, 6, 7, 8] | [Group?, Group#] | | | | 9873928 0.014768001934648714 | (Group7v2.85086227597182046-12, Group8v7.7981714753040946-11) | (Group7+2 5658660478346383E-11, Group8+6-238537180163275E-10) | [CARTPT, LEP] | [BBS2, BBS4, CARTPT, COX, CDHS1, GHSR, LEP, MKKS, NENF, NPFF, PPHRA, RIPK2, SPX, LICN] |
| 0032099 0 | GO Biologica/Process-681-UniProt-GOA 06.09.2018 00900 Inequirie resultation of appetite | [4.5.6.7.8.9] | (Group?, Group#) | 2 | - 1 | 14.285.714 0.0012306668 | 19872928 0.014768001934648714 | (Group?v2.860962275)?182046-12, Group8v?.7981714753040946-11) | (Group7+2-56586604780463806-11, Group8+6-2085371801632756-109 | TOWATRY, USPY | TBBS2, BBS4, CARTPT, CCX, CDHS1, GHGR, LEP, MKKS, NENF, NPFF, PPARA, RIPK2, SPX, LICN) |
| | GO, BiologicalProcess-Eib-UniProt-GOA, 06.09.2018, 00h00 regative regulation of response to nutrient lewis | [5, 6, 7] | [Group?, Groupil] | | 10.0 | | 7974373 0.025294261488788624 | | {Group7+2.5658660478946389E-11, Group8+6.238537180163275E-10} | | 18852 8854, CACYRP, CARTPT, COX CDH11, GHGR, KANKZ, LEP, MKKS, NENE, NPFF, PPHRA, RBF |
| | GO_BiologicalProcess-681-uniProt-GOA_08.09.2018_00h00 Cdot2 protein signal transduction | [2, 8, 9] | [Group?, Groupil] | | | | 1990647 0.016393177934368337 | | (Group?+2.56586604780463806-11. Group8+6.2385371801632756-10) | | (ABCA1 ABL1 APOA1 APOC3 APOC CDC12 HEATRE MTTP NAP1L1 NELL NRP1 NTN1 OPT |
| | | | (Group?, Group#) | | | | 10981433 0.013746499027275863 | | | | |
| | GO_BiologicalProcess-68I-UniProt-GOA_66.09.2018_00b00 vegulation of Cdo62 protein signal transduction | [8, 9, 10] | | | | 15.886.625 (J.0020576290) 10.191.010 | 7 #05411 0.012764699027274864 | | [Group7+2:5658660478346389E-11, Group8+6:238537180163275E-10] | | [ABCA1, ABL1, APOA1, APOC3, APOE, HEATRE, MTTP, NAPIL1, NELL1, NRP1, OPTN, RIT2, RNF7] |
| | GO_BiologicalProcess-68t-UniProt-GOA_66.09.2018_00b00 cell proliferation in midbrain | [3,4,6,7,8,9] | (Groupii) | . 2 | | | | (G104pG+8.796248070388876-8) | {Group5+6.1503701492722096-7} | [WNTS, WNTS] | [F208, F206, F209, INTS1, PITKS, PTKS, RYK, WINTS, WINTS, WINTSA, WINTSA] |
| | GO_BiologicalProcess-GBI-UniProt-GOA_08.09.3018_00h00 positive regulation of catecholamine secretion | [4, 5, 6, 7, 8, 9] | (Groups, Group?) | 2 | | 16.666.666 | 8,876+11 0.012556871568513055 | (GroupS-9.79624907098887K-9, Group7+2.8509622759718204E-12) | [Group5=6.1503701482722096-7, Group7+2.56586608783469836-11] | | [CARTFT, CHRNB2, CKCL12, GONF, GRK2, KONB1, NP/2R, CPRKS, CRT, CRTR, PINKS, STKSA] |
| 0034115 0 | GO_BiologicalProcess-Bit-UniProt-GOA_06.09.2018_00900 negative regulation of heterotypic cell-cell adhesion | [5, 6, 7, 8, 9] | (Groupk) | 2 | 1 | 14.285.714 0.0012306668 | 9873928 0.014768001934648714 | (Grouph/7.7981714752040946-11) | (Groupilinis 2385371801632756-10) | [APOA1, IL10] | [ADIPOQ, APOA1, IL10, IL181, IL18N, KLF4, MAP2KS, MAPK7, MBL2, MBP, MYADM, PRG2, WINKS |
