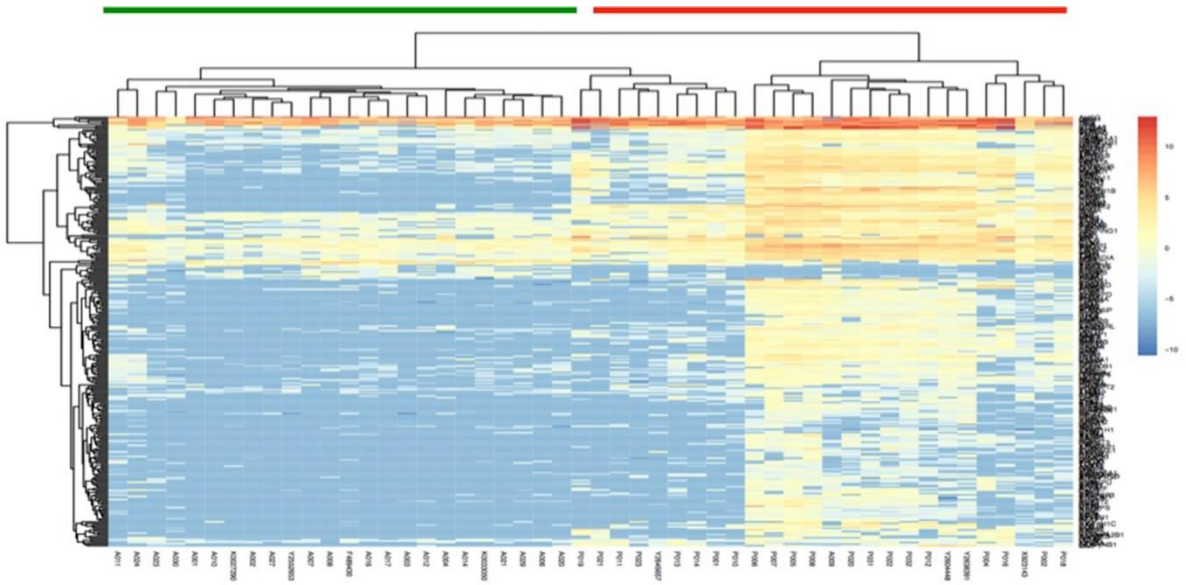
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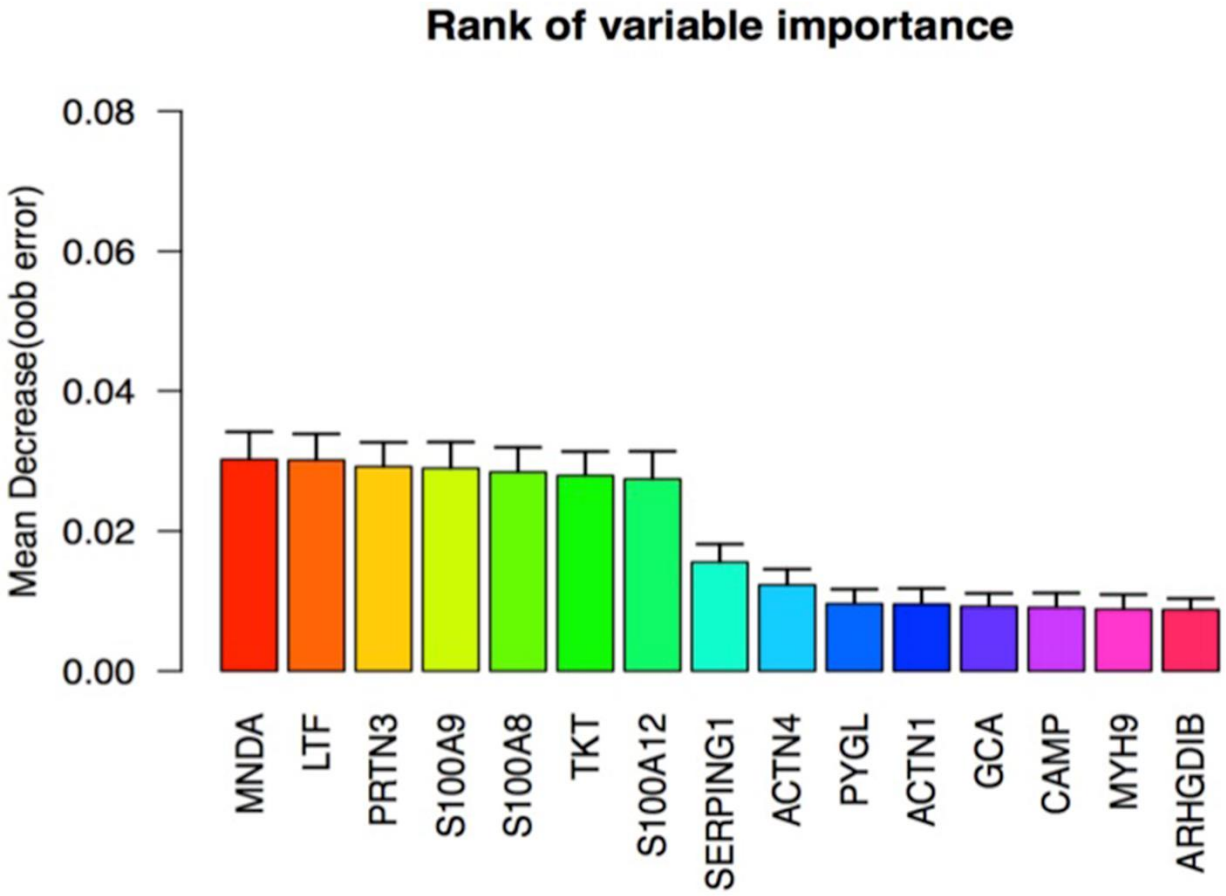
**Supplementary Figure 1. Hierarchical cluster analysis of variance genes between PJI and non-PJI patients.**



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**Supplementary Figure 2. The top 15 most important variables ranked by mean decrease in accuracy estimated from 1000 forests on oob (out of bag) samples.**



