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# Table S1. Study characteristics of the 17 public ovarian cancer datasets

|  |  |  |  |
| --- | --- | --- | --- |
| Study ID | Study title | Platform | Reference |
| GSE14764 | A Prognostic Gene Expression Index in Ovarian Cancer | Affymetrix Human Genome U133A Array | (1) |
| GSE23554 | Ovarian Cancer Dataset | Affymetrix Human Genome U133A Array | (2) |
| GSE26712 | A Gene Signature Predicting for Survival in Suboptimally Debulked Patients with Ovarian Cancer | Affymetrix Human Genome U133A Array | (3) |
| GSE3149 | Ovarian Cancer Dataset | Affymetrix Human Genome U133A Array | (4) |
| GSE18520 | Whole-genome oligonucleotide expression analysis of papillary serous ovarian adenocarcinomas | Affymetrix Human Genome U133 Plus 2.0 Array | (5) |
| GSE19829 | A gene expression profile of BRCAness that is associated with outcome in ovarian cancer | Affymetrix Human Genome U133 Plus 2.0 Array | (6) |
| GSE26193 | Control of oxidative stress by miRNA and impact on ovarian tumorigenesis | Affymetrix Human Genome U133 Plus 2.0 Array | (7) |
| GSE30161 | Genomic Multivariate Predictors of Response to Adjuvant Chemotherapy in Ovarian Carcinoma: Predicting Platinum Resistance | Affymetrix Human Genome U133 Plus 2.0 Array | (8) |
| GSE63885 | Gene expression profiling in ovarian cancer | Affymetrix Human Genome U133 Plus 2.0 Array | (9) |
| GSE9891 | Expression profile of 285 ovarian tumour samples | Affymetrix Human Genome U133 Plus 2.0 Array | (10) |
| GSE49997 | Validating the Impact of a Molecular Subtype in Epithelial Ovarian Cancer (EOC) on Progression Free and Overall Survival | ABI Human Genome Survey Microarray Version 2 | (11) |
| GSE13876 | Survival Related Profile, Pathways and Transcription Factors in Ovarian Cancer | Operon human v3 ~35K 70-mer two-color oligonucleotide microarrays | (12) |
| GSE17260 | Gene expression profile for predicting survival in advanced-stage serous ovarian cancer across two independent datasets | Agilent-014850 Whole Human Genome Microarray 4x44K G4112F | (13) |
| GSE32062 | Immune-activation as a therapeutic direction for patients with high-risk ovarian cancer based on gene expression signature | Agilent-014850 Whole Human Genome Microarray 4x44K G4112F | (14) |
| GSE53963 | Gene Expression Profiling of Human High-Grade Serous Ovarian Tumor Samples | Agilent-014850 Whole Human Genome Microarray 4x44K G4112F | (15) |
| GSE73614 | Can High Grade Serous Ovarian Cancer TCGA Gene Expression Signatures be seen in High Grade Endometrioid or Clear Cell Ovarian Cancer? | Agilent-014850 Whole Human Genome Microarray 4x44K G4112F | - |
| TCGA | TCGA ovarian cancer cohort | Affymetrix Human Genome U133A Array | (16) |

## Table S1. (Continued)

|  |  |  |  |
| --- | --- | --- | --- |
| Study ID | Raw sample size | QC sample size | Drop reason |
| GSE14764 | 80 | 80 | - |
| GSE23554 | 28 | 28 | - |
| GSE26712 | 195 | 185 | Normal tissue (n=10) |
| GSE3149 | 153 | 116 | Missing survival information (n=37) |
| GSE18520 | 63 | 53 | Normal tissue (n=10) |
| GSE19829 | 28 | 28 | - |
| GSE26193 | 107 | 107 | - |
| GSE30161 | 58 | 58 | - |
| GSE63885 | 101 | 75 | Missing survival information (n=26) |
| GSE9891 | 285 | 285 | - |
| GSE49997 | 204 | 194 | Missing survival information (n=10) |
| GSE13876 | 415 | 415 | - |
| GSE17260 | 110 | 110 | - |
| GSE32062 | 270 | 260 | Other platform (n=10) |
| GSE53963 | 174 | 160 | Duplicated samples (n=14) |
| GSE73614 | 107 | 107 | - |
| TCGA | 520 | 519 | Missing survival information (n=1) |