| 0034370 | GO_BiologicalProcess-681-UniProt-GOA_06.09.2018_00900 | [4, 6, 6, 7] | [Groupk] | 2 | | | 8015452 0.016433008072213907 | (Grouph/7.7981714752040946-11) | (Group8+6-2385971801692756-10) | [APOA1, APOR] | (ANAPC2, APC2, APOA1, APOA2, APOA4, APOA5, APOR, APOC2, APOC3, APOE, CETP, LCAT, LCP1, |
| 0034971 0 | GO Biologica/Process-681-UniProt-GOA 06.09.2018 00000 chilomicton remodeling | [5, 6, 7, 8] | (Groupk) | 2 | - 1 | S 384 615 0.00105742301 | 10981433 0.013746499027275863 | (Grouph/7,7981714752040945-11) | (Group#+6-2385371801632256-10) | [APOA1, APOR] | TANAPCZ, APCZ, APOA1, APOA2, APOA4, APOB, APOC2, APOC3, APOE, LCP1, LPAL2, LPL, SLC2SAC |
| 0034325 | GO Biologica/Process-681-UniProt-GOA 06.09.2018 00000 high-density lipportation particle remodeling | [4, 5, 6, 7] | [Groupk] | | | e non eng 'n mancassus: | 1300526 0.012255777349242105 | (Grouph/7,7981714752040945-11) | (Group#+6-2385371801632256-10) | [ALR. APDA1] | TABCAS, ABCG1, ALR. ANAPC2, APC2, APGA1, APGA2, APGA4, APGC1, APGC2, APGC3, APGS, AP |
| 9034279 V | GO BiologicalProcess-Bill-UniProt GOA, 08.09.2018, 00900 Chylomicson assembly | 14.5.6.71 | (Genunit) | | | 6 666 666 | 3 995+11 /3 /9911153/66646/36999 | (Garage 7 Not 7147CNA004C-11) | (Grounded, 1965)(1965)(1955, 48) | (APOA1, APOR, MTTP) | TANAPCZ, APCZ, APOA1, APOA2, APOA4, APOR, APOC2, APOC3, APO6, LPAL2, MT18, MTTP, PBH |
| 9034279 V | GO BiologicalProcess-68-uniProt GOA, 06.09.2018, 00th00 very-low-denoty (approximin particle accentity | 14.5.6.71 | (Group?, Groupit) | | | 6 000 000 to 0000 Table 1 | DOOGNG 00.0177557772463407405 | (Group?+2.65062275)7162065-12. Group8+7.7961714753040945-11) | (Group?+2.56586604783463836-11. Group8+6.2385371801632756-109 | MPOR MITTEL | TACAT'S ACATZ ACSS APOR APOCS APOCS APOCS ARE'S ARESPS CASOS CESS DEATS MIT |
| | GO_BiologicalProcess-681-uniProt-GOA_08.09.2018_00h00 Spoprosein transport | | (Group?, Group#) | | | | 8223114 0.010042877519466933 | | (Group?+2.56586604780463806-11. Group8+6.2385371801632756-10) | | (ANAPCE APCE APOR APOSECS APOSE ARVIT CSD. CDG. CURN. HPSR. URPS. MPSR. MRS. MC |
| 0065874 | AD_BiologicaProcess-san-craffice-scox_discretizationscoll repopulation transport | [5, 6, 7, 8] | | | | | 19274114 (3.030062977519896984 17974373 (3.045484351499794534 | | | | |
| | GO_BiologicalProcess-EBI-UniProt-GOA_04.04.09.2018_00h00 negative regulation of levatinocyte differentiation | [3, 4, 5, 6, 7, 8, 9] | (Group?) | | 10.0 | 0.0025323769 | | (Group7+2.85096227597182086-12) | (Group7+2.56586604788463836-11) | [REG3G, TP63] | (ASAPS, ASAP2, COSN, GRHL2, HHP, HORK?, LPINS, METTLR, MRPS30, MSX2, PAPOLA, PDAPS, R |