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**Supplementary Table 1. Detailed information about 256 increased proteins (red) and 14 decreased proteins (green) in PJI group.**

| Symbol | Description | pval | fc | Frequency (>=20%) | max_fot (>=1) |
|---|---|---|---|---|---|
| ATP6V1G1 | ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1 | 0.001126233 | 10.96703297 | 17 | 1.23 |
| ALYREF | Aly/REF export factor | 0.000833886 | 42.55 | 13 | 1.32 |
| IMPDH2 | IMP (inosine 5'-monophosphate) dehydrogenase 2 | 0.000543996 | Inf | 11 | 3.00 |
| RAB21 | RAB21, member RAS oncogene family | 0.00131912 | 26.28125 | 12 | 3.51 |
| APEX1 | APEX nuclease (multifunctional DNA repair enzyme) 1 | 0.002721485 | 15.28571429 | 11 | 1.14 |
| RAB10 | RAB10, member RAS oncogene family | 9.26E-06 | 21.7037037 | 21 | 1.24 |
| TCN1 | transcobalamin I (vitamin B12 binding protein, R binder family) | 0.001178466 | Inf | 10 | 1.26 |
| ERP29 | endoplasmic reticulum protein 29 | 0.001318489 | 13.75 | 13 | 1.32 |
| BST1 | bone marrow stromal cell antigen 1 | 0.000544683 | Inf | 10 | 1.42 |
| XPNPEP3 | X-prolyl aminopeptidase (aminopeptidase P) 3, putative | 0.003322088 | 5.113333333 | 18 | 1.76 |
| RAB8B | RAB8B, member RAS oncogene family | 7.61E-06 | Inf | 17 | 1.77 |
| H1FX | H1 histone family, member X | 0.001739011 | 44.08333333 | 11 | 2.06 |
| LAMC1 | laminin, gamma 1 (formerly LAMB2) | 0.00626351 | 103.25 | 16 | 2.22 |
| INHBA | inhibin, beta A | 0.029144894 | 22.47368421 | 14 | 2.78 |
| APEH | acylaminoacyl-peptide hydrolase | 0.015259075 | 5.644230769 | 14 | 3.37 |
| RNASET2 | ribonuclease T2 | 0.026281398 | 4.04048583 | 26 | 3.73 |

| | | | | | |
|---|---|---|---|---|---|
| SUB1 | SUB1 homolog (S. cerevisiae) | 0.003247959 | 16.78350515 | 14 | 3.89 |
| RNASE3 | ribonuclease, RNase A family, 3 | 0.002084972 | 37.84375 | 11 | 4.01 |
| PDLIM4 | PDZ and LIM domain 4 | 0.000307834 | 9.713815789 | 17 | 8.68 |
| CDA | cytidine deaminase | 1.87E-07 | 51.83448276 | 21 | 13.11 |
| COPB1 | coatomer protein complex, subunit beta 1 | 0.00049329 | 299.1428571 | 13 | 19.59 |
| PDXK | pyridoxal (pyridoxine, vitamin B6) kinase | 0.00422977 | 353.3 | 10 | 23.74 |
| RAB8A | RAB8A, member RAS oncogene family | 0.000107824 | Inf | 12 | 25.45 |
| NAPRT1 | nicotinate phosphoribosyltransferase domain containing 1 | 0.010806646 | 30 | 10 | 1.14 |
| RAB14 | RAB14, member RAS oncogene family | 4.60E-05 | Inf | 13 | 1.24 |
| PSMD2 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 | 0.0090801 | 64 | 15 | 1.32 |
| CYBB | cytochrome b-245, beta polypeptide | 0.000107751 | Inf | 12 | 1.36 |
| ARF4 | ADP-ribosylation factor 4 | 0.005970263 | 8.514285714 | 10 | 2.01 |
| PPIB | peptidylprolyl isomerase B (cyclophilin B) | 7.73E-05 | 8.153225806 | 18 | 2.07 |
| PGLS | 6-phosphogluconolactonase | 2.63E-06 | 392.3333333 | 18 | 2.53 |
| STX7 | syntaxin 7 | 0.002538548 | 24.2 | 13 | 2.63 |
| OSTF1 | osteoclast stimulating factor 1 | 0.001443116 | 13.16101695 | 13 | 3.50 |

| | | | | | |
|---|---|---|---|---|---|
| CBX3 | chromobox homolog 3 | 0.000955993 | 4.997101449 | 17 | 3.59 |
| BLVRA | biliverdin reductase A | 0.017393195 | 33.1875 | 15 | 3.61 |
| PDIA4 | protein disulfide isomerase family A, member 4 | 0.000876786 | 55.66666667 | 16 | 3.99 |
| AIF1 | allograft inflammatory factor 1 | 0.004186685 | 3.151898734 | 11 | 4.74 |
| TBCA | tubulin folding cofactor A | 0.018522843 | 4.893617021 | 17 | 4.85 |
| STK4 | serine/threonine kinase 4 | 7.60E-06 | Inf | 16 | 6.81 |
| RAB1B | RAB1B, member RAS oncogene family | 6.98E-05 | 225.5 | 20 | 9.31 |
| GMFG | glia maturation factor, gamma | 2.47E-06 | 3.691939346 | 21 | 12.53 |
| PRDX3 | peroxiredoxin 3 | 0.007559489 | 12.61702128 | 15 | 1.58 |
| SLC9A3R1 | solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 1 | 0.008331721 | 3.781021898 | 10 | 1.37 |
| RCSD1 | RCSD domain containing 1 | 0.000914678 | 118.4 | 12 | 1.64 |
| CCT8 | chaperonin containing TCP1, subunit 8 (theta) | 0.000352405 | 6.902439024 | 16 | 1.88 |
| RNH1 | ribonuclease/angiogenin inhibitor 1 | 0.018616175 | 3.112185687 | 28 | 2.43 |
| RAN | RAN, member RAS oncogene family | 8.27E-05 | 6.699588477 | 16 | 2.60 |
| EEF1G | eukaryotic translation elongation factor 1 gamma | 0.000246179 | 11.96226415 | 17 | 3.00 |

| | | | | | |
|---|---|---|---|---|---|
| KIF26A | kinesin family member 26A | 0.00702621 | 9.210526316 | 35 | 4.76 |
| PRSS3 | protease, serine, 3 | 0.006435003 | 4.381443299 | 21 | 8.90 |
| GLRX | glutaredoxin (thioltransferase) | 0.000749255 | 7.434715822 | 13 | 11.17 |
| MARCKS | myristoylated alanine-rich protein kinase C substrate | 0.000207798 | 16.62765957 | 34 | 19.69 |
| MIF | macrophage migration inhibitory factor (glycosylation-inhibiting factor) | 4.57E-05 | 7.175252112 | 39 | 92.90 |
| PARK7 | parkinson protein 7 | 0.00338566 | 24.16912488 | 22 | 117.61 |
| CPPED1 | calcineurin-like phosphoesterase domain containing 1 | 0.000567568 | 35.63333333 | 15 | 11.27 |
| ARG1 | arginase, liver | 4.59E-05 | Inf | 13 | 1.54 |
| PDIA6 | protein disulfide isomerase family A, member 6 | 0.005100566 | 3.527777778 | 18 | 1.76 |
| ATP6V1A | ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A | 0.001398842 | 7.12345679 | 18 | 1.81 |
| VPS29 | vacuolar protein sorting 29 homolog (S. cerevisiae) | 0.000353884 | 51 | 13 | 1.81 |
| CCT6A | chaperonin containing TCP1, subunit 6A (zeta 1) | 0.007673807 | 4.4 | 11 | 2.14 |
| F13B | coagulation factor XIII, B polypeptide | 0.020185434 | 3.080769231 | 43 | 2.35 |
| RAB2A | RAB2A, member RAS oncogene family | 0.003816678 | 9.503448276 | 13 | 4.27 |

