Supplementary Material

# Supplementary Methods

**Cell culture and transient transfection**

Human cervical cancer (CC) cell lines HeLa bought from Keygen Biotech (Nanjing, China) and SiHa bought from the Cell Resource Center, Peking Union Medical College (which is the headquarter of National Infrastructure of Cell Line Resource, NSTI). All cells were cultured in DMEM medium (HyClone, Logan, UT, USA) with 10% fetal bovine serum (Gibico, Carlsbad, CA, USA) and 1% penicillin-streptomycin solution in a humidified 37℃, 5% CO2 atmosphere. ZBTB32 overexpression plasmid and pcDNA3.1 empty vector (Generay Biotech, Shanghai, China) were transiently transfected using Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA) according to manufacturer’s instructions. Empty or overexpression plasmids after the cells were cultured for 48 hours, the cells were collected and RNA extracted or functionally analyzed. Briefly, 5 × 105 cells were plated in 6-well plates for 24 hours and subsequently incubated with the transfection mixture for 48 hours before cell collection and RNA extraction or functional analysis.

The sequence of ZBTB32 over-expression plasmid is as follows (Forward):

|  |  |
| --- | --- |
| 15110115120125130135140145150155160165170175180185190195110011051110111511201125113011351140114511501155116011651170117511801185119011951200120512101215122012251230123512401245125012551260126512701275128012851290129513001305131013151320132513301335134013451350135513601365137013751380138513901395140014051410141514201425143014351440144514501455146014651470147514801485149014951500150515101515152015251530153515401545155015551560156515701575158015851590159516001 | GACGGATCGG GAGATCTCCC GATCCCCTAT GGTGCACTCT CAGTACAATCTGCTCTGATG CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTTGGAGGTCGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA ACAAGGCAAGGCTTGACCGA CAATTGCATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCGCTGCTTCGCG ATGTACGGGC CAGATATACG CGTTGACATT GATTATTGACTAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATATGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCGCCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGTAACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGTAAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCCCCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTACATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCATCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGATAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAATGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTAACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAGGTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTGGCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGCGTTTAAACTT AAGCTTGGTA CCGAGCTCGG ATCCGCCACC ATGGAAGAGTCTGATCAGGG GCACACAGGC GCACTTGCAA CCTGTGCGGG TCATGAGGACAAGGCAGGCT GCCCACCTCG CCCGCACCCT CCCCCGGCCC CTCCTGCTCGGTCTCGGCCC TATGCGTGCT CTGTCTGTGG AAAGAGGTTT TCACTCAAGCATCAGATGGA GACGCACTAC CGAGTCCACA CAGGAGAGAA GCCCTTCTCCTGTAGCCTTT GTCCTCAGCG CTCCCGGGAC TTCTCGGCCA TGACCAAGCACCTGCGGACA CACGGGGCCG CTCCGTACCG CTGCTCCCTG TGCGGGGCCGGCTGTCCCAG CCTGGCCTCC ATGCAGGCGC ACATGCGCGG TCACTCGCCCAGCCAACTCC CGCCCGGATG GACCATCCGC TCCACCTTCC TCTACTCCTCCTCGAGGCCG TCTCGGCCCT CGACCTCTCC CTGTTGTCCT TCTTCCTCCACCACCTGAGA ATTCTGCAGA TATCCAGCAC AGTGGCGGCC GCTCGAGTCTAGAGGGCCCG TTTAAACCCG CTGATCAGCC TCGACTGTGC CTTCTAGTTGCCAGCCATCT GTTGTTTGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAGGTGCCACTCC CACTGTCCTT TCCTAATAAA ATGAGGAAAT TGCATCGCATTGTCTGAGTA GGTGTCATTC TATTCTGGGG GGTGGGGTGG GGCAGGACAGCAAGGGGGAG GATTGGGAAG ACAATAGCAG GCATGCTGGG GATGCGGTGGGCTCTATGGC TTCTGAGGCG GAAAGAACCA GCTGGGGCTC TAGGGGGTATCCCCACGCGC CCTGTAGCGG CGCATTAAGC GCGGCGGGTG TGGTGGTTACGCGCAGCGTG ACCGCTACAC TTGCCAGCGC CCTAGCGCCC GCTCCTTTCGCTTTCTTCCC TTCCTTTCTC GCCACGTTCG CCGGCTTTCC CCGTCAAGCTCTAAATCGGG GGCTCCCTTT AGGGTTCCGA TTTAGTGCTT TACGGCACCTCGACCCCAAA AAACTTGATT AGGGTGATGG TTCACGTAGT GGGCCATCGCCCTGATAGAC GGTTTTTCGC CCTTTGACGT TGGAGTCCAC GTTCTTTAATAGTGGACTCT TGTTCCAAAC TGGAACAACA CTCAACCCTA TCTCGGTCTATTCTTTTGAT TTATAAGGGA TTTTGCCGAT TTCGGCCTAT TGGTTAAAAAATGAGCTGAT TTAACAAAAA TTTAACGCGA ATTAATTCTG TGGAATGTGTGTCAGTTAGG GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATGCAAAGCATGC ATCTCAATTA GTCAGCAACC AGGTGTGGAA AGTCCCCAGGCTCCCCAGCA GGCAGAAGTA TGCAAAGCAT GCATCTCAAT TAGTCAGCAACCATAGTCCC GCCCCTAACT CCGCCCATCC CGCCCCTAAC TCCGCCCAGTTCCGCCCATT CTCCGCCCCA TGGCTGACTA ATTTTTTTTA TTTATGCAGAGGCCGAGGCC GCCTCTGCCT CTGAGCTATT CCAGAAGTAG TGAGGAGGCTTTTTTGGAGG CCTAGGCTTT TGCAAAAAGC TCCCGGGAGC TTGTATATCCATTTTCGGAT CTGATCAAGA GACAGGATGA GGATCGTTTC GCATGATTGAACAAGATGGA TTGCACGCAG GTTCTCCGGC CGCTTGGGTG GAGAGGCTATTCGGCTATGA CTGGGCACAA CAGACAATCG GCTGCTCTGA TGCCGCCGTGTTCCGGCTGT CAGCGCAGGG GCGCCCGGTT CTTTTTGTCA AGACCGACCTGTCCGGTGCC CTGAATGAAC TGCAGGACGA GGCAGCGCGG CTATCGTGGCTGGCCACGAC GGGCGTTCCT TGCGCAGCTG TGCTCGACGT TGTCACTGAAGCGGGAAGGG ACTGGCTGCT ATTGGGCGAA GTGCCGGGGC AGGATCTCCTGTCATCTCAC CTTGCTCCTG CCGAGAAAGT ATCCATCATG GCTGATGCAATGCGGCGGCT GCATACGCTT GATCCGGCTA CCTGCCCATT CGACCACCAAGCGAAACATC GCATCGAGCG AGCACGTACT CGGATGGAAG CCGGTCTTGTCGATCAGGAT GATCTGGACG AAGAGCATCA GGGGCTCGCG CCAGCCGAACTGTTCGCCAG GCTCAAGGCG CGCATGCCCG ACGGCGAGGA TCTCGTCGTGACCCATGGCG ATGCCTGCTT GCCGAATATC ATGGTGGAAA ATGGCCGCTTTTCTGGATTC ATCGACTGTG GCCGGCTGGG TGTGGCGGAC CGCTATCAGGACATAGCGTT GGCTACCCGT GATATTGCTG AAGAGCTTGG CGGCGAATGGGCTGACCGCT TCCTCGTGCT TTACGGTATC GCCGCTCCCG ATTCGCAGCGCATCGCCTTC TATCGCCTTC TTGACGAGTT CTTCTGAGCG GGACTCTGGGGTTCGAAATG ACCGACCAAG CGACGCCCAA CCTGCCATCA CGAGATTTCGATTCCACCGC CGCCTTCTAT GAAAGGTTGG GCTTCGGAAT CGTTTTCCGGGACGCCGGCT GGATGATCCT CCAGCGCGGG GATCTCATGC TGGAGTTCTTCGCCCACCCC AACTTGTTTA TTGCAGCTTA TAATGGTTAC AAATAAAGCAATAGCATCAC AAATTTCACA AATAAAGCAT TTTTTTCACT GCATTCTAGTTGTGGTTTGT CCAAACTCAT CAATGTATCT TATCATGTCT GTATACCGTCGACCTCTAGC TAGAGCTTGG CGTAATCATG GTCATAGCTG TTTCCTGTGTGAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC CGGAAGCATAAAGTGTAAAG CCTGGGGTGC CTAATGAGTG AGCTAACTCA CATTAATTGCGTTGCGCTCA CTGCCCGCTT TCCAGTCGGG AAACCTGTCG TGCCAGCTGCATTAATGAAT CGGCCAACGC GCGGGGAGAG GCGGTTTGCG TATTGGGCGCTCTTCCGCTT CCTCGCTCAC TGACTCGCTG CGCTCGGTCG TTCGGCTGCGGCGAGCGGTA TCAGCTCACT CAAAGGCGGT AATACGGTTA TCCACAGAATCAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA GCAAAAGGCCAGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTTCCATA GGCTCCGCCCCCCTGACGAG CATCACAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACCCGACAGGACT ATAAAGATAC CAGGCGTTTC CCCCTGGAAG CTCCCTCGTGCGCTCTCCTG TTCCGACCCT GCCGCTTACC GGATACCTGT CCGCCTTTCTCCCTTCGGGA AGCGTGGCGC TTTCTCATAG CTCACGCTGT AGGTATCTCAGTTCGGTGTA GGTCGTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCCGTTCAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAACCCGGTAAGA CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGATTAGCAGAGC GAGGTATGTA GGCGGTGCTA CAGAGTTCTT GAAGTGGTGGCCTAACTACG GCTACACTAG AAGAACAGTA TTTGGTATCT GCGCTCTGCTGAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTCTTGA TCCGGCAAACAAACCACCGC TGGTAGCGGT TTTTTTGTTT GCAAGCAGCA GATTACGCGCAGAAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGACGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC ATGAGATTATCAAAAAGGAT CTTCACCTAG ATCCTTTTAA ATTAAAAATG AAGTTTTAAATCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT ACCAATGCTTAATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAGTTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCATCTGGCCCCA GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCCAGATTTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG CGCAGAAGTGGTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAAGCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG TTGTTGCCATTGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCAGCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGCAAAAAAGCGG TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTTGGCCGCAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT AATTCTCTTACTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGACTGGTGA GTACTCAACCAAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT CTTGCCCGGCGTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCATCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTGTTGAGATCCA GTTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGCATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA GGAAGGCAAAATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATACTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT ATTGTCTCATGAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTCCGCGCACATT TCCCCGAAAA GTGCCACCTG ACGTC |

**RNA extraction and qRT-PCR**

Total RNA was isolated by TRIzol reagent (Invitrogen) and subsequently reverse transcribed with application of cDNA Reverse Transcription Kit (Vazyme Biotech, Nanjing, China). Real-time PCR was carried out using SYBR® Green PCR kit (Vazyme Biotech, Nanjing, China). The housekeeping gene GAPDH was used as loading controls. Premier sequences were listed in Table S2.

**CCK-8 assays and Transwell assays**

The transfected cells (5 × 103 cells/well) were seeded in 96-well plates and cells of each group were set up in parallel with 6 duplicate holes. At 24, 36, 48 or 60 hours respectively, 10μl CCK-8 reagent (Vazyme Biotech, Nanjing, China) was added to each plate for another 2 hours of incubation at 37°C. The absorbance was then tested at a wavelength of 450 nm (OD 450 value). For invasion assays, after 48 hours of transfection, 4×105 cells were added to the upper compartment of Matrigel-coated (BD, Franklin Lakes, NJ, USA) invasion chambers (8-mm pore size, Corning, New York, USA) and 600 μL of DMEM supplemented with 15% FBS was added to the lower chamber. After 24 hours, cells at the bottom of the chamber were fixed with 100% methanol and stained with 0.1% crystal violet. Air dried cells counted under a microscope and five randomly fields were counted randomly in each well. Migration was also measured according to the above method without Matrigel.

**Immunohistochemistry staining**

Human CC tissues were used for immunohistochemistry experiments, and the adjacent tissues from this patient were used as normal tissue controls. ZBTB32 and PALB2 antibody used were purchased from Novus Biologicals (NBP2-62707, NBP2-50232; US) at a dilution of 1:500. After the staining was completed, scanning analysis was performed using CaseViewer v2.4 software, and the proportion of brown areas was used as the basis for judging the expression amount of target proteins in each tissue.

# Supplementary Figure Legends

**Figure S1 Pan-cancer analyses of extremely significant FARGs among tumors.**

A) The RNA pattern of RPS27AP11 among 33 cancers. B) The association between OS and methylation level. C-D) Drug sensitive analysis between extremely significant FARGs expression obtained from cancer cell lines and GDSC (C) and CTRP (D) database.

**Figure S2 Pan-cancer analyses of general significant FARGs among tumors.**

A-B) The PPI network (A) and the edge numbers involved in network (B). C) The relation between FARGs and overall survival among cancers. D) Type and frequency analysis of CNV mutations in extremely significant FARGs (Top 10). E) Pearson correlation between CNV and RNA expression. F) General significant FARGs methylation level comparison between cancers and normal samples. G) The association between OS and methylation level. H) Spearman correlation analyses of gene methylation and expression. I) The essential pathway enrichment analyses of general significant FARGs by GSVA. J-K) Drug sensitive analysis between extremely significant FARGs expression obtained from cancer cell lines and GDSC (J) and CTRP (K) database.

**Figure S3 Pan-cancer analyses of not significant FARGs among tumors.**

A-B) The PPI network (A) and the edge numbers involved in network (B). C) The relation between FARGs and overall survival among cancers. D) Type and frequency analysis of CNV mutations in extremely significant FARGs (Top 10). E) Pearson correlation between CNV and RNA expression. F) Not significant FARGs methylation level comparison between cancers and normal samples. G) The association between OS and methylation level. H) Spearman correlation analyses of gene methylation and expression. I) The essential pathway enrichment analyses of not significant FARGs by GSVA. J-K) Drug sensitive analysis between extremely significant FARGs expression obtained from cancer cell lines and GDSC (J) and CTRP (K) database.

**Figure S4 Establishment of FPS in CC.**

A) The correlation between HPV integration hot pot genes and FARGs. B-C) The fitting process of LASSO-Cox regression for both OS (B) and RFS (C). D-E) The nomogram prognosis prediction model containing Age, HPV\_Status, Grade, Stage, and FPS for both OS (D, left) and RFS (E, left). The calibration plots suggested the comparison between prediction and actual outcome for 2-, 3-, and 5-year survival probabilities in the nomogram model for both OS (D, right) and RFS (E, right). F-G) Decision curve analysis for the evaluation of the net benefits of FPS, Age, HPV\_Status, Grade, and Stage at 2-, 3-, and 5-year for both OS model (F) and RFS model (G).

**Figure S5 Survival curves and heatmap of candidate genes.**

A-B) Distribution of the FPS, survival status, and the relative expression of candidate genes among CC patients for both OS (A) and RFS (B). C-D) The heatmap showed the different expression level of FARGs in both OS (C) and RFS (D) groups.