| | GO_BiologicalProcess-68i-UniProceGOA_06.09.2018_00h00 negative regulation of oxecutant differentiation | [6, 7, 8, 9, 10, 11, 12] | (Group?) | | 12.5 | | 6,075+09 | 1,846+12 (Group7v2.86096227537182065-12) | (Group7+2-56586604789463836-11) | [CALCA, CARTIFT, GPRSS, SFRP1] | [ATR, CALCA, CARTPT, CCLR, CLON1R, FBIN1, FBINDM, FBIXW7, FSTL1, FSTL1, GPRSS, IL4, INHBA, |
| 0045779 0 | GO_BiologicalProcess-Bit-UniProt-GOA_06.09.2018_00t00 negative regulation of bone recorption | [4, 6, 6, 7, 8] | [Group6, Group7] | 2 | 1 | 14.285.714 0.0012306668 | 9873928 0.014768001934648714 | (Group6+4.8542074826216466-7, Group7+2.85096227637182046-12) | (Group6+2.912524489572987K-6, Group7+2.5658660478346383E-11) | [CALCA, CARTIPT] | [BTF3P11, CALCA, CARTPT, CDGR, CLDN1R, CSK, FSHR, IAPP, E.G., INPPSD, P2RX7, TNFAIP3, TNFR1 |
| 0090908 0 | GO_BiologicalProcess-681-UniProt-GOA_06.09.2018_00h00 detection of light stimulus involved in visual perception | [5, 6, 7] | [Groupt] | 2 | 1 | 11 111 111 0 0020495472 | 1283542 0.016393177834268337 | (Groups+0.002089147229283642) | (Groups +0.002069147229282642) | [GRM6, RGS98P] | (ATPRAZ, BEST1, CACNA1F, CACNA2DA, CCDCGG, CNGB1, EYS, GIA10, GIAR, GNAT1, GNAT2, GR |
| 0055008 0 | GO_BiologicalProcess-681-UniProt-GOA_06.09.2018_00900 cardiac myofibril assembly | [5, 6, 7, 8, 9, 10] | [Group6] | 2 | | 8 333 333 0 0036431181 | 6800764 0.00728623628936253 | (Groups-4.8542074826216466-7) | (Grpup6+2.9125244899729876-6) | [MUC2, MO2-5] | (ACTC1, CALMLR, COTL1, CSRPR, FHOOR, FMNLR, MARCKSL1, MEF2A, MUCZ, MYLZ, MYLR, MYLK |
| | GO, BiologicalProcess-SBI-UniProt-GOA, 08.09.3018, 00h00 primary lung bud formation | [4, 5, 6, 7, 8, 9, 20] | [Grouph] | | 40.0 | | 1 395413 0 000041035549439539 | 1G10446-8.786243070388876-8 | 16/rpup5+6.1503701492722096-75 | IPRIH WNT2I | THIREX, PRIJH, ROHGO, WINTZ, WINTZRI |
| 0060535 | GO, BiologicalProcess-Eili-UniProt-GOA, 06.09.2018, 00h00 proctate glandular acinux development | [4, 5, 6, 7, 8] | 16rpup?1 | | | 4 200 Te 4 0 004 22000000 | 19972929 0.014769001924649714 | 3Garus 7v.7 9G86G2222G2748269G-125 | 16mm/3/2 66686604393463936.111 | NGRIN TRGIT | TATE COST COCES COVER CECT COTTS MOVERS MOVED INMER NOTICES BYEN COST TEC |
| | SO Biologica/Pozero-Ell-UniProt GOA 60.09.2018 00000 Incontingention of an eathering but | [6.7] | (Groupi) | | 15.0 | DE 281.724 D.00123000000. | 5 535+10 0 0014339999179919700 | Group's 29624007098875-80 | (Group's 5500791492722096-7) | IPRIH TPGS, WNT21 | TAXRIBL AR AREG BMP4 BMP7 FGF10 FGFR2 GLIZ HHEX NOG PRIH ROHID SHK SOSTO |
| | SO Biologica/Pozes-68-UniProt GOA 0.09.2018 00000 incurrent secretion | | | | | | 19873939 (1.03476900+93464974.4 | | (Group?+2.56596604790463905-11. Group8+6.2395371901632756-10) | | TAMP1 CIOTNET CARTET CON11 CRH SMI2 FAMSO GIP, GNA2 ILE LEP PASK STKSR SYT |
| | | [6,7,8,9] | [Group?, Groupil] | | | | | | | | |