# Table S2. Gene list and immune category for IPSOV

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | genelist | ID | Name | Category |
| 1 | ACVR2B | 93 | activin A receptor, type IIB | TGFb\_Family\_Member\_Receptor, Cytokine\_Receptors |
| 2 | ADIPOR2 | 79602 | adiponectin receptor 2 | Cytokine\_Receptors |
| 3 | AKT2 | 208 | v-akt murine thymoma viral oncogene homolog 2 | BCRSignalingPathway, TCRsignalingPathway |
| 4 | ALB | 213 | albumin | Antimicrobials |
| 5 | AMBN | 258 | ameloblastin (enamel matrix protein) | Cytokines |
| 6 | AQP9 | 366 | aquaporin 9 | Antimicrobials |
| 7 | ARTN | 9048 | artemin | Cytokines |
| 8 | AVP | 551 | arginine vasopressin | Cytokines |
| 9 | AVPR1B | 553 | arginine vasopressin receptor 1B | Cytokine\_Receptors |
| 10 | B2M | 567 | beta-2-microglobulin | Antigen\_Processing\_and\_Presentation, Antimicrobials |
| 11 | BIRC5 | 332 | baculoviral IAP repeat-containing 5 | Antimicrobials |
| 12 | BMP15 | 9210 | bone morphogenetic protein 15 | Cytokines, TGFb\_Family\_Member |
| 13 | BMP2 | 650 | bone morphogenetic protein 2 | Cytokines, TGFb\_Family\_Member |
| 14 | BMP7 | 655 | bone morphogenetic protein 7 | TGFb\_Family\_Member, Cytokines |
| 15 | BMP8B | 656 | bone morphogenetic protein 8b | TGFb\_Family\_Member, Cytokines |
| 16 | C19orf10 | 56005 | chromosome 19 open reading frame 10 | Cytokines |
| 17 | C5AR1 | 728 | complement component 5a receptor 1 | Cytokine\_Receptors, Chemokine\_Receptors |
| 18 | CALR | 811 | calreticulin | Antigen\_Processing\_and\_Presentation |
| 19 | CBL | 867 | Cas-Br-M (murine) ecotropic retroviral transforming sequence | TCRsignalingPathway |
| 20 | CCL13 | 6357 | chemokine (C-C motif) ligand 13 | Chemokines, Antimicrobials, Cytokines, Antimicrobials |
| 21 | CCL18 | 6362 | chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) | Cytokines, Chemokines, Antimicrobials |
| 22 | CCR7 | 1236 | chemokine (C-C motif) receptor 7 | Cytokine\_Receptors, Antimicrobials, Chemokine\_Receptors |
| 23 | CCR9 | 10803 | chemokine (C-C motif) receptor 9 | Chemokine\_Receptors, Cytokine\_Receptors |
| 24 | CD1B | 910 | CD1b molecule | Antigen\_Processing\_and\_Presentation |
| 25 | CD3G | 917 | CD3g molecule, gamma (CD3-TCR complex) | TCRsignalingPathway |
| 26 | CDC42 | 998 | cell division cycle 42 (GTP binding protein, 25kDa) | TCRsignalingPathway |
| 27 | CMKLR1 | 1240 | chemokine-like receptor 1 | Cytokine\_Receptors, Chemokine\_Receptors |
| 28 | CORT | 1325 | cortistatin | Cytokines |
| 29 | CRHR1 | 1394 | corticotropin releasing hormone receptor 1 | Cytokine\_Receptors |
| 30 | CX3CR1 | 1524 | chemokine (C-X3-C motif) receptor 1 | Cytokine\_Receptors, Chemokine\_Receptors |
| 31 | CXCL13 | 10563 | chemokine (C-X-C motif) ligand 13 | Antimicrobials, Cytokines, Chemokines |
| 32 | CXCL9 | 4283 | chemokine (C-X-C motif) ligand 9 | Chemokines, Cytokines, Antimicrobials |
| 33 | CYLD | 1540 | cylindromatosis (turban tumor syndrome) | Antimicrobials |
| 34 | CYSLTR1 | 10800 | cysteinyl leukotriene receptor 1 | Cytokine\_Receptors, Chemokine\_Receptors |
| 35 | CYSLTR2 | 57105 | cysteinyl leukotriene receptor 2 | Chemokine\_Receptors, Cytokine\_Receptors |
| 36 | DES | 1674 | desmin | Antimicrobials |
| 37 | DKK1 | 22943 | dickkopf homolog 1 (Xenopus laevis) | Cytokines |
| 38 | DMBT1 | 1755 | deleted in malignant brain tumors 1 | Antimicrobials |
| 39 | EDNRB | 1910 | endothelin receptor type B | Chemokine\_Receptors, Cytokine\_Receptors |
| 40 | EGFR | 1956 | epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) | Cytokine\_Receptors |
| 41 | ENG | 2022 | endoglin | Cytokine\_Receptors |
| 42 | EPOR | 2057 | erythropoietin receptor | Cytokine\_Receptors |
| 43 | EREG | 2069 | epiregulin | Cytokines |
| 44 | ESM1 | 11082 | endothelial cell-specific molecule 1 | Cytokines |
| 45 | ESR2 | 2100 | estrogen receptor 2 (ER beta) | Cytokine\_Receptors |
| 46 | ESRRB | 2103 | estrogen-related receptor beta | Cytokine\_Receptors |
| 47 | F2R | 2149 | coagulation factor II (thrombin) receptor | Antimicrobials |
| 48 | FABP7 | 2173 | fatty acid binding protein 7, brain | Antimicrobials |
| 49 | FAS | 355 | Fas (TNF receptor superfamily, member 6) | NaturalKiller\_Cell\_Cytotoxicity |
| 50 | FGF14 | 2259 | fibroblast growth factor 14 | Cytokines |
| 51 | FGF18 | 8817 | fibroblast growth factor 18 | Cytokines |
| 52 | FGF7 | 2252 | fibroblast growth factor 7 (keratinocyte growth factor) | Cytokines |
| 53 | FGF9 | 2254 | fibroblast growth factor 9 (glia-activating factor) | Cytokines |
| 54 | FGFR2 | 2263 | fibroblast growth factor receptor 2 | Cytokine\_Receptors |
| 55 | FGFR4 | 2264 | fibroblast growth factor receptor 4 | Cytokine\_Receptors |
| 56 | FURIN | 5045 | furin (paired basic amino acid cleaving enzyme) | Antimicrobials |
| 57 | GDF11 | 10220 | growth differentiation factor 11 | Cytokines, TGFb\_Family\_Member |
| 58 | GHRH | 2691 | growth hormone releasing hormone | Cytokines |
| 59 | GLP1R | 2740 | glucagon-like peptide 1 receptor | Cytokine\_Receptors |
| 60 | GRB2 | 2885 | growth factor receptor-bound protein 2 | NaturalKiller\_Cell\_Cytotoxicity, TCRsignalingPathway |
| 61 | HDGFRP3 | 50810 | hepatoma-derived growth factor, related protein 3 | Cytokines |
| 62 | HGF | 3082 | hepatocyte growth factor (hepapoietin A; scatter factor) | Antimicrobials, Cytokines |
| 63 | HLA-DOB | 3112 | major histocompatibility complex, class II, DO beta | Antigen\_Processing\_and\_Presentation |
| 64 | HNF4A | 3172 | hepatocyte nuclear factor 4, alpha | Cytokine\_Receptors |
| 65 | HNF4G | 3174 | hepatocyte nuclear factor 4, gamma | Cytokine\_Receptors |
| 66 | HSPA4 | 3308 | heat shock 70kDa protein 4 | Antigen\_Processing\_and\_Presentation |
| 67 | IL12RB2 | 3595 | interleukin 12 receptor, beta 2 | Cytokine\_Receptors, Interleukins\_Receptor |
| 68 | IL17A | 3605 | interleukin 17A | Interleukins, Antimicrobials, Cytokines |