| | | | | | |
|---|---|---|---|---|---|
| ANP32B | acidic (leucine-rich) nuclear phosphoprotein 32 family, member B | 0.000898309 | 6.78600823 | 13 | 4.61 |
| EFHD2 | EF-hand domain family, member D2 | 0.003602363 | 8.451505017 | 26 | 4.86 |
| MMP8 | matrix metallopeptidase 8 (neutrophil collagenase) | 3.73E-07 | 3.661016949 | 25 | 5.84 |
| SH3BGRL | SH3 domain binding glutamic acid-rich protein like | 0.000616389 | 3.928486293 | 23 | 7.45 |
| KCTD12 | potassium channel tetramerization domain containing 12 | 0.023674384 | 22.71052632 | 23 | 8.36 |
| APOD | apolipoprotein D | 0.016007033 | 11.75333333 | 11 | 9.22 |
| S100P | S100 calcium binding protein P | 9.56E-05 | 55.95959596 | 15 | 38.26 |
| S100A11 | S100 calcium binding protein A11 | 9.28E-06 | 29.54166667 | 26 | 54.14 |
| ATP6V1E1 | ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1 | 0.006493288 | 10.55813953 | 10 | 1.57 |
| NCL | nucleolin | 3.29E-05 | 9.466666667 | 21 | 1.30 |
| APMAP | adipocyte plasma membrane associated protein | 0.00322983 | 5.699115044 | 29 | 1.39 |
| HSPA4 | heat shock 70kDa protein 4 | 0.017359258 | 6.368421053 | 19 | 1.66 |
| VASP | vasodilator-stimulated phosphoprotein | 0.00015573 | 10.07051282 | 16 | 3.87 |

| | | | | | |
|---|---|---|---|---|---|
| BID | BH3 interacting domain death agonist | 2.07E-05 | 71.03225806 | 18 | 4.99 |
| RAB7A | RAB7A, member RAS oncogene family | 6.71E-05 | 6.839669421 | 18 | 8.04 |
| GLIPR2 | GLI pathogenesis-related 2 | 0.033914927 | 3.237518911 | 41 | 12.11 |
| CRP | C-reactive protein, pentraxin-related | 6.93E-05 | 10.94508512 | 33 | 36.53 |
| CCT3 | chaperonin containing TCP1, subunit 3 (gamma) | 0.002721485 | 714.5 | 12 | 202.32 |
| COTL1 | coactosin-like 1 (Dictyostelium) | 0.001229306 | 86.91332471 | 20 | 341.91 |
| ALDH16A1 | aldehyde dehydrogenase 16 family, member A1 | 0.001171273 | 32.4 | 16 | 1.16 |
| MMP2 | matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) | 0.047364411 | 12.84615385 | 30 | 2.61 |
| DCN | decorin | 0.028229537 | 16.29411765 | 10 | 2.64 |
| RAD23B | RAD23 homolog B (S. cerevisiae) | 0.006283481 | 44 | 12 | 6.20 |
| MVP | major vault protein | 0.000822306 | 51.66666667 | 14 | 1.17 |
| DYNC1H1 | dynein, cytoplasmic 1, heavy chain 1 | 0.00524231 | 75.5 | 13 | 1.19 |
| PRKCD | protein kinase C, delta | 1.90E-05 | Inf | 15 | 1.53 |
| NAGK | N-acetylglucosamine kinase | 0.000315343 | 17.42307692 | 15 | 2.99 |
| RNPEP | arginyl aminopeptidase (aminopeptidase B) | 0.007341984 | 45.61111111 | 12 | 5.60 |

| | | | | | |
|---|---|---|---|---|---|
| GBE1 | glucan (1,4-alpha-), branching enzyme 1 | 0.000260845 | 40.68831169 | 14 | 9.04 |
| CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | 8.85E-06 | 7.698854337 | 26 | 9.62 |
| CAMP | cathelicidin antimicrobial peptide | 1.56E-07 | 7.044169611 | 36 | 10.48 |
| RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | 0.003239643 | 7.933263816 | 11 | 13.48 |
| STOM | stomatin | 0.010291071 | 7.053691275 | 18 | 2.75 |
| FKBP1A | FK506 binding protein 1A, 12kDa | 7.30E-06 | 5.094457014 | 36 | 80.25 |
| NPEPPS | aminopeptidase puromycin sensitive | 0.000368339 | 18.92307692 | 16 | 1.59 |
| HNRNPU | heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) | 0.01381913 | 3.407407407 | 18 | 2.21 |
| PRKCSH | protein kinase C substrate 80K-H | 0.011384987 | 5.776744186 | 16 | 2.72 |
| ADSS | adenylosuccinate synthase | 9.56E-06 | 10.55 | 18 | 3.46 |
| CALR | calreticulin | 0.001303684 | 4.959627329 | 25 | 3.80 |
| BIN2 | bridging integrator 2 | 3.19E-06 | 17.44339623 | 22 | 3.86 |
| BPI | bactericidal/permeability-increasing protein | 5.56E-08 | 19.04733728 | 23 | 5.64 |
| PON3 | paraoxonase 3 | 0.002796547 | 3.165814463 | 46 | 6.72 |