| | GO_BiologicalProcess-Bit-UniProt-GOA_08.09.2018_00h00 regulation of glucagon secretion | [5, 6, 7, 8, 9, 10] | [Group?, Groupil] | | | 15.384.615 (0.0010574230) | 10981433 0.013746499027275863 | | (Group7+2 56586604783463836-11, Group8+6 2385371801632756-10) | | [AMP1, C1QTNF1, CARTFT, CDH11, CRH, EM12, FAM90, GIP, GNAI2, LEP, PASK, STK99, SYT7] |
| 0070098 | GO_BiologicalProcess-Bit-UniProt-GOA_06.09.2018_00900 regative regulation of glucagon secretion | [5, 6, 7, 8, 9, 10, 11] | [Group?, Groupii] | 2 | 40.0 | | 1,385+12 0.000041076548479579 | (Group?v2.85096227587182086-12, Group8v7.7981714753040946-11) | {Group3+2.56586604783463836-11, Group8+6.2385371801632756-10} | [CARTPT, LEP] | [GARTPT, CDH11, CRH, FAMRD, LEP] |
| 0070365 | GO_BiologicalProcess-681-UniProt-GOA_06.09.2018_00900 hegatocyte differentiation | [5, 6, 7, 8] | [Grouph] | 3 | 1 | 13.063.478 | 8,586+10 0.0059616368911192 | (GroupS-9, 7962 63070388879-9) | {Group5+6.1509701492722096-7} | [PRIH, SERP1, WNT1] | [ANNA1, CP61, CYP1A1, CYP21A2, E2F7, E2FR, FRZR, FSTL1, HHEX, HNF1A, HNF1R, HNF4A, INHR |
| | GO, BiologicalProcess-EBI UniProt-GOA, 06.09.3018, 00h00 cell-cell adhesion involved in gastrulation | [5, 6, 7] | [Groupk] | 2 | - 1 | 13 333 333 0.001416556 | 1588434 0.015582111847582775 | (Groupk/7.7981714752040946-11) | (Group®=6.2385971801692756-10) | [APOA1, ILSO] | (ADIPOQ, APOA1, IL10, IL181, IL18N, KLF4, MAP2KS, MAPK7, MBL2, MBP, MYADM, PRG2, RICRA |
| | GO, BiologicalProcess-68th-UniProt-GOA, 06.09.2018, 00th00 regulation of cell-cell adherion involved in gastrulation | [4, 5, 6, 7, 8] | [Groupk] | | | | 19872929 0.014769001924648714 | (Grouph/7.7981714752040946-11) | (Grouph 6.2385371801632756-10) | (APOA1, ILIO) | TADPOD, APOAT, ILSO, ILSRS, ILSRS, KIEFA, MAPZKS, MAPK?, MBIZ, MBP, MYADM, PRGZ, WINKS |
| | GO_BiologicalProcess-681-uniProt-GOA_08.09.2018_00h00 striated muscle myosin thick filament assembly | [4,5,6,7,6] | (Groups) | | | | 10001433 0.012746400027775063 | Groupe 0.0052806682798799281 | (Groups 0.002 6513336657747856) | DANGER MINISTER | DISCOST MANGEST MANGES |
| | | | Marriages; Security | | | 22.322.321 | 4 935411 0 009277779913199535 | | (Group?+2.56586604780463806-11. Group8+6.2385371801632756-10) | | Tabrics abrics about about about about must like that? |
| | GO_BiologicalProcess-68I-UniProt-GOA_66.09.2018_00b00 vegulation of interstnal lipid absorption | [5, 6, 7] | | | | 12 525 254 | 7.465+10.0.006877772913190525 | | | | |
| | GO_BiologicalProcess-GBI-UniProt-GOA_06.09.2018_00900 midbrain departments reward differentiation | [4, 6, 7, 8, 9, 10] | (Groupii) | - 3 | | | | GroupSi-8.796243070388876-0 | (Group5+6.1503701492722096-7) | [SFRPI, WNT1, WNT2] | [ATR, CSNIED, CSNIEE, CTNNEE, DIKEL, FSTLE, F2DS, INHRA, INTSE, INTSE, LMIELA, LIPPE, NRAK |