| 69 | IL6R | 3570 | interleukin 6 receptor | Interleukins\_Receptor, Cytokine\_Receptors |
| 70 | IRF5 | 3663 | interferon regulatory factor 5 | Antimicrobials |
| 71 | JUN | 3725 | jun oncogene | TCRsignalingPathway, BCRSignalingPathway, Antimicrobials |
| 72 | KAL1 | 3730 | Kallmann syndrome 1 sequence | Antimicrobials |
| 73 | KRAS | 3845 | v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog | TCRsignalingPathway, BCRSignalingPathway, NaturalKiller\_Cell\_Cytotoxicity |
| 74 | LBP | 3929 | lipopolysaccharide binding protein | Antimicrobials |
| 75 | LTBP1 | 4052 | latent transforming growth factor beta binding protein 1 | Cytokines, Antimicrobials |
| 76 | MAP2K1 | 5604 | mitogen-activated protein kinase kinase 1 | Antimicrobials, NaturalKiller\_Cell\_Cytotoxicity |
| 77 | MAPT | 4137 | microtubule-associated protein tau | Antimicrobials |
| 78 | MASP1 | 5648 | mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor) | Antimicrobials |
| 79 | MIF | 4282 | macrophage migration inhibitory factor (glycosylation-inhibiting factor) | Antimicrobials, Cytokines |
| 80 | MMP9 | 4318 | matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) | Antimicrobials, Antimicrobials |
| 81 | MPL | 4352 | myeloproliferative leukemia virus oncogene | Cytokine\_Receptors |
| 82 | MSR1 | 4481 | macrophage scavenger receptor 1 | Antimicrobials |
| 83 | NAMPT | 10135 | nicotinamide phosphoribosyltransferase | Cytokines |
| 84 | NFATC3 | 4775 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 | NaturalKiller\_Cell\_Cytotoxicity, BCRSignalingPathway, TCRsignalingPathway |
| 85 | NFKB1 | 4790 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 | TCRsignalingPathway, BCRSignalingPathway, Antimicrobials |
| 86 | NLRX1 | 79671 | NLR family member X1 | Antimicrobials |
| 87 | NR0B1 | 190 | nuclear receptor subfamily 0, group B, member 1 | Cytokine\_Receptors |
| 88 | OBP2A | 29991 | odorant binding protein 2A | Antimicrobials |
| 89 | PAEP | 5047 | progestagen-associated endometrial protein | Antimicrobials |
| 90 | PDGFA | 5154 | platelet-derived growth factor alpha polypeptide | Cytokines |
| 91 | PGLYRP1 | 8993 | peptidoglycan recognition protein 1 | Antimicrobials |
| 92 | PI3 | 5266 | peptidase inhibitor 3, skin-derived | Antimicrobials |
| 93 | PMCH | 5367 | pro-melanin-concentrating hormone | Cytokines |
| 94 | PPARA | 5465 | peroxisome proliferator-activated receptor alpha | Cytokine\_Receptors |
| 95 | PPP3CA | 5530 | protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform | NaturalKiller\_Cell\_Cytotoxicity, BCRSignalingPathway, TCRsignalingPathway |
| 96 | PPP3R1 | 5534 | protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform | BCRSignalingPathway, TCRsignalingPathway, NaturalKiller\_Cell\_Cytotoxicity |
| 97 | PSMC2 | 5701 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 | Antigen\_Processing\_and\_Presentation |
| 98 | PSMD11 | 5717 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 | Antigen\_Processing\_and\_Presentation |
| 99 | PSMD4 | 5710 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 | Antigen\_Processing\_and\_Presentation |
| 100 | PTGER2 | 5732 | prostaglandin E receptor 2 (subtype EP2), 53kDa | Cytokine\_Receptors |
| 101 | PTGFR | 5737 | prostaglandin F receptor (FP) | Cytokine\_Receptors |
| 102 | PTPN11 | 5781 | protein tyrosine phosphatase, non-receptor type 11 | NaturalKiller\_Cell\_Cytotoxicity |
| 103 | PYY | 5697 | peptide YY | Cytokines |
| 104 | RAC1 | 5879 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) | NaturalKiller\_Cell\_Cytotoxicity, BCRSignalingPathway |
| 105 | RARG | 5916 | retinoic acid receptor, gamma | Cytokine\_Receptors |
| 106 | RNASE2 | 6036 | ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) | Antimicrobials, Cytokines, Chemokines |
| 107 | RXRB | 6257 | retinoid X receptor, beta | Cytokine\_Receptors |
| 108 | S100A5 | 6276 | S100 calcium binding protein A5 | Antimicrobials |
| 109 | SEMA4G | 57715 | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G | Cytokines, Chemokines |
| 110 | SORT1 | 6272 | sortilin 1 | Cytokine\_Receptors |
| 111 | SOS1 | 6654 | son of sevenless homolog 1 (Drosophila) | NaturalKiller\_Cell\_Cytotoxicity, TCRsignalingPathway |
| 112 | SST | 6750 | somatostatin | Cytokines |
| 113 | SSTR1 | 6751 | somatostatin receptor 1 | Cytokine\_Receptors |
| 114 | STAB2 | 55576 | stabilin 2 | Antimicrobials |
| 115 | TGFA | 7039 | transforming growth factor, alpha | Cytokines |
| 116 | TGFB2 | 7042 | transforming growth factor, beta 2 | Cytokines, TGFb\_Family\_Member |
| 117 | TGFBR2 | 7048 | transforming growth factor, beta receptor II (70/80kDa) | TGFb\_Family\_Member\_Receptor, Cytokine\_Receptors |
| 118 | TMSB4Y | 9087 | thymosin beta 4, Y-linked | Antimicrobials |
| 119 | TNFRSF10D | 8793 | tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain | TNF\_Family\_Members\_Receptors, NaturalKiller\_Cell\_Cytotoxicity, Cytokine\_Receptors |
| 120 | TNFRSF4 | 7293 | tumor necrosis factor receptor superfamily, member 4 | TNF\_Family\_Members\_Receptors, Cytokine\_Receptors |
| 121 | TNFRSF8 | 943 | tumor necrosis factor receptor superfamily, member 8 | Cytokine\_Receptors, TNF\_Family\_Members\_Receptors |
| 122 | TNFRSF9 | 3604 | tumor necrosis factor receptor superfamily, member 9 | TNF\_Family\_Members\_Receptors, Cytokine\_Receptors |
| 123 | TNFSF11 | 8600 | tumor necrosis factor (ligand) superfamily, member 11 | Antimicrobials, TNF\_Family\_Members, Cytokines |
| 124 | TRH | 7200 | thyrotropin-releasing hormone | Cytokines |
| 125 | TRHR | 7201 | thyrotropin-releasing hormone receptor | Cytokine\_Receptors |
| 126 | TRIM27 | 5987 | tripartite motif-containing 27 | Antimicrobials |
| 127 | TSHR | 7253 | thyroid stimulating hormone receptor | Cytokine\_Receptors |
| 128 | VDR | 7421 | vitamin D (1,25- dihydroxyvitamin D3) receptor | Cytokine\_Receptors, Antimicrobials |
| 129 | VIPR2 | 7434 | vasoactive intestinal peptide receptor 2 | Cytokine\_Receptors |