| | | | | | |
|---|---|---|---|---|---|
| RHOG | ras homolog family member G | 1.91E-05 | 22.41780822 | 17 | 7.70 |
| PRDX5 | peroxiredoxin 5 | 2.12E-05 | 12.94313725 | 17 | 9.88 |
| ARHGAP25 | Rho GTPase activating protein 25 | 2.22E-05 | 103.1666667 | 16 | 1.57 |
| ZYX | zyxin | 0.00028673 | 30.75862069 | 15 | 2.26 |
| LDHB | lactate dehydrogenase B | 0.002057046 | 5.517571885 | 43 | 6.57 |
| GPX3 | glutathione peroxidase 3 (plasma) | 0.000903652 | 3.202480222 | 46 | 41.87 |
| PRTN3 | proteinase 3 | 2.30E-08 | 10.93389214 | 32 | 157.72 |
| GRB2 | growth factor receptor-bound protein 2 | 0.000385492 | 7.655487805 | 16 | 4.62 |
| HNRNPA2B1 | heterogeneous nuclear ribonucleoprotein A2/B1 | 6.80E-05 | 8.414141414 | 17 | 5.10 |
| CLTC | clathrin, heavy chain (Hc) | 0.000727209 | 11.4 | 17 | 1.24 |
| ARHGAP1 | Rho GTPase activating protein 1 | 3.65E-06 | 191.75 | 18 | 1.66 |
| HSP90B1 | heat shock protein 90kDa beta (Grp94), member 1 | 0.048483774 | 3.043352601 | 35 | 2.03 |
| IDH1 | isocitrate dehydrogenase 1 (NADP+), soluble | 0.017515668 | 6.271008403 | 34 | 5.07 |
| GCA | grancalcin, EF-hand calcium binding protein | 1.42E-08 | 28.90540541 | 24 | 6.39 |

| | | | | | |
|---|---|---|---|---|---|
| XRCC6 | X-ray repair complementing defective repair in Chinese hamster cells 6 | 0.000177263 | 98.83333333 | 15 | 10.60 |
| FTO | fat mass and obesity associated | 0.013690681 | 21.07784431 | 13 | 10.74 |
| CNN2 | calponin 2 | 3.38E-06 | 17.77076412 | 20 | 11.37 |
| PPIA | peptidylprolyl isomerase A (cyclophilin A) | 0.000166451 | 4.251518987 | 46 | 61.76 |
| VCAN | versican | 0.00666626 | 4.350649351 | 33 | 1.22 |
| EEF1D | eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) | 0.000329087 | 5.306358382 | 20 | 1.98 |
| GYG1 | glycogenin 1 | 0.000389671 | 55.54166667 | 14 | 4.43 |
| ARHGDIA | Rho GDP dissociation inhibitor (GDI) alpha | 3.50E-07 | 3.921884086 | 48 | 30.60 |
| GNAI2 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 | 0.001100101 | 13.60294118 | 12 | 1.44 |
| FERMT3 | fermitin family member 3 | 6.36E-05 | 42.94444444 | 17 | 1.65 |
| UBA1 | ubiquitin-like modifier activating enzyme 1 | 8.29E-05 | 11.85714286 | 22 | 2.08 |
| EHD1 | EH-domain containing 1 | 0.000102568 | 12.22727273 | 18 | 2.23 |
| F13A1 | coagulation factor XIII, A1 polypeptide | 0.012866784 | 5.755555556 | 31 | 2.39 |

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|---|---|---|---|---|---|
| HCLS1 | hematopoietic cell-specific Lyn substrate 1 | 0.000278173 | 3.441489362 | 21 | 3.34 |
| YWHAQ | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide | 0.002664997 | 3.003259984 | 42 | 5.44 |
| ARPC3 | actin related protein 2/3 complex, subunit 3, 21kDa | 3.68E-06 | 17.1799591 | 26 | 16.08 |
| WDR1 | WD repeat domain 1 | 5.58E-06 | 13.4114053 | 24 | 22.84 |
| TXN | thioredoxin | 9.13E-06 | 64.08064516 | 24 | 88.94 |
| EIF4A1 | eukaryotic translation initiation factor 4A1 | 0.026569938 | 12.03773585 | 14 | 3.25 |
| AHCY | adenosylhomocysteinase | 0.000352574 | 9.761261261 | 16 | 4.35 |
| APOBR | apolipoprotein B receptor | 1.85E-05 | 7.704166667 | 32 | 4.23 |
| FAM49B | family with sequence similarity 49, member B | 1.96E-06 | 21.93506494 | 21 | 5.63 |
| ANXA3 | annexin A3 | 9.22E-08 | 1246.5 | 21 | 7.10 |
| SERPINB1 | serpin peptidase inhibitor, clade B (ovalbumin), member 1 | 3.46E-07 | 98.27272727 | 23 | 8.65 |
| PYCARD | PYD and CARD domain containing | 2.58E-07 | 37.80740741 | 31 | 11.57 |
| CLIC1 | chloride intracellular channel 1 | 0.001344218 | 6.522210184 | 30 | 16.77 |
| VAT1 | vesicle amine transport protein 1 homolog (T. californica) | 8.56E-06 | 11.08528785 | 31 | 22.53 |

| | | | | | |
|---|---|---|---|---|---|
| ARPC1B | actin related protein 2/3 complex, subunit 1B, 41kDa | 4.28E-06 | 17.09511111 | 30 | 32.57 |
| GSTP1 | glutathione S-transferase pi 1 | 3.66E-06 | 5.454403498 | 34 | 32.77 |
| ARPC4 | actin related protein 2/3 complex, subunit 4, 20kDa | 0.000346429 | 7.253721683 | 14 | 37.68 |
| ACLY | ATP citrate lyase | 6.95E-06 | 30.53333333 | 19 | 1.82 |
| HNRNPK | heterogeneous nuclear ribonucleoprotein K | 2.23E-06 | 7.23255814 | 32 | 2.93 |
| LMNB1 | lamin B1 | 6.53E-05 | 7.262295082 | 27 | 2.96 |
| GSTO1 | glutathione S-transferase omega 1 | 4.00E-05 | 6.68 | 33 | 7.89 |
| WARS | tryptophanyl-tRNA synthetase | 0.02865007 | 3.96969697 | 25 | 2.45 |
| HMGB1 | high mobility group box 1 | 4.66E-06 | 10.61842105 | 19 | 19.80 |
| ARPC5 | actin related protein 2/3 complex, subunit 5, 16kDa | 1.34E-05 | 9.195228822 | 23 | 29.34 |
| APCS | amyloid P component, serum | 2.61E-07 | 5.344537121 | 50 | 85.41 |
| HNRNPC | heterogeneous nuclear ribonucleoprotein C (C1/C2) | 0.001383197 | 10.87234043 | 14 | 1.78 |
| NCF2 | neutrophil cytosolic factor 2 | 2.92E-05 | 9.443661972 | 20 | 2.74 |
| HDGF | hepatoma-derived growth factor | 1.61E-05 | 13.38955823 | 19 | 3.95 |

