SUPPLEMENTARY DATA

**Supplementary Table 1.**

Subject characteristics in the 1st micro array

| | Control Subjects | IR Offspring | *P*-value |
|---|---|---|---|
| Gender | 4F, 1M | 5F, 1M | |
| Age (years) | 27±3 | 28±5 | 0.96 |
| Height (m) | 1.65±0.04 | 1.65±0.07 | 0.98 |
| Body Weight (kg) | 53.4±4.5 | 68.8±7.3 | 0.09 |
| BMI (kg/m$^2$) | 19.4±0.8 | 24.9±0.8 | 0.001 |
| Fasting Plasma Glucose (mg/dL) | 82±3 | 97±4 | 0.01 |
| Fasting Plasma Insulin (μU/mL) | 4.0±0.8 | 16.6±1.1 | <0.0001 |
| Mitochondrial density (%) | 2.90±0.22 | 2.20±0.18 | 0.05 |

2nd Microarray using double amplification

| | Control Subjects | IR Offspring | *P*-value |
|---|---|---|---|
| Gender | 7F, 2M | 8F, 1M | |
| Age (years) | 27±3 | 23±1 | 0.18 |
| Height (m) | 1.67±0.04 | 1.66±0.05 | 0. 85 |
| Body Weight (kg) | 61.6±6.5 | 63.6±6.1 | 0.78 |
| BMI (kg/m$^2$) | 21.8±1.4 | 22.9±1.1 | 0.45 |
| Fasting Plasma Glucose (mg/dL) | 80±2 | 91±3 | 0.016 |
| Fasting Plasma Insulin (μU/mL) | 6.0±0.8 | 16.6±1.1 | <0.0001 |
| Mitochondrial density (%) | 2.79±0.02 | 2.07±0.02 | 0.0068 |

SUPPLEMENTARY DATA

**Supplementary Table 2.** Probe sets constituting the insulin resistance signature

## 2.1 Probe sets showing a higher average expression level in IR offspring

| fold | p-value | IS | IR | Gene Symbol | Gene Title |
|---|---|---|---|---|---|
| 3.91 | 0.040639 | 422 | 1099 | C21orf82 | chromosome 21 open reading frame 82 |
| 2.78 | 0.016364 | 394 | 1013 | HIST1H3C | histone 1, H3c |
| 2.66 | 0.022924 | 395 | 1118 | MGC3101 | hypothetical protein MGC3101 |
| 2.64 | 0.01495 | 708 | 1562 | FBXO6 | F-box only protein 6 |
| 2.6 | 0.009525 | 106 | 242 | ACOX3 | acyl-Coenzyme A oxidase 3, pristanoyl |
| 2.5 | 0.005599 | 932 | 2109 | GDF8 | growth differentiation factor 8 |
| 2.4 | 0.037437 | 178 | 340 | LOC340719 | Homo sapiens similar to nanos (LOC375939), mRNA |
| 2.33 | 0.023896 | 226 | 456 | CES1 | carboxylesterase 1 (monocyte/macrophage serine esterase 1) |
| 2.25 | 0.002841 | 125 | 263 | MGC23920 | hypothetical protein MGC23920 |
| 2.23 | 0.029937 | 3370 | 7210 | LOC340719 | Homo sapiens similar to nanos (LOC375939), mRNA |
| 2.23 | 0.02289 | 270 | 508 | MCAM | melanoma cell adhesion molecule |
| 2.21 | 0.017703 | 177 | 344 | NCDN | neurochondrin |
| 2.19 | 0.003083 | 283 | 565 |  | weak similarity to hypothetical protein FLJ20378 [Homo sapiens] |
| 2.16 | 0.008468 | 127 | 244 |  | Homo sapiens clone IMAGE:111705 mRNA sequence |
| 2.1 | 0.028557 | 596 | 1290 | GALNAC4S-6ST | B cell RAG associated protein |
| 2.09 | 0.026686 | 2483 | 5132 | GLRX | glutaredoxin (thioltransferase) |
| 2.08 | 0.03774 | 109 | 206 |  | Homo sapiens neuroglycan C mRNA |
| 2.07 | 0.005792 | 293 | 536 | KIAA0493 | Homo sapiens cDNA FLJ39739 fis, clone SMINT2016440. |
| 2.05 | 0.034608 | 124 | 219 | NDUFS7 | NADH dehydrogenase (ubiquinone) Fe-S protein 7, |
| 2 | 0.02552 | 313 | 533 | FLJ20401 | FLJ20401 protein |
| 1.99 | 0.01081 | 2369 | 4476 | GLRX | glutaredoxin (thioltransferase) |
| 1.95 | 0.035951 | 234 | 379 | C22orf1; 239AB; FAM1A | Homo sapiens cDNA clone MGC:5619 IMAGE:3462332 |
| 1.95 | 0.008328 | 320 | 554 | C10orf33 | chromosome 10 open reading frame 33 |
| 1.93 | 5.12E-04 | 142 | 258 | MGC20481 | cDNA DKFZp451P134 (from clone DKFZp451P134). |
| 1.91 | 0.008589 | 949 | 1675 | P8 | p8 protein (candidate of metastasis 1) |
| 1.87 | 0.027144 | 189 | 322 | psMAGEA | Homo sapiens chromosome X multiple clones map q28 |
| 1.86 | 0.023307 | 6962 | 11540 | TncRNA | Homo sapiens mRNA; cDNA DKFZp686L01105 |

| | | | | | |
|---|---|---|---|---|---|
| 1.85 | 0.022383 | 114 | 202 | B3GTL | beta 3-glycosyltransferase-like |
| 1.85 | 0.007953 | 283 | 501 | USP7 | ubiquitin specific protease 7 (herpes virus-associated) |
| 1.85 | 0.02125 | 641 | 1076 | TNS | tensin |
| 1.84 | 0.012589 | 193 | 331 | CCNG2 | cyclin G2 |
| 1.82 | 0.004557 | 182 | 308 | LOC157697 | hypothetical protein LOC157697 |
| 1.81 | 0.027866 | 218 | 365 | HIST1H2BC | histone 1, H2bc |
| 1.8 | 0.037885 | 134 | 215 | FMO3 | flavin containing monooxygenase 3 |
| 1.78 | 0.030215 | 465 | 774 | | Homo sapiens, clone IMAGE:4819084, mRNA |
| 1.77 | 0.027762 | 269 | 437 | FLJ20674 | hypothetical protein FLJ20674 |
| 1.76 | 0.038131 | 181 | 286 | FCGR2A | Fc fragment of IgG, low affinity IIa, receptor for (CD32) |
| 1.76 | 0.034264 | 2927 | 4794 | LMOD1 | leiomodin 1 (smooth muscle) |
| 1.75 | 0.04101 | 1088 | 1857 | DKFZP564O0823 | DKFZP564O0823 protein |
| 1.75 | 0.046698 | 281 | 429 | | Cluster Incl. AI278629:qm47b10.x1 Homo sapiens cDNA |
| 1.73 | 0.03127 | 189 | 290 | KIAA0967 | KIAA0967 protein |
| 1.72 | 0.036325 | 152 | 231 | | Homo sapiens transcribed sequences |
| 1.72 | 0.048509 | 329 | 529 | FLJ40432 | hypothetical protein FLJ40432 |
| 1.71 | 0.009395 | 142 | 229 | PVRL3 | poliovirus receptor-related 3 |
| 1.71 | 0.002146 | 234 | 382 | D8S2298E | reproduction 8 |
| 1.7 | 0.038473 | 1125 | 1832 | PRKAG3 | protein kinase, AMP-activated, gamma 3 non-catalytic subunit |
| 1.7 | 0.033182 | 238 | 363 | | weak similarity to protein sp:P23961 (H.sapiens) |
| 1.7 | 0.023385 | 271 | 410 | BHLHB2 | basic helix-loop-helix domain containing, class B, 2 |
| 1.69 | 0.03811 | 148 | 221 | RPESP | RPE-spondin |
| 1.69 | 0.021764 | 398 | 645 | LOC55954 | hypothetical protein LOC55954 |
| 1.68 | 0.030424 | 746 | 1108 | RXRG | retinoid X receptor, gamma |
| 1.67 | 0.018507 | 471 | 731 | HS6ST2 | heparan sulfate 6-O-sulfotransferase 2 |
| 1.66 | 0.030039 | 470 | 740 | | moderate similarity to protein pdb:1BGM (E. coli) |
| 1.66 | 0.035378 | 408 | 659 | FLNA | filamin A, alpha (actin binding protein 280) |
| 1.66 | 0.03585 | 312 | 510 | GNPDA2 | glucosamine-6-phosphate deaminase 2 |
| 1.65 | 0.037207 | 957 | 1541 | PNMA1 | paraneoplastic antigen MA1 |
| 1.65 | 0.036139 | 140 | 204 | SCARF1 | scavenger receptor class F, member 1 |
| 1.65 | 0.023149 | 597 | 948 | NDFIP2 | Nedd4 family interacting protein 2 |

| | | | | | |
|---|---|---|---|---|---|
| 1.63 | 0.023647 | 210 | 312 | FLJ37562 | hypothetical protein FLJ37562 |
| 1.62 | 0.046232 | 3695 | 5822 | MRPS6 | mitochondrial ribosomal protein S6 |
| 1.6 | 0.016355 | 201 | 289 | AGA | aspartylglucosaminidase |
| 1.59 | 0.048232 | 157 | 244 | RRBP1 | ribosome binding protein 1 homolog 180kDa (dog) |
| 1.59 | 0.006843 | 1199 | 1799 | DSCR2 | Down syndrome critical region gene 2 |
| 1.58 | 0.040236 | 192 | 285 | ZNF174 | zinc finger protein 174 |
| 1.58 | 0.011134 | 251 | 373 | FLJ45246 | FLJ45246 protein |
| 1.58 | 0.027474 | 157 | 227 | FLJ14681 | hypothetical protein FLJ14681 |
| 1.57 | 0.013959 | 466 | 700 | RFX5 | regulatory factor X, 5 (influences HLA class II expression) |
| 1.56 | 0.029873 | 1682 | 2503 | | moderate similarity to protein ref:NP_060312.1 (H.sapiens) |
| 1.56 | 0.008387 | 528 | 776 | AP3D1 | adaptor-related protein complex 3, delta 1 subunit |
| 1.56 | 0.034047 | 234 | 353 | PTPRC | protein tyrosine phosphatase, receptor type, C |
| 1.55 | 0.002245 | 368 | 544 | SERPINB1 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 |
| 1.55 | 0.020561 | 173 | 247 | SIP | Siah-interacting protein |
| 1.55 | 0.044429 | 149 | 212 | TM4SF11 | transmembrane 4 superfamily member 11 (plasmolipin) |
| 1.54 | 0.034834 | 4365 | 6134 | C1orf24 | chromosome 1 open reading frame 24 |
| 1.54 | 0.043659 | 1161 | 1739 | LMO4 | LIM domain only 4 |
| 1.54 | 0.014638 | 578 | 821 | ACOX2 | acyl-Coenzyme A oxidase 2, branched chain |
| 1.53 | 0.02261 | 500 | 731 | KPNB2 | karyopherin (importin) beta 2 |
| 1.53 | 0.009932 | 183 | 268 | ABCC9 | ATP-binding cassette, sub-family C (CFTR/MRP), member 9 |
| 1.52 | 0.045869 | 164 | 230 | C14orf45 | chromosome 14 open reading frame 45 |
| 1.52 | 0.012629 | 279 | 387 | | Cluster Incl. U87408:Human clone IMAGE-74593 unknown protein mRNA2 |
| 1.52 | 0.01725 | 3620 | 5341 | GATM | glycine amidinotransferase (L-arginine:glycine amidinotransferase) |
| 1.52 | 0.037012 | 314 | 454 | TUBA4 | tubulin, alpha 4 |
| 1.52 | 0.028351 | 1731 | 2506 | LSM7 | LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae) |
| 1.52 | 0.031926 | 339 | 473 | VCY2IP1 | VCY2 interacting protein 1 |
| 1.52 | 0.041478 | 618 | 863 | TBC1D1 | TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 |
| 1.51 | 0.048309 | 320 | 463 | PTPRC | protein tyrosine phosphatase, receptor type, C |
| 1.51 | 0.019486 | 270 | 382 | TBRG1 | likely ortholog of mouse transforming growth factor beta regulated gene 1 |
| 1.51 | 0.010613 | 9382 | 13309 | ENIGMA | enigma (LIM domain protein) |