# Table S3. Coefficients for each immune category of IPSOV

|  |  |
| --- | --- |
| **Immune process** | **Coefficients** |
| Antigen\_Processing\_and\_Presentation | -0.62862534 |
| Antimicrobials | -1.29245906 |
| BCRSignalingPathway | 1.36898914 |
| Chemokine\_Receptors | 0.46894412 |
| Chemokines | -0.4701052 |
| Cytokine\_Receptors | -3.52173127 |
| Cytokines | -4.74485899 |
| Interleukins | -0.11913731 |
| Interleukins\_Receptor | -0.37665861 |
| NaturalKiller\_Cell\_Cytotoxicity | 0.07553575 |
| TCRsignalingPathway | -1.41367648 |
| TGFb\_Family\_Member | 0.69202647 |
| TGFb\_Family\_Member\_Receptor | -0.92595914 |
| TNF\_Family\_Members | 0.89442583 |
| TNF\_Family\_Members\_Receptors | -0.07715177 |

# Table S4. Cox regression analysis for the IPSOV and clinical characteristics

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characteristicsa** | Training set | | | | Validation set 1 | | | | Validation set 2 | | | |
| Univariable | | Multivariable | | Univariable | | Multivariable | | Univariable | | Multivariable | |
| HR (95% CI) | P | HR (95% CI) | P | HR (95% CI) | P | HR (95% CI) | P | HR (95% CI) | P | HR (95% CI) | P |
| **High IPSOV group** | 1.82 (1.43-2.30) | 9.19×10-7 | 1.71 (1.32-2.19) | 4.04×10-5 | 1.66 (1.27-2.15) | 1.84×10-4 | 2.86 (1.72-4.74) | 4.89×10-5 | 1.66 (1.29-2.12) | 6.20×10-5 | 2.31 (1.52-3.49) | 7.30×10-5 |
| **Age (per year)** | 1.02 (1.01-1.04) | 6.32×10-5 | 1.01 (1.00-1.03) | 0.025 | - | - | - | - | 1.00 (0.97-1.02) | 0.799 | -b | - b |
| **FIGO Stage (per stage)** | 1.67 (1.41-1.97) | 2.54×10-9 | 1.78 (1.25-2.55) | 0.001 | 2.20 (1.31-3.68) | 0.002 | 2.20 (1.24-3.90) | 0.006 | 1.76 (1.46-2.12) | 1.77×10-9 | 1.26 (0.90-1.76) | 0.163 |
| **Grade (per grade)** | 1.42 (1.23-1.64) | 1.70×10-6 | 1.30 (0.93-1.81) | 0.117 | 1.15 (0.83-1.58) | 0.389 | 1.31 (0.86-1.98) | 0.200 | 1.64 (1.34-2.00) | 1.10×10-6 | 1.78 (1.22-2.59) | 0.002 |
| **Debulking status (Optimal)** | 0.58 (0.46-0.73) | 5.17×10-6 | 0.44 (0.30-0.65) | 4.19×10-5 | 0.54 (0.41-0.71) | 1.95×10-5 | 0.47 (0.29-0.77) | 0.002 | 0.53 (0.38-0.75) | 3.22×10-4 | 0.71 (0.50-1.2) | 0.068 |