**Figure S6 Validation of FPS in HPV-related cancers and major gynecologic tumors.**

A-D) Kaplan-Meier survival curves and ROC curves showed a reasonable discriminative effect of FPS-OS in both BRCA (A), HNSC (B), OV (C) and UCEC (D). E) The FPS-RFS validation by GSE4401, a CC dataset.

**Figure S7 Immune infiltration in CESC among the two risk FPS groups.**

A) Volcano plot of DEGs in high-FPS (n = 117) compared to low-FPS (n = 117) groups, |log2FC| > 1 and P-value < 0.05 served as the cutoff. B-C) The GO terms (B) and KEGG pathways (C) enriched based on the DEGs. D) Spearman correlation analysis of the 22 immune cells in 309 CC patients. E) Violin plot showed the abundance and comparison of different immune cells in different FPS groups. F) Kaplan-Meier survival curves for patients with significant infiltrated features (P < 0.05). G) Spearman correlation analysis among FARGs and IPS-associated signatures at RNA level (Rs > 0.3, Ps < 0.05).

**Figure S8 Construction immune signature IPS based on FARGs.**

A-B) The fitting process of LASSO-Cox regression for both OS (A) and RFS (B) based on immune signatures. C) Kaplan-Meier survival curves for patients RFS with high and low IPS based on immune signature. D) The ROC curves based on IPS for 2-, 3- and 5-year RFS probabilities. E-F) Distribution of the IPS, survival status, and the relative expression of candidate genes among CC patients for both OS (E) and RFS (F).

**Figure S9 Identification and characteristic description of the consensus cluster and build cell adhesion signature APS based on FARGs.**

A) Line chart showed the optimal number selection and the change of total within sum of square. B) Kaplan-Meier RFS curve for patients in different clusters. C) Volcano plot of DEGs in each of the two clusters comparison. D) Kaplan-Meier RFS curves for patients with high and low FacScore. E-F) The fitting process of LASSO-Cox regression for both OS (E) and RFS (F) based on cell adhesion signatures. G) The signature coefficients of RFS. H) Kaplan-Meier survival curves for patients RFS with high and low APS based on immune signature. I) The ROC curves based on APS for 2-, 3- and 5-year RFS probabilities.

**Figure S10 Comprehensive signature was identified based on FARGs and played vital roles in the prognosis of CC.**

A) The fitting process of LASSO-Cox regression for CC OS based on the FPS-, IPS- and APS- signatures. B) Distribution of the CPS, OS, survival status, and the relative expression of candidate genes among CC patients. C) ROC curve comparison at 2-, 3-, and 5-year survival probabilities. D) Heatmap showed FARGs expression pattern in low- and high- CPS groups. E) Heatmap showed that FARGs expression pattern in CC clinical features including FPS, IPS, APS and CPS.

**Figure S11 Machine learning-based CC prognostic predictor for both OS and RFS.**

A) The decision tree for OS prognostic model fitting of CC patients based on FARGs. B) The process of tree number determination in random forest fitting process for OS outcome. C) The decision tree for RFS prognostic model fitting of CC patients based on FARGs. D-E) Variable importance screening based on decision tree (D) and naïve bayes (E) algorithm fitting process. F) The process of tree number determination in random forest fitting process for RFS outcome. G) Variable importance screening based on random forest algorithm fitting progress. H-I) Kaplan-Meier OS curves for patients with ZBTB32 (H) and CENPS (I). J-K) Kaplan-Meier RFS curves for patients with PALB2 (J) and BRCA2 (K).

**Figure S12 Further bioinformation analyses and validation of the four essential FARGs related to CC prognosis.**

A) The expression pattern of ZBTB32, PALB2, CENPS, and BRCA2 between CC patients and normal control at RNA level from TCGA-CESC. B) The expression pattern of ZBTB32, PALB2, CENPS, and BRCA2 between CC patients and normal control at RNA level from GSE63514. C) The expression pattern of ZBTB32, PALB2, and BRCA2 between CC tissues and paired normal tissues by immunohistochemistry. D) The PPI networks of CENPS, PALB2, and BRCA2. E) The violin plots showed CENPS, PALB2, and BRCA2 mRNA expression in various clinical stages of CC. F-G) GSEA analyses of ZBTB32 using GO terms (F) and KEGG pathways (G). H-I) Spearman correlation between ZBTB32, CENPS, PALB2, and BRCA2 mRNA expression level and immune checkpoints (H) and P values (I).

**Figure S13 ZBTB32 overexpression inhibited CC cells proliferation.**

A) Structural diagram of ZBTB32 overexpression plasmid. B) QRT-PCR determined expression efficiency of transfection with ZBTB32 in HeLa and SiHa cells. C-D) The CCK-8 assay was conducted to measure cell proliferation in HeLa (C) and SiHa (D) cells after transfection with ZBTB32. E-F) Transwell assays were used for testing the migration and invasion ability of HeLa and SiHa cells after transfection with ZBTB32. G-H) QRT-PCR was performed for detecting key genes expression. OE, overexpression; \* *P* < 0.05, \*\* *P* < 0.01, \*\*\* *P* < 0.001, \*\*\*\* *P* < 0.0001.

# Supplementary Tables

## Table S1. Details of human tissue samples used for qPCR assays

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **ID** | **Type** | **Age** | **Gender** | **Pathology** |
| C01 | Ca | 72 | female | Uterine squamous cell carcinoma stage IIA1 |
| C02 | Ca | 41 | female | Right pelvic lymph node showed cancer metastasis 1 / 1 |
| C03 | Ca | 53 | female | Squamous cell carcinoma grade II-III; >Full thickness of 2 / 3 cervix; left pelvic lymph node can be seen cancer metastasis 1 / 12 |
| C04 | Ca | 49 | female | Squamous cell carcinoma grade III, the depth of cancer tissue invasion approximately 9 / 13 of the full thickness of the cervical wall, visible multifocal intravascular tumor thrombus; left and right pelvic cavity, left and right common iliac, presacral lymph node cancer metastasis T1B2N1 |
| C05 | Ca | 74 | female | Squamous cell carcinoma; full thickness of the muscular wall of the cervical canal (outer 1 / 2) |
| C06 | Ca | 66 | female | Squamous cell carcinoma Grade I |
| C07 | Ca | 46 | female | Squamous cell carcinoma; 1 / 2 layer within fibromuscular layer |
| C08 | Ca | 53 | female | Squamous cell carcinoma; stage IB1 |
| C09 | Ca | 53 | female | Squamous cell carcinoma; full thickness of cervical wall |
| C10 | Ca | 77 | female | Invasive squamous cell carcinoma  |
| C11 | Ca | 50 | female | Cervical squamous cell carcinoma |
| C12 | Ca | 32 | female | Cervical squamous cell carcinoma |
| C13 | Ca | 34 | female | Cervical squamous cell carcinoma |
| C14 | Ca | 64 | female | Cervical squamous cell carcinoma |
| C15 | Ca | 57 | female | Cervical squamous cell carcinoma |
| C16 | Ca | 53 | female | Cervical squamous cell carcinoma |
| C17 | Ca | 66 | female | Cervical squamous cell carcinoma |
| C18 | Ca | 45 | female | Cervical squamous cell carcinoma |
| C19 | Ca | 43 | female | Cervical squamous cell carcinoma |
| N01 | N | 48 | female | Fibroid, normal CC tissue |
| N02 | N | 63 | female | Fibroid, normal CC tissue |
| N03 | N | 42 | female | Fibroids; cavity occupation, endometrial polyps; chronic cervicitis |
| N04 | N | 54 | female | Fibroid; intrauterine ring |
| N05 | N | 43 | female | Multiple fibroids in uterus; cyst in left ovary |
| N06 | N | 46 | female | Fibroid, normal CC tissue |
| N07 | N | 61 | female | Uterine prolapse III degree |
| N08 | N | 47 | female | Fibroids; adenomyosis |
| N09 | N | 41 | female | Chronic inflammation, squamous metaplasia |
| N10 | N | 50 | female | Paracancerous tissues |
| N11 | N | 32 | female | Paracancerous tissues |
| N12 | N | 34 | female | Normal cervical tissue |
| N13 | N | 62 | female | Fibroid, normal CC tissue |
| N14 | N | 64 | female | Normal cervical tissue |
| N15 | N | 57 | female | Paracancerous tissues |
| N16 | N | 53 | female | Paracancerous tissues |
| N17 | N | 66 | female | Paracancerous tissues |
| N18 | N | 53 | female | Normal cervical tissue |
| N19 | N | 45 | female | Paracancerous tissues |
| N20 | N | 43 | female | Paracancerous tissues |
| N21 | N | 48 | female | Normal cervical tissue |
| N22 | N | 49 | female | Uterine fibroid, normal cervical cancer tissue |

## Table S2. Primer sequences of key signatures for qPCR

|  |  |  |
| --- | --- | --- |
| **GeneSymbol** | **Premier\_Sequence** |  |
| ZBTB32 | TGGCTCTGATCGGCTGGTACAG | Forward |
| CTCCTGGCTCCCTACGGTGATC | Reverse |
| ZAP70 | GAAGGCAGACACGGAAGAGATGATG | Forward |
| CCAATGAGCCGCACGATGTAGG | Reverse |
| VCAM1 | ACACACAGGTGGGACACAAATAAGG | Forward |
| GCTCCAAGGATCACGACCATCTTC | Reverse |
| RPA2 | CTGCTTTCTGCCACTTTGGTTGATG | Forward |
| ACAATGTTGGTTGGAGCCTTCTCTG | Reverse |
| PSTPIP1 | TGCGTTCTGTTCTCCTTGGTGTG | Forward |
| CTTCCCTTGTTCCTTTGCCTCCTC | Reverse |
| RFC3 | AGCCTCTGGGTGGACAAGTATCG | Forward |
| GCACCTGATGGTCCGTACACTAAC | Reverse |
| PCDHGB3 | GGGCAGAGGCGAATGCTATTTCTC | Forward |
| GGAATAGCGTAGCGGATCGGTTC | Reverse |
| PCDHGA7 | AAGCAAGAGAAGCAGGACGACTATG | Forward |
| AGGAGGATGGAGAGCAGGAAGAATC | Reverse |
| PCDHB5 | AGGTACAGGTGCCCGAGAACAG | Forward |
| TGGTTGAGTAACTTCATCGCCTTGG | Reverse |
| PCDHB12 | GAGCAGAGCCGAGTACAACATCAC | Forward |
| CGAACAGGGCGTAGGAAGTTTGG | Reverse |
| PCDHAC2 | CGGGAGTTCTTTGTGACTGTGGAG | Forward |
| GGCTGCTGACGAGTTGGTTGAG | Reverse |
| PCDHA11 | CCGTTCGGCTGTTAGTCCAAGTC | Forward |
| TCGGTCTGTGGCGTTTAGTTTGAG | Reverse |
| NECTIN3 | AGGTGGGCAGGGTGTAGAATGG | Forward |
| CGGCTTTCAGTCAATAGGGTCTTCC | Reverse |
| ITGA5 | CCTCCCAATTTCAGACTCCCATTCC | Forward |
| CCGTCAGCACCTTCAAGAAGTACC | Reverse |
| ITGA2B | GCAATTCTAGCCACCATGAGTCCAG | Forward |
| CTCCTCCTCCTTCCCTTCAGATTCC | Reverse |
| CXCL8 | AACTTTCAGAGACAGCAGAGCACAC | Forward |
| CACACAGTGAGATGGTTCCTTCCG | Reverse |
| CENPS | ACAGAGGCTAAAGGCAGCAGT | Forward |
| GCCGCAATGGTCTGTTTGCT | Reverse |
| CD6 | CCACCGACAACGATGACTACGATG | Forward |
| GGAAAGGGAGTAGGTAGAGCAGGAG | Reverse |
| CD244 | GTGGCTCTGTCTTGCTTGGTCTC | Forward |
| CTCGTCCAGGTAGGTGAGGTTCC | Reverse |
| CCR7 | GCTGTGGTCGTGGTCTTCATAGTC | Forward |
| AGGCGATGTTGAGTTGCTTACTGAG | Reverse |
| CCL1 | CGCCTTGGACACAGTTGGATGG | Forward |
| GAATGGTGTAGGGCTGGTAGTTTCG | Reverse |
| CAMP | ATGCTAACCTCTACCGCCTCCTG | Forward |
| CAATCCTCTGGTGACTGCTGTGTC | Reverse |
| BRCA2 | AGGGAAGCTTCATAAGTCAGTCTCA | Forward |
| TGAAGCATCTGATACCTGGACAGA | Reverse |
| PALB2 | GGATCTCTCACCGCAGCTAA | Forward |
| ACTCAGGCCCAACATCAAGT | Reverse |
| β-actin | ATCCGCAAAGACCTGT | Forward |
| GGGTGTAACGCAACTAAG | Reverse |