| | | | | | |
|---|---|---|---|---|---|
| 1.5 | 0.002948 | 422 | 600 | IRF2 | interferon regulatory factor 2 |
| 1.5 | 0.021426 | 279 | 398 | | Homo sapiens cDNA clone IMAGE:5607466 5', mRNA sequence. |
| 1.5 | 0.021625 | 265 | 374 | KIAA1237 | KIAA1237 protein |
| 1.5 | 0.022072 | 300 | 426 | cig5 | viperin |
| 1.5 | 0.033857 | 347 | 487 | TXNL | thioredoxin-like, 32kDa |
| 1.5 | 0.030136 | 190 | 259 | | Homo sapiens transcribed sequences |
| 1.5 | 0.043378 | 2039 | 2861 | KIAA1161 | Homo sapiens mRNA for KIAA1161 protein, partial cds. |
| 1.49 | 0.026668 | 692 | 977 | DKFZp762O076 | hypothetical protein DKFZp762O076 |
| 1.49 | 0.045749 | 204 | 276 | OCRL | oculocerebrorenal syndrome of Lowe |
| 1.49 | 0.014745 | 230 | 327 | PDLIM2 | PDZ and LIM domain 2 (mystique) |
| 1.49 | 0.032342 | 379 | 530 | VIPR2 | vasoactive intestinal peptide receptor 2 |
| 1.49 | 0.003067 | 170 | 237 | NOD3 | NOD3 protein |
| 1.49 | 0.04642 | 346 | 480 | DJ159A19.3 | hypothetical protein DJ159A19.3 (DJ159A19.3), mRNA. |
| 1.49 | 0.021729 | 357 | 499 | KIAA0692 | KIAA0692 protein |
| 1.48 | 0.045526 | 1036 | 1449 | SEC61A1 | Sec61 alpha 1 subunit (S. cerevisiae) |
| 1.48 | 0.049695 | 387 | 534 | KPNA5 | karyopherin alpha 5 (importin alpha 6) |
| 1.48 | 0.025565 | 332 | 462 | DKFZp761G2113 | hypothetical protein DKFZp761G2113 |
| 1.48 | 0.038966 | 672 | 950 | MGEA6 | meningioma expressed antigen 6 (coiled-coil proline-rich) |
| 1.48 | 0.047946 | 162 | 221 | | Homo sapiens transcribed sequences |
| 1.48 | 0.027893 | 244 | 335 | SLIT2 | slit homolog 2 (Drosophila) |
| 1.48 | 0.006446 | 237 | 324 | CAB2 | CAB2 protein |
| 1.47 | 0.007497 | 717 | 984 | ATP9B | ATPase, Class II, type 9B |
| 1.47 | 0.045679 | 198 | 275 | SLA | Src-like-adaptor |
| 1.47 | 0.04453 | 197 | 278 | LYN | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog |
| 1.47 | 0.036285 | 2770 | 3794 | SLC16A10 | solute carrier family 16 (monocarboxylic acid transporters), member 10 |
| 1.47 | 0.018918 | 1075 | 1477 | SSA2 | Sjogren syndrome antigen A2 (60kDa, SS-A/Ro) |
| 1.46 | 0.013065 | 1044 | 1434 | DUSP3 | dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) |
| 1.46 | 0.027522 | 285 | 383 | SLC35C2 | solute carrier family 35, member C2 |
| 1.46 | 0.00331 | 1024 | 1399 | | Homo sapiens KIAA0397 mRNA, complete cds |
| 1.46 | 0.042708 | 440 | 585 | ZNF213 | zinc finger protein 213 |

| | | | | | |
|---|---|---|---|---|---|
| 1.46 | 0.033616 | 231 | 331 | na | Homo sapiens cDNA FLJ11701 fis, clone HEMBA1005062. |
| 1.46 | 0.011675 | 195 | 272 | | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0496. |
| 1.46 | 0.033013 | 153 | 213 | SRD5A1 | steroid-5-alpha-reductase, alpha polypeptide 1 |
| 1.46 | 0.02426 | 305 | 413 | ZNF23 | zinc finger protein 23 (KOX 16) |
| 1.46 | 0.013607 | 242 | 336 | TTBK2 | Homo sapiens, clone IMAGE:5267224, mRNA |
| 1.46 | 0.036484 | 689 | 944 | MSCP | mitochondrial solute carrier protein |
| 1.46 | 0.007475 | 223 | 304 | FLJ30313 | hypothetical protein FLJ30313 |
| 1.45 | 0.029012 | 576 | 797 | FLJ10439 | hypothetical protein FLJ10439 |
| 1.45 | 0.014805 | 1263 | 1759 | EIF4EL3 | eukaryotic translation initiation factor 4E-like 3 |
| 1.45 | 0.009053 | 801 | 1085 | DNAJB2 | DnaJ (Hsp40) homolog, subfamily B, member 2 |
| 1.45 | 0.047878 | 230 | 308 | MGC39350 | hypothetical protein MGC39350 |
| 1.45 | 0.03532 | 347 | 459 | FLJ31821 | hypothetical protein FLJ31821 |
| 1.45 | 0.028346 | 256 | 350 | UEV3 | ubiquitin-conjugating enzyme E2-like |
| 1.45 | 0.027689 | 774 | 1038 | MLLT6 | myeloid/lymphoid or mixed-lineage leukemia |
| 1.44 | 0.011076 | 265 | 359 | SDS3 | likely ortholog of mouse Sds3 |
| 1.44 | 0.014257 | 653 | 894 | RFX5 | regulatory factor X, 5 (influences HLA class II expression) |
| 1.44 | 0.024917 | 252 | 345 | | Homo sapiens cDNA FLJ42331 fis, clone TSTOM2000588 |
| 1.44 | 0.028501 | 6265 | 8442 | SPARC | secreted protein, acidic, cysteine-rich (osteonectin) |
| 1.44 | 0.031847 | 184 | 246 | MGC3771 | hypothetical protein MGC3771 |
| 1.43 | 0.019031 | 392 | 537 | | weak similarity to protein pir:S57447 (H.sapiens) S57447 HPBRII-7 protein |
| 1.43 | 0.018429 | 593 | 790 | DKFZp762N1910 | hypothetical protein DKFZp762N1910 |
| 1.43 | 0.01061 | 349 | 472 | KIAA1545 | KIAA1545 protein |
| 1.43 | 0.044952 | 427 | 566 | FLJ14281 | hypothetical protein FLJ14281 |
| 1.43 | 0.035137 | 217 | 292 | | AL577977 |
| 1.43 | 0.046044 | 579 | 794 | TOPORS | topoisomerase I binding, arginine/serine-rich |
| 1.43 | 0.040852 | 385 | 513 | ZNF92 | zinc finger protein 92 (HTF12) |
| 1.43 | 0.014063 | 667 | 892 | | Cluster Incl. AI733019:oh64e12.x5 |
| 1.43 | 0.044053 | 567 | 769 | | ow12a02.s1 Soares_parathyroid_tumor_NbHPA |
| 1.43 | 0.022938 | 1073 | 1437 | BIVM | basic, immunoglobulin-like variable motif containing |
| 1.42 | 0.028835 | 546 | 724 | BIG1 | brefeldin A-inhibited guanine nucleotide-exchange protein 1 |

| | | | | | |
|---|---|---|---|---|---|
| 1.42 | 0.026586 | 1751 | 2387 | F8A | coagulation factor VIII-associated (intronic transcript) |
| 1.42 | 0.029815 | 233 | 317 | IFI35 | interferon-induced protein 35 |
| 1.42 | 0.031923 | 1874 | 2505 | MGC35274 | hypothetical protein MGC35274 |
| 1.42 | 0.006313 | 397 | 534 | IRF3 | interferon regulatory factor 3 |
| 1.42 | 0.013933 | 247 | 339 | na | Homo sapiens cDNA FLJ37848 fis, clone BRSSN2013544. |
| 1.42 | 0.031243 | 258 | 336 | LCHN | LCHN protein |
| 1.42 | 0.021167 | 952 | 1246 | | Homo sapiens transcribed sequences |
| 1.42 | 1.14E-04 | 3920 | 5268 | BHLHB2 | basic helix-loop-helix domain containing, class B, 2 |
| 1.41 | 0.035311 | 5813 | 7684 | MONDOA | Mlx interactor |
| 1.41 | 0.048612 | 314 | 420 | MTF1 | metal-regulatory transcription factor 1 |
| 1.41 | 0.003335 | 243 | 324 | CTNND1 | catenin (cadherin-associated protein), delta 1 |
| 1.41 | 0.04509 | 251 | 336 | LOC113655 | hypothetical protein BC011982 |
| 1.41 | 0.012522 | 745 | 1002 | KIAA0478 | KIAA0478 gene product |
| 1.4 | 0.026926 | 260 | 340 | LYN | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog |
| 1.4 | 0.026588 | 676 | 889 | FLJ10904 | hypothetical protein FLJ10904 |
| 1.4 | 0.013871 | 2716 | 3618 | C6orf107 | chromosome 6 open reading frame 107 |
| 1.4 | 0.046106 | 1501 | 2037 | NUCB2 | nucleobindin 2 |
| 1.4 | 0.033282 | 361 | 476 | HATH6 | basic helix-loop-helix transcription factor 6 |
| 1.4 | 0.018684 | 882 | 1174 | RNF41 | ring finger protein 41 |
| 1.39 | 0.003069 | 600 | 799 | FKRP | fukutin related protein |
| 1.39 | 0.021391 | 328 | 432 | FCMD | Fukuyama type congenital muscular dystrophy (fukutin) |
| 1.39 | 0.014835 | 932 | 1226 | | FLJ11583.1 |
| 1.39 | 0.009957 | 957 | 1266 | MGC10526 | hypothetical protein MGC10526 |
| 1.39 | 0.004968 | 497 | 651 | MGAT4B | mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, |
| 1.39 | 0.023362 | 4865 | 6350 | PPP1R1A | protein phosphatase 1, regulatory (inhibitor) subunit 1A |
| 1.39 | 0.020692 | 631 | 831 | ZYX | zyxin |
| 1.39 | 0.027569 | 568 | 749 | UBE2J1 | ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast) |
| 1.38 | 0.026749 | 688 | 901 | MAN2A1 | mannosidase, alpha, class 2A, member 1 |
| 1.38 | 0.00468 | 18153 | 23670 | CALM1 | calmodulin 1 (phosphorylase kinase, delta) |
| 1.38 | 0.046648 | 675 | 886 | MTX1 | metaxin 1 |
| 1.38 | 0.036501 | 552 | 702 | SPPL3 | signal peptide peptidase 3 |

| | | | | | |
|---|---|---|---|---|---|
| 1.38 | 0.041083 | 249 | 319 | C9orf12 | chromosome 9 open reading frame 12 |
| 1.38 | 0.005884 | 762 | 998 | AEBP2 | AE(adipocyte enhancer)-binding protein 2 |
| 1.38 | 0.026259 | 1111 | 1467 | SP2 | Sp2 transcription factor |
| 1.38 | 0.043203 | 402 | 516 | DNAJ | DnaJ protein |
| 1.38 | 0.022636 | 708 | 927 | SGCD | sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) |
| 1.38 | 0.038344 | 290 | 383 | KIAA1345 | KIAA1345 protein |
| 1.38 | 0.033435 | 333 | 426 | POMT1 | protein-O-mannosyltransferase 1 |
| 1.38 | 0.017765 | 283 | 365 | na | Homo sapiens cDNA clone IMAGE:5269484 |
| 1.38 | 0.030733 | 274 | 355 | | Cluster Incl. AA402435:zt60g10.r1 |
| 1.38 | 0.008667 | 1845 | 2415 | CAT | catalase |
| 1.37 | 0.001071 | 664 | 859 | | C:H.sapiens mRNA for CLC-7 chloride channel protein |
| 1.37 | 0.045411 | 453 | 592 | NMT2 | N-myristoyltransferase 2 |
| 1.37 | 0.049888 | 496 | 633 | CD53 | CD53 antigen |
| 1.37 | 0.004542 | 158 | 205 | KIAA1018 | KIAA1018 protein |
| 1.37 | 0.008309 | 3672 | 4810 | HP1-BP74 | HP1-BP74 |
| 1.37 | 0.041636 | 1826 | 2356 | C1orf19 | chromosome 1 open reading frame 19 |
| 1.37 | 0.040801 | 531 | 693 | TFDP2 | transcription factor Dp-2 (E2F dimerization partner 2) |
| 1.37 | 0.008504 | 436 | 563 | PIM1 | pim-1 oncogene |
| 1.37 | 0.011927 | 577 | 750 | PIP5K1C | phosphatidylinositol-4-phosphate 5-kinase, type I, gamma |
| 1.37 | 0.016689 | 213 | 272 | | Homo sapiens cDNA FLJ13558 fis, clone PLACE1007743. |
| 1.37 | 0.031507 | 413 | 525 | CORO1C | coronin, actin binding protein, 1C |
| 1.37 | 0.049068 | 2360 | 3090 | ENIGMA | enigma (LIM domain protein) |
| 1.37 | 0.031991 | 907 | 1176 | RIF1 | receptor-interacting factor 1 |
| 1.37 | 0.019442 | 321 | 417 | NOC4 | neighbor of COX4 |
| 1.36 | 0.015589 | 556 | 717 | Rab11-FIP2 | KIAA0941 protein |
| 1.36 | 0.018179 | 477 | 611 | P38IP | transcription factor (p38 interacting protein) |
| 1.36 | 0.016882 | 329 | 426 | FNBP3 | formin binding protein 3 |
| 1.36 | 0.01963 | 2707 | 3501 | TRA1 | tumor rejection antigen (gp96) 1 |
| 1.36 | 0.027349 | 810 | 1012 | PGPEP1 | pyroglutamyl-peptidase I |
| 1.36 | 0.02404 | 1670 | 2133 | PIK3CB | phosphoinositide-3-kinase, catalytic, beta polypeptide |
| 1.36 | 0.005945 | 505 | 645 | FLJ10534 | hypothetical protein FLJ10534 |