## Table S4. (Continued)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characteristicsa** | Validation set 3 | | | | Validation set 4 | | | | Validation set 5 | | | |
| Univariable | | Multivariable | | Univariable | | Multivariable | | Univariable | | Multivariable | |
| HR (95% CI) | P | HR (95% CI) | P | HR (95% CI) | P | HR (95% CI) | P | HR (95% CI) | P | HR (95% CI) | P |
| **High IPSOV group** | 1.67 (1.35-2.05) | 1.64×10-6 | 1.73 (1.36-2.17) | 3.64×10-6 | 2.04 (1.60-2.59) | 7.02×10-9 | 2.07 (1.62-2.64) | 3.98×10-9 | 2.36 (1.38-4.00) | 0.001 | 2.62 (1.53-4.47) | 4.48×10-4 |
| **Age (per year)** | 1.01 (1.00-1.03) | 6.50×10-4 | 1.01 (1.00-1.03) | 4.65×10-4 | 1.00 (0.99-1.01) | 0.313 | 1.00 (0.99-1.01) | 0.382 | 1.03 (1.00-1.05) | 0.007 | 1.03 (1.00-1.05) | 0.012 |
| **FIGO Stage (per stage)** | 1.51 (1.20-1.90) | 5.11×10-4 | 1.53 (1.20-1.94) | 4.96×10-4 | - | - | - | - | 1.89 (1.07-3.36) | 0.028 | 1.75 (0.98-3.13) | 0.058 |
| **Grade (per grade)** | 1.39 (1.02-1.90) | 0.034 | 1.20 (0.88-1.65) | 0.236 | - | - | - | - | - | - | - | - |
| **Debulking status (Optimal)** | 0.75 (0.57-0.97) | 0.033 | 0.86 (0.65-1.13) | 0.293 | - | - | - | - | - | - | - | - |

aThe histology type for most cases is serous, the sample size for other subtypes is too small to adjust.

bThe missing rate is too high (>50%), which is not included in the multivariable model.

# Table S5. C-index (standard error) of the prognostic signatures and clinical characteristics in the eight datasets.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Signature** | Training set | Validation 1 | Validation 2 | Validation 3 | Validation 4 | Validation 5 | **Overall C-index** |
| **N** | 519 | 409 | 606 | 634 | 415 | 194 | **2777** |
| **IPSOV** | 0.622 (0.021) | 0.614 (0.017) | 0.625 (0.02) | 0.623 (0.017) | 0.630 (0.019) | 0.650 (0.016) | **0.625** |
| **Sabatier 2011** | 0.555 (0.021) | 0.575 (0.017) | 0.567 (0.02) | 0.536 (0.017) | 0.504 (0.019) | 0.534 (0.042) | **0.550** |
| **Hernandez 2010** | 0.526 (0.021) | 0.515 (0.017) | 0.497 (0.02) | 0.524 (0.017) | 0.498 (0.019) | 0.514 (0.042) | **0.516** |
| **Kernagis 2012** | 0.54 (0.021) | 0.588 (0.017) | 0.55 (0.02) | 0.561 (0.017) | 0.528 (0.019) | 0.576 (0.042) | **0.560** |
| **Kang 2012** | 0.542 (0.021) | 0.516 (0.017) | 0.557 (0.02) | 0.512 (0.017) | 0.503 (0.019) | 0.483 (0.042) | **0.523** |
| **Konstantinopoulos 2010** | 0.495 (0.021) | 0.553 (0.017) | 0.515 (0.02) | 0.502 (0.017) | 0.529 (0.019) | 0.546 (0.042) | **0.525** |
| **Crijns 2009** | 0.54 (0.021) | 0.585 (0.017) | 0.523 (0.02) | 0.554 (0.017) | 0.615 (0.019) | 0.513 (0.042) | **0.559** |
| **Yoshihara 2012** | 0.592 (0.021) | 0.557 (0.017) | 0.557 (0.02) | 0.652 (0.018) | 0.608 (0.019) | 0.507 (0.042) | **0.583** |
| **TCGA 2011** | 0.606 (0.021) | 0.607 (0.017) | 0.652 (0.02) | 0.608 (0.018) | 0.541 (0.019) | 0.6 (0.042) | **0.602** |
| **Denkert 2009** | 0.566 (0.021) | 0.538 (0.02) | 0.556 (0.017) | 0.49 (0.02) | 0.486 (0.019) | 0.637 (0.042) | **0.524** |
|  |  |  |  |  |  |  |  |
| **Stagea** | 0.572 (0.021) | 0.571 (0.016) | 0.558 (0.014) | 0.569 (0.013) | - | 0.549 (0.029) | **0.564** |
| **Gradea** | 0.522 (0.028) | 0.552 (0.015) | 0.534 (0.013) | 0.584 (0.015) | - | - | **0.555** |
| **Debulking statusa** | 0.599 (0.019) | 0.596 (0.022) | 0.546 (0.016) | 0.575 (0.016) | - | - | **0.583** |