## Table S3. GSVA analysis of FARGs in cervical cancer data

|  |  |  |  |
| --- | --- | --- | --- |
| **id** | **logFC** | ***P*-value** | **adj.*P*.Val** |
| GOCC\_NUCLEOLUS | 0.387  | 0.000  | 0.000  |
| HP\_HYPERTONIA | 0.366  | 0.000  | 0.000  |
| HP\_UPPER\_MOTOR\_NEURON\_DYSFUNCTION | 0.366  | 0.000  | 0.000  |
| HP\_ABNORMALITY\_OF\_THE\_SYNOVIA | -0.244  | 0.000  | 0.000  |
| HP\_JOINT\_DISLOCATION | -0.236  | 0.000  | 0.001  |
| HP\_LOWER\_EXTREMITY\_JOINT\_DISLOCATION | -0.236  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_LOWER\_LIMB\_JOINT | -0.236  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_CALVARIA | -0.258  | 0.000  | 0.001  |
| GOMF\_ENDONUCLEASE\_ACTIVITY | 0.310  | 0.000  | 0.001  |
| HP\_ABNORMAL\_SIZE\_OF\_THE\_PALPEBRAL\_FISSURES | -0.229  | 0.000  | 0.001  |
| HP\_ABNORMAL\_PENIS\_MORPHOLOGY | -0.254  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_URETHRA | -0.254  | 0.000  | 0.001  |
| HP\_PES\_PLANUS | -0.254  | 0.000  | 0.001  |
| HP\_HYPERTROPHIC\_CARDIOMYOPATHY | -0.255  | 0.000  | 0.001  |
| HP\_ABNORMAL\_BONE\_STRUCTURE | -0.255  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_BONE\_MINERAL\_DENSITY | -0.255  | 0.000  | 0.001  |
| HP\_FACIAL\_ASYMMETRY | -0.264  | 0.000  | 0.001  |
| HP\_SHORT\_LONG\_BONE | -0.264  | 0.000  | 0.001  |
| HP\_UPPER\_LIMB\_UNDERGROWTH | -0.264  | 0.000  | 0.001  |
| HP\_LIMB\_UNDERGROWTH | -0.264  | 0.000  | 0.001  |
| HP\_ABNORMAL\_FOREARM\_BONE\_MORPHOLOGY | -0.264  | 0.000  | 0.001  |
| HP\_DISPLACEMENT\_OF\_THE\_URETHRAL\_MEATUS | -0.264  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_GLOBE\_SIZE | -0.234  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_LONG\_BONE\_MORPHOLOGY | -0.229  | 0.000  | 0.001  |
| HP\_HYPERREFLEXIA | -0.242  | 0.000  | 0.001  |
| HP\_HYDROURETER | -0.269  | 0.000  | 0.001  |
| HP\_HYDROCEPHALUS | -0.269  | 0.000  | 0.001  |
| HP\_PROPTOSIS | -0.269  | 0.000  | 0.001  |
| HP\_BICORNUATE\_UTERUS | -0.269  | 0.000  | 0.001  |
| HP\_TRIPHALANGEAL\_THUMB | -0.269  | 0.000  | 0.001  |
| HP\_CLUBBING | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMAL\_ILEUM\_MORPHOLOGY | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_AMNIOTIC\_FLUID | -0.269  | 0.000  | 0.001  |
| HP\_OLIGOHYDRAMNIOS | -0.269  | 0.000  | 0.001  |
| HP\_SIDEROBLASTIC\_ANEMIA | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_SMALL\_INTESTINE | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMAL\_DUODENUM\_MORPHOLOGY | -0.269  | 0.000  | 0.001  |
| HP\_AGANGLIONIC\_MEGACOLON | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_FEMUR\_MORPHOLOGY | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_CEREBROSPINAL\_FLUID | -0.269  | 0.000  | 0.001  |
| HP\_PYRIDOXINE\_RESPONSIVE\_SIDEROBLASTIC\_ANEMIA | -0.269  | 0.000  | 0.001  |
| HP\_APLASIA\_HYPOPLASIA\_OF\_THE\_ULNA | -0.269  | 0.000  | 0.001  |
| HP\_EXTERNAL\_EAR\_MALFORMATION | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_PHALANGES\_OF\_THE\_TOES | -0.269  | 0.000  | 0.001  |
| HP\_APLASIA\_HYPOPLASIA\_OF\_THE\_UVULA | -0.269  | 0.000  | 0.001  |
| HP\_ABSENT\_TESTIS | -0.269  | 0.000  | 0.001  |
| HP\_ANEMIA\_OF\_INADEQUATE\_PRODUCTION | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMAL\_SHAPE\_OF\_THE\_FRONTAL\_REGION | -0.269  | 0.000  | 0.001  |
| HP\_SHORT\_PALPEBRAL\_FISSURE | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMAL\_URETER\_MORPHOLOGY | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_TESTIS\_SIZE | -0.269  | 0.000  | 0.001  |
| HP\_ARTERIOVENOUS\_MALFORMATION | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_PREPUTIUM | -0.269  | 0.000  | 0.001  |
| HP\_CLUBBING\_OF\_TOES | -0.269  | 0.000  | 0.001  |
| HP\_DUODENAL\_STENOSIS | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMAL\_SHAPE\_OF\_THE\_PALPEBRAL\_FISSURE | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_PERIPHERAL\_NERVOUS\_SYSTEM | -0.269  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_URETER | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_IRIS\_MORPHOLOGY | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_PRENATAL\_DEVELOPMENT\_OR\_BIRTH | -0.259  | 0.000  | 0.001  |
| HP\_TETRALOGY\_OF\_FALLOT | -0.259  | 0.000  | 0.001  |
| HP\_PATENT\_DUCTUS\_ARTERIOSUS | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMAL\_AORTIC\_VALVE\_MORPHOLOGY | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMAL\_HEART\_VALVE\_MORPHOLOGY | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_SPINAL\_CORD | -0.259  | 0.000  | 0.001  |
| HP\_TRACHEOESOPHAGEAL\_FISTULA | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMAL\_TRACHEA\_MORPHOLOGY | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMAL\_CAROTID\_ARTERY\_MORPHOLOGY | -0.259  | 0.000  | 0.001  |
| HP\_SPINAL\_DYSRAPHISM | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMAL\_CONNECTION\_OF\_THE\_CARDIAC\_SEGMENTS | -0.259  | 0.000  | 0.001  |
| HP\_CONGENITAL\_MALFORMATION\_OF\_THE\_GREAT\_ARTERIES | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMAL\_LOCALIZATION\_OF\_KIDNEY | -0.259  | 0.000  | 0.001  |
| HP\_ABNORMAL\_NEURAL\_TUBE\_MORPHOLOGY | -0.259  | 0.000  | 0.001  |
| HP\_APLASIA\_HYPOPLASIA\_AFFECTING\_THE\_EYE | -0.231  | 0.000  | 0.001  |
| HP\_ABNORMALITY\_OF\_THE\_FOREARM | -0.223  | 0.000  | 0.001  |
| HP\_HYPERPIGMENTATION\_OF\_THE\_SKIN | -0.247  | 0.000  | 0.001  |
| HP\_ABNORMAL\_MYOCARDIUM\_MORPHOLOGY | -0.241  | 0.000  | 0.002  |
| HP\_ABNORMALITY\_OF\_THE\_UVULA | -0.258  | 0.000  | 0.002  |
| HP\_ABNORMAL\_SOFT\_PALATE\_MORPHOLOGY | -0.258  | 0.000  | 0.002  |
| HP\_ABNORMAL\_UVEA\_MORPHOLOGY | -0.247  | 0.000  | 0.002  |
| HP\_GAIT\_DISTURBANCE | 0.313  | 0.000  | 0.002  |
| HP\_RENAL\_INSUFFICIENCY | -0.232  | 0.000  | 0.002  |
| HP\_ABNORMAL\_RENAL\_PHYSIOLOGY | -0.232  | 0.000  | 0.002  |
| HP\_IRREGULAR\_HYPERPIGMENTATION | -0.244  | 0.000  | 0.003  |
| HP\_ABNORMAL\_JOINT\_MORPHOLOGY | -0.208  | 0.000  | 0.003  |
| HP\_ABNORMALITY\_OF\_TOE | -0.207  | 0.000  | 0.003  |
| HP\_ABNORMALITY\_OF\_PELVIC\_GIRDLE\_BONE\_MORPHOLOGY | -0.207  | 0.000  | 0.003  |
| HP\_ABNORMALITY\_OF\_THE\_CURVATURE\_OF\_THE\_VERTEBRAL\_COLUMN | -0.207  | 0.000  | 0.003  |
| HP\_CRYPTORCHIDISM | -0.216  | 0.000  | 0.004  |
| HP\_HYPOPIGMENTATION\_OF\_THE\_SKIN | -0.254  | 0.000  | 0.004  |
| HP\_ABNORMAL\_LOWER\_LIMB\_BONE\_MORPHOLOGY | -0.211  | 0.000  | 0.004  |
| HP\_ABNORMALITY\_OF\_THE\_ABDOMINAL\_WALL | -0.223  | 0.000  | 0.004  |
| HP\_ABNORMAL\_REFLEX | -0.214  | 0.000  | 0.005  |
| HP\_ABNORMAL\_FINGER\_PHALANX\_MORPHOLOGY | -0.219  | 0.000  | 0.005  |
| HP\_ABNORMALITY\_OF\_THE\_LOWER\_URINARY\_TRACT | -0.220  | 0.000  | 0.006  |
| HP\_ABNORMAL\_UMBILICUS\_MORPHOLOGY | -0.227  | 0.000  | 0.006  |
| HP\_ABNORMAL\_CARDIAC\_SEPTUM\_MORPHOLOGY | -0.227  | 0.000  | 0.006  |
| HP\_ABNORMAL\_AORTIC\_MORPHOLOGY | -0.227  | 0.000  | 0.006  |
| HP\_ABNORMAL\_CARDIAC\_ATRIUM\_MORPHOLOGY | -0.227  | 0.000  | 0.006  |
| HP\_APLASIA\_HYPOPLASIA\_AFFECTING\_THE\_ANTERIOR\_SEGMENT\_OF\_THE\_EYE | -0.227  | 0.000  | 0.006  |
| HP\_RENAL\_HYPOPLASIA\_APLASIA | -0.227  | 0.000  | 0.006  |
| HP\_ABNORMAL\_SYSTEMIC\_ARTERIAL\_MORPHOLOGY | -0.227  | 0.000  | 0.006  |
| HP\_ABNORMALITY\_OF\_THE\_CURVATURE\_OF\_THE\_CORNEA | -0.227  | 0.000  | 0.006  |
| HP\_HERNIA | -0.227  | 0.000  | 0.006  |
| HP\_SLOPING\_FOREHEAD | -0.228  | 0.000  | 0.006  |
| HP\_ABNORMALITY\_OF\_THE\_FOREHEAD | -0.197  | 0.000  | 0.006  |
| HP\_ABNORMAL\_ESOPHAGUS\_MORPHOLOGY | -0.243  | 0.000  | 0.006  |
| HP\_ASTIGMATISM | -0.234  | 0.000  | 0.006  |
| HP\_TRIANGULAR\_SHAPED\_PHALANGES\_OF\_THE\_HAND | -0.234  | 0.000  | 0.006  |
| HP\_DECREASED\_FERTILITY | -0.250  | 0.000  | 0.007  |
| HP\_DOLICHOCEPHALY | -0.250  | 0.000  | 0.007  |
| HP\_HYPOPIGMENTED\_SKIN\_PATCHES | -0.250  | 0.000  | 0.007  |
| HP\_MYELODYSPLASIA | -0.250  | 0.000  | 0.007  |
| HP\_DECREASED\_FERTILITY\_IN\_MALES | -0.250  | 0.000  | 0.007  |
| HP\_ABNORMALITY\_OF\_THE\_LENS | -0.208  | 0.000  | 0.007  |
| HP\_OCULAR\_ANTERIOR\_SEGMENT\_DYSGENESIS | -0.208  | 0.000  | 0.007  |
| HP\_FUNCTIONAL\_ABNORMALITY\_OF\_MALE\_INTERNAL\_GENITALIA | -0.218  | 0.000  | 0.007  |
| HP\_ABNORMAL\_MALE\_REPRODUCTIVE\_SYSTEM\_PHYSIOLOGY | -0.218  | 0.000  | 0.007  |
| HP\_NEUROLOGICAL\_SPEECH\_IMPAIRMENT | 0.299  | 0.000  | 0.007  |
| HP\_ABNORMALITY\_OF\_GLOBE\_LOCATION | -0.211  | 0.000  | 0.007  |
| HP\_ABNORMAL\_PERIPHERAL\_NERVOUS\_SYSTEM\_MORPHOLOGY | 0.294  | 0.000  | 0.007  |
| HP\_ABNORMALITY\_OF\_SKIN\_PIGMENTATION | -0.217  | 0.000  | 0.008  |
| HP\_ABNORMALITY\_OF\_THE\_CHOANAE | -0.231  | 0.000  | 0.008  |
| HP\_ABNORMAL\_THROMBOCYTE\_MORPHOLOGY | -0.231  | 0.000  | 0.008  |
| HP\_ABNORMAL\_ERYTHROCYTE\_MORPHOLOGY | -0.231  | 0.000  | 0.008  |
| HP\_ANAL\_ATRESIA | -0.231  | 0.000  | 0.008  |
| HP\_ABNORMALITY\_OF\_THE\_ANUS | -0.231  | 0.000  | 0.008  |
| HP\_ABNORMAL\_UPPER\_LIMB\_BONE\_MORPHOLOGY | -0.192  | 0.000  | 0.010  |
| HP\_APLASIA\_HYPOPLASIA\_OF\_THE\_RADIUS | -0.223  | 0.000  | 0.010  |
| HP\_APLASIA\_HYPOPLASIA\_INVOLVING\_FOREARM\_BONES | -0.223  | 0.000  | 0.010  |
| HP\_CLINICAL\_COURSE | 0.286  | 0.000  | 0.010  |
| HP\_ABNORMAL\_TESTIS\_MORPHOLOGY | -0.193  | 0.000  | 0.010  |
| HP\_ABNORMAL\_EXTERNAL\_GENITALIA | -0.193  | 0.000  | 0.010  |
| HP\_ABNORMALITY\_OF\_THE\_LIVER | -0.195  | 0.000  | 0.013  |
| HP\_EPICANTHUS | -0.217  | 0.000  | 0.014  |
| HP\_ABNORMALITY\_OF\_THE\_ULNA | -0.217  | 0.000  | 0.014  |
| HP\_INTRAUTERINE\_GROWTH\_RETARDATION | -0.196  | 0.000  | 0.014  |
| HP\_FINGER\_SYNDACTYLY | -0.225  | 0.000  | 0.015  |
| HP\_APLASIA\_HYPOPLASIA\_OF\_FINGERS | -0.225  | 0.000  | 0.015  |
| HP\_ABNORMAL\_CRANIAL\_NERVE\_PHYSIOLOGY | -0.225  | 0.000  | 0.015  |
| HP\_ABNORMAL\_THUMB\_MORPHOLOGY | -0.194  | 0.000  | 0.017  |
| HP\_ABNORMALITY\_OF\_THE\_UTERUS | -0.215  | 0.000  | 0.017  |
| HP\_ABNORMAL\_UTERUS\_MORPHOLOGY | -0.215  | 0.000  | 0.017  |
| HP\_ABNORMALITY\_OF\_THE\_OUTER\_EAR | -0.190  | 0.000  | 0.018  |
| HP\_ABNORMALITY\_OF\_THE\_CEREBRAL\_VENTRICLES | -0.212  | 0.000  | 0.018  |
| HP\_VENTRICULOMEGALY | -0.212  | 0.000  | 0.018  |
| HP\_ABNORMALITY\_OF\_THE\_PALPEBRAL\_FISSURES | -0.181  | 0.000  | 0.018  |
| HP\_ABNORMAL\_SPERMATOGENESIS | -0.220  | 0.000  | 0.020  |
| GOBP\_MITOTIC\_DNA\_INTEGRITY\_CHECKPOINT | 0.226  | 0.000  | 0.021  |
| HP\_ABNORMAL\_VASCULAR\_MORPHOLOGY | -0.204  | 0.000  | 0.022  |
| HP\_ABNORMAL\_MORPHOLOGY\_OF\_THE\_GREAT\_VESSELS | -0.204  | 0.000  | 0.022  |
| HP\_HYPERTELORISM | -0.208  | 0.000  | 0.025  |
| HP\_TOE\_SYNDACTYLY | -0.208  | 0.000  | 0.025  |
| HP\_RECURRENT\_URINARY\_TRACT\_INFECTIONS | -0.209  | 0.000  | 0.029  |
| GOMF\_ENDODEOXYRIBONUCLEASE\_ACTIVITY | 0.255  | 0.000  | 0.029  |
| HP\_UPSLANTED\_PALPEBRAL\_FISSURE | -0.203  | 0.000  | 0.032  |
| GOBP\_REGULATION\_OF\_TELOMERE\_MAINTENANCE | 0.267  | 0.000  | 0.033  |
| HP\_LEUKOPENIA | -0.199  | 0.000  | 0.037  |
| HP\_APLASIA\_HYPOPLASIA\_INVOLVING\_BONES\_OF\_THE\_UPPER\_LIMBS | -0.195  | 0.000  | 0.039  |
| HP\_HYPOGONADISM | -0.181  | 0.000  | 0.046  |