| | | | | | |
|---|---|---|---|---|---|
| 1.36 | 0.014997 | 1092 | 1409 | TBCC | tubulin-specific chaperone c |
| 1.36 | 0.018236 | 866 | 1110 | PKP4 | plakophilin 4 |
| 1.36 | 0.018824 | 1055 | 1365 | UBN1 | ubinuclein 1 |
| 1.36 | 0.028595 | 2479 | 3178 | TAX1BP1 | Tax1 (human T-cell leukemia virus type I) binding protein 1 |
| 1.36 | 0.003043 | 598 | 767 | MGC5309 | hypothetical protein MGC5309 |
| 1.36 | 0.020384 | 1040 | 1328 | SCYL1 | SCY1-like 1 (S. cerevisiae) |
| 1.36 | 0.047179 | 2741 | 3456 | QKI | quaking homolog, KH domain RNA binding (mouse) |
| 1.36 | 0.00223 | 429 | 547 | | cDNA DKFZp586N1918 (from clone DKFZp586N1918) |
| 1.36 | 0.037574 | 5659 | 7306 | TEB4 | similar to S. cerevisiae SSM4 |
| 1.35 | 0.048242 | 793 | 1030 | KIAA1522 | KIAA1522 protein |
| 1.35 | 0.039065 | 1268 | 1652 | CCNG2 | cyclin G2 |
| 1.35 | 0.034163 | 3302 | 4199 | NOS1 | nitric oxide synthase 1 (neuronal) |
| 1.35 | 0.043885 | 689 | 873 | LAMP2 | lysosomal-associated membrane protein 2 |
| 1.35 | 0.02889 | 1742 | 2245 | FBXO30 | F-box protein 30 |
| 1.35 | 0.045721 | 566 | 716 | FLJ12666 | hypothetical protein FLJ12666 |
| 1.35 | 0.018551 | 3297 | 4217 | LOC283820 | hypothetical protein LOC283820 |
| 1.35 | 0.02783 | 1315 | 1685 | LOC154807 | hypothetical protein LOC154807 |
| 1.35 | 0.029148 | 5518 | 7014 | TM4SF10 | transmembrane 4 superfamily member 10 |
| 1.34 | 0.004123 | 3003 | 3818 | PSMD3 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 |
| 1.34 | 0.03345 | 296 | 377 | KIF3C | kinesin family member 3C |
| 1.34 | 0.017498 | 952 | 1213 | CPR8 | cell cycle progression 8 protein |
| 1.34 | 0.048879 | 214 | 270 | FLJ20366 | hypothetical protein FLJ20366 |
| 1.34 | 0.013305 | 967 | 1222 | | ok92b01.s1 NCI_CGAP_Lu5 |
| 1.34 | 0.010744 | 416 | 528 | ISGF3G | interferon-stimulated transcription factor 3, gamma 48kDa |
| 1.34 | 0.014949 | 840 | 1051 | CTMP | C-terminal modulator protein |
| 1.34 | 0.022681 | 512 | 641 | FLJ10357 | Homo sapiens hypothetical protein FLJ10357 (FLJ10357), mRNA. |
| 1.33 | 0.044393 | 228 | 286 | ZXDA | zinc finger, X-linked, duplicated A |
| 1.33 | 0.034636 | 538 | 676 | HLF | hepatic leukemia factor |
| 1.33 | 0.027812 | 335 | 425 | | Homo sapiens full length insert cDNA YI38B04 |
| 1.33 | 0.01529 | 808 | 1026 | MIR | c-mir, cellular modulator of immune recognition |
| 1.33 | 0.032507 | 1785 | 2224 | SIAT9 | sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase) |

| | | | | | |
|---|---|---|---|---|---|
| 1.33 | 0.031122 | 997 | 1260 | | Cluster Incl. AA522816:ni40e12.s1 |
| 1.33 | 0.010626 | 1267 | 1597 | | Cluster Incl. AI669655:wc12a05.x1 |
| 1.33 | 0.027462 | 1036 | 1307 | MGC33864 | ADP-ribosylation-like factor 6-interacting protein 6 |
| 1.33 | 0.048712 | 9523 | 11745 | OPHN1 | oligophrenin 1 |
| 1.33 | 0.027506 | 1145 | 1416 | MGC3048 | hypothetical protein MGC3048 |
| 1.33 | 0.023687 | 6849 | 8706 | MO25 | MO25 protein |
| 1.33 | 0.042844 | 291 | 369 | DKFZp313A2432 | hypothetical protein DKFZp313A2432 |
| 1.33 | 0.004189 | 409 | 522 | COL27A1 | collagen, type XXVII, alpha 1 |
| 1.33 | 0.027765 | 349 | 440 | STRBP | spermatid perinuclear RNA binding protein |
| 1.33 | 0.005231 | 848 | 1078 | | Cluster Incl. AB002319: |
| 1.33 | 0.014343 | 300 | 382 | | Human DNA sequence from clone RP4-581F12 on chromosome Xq21 |
| 1.33 | 0.021626 | 471 | 584 | HRASLS3 | HRAS-like suppressor 3 |
| 1.33 | 0.041068 | 3683 | 4624 | WDR26 | WD repeat domain 26 |
| 1.32 | 0.037754 | 4498 | 5658 | HADHA | hydroxyacyl-Coenzyme A dehydrogenase, alpha subunit |
| 1.32 | 0.025313 | 950 | 1186 | FLJ20296 | hypothetical protein FLJ20296 |
| 1.32 | 0.042952 | 605 | 758 | TERE1 | transitional epithelia response protein |
| 1.32 | 0.017555 | 1013 | 1267 | KPNA6 | karyopherin alpha 6 (importin alpha 7) |
| 1.32 | 0.042977 | 543 | 686 | MGC5178 | hypothetical protein MGC5178 |
| 1.32 | 0.032438 | 432 | 536 | VTI1B | vesicle transport through interaction with t-SNAREs homolog 1B (yeast) |
| 1.32 | 0.011467 | 738 | 909 | FARS1 | phenylalanine-tRNA synthetase 1 (mitochondrial) |
| 1.32 | 0.017511 | 845 | 1067 | PURB | purine-rich element binding protein B |
| 1.32 | 0.047708 | 432 | 533 | SEC6 | Sec 6 (S. cerevisiae) homolog |
| 1.31 | 0.041776 | 755 | 926 | FLJ90024 | fasting-inducible integral membrane protein TM6P1 |
| 1.31 | 0.041951 | 267 | 328 | | Homo sapiens cDNA FLJ44231 fis, clone THYMU3006767 |
| 1.31 | 0.047958 | 1061 | 1311 | DTNBP1 | dystrobrevin binding protein 1 |
| 1.31 | 0.0318 | 1791 | 2238 | KLHL8 | kelch-like 8 (Drosophila) |
| 1.31 | 0.019487 | 1572 | 1960 | LOC151194 | similar to hepatocellular carcinoma-associated antigen HCA557b |
| 1.31 | 9.09E-05 | 841 | 1047 | SCAND1 | SCAN domain containing 1 |
| 1.31 | 0.015477 | 577 | 717 | DJ1042K10.2 | hypothetical protein DJ1042K10.2 |
| 1.31 | 0.021146 | 842 | 1049 | CUGBP1 | CUG triplet repeat, RNA binding protein 1 |

| | | | | | |
|---|---|---|---|---|---|
| 1.31 | 0.036575 | 2601 | 3233 | C5orf7 | chromosome 5 open reading frame 7 |
| 1.31 | 0.043359 | 2338 | 2912 | KLHL8 | kelch-like 8 (Drosophila) |
| 1.31 | 0.039257 | 10815 | 13643 | CACNA1S | calcium channel, voltage-dependent, L type, alpha 1S subunit |
| 1.31 | 0.048486 | 457 | 550 | SRR | serine racemase |
| 1.3 | 0.025623 | 1039 | 1280 | MFN1 | mitofusin 1 |
| 1.3 | 0.005766 | 1317 | 1624 | EIF2C2 | eukaryotic translation initiation factor 2C, 2 |
| 1.3 | 0.01611 | 2222 | 2743 | PHC2 | polyhomeotic-like 2 (Drosophila) |
| 1.3 | 0.024929 | 8530 | 10494 | PM5 | pM5 protein |
| 1.3 | 0.023784 | 299 | 363 | VAPA | Homo sapiens cDNA FLJ10056 fis |
| 1.3 | 0.03401 | 1730 | 2119 | | cDNA DKFZp667N1113 (from clone DKFZp667N1113) |
| 1.3 | 0.038585 | 968 | 1195 | | Cluster Incl. D50928:Human mRNA for KIAA0138 gene, complete cds |
| 1.3 | 0.038772 | 1567 | 1911 | MGC45594 | hypothetical protein MGC45594 |
| 1.3 | 0.025864 | 549 | 680 | DJ122O8.2 | hypothetical protein dJ122O8.2 |
| 1.3 | 0.02805 | 500 | 610 | PEMT | phosphatidylethanolamine N-methyltransferase |
| 1.3 | 0.039896 | 801 | 994 | MYL6 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle |
| 1.29 | 0.041788 | 4970 | 6126 | | Homo sapiens cDNA clone IMAGE:3915844 3', mRNA sequence. |
| 1.29 | 0.038669 | 630 | 773 | | Homo sapiens PAC clone RP5-988G15 from 7q33-q35 |
| 1.29 | 0.020212 | 1687 | 2076 | OBRGRP | Homo sapiens leptin receptor gene-related protein (OBRGRP), mRNA. |
| 1.29 | 0.037962 | 814 | 1014 | | Homo sapiens cDNA clone IMAGE:3885682 3', mRNA sequence. |
| 1.29 | 0.033323 | 1139 | 1400 | USP30 | ubiquitin specific protease 30 |
| 1.29 | 0.024834 | 6087 | 7470 | LAMP2 | lysosomal-associated membrane protein 2 |
| 1.29 | 0.015782 | 1437 | 1764 | UBQLN1 | ubiquilin 1 |
| 1.29 | 0.016646 | 751 | 914 | CLPTM1 | cleft lip and palate associated transmembrane protein 1 |
| 1.29 | 0.022512 | 1888 | 2303 | ILK | integrin-linked kinase |
| 1.29 | 0.041161 | 1504 | 1830 | FLJ30596 | hypothetical protein FLJ30596 |
| 1.29 | 0.009615 | 1300 | 1591 | SURF4 | surfeit 4 |
| 1.29 | 0.046356 | 3413 | 4196 | DPP8 | dipeptidylpeptidase 8 |
| 1.29 | 0.034969 | 3712 | 4549 | RAC1 | ras-related C3 botulinum toxin substrate 1 |
| 1.29 | 0.048394 | 410 | 503 | na | Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133. |
| 1.29 | 0.043314 | 1345 | 1627 | DAZAP1 | DAZ associated protein 1 |