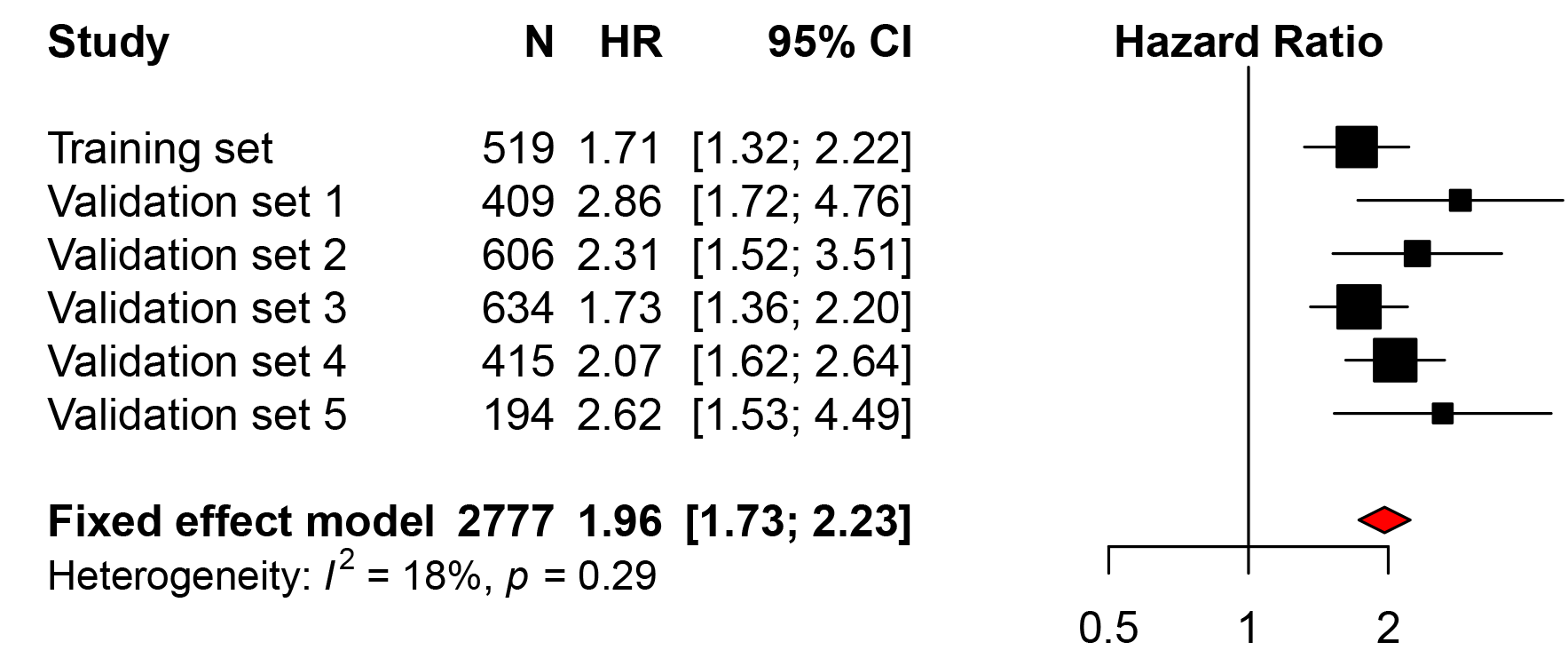
aWeights were recalculated after removing the missing dataset.