## Table S4. Significant FARGs screened out by univariable cox regression analysis for IPS model fitting

|  |  |  |
| --- | --- | --- |
| **OS related gene** |  | **RFS related gene** |
| **id** | **HR** | **HR.95L** | **HR.95H** | ***P*-value** |  | **id** | **HR** | **HR.95L** | **HR.95H** | ***P*-value** |
| ANGPTL5 | 60.021  | 6.596  | 546.162  | 0.000  |  | REG1A | 1.281  | 1.067  | 1.538  | 0.008  |
| C8G | 0.585  | 0.369  | 0.930  | 0.023  |  | BMP3 | 1.377  | 1.064  | 1.781  | 0.015  |
| CAMP | 0.632  | 0.420  | 0.952  | 0.028  |  | CCL1 | 0.000  | 0.000  | 0.239  | 0.019  |
| CCL19 | 0.816  | 0.713  | 0.933  | 0.003  |  | INSL4 | 1.597  | 1.074  | 2.377  | 0.021  |
| CCL5 | 0.820  | 0.714  | 0.941  | 0.005  |  | CLEC4M | 0.002  | 0.234  | 0.000  | 0.021  |
| CCR7 | 0.569  | 0.421  | 0.769  | 0.000  |  | NCR1 | 0.095  | 0.012  | 0.741  | 0.025  |
| CD19 | 0.489  | 0.287  | 0.833  | 0.009  |  | UCN2 | 0.629  | 0.416  | 0.949  | 0.027  |
| CD3D | 0.746  | 0.627  | 0.889  | 0.001  |  | GNLY | 0.733  | 0.556  | 0.967  | 0.028  |
| CD48 | 0.687  | 0.538  | 0.876  | 0.003  |  | ZAP70 | 0.578  | 0.353  | 0.944  | 0.029  |
| CD79A | 0.803  | 0.671  | 0.960  | 0.016  |  | CD244 | 0.324  | 0.118  | 0.894  | 0.029  |
| CD79B | 0.626  | 0.443  | 0.883  | 0.008  |  | IL18RAP | 0.344  | 0.123  | 0.957  | 0.041  |
| CD8A | 0.740  | 0.607  | 0.902  | 0.003  |  | XCL2 | 0.582  | 0.345  | 0.982  | 0.043  |
| CD8B | 0.770  | 0.625  | 0.947  | 0.013  |  | FASLG | 0.553  | 0.309  | 0.988  | 0.046  |
| CHIT1 | 0.591  | 0.420  | 0.832  | 0.003  |  | TNFRSF9 | 0.378  | 0.144  | 0.989  | 0.047  |
| CRP | 2.310  | 1.502  | 3.554  | 0.000  |  |  |  |  |  |  |
| CSF2 | 1.291  | 1.048  | 1.591  | 0.016  |  |  |  |  |  |  |
| CTLA4 | 0.651  | 0.481  | 0.881  | 0.005  |  |  |  |  |  |  |
| CXCL2 | 1.242  | 1.088  | 1.418  | 0.001  |  |  |  |  |  |  |
| CXCL8 | 1.290  | 1.142  | 1.457  | 0.000  |  |  |  |  |  |  |
| CXCL9 | 0.894  | 0.799  | 0.999  | 0.048  |  |  |  |  |  |  |
| CXCR3 | 0.672  | 0.514  | 0.879  | 0.004  |  |  |  |  |  |  |
| CXCR6 | 0.612  | 0.452  | 0.827  | 0.001  |  |  |  |  |  |  |
| EREG | 1.401  | 1.163  | 1.687  | 0.000  |  |  |  |  |  |  |
| FGF5 | 2.019  | 1.156  | 3.527  | 0.014  |  |  |  |  |  |  |
| GALP | 11.882  | 1.478  | 95.502  | 0.020  |  |  |  |  |  |  |
| GUCA2A | 1.263  | 1.019  | 1.565  | 0.033  |  |  |  |  |  |  |
| HCST | 0.789  | 0.645  | 0.965  | 0.021  |  |  |  |  |  |  |
| ICOS | 0.524  | 0.342  | 0.803  | 0.003  |  |  |  |  |  |  |
| IL11 | 1.238  | 1.024  | 1.498  | 0.028  |  |  |  |  |  |  |
| IL17C | 1.982  | 1.185  | 3.316  | 0.009  |  |  |  |  |  |  |
| IL22RA2 | 0.408  | 0.193  | 0.861  | 0.019  |  |  |  |  |  |  |
| IL6 | 1.187  | 1.003  | 1.404  | 0.046  |  |  |  |  |  |  |
| INSL4 | 1.396  | 1.010  | 1.930  | 0.043  |  |  |  |  |  |  |
| LBP | 1.305  | 1.065  | 1.599  | 0.010  |  |  |  |  |  |  |
| LTA | 0.536  | 0.301  | 0.955  | 0.034  |  |  |  |  |  |  |
| PAEP | 1.240  | 1.082  | 1.421  | 0.002  |  |  |  |  |  |  |
| PF4 | 1.393  | 1.012  | 1.917  | 0.042  |  |  |  |  |  |  |
| PGC | 1.297  | 1.001  | 1.681  | 0.049  |  |  |  |  |  |  |
| PTGS2 | 1.202  | 1.040  | 1.390  | 0.013  |  |  |  |  |  |  |
| PTX3 | 1.405  | 1.062  | 1.860  | 0.017  |  |  |  |  |  |  |
| REG1A | 1.217  | 1.054  | 1.406  | 0.008  |  |  |  |  |  |  |
| SERPINA3 | 1.682  | 1.191  | 2.376  | 0.003  |  |  |  |  |  |  |
| SH2D1A | 0.563  | 0.387  | 0.819  | 0.003  |  |  |  |  |  |  |
| STC1 | 1.239  | 1.080  | 1.421  | 0.002  |  |  |  |  |  |  |
| TNFRSF11B | 1.295  | 1.087  | 1.544  | 0.004  |  |  |  |  |  |  |
| TNFRSF13B | 0.281  | 0.105  | 0.756  | 0.012  |  |  |  |  |  |  |
| UCN3 | 1.622  | 1.122  | 2.345  | 0.010  |  |  |  |  |  |  |
| VCAM1 | 0.692  | 0.531  | 0.902  | 0.007  |  |  |  |  |  |  |
| XCR1 | 0.364  | 0.136  | 0.972  | 0.044  |  |  |  |  |  |  |
| ZAP70 | 0.554  | 0.406  | 0.756  | 0.000  | 　 | 　 | 　 | 　 | 　 | 　 |

## Table S5. Significant FARGs screened out by univariable cox regression analysis for APS model fitting

|  |  |  |
| --- | --- | --- |
| **OS related gene** |  | **RFS related gene** |
| **id** | **HR** | **HR.95L** | **HR.95H** | ***P*-value** |  | **id** | **HR** | **HR.95L** | **HR.95H** | ***P*-value** |
| ADAM17 | 1.423  | 1.039  | 1.950  | 0.028  |  | ADAM12 | 1.446  | 1.003  | 2.084  | 0.048  |
| ADAM9 | 1.652  | 1.201  | 2.273  | 0.002  |  | CDH11 | 1.566  | 1.107  | 2.216  | 0.011  |
| CD6 | 0.486  | 0.339  | 0.699  | 0.000  |  | CDH5 | 2.287  | 1.553  | 3.368  | 0.000  |
| CDH5 | 1.364  | 1.035  | 1.798  | 0.027  |  | COL3A1 | 1.280  | 1.030  | 1.591  | 0.026  |
| COL4A1 | 1.326  | 1.083  | 1.623  | 0.006  |  | DDR2 | 1.794  | 1.104  | 2.915  | 0.018  |
| COL4A6 | 1.249  | 1.037  | 1.504  | 0.019  |  | HRAS | 0.553  | 0.315  | 0.969  | 0.039  |
| DGCR6 | 0.410  | 0.215  | 0.783  | 0.007  |  | MFAP4 | 1.418  | 1.107  | 1.815  | 0.006  |
| FAT1 | 1.275  | 1.002  | 1.623  | 0.048  |  | MPDZ | 1.998  | 1.177  | 3.392  | 0.010  |
| HES5 | 0.643  | 0.416  | 0.992  | 0.046  |  | PCDHA11 | 4.348  | 1.183  | 15.987  | 0.027  |
| HLA-DMA | 0.851  | 0.728  | 0.995  | 0.043  |  | PCDHAC2 | 2.350  | 1.044  | 5.289  | 0.039  |
| HLA-DPB1 | 0.805  | 0.692  | 0.935  | 0.005  |  | PCDHB6 | 2.755  | 1.313  | 5.781  | 0.007  |
| HLA-DRB1 | 0.862  | 0.758  | 0.979  | 0.023  |  | PCDHB8 | 1.904  | 1.100  | 3.294  | 0.021  |
| HSPG2 | 1.324  | 1.048  | 1.672  | 0.019  |  | PCDHGB7 | 4.159  | 1.574  | 10.988  | 0.004  |
| ILK | 1.585  | 1.004  | 2.501  | 0.048  |  | PDGFD | 1.900  | 1.147  | 3.147  | 0.013  |
| ITGA2B | 0.684  | 0.478  | 0.977  | 0.037  |  | PDGFRA | 1.726  | 1.173  | 2.539  | 0.006  |
| ITGA5 | 1.510  | 1.268  | 1.797  | 0.000  |  | POSTN | 1.255  | 1.034  | 1.522  | 0.022  |
| ITGB1 | 1.517  | 1.169  | 1.969  | 0.002  |  | PTPRM | 1.514  | 1.006  | 2.279  | 0.047  |
| ITGB1.1 | 1.517  | 1.169  | 1.969  | 0.002  |  | S1PR1 | 1.855  | 1.107  | 3.109  | 0.019  |
| LAMC2 | 1.170  | 1.014  | 1.350  | 0.032  |  | SORBS1 | 1.881  | 1.046  | 3.383  | 0.035  |
| MPDZ | 1.485  | 1.066  | 2.070  | 0.020  |  | SPOCK1 | 1.356  | 1.006  | 1.829  | 0.046  |
| NECTIN3 | 1.344  | 1.029  | 1.755  | 0.030  |  | SUSD5 | 2.379  | 1.372  | 4.126  | 0.002  |
| PCDHA11 | 4.606  | 1.965  | 10.794  | 0.000  |  | VCAN | 1.374  | 1.051  | 1.797  | 0.020  |
| PCDHAC2 | 2.224  | 1.234  | 4.009  | 0.008  |  |  |  |  |  |  |
| PCDHB12 | 2.267  | 1.203  | 4.272  | 0.011  |  |  |  |  |  |  |
| PCDHB5 | 1.864  | 1.173  | 2.961  | 0.008  |  |  |  |  |  |  |
| PCDHGA10 | 1.556  | 1.056  | 2.293  | 0.025  |  |  |  |  |  |  |
| PCDHGA5 | 5.508  | 1.260  | 24.075  | 0.023  |  |  |  |  |  |  |
| PCDHGA7 | 4.978  | 1.229  | 20.165  | 0.025  |  |  |  |  |  |  |
| PCDHGB2 | 1.556  | 1.005  | 2.411  | 0.048  |  |  |  |  |  |  |
| PCDHGB3 | 17.254  | 2.300  | 129.445  | 0.006  |  |  |  |  |  |  |
| PCDHGB6 | 5.321  | 1.013  | 27.941  | 0.048  |  |  |  |  |  |  |
| PCDHGC3 | 1.354  | 1.071  | 1.712  | 0.011  |  |  |  |  |  |  |
| PCDHGC4 | 72.926  | 1.883  | 2823.912  | 0.021  |  |  |  |  |  |  |
| PIK3R2 | 0.099  | 0.021  | 0.468  | 0.004  |  |  |  |  |  |  |
| POSTN | 1.185  | 1.046  | 1.342  | 0.008  |  |  |  |  |  |  |
| PSTPIP1 | 0.556  | 0.387  | 0.799  | 0.002  |  |  |  |  |  |  |
| PTPRM | 1.368  | 1.058  | 1.769  | 0.017  |  |  |  |  |  |  |
| SPON1 | 1.211  | 1.011  | 1.449  | 0.037  |  |  |  |  |  |  |
| VCAM1 | 0.692  | 0.531  | 0.902  | 0.007  | 　 | 　 | 　 | 　 | 　 | 　 |

## Table S6. GSEA analysis of *ZBTB32* using KEGG pathways in CC

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **ID** | **setSize** | **enrichmentScore** | **NES** | ***P*-value** | **rank** |
| KEGG\_OLFACTORY\_TRANSDUCTION | 383 | -0.476  | -1.338  | 0.014  | 4832  |
| KEGG\_HEMATOPOIETIC\_CELL\_LINEAGE | 85 | 0.667  | 1.723  | 0.020  | 9181  |
| KEGG\_PRIMARY\_IMMUNODEFICIENCY | 35 | 0.760  | 1.661  | 0.020  | 7933  |
| KEGG\_MATURITY\_ONSET\_DIABETES\_OF\_THE\_YOUNG | 25 | -0.764  | -1.503  | 0.022  | 8042  |
| KEGG\_B\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 75 | 0.640  | 1.583  | 0.022  | 10403  |
| KEGG\_CELL\_ADHESION\_MOLECULES\_CAMS | 131 | 0.549  | 1.454  | 0.024  | 13761  |
| KEGG\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 108 | 0.672  | 1.713  | 0.024  | 10403  |
| KEGG\_CYTOKINE\_CYTOKINE\_RECEPTOR\_INTERACTION | 264 | 0.483  | 1.395  | 0.026  | 9920  |
| KEGG\_ASTHMA | 28 | 0.690  | 1.489  | 0.038  | 14235  |
| KEGG\_ALLOGRAFT\_REJECTION | 35 | 0.712  | 1.555  | 0.041  | 12798  |
| KEGG\_GLYOXYLATE\_AND\_DICARBOXYLATE\_METABOLISM | 16 | 0.818  | 1.605  | 0.041  | 2738  |
| KEGG\_GRAFT\_VERSUS\_HOST\_DISEASE | 37 | 0.717  | 1.567  | 0.043  | 12798  |
| KEGG\_LEISHMANIA\_INFECTION | 69 | 0.623  | 1.496  | 0.043  | 14235  |
| KEGG\_INTESTINAL\_IMMUNE\_NETWORK\_FOR\_IGA\_PRODUCTION | 46 | 0.701  | 1.571  | 0.043  | 12805  |
| KEGG\_SYSTEMIC\_LUPUS\_ERYTHEMATOSUS | 135 | 0.517  | 1.378  | 0.048  | 15087  |
| KEGG\_NATURAL\_KILLER\_CELL\_MEDIATED\_CYTOTOXICITY | 132 | 0.530  | 1.401  | 0.049  | 10313  |