| 1906953 | GO_BiologicalProcess-68H-UniProt-GOA_08.09.3018_00h00 Wirt signaling pathway involved in midbrain doparminergic neuron differentiation | [5, 6, 7, 8, 9, 10, 11] | (Groupli) | . 2 | | | 9872928 0.014768001934648714 | (GroupS-9.796243070388876-9) | {Group5=6.1503701482722096-7} | [WNTs, WNT2] | [CSNK1D, CSNK16, CTNN61, FZDS, INTS1, INTS4, URP6, RYK, WNT1, WNT2, WNT3, WNT3A, WN |
| | GO_BiologicalProcess-Bit-UniProt-GOA_06.09.2018_00h00 canonical Wire signaling pathway involved in midbrain departments reuron differentiation | | (Groupli) | 2 | | 33.333.332 | 2,075+12 0.009929997129045433 | (G10upS-9.796243070388876-8) | (GroupS=6.1503701492722096-7) | [WNTs, WNT2] | [CTNNR1, INTS1, INTS4, WNT1, WNT2, WNT3] |
| 1906276 | GO_BiologicalProcess-681-UniProt-GOA_06.09.2018_00900 regulation of epithelial tube formation | [4, 6, 6, 7, 8] | [Groupi, Group?] | 2 | | 9.090.909 0.0030639443 | 13:0526 0.012255777349242105 | (GroupS+R 79624307038887N-R, Group7+2 8509622753718204E-12) | (Group5+6.1503701492722096-7, Group7+2.56586604793463836-11) | [GDNF, SFRP1] | [ATR, CELSRS, DVL1, DVL1P1, DVL2, DVL3, FSTL1, F2D1, F2D2, GATAR, GDNF, GRHL3, INHRA, NP |
| | GO_BiologicalProcess-681-UniProt-GOA_06.09.2018_00900 activation of protein kinase Cactivity | [8, 10, 11, 12] | [Group?, Groupil] | 2 | 50.0 | | 8,315+10 0.001995375989682884 | (Group7v2.96096227527182046-12, Group8v7.7981714752040946-11) | {Group7+2.56586604783463886-11, Group8+6.2385371801632756-10} | [LEP, MTTP] | [ABL1, CDH11, LEP, MITTP] |
| | 60 BiologicalProcess 68t UniProt 60A 06.09.2018 00b00 positive regulation of non-canonical Writ signaling pathway | [5, 6, 7, 8, 9, 10] | (Group?, Group#) | 2 | 12.5 | | 6279086 0.036169946876279084 | | (Group?+2.56586604783462886-11, Group8+6.2385371801632756-10) | | [ABL1, ANWRON, ATR, CSMILD, CSMILE, DARR, DWIL, FSTL1, GPCR, INHRA, MILTR, MTTP, NKD1, |
| 2000095 (| GO, BiologicalProcess-GBI-UniProt-GOA, 08.09.2018, 00h00 pregulation of Witt signaling pathway, planar cell polarity pathway | 16.7.8.9.101 | Kirpup?, Group#1 | 2 | - 1 | 11.111.111.0.0020495472 | 1283542 0.016393177834268337 | 1G10up7-2.86096227527182046-12. G10up8-7.7981714752040946-11) | (Group)+2.56586604780463886-11. Group8+6.2385371801632756-109 | [MTP, SFRPS] | TABLE ANGEDS ATK DARR DACTE DIKE FETEL GPC3. INHIBA MISSEMILTE MITTE NICES NO |
| | GO, BiologicalProcess-Eile-UniProt-GOA, 06.09.2018, 00h00 inguistion of Fibroblam apoptatic process | [6.7] | 16rpup?1 | | | | 283542 0.016393177834268337 | (Group?v2.850962275)7182095-121 | (Group7+2 56586604783463836-11) | SERPS, TPGIT | TAPIS ATR. BCL3L11. BID. BTG1. CFDP1. FSTL1. GASG. IERBP1. INHBA. PIKRCA. PIKRCS. PROMIS |