# Table S6. Pathway enrichment analysis for IPSOV genes from KEGG and GO (top20 of BP, MF and CC) database

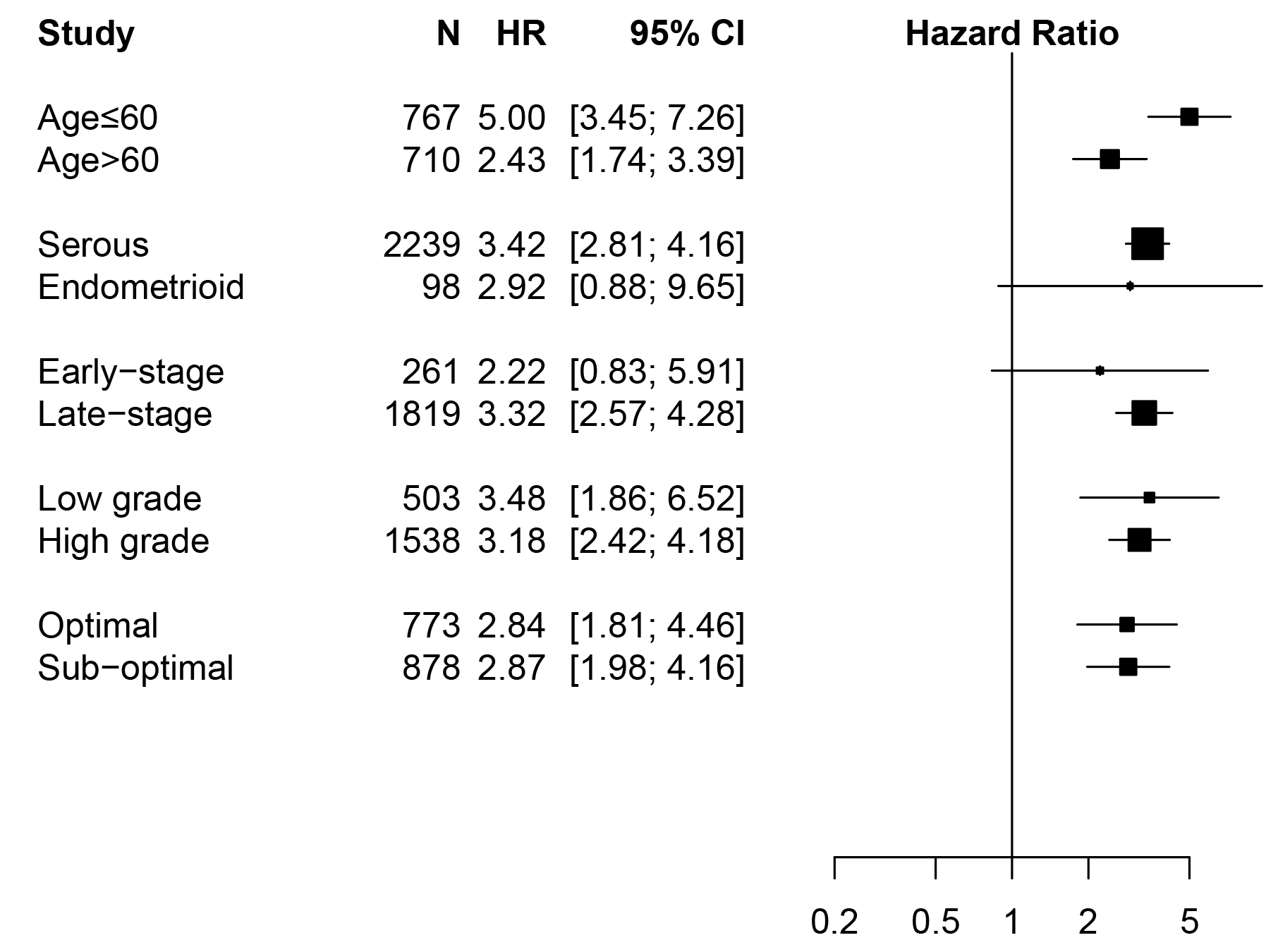
|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Database | ID | Pathway name | Gene Ratio | Raw *P* value | Adjusted *P* value | Gene Entrez ID |
| KEGG | hsa04060 | Cytokine-cytokine receptor interaction | 26/106 | 2.32E-14 | 2.39E-12 | 93/9210/650/655/656/6357/6362/1236/10803/1524/10563/4283/2057/355/10220/3595/3605/3570/4352/7042/7048/8793/7293/943/3604/8600 |
| KEGG | hsa04010 | MAPK signaling pathway | 26/106 | 2.52E-14 | 2.39E-12 | 208/998/1956/2069/355/8817/2252/2254/2263/2264/2885/3082/3725/3845/5604/4137/4775/4790/5154/5530/5534/5879/6654/7039/7042/7048 |
| KEGG | hsa05211 | Renal cell carcinoma | 12/106 | 1.59E-10 | 7.84E-09 | 208/998/2885/3082/3725/3845/5604/5781/5879/6654/7039/7042 |
| KEGG | hsa05210 | Colorectal cancer | 13/106 | 1.65E-10 | 7.84E-09 | 208/332/1956/2069/2885/3725/3845/5604/5879/6654/7039/7042/7048 |
| KEGG | hsa04014 | Ras signaling pathway | 18/106 | 3.19E-09 | 1.11E-07 | 208/998/1956/8817/2252/2254/2263/2264/2885/3082/3845/5604/4790/5154/5781/5879/6654/7039 |
| KEGG | hsa04662 | B cell receptor signaling pathway | 11/106 | 3.50E-09 | 1.11E-07 | 208/2885/3725/3845/5604/4775/4790/5530/5534/5879/6654 |
| KEGG | hsa01521 | EGFR tyrosine kinase inhibitor resistance | 11/106 | 1.13E-08 | 3.05E-07 | 208/1956/2263/2885/3082/3570/3845/5604/5154/6654/7039 |
| KEGG | hsa04660 | T cell receptor signaling pathway | 12/106 | 1.48E-08 | 3.52E-07 | 208/917/998/2885/3725/3845/5604/4775/4790/5530/5534/6654 |
| KEGG | hsa05226 | Gastric cancer | 14/106 | 1.87E-08 | 3.95E-07 | 208/1956/8817/2252/2254/2263/2885/3082/3845/5604/6257/6654/7042/7048 |
| KEGG | hsa04062 | Chemokine signaling pathway | 15/106 | 5.53E-08 | 1.05E-06 | 208/6357/6362/1236/10803/998/1524/10563/4283/2885/3845/5604/4790/5879/6654 |
| KEGG | hsa05212 | Pancreatic cancer | 10/106 | 8.30E-08 | 1.27E-06 | 208/998/1956/3845/5604/4790/5879/7039/7042/7048 |
| KEGG | hsa04151 | PI3K-Akt signaling pathway | 20/106 | 8.84E-08 | 1.27E-06 | 208/1956/2057/2069/2149/8817/2252/2254/2263/2264/2885/3082/3570/3845/5604/4790/5154/5879/6654/7039 |
| KEGG | hsa05163 | Human cytomegalovirus infection | 16/106 | 8.97E-08 | 1.27E-06 | 208/567/811/1956/355/2885/3570/3845/5604/4775/4790/5530/5534/5732/5879/6654 |
| KEGG | hsa05220 | Chronic myeloid leukemia | 10/106 | 9.44E-08 | 1.27E-06 | 208/867/2885/3845/5604/4790/5781/6654/7042/7048 |
| KEGG | hsa05215 | Prostate cancer | 11/106 | 1.00E-07 | 1.27E-06 | 208/1956/2263/2885/3845/5604/4318/4790/5154/6654/7039 |
| KEGG | hsa04380 | Osteoclast differentiation | 12/106 | 2.15E-07 | 2.55E-06 | 208/1540/2885/3725/5604/4790/5530/5534/5879/7042/7048/8600 |
| KEGG | hsa04659 | Th17 cell differentiation | 11/106 | 2.77E-07 | 2.94E-06 | 917/3112/3605/3570/3725/4775/4790/5530/5534/6257/7048 |
| KEGG | hsa04012 | ErbB signaling pathway | 10/106 | 2.78E-07 | 2.94E-06 | 208/867/1956/2069/2885/3725/3845/5604/6654/7039 |
| KEGG | hsa05218 | Melanoma | 9/106 | 6.71E-07 | 6.71E-06 | 208/1956/8817/2252/2254/3082/3845/5604/5154 |
|  |  |  |  |  |  |  |
| GO (BP) | GO:0050900 | leukocyte migration | 23/126 | 3.35E-15 | 1.03E-11 | 9048/728/811/6357/6362/1236/998/1240/1524/10563/4283/1910/2885/3570/3845/3929/4282/4318/5781/5879/6654/7042/8600 |
| GO (BP) | GO:0070374 | positive regulation of ERK1 and ERK2 cascade | 17/126 | 1.10E-14 | 1.19E-11 | 650/728/6357/6362/1236/57105/1956/2149/8817/2263/2264/3725/5604/4282/5154/5781/8600 |