## Table S7. GSEA analysis of ZBTB32 using GO geneset in CC

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **ID** | **setSize** | **enrichmentScore** | **NES** | ***P*-value** | **rank** |
| GOMF\_BASAL\_TRANSCRIPTION\_MACHINERY\_BINDING | 68 | -0.699  | -1.533  | 0.018  | 294 |
| GOMF\_RNA\_POLYMERASE\_BINDING | 72 | -0.672  | -1.489  | 0.018  | 294 |
| GOBP\_REGULATION\_OF\_CYTOPLASMIC\_TRANSLATION | 21 | -0.831  | -1.562  | 0.018  | 3112 |
| GOBP\_RESPONSE\_TO\_PLATELET\_DERIVED\_GROWTH\_FACTOR | 21 | -0.821  | -1.544  | 0.018  | 147 |
| GOMF\_PROTEIN\_DISULFIDE\_ISOMERASE\_ACTIVITY | 19 | -0.818  | -1.556  | 0.018  | 1107 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_METALLOPEPTIDASE\_ACTIVITY | 10 | -0.926  | -1.632  | 0.018  | 128 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CHOLESTEROL\_METABOLIC\_PROCESS | 10 | -0.900  | -1.586  | 0.018  | 39 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CYTOPLASMIC\_TRANSLATION | 12 | -0.911  | -1.594  | 0.018  | 3112 |
| GOBP\_CD4\_POSITIVE\_ALPHA\_BETA\_T\_CELL\_DIFFERENTIATION | 80 | 0.632  | 1.635  | 0.019  | 8631 |
| GOBP\_CELLULAR\_RESPONSE\_TO\_STEROL | 24 | -0.736  | -1.427  | 0.019  | 39 |
| GOBP\_POSITIVE\_REGULATION\_OF\_INTERLEUKIN\_6\_PRODUCTION | 84 | 0.577  | 1.490  | 0.019  | 16066 |
| GOBP\_REGULATION\_OF\_ACUTE\_INFLAMMATORY\_RESPONSE\_TO\_ANTIGENIC\_STIMULUS | 14 | 0.839  | 1.489  | 0.019  | 5014 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_APOPTOTIC\_PROCESS | 80 | 0.637  | 1.647  | 0.019  | 14858 |
| HP\_HEPATITIS | 84 | 0.600  | 1.550  | 0.019  | 7599 |
| GOBP\_CELL\_ADHESION\_MOLECULE\_PRODUCTION | 23 | -0.763  | -1.440  | 0.019  | 498 |
| GOBP\_ESTABLISHMENT\_OF\_LYMPHOCYTE\_POLARITY | 13 | 0.844  | 1.475  | 0.019  | 6952 |
| GOBP\_PROTEIN\_MATURATION\_BY\_IRON\_SULFUR\_CLUSTER\_TRANSFER | 16 | 0.930  | 1.675  | 0.019  | 189 |
| GOBP\_REGULATION\_OF\_METALLOPEPTIDASE\_ACTIVITY | 17 | -0.867  | -1.558  | 0.019  | 128 |
| GOBP\_MYELOID\_DENDRITIC\_CELL\_ACTIVATION | 29 | 0.754  | 1.517  | 0.020  | 9900 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_ANTIGEN\_RECEPTOR\_MEDIATED\_SIGNALING\_PATHWAY | 29 | 0.743  | 1.495  | 0.020  | 10363 |
| GOBP\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE\_TO\_ANTIGENIC\_STIMULUS | 29 | 0.786  | 1.582  | 0.020  | 5634 |
| GOBP\_B\_CELL\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | 79 | 0.679  | 1.724  | 0.020  | 8434 |
| GOBP\_IRON\_ION\_HOMEOSTASIS | 86 | 0.570  | 1.473  | 0.020  | 5180 |
| GOBP\_LEUKOCYTE\_HOMEOSTASIS | 79 | 0.622  | 1.579  | 0.020  | 14574 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_CHOLESTEROL\_EFFLUX | 15 | -0.822  | -1.459  | 0.020  | 8352 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_INTERLEUKIN\_12\_PRODUCTION | 17 | 0.824  | 1.483  | 0.020  | 6585 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_PHOSPHATIDYLINOSITOL\_3\_KINASE\_SIGNALING | 15 | -0.832  | -1.477  | 0.020  | 57 |
| GOBP\_PHAGOCYTOSIS\_RECOGNITION | 87 | 0.771  | 2.019  | 0.020  | 8498 |
| GOBP\_REGULATION\_OF\_T\_CELL\_MEDIATED\_IMMUNITY | 76 | 0.649  | 1.638  | 0.020  | 12798 |
| GOCC\_EXTRINSIC\_COMPONENT\_OF\_MITOCHONDRIAL\_INNER\_MEMBRANE | 15 | -0.817  | -1.450  | 0.020  | 1698 |
| GOCC\_TRANSCRIPTIONALLY\_ACTIVE\_CHROMATIN | 23 | 0.843  | 1.647  | 0.020  | 3079 |
| GOBP\_IRON\_SULFUR\_CLUSTER\_ASSEMBLY | 24 | 0.890  | 1.706  | 0.020  | 189 |
| GOBP\_POSITIVE\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE | 128 | 0.580  | 1.643  | 0.020  | 11382 |
| GOBP\_POSITIVE\_REGULATION\_OF\_INTERLEUKIN\_2\_PRODUCTION | 30 | 0.736  | 1.505  | 0.020  | 10403 |
| GOBP\_POSITIVE\_REGULATION\_OF\_NATURAL\_KILLER\_CELL\_MEDIATED\_CYTOTOXICITY | 26 | 0.821  | 1.561  | 0.020  | 7846 |
| GOBP\_POSITIVE\_REGULATION\_OF\_T\_CELL\_MIGRATION | 30 | 0.711  | 1.455  | 0.020  | 9395 |
| GOBP\_REGULATION\_OF\_B\_CELL\_DIFFERENTIATION | 30 | 0.720  | 1.473  | 0.020  | 11505 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_CYTOTOXICITY | 78 | 0.716  | 1.806  | 0.020  | 10312 |
| GOBP\_SOMATIC\_DIVERSIFICATION\_OF\_IMMUNE\_RECEPTORS | 75 | 0.612  | 1.539  | 0.020  | 7331 |
| GOBP\_T\_CELL\_CHEMOTAXIS | 27 | 0.747  | 1.435  | 0.020  | 8703 |
| GOBP\_TYPE\_I\_INTERFERON\_PRODUCTION | 128 | 0.540  | 1.530  | 0.020  | 13967 |
| HP\_GASTROINTESTINAL\_STROMA\_TUMOR | 18 | 0.819  | 1.500  | 0.020  | 2827 |
| HP\_SEVERE\_INFECTION | 28 | 0.732  | 1.429  | 0.020  | 11815 |
| GOBP\_B\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 120 | 0.797  | 2.219  | 0.021  | 8685 |
| GOBP\_COLLAGEN\_ACTIVATED\_TYROSINE\_KINASE\_RECEPTOR\_SIGNALING\_PATHWAY | 12 | 0.857  | 1.454  | 0.021  | 834 |
| GOBP\_GRANULOCYTE\_CHEMOTAXIS | 120 | 0.586  | 1.631  | 0.021  | 12618 |
| GOBP\_MEIOTIC\_CELL\_CYCLE\_PHASE\_TRANSITION | 10 | 0.842  | 1.369  | 0.021  | 2183 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS | 125 | 0.566  | 1.588  | 0.021  | 8703 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION | 88 | 0.615  | 1.596  | 0.021  | 10037 |
| GOBP\_POSITIVE\_REGULATION\_OF\_NATURAL\_KILLER\_CELL\_MEDIATED\_IMMUNITY | 31 | 0.789  | 1.606  | 0.021  | 7846 |
| GOCC\_U1\_SNRNP | 31 | 0.708  | 1.442  | 0.021  | 5059 |
| HP\_CHRONIC\_MUCOCUTANEOUS\_CANDIDIASIS | 31 | 0.715  | 1.456  | 0.021  | 10831 |
| HP\_MENINGITIS | 73 | 0.693  | 1.738  | 0.021  | 13110 |
| GOBP\_CELLULAR\_EXTRAVASATION | 69 | 0.601  | 1.476  | 0.022  | 15081 |
| GOBP\_INTERFERON\_GAMMA\_MEDIATED\_SIGNALING\_PATHWAY | 89 | 0.584  | 1.515  | 0.022  | 17572 |
| GOBP\_NEUTROPHIL\_MIGRATION | 118 | 0.593  | 1.639  | 0.022  | 12618 |
| GOBP\_POSITIVE\_REGULATION\_OF\_MITOCHONDRIAL\_MEMBRANE\_POTENTIAL | 11 | 0.849  | 1.392  | 0.022  | 1434 |
| GOBP\_POSITIVE\_REGULATION\_OF\_TUMOR\_NECROSIS\_FACTOR\_SUPERFAMILY\_CYTOKINE\_PRODUCTION | 89 | 0.587  | 1.522  | 0.022  | 12340 |
| GOBP\_REGULATION\_OF\_PHAGOCYTOSIS | 92 | 0.589  | 1.533  | 0.022  | 10965 |
| GOCC\_CHAPERONIN\_CONTAINING\_T\_COMPLEX | 11 | 0.875  | 1.433  | 0.022  | 1278 |
| HP\_LEUKOCYTOSIS | 118 | 0.494  | 1.364  | 0.022  | 13660 |
| HP\_LYMPHOPENIA | 121 | 0.620  | 1.727  | 0.022  | 13185 |
| HP\_SEPSIS | 92 | 0.532  | 1.384  | 0.022  | 13110 |
| HP\_UNUSUAL\_INFECTION\_BY\_ANATOMICAL\_SITE | 92 | 0.632  | 1.644  | 0.022  | 13110 |
| GOBP\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION\_OF\_PEPTIDE\_ANTIGEN\_VIA\_MHC\_CLASS\_I | 99 | 0.533  | 1.429  | 0.022  | 19771 |
| GOBP\_CHEMOKINE\_PRODUCTION | 93 | 0.505  | 1.311  | 0.022  | 18240 |
| GOBP\_CYTOKINE\_PRODUCTION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | 93 | 0.573  | 1.489  | 0.022  | 12763 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_LEUKOCYTE\_CELL\_CELL\_ADHESION | 136 | 0.578  | 1.647  | 0.022  | 13917 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_RESPONSE\_TO\_BIOTIC\_STIMULUS | 99 | 0.518  | 1.388  | 0.022  | 14135 |
| GOBP\_NEUTROPHIL\_CHEMOTAXIS | 99 | 0.597  | 1.599  | 0.022  | 12618 |
| GOBP\_POSITIVE\_REGULATION\_OF\_PRODUCTION\_OF\_MOLECULAR\_MEDIATOR\_OF\_IMMUNE\_RESPONSE | 99 | 0.573  | 1.535  | 0.022  | 12763 |
| GOBP\_REGULATION\_OF\_ALPHA\_BETA\_T\_CELL\_ACTIVATION | 99 | 0.642  | 1.719  | 0.022  | 8703 |
| GOBP\_REGULATION\_OF\_MONONUCLEAR\_CELL\_MIGRATION | 111 | 0.628  | 1.727  | 0.022  | 15081 |
| GOBP\_T\_CELL\_DIFFERENTIATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | 72 | 0.645  | 1.597  | 0.022  | 8419 |
| GOCC\_TERTIARY\_GRANULE\_MEMBRANE | 72 | 0.607  | 1.504  | 0.022  | 10032 |
| GOMF\_CYTOKINE\_BINDING | 136 | 0.523  | 1.492  | 0.022  | 14965 |
| GOMF\_IMMUNOGLOBULIN\_RECEPTOR\_BINDING | 68 | 0.833  | 2.042  | 0.022  | 8882 |
| HP\_INCREASED\_CSF\_LACTATE | 99 | 0.530  | 1.418  | 0.022  | 397 |
| HP\_LYMPHOMA | 99 | 0.617  | 1.653  | 0.022  | 9427 |
| HP\_RECURRENT\_SKIN\_INFECTIONS | 99 | 0.651  | 1.744  | 0.022  | 11698 |
| HP\_RECURRENT\_UPPER\_RESPIRATORY\_TRACT\_INFECTIONS | 124 | 0.530  | 1.468  | 0.022  | 7933 |
| GOBP\_B\_CELL\_DIFFERENTIATION | 137 | 0.518  | 1.464  | 0.023  | 8596 |
| GOBP\_DENDRITIC\_CELL\_DIFFERENTIATION | 46 | 0.667  | 1.497  | 0.023  | 11161 |
| GOBP\_INFLAMMATORY\_RESPONSE\_TO\_ANTIGENIC\_STIMULUS | 59 | 0.666  | 1.537  | 0.023  | 13761 |
| GOBP\_INTERFERON\_GAMMA\_PRODUCTION | 110 | 0.659  | 1.804  | 0.023  | 13771 |
| GOBP\_INTERLEUKIN\_10\_PRODUCTION | 61 | 0.646  | 1.504  | 0.023  | 13771 |
| GOBP\_INTERLEUKIN\_12\_PRODUCTION | 59 | 0.701  | 1.617  | 0.023  | 7823 |
| GOBP\_LEUKOCYTE\_MEDIATED\_CYTOTOXICITY | 110 | 0.686  | 1.877  | 0.023  | 10312 |
| GOBP\_LYMPHOCYTE\_APOPTOTIC\_PROCESS | 71 | 0.681  | 1.669  | 0.023  | 8251 |
| GOBP\_LYMPHOCYTE\_COSTIMULATION | 59 | 0.710  | 1.639  | 0.023  | 7846 |
| GOBP\_MEMBRANE\_INVAGINATION | 132 | 0.761  | 2.143  | 0.023  | 8685 |
| GOBP\_MONOCYTE\_CHEMOTAXIS | 66 | 0.649  | 1.588  | 0.023  | 11559 |
| GOBP\_NATURAL\_KILLER\_CELL\_MEDIATED\_IMMUNITY | 67 | 0.726  | 1.785  | 0.023  | 9736 |
| GOBP\_POSITIVE\_REGULATION\_OF\_ALPHA\_BETA\_T\_CELL\_ACTIVATION | 64 | 0.639  | 1.529  | 0.023  | 8703 |
| GOBP\_POSITIVE\_REGULATION\_OF\_INTERFERON\_GAMMA\_PRODUCTION | 64 | 0.723  | 1.731  | 0.023  | 11200 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_CHEMOTAXIS | 91 | 0.617  | 1.606  | 0.023  | 12164 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_IMMUNITY | 123 | 0.673  | 1.858  | 0.023  | 7949 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LYMPHOCYTE\_DIFFERENTIATION | 100 | 0.574  | 1.544  | 0.023  | 15003 |
| GOBP\_POSITIVE\_REGULATION\_OF\_PHAGOCYTOSIS | 65 | 0.641  | 1.557  | 0.023  | 10691 |
| GOBP\_REGULATION\_OF\_ALPHA\_BETA\_T\_CELL\_DIFFERENTIATION | 66 | 0.627  | 1.535  | 0.023  | 7879 |
| GOBP\_REGULATION\_OF\_B\_CELL\_PROLIFERATION | 61 | 0.695  | 1.619  | 0.023  | 12658 |
| GOBP\_REGULATION\_OF\_CD4\_POSITIVE\_ALPHA\_BETA\_T\_CELL\_ACTIVATION | 65 | 0.638  | 1.547  | 0.023  | 13771 |
| GOBP\_REGULATION\_OF\_HUMORAL\_IMMUNE\_RESPONSE | 137 | 0.732  | 2.067  | 0.023  | 9680 |
| GOBP\_REGULATION\_OF\_IMMUNOGLOBULIN\_PRODUCTION | 67 | 0.639  | 1.570  | 0.023  | 8703 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_CHEMOTAXIS | 117 | 0.610  | 1.674  | 0.023  | 12340 |
| GOBP\_SOMATIC\_DIVERSIFICATION\_OF\_IMMUNOGLOBULINS | 64 | 0.657  | 1.572  | 0.023  | 7331 |
| GOBP\_T\_CELL\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | 110 | 0.516  | 1.411  | 0.023  | 7879 |
| GOBP\_T\_CELL\_MEDIATED\_CYTOTOXICITY | 45 | 0.660  | 1.476  | 0.023  | 12798 |
| GOBP\_T\_CELL\_MEDIATED\_IMMUNITY | 100 | 0.638  | 1.715  | 0.023  | 12798 |
| GOBP\_T\_CELL\_MIGRATION | 66 | 0.682  | 1.671  | 0.023  | 11892 |
| GOBP\_T\_HELPER\_17\_TYPE\_IMMUNE\_RESPONSE | 32 | 0.700  | 1.444  | 0.023  | 8251 |
| GOCC\_IMMUNOGLOBULIN\_COMPLEX\_CIRCULATING | 66 | 0.837  | 2.050  | 0.023  | 8498 |
| GOCC\_KERATIN\_FILAMENT | 94 | 0.516  | 1.339  | 0.023  | 6703 |
| GOCC\_SM\_LIKE\_PROTEIN\_FAMILY\_COMPLEX | 110 | 0.483  | 1.322  | 0.023  | 466 |
| GOCC\_SPECIFIC\_GRANULE\_MEMBRANE | 90 | 0.572  | 1.475  | 0.023  | 9918 |
| GOCC\_T\_CELL\_RECEPTOR\_COMPLEX | 135 | 0.874  | 2.466  | 0.023  | 6546 |