| | GO, BiologicalProcess-68-UniProt-GOA, 06.09.2018, 00h00 positive regulation of fibroblast apaptotic process | [6, 7, 8] | [Group?] | | | 10 101 010 | 7.695+11.0.011739736695999749 | (Group?v2.850962275)?182095-121 | (Graup7+2 56586604788463836-11) | SFRPs, TPGIT | TATR. BCL2L11. BID. BTG1. FSTL1. NHBA. PROMIS. SFRPS. STKS7A. STKS7B. TPGH |
| | | [-1] | (Group) | - 1 | | 4.694.147 | 9.165+06 | | | | |
| 1000271 0 | | | | | | | | 3,116+08 (Group8r7.7981714752040946-11) | (Group8:6.2385371801632756-10) | | [ABCA1, ABCGS, ABCGS, ACKT2, AGPKT1, AGPKT2, APOA1, APOA4, APOB, CD96, CEL, CLP5, DGA |
| 5:00975 R | KEGG_04.09.2008 Fat digretion and absorption | | | | | | 6800764 0.00728623628936253 | (Grouph/7.7981714752040946-11) | {Group8=6.2385971801692756-10} | [APOA1, APOR] | (ABCCS, APOAS, APOA, APOB, AWATZ, BTD, CUBN, FOLKS, GF, LMBRDS, LRAT, MMACHC, PLB |
| 5:00975 × 5:00977 × | KEGG_04.09.200k Fat digretion and absorption KEGG_04.09.200k Vitamin digretion and absorption | [-1] | (Groupk) | - 2 | | | | | | | |
| G:00975 6 G:00977 8 GA:2168880 6 | KKGGG, 04.098.2009 Fat digretion and absorption KKGGG, 04.098.2009 Vitamin digretion and absorption KKGCTOME, Pathways, 04.09.2009 Vitamin digretion and absorption KKGCTOME, Pathways, 04.09.2009 Vitamin digretion and absorption | [-1] | (Groupk) | 1 | - 2 | 23.076.923 | 1,416+11 | 4,8%+12 (Groupk/7.7981714752040946-11) | {Group8=6.2385971801692756-10} | [ALR, APOA1, JOHAN] | [ALR, AMRP, APOA1, APOL1, COLGE, HEA1, HEA2, HEB, HP, HPK, HPK, JOHAN, LRF1] |
| G 00975 H G 00977 H G 2168880 H G 2173782 H | Visidi, Octob Artical Visidi (Aced Artical | [-1] [-1] [-1] | (Groupk) | 3 | 2 | 9.523.809 | 1,845+10 | 5,516+11 (Groupik/7.7981714752040946-11) | (Group8+6-2385871801682756-10) | [ALB, APOA1, APOR, ICHNIN] | (AUR, AMBP, APOA1, APOR, APOE, APOL1, CAUR, CD16R, CD16R, CDL1A1, COL1A2, COL3A1, CDL0A |
| G 00975 8 G 00977 8 IA 2168880 8 IA 2172782 8 IA 2852902 8 | First digestion and absorption First digestion and absorption | [-1] | (Groupk) | 2 4 | 1 | 9.523.809 13.063.478 | 1,845+10 8,535+10 0.0019616368911192 | 5,516+11 (Grouph-7.7981714753040946-11) (Grouph-9.5288560483443476-5) | | | |
| G 06975 8 G 06977 8 SA 2168890 8 SA 2173792 8 SA 2653902 8 | Visidi, Octob Artical Visidi (Aced Artical | [-1] [-1] [-1] | (Groupi) (Groupi) (Groupi) | 3 4 3 | 1 | 9.523.809 | 1,845+10 | 5,516+11 (Groupik/7.7981714752040946-11) | (Group8+6-2385871801682756-10) | [ALB, APOA1, APOR, ICHNIN] | (AUR, AMBP, APOA1, APOR, APOE, APOL1, CAUR, CD16R, CD16R, CDL1A1, COL1A2, COL3A1, CDL0A |
| G 00975 8 G 00977 8 IA 2168880 9 IA 2179792 9 IA 265990 9 IA 3000071 9 | First digestion and absorption First digestion and absorption | [-1] [-1] [-1] | (Groupk) | 2 4 3 | 1 2 | 23.076.923 9.523.909 13.063.478 23.333.332 | 1,845+10 8,535+10 0.0019616368911192 | 5,516+11 (Grouph-7.7981714753040946-11) (Grouph-9.5288560483443476-5) | [Group8:6.2385871801632766-18] [Group3:0.411624180377296-0] | [ALB, APOA1, APOB, JOHNIN] [ABCA4, ROHR, SDRSCT] | (AUR, AMREY, APONS, APOR, APOLS, CALR, CDSER, CDSE, CDLTAS, CD |