| | | | | | |
|---|---|---|---|---|---|
| 1.29 | 0.023027 | 2687 | 3263 | ZNF207 | zinc finger protein 207 |
| 1.29 | 0.031894 | 580 | 706 | | GHRH gene for growth hormone releasing hormone (somatocrinin) |
| 1.29 | 0.0423 | 586 | 702 | SNX24 | sorting nexing 24 |
| 1.28 | 0.007346 | 851 | 1051 | CLK3 | CDC-like kinase 3 |
| 1.28 | 0.012364 | 1227 | 1495 | SHMT1 | serine hydroxymethyltransferase 1 (soluble) |
| 1.28 | 0.002102 | 1502 | 1822 | STARD10 | START domain containing 10 |
| 1.28 | 0.017725 | 1509 | 1843 | PDCD6IP | programmed cell death 6 interacting protein |
| 1.28 | 0.014614 | 1403 | 1703 | | Homo sapiens cDNA clone IMAGE:2258219 3', mRNA sequence. |
| 1.28 | 0.046018 | 2597 | 3144 | | Homo sapiens cDNA clone IMAGE:4248227 5', mRNA sequence. |
| 1.28 | 0.005699 | 2959 | 3601 | DKFZP762D096 | hypothetical protein DKFZp762D096 |
| 1.28 | 0.034486 | 2190 | 2642 | RP42 | RP42 homolog |
| 1.28 | 0.007791 | 676 | 828 | | Homo sapiens mRNA for hSLP-1 protein |
| 1.28 | 0.013111 | 2487 | 3041 | TRIM8 | tripartite motif-containing 8 |
| 1.28 | 0.043167 | 720 | 876 | VAPA | VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa |
| 1.28 | 0.017132 | 1212 | 1468 | | Homo sapiens cDNA clone IMAGE:117868 3', mRNA sequence. |
| 1.28 | 0.040376 | 459 | 559 | TFDP2 | transcription factor Dp-2 (E2F dimerization partner 2) |
| 1.28 | 0.015622 | 1446 | 1753 | UBE2L3 | ubiquitin-conjugating enzyme E2L 3 |
| 1.28 | 0.014465 | 792 | 963 | KIAA0685 | KIAA0685 |
| 1.28 | 0.02618 | 333 | 398 | ELMO2 | engulfment and cell motility 2 (ced-12 homolog, C. elegans) |
| 1.28 | 0.017363 | 2318 | 2806 | HT014 | HT014 |
| 1.28 | 0.012066 | 20067 | 24258 | CALM1 | calmodulin 1 (phosphorylase kinase, delta) |
| 1.28 | 0.016359 | 3474 | 4186 | FLJ25476 | FLJ25476 protein |
| 1.28 | 0.029186 | 1309 | 1573 | NFIA | nuclear factor I/A |
| 1.28 | 0.042526 | 489 | 599 | | DKFZp434D0918 |
| 1.28 | 0.037922 | 769 | 925 | FLJ20618 | hypothetical protein FLJ20618 |
| 1.28 | 0.034484 | 243 | 293 | CTPS2 | CTP synthase II |
| 1.27 | 0.042953 | 1583 | 1934 | SEC61B | Sec61 beta subunit |
| 1.27 | 0.020012 | 6594 | 7946 | RAF1 | v-raf-1 murine leukemia viral oncogene homolog 1 |
| 1.27 | 0.032844 | 2462 | 2969 | STK25 | serine/threonine kinase 25 (STE20 homolog, yeast) |
| 1.27 | 0.046162 | 2152 | 2585 | MAST205 | microtubule associated testis specific serine/threonine protein kinase |

| | | | | | |
|---|---|---|---|---|---|
| 1.27 | 0.017436 | 208 | 251 | YT521 | splicing factor YT521-B |
| 1.27 | 0.017322 | 1116 | 1342 | LOC51619 | ubiquitin-conjugating enzyme HBUCE1 |
| 1.27 | 0.006467 | 10882 | 13014 | RTN2 | reticulon 2 |
| 1.27 | 0.013493 | 583 | 688 | CARD10 | caspase recruitment domain family, member 10 |
| 1.26 | 0.003138 | 2100 | 2519 | | Human transducin-like enhancer protein (TLE2) mRNA |
| 1.26 | 0.012897 | 1446 | 1731 | FLJ10702 | hypothetical protein FLJ10702 |
| 1.26 | 0.01822 | 2162 | 2598 | PPP2R5E | protein phosphatase 2, regulatory subunit B (B56), epsilon isoform |
| 1.26 | 0.04741 | 4814 | 5760 | ENTH | enthoprotin |
| 1.26 | 0.007143 | 605 | 725 | | Human DNA sequence from clone RP4-620E11 on chromosome 20q11 |
| 1.26 | 0.0408 | 1821 | 2165 | SPS2 | selenophosphate synthetase 2 |
| 1.26 | 0.008071 | 608 | 728 | BET1 | BET1 homolog (S. cerevisiae) |
| 1.26 | 0.039808 | 2792 | 3340 | MBD4 | methyl-CpG binding domain protein 4 |
| 1.26 | 0.040299 | 756 | 904 | CIRBP | cold inducible RNA binding protein |
| 1.26 | 0.003235 | 350 | 420 | MGC15677 | hypothetical protein MGC15677 |
| 1.26 | 0.012895 | 3061 | 3637 | ZNF148 | zinc finger protein 148 (pHZ-52) |
| 1.26 | 0.04391 | 740 | 892 | CRSP9 | cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa |
| 1.26 | 0.044863 | 687 | 823 | TIX1 | triple homeobox 1 |
| 1.26 | 0.031267 | 918 | 1091 | SMARCC2 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, |
| 1.25 | 0.02618 | 1408 | 1672 | MGC33867 | hypothetical protein MGC33867 |
| 1.25 | 0.031027 | 1177 | 1419 | KIAA0116 | KIAA0116 protein |
| 1.25 | 0.045198 | 726 | 854 | SMARCB1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, |
| 1.25 | 0.037178 | 199 | 234 | MGC3248 | dynactin 4 |
| 1.25 | 0.011163 | 744 | 874 | | hypothetical protein FLJ20378 [Homo sapiens] |
| 1.25 | 0.026771 | 730 | 875 | NFIC | nuclear factor I/C (CCAAT-binding transcription factor) |
| 1.25 | 0.00226 | 1180 | 1394 | ADPRHL2 | ADP-ribosylhydrolase like 2 |
| 1.25 | 0.038581 | 516 | 600 | SMARCC1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin |
| 1.25 | 0.032669 | 797 | 941 | | AL566034 |
| 1.25 | 0.021224 | 618 | 730 | FLJ20555 | hypothetical protein FLJ20555 |
| 1.25 | 0.025941 | 1050 | 1253 | DAZAP1 | DAZ associated protein 1 |

| | | | | | |
|---|---|---|---|---|---|
| 1.24 | 0.042655 | 2629 | 3136 | ZAP128 | peroxisomal long-chain acyl-coA thioesterase |
| 1.24 | 0.026498 | 4214 | 4993 | RBAF600 | retinoblastoma-associated factor 600 |
| 1.24 | 0.028187 | 637 | 748 | ULK1 | unc-51-like kinase 1 (C. elegans) |
| 1.24 | 0.032664 | 447 | 524 | CDV-1 | carnitine deficiency-associated gene expressed in ventricle 1 |
| 1.24 | 0.021861 | 711 | 831 | GOLGB1 | cDNA DKFZp686F09142 (from clone DKFZp686F09142) |
| 1.24 | 0.027321 | 11836 | 13895 | LOC284612 | hypothetical protein LOC284612 |
| 1.24 | 0.03435 | 3164 | 3692 | IFRD2 | interferon-related developmental regulator 2 |
| 1.24 | 0.041531 | 5186 | 6087 | HSPC063 | HSPC063 protein |
| 1.24 | 0.023749 | 570 | 663 | CSNK1E | casein kinase 1, epsilon |
| 1.24 | 0.015327 | 961 | 1115 | TAF11 | TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor |
| 1.23 | 0.027282 | 2492 | 2921 | C5orf6 | chromosome 5 open reading frame 6 |
| 1.23 | 0.011244 | 1240 | 1441 | SUPT6H | suppressor of Ty 6 homolog (S. cerevisiae) |
| 1.23 | 0.028998 | 1374 | 1610 | MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) |
| 1.23 | 0.002445 | 814 | 954 | VPS39 | vacuolar protein sorting 39 (yeast) |
| 1.23 | 0.021509 | 858 | 1010 | ERAL1 | Era G-protein-like 1 (E. coli) |
| 1.23 | 0.043062 | 391 | 463 | ATPAF2 | ATP synthase mitochondrial F1 complex assembly factor 2 |
| 1.23 | 0.034495 | 7436 | 8698 | | Homo sapiens cDNA clone IMAGE:6503168, partial cds |
| 1.23 | 0.037403 | 903 | 1039 | DAZAP2 | DAZ associated protein 2 |
| 1.23 | 0.024772 | 708 | 818 | PTBP1 | polypyrimidine tract binding protein 1 |
| 1.23 | 0.024837 | 176 | 205 | | hypothetical protein FLJ20837 [Homo sapiens] |
| 1.23 | 0.022704 | 1150 | 1351 | RBM4 | RNA binding motif protein 4 |
| 1.23 | 0.045725 | 6236 | 7286 | HNRPDL | heterogeneous nuclear ribonucleoprotein D-like |
| 1.23 | 0.046288 | 2374 | 2769 | SEC10L1 | SEC10-like 1 (S. cerevisiae) |
| 1.22 | 0.014122 | 1345 | 1567 | SEC24C | SEC24 related gene family, member C (S. cerevisiae) |
| 1.22 | 0.017348 | 842 | 970 | DAB2IP | DAB2 interacting protein |
| 1.22 | 0.015685 | 1544 | 1795 | STX17 | syntaxin 17 |
| 1.22 | 0.044122 | 623 | 709 | | IMAGE-2276188 |
| 1.22 | 0.027138 | 3700 | 4289 | PRO0149 | PRO0149 protein |
| 1.22 | 0.044374 | 665 | 765 | MGC20255 | hypothetical protein MGC20255 |
| 1.22 | 0.035424 | 7134 | 8246 | GNA13 | guanine nucleotide binding protein (G protein), alpha 13 |

| | | | | | |
|---|---|---|---|---|---|
| 1.22 | 0.033215 | 987 | 1129 | TAPBP | TAP binding protein (tapasin) |
| 1.22 | 0.017931 | 3672 | 4202 | C20orf108 | chromosome 20 open reading frame 108 |
| 1.22 | 0.034744 | 2007 | 2323 | | Homo sapiens cDNA FLJ11723 fis, clone HEMBA1005314. |
| 1.22 | 0.013791 | 8450 | 9728 | SQSTM1 | sequestosome 1 |
| 1.22 | 0.035963 | 691 | 798 | DDX5 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 |
| 1.22 | 0.037644 | 1109 | 1284 | | Homo sapiens cDNA clone IMAGE:83358 3', mRNA sequence. |
| 1.22 | 0.038148 | 822 | 942 | CPNE1 | copine I |
| 1.22 | 0.032408 | 5630 | 6490 | PSAP | prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) |
| 1.22 | 0.007543 | 2117 | 2441 | | Homo sapiens cDNA clone IMAGE:3866021 3', mRNA sequence. |
| 1.21 | 0.016921 | 2387 | 2749 | PTD012 | PTD012 protein |
| 1.21 | 0.04504 | 898 | 1042 | MGC2747 | hypothetical protein MGC2747 |
| 1.21 | 0.023294 | 416 | 472 | na | Homo sapiens, clone IMAGE:5302722, mRNA |
| 1.21 | 0.047218 | 6986 | 8019 | G3BP | Ras-GTPase-activating protein SH3-domain-binding protein |
| 1.2 | 0.024545 | 936 | 1065 | FTSJ3 | FtsJ homolog 3 (E. coli) |
| 1.2 | 0.011746 | 652 | 740 | MGC10084 | hypothetical protein MGC10084 |
| 1.2 | 0.048159 | 3846 | 4380 | TGOLN2 | trans-golgi network protein 2 |
| 1.2 | 0.0336 | 3750 | 4268 | LOC51255 | hypothetical protein LOC51255 |