| | | | | | |
|---|---|---|---|---|---|
| PSME1 | proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) | 0.009699966 | 6.783505155 | 28 | 4.06 |
| TUBB | tubulin, beta class I | 0.000385492 | 8.746938776 | 16 | 5.69 |
| PDIA3 | protein disulfide isomerase family A, member 3 | 0.000550801 | 33.84705882 | 33 | 23.13 |
| ALDOC | aldolase C, fructose-bisphosphate | 0.012644588 | 3.660273369 | 47 | 50.07 |
| ELANE | elastase, neutrophil expressed | 4.62E-08 | 9.138663172 | 25 | 180.49 |
| DBNL | drebrin-like | 8.48E-05 | 49.88235294 | 17 | 1.62 |
| FBLN1 | fibulin 1 | 0.002978775 | 3.020477816 | 48 | 4.40 |
| MMP9 | matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) | 4.63E-06 | 4.25 | 31 | 4.47 |
| NCF1 | neutrophil cytosolic factor 1 | 8.61E-06 | 14.59375 | 18 | 7.93 |
| YWHAH | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide | 5.38E-05 | 4.493112948 | 33 | 8.65 |
| EEF2 | eukaryotic translation elongation factor 2 | 0.004534899 | 23.85416667 | 31 | 27.97 |
| LBP | lipopolysaccharide binding protein | 3.87E-06 | 6.170636639 | 50 | 30.48 |
| ANXA6 | annexin A6 | 0.001203852 | 23.81818182 | 13 | 1.04 |
| CDC42 | cell division cycle 42 | 5.88E-09 | 157.8735632 | 28 | 37.16 |

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|---|---|---|---|---|---|
| F5 | coagulation factor V (proaccelerin, labile factor) | 0.003798291 | 4.533333333 | 27 | 1.16 |
| PGM1 | phosphoglucomutase 1 | 0.00022547 | 9.802197802 | 23 | 2.91 |
| PLIN3 | perilipin 3 | 0.009501019 | 6.81871345 | 27 | 4.76 |
| PCMT1 | protein-L-isoaspartate (D-aspartate) O-methyltransferase | 0.003083685 | 11.30578512 | 23 | 2.91 |
| VCP | valosin containing protein | 0.002878648 | 5.808333333 | 23 | 4.92 |
| UGP2 | UDP-glucose pyrophosphorylase 2 | 1.42E-05 | 19.01408451 | 28 | 5.80 |
| NUCB1 | nucleobindin 1 | 0.00724417 | 5.333905579 | 41 | 17.24 |
| MYL6 | myosin, light chain 6, alkali, smooth muscle and non-muscle | 7.12E-06 | 10.29722539 | 40 | 28.21 |
| HIST1H1C | histone cluster 1, H1c | 0.000245739 | Inf | 11 | 50.53 |
| MMP1 | matrix metallopeptidase 1 (interstitial collagenase) | 1.24E-07 | 319.9361702 | 26 | 65.26 |
| CTSG | cathepsin G | 6.44E-08 | 1311.321429 | 22 | 143.99 |
| PGAM1 | phosphoglycerate mutase 1 (brain) | 0.001924586 | 6.916195037 | 39 | 157.82 |
| FCN3 | ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen) | 4.62E-06 | 3.375185957 | 45 | 20.95 |
| CAPZB | capping protein (actin filament) muscle Z-line, beta | 2.04E-05 | 7.599310345 | 21 | 24.77 |

| | | | | | |
|---|---|---|---|---|---|
| HNRNPD | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) | 0.000482049 | 14.24324324 | 20 | 4.94 |
| YWHAB | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide | 0.000142768 | 4.635670357 | 48 | 32.07 |
| CPN2 | carboxypeptidase N, polypeptide 2 | 0.010769762 | 3.111804223 | 50 | 49.93 |
| HMGB2 | high mobility group box 2 | 8.61E-06 | 15.44045608 | 18 | 76.19 |
| LRRFIP1 | leucine rich repeat (in FLII) interacting protein 1 | 8.33E-05 | 7.93129771 | 36 | 1.77 |
| PDCD6IP | programmed cell death 6 interacting protein | 1.18E-05 | 9.711711712 | 18 | 2.58 |
| GDI2 | GDP dissociation inhibitor 2 | 0.000479237 | 11.35222672 | 27 | 5.22 |
| NAMPT | nicotinamide phosphoribosyltransferase | 8.93E-08 | 15.21973929 | 26 | 14.97 |
| P4HB | prolyl 4-hydroxylase, beta polypeptide | 8.79E-05 | 11.84979138 | 47 | 24.55 |
| TUBA4A | tubulin, alpha 4a | 0.000188553 | 7.484076433 | 15 | 2.17 |
| PGD | phosphogluconate dehydrogenase | 4.17E-07 | 7.690920938 | 26 | 56.84 |
| LCN2 | lipocalin 2 | 1.68E-07 | 245.375 | 24 | 90.65 |
| S100A12 | S100 calcium binding protein A12 | 1.18E-08 | 4.929368753 | 32 | 251.00 |

| | | | | | |
|---|---|---|---|---|---|
| VCL | vinculin | 2.99E-06 | 12.39568345 | 34 | 4.44 |
| MNDA | myeloid cell nuclear differentiation antigen | 4.57E-09 | 8.864250614 | 28 | 52.13 |
| TALDO1 | transaldolase 1 | 4.20E-07 | 10.28786496 | 41 | 63.23 |
| ARHGDIB | Rho GDP dissociation inhibitor (GDI) beta | 9.10E-08 | 4.910482789 | 37 | 84.96 |
| EZR | ezrin | 0.011730417 | 4.903398927 | 26 | 4.79 |
| H2AFY | H2A histone family, member Y | 2.88E-06 | 48.61165049 | 22 | 8.46 |
| YWHAZ | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide | 2.26E-07 | 4.635608253 | 50 | 56.92 |
| HIST1H1B | histone cluster 1, H1b | 4.91E-06 | 43.26294278 | 20 | 209.52 |
| G6PD | glucose-6-phosphate dehydrogenase | 1.99E-06 | 8.565345081 | 20 | 10.91 |
| IQGAP1 | IQ motif containing GTPase activating protein 1 | 7.56E-07 | 18.43564356 | 34 | 5.26 |
| ACTR2 | ARP2 actin-related protein 2 homolog (yeast) | 2.76E-07 | 6.33406775 | 34 | 33.39 |
| C1S | complement component 1, s subcomponent | 6.96E-05 | 3.431847685 | 50 | 38.82 |
| ARPC2 | actin related protein 2/3 complex, subunit 2, 34kDa | 1.72E-07 | 10.22548028 | 37 | 45.26 |