| GOMF\_METAL\_CLUSTER\_BINDING | 67 | 0.656  | 1.612  | 0.023  | 189 |
| HP\_ABNORMAL\_CIRCULATING\_IGG\_LEVEL | 64 | 0.670  | 1.605  | 0.023  | 13556 |
| HP\_ABNORMAL\_CIRCULATING\_IGM\_LEVEL | 60 | 0.641  | 1.500  | 0.023  | 13556 |
| HP\_ECZEMA | 134 | 0.520  | 1.466  | 0.023  | 13704 |
| HP\_GASTROINTESTINAL\_INFLAMMATION | 100 | 0.553  | 1.487  | 0.023  | 9322 |
| HP\_HEMOLYTIC\_ANEMIA | 123 | 0.556  | 1.535  | 0.023  | 7412 |
| HP\_HEPATOSPLENOMEGALY | 117 | 0.526  | 1.443  | 0.023  | 7970 |
| HP\_INCREASED\_CIRCULATING\_ANTIBODY\_LEVEL | 91 | 0.521  | 1.354  | 0.023  | 13274 |
| HP\_NEPHRITIS | 61 | 0.662  | 1.540  | 0.023  | 9680 |
| HP\_RECURRENT\_LOWER\_RESPIRATORY\_TRACT\_INFECTIONS | 110 | 0.566  | 1.549  | 0.023  | 7933 |
| HP\_RECURRENT\_PAROXYSMAL\_HEADACHE | 32 | 0.713  | 1.471  | 0.023  | 397 |
| HP\_SKIN\_RASH | 115 | 0.546  | 1.504  | 0.023  | 13274 |
| HP\_SYSTEMIC\_LUPUS\_ERYTHEMATOSUS | 32 | 0.698  | 1.439  | 0.023  | 13813 |
| HP\_T\_LYMPHOCYTOPENIA | 45 | 0.708  | 1.583  | 0.023  | 13185 |
| HP\_VASCULITIS | 65 | 0.669  | 1.625  | 0.023  | 13185 |
| GOBP\_B\_CELL\_PROLIFERATION | 96 | 0.565  | 1.476  | 0.023  | 7288 |
| GOBP\_CELLULAR\_IRON\_ION\_HOMEOSTASIS | 70 | 0.611  | 1.496  | 0.023  | 5180 |
| GOBP\_FC\_RECEPTOR\_MEDIATED\_STIMULATORY\_SIGNALING\_PATHWAY | 144 | 0.790  | 2.193  | 0.023  | 9244 |
| GOBP\_GRANULOCYTE\_MIGRATION | 143 | 0.590  | 1.643  | 0.023  | 12340 |
| GOBP\_LYMPHOCYTE\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | 188 | 0.546  | 1.565  | 0.023  | 8474 |
| GOBP\_LYMPHOCYTE\_HOMEOSTASIS | 57 | 0.665  | 1.518  | 0.023  | 9223 |
| GOBP\_LYMPHOCYTE\_MIGRATION | 116 | 0.674  | 1.848  | 0.023  | 12981 |
| GOBP\_MONONUCLEAR\_CELL\_MIGRATION | 188 | 0.634  | 1.818  | 0.023  | 13917 |
| GOBP\_POSITIVE\_REGULATION\_OF\_B\_CELL\_ACTIVATION | 139 | 0.770  | 2.153  | 0.023  | 9260 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CHEMOTAXIS | 139 | 0.505  | 1.410  | 0.023  | 12547 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_MIGRATION | 133 | 0.591  | 1.659  | 0.023  | 14449 |
| GOBP\_POSITIVE\_REGULATION\_OF\_MITOTIC\_CELL\_CYCLE | 116 | 0.552  | 1.513  | 0.023  | 8401 |
| GOBP\_POSITIVE\_REGULATION\_OF\_MONONUCLEAR\_CELL\_MIGRATION | 63 | 0.657  | 1.559  | 0.023  | 9395 |
| GOBP\_POSITIVE\_T\_CELL\_SELECTION | 36 | 0.715  | 1.487  | 0.023  | 8631 |
| GOBP\_REGULATION\_OF\_ANTIGEN\_RECEPTOR\_MEDIATED\_SIGNALING\_PATHWAY | 63 | 0.732  | 1.737  | 0.023  | 10889 |
| GOBP\_REGULATION\_OF\_COMPLEMENT\_ACTIVATION | 114 | 0.751  | 2.068  | 0.023  | 9680 |
| GOBP\_REGULATION\_OF\_LYMPHOCYTE\_MIGRATION | 63 | 0.663  | 1.573  | 0.023  | 14965 |
| GOBP\_REGULATION\_OF\_NATURAL\_KILLER\_CELL\_MEDIATED\_IMMUNITY | 48 | 0.777  | 1.731  | 0.023  | 7846 |
| GOBP\_REGULATION\_OF\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 40 | 0.710  | 1.527  | 0.023  | 10403 |
| GOBP\_RESPONSE\_TO\_CHEMOKINE | 95 | 0.578  | 1.500  | 0.023  | 10829 |
| GOBP\_RESPONSE\_TO\_INTERLEUKIN\_12 | 50 | 0.711  | 1.556  | 0.023  | 6130 |
| GOBP\_T\_CELL\_SELECTION | 48 | 0.698  | 1.556  | 0.023  | 10831 |
| GOMF\_IMMUNE\_RECEPTOR\_ACTIVITY | 133 | 0.619  | 1.739  | 0.023  | 12805 |
| HP\_ABNORMAL\_T\_CELL\_SUBSET\_DISTRIBUTION | 47 | 0.719  | 1.605  | 0.023  | 8786 |
| HP\_ANTINUCLEAR\_ANTIBODY\_POSITIVITY | 37 | 0.703  | 1.450  | 0.023  | 10698 |
| HP\_SKIN\_ULCER | 116 | 0.498  | 1.365  | 0.023  | 13188 |
| GOBP\_CD4\_POSITIVE\_ALPHA\_BETA\_T\_CELL\_ACTIVATION | 98 | 0.618  | 1.638  | 0.024  | 8703 |
| GOBP\_CELLULAR\_DEFENSE\_RESPONSE | 53 | 0.707  | 1.562  | 0.024  | 10037 |
| GOBP\_HUMORAL\_IMMUNE\_RESPONSE\_MEDIATED\_BY\_CIRCULATING\_IMMUNOGLOBULIN | 145 | 0.784  | 2.180  | 0.024  | 8600 |
| GOBP\_IMMUNOGLOBULIN\_PRODUCTION\_INVOLVED\_IN\_IMMUNOGLOBULIN\_MEDIATED\_IMMUNE\_RESPONSE | 54 | 0.654  | 1.444  | 0.024  | 9838 |
| GOBP\_LYMPHOCYTE\_CHEMOTAXIS | 62 | 0.682  | 1.588  | 0.024  | 10884 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_CELL\_ADHESION | 187 | 0.544  | 1.553  | 0.024  | 13917 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION | 152 | 0.601  | 1.652  | 0.024  | 10334 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_KILLING | 62 | 0.733  | 1.707  | 0.024  | 10312 |
| GOBP\_POSITIVE\_REGULATION\_OF\_T\_CELL\_PROLIFERATION | 98 | 0.667  | 1.768  | 0.024  | 11071 |
| GOBP\_REGULATION\_OF\_LYMPHOCYTE\_APOPTOTIC\_PROCESS | 54 | 0.701  | 1.546  | 0.024  | 8251 |
| GOBP\_REGULATION\_OF\_LYMPHOCYTE\_MEDIATED\_IMMUNITY | 155 | 0.653  | 1.806  | 0.024  | 8703 |
| GOBP\_REGULATION\_OF\_T\_CELL\_DIFFERENTIATION | 145 | 0.572  | 1.592  | 0.024  | 14449 |
| GOBP\_REGULATION\_OF\_T\_HELPER\_CELL\_DIFFERENTIATION | 38 | 0.701  | 1.473  | 0.024  | 7879 |
| GOBP\_SOMATIC\_RECOMBINATION\_OF\_IMMUNOGLOBULIN\_GENE\_SEGMENTS | 54 | 0.671  | 1.480  | 0.024  | 7331 |
| GOBP\_TUMOR\_NECROSIS\_FACTOR\_MEDIATED\_SIGNALING\_PATHWAY | 172 | 0.493  | 1.389  | 0.024  | 14375 |
| GOCC\_BLOOD\_MICROPARTICLE | 145 | 0.625  | 1.739  | 0.024  | 10432 |
| GOCC\_SMALL\_NUCLEAR\_RIBONUCLEOPROTEIN\_COMPLEX | 98 | 0.503  | 1.333  | 0.024  | 466 |
| GOMF\_MHC\_PROTEIN\_BINDING | 39 | 0.796  | 1.692  | 0.024  | 7081 |
| HP\_ABNORMAL\_CIRCULATING\_IGA\_LEVEL | 62 | 0.664  | 1.546  | 0.024  | 10403 |
| HP\_ABNORMAL\_CONJUNCTIVA\_MORPHOLOGY | 142 | 0.522  | 1.443  | 0.024  | 12798 |
| HP\_ABNORMAL\_T\_CELL\_MORPHOLOGY | 62 | 0.693  | 1.614  | 0.024  | 13185 |
| HP\_ABNORMALITY\_OF\_BONE\_MARROW\_CELL\_MORPHOLOGY | 172 | 0.499  | 1.405  | 0.024  | 13882 |
| HP\_ABNORMALITY\_OF\_THE\_PHARYNX | 172 | 0.479  | 1.349  | 0.024  | 8212 |
| HP\_AUTOIMMUNE\_ANTIBODY\_POSITIVITY | 62 | 0.674  | 1.568  | 0.024  | 10698 |
| HP\_AUTOIMMUNE\_THROMBOCYTOPENIA | 39 | 0.702  | 1.492  | 0.024  | 7283 |
| HP\_DECREASED\_CIRCULATING\_IGA\_LEVEL | 39 | 0.699  | 1.485  | 0.024  | 12658 |
| HP\_DECREASED\_CIRCULATING\_IGG\_LEVEL | 54 | 0.688  | 1.517  | 0.024  | 13556 |
| HP\_PANCYTOPENIA | 109 | 0.522  | 1.417  | 0.024  | 13660 |
| HP\_RECURRENT\_VIRAL\_INFECTIONS | 56 | 0.690  | 1.553  | 0.024  | 7933 |
| HP\_UNUSUAL\_FUNGAL\_INFECTION | 62 | 0.643  | 1.496  | 0.024  | 13110 |
| GOBP\_ALPHA\_BETA\_T\_CELL\_ACTIVATION | 147 | 0.630  | 1.740  | 0.024  | 8703 |
| GOBP\_ALPHA\_BETA\_T\_CELL\_DIFFERENTIATION | 106 | 0.621  | 1.665  | 0.024  | 8631 |
| GOBP\_CELL\_KILLING | 176 | 0.557  | 1.564  | 0.024  | 7949 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_B\_CELL\_ACTIVATION | 33 | 0.724  | 1.480  | 0.024  | 10334 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_IMMUNE\_RESPONSE | 146 | 0.549  | 1.521  | 0.024  | 13917 |
| GOBP\_POSITIVE\_REGULATION\_OF\_HEMOPOIESIS | 153 | 0.507  | 1.384  | 0.024  | 15081 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION | 147 | 0.634  | 1.750  | 0.024  | 11685 |
| GOBP\_REGULATION\_OF\_B\_CELL\_ACTIVATION | 182 | 0.755  | 2.156  | 0.024  | 9260 |
| GOBP\_REGULATION\_OF\_CELL\_KILLING | 97 | 0.712  | 1.852  | 0.024  | 10312 |
| GOBP\_REGULATION\_OF\_LYMPHOCYTE\_DIFFERENTIATION | 174 | 0.582  | 1.639  | 0.024  | 15003 |
| GOBP\_REGULATION\_OF\_NATURAL\_KILLER\_CELL\_ACTIVATION | 33 | 0.679  | 1.388  | 0.024  | 13553 |
| GOBP\_REGULATION\_OF\_PRODUCTION\_OF\_MOLECULAR\_MEDIATOR\_OF\_IMMUNE\_RESPONSE | 146 | 0.580  | 1.607  | 0.024  | 12763 |
| GOBP\_T\_CELL\_PROLIFERATION | 194 | 0.615  | 1.753  | 0.024  | 12946 |
| GOBP\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 202 | 0.591  | 1.689  | 0.024  | 12829 |
| GOCC\_IMMUNOGLOBULIN\_COMPLEX | 153 | 0.845  | 2.308  | 0.024  | 7776 |
| GOMF\_ANTIGEN\_BINDING | 153 | 0.798  | 2.180  | 0.024  | 8498 |
| GOMF\_CHEMOKINE\_BINDING | 33 | 0.712  | 1.454  | 0.024  | 8420 |
| GOMF\_CYTOKINE\_RECEPTOR\_ACTIVITY | 97 | 0.605  | 1.573  | 0.024  | 12805 |
| HP\_ABNORMAL\_NEUTROPHIL\_COUNT | 175 | 0.555  | 1.562  | 0.024  | 8786 |
| HP\_ABNORMAL\_PHARYNX\_MORPHOLOGY | 147 | 0.502  | 1.387  | 0.024  | 8212 |
| HP\_AUTOIMMUNITY | 171 | 0.551  | 1.542  | 0.024  | 13185 |
| HP\_DECREASED\_CIRCULATING\_ANTIBODY\_LEVEL | 153 | 0.627  | 1.712  | 0.024  | 8350 |
| HP\_PURPURA | 106 | 0.555  | 1.488  | 0.024  | 13882 |
| GOBP\_CELLULAR\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN | 201 | 0.570  | 1.630  | 0.025  | 13761 |
| GOBP\_IMMUNOGLOBULIN\_PRODUCTION | 197 | 0.815  | 2.322  | 0.025  | 7406 |
| GOBP\_POSITIVE\_REGULATION\_OF\_ADAPTIVE\_IMMUNE\_RESPONSE | 101 | 0.608  | 1.607  | 0.025  | 12798 |
| GOBP\_POSITIVE\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS | 216 | 0.600  | 1.732  | 0.025  | 12798 |
| GOBP\_RECEPTOR\_MEDIATED\_ENDOCYTOSIS | 324 | 0.618  | 1.865  | 0.025  | 9807 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_MIGRATION | 201 | 0.580  | 1.658  | 0.025  | 15168 |
| GOBP\_REGULATION\_OF\_T\_CELL\_ACTIVATION | 324 | 0.604  | 1.822  | 0.025  | 12946 |
| GOBP\_REGULATION\_OF\_T\_CELL\_APOPTOTIC\_PROCESS | 34 | 0.704  | 1.444  | 0.025  | 8251 |
| GOBP\_REGULATORY\_T\_CELL\_DIFFERENTIATION | 35 | 0.695  | 1.447  | 0.025  | 10107 |
| GOBP\_RESPONSE\_TO\_INTERFERON\_GAMMA | 193 | 0.552  | 1.566  | 0.025  | 14745 |
| GOCC\_FICOLIN\_1\_RICH\_GRANULE | 184 | 0.504  | 1.434  | 0.025  | 15666 |
| HP\_ABNORMAL\_GRANULOCYTE\_COUNT | 216 | 0.574  | 1.655  | 0.025  | 13660 |
| HP\_ABNORMAL\_LYMPHOCYTE\_MORPHOLOGY | 158 | 0.613  | 1.691  | 0.025  | 13185 |
| HP\_ABNORMALITY\_OF\_THE\_LYMPH\_NODES | 197 | 0.570  | 1.624  | 0.025  | 13660 |
| HP\_ARTHRITIS | 197 | 0.491  | 1.399  | 0.025  | 10939 |
| HP\_DECREASED\_CIRCULATING\_TOTAL\_IGM | 35 | 0.690  | 1.436  | 0.025  | 13556 |
| HP\_IMMUNODEFICIENCY | 205 | 0.617  | 1.766  | 0.025  | 13110 |
| HP\_INFLAMMATORY\_ABNORMALITY\_OF\_THE\_EYE | 195 | 0.557  | 1.582  | 0.025  | 13185 |
| HP\_RECURRENT\_INFECTION\_OF\_THE\_GASTROINTESTINAL\_TRACT | 34 | 0.693  | 1.422  | 0.025  | 7664 |
| HP\_RED\_EYE | 101 | 0.604  | 1.598  | 0.025  | 12798 |
| GOBP\_COMPLEMENT\_ACTIVATION | 167 | 0.759  | 2.102  | 0.026  | 9488 |
| GOBP\_FC\_EPSILON\_RECEPTOR\_SIGNALING\_PATHWAY | 168 | 0.782  | 2.154  | 0.026  | 8498 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_ACTIVATION | 199 | 0.584  | 1.666  | 0.026  | 13917 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_CELL\_ADHESION | 272 | 0.573  | 1.709  | 0.026  | 12829 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_CYCLE\_PHASE\_TRANSITION | 105 | 0.599  | 1.605  | 0.026  | 11091 |
| GOBP\_REGULATION\_OF\_ADAPTIVE\_IMMUNE\_RESPONSE | 167 | 0.600  | 1.660  | 0.026  | 12798 |
| GOBP\_TUMOR\_NECROSIS\_FACTOR\_SUPERFAMILY\_CYTOKINE\_PRODUCTION | 164 | 0.488  | 1.347  | 0.026  | 11328 |
| GOCC\_SPECIFIC\_GRANULE | 159 | 0.480  | 1.314  | 0.026  | 9918 |
| GOCC\_TERTIARY\_GRANULE | 163 | 0.526  | 1.452  | 0.026  | 10032 |
| HP\_ABNORMAL\_RENAL\_GLOMERULUS\_MORPHOLOGY | 167 | 0.485  | 1.342  | 0.026  | 9778 |
| GOBP\_B\_CELL\_MEDIATED\_IMMUNITY | 215 | 0.761  | 2.189  | 0.026  | 9838 |
| GOBP\_LEUKOCYTE\_APOPTOTIC\_PROCESS | 102 | 0.615  | 1.618  | 0.026  | 13103 |