## 2.2 Probe sets showing a lower average expression level in IR offspring

| fold | p-value | IS | IR | Gene Symbol | Gene Title |
|---|---|---|---|---|---|
| -2.73 | 0.041618 | 265 | 115 | GPRC5B | G protein-coupled receptor, family C, group 5, member B |
| -2.6 | 4.90E-05 | 390 | 141 | MGC40053 | hypothetical protein MGC40053 |
| -2.27 | 0.011031 | 6796 | 2801 | LPL | lipoprotein lipase |
| -2.26 | 0.025928 | 350 | 138 |  | Homo sapiens transcribed sequences |
| -1.94 | 0.043594 | 221 | 117 | ZNF19 | zinc finger protein 19 (KOX 12) |
| -1.92 | 0.028766 | 5622 | 2765 | LPL | lipoprotein lipase |
| -1.9 | 0.025167 | 283 | 147 | KIAA0831 | KIAA0831 |
| -1.85 | 0.010548 | 316 | 159 | VR22 | alpha-catenin-like protein |
| -1.83 | 0.020334 | 218 | 119 | CDC42BPA | CDC42 binding protein kinase alpha (DMPK-like) |
| -1.82 | 0.008891 | 223 | 117 |  | Homo sapiens cDNA FLJ46713 fis, clone TRACH3016885 |
| -1.8 | 0.001782 | 263 | 137 | C10orf13 | chromosome 10 open reading frame 13 |
| -1.8 | 0.008551 | 4766 | 2452 | PANX1 | pannexin 1 |
| -1.76 | 0.031594 | 333 | 186 |  | Homo sapiens cDNA clone IMAGE:21583 3', mRNA sequence. |
| -1.76 | 0.0128 | 622 | 339 |  | Homo sapiens transcribed sequences |
| -1.75 | 0.041239 | 334 | 189 | ANGPT2 | angiopoietin 2 |
| -1.73 | 0.03574 | 290 | 151 | CPN2 | carboxypeptidase N, polypeptide 2, 83kD |
| -1.73 | 0.001214 | 391 | 211 | ENPEP | glutamyl aminopeptidase (aminopeptidase A) |
| -1.72 | 0.011236 | 204 | 108 | MGC34290 | hypothetical protein MGC34290 |
| -1.7 | 0.0389 | 599 | 328 |  | septin 10 |
| -1.7 | 0.011663 | 223 | 124 | CAPNS2 | calpain small subunit 2 |
| -1.69 | 0.030575 | 729 | 379 | PANX1 | pannexin 1 |
| -1.67 | 0.011468 | 304 | 172 | CUGBP1 | CUG triplet repeat, RNA binding protein 1 |
| -1.64 | 0.011255 | 460 | 263 | na | Homo sapiens, clone IMAGE:5111803, mRNA |
| -1.64 | 0.027024 | 210 | 126 | UQCRC2 | ubiquinol-cytochrome c reductase core protein II |
| -1.63 | 0.010469 | 686 | 414 | DHTKD1 | dehydrogenase E1 and transketolase domain containing 1 |
| -1.61 | 0.010449 | 218 | 128 | FLJ20989 | hypothetical protein FLJ20989 |

| | | | | | |
|---|---|---|---|---|---|
| -1.6 | 0.006026 | 292 | 174 | | weak similarity to protein ref:NP_009056.1 (H.sapiens) |
| -1.6 | 0.028722 | 349 | 205 | MSI2 | musashi homolog 2 (Drosophila) |
| -1.6 | 0.034293 | 1709 | 985 | TM4SF13 | transmembrane 4 superfamily member 13 |
| -1.58 | 0.035901 | 466 | 293 | LPAAT-e | acid acyltransferase-epsilon |
| -1.58 | 0.04008 | 588 | 342 | PANX1 | pannexin 1 |
| -1.58 | 0.022348 | 559 | 345 | ZNF207 | zinc finger protein 207 |
| -1.57 | 0.005992 | 288 | 174 | | similar to Homo sapiens putative secreted protein (SIG11) |
| -1.54 | 0.015648 | 825 | 493 | HMGN1 | high-mobility group nucleosome binding domain 1 |
| -1.54 | 0.016385 | 429 | 269 | | A32422 dihydrolipoamide S-(2-methylpropanoyl)transferase (EC 2.3.1.-) |
| -1.54 | 0.035209 | 2540 | 1476 | HCFC1R1 | host cell factor C1 regulator 1 (XPO1 dependant) |
| -1.54 | 0.040769 | 242 | 152 | C13orf10 | chromosome 13 open reading frame 10 |
| -1.53 | 0.01243 | 1937 | 1201 | WDR5B | WD repeat domain 5B |
| -1.53 | 0.016035 | 500 | 314 | SH3BGRL2 | SH3BGRL2 gene for SH3 domain binding glutamic acid-rich protein-like 2 |
| -1.53 | 0.001127 | 835 | 515 | PHLDA3 | pleckstrin homology-like domain, family A, member 3 |
| -1.53 | 0.032258 | 321 | 207 | APC10 | anaphase-promoting complex subunit 10 |
| -1.52 | 0.033126 | 475 | 296 | SIP1 | survival of motor neuron protein interacting protein 1 |
| -1.51 | 0.002094 | 648 | 408 | TM6SF1 | transmembrane 6 superfamily member 1 |
| -1.5 | 0.041059 | 2434 | 1504 | H19 | H19, imprinted maternally expressed untranslated mRNA |
| -1.5 | 0.020117 | 280 | 174 | | hypothetical protein FLJ20489 [Homo sapiens] |
| -1.49 | 0.036475 | 6142 | 3889 | | gb=AA436930 |
| -1.48 | 0.014755 | 254 | 165 | PRKACB | protein kinase, cAMP-dependent, catalytic, beta |
| -1.48 | 0.032721 | 291 | 191 | ZTL1 | hZTL1; Homo sapiens zinc transporter ZTL1 (ZTL1) mRNA, complete cds. |
| -1.47 | 0.032212 | 310 | 202 | C14orf116 | chromosome 14 open reading frame 116 |
| -1.47 | 0.044601 | 340 | 223 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 |
| -1.47 | 0.028463 | 498 | 314 | FLJ21603 | hypothetical protein FLJ21603 |
| -1.46 | 0.046988 | 1645 | 1107 | STN2 | stonin 2 |
| -1.46 | 0.012708 | 319 | 211 | LOC285989 | hypothetical protein LOC285989 |

| | | | | | |
|---|---|---|---|---|---|
| -1.45 | 0.035498 | 219 | 141 | PRKAA1 | protein kinase, AMP-activated, alpha 1 catalytic subunit |
| -1.45 | 0.033651 | 704 | 456 | SNAP23 | synaptosomal-associated protein, 23kDa |
| -1.43 | 0.014219 | 663 | 441 | KIAA1458 | KIAA1458 protein |
| -1.43 | 0.04741 | 605 | 401 | LOC92270 | hypothetical protein LOC92270 |
| -1.41 | 0.02834 | 400 | 267 | PDCD2 | programmed cell death 2 |
| -1.4 | 0.031966 | 649 | 448 | LDHD | lactate dehydrogenase D |
| -1.4 | 0.001625 | 357 | 244 | TM9SF1 | transmembrane 9 superfamily member 1 |
| -1.4 | 0.004631 | 2084 | 1420 | DHTKD1 | dehydrogenase E1 and transketolase domain containing 1 |
| -1.4 | 0.034484 | 754 | 517 | | Homo sapiens transcribed sequences |
| -1.4 | 0.016161 | 1099 | 729 | | FabG (beta-ketoacyl-(acyl-carrier-protein) reductase, E coli) |
| -1.39 | 0.036375 | 709 | 496 | RRM1 | ribonucleotide reductase M1 polypeptide |
| -1.39 | 0.034109 | 646 | 444 | AP2A2 | adaptor-related protein complex 2, alpha 2 subunit |
| -1.38 | 0.010238 | 251 | 172 | LOC220929 | hypothetical protein LOC220929 |
| -1.37 | 0.035389 | 491 | 344 | IRF1 | interferon regulatory factor 1 |
| -1.37 | 0.029335 | 2337 | 1621 | MIB | Homo sapiens mRNA; cDNA DKFZp779F0655 (from clone DKFZp779F0655) |
| -1.36 | 0.04609 | 424 | 301 | LOC90799 | hypothetical protein BC009518 |
| -1.36 | 0.037209 | 2948 | 2080 | KIAA0114 | KIAA0114 gene product |
| -1.36 | 0.028297 | 1069 | 748 | | Homo sapiens cDNA clone IMAGE:4183999 5', mRNA sequence. |
| -1.35 | 0.003033 | 460 | 326 | KIAA0930 | KIAA0930 protein |
| -1.35 | 0.041413 | 1078 | 753 | PRO1073 | PRO1073 protein |
| -1.35 | 0.045962 | 592 | 419 | C20orf162 | chromosome 20 open reading frame 162 |
| -1.34 | 0.041978 | 668 | 478 | | Homo sapiens cDNA clone IMAGE:984135 3', mRNA sequence. |
| -1.34 | 0.015105 | 359 | 252 | | Homo sapiens transcribed sequences |
| -1.34 | 0.034452 | 484 | 347 | SLC25A27 | solute carrier family 25, member 27 |
| -1.32 | 0.019967 | 463 | 334 | TUBE1 | tubulin, epsilon 1 |
| -1.32 | 0.037727 | 588 | 421 | FLJ12519 | hypothetical protein FLJ12519 |
| -1.32 | 0.046511 | 455 | 332 | LOC283337 | Homo sapiens cDNA clone MGC:61706 IMAGE:6162269, complete cds |
| -1.32 | 0.01165 | 592 | 429 | MGC61716 | hypothetical protein MGC61716 |

| | | | | | |
|---|---|---|---|---|---|
| -1.32 | 0.038673 | 477 | 344 | FLJ12903 | hypothetical protein FLJ12903 |
| -1.31 | 0.041399 | 417 | 299 | TUBGCP5 | tubulin, gamma complex associated protein 5 |
| -1.31 | 0.047673 | 1444 | 1068 | HNLF | putative NFkB activating protein HNLF |
| -1.31 | 0.036271 | 274 | 193 | SEC5 | homolog of yeast Sec5 |
| -1.3 | 0.029231 | 931 | 686 | PPP2R5E | protein phosphatase 2, regulatory subunit B (B56), epsilon isoform |
| -1.3 | 0.017072 | 17397 | 12641 | | Homo sapiens mRNA; cDNA DKFZp779F0655 (from clone DKFZp779F0655) |
| -1.3 | 0.03853 | 342 | 246 | HSPC129 | hypothetical protein HSPC129 |
| -1.3 | 0.039358 | 562 | 404 | CBFA2T2 | core-binding factor, runt domain, alpha subunit 2; translocated to, 2 |
| -1.28 | 0.040276 | 1052 | 785 | FLJ10490 | hypothetical protein FLJ10490 |
| -1.28 | 0.042933 | 703 | 528 | AF311304 | hypothetical protein AF311304 |
| -1.27 | 0.032061 | 3842 | 2889 | CLTA | clathrin, light polypeptide (Lca) |
| -1.27 | 0.033279 | 613 | 454 | PRSC2 | protease, cysteine, 2 (NEDD8 specific) |
| -1.27 | 0.041491 | 7771 | 5770 | na | Homo sapiens, clone IMAGE:5314816, mRNA |
| -1.26 | 0.027258 | 863 | 657 | LSR7 | lipopolysaccharide specific response-7 protein |
| -1.23 | 0.049324 | 500 | 393 | | Human DNA sequence from clone RP1-101G11 on chromosome 22q12 |
| -1.22 | 0.006087 | 1050 | 816 | SKB1 | SKB1 homolog (S. pombe) |
| -1.22 | 0.016254 | 809 | 634 | SMYD3 | SET and MYND domain containing 3 |
| -1.22 | 0.037461 | 1029 | 806 | ABCC5 | ATP-binding cassette, sub-family C (CFTR/MRP), member 5 |
| -1.22 | 0.036174 | 831 | 648 | KIAA0141 | KIAA0141 gene product |
| -1.21 | 0.038202 | 231 | 179 | PPA2 | inorganic pyrophosphatase 2 |
| -1.21 | 0.022662 | 578 | 448 | NOL5A | nucleolar protein 5A (56kDa with KKE/D repeat) |
| -1.2 | 0.035265 | 1556 | 1230 | RPL27A | ribosomal protein L27a |