| | | | | | |
|---|---|---|---|---|---|
| CORO1A | coronin, actin binding protein, 1A | 8.91E-08 | 8.018788727 | 40 | 47.54 |
| LSP1 | lymphocyte-specific protein 1 | 3.87E-05 | 8.234146341 | 27 | 13.27 |
| SERPING1 | serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 | 1.46E-08 | 11.82815598 | 48 | 36.42 |
| CAT | catalase | 4.77E-05 | 3.576416103 | 47 | 12.74 |
| PTPN6 | protein tyrosine phosphatase, non-receptor type 6 | 2.18E-05 | 12.90909091 | 19 | 12.16 |
| CAP1 | CAP, adenylate cyclase-associated protein 1 (yeast) | 1.25E-07 | 6.678246927 | 33 | 17.99 |
| MPO | myeloperoxidase | 2.91E-08 | 7.168127231 | 35 | 37.47 |
| SAA1 | serum amyloid A1 | 7.33E-05 | 9.025179993 | 35 | 1151.61 |
| TPI1 | triosephosphate isomerase 1 | 1.87E-06 | 5.161999398 | 50 | 23.27 |
| SPTBN1 | spectrin, beta, non-erythrocytic 1 | 6.25E-06 | 38.8125 | 18 | 2.01 |
| ACTN4 | actinin, alpha 4 | 2.50E-08 | 19.67042254 | 34 | 12.26 |
| PGK1 | phosphoglycerate kinase 1 | 2.66E-05 | 3.540204905 | 49 | 51.70 |
| BASP1 | brain abundant, membrane attached signal protein 1 | 3.52E-06 | 6.618039362 | 48 | 105.80 |
| ANXA1 | annexin A1 | 7.31E-06 | 11.34326669 | 46 | 44.07 |

| | | | | | |
|---|---|---|---|---|---|
| GPI | glucose-6-phosphate isomerase | 1.20E-06 | 44.18656716 | 26 | 25.01 |
| LTA4H | leukotriene A4 hydrolase | 8.99E-07 | 5.236263736 | 34 | 14.74 |
| HSP90AA1 | heat shock protein 90kDa alpha (cytosolic), class A member 1 | 0.000273332 | 4.291543756 | 47 | 13.06 |
| HSPA8 | heat shock 70kDa protein 8 | 5.00E-05 | 4.348450245 | 49 | 20.17 |
| TLN1 | talin 1 | 1.41E-05 | 7.152284264 | 38 | 5.26 |
| HSP90AB1 | heat shock protein 90kDa alpha (cytosolic), class B member 1 | 0.003068576 | 3.228684359 | 45 | 10.13 |
| C8B | complement component 8, beta polypeptide | 0.000295966 | 3.022024651 | 50 | 22.83 |
| PLTP | phospholipid transfer protein | 0.002024026 | 7.574827322 | 47 | 19.04 |
| TPM1 | tropomyosin 1 (alpha) | 0.000134873 | 5.288955224 | 34 | 16.34 |
| S100A8 | S100 calcium binding protein A8 | 2.82E-08 | 51.76838618 | 45 | 7826.89 |
| SPTAN1 | spectrin, alpha, non-erythrocytic 1 | 4.07E-07 | 509.625 | 25 | 23.55 |
| LDHA | lactate dehydrogenase A | 6.79E-07 | 6.748472304 | 50 | 96.17 |
| PYGL | phosphorylase, glycogen, liver | 1.73E-08 | 7.256260434 | 27 | 16.36 |
| LCP1 | lymphocyte cytosolic protein 1 (L-plastin) | 2.00E-06 | 9.285640629 | 49 | 106.66 |

| | | | | | |
|---|---|---|---|---|---|
| S100A9 | S100 calcium binding protein A9 | 1.04E-08 | 52.63080994 | 47 | 7154.33 |
| TKT | transketolase | 8.39E-09 | 19.46872461 | 41 | 21.84 |
| MSN | moesin | 6.44E-06 | 8.664498141 | 48 | 60.90 |
| GAPDH | glyceraldehyde-3-phosphate dehydrogenase | 9.15E-07 | 3.51113143 | 50 | 420.32 |
| LTF | lactotransferrin | 4.72E-10 | 84.71052632 | 27 | 39.98 |
| HPR | haptoglobin-related protein | 0.024883399 | 3.788765476 | 39 | 6808.79 |
| ENO1 | enolase 1, (alpha) | 5.56E-05 | 3.161821787 | 50 | 254.70 |
| ACTN1 | actinin, alpha 1 | 9.84E-09 | 27.45321637 | 32 | 18.46 |
| FLNA | filamin A, alpha | 2.04E-05 | 5.563442768 | 50 | 7.35 |
| ORM1 | orosomucoid 1 | 9.58E-06 | 19.73690395 | 49 | 5846.34 |
| TPM3 | tropomyosin 3 | 6.41E-06 | 6.588388215 | 47 | 55.52 |
| HP | haptoglobin | 2.25E-05 | 5.794077559 | 49 | 6544.01 |
| FGG | fibrinogen gamma chain | 3.35E-09 | 4.958265028 | 50 | 3815.02 |
| PKM | pyruvate kinase, muscle | 1.13E-06 | 5.714993278 | 50 | 116.05 |

| | | | | | |
|---|---|---|---|---|---|
| MYH9 | myosin, heavy chain 9, non-muscle | 1.30E-08 | 17.33259546 | 47 | 40.80 |
| FGB | fibrinogen beta chain | 9.44E-08 | 4.906916508 | 50 | 2399.74 |
| S100A10 | | 0.002147621 | 0.020531401 | 13 | 6.72 |
| PIKFYVE | phosphoinositide kinase, FYVE finger containing | 0.041498799 | 0.213778409 | 16 | 12.70 |
| HTRA1 | HtrA serine peptidase 1 | 0.005638702 | 0.148975791 | 23 | 2.77 |
| GPNMB | | 1.90E-05 | 0 | 14 | 2.54 |
| GM2A | GM2 ganglioside activator | 0.000944178 | 0.109659091 | 25 | 3.51 |
| ENO2 | enolase 2 (gamma, neuronal) | 5.01E-05 | 0.02919708 | 18 | 4.73 |
| DKK3 | dickkopf WNT signaling pathway inhibitor 3 | 0.000112715 | 0.127593066 | 29 | 6.41 |
| CD109 | | 0.000129661 | 0.02739726 | 18 | 2.91 |
| TNXB | tenascin XB | 0.01980318 | 0.263157895 | 36 | 2.29 |
| SOD2 | superoxide dismutase 2, mitochondrial | 0.040772122 | 0.273271247 | 35 | 169.96 |
| AHSG | alpha-2-HS-glycoprotein | 6.75E-07 | 0.161646835 | 50 | 2603.26 |
| CRTAC1 | cartilage acidic protein 1 | 0.000209056 | 0.164549277 | 45 | 81.91 |