| GOBP\_MYELOID\_LEUKOCYTE\_MIGRATION | 211 | 0.537  | 1.532  | 0.026  | 11892 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_DIFFERENTIATION | 277 | 0.517  | 1.541  | 0.026  | 13771 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_IMMUNITY | 207 | 0.637  | 1.816  | 0.026  | 9049 |
| GOCC\_PLASMA\_MEMBRANE\_SIGNALING\_RECEPTOR\_COMPLEX | 301 | 0.765  | 2.288  | 0.027  | 7015 |
| GOBP\_CELL\_RECOGNITION | 221 | 0.601  | 1.717  | 0.028  | 8645 |
| GOBP\_FC\_RECEPTOR\_SIGNALING\_PATHWAY | 238 | 0.750  | 2.153  | 0.028  | 9244 |
| GOBP\_LEUKOCYTE\_CHEMOTAXIS | 221 | 0.557  | 1.592  | 0.028  | 12618 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_CELL\_CELL\_ADHESION | 230 | 0.604  | 1.743  | 0.028  | 12829 |
| GOBP\_PRODUCTION\_OF\_MOLECULAR\_MEDIATOR\_OF\_IMMUNE\_RESPONSE | 285 | 0.757  | 2.241  | 0.028  | 7406 |
| GOBP\_T\_CELL\_DIFFERENTIATION | 245 | 0.594  | 1.735  | 0.028  | 10403 |
| GOCC\_EXTERNAL\_SIDE\_OF\_PLASMA\_MEMBRANE | 390 | 0.622  | 1.882  | 0.028  | 8498 |
| HP\_LEUKOPENIA | 220 | 0.569  | 1.623  | 0.028  | 13660 |
| GOMF\_OLFACTORY\_RECEPTOR\_ACTIVITY | 417 | -0.480  | -1.349  | 0.028  | 3098 |
| GOBP\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | 232 | 0.493  | 1.417  | 0.029  | 14546 |
| GOBP\_ANTIGEN\_RECEPTOR\_MEDIATED\_SIGNALING\_PATHWAY | 307 | 0.701  | 2.089  | 0.029  | 10403 |
| GOBP\_B\_CELL\_ACTIVATION | 314 | 0.682  | 2.025  | 0.029  | 8685 |
| GOBP\_CELL\_CHEMOTAXIS | 298 | 0.518  | 1.533  | 0.029  | 12618 |
| GOBP\_CELLULAR\_RESPONSE\_TO\_BIOTIC\_STIMULUS | 225 | 0.564  | 1.602  | 0.029  | 13761 |
| GOBP\_LEUKOCYTE\_PROLIFERATION | 311 | 0.566  | 1.681  | 0.029  | 12680 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_IMMUNE\_SYSTEM\_PROCESS | 394 | 0.546  | 1.643  | 0.029  | 15372 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_ACTIVATION | 396 | 0.668  | 2.015  | 0.029  | 9260 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION | 240 | 0.620  | 1.773  | 0.029  | 12798 |
| GOBP\_RESPONSE\_TO\_TUMOR\_NECROSIS\_FACTOR | 314 | 0.499  | 1.481  | 0.029  | 13038 |
| HP\_ABNORMAL\_LYMPHOCYTE\_PHYSIOLOGY | 247 | 0.561  | 1.633  | 0.029  | 12798 |
| HP\_ABNORMAL\_MYELOID\_LEUKOCYTE\_MORPHOLOGY | 314 | 0.492  | 1.460  | 0.029  | 13660 |
| HP\_ABNORMALITY\_OF\_HUMORAL\_IMMUNITY | 250 | 0.572  | 1.658  | 0.029  | 12931 |
| HP\_ABNORMALITY\_OF\_NEUTROPHILS | 250 | 0.470  | 1.362  | 0.029  | 13660 |
| HP\_HEMATOLOGICAL\_NEOPLASM | 241 | 0.516  | 1.485  | 0.029  | 13185 |
| GOBP\_SENSORY\_PERCEPTION\_OF\_SMELL | 441 | -0.479  | -1.358  | 0.029  | 4832 |
| GOBP\_HUMORAL\_IMMUNE\_RESPONSE | 369 | 0.549  | 1.634  | 0.029  | 8600 |
| GOBP\_PHAGOCYTOSIS | 368 | 0.688  | 2.045  | 0.029  | 9680 |
| GOMF\_CYTOKINE\_ACTIVITY | 233 | 0.446  | 1.270  | 0.029  | 10829 |
| GOBP\_ADAPTIVE\_IMMUNE\_RESPONSE\_BASED\_ON\_SOMATIC\_RECOMBINATION\_OF\_IMMUNE\_RECEPTORS\_BUILT\_FROM\_IMMUNOGLOBULIN\_SUPERFAMILY\_DOMAINS | 351 | 0.723  | 2.161  | 0.030  | 10341 |
| GOBP\_POSITIVE\_REGULATION\_OF\_DEFENSE\_RESPONSE | 352 | 0.493  | 1.474  | 0.030  | 11455 |
| GOBP\_REGULATION\_OF\_CELL\_CELL\_ADHESION | 432 | 0.549  | 1.649  | 0.030  | 12829 |
| GOBP\_LYMPHOCYTE\_MEDIATED\_IMMUNITY | 345 | 0.731  | 2.186  | 0.031  | 9488 |
| GOBP\_MONONUCLEAR\_CELL\_DIFFERENTIATION | 409 | 0.554  | 1.664  | 0.031  | 10517 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CYTOKINE\_PRODUCTION | 431 | 0.562  | 1.685  | 0.031  | 12763 |
| GOBP\_POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_BIOTIC\_STIMULUS | 253 | 0.498  | 1.437  | 0.031  | 10037 |
| GOBP\_REGULATION\_OF\_HEMOPOIESIS | 411 | 0.493  | 1.482  | 0.031  | 15081 |
| GOBP\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS | 461 | 0.658  | 1.988  | 0.031  | 10408 |
| GOBP\_REGULATION\_OF\_RESPONSE\_TO\_BIOTIC\_STIMULUS | 414 | 0.496  | 1.486  | 0.031  | 13361 |
| GOBP\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN | 337 | 0.516  | 1.541  | 0.031  | 13771 |
| GOBP\_LEUKOCYTE\_CELL\_CELL\_ADHESION | 360 | 0.597  | 1.758  | 0.032  | 12981 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_ADHESION | 420 | 0.496  | 1.482  | 0.032  | 15081 |
| GOBP\_REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION | 494 | 0.664  | 2.023  | 0.032  | 10499 |
| GOBP\_T\_CELL\_ACTIVATION | 471 | 0.560  | 1.679  | 0.032  | 10499 |
| HP\_ABNORMAL\_LEUKOCYTE\_COUNT | 356 | 0.530  | 1.577  | 0.032  | 13660 |
| GOBP\_IMMUNE\_RESPONSE\_REGULATING\_SIGNALING\_PATHWAY | 500 | 0.665  | 2.030  | 0.033  | 10403 |
| GOBP\_LEUKOCYTE\_MIGRATION | 500 | 0.624  | 1.904  | 0.033  | 11261 |
| GOBP\_POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_EXTERNAL\_STIMULUS | 500 | 0.495  | 1.512  | 0.033  | 12837 |
| GOMF\_RNA\_POLYMERASE\_CORE\_ENZYME\_BINDING | 56 | -0.699  | -1.617  | 0.033  | 294 |
| HP\_ABNORMAL\_WAIST\_TO\_HIP\_RATIO | 37 | -0.668  | -1.438  | 0.034  | 11689 |
| GOBP\_REGULATION\_OF\_CHOLESTEROL\_EFFLUX | 41 | -0.704  | -1.540  | 0.034  | 8352 |
| GOBP\_REGULATION\_OF\_VASCULAR\_ASSOCIATED\_SMOOTH\_MUSCLE\_CELL\_PROLIFERATION | 72 | -0.651  | -1.443  | 0.035  | 454 |
| GOBP\_CELLULAR\_RESPONSE\_TO\_CHOLESTEROL | 19 | -0.778  | -1.479  | 0.036  | 39 |
| GOBP\_REGULATION\_OF\_VASCULAR\_WOUND\_HEALING | 11 | -0.852  | -1.508  | 0.036  | 147 |
| GOBP\_VASCULAR\_WOUND\_HEALING | 19 | -0.777  | -1.477  | 0.036  | 147 |
| GOBP\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION\_OF\_EXOGENOUS\_PEPTIDE\_ANTIGEN\_VIA\_MHC\_CLASS\_I | 80 | 0.562  | 1.454  | 0.038  | 13214 |
| GOBP\_PRODUCTION\_OF\_MOLECULAR\_MEDIATOR\_INVOLVED\_IN\_INFLAMMATORY\_RESPONSE | 81 | 0.570  | 1.468  | 0.038  | 7680 |
| GOBP\_IMMUNOLOGICAL\_SYNAPSE\_FORMATION | 13 | 0.832  | 1.455  | 0.038  | 6952 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_STEROL\_TRANSPORT | 23 | -0.701  | -1.324  | 0.038  | 8352 |
| GOBP\_DENDRITIC\_CELL\_MIGRATION | 29 | 0.702  | 1.413  | 0.039  | 11568 |
| GOBP\_REGULATION\_OF\_DEFENSE\_RESPONSE\_TO\_VIRUS\_BY\_VIRUS | 29 | 0.710  | 1.429  | 0.039  | 9575 |
| HP\_AUTOIMMUNE\_HEMOLYTIC\_ANEMIA | 29 | 0.697  | 1.402  | 0.039  | 13185 |
| HP\_INTESTINAL\_PSEUDO\_OBSTRUCTION | 29 | 0.703  | 1.415  | 0.039  | 397 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_B\_CELL\_PROLIFERATION | 17 | 0.786  | 1.414  | 0.040  | 10037 |
| GOBP\_PRE\_MIRNA\_PROCESSING | 15 | -0.794  | -1.410  | 0.040  | 1340 |
| GOBP\_REGULATION\_OF\_RESPONSE\_TO\_TUMOR\_CELL | 17 | 0.783  | 1.409  | 0.040  | 7601 |
| GOBP\_T\_HELPER\_CELL\_LINEAGE\_COMMITMENT | 17 | 0.770  | 1.386  | 0.040  | 7879 |
| GOBP\_REGULATION\_OF\_MYOBLAST\_PROLIFERATION | 18 | 0.780  | 1.429  | 0.041  | 499 |
| GOBP\_TOLERANCE\_INDUCTION | 28 | 0.729  | 1.424  | 0.041  | 6908 |
| GOCC\_CHAPERONE\_COMPLEX | 28 | 0.706  | 1.379  | 0.041  | 1278 |
| GOMF\_C\_C\_CHEMOKINE\_BINDING | 24 | 0.760  | 1.457  | 0.041  | 8420 |
| HP\_ABNORMAL\_CELL\_PROLIFERATION | 27 | 0.717  | 1.377  | 0.041  | 10313 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LYMPHOCYTE\_CHEMOTAXIS | 20 | 0.745  | 1.405  | 0.042  | 8703 |
| GOBP\_REGULATION\_OF\_B\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 25 | 0.762  | 1.426  | 0.042  | 10889 |
| GOCC\_TRIGLYCERIDE\_RICH\_PLASMA\_LIPOPROTEIN\_PARTICLE | 20 | 0.739  | 1.393  | 0.042  | 11644 |
| GOBP\_DETECTION\_OF\_CHEMICAL\_STIMULUS | 495 | -0.460  | -1.320  | 0.042  | 4832 |
| GOBP\_MATURE\_B\_CELL\_DIFFERENTIATION | 31 | 0.685  | 1.395  | 0.043  | 8434 |
| GOMF\_PEPTIDE\_ANTIGEN\_BINDING | 31 | 0.690  | 1.405  | 0.043  | 14802 |
| HP\_POSTERIOR\_PHARYNGEAL\_CLEFT | 12 | 0.837  | 1.420  | 0.043  | 2827 |
| GOBP\_MYOBLAST\_PROLIFERATION | 22 | 0.769  | 1.452  | 0.043  | 499 |
| GOBP\_POSITIVE\_REGULATION\_OF\_ANTIGEN\_RECEPTOR\_MEDIATED\_SIGNALING\_PATHWAY | 21 | 0.769  | 1.449  | 0.043  | 6794 |
| GOBP\_REGULATION\_OF\_DEFENSE\_RESPONSE\_TO\_VIRUS | 69 | 0.595  | 1.462  | 0.043  | 14216 |
| GOMF\_SIALIC\_ACID\_BINDING | 22 | 0.775  | 1.464  | 0.043  | 7393 |
| HP\_AGAMMAGLOBULINEMIA | 19 | 0.758  | 1.387  | 0.043  | 7933 |
| HP\_DECREASED\_LDL\_CHOLESTEROL\_CONCENTRATION | 11 | 0.846  | 1.386  | 0.043  | 4267 |
| HP\_DISTAL\_PERIPHERAL\_SENSORY\_NEUROPATHY | 19 | 0.746  | 1.364  | 0.043  | 397 |
| HP\_ERYTHEMA | 118 | 0.466  | 1.289  | 0.043  | 13621 |
| GOBP\_POSITIVE\_REGULATION\_OF\_G1\_S\_TRANSITION\_OF\_MITOTIC\_CELL\_CYCLE | 43 | 0.674  | 1.516  | 0.044  | 11963 |
| GOBP\_REGULATION\_OF\_T\_CELL\_MIGRATION | 43 | 0.671  | 1.509  | 0.044  | 9395 |
| GOBP\_INTERLEUKIN\_1\_PRODUCTION | 123 | 0.482  | 1.331  | 0.045  | 11030 |
| GOBP\_INTERLEUKIN\_2\_PRODUCTION | 61 | 0.638  | 1.486  | 0.045  | 10403 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_T\_CELL\_PROLIFERATION | 66 | 0.580  | 1.421  | 0.045  | 8703 |
| GOBP\_POSITIVE\_REGULATION\_OF\_B\_CELL\_PROLIFERATION | 40 | 0.658  | 1.415  | 0.047  | 12658 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CD4\_POSITIVE\_ALPHA\_BETA\_T\_CELL\_ACTIVATION | 37 | 0.661  | 1.364  | 0.047  | 14235 |
| GOBP\_POSITIVE\_REGULATION\_OF\_INTERLEUKIN\_1\_PRODUCTION | 63 | 0.624  | 1.481  | 0.047  | 11637 |
| GOBP\_POSITIVE\_REGULATION\_OF\_INTERLEUKIN\_12\_PRODUCTION | 40 | 0.672  | 1.447  | 0.047  | 13771 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LYMPHOCYTE\_MIGRATION | 37 | 0.680  | 1.402  | 0.047  | 13917 |
| GOBP\_REGULATION\_OF\_CD4\_POSITIVE\_ALPHA\_BETA\_T\_CELL\_DIFFERENTIATION | 50 | 0.664  | 1.453  | 0.047  | 7879 |
| GOBP\_REGULATION\_OF\_T\_CELL\_MEDIATED\_CYTOTOXICITY | 37 | 0.670  | 1.383  | 0.047  | 12798 |
| GOBP\_T\_CELL\_APOPTOTIC\_PROCESS | 49 | 0.672  | 1.484  | 0.047  | 8251 |
| GOBP\_T\_CELL\_HOMEOSTASIS | 36 | 0.667  | 1.389  | 0.047  | 8474 |
| GOCC\_DNA\_PACKAGING\_COMPLEX | 113 | 0.474  | 1.297  | 0.047  | 17869 |
| HP\_ABNORMAL\_METABOLIC\_BRAIN\_IMAGING\_BY\_MRS | 37 | 0.675  | 1.392  | 0.047  | 397 |
| HP\_STOMATITIS | 58 | 0.624  | 1.443  | 0.047  | 13967 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_PRODUCTION\_OF\_MOLECULAR\_MEDIATOR\_OF\_IMMUNE\_RESPONSE | 39 | 0.647  | 1.375  | 0.048  | 8703 |
| GOBP\_POSITIVE\_REGULATION\_OF\_B\_CELL\_MEDIATED\_IMMUNITY | 38 | 0.666  | 1.399  | 0.048  | 8703 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_CYCLE\_G1\_S\_PHASE\_TRANSITION | 54 | 0.639  | 1.409  | 0.048  | 11963 |
| GOBP\_POSITIVE\_REGULATION\_OF\_INTERLEUKIN\_10\_PRODUCTION | 38 | 0.660  | 1.386  | 0.048  | 8703 |
| HP\_ABNORMAL\_B\_CELL\_MORPHOLOGY | 38 | 0.684  | 1.436  | 0.048  | 13185 |
| HP\_ABNORMAL\_EOSINOPHIL\_MORPHOLOGY | 56 | 0.644  | 1.448  | 0.048  | 13473 |
| HP\_ABNORMALITY\_OF\_T\_CELL\_PHYSIOLOGY | 53 | 0.653  | 1.441  | 0.048  | 7283 |
| HP\_INFLAMMATION\_OF\_THE\_LARGE\_INTESTINE | 62 | 0.628  | 1.461  | 0.048  | 9322 |
| HP\_ORAL\_ULCER | 39 | 0.690  | 1.468  | 0.048  | 7107 |
| GOBP\_INTERLEUKIN\_1\_BETA\_PRODUCTION | 106 | 0.478  | 1.283  | 0.049  | 11637 |
| GOBP\_MYELOID\_LEUKOCYTE\_DIFFERENTIATION | 203 | 0.424  | 1.217  | 0.049  | 13661 |
| GOBP\_PATTERN\_RECOGNITION\_RECEPTOR\_SIGNALING\_PATHWAY | 203 | 0.441  | 1.266  | 0.049  | 14110 |
| GOCC\_INTERMEDIATE\_FILAMENT | 203 | 0.420  | 1.207  | 0.049  | 6703 |
| HP\_NEOPLASM\_OF\_THE\_SKIN | 182 | 0.433  | 1.236  | 0.049  | 19247 |