SUPPLEMENTARY DATA

## 2.3 Probe sets showing a higher significance between IR offspring and control

| p-value | IS | IR | Gene Symbol | Gene Title |
|---:|---:|---:|---|---|
| 4.90E-05 | 390 | 141 | MGC40053 | hypothetical protein MGC40053 |
| 9.09E-05 | 841 | 1047 | SCAND1 | SCAN domain containing 1 |
| 1.14E-04 | 3920 | 5268 | BHLHB2 | basic helix-loop-helix domain containing, class B, 2 |
| 5.12E-04 | 142 | 258 | MGC20481 | Homo sapiens mRNA; cDNA DKFZp451P134 (from clone DKFZp451P134). |
| 0.0010708 | 664 | 859 |  | H.sapiens mRNA for CLC-7 chloride channel protein |
| 0.0011273 | 835 | 515 | PHLDA3 | pleckstrin homology-like domain, family A, member 3 |
| 0.0012136 | 391 | 211 | ENPEP | glutamyl aminopeptidase (aminopeptidase A) |
| 0.0016247 | 357 | 244 | TM9SF1 | transmembrane 9 superfamily member 1 |
| 0.0017825 | 263 | 137 | C10orf13 | chromosome 10 open reading frame 13 |
| 0.0020943 | 648 | 408 | TM6SF1 | transmembrane 6 superfamily member 1 |
| 0.0021025 | 1502 | 1822 | STARD10 | START domain containing 10 |
| 0.0021464 | 234 | 382 | D8S2298E | reproduction 8 |
| 0.0022297 | 429 | 547 |  | Homo sapiens mRNA; cDNA DKFZp586N1918 (from clone DKFZp586N1918) |
| 0.0022452 | 368 | 544 | SERPINB1 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 |
| 0.0022599 | 1180 | 1394 | ADPRHL2 | ADP-ribosylhydrolase like 2 |
| 0.0024451 | 814 | 954 | VPS39 | vacuolar protein sorting 39 (yeast) |
| 0.0028407 | 125 | 263 | MGC23920 | hypothetical protein MGC23920 |
| 0.0029477 | 422 | 600 | IRF2 | interferon regulatory factor 2 |
| 0.0030335 | 460 | 326 | KIAA0930 | KIAA0930 protein |
| 0.0030429 | 598 | 767 | MGC5309 | hypothetical protein MGC5309 |
| 0.0030666 | 170 | 237 | NOD3 | NOD3 protein |
| 0.0030689 | 600 | 799 | FKRP | fukutin related protein |
| 0.0030829 | 283 | 565 |  | hypothetical protein FLJ20378 [Homo sapiens] |
| 0.0031379 | 2100 | 2519 |  | Human transducin-like enhancer protein (TLE2) mRNA, complete cds |
| 0.0032352 | 350 | 420 | MGC15677 | hypothetical protein MGC15677 |
| 0.0033101 | 1024 | 1399 |  | Homo sapiens KIAA0397 mRNA, complete cds |
| 0.0033352 | 243 | 324 | CTNND1 | catenin (cadherin-associated protein), delta 1 |
| 0.0041226 | 3003 | 3818 | PSMD3 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 |
| 0.0041892 | 409 | 522 | COL27A1 | collagen, type XXVII, alpha 1 |

| | | | | |
|---|---|---|---|---|
| 0.0045425 | 158 | 205 | KIAA1018 | KIAA1018 protein |
| 0.0045568 | 182 | 308 | LOC157697 | hypothetical protein LOC157697 |
| 0.0046307 | 2084 | 1420 | DHTKD1 | dehydrogenase E1 and transketolase domain containing 1 |
| 0.0046805 | 18153 | 23670 | CALM1 | calmodulin 1 (phosphorylase kinase, delta) |
| 0.004968 | 497 | 651 | MGAT4B | mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B |
| 0.0052313 | 848 | 1078 | | Human mRNA for KIAA0321 gene, partial cds |
| 0.0055987 | 932 | 2109 | GDF8 | growth differentiation factor 8 |
| 0.005699 | 2959 | 3601 | DKFZP762D096 | hypothetical protein DKFZp762D096 |
| 0.0057658 | 1317 | 1624 | EIF2C2 | eukaryotic translation initiation factor 2C, 2 |
| 0.0057923 | 293 | 536 | KIAA0493 | Homo sapiens cDNA FLJ39739 fis, clone SMINT2016440. |
| 0.0058844 | 762 | 998 | AEBP2 | AE(adipocyte enhancer)-binding protein 2 |
| 0.0059446 | 505 | 645 | FLJ10534 | hypothetical protein FLJ10534 |
| 0.0059917 | 288 | 174 | | similar to Homo sapiens putative secreted protein (SIG11) |
| 0.0060265 | 292 | 174 | | Ubiquitously transcribed TPR gene on Y chromosome [Homo sapiens] |
| 0.0060868 | 1050 | 816 | SKB1 | SKB1 homolog (S. pombe) |
| 0.006313 | 397 | 534 | IRF3 | interferon regulatory factor 3 |
| 0.0064463 | 237 | 324 | CAB2 | CAB2 protein |
| 0.0064672 | 10882 | 13014 | RTN2 | reticulon 2 |
| 0.0068427 | 1199 | 1799 | DSCR2 | Down syndrome critical region gene 2 |
| 0.0071432 | 605 | 725 | | Human DNA sequence from clone RP4-620E11 on chromosome 20q11.2-12. |
| 0.0073456 | 851 | 1051 | CLK3 | CDC-like kinase 3 |
| 0.0074745 | 223 | 304 | FLJ30313 | hypothetical protein FLJ30313 |
| 0.0074966 | 717 | 984 | ATP9B | ATPase, Class II, type 9B |
| 0.0075432 | 2117 | 2441 | | Homo sapiens cDNA clone IMAGE:3866021 3', mRNA sequence. |
| 0.0077911 | 676 | 828 | | Homo sapiens mRNA for hSLP-1 protein |
| 0.0079534 | 283 | 501 | USP7 | ubiquitin specific protease 7 (herpes virus-associated) |
| 0.0080713 | 608 | 728 | BET1 | BET1 homolog (S. cerevisiae) |
| 0.0083089 | 3672 | 4810 | HP1-BP74 | HP1-BP74 |
| 0.0083283 | 320 | 554 | C10orf33 | chromosome 10 open reading frame 33 |
| 0.0083868 | 528 | 776 | AP3D1 | adaptor-related protein complex 3, delta 1 subunit |
| 0.0084684 | 127 | 244 | | Homo sapiens clone IMAGE:111705 mRNA sequence |

| | | | | |
|---|---|---|---|---|
| 0.0085038 | 436 | 563 | PIM1 | pim-1 oncogene |
| 0.0085505 | 4766 | 2452 | PANX1 | pannexin 1 |
| 0.0085891 | 949 | 1675 | P8 | p8 protein (candidate of metastasis 1) |
| 0.0086669 | 1845 | 2415 | CAT | catalase |
| 0.0088908 | 223 | 117 | | Homo sapiens cDNA FLJ46713 fis, clone TRACH3016885 |
| 0.0090526 | 801 | 1085 | DNAJB2 | DnaJ (Hsp40) homolog, subfamily B, member 2 |
| 0.0093947 | 142 | 229 | PVRL3 | poliovirus receptor-related 3 |
| 0.0095245 | 106 | 242 | ACOX3 | acyl-Coenzyme A oxidase 3, pristanoyl |
| 0.009615 | 1300 | 1591 | SURF4 | surfeit 4 |
| 0.0099315 | 183 | 268 | ABCC9 | ATP-binding cassette, sub-family C (CFTR/MRP), member 9 |
| 0.0099572 | 957 | 1266 | MGC10526 | hypothetical protein MGC10526 |
| 0.0102376 | 251 | 172 | LOC220929 | hypothetical protein LOC220929 |
| 0.0104487 | 218 | 128 | FLJ20989 | hypothetical protein FLJ20989 |
| 0.010469 | 686 | 414 | DHTKD1 | dehydrogenase E1 and transketolase domain containing 1 |
| 0.0105482 | 316 | 159 | VR22 | alpha-catenin-like protein |
| 0.0106105 | 349 | 472 | KIAA1545 | KIAA1545 protein |
| 0.0106125 | 9382 | 13309 | ENIGMA | enigma (LIM domain protein) |
| 0.0106264 | 1267 | 1597 | | Homo sapiens cDNA, IMAGE-2314928 |
| 0.0107438 | 416 | 528 | ISGF3G | interferon-stimulated transcription factor 3, gamma 48kDa |
| 0.0108105 | 2369 | 4476 | GLRX | glutaredoxin (thioltransferase) |
| 0.0110309 | 6796 | 2801 | LPL | lipoprotein lipase |
| 0.0110763 | 265 | 359 | SDS3 | likely ortholog of mouse Sds3 |
| 0.0111337 | 251 | 373 | FLJ45246 | FLJ45246 protein |
| 0.0111634 | 744 | 874 | | weak similarity to hypothetical protein FLJ20378 [Homo sapiens] |
| 0.011236 | 204 | 108 | MGC34290 | hypothetical protein MGC34290 |
| 0.0112442 | 1240 | 1441 | SUPT6H | suppressor of Ty 6 homolog (S. cerevisiae) |
| 0.011255 | 460 | 263 | na | Homo sapiens, clone IMAGE:5111803, mRNA |
| 0.0114672 | 738 | 909 | FARS1 | phenylalanine-tRNA synthetase 1 (mitochondrial) |
| 0.0114678 | 304 | 172 | CUGBP1 | CUG triplet repeat, RNA binding protein 1 |
| 0.0116498 | 592 | 429 | MGC61716 | hypothetical protein MGC61716 |
| 0.0116628 | 223 | 124 | CAPNS2 | calpain small subunit 2 |

| | | | | |
|---|---|---|---|---|
| 0.0116747 | 195 | 272 | | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0496. |
| 0.0117462 | 652 | 740 | MGC10084 | hypothetical protein MGC10084 |
| 0.0119267 | 577 | 750 | PIP5K1C | phosphatidylinositol-4-phosphate 5-kinase, type I, gamma |
| 0.0120659 | 20067 | 24258 | CALM1 | calmodulin 1 (phosphorylase kinase, delta) |
| 0.0123644 | 1227 | 1495 | SHMT1 | serine hydroxymethyltransferase 1 (soluble) |
| 0.0124299 | 1937 | 1201 | WDR5B | WD repeat domain 5B |
| 0.012522 | 745 | 1002 | KIAA0478 | KIAA0478 gene product |
| 0.0125885 | 193 | 331 | CCNG2 | cyclin G2 |
| 0.012629 | 279 | 387 | | Human clone IMAGE-74593 unknown protein mRNA, partial cds |
| 0.0127085 | 319 | 211 | LOC285989 | hypothetical protein LOC285989 |
| 0.0127996 | 622 | 339 | | Homo sapiens transcribed sequences |
| 0.0128946 | 3061 | 3637 | ZNF148 | zinc finger protein 148 (pHZ-52) |
| 0.0128975 | 1446 | 1731 | FLJ10702 | hypothetical protein FLJ10702 |
| 0.0130651 | 1044 | 1434 | DUSP3 | dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) |
| 0.0131112 | 2487 | 3041 | TRIM8 | tripartite motif-containing 8 |
| 0.0133048 | 967 | 1222 | | Homo sapiens cDNA clone IMAGE:1521385 3', mRNA sequence. |
| 0.0134927 | 583 | 688 | CARD10 | caspase recruitment domain family, member 10 |
| 0.0136074 | 242 | 336 | TTBK2 | Homo sapiens, clone IMAGE:5267224, mRNA |
| 0.0137913 | 8450 | 9728 | SQSTM1 | sequestosome 1 |
| 0.0138713 | 2716 | 3618 | C6orf107 | chromosome 6 open reading frame 107 |
| 0.0139329 | 247 | 339 | na | Homo sapiens cDNA FLJ37848 fis, clone BRSSN2013544. |
| 0.0139591 | 466 | 700 | RFX5 | regulatory factor X, 5 (influences HLA class II expression) |
| 0.0140629 | 667 | 892 | | Homo sapiens cDNA, IMAGE-1471822 |
| 0.0141222 | 1345 | 1567 | SEC24C | SEC24 related gene family, member C (S. cerevisiae) |
| 0.0142192 | 663 | 441 | KIAA1458 | KIAA1458 protein |
| 0.0142565 | 653 | 894 | RFX5 | regulatory factor X, 5 (influences HLA class II expression) |
| 0.0143427 | 300 | 382 | | Human DNA sequence from clone RP4-581F12 on chromosome Xq21 |
| 0.0144646 | 792 | 963 | KIAA0685 | KIAA0685 |
| 0.0146141 | 1403 | 1703 | | Homo sapiens cDNA clone IMAGE:2258219 3', mRNA sequence. |
| 0.0146379 | 578 | 821 | ACOX2 | acyl-Coenzyme A oxidase 2, branched chain |
| 0.0147448 | 230 | 327 | PDLIM2 | PDZ and LIM domain 2 (mystique) |