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|---|---|---|---|---|---|
| SPP1 | secreted phosphoprotein 1 | 4.38E-05 | 0.205506557 | 41 | 143.75 |
| PRG4 | proteoglycan 4 | 0.000132032 | 0.113040238 | 49 | 27.86 |

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**Supplementary Table 2. Full list of genes in GO enrichment analysis of significantly increased proteins in PJI group.**

| Category | Term | Count | % | PValue | Genes | List Total | FDR |
|---|---|---|---|---|---|---|---|
| GOTERM_BP_FAT | GO:0017015~regulation of transforming growth factor beta receptor signaling pathway | 3 | 21.42857143 | 0.002667995 | DKK3, HTRA1, CD109 | 14 | 4.107767359 |
| GOTERM_BP_FAT | GO:1903844~regulation of cellular response to transforming growth factor beta stimulus | 3 | 21.42857143 | 0.002667995 | DKK3, HTRA1, CD109 | 14 | 4.107767359 |
| GOTERM_BP_FAT | GO:0048585~negative regulation of response to stimulus | 6 | 42.85714286 | 0.002739909 | DKK3, HTRA1, CD109, SPP1, AHSG, SOD2 | 14 | 4.216270852 |
| GOTERM_BP_FAT | GO:0031214~biomineral tissue development | 3 | 21.42857143 | 0.004731605 | GPNMB, SPP1, AHSG | 14 | 7.176052918 |
| GOTERM_BP_FAT | GO:0009968~negative regulation of signal transduction | 5 | 35.71428571 | 0.008075761 | DKK3, HTRA1, CD109, AHSG, SOD2 | 14 | 11.95387489 |
| GOTERM_BP_FAT | GO:0010648~negative regulation of cell communication | 5 | 35.71428571 | 0.010755795 | DKK3, HTRA1, CD109, AHSG, SOD2 | 14 | 15.61559624 |
| GOTERM_BP_FAT | GO:0023057~negative regulation of signaling | 5 | 35.71428571 | 0.010882778 | DKK3, HTRA1, CD109, AHSG, SOD2 | 14 | 15.78550289 |
| GOTERM_BP_FAT | GO:0090092~regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 3 | 21.42857143 | 0.011475555 | DKK3, HTRA1, CD109 | 14 | 16.57442861 |
| GOTERM_BP_FAT | GO:0071560~cellular response to transforming growth factor beta stimulus | 3 | 21.42857143 | 0.011579238 | DKK3, HTRA1, CD109 | 14 | 16.71170609 |
| GOTERM_BP_FAT | GO:0071559~response to transforming growth factor beta | 3 | 21.42857143 | 0.01178786 | DKK3, HTRA1, CD109 | 14 | 16.98728524 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| GOTERM_BP_FAT | GO:0090287~regulation of cellular response to growth factor stimulus | 3 | 21.42857143 | 0.013965268 | DKK3, HTRA1, CD109 | 14 | 19.81302266 |
| GOTERM_BP_FAT | GO:0080134~regulation of response to stress | 5 | 35.71428571 | 0.014350696 | HTRA1, CD109, SPP1, AHSG, SOD2 | 14 | 20.30373267 |
| GOTERM_BP_FAT | GO:0009605~response to external stimulus | 6 | 42.85714286 | 0.016169974 | HTRA1, CD109, GPNMB, SPP1, AHSG, SOD2 | 14 | 22.58223562 |
| GOTERM_BP_FAT | GO:0032101~regulation of response to external stimulus | 4 | 28.57142857 | 0.016704877 | HTRA1, CD109, SPP1, AHSG | 14 | 23.24046633 |
| GOTERM_BP_FAT | GO:0032102~negative regulation of response to external stimulus | 3 | 21.42857143 | 0.017784967 | HTRA1, CD109, SPP1 | 14 | 24.55364094 |
| GOTERM_BP_FAT | GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway | 3 | 21.42857143 | 0.025265832 | DKK3, HTRA1, CD109 | 14 | 33.08767891 |
| GOTERM_BP_FAT | GO:0009719~response to endogenous stimulus | 5 | 35.71428571 | 0.026861474 | DKK3, HTRA1, CD109, SPP1, AHSG | 14 | 34.78691843 |
| GOTERM_BP_FAT | GO:0030198~extracellular matrix organization | 3 | 21.42857143 | 0.027044334 | TNXB, HTRA1, SPP1 | 14 | 34.9790497 |
| GOTERM_BP_FAT | GO:0043062~extracellular structure organization | 3 | 21.42857143 | 0.027194827 | TNXB, HTRA1, SPP1 | 14 | 35.13677391 |
| GOTERM_BP_FAT | GO:0001503~ossification | 3 | 21.42857143 | 0.030910039 | GPNMB, SPP1, AHSG | 14 | 38.91879566 |
| GOTERM_BP_FAT | GO:0007167~enzyme linked receptor protein signaling pathway | 4 | 28.57142857 | 0.034828694 | DKK3, HTRA1, CD109, AHSG | 14 | 42.68354878 |
| GOTERM_BP_FAT | GO:0048678~response to axon injury | 2 | 14.28571429 | 0.044366424 | SPP1, SOD2 | 14 | 50.95865074 |
| GOTERM_BP_FAT | GO:0009966~regulation of signal transduction | 6 | 42.85714286 | 0.04789333 | DKK3, HTRA1, CD109, GPNMB, AHSG, SOD2 | 14 | 53.72457187 |