## Table S8. Correlation analysis of four key genes and immune checkpoints

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene** | **Checkpoint** | **Alias** | **Rs(Spearman)** | ***P*value** |
| ZBTB32 | A2AR |  | 0.54 | 9.20E-25 |
| ZBTB32 | CD122 |  | 0.48 | 4.20E-19 |
| ZBTB32 | CD134 | OX40 | 0.57 | 3.20E-27 |
| ZBTB32 | CD137 |  | 0.52 | 9.50E-23 |
| ZBTB32 | CD152 | CTLA-4 | 0.59 | 4.00E-30 |
| ZBTB32 | CD159A | KLRC1 | 0.24 | 2.60E-05 |
| ZBTB32 | CD172A | SIRPA | 0.24 | 2.80E-05 |
| ZBTB32 | CD2 |  | 0.57 | 3.00E-27 |
| ZBTB32 | CD200R1 |  | 0.42 | 2.20E-14 |
| ZBTB32 | CD223 | LAG3 | 0.57 | 7.40E-28 |
| ZBTB32 | CD244 |  | 0.41 | 3.70E-14 |
| ZBTB32 | CD27 |  | 0.62 | 4.00E-34 |
| ZBTB32 | CD272 | BTLA | 0.52 | 3.90E-22 |
| ZBTB32 | CD278 | ICOS | 0.64 | 1.20E-36 |
| ZBTB32 | CD279 | PD-1 | 0.58 | 2.20E-29 |
| ZBTB32 | CD28 |  | 0.58 | 2.60E-29 |
| ZBTB32 | CD357 | GITR | 0.17 | 2.70E-03 |
| ZBTB32 | CD366 | TIM-3 | 0.53 | 1.20E-23 |
| ZBTB32 | CD40 |  | 0.31 | 4.60E-08 |
| ZBTB32 | CD80 |  | 0.54 | 3.20E-24 |
| ZBTB32 | CD94 | KLRD1 | 0.44 | 4.00E-16 |
| ZBTB32 | TIGIT |  | 0.56 | 3.40E-26 |
| ZBTB32 | IDO |  | 0.37 | 1.50E-11 |
| PALB2 | A2AR |  | -0.096 | 0.095 |
| PALB2 | CD122 |  | 0.097 | 0.09 |
| PALB2 | CD134 | OX40 | -0.077 | 0.18 |
| PALB2 | CD137 |  | 0.086 | 0.13 |
| PALB2 | CD152 | CTLA-4 | 0.11 | 0.053 |
| PALB2 | CD159A | KLRC1 | 0.13 | 0.027 |
| PALB2 | CD172A | SIRPA | -0.066 | 0.25 |
| PALB2 | CD2 |  | 0.13 | 0.024 |
| PALB2 | CD200R1 |  | 0.21 | 0.00026 |
| PALB2 | CD223 | LAG3 | 0.089 | 0.12 |
| PALB2 | CD244 |  | 0.099 | 0.082 |
| PALB2 | CD27 |  | 0.049 | 0.4 |
| PALB2 | CD272 | BTLA | 0.13 | 0.021 |
| PALB2 | CD278 | ICOS | 0.082 | 0.15 |
| PALB2 | CD279 | PD-1 | 0.06 | 0.29 |
| PALB2 | CD28 |  | 0.028 | 0.63 |
| PALB2 | CD357 | GITR | 0.24 | 3.10E-05 |
| PALB2 | CD366 | TIM-3 | 0.13 | 0.023 |
| PALB2 | CD40 |  | 0.16 | 0.0044 |
| PALB2 | CD80 |  | 0.11 | 0.06 |
| PALB2 | CD94 | KLRD1 | 0.12 | 0.041 |
| PALB2 | TIGIT |  | 0.15 | 0.0095 |
| PALB2 | IDO |  | 0.17 | 0.0029 |
| BRCA2 | A2AR |  | 0.085 | 0.14 |
| BRCA2 | CD122 |  | 0.23 | 5.30E-05 |
| BRCA2 | CD134 | OX40 | -0.1 | 0.078 |
| BRCA2 | CD137 |  | 0.12 | 0.039 |
| BRCA2 | CD152 | CTLA-4 | -0.066 | 0.25 |
| BRCA2 | CD159A | KLRC1 | 0.013 | 0.81 |
| BRCA2 | CD172A | SIRPA | 0.018 | 0.75 |
| BRCA2 | CD2 |  | -0.013 | 0.82 |
| BRCA2 | CD200R1 |  | 0.19 | 0.00075 |
| BRCA2 | CD223 | LAG3 | -0.13 | 0.02 |
| BRCA2 | CD244 |  | 0.057 | 0.32 |
| BRCA2 | CD27 |  | -0.079 | 0.17 |
| BRCA2 | CD272 | BTLA | -0.045 | 0.43 |
| BRCA2 | CD278 | ICOS | 0.015 | 0.79 |
| BRCA2 | CD279 | PD-1 | -0.02 | 0.73 |
| BRCA2 | CD28 |  | 0.099 | 0.083 |
| BRCA2 | CD357 | GITR | -0.015 | 0.79 |
| BRCA2 | CD366 | TIM-3 | -0.039 | 0.5 |
| BRCA2 | CD40 |  | 0.028 | 0.63 |
| BRCA2 | CD80 |  | -0.0086 | 0.88 |
| BRCA2 | CD94 | KLRD1 | 0.025 | 0.67 |
| BRCA2 | TIGIT |  | 0.036 | 0.53 |
| BRCA2 | IDO |  | 0.12 | 0.041 |
| CENPS | A2AR |  | 0.035 | 0.54 |
| CENPS | CD122 |  | -0.035 | 0.54 |
| CENPS | CD134 | OX40 | -0.073 | 0.2 |
| CENPS | CD137 |  | -0.01 | 0.86 |
| CENPS | CD152 | CTLA-4 | -0.096 | 0.094 |
| CENPS | CD159A | KLRC1 | -0.061 | 0.29 |
| CENPS | CD172A | SIRPA | -0.19 | 0.00062 |
| CENPS | CD2 |  | -0.051 | 0.37 |
| CENPS | CD200R1 |  | 0.036 | 0.53 |
| CENPS | CD223 | LAG3 | -0.15 | 0.011 |
| CENPS | CD244 |  | -0.11 | 0.06 |
| CENPS | CD27 |  | -0.063 | 0.27 |
| CENPS | CD272 | BTLA | -0.027 | 0.64 |
| CENPS | CD278 | ICOS | -0.082 | 0.15 |
| CENPS | CD279 | PD-1 | -0.085 | 0.14 |
| CENPS | CD28 |  | -0.035 | 0.54 |
| CENPS | CD357 | GITR | 0.14 | 0.011 |
| CENPS | CD366 | TIM-3 | -0.1 | 0.082 |
| CENPS | CD40 |  | -0.033 | 0.57 |
| CENPS | CD80 |  | -0.038 | 0.51 |
| CENPS | CD94 | KLRD1 | -0.074 | 0.2 |
| CENPS | TIGIT |  | -0.04 | 0.49 |
| CENPS | IDO | 　 | 0.048 | 0.41 |