| | | | | |
|---|---|---|---|---|
| 0.0147549 | 254 | 165 | PRKACB | protein kinase, cAMP-dependent, catalytic, beta |
| 0.0148045 | 1263 | 1759 | EIF4EL3 | eukaryotic translation initiation factor 4E-like 3 |
| 0.0148351 | 932 | 1226 | | STX16 gene for syntaxin 16 and a novel gene for a protein similar to fly CG7340 |
| 0.0149495 | 840 | 1051 | CTMP | C-terminal modulator protein |
| 0.0149501 | 708 | 1562 | FBXO6 | F-box only protein 6 |
| 0.0149971 | 1092 | 1409 | TBCC | tubulin-specific chaperone c |
| 0.0151046 | 359 | 252 | | Homo sapiens transcribed sequences |
| 0.0152904 | 808 | 1026 | MIR | c-mir, cellular modulator of immune recognition |
| 0.0153267 | 961 | 1115 | TAF11 | TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa |
| 0.0154769 | 577 | 717 | DJ1042K10.2 | hypothetical protein DJ1042K10.2 |
| 0.015589 | 556 | 717 | Rab11-FIP2 | KIAA0941 protein |
| 0.0156216 | 1446 | 1753 | UBE2L3 | ubiquitin-conjugating enzyme E2L 3 |
| 0.0156483 | 825 | 493 | HMGN1 | high-mobility group nucleosome binding domain 1 |
| 0.0156853 | 1544 | 1795 | STX17 | syntaxin 17 |
| 0.0157818 | 1437 | 1764 | UBQLN1 | ubiquilin 1 |
| 0.0160349 | 500 | 314 | SH3BGRL2 | SH3 domain binding glutamic acid-rich protein-like 2, complete sequence. |
| 0.0161098 | 2222 | 2743 | PHC2 | polyhomeotic-like 2 (Drosophila) |
| 0.0161609 | 1099 | 729 | | GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene |
| 0.0162536 | 809 | 634 | SMYD3 | SET and MYND domain containing 3 |
| 0.0163552 | 201 | 289 | AGA | aspartylglucosaminidase |
| 0.0163588 | 3474 | 4186 | FLJ25476 | FLJ25476 protein |
| 0.0163643 | 394 | 1013 | HIST1H3C | histone 1, H3c |
| 0.016385 | 429 | 269 | | A32422 dihydrolipoamide S-(2-methylpropanoyl)transferase |
| 0.0166463 | 751 | 914 | CLPTM1 | cleft lip and palate associated transmembrane protein 1 |
| 0.0166894 | 213 | 272 | | Homo sapiens cDNA FLJ13558 fis, clone PLACE1007743. |
| 0.0168818 | 329 | 426 | FNBP3 | formin binding protein 3 |
| 0.0169206 | 2387 | 2749 | PTD012 | PTD012 protein |
| 0.0170719 | 17397 | 12641 | | Homo sapiens mRNA; cDNA DKFZp779F0655 (from clone DKFZp779F0655) |
| 0.0171322 | 1212 | 1468 | | Homo sapiens cDNA clone IMAGE:117868 3', mRNA sequence. |
| 0.0172502 | 3620 | 5341 | GATM | glycine amidinotransferase (L-arginine:glycine amidinotransferase) |
| 0.0173217 | 1116 | 1342 | LOC51619 | ubiquitin-conjugating enzyme HBUCE1 |

| | | | | |
|---|---|---|---|---|
| 0.0173475 | 842 | 970 | DAB2IP | DAB2 interacting protein |
| 0.0173631 | 2318 | 2806 | HT014 | HT014 |
| 0.0174362 | 208 | 251 | YT521 | splicing factor YT521-B |
| 0.0174979 | 952 | 1213 | CPR8 | cell cycle progression 8 protein |
| 0.0175112 | 845 | 1067 | PURB | purine-rich element binding protein B |
| 0.017555 | 1013 | 1267 | KPNA6 | karyopherin alpha 6 (importin alpha 7) |
| 0.0177029 | 177 | 344 | NCDN | neurochondrin |
| 0.0177252 | 1509 | 1843 | PDCD6IP | programmed cell death 6 interacting protein |
| 0.0177652 | 283 | 365 | na | Homo sapiens cDNA clone IMAGE:5269484 |
| 0.0179308 | 3672 | 4202 | C20orf108 | chromosome 20 open reading frame 108 |
| 0.0181792 | 477 | 611 | P38IP | transcription factor (p38 interacting protein) |
| 0.0182197 | 2162 | 2598 | PPP2R5E | protein phosphatase 2, regulatory subunit B (B56), epsilon isoform |
| 0.0182357 | 866 | 1110 | PKP4 | plakophilin 4 |
| 0.018429 | 593 | 790 | DKFZp762N1910 | hypothetical protein DKFZp762N1910 |
| 0.0185068 | 471 | 731 | HS6ST2 | heparan sulfate 6-O-sulfotransferase 2 |
| 0.0185507 | 3297 | 4217 | LOC283820 | hypothetical protein LOC283820 |
| 0.0186835 | 882 | 1174 | RNF41 | ring finger protein 41 |
| 0.0188238 | 1055 | 1365 | UBN1 | ubinuclein 1 |
| 0.0189178 | 1075 | 1477 | SSA2 | Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro) |
| 0.0190309 | 392 | 537 | | weak similarity to protein pir:S57447 (H.sapiens) S57447 HPBRII-7 protein - human |
| 0.0194419 | 321 | 417 | NOC4 | neighbor of COX4 |
| 0.0194859 | 270 | 382 | TBRG1 | likely ortholog of mouse transforming growth factor beta regulated gene 1 |
| 0.0194872 | 1572 | 1960 | LOC151194 | similar to hepatocellular carcinoma-associated antigen HCA557b |
| 0.0196303 | 2707 | 3501 | TRA1 | tumor rejection antigen (gp96) 1 |
| 0.019967 | 463 | 334 | TUBE1 | tubulin, epsilon 1 |

## 2.4 Probe sets overlapped in 1st and 2nd DNA chip.

| Affimetrix ID | fold change | p-value | Gene Symbol | Gene Title |
|---|---|---|---|---|
| 203549_s_at | -1.89 | 0.0404 | LPL | lipoprotein lipase |
| 203548_s_at | -1.76 | 0.0325 | LPL | lipoprotein lipase |
| 1558648_at | -1.63 | 0.00321 | MGC20481 | hypothetical protein MGC20481 |
| 227510_x_at | -1.56 | 0.0408 | PRO1073 | PRO1073 protein |
| 227461_at | -1.53 | 0.000203 | STN2 | stonin 2 |
| 224870_at | -1.5 | 0.000744 | KIAA0114 | KIAA0114 gene product |
| 204844_at | -1.47 | 0.0439 | ENPEP | glutamyl aminopeptidase (aminopeptidase A) |
| 227210_at | -1.42 | 0.0135 | SFMBT2 | Scm-like with four mbt domains 2 |
| 203279_at | -1.4 | 0.0265 | EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 |
| 227094_at | -1.38 | 0.000105 | DHTKD1 | dehydrogenase E1 and transketolase domain containing 1 |
| 212044_s_at | -1.37 | 0.0451 | RPL27A | Hypothetical protein MGC10850 |
| 213540_at | -1.37 | 0.0207 | HSD17B8 | hydroxysteroid (17-beta) dehydrogenase 8 |
| 212176_at | -1.36 | 0.0109 | C6orf111 | chromosome 6 open reading frame 111 |
| 219092_s_at | -1.26 | 0.0184 | C9orf12 | chromosome 9 open reading frame 12 |
| 218476_at | -1.23 | 0.0396 | POMT1 | protein-O-mannosyltransferase 1 |
| 226363_at | -1.23 | 0.0258 | ABCC5 | ATP-binding cassette, sub-family C (CFTR/MRP), member 5 |
| 212337_at | -1.22 | 0.035 | TI-227H | hypothetical protein TI-227H |
| 218788_s_at | -1.21 | 0.0337 | SMYD3 | SET and MYND domain containing 3 |
| 201769_at | 1.21 | 0.00847 | ENTH | enthoprotin |
| 217515_s_at | 1.22 | 0.00571 | CACNA1S | calcium channel, voltage-dependent, L type, alpha 1S subunit |
| 226152_at | 1.22 | 0.0351 | TTC7B | tetratricopeptide repeat domain 7B |
| 220235_s_at | 1.23 | 0.0482 | C1orf103 | chromosome 1 open reading frame 103 |
| 229483_at | 1.25 | 0.0418 | UBE2H | Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) |
| 36129_at | 1.26 | 0.0154 | RUTBC1 | RUN and TBC1 domain containing 1 |
| 227630_at | 1.27 | 0.0239 | PPP2R5E | Protein phosphatase 2, regulatory subunit B (B56), epsilon isoform |
| 228452_at | 1.29 | 0.0475 | C17orf39 | chromosome 17 open reading frame 39 |
| 206241_at | 1.29 | 0.0231 | KPNA5 | karyopherin alpha 5 (importin alpha 6) |
| 227718_at | 1.3 | 0.0471 | PURB | purine-rich element binding protein B |
| 209149_s_at | 1.3 | 0.0479 | TM9SF1 | transmembrane 9 superfamily member 1 |
| 229253_at | 1.3 | 0.024 | CTMP | C-terminal modulator protein |
| 238549_at | 1.31 | 0.0195 | CBFA2T2 | core-binding factor, runt domain, alpha subunit 2; translocated to, 2 |
| 228810_at | 1.32 | 0.0192 | FLJ40432 | hypothetical protein FLJ40432 |
| 1553743_at | 1.33 | 0.0125 | LOC151194 | similar to hepatocellular carcinoma-associated antigen HCA557b |
| 203275_at | 1.33 | 0.00689 | IRF2 | interferon regulatory factor 2 |
| 235456_at | 1.36 | 0.0475 | --- | --- |
| 201928_at | 1.36 | 0.00672 | PKP4 | plakophilin 4 |
| 232244_at | 1.37 | 0.0482 | KIAA1161 | KIAA1161 |
| 228700_at | 1.44 | 0.00108 | CXorf38 | Chromosome X open reading frame 38 |
| 223641_at | 1.48 | 0.043 | FLJ39207 | C219-reactive peptide |

| | | | | |
|---|---|---|---|---|
| 203766_s_at | 1.68 | 0.0242 | LMOD1 | leiomodin 1 (smooth muscle) |
| 236278_at | 1.8 | 0.0261 | --- | --- |
| 227083_at | 1.86 | 0.0369 | B3GTL | beta 3-glycosyltransferase-like |
| 228523_at | 1.96 | 0.0161 | NANOS1 | nanos homolog 1 (Drosophila) |
| 207145_at | 2.21 | 0.00725 | GDF8 | growth differentiation factor 8 |
| 237326_at | 2.3 | 0.00216 | C21orf82 | chromosome 21 open reading frame 82 |

SUPPLEMENTARY DATA

## 2.5 Summary of the EASE analysis related to mitochondria in 1st and 2nd DNA chip.

| 1st chip Genespring | | | | 2nd Chip Genespring2 | | | |
|---|---|---|---|---|---|---|---|
| **Gene Category** | **List Hits** | **List Total** | **Fisher Exact Probability** | **Gene Category** | **List Hits** | **List Total** | **Fisher Exact Probability** |
| Hs_Fatty Acid Degradation | 4 | 29 | 0.0015 | cytochrome-c oxidase activity | 6 | 479 | 0.0001 |
| regulation of fatty acid oxidation | 1 | 376 | 0.02984 | mitochondrion | 44 | 452 | 0.0012 |
| positive regulation of fatty acid metabolism | 1 | 376 | 0.02984 | thyroid hormone receptor binding | 4 | 479 | 0.0038 |
| positive regulation of fatty acid oxidation | 1 | 376 | 0.02984 | Hs_Electron Transport Chain | 8 | 41 | 0.0052 |
| | | | | NAD(P)H dehydrogenase (quinone) activity | 2 | 479 | 0.0014 |
| | | | | Hs_Electron Transport Chain | 8 | 41 | 0.0052 |
| | | | | electron transport | 26 | 473 | 0.0167 |
| | | | | electron transporter activity | 20 | 479 | 0.0287 |
| | | | | electron transfer flavoprotein | 2 | 479 | 0.0332 |
| | | | | NADPH dehydrogenase (quinone) activity | 1 | 479 | 0.0371 |
| | | | | mitochondrial electron transport\, NADH to ubiquinone | 3 | 473 | 0.0423 |

Gene ontology enrichment analysis was performed using EASE (http://david.abcc.ncifcrf.gov/ease/ease.jsp). The enrichment p-values were calculated using Fisher Exact test. Only the genes changed more than 1.2x and p<0.05 were used in this analysis