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|---|---|---|---|---|---|---|---|
| GOTERM_BP_FAT | GO:0008283~cell proliferation | 5 | 35.71428571 | 0.048693697 | PRG4, HTRA1, CD109, GPNMB, SOD2 | 14 | 54.33157369 |
| GOTERM_BP_FAT | GO:0030512~negative regulation of transforming growth factor beta receptor signaling pathway | 2 | 14.28571429 | 0.051085696 | HTRA1, CD109 | 14 | 56.10154132 |
| GOTERM_BP_FAT | GO:1903845~negative regulation of cellular response to transforming growth factor beta stimulus | 2 | 14.28571429 | 0.051085696 | HTRA1, CD109 | 14 | 56.10154132 |
| GOTERM_BP_FAT | GO:0034103~regulation of tissue remodeling | 2 | 14.28571429 | 0.051829583 | GPNMB, SPP1 | 14 | 56.63875379 |
| GOTERM_BP_FAT | GO:1903035~negative regulation of response to wounding | 2 | 14.28571429 | 0.051829583 | CD109, SPP1 | 14 | 56.63875379 |
| GOTERM_BP_FAT | GO:0010033~response to organic substance | 6 | 42.85714286 | 0.054409881 | DKK3, HTRA1, CD109, SPP1, AHSG, SOD2 | 14 | 58.45484071 |
| GOTERM_BP_FAT | GO:0065009~regulation of molecular function | 6 | 42.85714286 | 0.057419279 | GM2A, CRTAC1, CD109, S100A10, AHSG, SOD2 | 14 | 60.48291562 |
| GOTERM_BP_FAT | GO:0071495~cellular response to endogenous stimulus | 4 | 28.57142857 | 0.06008958 | DKK3, HTRA1, CD109, AHSG | 14 | 62.20448003 |
| GOTERM_BP_FAT | GO:0033273~response to vitamin | 2 | 14.28571429 | 0.065127848 | SPP1, SOD2 | 14 | 65.26308458 |
| GOTERM_BP_FAT | GO:0022617~extracellular matrix disassembly | 2 | 14.28571429 | 0.066594756 | HTRA1, SPP1 | 14 | 66.10905943 |
| GOTERM_BP_FAT | GO:0030282~bone mineralization | 2 | 14.28571429 | 0.06805954 | GPNMB, AHSG | 14 | 66.9345301 |
| GOTERM_BP_FAT | GO:0010646~regulation of cell communication | 6 | 42.85714286 | 0.069897171 | DKK3, HTRA1, CD109, GPNMB, AHSG, SOD2 | 14 | 67.94350142 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| GOTERM_BP_FAT | GO:0023051~regulation of signaling | 6 | 42.85714286 | 0.074191994 | DKK3, HTRA1, CD109, GPNMB, AHSG, SOD2 | 14 | 70.19032219 |
| GOTERM_BP_FAT | GO:0090101~negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 2 | 14.28571429 | 0.079701648 | HTRA1, CD109 | 14 | 72.85707109 |
| GOTERM_BP_FAT | GO:0071310~cellular response to organic substance | 5 | 35.71428571 | 0.079901417 | DKK3, HTRA1, CD109, AHSG, SOD2 | 14 | 72.94943046 |
| GOTERM_BP_FAT | GO:0071363~cellular response to growth factor stimulus | 3 | 21.42857143 | 0.080047395 | DKK3, HTRA1, CD109 | 14 | 73.01673424 |
| GOTERM_BP_FAT | GO:0051336~regulation of hydrolase activity | 4 | 28.57142857 | 0.080518132 | GM2A, CD109, S100A10, AHSG | 14 | 73.23270371 |
| GOTERM_BP_FAT | GO:0016310~phosphorylation | 5 | 35.71428571 | 0.084686178 | PIKFYVE, CD109, ENO2, GPNMB, AHSG | 14 | 75.07559423 |
| GOTERM_BP_FAT | GO:0070848~response to growth factor | 3 | 21.42857143 | 0.085573783 | DKK3, HTRA1, CD109 | 14 | 75.45238386 |
| GOTERM_BP_FAT | GO:0009611~response to wounding | 3 | 21.42857143 | 0.089088839 | CD109, SPP1, SOD2 | 14 | 76.8927789 |
| GOTERM_BP_FAT | GO:0008285~negative regulation of cell proliferation | 3 | 21.42857143 | 0.089560968 | CD109, GPNMB, SOD2 | 14 | 77.08010405 |
| GOTERM_BP_FAT | GO:0006897~endocytosis | 3 | 21.42857143 | 0.092888174 | PRG4, PIKFYVE, AHSG | 14 | 78.36046086 |
| GOTERM_BP_FAT | GO:0090288~negative regulation of cellular response to growth factor stimulus | 2 | 14.28571429 | 0.09477821 | HTRA1, CD109 | 14 | 79.05762609 |
| GOTERM_BP_FAT | GO:0051128~regulation of cellular component organization | 5 | 35.71428571 | 0.095669999 | HTRA1, PIKFYVE, S100A10, SPP1, AHSG | 14 | 79.3792203 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| GOTERM_BP_FAT | GO:0050790~regulation of catalytic activity | 5 | 35.71428571 | 0.099817923 | GM2A, CD109, S100A10, AHSG, SOD2 | 14 | 80.81518795 |
| GOTERM_CC_FAT | GO:0005576~extracellular region | 12 | 85.71428571 | 1.32E-04 | DKK3, TNXB, GM2A, PRG4, HTRA1, CRTAC1, CD109, ENO2, S100A10, SPP1, AHSG, SOD2 | 0.14490594 | 85.71428571 |
| GOTERM_CC_FAT | GO:0044421~extracellular region part | 11 | 78.57142857 | 2.27E-04 | DKK3, TNXB, GM2A, HTRA1, CRTAC1, CD109, ENO2, S100A10, SPP1, AHSG, SOD2 | 0.24962831 | 78.57142857 |
| GOTERM_CC_FAT | GO:0005615~extracellular space | 7 | 50 | 8.85E-04 | DKK3, TNXB, HTRA1, CD109, ENO2, SPP1, AHSG | 0.96811573 | 50 |
| GOTERM_CC_FAT | GO:0031988~membrane-bounded vesicle | 10 | 71.42857143 | 9.40E-04 | TNXB, GM2A, HTRA1, CRTAC1, ENO2, S100A10, GPNMB, SPP1, AHSG, SOD2 | 1.02888006 | 71.42857143 |
| GOTERM_CC_FAT | GO:0070062~extracellular exosome | 9 | 64.28571429 | 9.84E-04 | TNXB, GM2A, HTRA1, CRTAC1, ENO2, S100A10, SPP1, AHSG, SOD2 | 1.07657034 | 64.28571429 |
| GOTERM_CC_FAT | GO:1903561~extracellular vesicle | 9 | 64.28571429 | 0.001018971 | TNXB, GM2A, HTRA1, CRTAC1, ENO2, S100A10, SPP1, AHSG, SOD2 | 1.11437340 | 64.28571429 |

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|---|---|---|---|---|---|---|---|
| GOTERM_CC_FAT | GO:0043230~extracellular organelle | 9 | 64.28571429 | 0.001021491 | TNXB, GM2A, HTRA1, CRTAC1, ENO2, S100A10, SPP1, AHSG, SOD2 | 1.11711501 | 64.28571429 |
| GOTERM_CC_FAT | GO:0031012~extracellular matrix | 4 | 28.57142857 | 0.010506919 | TNXB, HTRA1, CRTAC1, AHSG | 10.9617007 | 28.57142857 |
| GOTERM_MF_FAT | GO:0005178~integrin binding | 2 | 14.28571429 | 0.079182371 | TNXB, GPNMB | 60.1096093 | |
| GOTERM_MF_FAT | GO:0019838~growth factor binding | 2 | 14.28571429 | 0.094878253 | HTRA1, CD109 | 67.0629512 | |