| 5:08975 8 5:08977 8 A:2168880 8 A:2172792 8 A:2653902 8 A:2000675 8 | Visit digents and desception Visit | [-1] [-2] [-3] [-4] [-4] | (Groupk) (Groupk) (Groupk) (Groupk) (Groupk) | 3 4 3 2 2 | 1 3 | 22.076.923 9.523.909 13.063.478 22.323.322 10.526.356 (0.0022846728) | 1,845+10 8,535+10 0.0009616368911182 2,075+12 0.003929987129085433 6662155 0.01599271682152251 | 5,516+13 (Sinospin 7,7981714753040946-11) (Sinospin 6,5385504884437K-6) (Sinospin 7,7981714753040946-11) (Sinospin 7,7981714753040946-11) | Grouphis.226537380562756-15 Grouphis.415625188277286-0 Grouphis.236537380562756-15 Grouphis.236537380562756-15 | [ALB, APOA1, APOB, ICHNIN] [ABCA4, ROHE, SDRRCT] [APOA1, APOB] [APOA1, APOB] | JALIB, AMBP, JAPOAT, APOB, JAPOB, JAPOB, CADIS, COLGE, COLGE, COLLAS, COLLAS, COLGAS, CAPPAD, JAPOB, CADIG, CADIG, SAMS, SCARGES, SCASCO, SCASCO, COLGAS, COLG |
| 5 00975 8 5 00977 9 A 2168880 9 A 2179792 9 A 2453902 9 A 2000475 A 2000480 9 A 2772470 9 | Vir. digestion and advancem Vir. digestion digestion by lacenage Vir. digestion digestion digestion Vir. digestion | [4] [4] [4] | Groupi Groupi Groupi Groupi Groupi Groupi | 3 4 3 2 2 | 1 3 1 | 22.076.923 9.523.909 13.063.478 22.323.322 10.526.356 (0.0022846728) | 1,865+10 8,535+10 0.0010616368911182 2,075+12 0.003029987129045633 5662155 0.01508271682152951 188834 0.015582111847582775 | \$,548-11 [Sinsupler, 7.98272475040964-11] \$6700pler, \$2.786566048046417-5] \$6700pler, 7.98272475040964-12] \$6700pler, 7.98272475040964-12] \$6700pler, 7.98272475040964-12] | Groups 2 28537180542756-10 Groups 3 x 1116431827726-0 Groups 2 285371805427726-0 Groups 2 28537180542776-10 Groups 2 28537180542776-10 | [ALB, APOA1, APOB, IOHIN] [ABCA4, ROSE, SDRSCT] [APOA1, APOB] [APOA1, APOB] [DXX2, SPRS1] | Sala, ANDP, APOLA, APOR, APOL, APOLE, CORE, COSE, COSE, COLEA, CO |
| 5:00975 1 5:00977 1 A:2168880 1 A:2179792 1 A:2052900 1 A:3000871 1 A:3000880 1 A:3772870 1 A:3866428 1 | GEO, (ASE 2002). Per dipetion set discopron. February St. | [-1] [-2] [-3] [-4] [-4] | Groupi Groupi Groupi Groupi Groupi Groupi Groupi | 3 4 3 2 2 2 2 | 1 2 1 1 | 23.0%.923 9.523.609 13.082.478 83.383.382 10.526.356 0.0022846738 13.383.383 0.0014166566 | 1,865+10 8,516+10 0.0009616368911182 2,876+12 0.0009998729905635 6962155 0.01598271682152951 588838 0.015582111847582775 1,886+12 0.00001076568829579 | 5,544-11 [Smaple7.7H827.67/30.00464-11] (Smaple7.7H827.67/30.00464-11) (Smaple7.7H827.67/30.00464-11) (Smaple7.7H827.67/30.00464-11) (Smaple7.2H827.67/30.00464-11) (Smaple7.2H8662.2297.12.1066-12) (Smaple7.2H8662.2297.12.1066-12) | Groupin. 226537180162276-187 Groupin. 24.115421827796-0 Groupin. 2365373861627766-187 Groupin. 236537386162776-187 Groupin. 236537386162776-187 Groupin. 2.5656660738616286-11 Groupin. 2.5666660738616286-11 | [ALB, APOAS, APOB, ICHANN] [ALCAL, ROAD, SONGCT] [APOAS, APOB] [APOAS, APOB] [DIXCS, SERPS] [APOB, MITTP] | EMB, AMBP, AFORE, MODE, AFOE, SCHOLL, CHEE, CODER, |