SUPPLEMENTARY DATA

## 2.6 Gene Set Enrichment Analysis (GSEA) and Random Forest classification for pathway analysis in 2nd DNA chip

**GSEA(**http://www.broad.mit.edu/gsea/index.html):

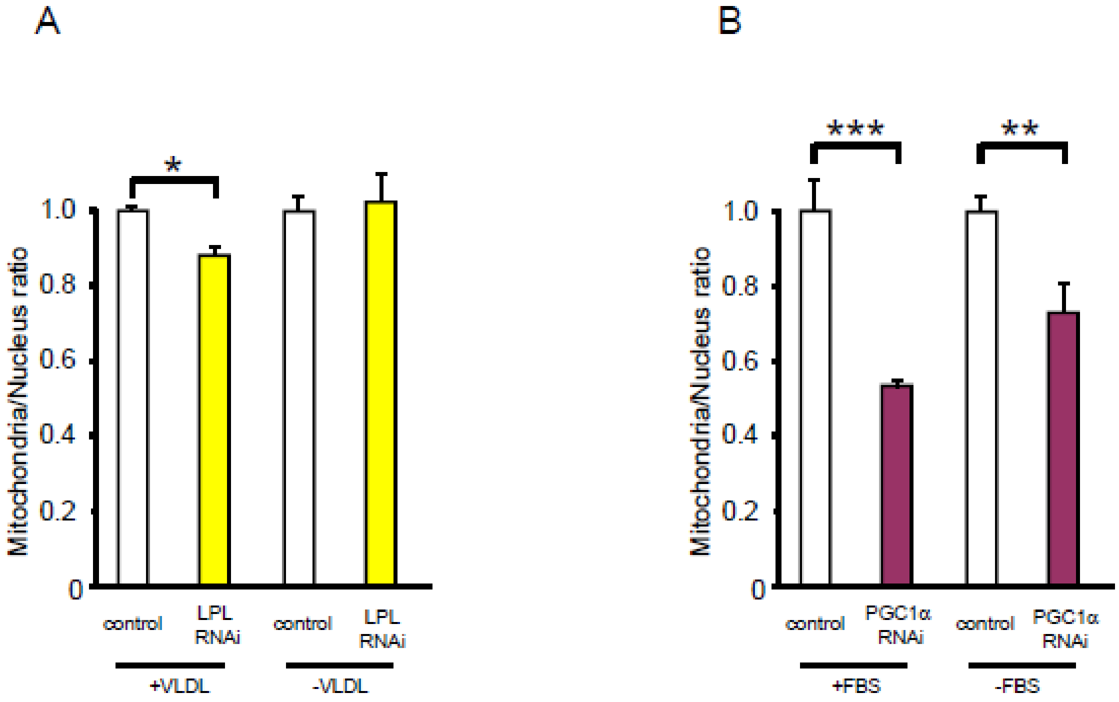
**Random Forest Classification (Pang, Hongyu Zhao et al, Bioinformatics 2006)**:

| |
|---|
| **RF error rate: classification error rate based on Random Forest(RF)** |
| **IR Enrichment: p-values based on GSEA** |
| **IS enrichment: p-values based on GSEA** |
| **BC- pathway from BioCarta** |
| **GM- pathway from GeneMapp** |

| **pathway** | **RF error rate** | **IR Enrichment** | **IS enrichment** | **num_of_genes in pathway** | |
|---|---|---|---|---|---|
| BC-Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling_ | 0.3889 | | 0.0023 | 124 | 32 |
| Huntington's disease_ | 0.6111 | | 0.005 | 108 | 313 |
| BC-T Cell Receptor Signaling Pathway_ | 0.5 | | 0.0051 | 142 | 187 |
| BC-Fc Epsilon Receptor I Signaling in Mast Cells_ | 0.5 | | 0.0052 | 123 | 144 |
| BC-BCR Signaling Pathway_ | 0.6111 | | 0.0066 | 116 | 291 |
| BC-Role of Ran in mitotic spindle regulation_ | 0.5556 | | 0.0267 | 31 | 268 |
| BC-Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor_ | 0.5 | | 0.0284 | 79 | 122 |
| BC-T Cell Receptor and CD3 Complex_ | 0.3333 | | 0.0288 | 12 | 27 |
| BC-Signaling Pathway from G-Protein Families_ | 0.4444 | | 0.0332 | 126 | 109 |
| O-Glycans biosynthesis_ | 0.3889 | | 0.0364 | 84 | 55 |
| BC-Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation_ | 0.5556 | | 0.0375 | 66 | 242 |
| BC-Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility_ | 0.6111 | | 0.041 | 63 | 344 |
| Globoside metabolism_ | 0.5 | | 0.0438 | 76 | 147 |
| Blood group glycolipid biosynthesis-neolactoseries_ | 0.3333 | | 0.0479 | 73 | 14 |
| Propanoate metabolism_ | 0.3889 | 0 | | 71 | 58 |
| Porphyrin and chlorophyll metabolism_ | 0.4444 | 0 | | 55 | 103 |
| Fatty acid metabolism_ | 0.6667 | 0 | | 176 | 374 |
| Inositol metabolism_ | 0.1111 | 0.00297 | | 8 | 1 |
| BC-Erythropoietin mediated neuroprotection through NF-kB_ | 0.3333 | 0.00975 | | 39 | 18 |
| Benzoate degradation via hydroxylation_ | 0.6111 | 0.01029 | | 10 | 292 |
| Glycolysis - Gluconeogenesis_ | 0.4444 | 0.02618 | | 157 | 89 |
| Glycosaminoglycan degradation_ | 0.3889 | 0.02862 | | 44 | 45 |
| BC-Acetylation and Deacetylation of RelA in The Nucleus_ | 0.6111 | 0.02869 | | 44 | 280 |
| Bile acid biosynthesis_ | 0.6111 | 0.03069 | | 85 | 293 |
| GM-Synthesis and Degradation of Ketone Bodies_ | 0.4444 | 0.03237 | | 8 | 114 |
| Arginine and proline metabolism_ | 0.5556 | 0.03602 | | 137 | 204 |
| BC-Regulation of hematopoiesis by cytokines_ | 0.7778 | 0.03636 | | 33 | 468 |
| BC-Activation of PKC through G protein coupled receptor_ | 0.2778 | 0.03746 | | 28 | 5 |
| Valine, leucine and isoleucine degradation_ | 0.5 | 0.04564 | | 101 | 196 |

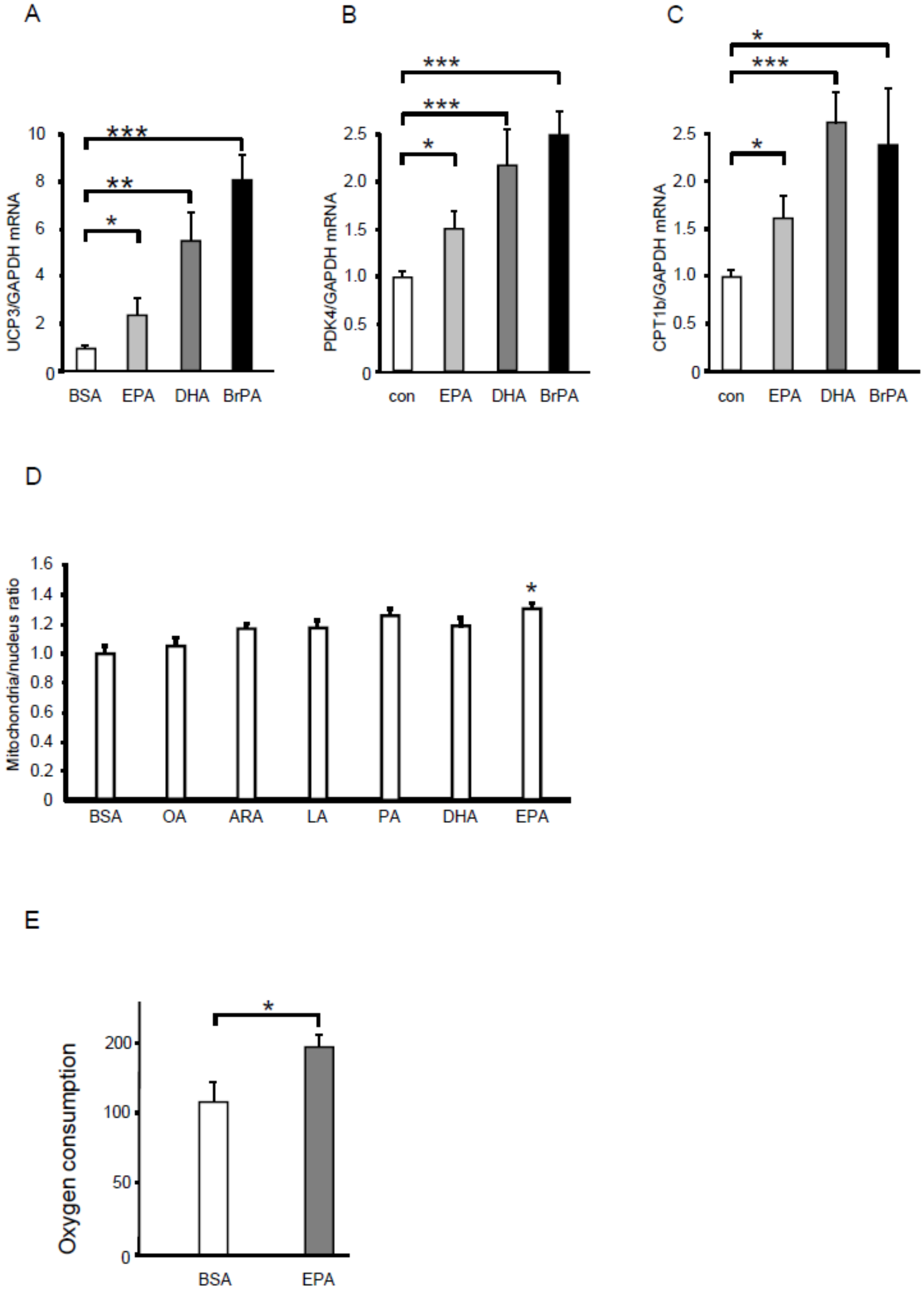
| | | | | | |
|---|---|---|---|---|---|
| BC-G-Protein Signaling Through Tubby Proteins_ | 0.2778 | 0.04625 | | 19 | 6 |
| BC-Nuclear recep1 _ | 0.6111 | 0.04695 | | 58 | 328 |
| BC-Nuclear Receptors2 _ | 0.6111 | 0.04743 | | 102 | 329 |

**Supplementary Figure 1.** Mitochondrial density measured by fluorescence dyes. (A) RC13 cells were treated with RNAi reagents against either LPL or non-targeting control (50 nM), maintained in 10%FBS RPMI for 48 hours, fixed with 1% formaldehyde, stained with mitochondria-specific Mitotracker Green, which stain mitochondria specifically and scanned with multi fluorescence reader. Nuclei were stained by DAPI. The intensity of Mitotracker dye was divided by DAPI signal to normalize cell number. RC13 cell were maintained in either FBS free RPMI or VLDL enriched RPMI. (B) RC13 cell were treated with PGC-1α RNAi reagent and maintained in either FBS free RPMI or 10% FBS RPMI.



SUPPLEMENTARY DATA

**Supplementary Figure 2.** Polyunsaturated fatty acids stimulate fat oxidation. (A)-(C) L6 myotubes were incubated with EPA (50 μM), DHA (50 μM), 2-bromopalmitate (5μM) or 0.125%BSA for 48 hours and measured mRNA expression of uncoupling protein 3 (UCP-3), pyruvate dehydrogenase kinase 4 (PDK4), and carnitine palmitoyltransferase 1B (Cpt1b) by RT-qPCR. (D) L6 myotubes were incubated with 50 μM of EPA, DHA, palmitic acid, linoleic acid, arachidonic acid, oleic acid or BSA (0.125%) for 48 hours and measured Mitochondria/Nucleus ratio by fluorescence dyes. Results presented as mean ± SEM; *P<0.05(E) L6 myotubes were incubated with 50 μM of EPA or 0.125%BSA for 48 hours. Oxygen consumption was measured with Seahorse Bioscience XF24-3 Extracellular Flux Analyzer.



**Supplementary Figure 3.** GW501516 stimulates fat oxidation and mitochondria biogenesis in rat L6 myotubes. (A)-(C) L6 myotubes were incubated with GW501516 (1μM), PPARδ activator, orBSA (0.125%) for 48 hours and measured mRNA expression of uncoupling protein 3 (UCP-3), pyruvate dehydrogenase kinase 4 (PDK4), and carnitine palmitoyltransferase 1B (Cpt1b) by RT-qPCR. (D) Protein expression of MTCOI was assessed by western blotting 48 hours after RNAi treatment against either non-targeting control (n=6) and LPL (n=6) with and withoutGW501516 (1μM). (E) L6 myotubes were treated with and without RNAi against PPARδ. Oxygen consumption was measured with Seahorse Bioscience XF24-3 Extracellular Flux Analyzer. Results presented as mean ± SEM; *P< 0.05, **P<0.005, ***P<0.0005.