| G 108975 8 G 108977 8 A 2568880 8 A 2573782 8 A 2653902 8 A 3000875 8 A 3000880 8 A 39773870 8 A 3866622 8 A 3963888 8 A 39638888 8 A 39638888 8 A 39638888 8 A 3963888 8 A 3963888 8 A 3963888 8 A 3963888 8 | Fried Spellan and American Conference Confer | [-1] [-2] [-3] [-4] [-4] | Groupi Groupi | 2 4 3 2 2 2 2 2 3 | 2 3 1 1 40.0 | 22.0%-923 9.523.809 13.082.438 82.323.322 10.526.356 0.0022846738 12.323.323 0.0014165566 83.323.323 | 1,865+10 8,585-10-0.0009616368911192 2,875-12-0.00099897199086823 5665255 0.01599279682152951 188688 0.015582111847582775 1,865+12-0.000081076588879579 4,205+09 | \$,544-11 [6/cmp6/7-78627-6/DOS0066-12] [6/cmp6/7-78627-6/DOS0066-12] [6/cmp6/7-78627-6/DOS0066-12] [6/cmp6/7-78627-6/DOS0066-12] [6/cmp6/7-78627-6/DOS0066-12] [6/cmp6/7-78627-6/DOS0066-13] [6/cmp6/7-78627-6/DOS0066-13] [6/cmp6/7-78627-6/DOS0066-13] | Georgia 2865794865427956-52] Georgia 241552818277906-0] Georgia 28657186642796-0] Georgia 28657186642796-12] Georgia 28657186642796-12] Georgia 26656078868828-1] Georgia 2665607886828-1] Georgia 26656078868296-1] | [ALB, APOAT, APOB, ICHNIN] ABICAL, RISHE, SERICT] JAPOAT, APOB] [DICKZ, SFRPT] JAPOAT, APOB, MITTP] JAPOAT, APOB, MITTP] | [MA] AMMY AMMA, AMMA, AMMA, CHAIR, COMBA, CO |
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| G 00075 1 G 00077 1 G 0007 | The Control of Control | [-1] [-2] [-3] [-4] [-4] | Groupi Groupi | 3 | 2 1 2 1 1 40.0 3 1 | 22.0%-923 9.523.809 13.082.438 82.323.322 10.526.356 0.0022846738 12.323.323 0.0014165566 83.323.323 | 1,866+10 8,556-10 0.0009615368911182 3,076+12 0.00092999719005483 5665155 0.0159827568215281 588634 0.015982111847582775 1,386-12 0.000011005488479579 4,006-09 3,868-11 0.00011538666666080 | 5,544-13 [Graught-79827-0750400661-13] [Straught-8.1585064014541-5] [Straught-79827-075040661-13] [Straught-79827-075040661-13] [Straught-8.056622977-120661-12] [Straught-8.056622977-120661-12] [Straught-8.056622977-120661-12] [Straught-79827-075040661-13] | [Grouphic 200071900327976-05] [Grouphic 15105072100327976-0] [Grouphic 200071900327976-05] [Grouphic 20007190032797-05] [Grouphic 20007190032797-05] [Grouphic 20007190032797-05] [Grouphic 2000719003297-05] [Grouphic 2000719003297-05] | [ALE, AFOAL, AFOA, CHANN) [ARCAA, ROHA, SONICT] [AFOAL, AFOB) [AFOAL, AFOB) [AFOAL, AFOB) [AFOAL, AFOB, MITTP] [AFOAL, AFOB, MITTP] | THAN ARMY APPOLY, APPO |

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 \pm 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) | | |
| | | | | |