| GO (BP) | GO:0043410 | positive regulation of MAPK cascade | 25/126 | 1.17E-14 | 1.19E-11 | 650/728/6357/6362/1236/998/57105/1956/2149/355/8817/2254/2263/2264/3082/3725/3845/5604/4282/5154/5781/7039/7042/7293/8600 |
| GO (BP) | GO:0002237 | response to molecule of bacterial origin | 21/126 | 1.82E-14 | 1.39E-11 | 567/728/1236/1524/10563/4283/1910/2149/355/3595/3663/3725/3929/4282/4790/5732/5737/8793/7293/943/3604 |
| GO (BP) | GO:0040017 | positive regulation of locomotion | 23/126 | 5.04E-14 | 3.09E-11 | 208/9048/650/728/811/1236/1240/10563/4283/1956/2149/8817/2252/3082/3570/3725/3929/4318/5154/5879/57715/7042/7048 |
| GO (BP) | GO:0032496 | response to lipopolysaccharide | 20/126 | 9.07E-14 | 4.63E-11 | 567/728/1236/1524/10563/4283/1910/2149/355/3595/3725/3929/4282/4790/5732/5737/8793/7293/943/3604 |
| GO (BP) | GO:0030335 | positive regulation of cell migration | 22/126 | 1.31E-13 | 5.75E-11 | 208/650/728/811/1236/1240/10563/4283/1956/2149/8817/2252/3082/3570/3725/3929/4318/5154/5879/57715/7042/7048 |
| GO (BP) | GO:2000147 | positive regulation of cell motility | 22/126 | 2.57E-13 | 9.83E-11 | 208/650/728/811/1236/1240/10563/4283/1956/2149/8817/2252/3082/3570/3725/3929/4318/5154/5879/57715/7042/7048 |
| GO (BP) | GO:0051272 | positive regulation of cellular component movement | 22/126 | 4.23E-13 | 1.41E-10 | 208/650/728/811/1236/1240/10563/4283/1956/2149/8817/2252/3082/3570/3725/3929/4318/5154/5879/57715/7042/7048 |
| GO (BP) | GO:0009755 | hormone-mediated signaling pathway | 17/126 | 4.60E-13 | 1.41E-10 | 79602/655/811/2100/2103/3172/3174/190/5465/5781/5916/6257/6750/6751/7200/7253/7421 |
| GO (BP) | GO:0070371 | ERK1 and ERK2 cascade | 18/126 | 5.64E-13 | 1.57E-10 | 551/650/728/6357/6362/1236/57105/1956/2149/8817/2263/2264/3725/5604/4282/5154/5781/8600 |
| GO (BP) | GO:0070372 | regulation of ERK1 and ERK2 cascade | 17/126 | 2.60E-12 | 6.64E-10 | 650/728/6357/6362/1236/57105/1956/2149/8817/2263/2264/3725/5604/4282/5154/5781/8600 |
| GO (BP) | GO:0014066 | regulation of phosphatidylinositol 3-kinase signaling | 14/126 | 3.06E-12 | 6.96E-10 | 867/1956/2069/2149/8817/2252/2254/2263/2264/2885/3082/5154/5781/7042 |
| GO (BP) | GO:0060326 | cell chemotaxis | 17/126 | 3.18E-12 | 6.96E-10 | 728/811/6357/6362/1236/1240/1524/10563/4283/1910/8817/3082/3570/3929/5879/7042/8600 |
| GO (BP) | GO:0048545 | response to steroid hormone | 20/126 | 4.78E-12 | 9.75E-10 | 655/811/1956/2022/2100/2103/355/3172/3174/3845/190/5465/5732/5916/6257/6750/7042/7048/7200/7421 |
| GO (BP) | GO:0030595 | leukocyte chemotaxis | 15/126 | 8.08E-12 | 1.55E-09 | 728/811/6357/6362/1236/1240/1524/10563/4283/1910/3570/3929/5879/7042/8600 |
| GO (BP) | GO:0032103 | positive regulation of response to external stimulus | 17/126 | 1.22E-11 | 2.20E-09 | 9048/728/811/6357/6362/1236/1240/10563/4283/1956/8817/3605/3570/3929/4282/5879/8600 |
| GO (BP) | GO:0014065 | phosphatidylinositol 3-kinase signaling | 14/126 | 1.59E-11 | 2.70E-09 | 867/1956/2069/2149/8817/2252/2254/2263/2264/2885/3082/5154/5781/7042 |
| GO (BP) | GO:2000027 | regulation of organ morphogenesis | 16/126 | 4.92E-11 | 7.92E-09 | 650/655/998/22943/2022/2252/2263/3082/5154/5701/5717/5710/5879/7042/7048/7421 |
|  |  |  |  |  |  |  |
| GO (MF) | GO:0008083 | growth factor activity | 18/127 | 4.37E-16 | 1.41E-13 | 258/9048/9210/650/655/656/22943/2069/2259/8817/2252/2254/10220/50810/3082/5154/7039/7042 |
| GO (MF) | GO:0019838 | growth factor binding | 13/127 | 1.68E-11 | 2.72E-09 | 93/10563/1956/2022/11082/2263/2264/5045/3570/4052/5154/6272/7048 |
| GO (MF) | GO:0005126 | cytokine receptor binding | 17/127 | 2.96E-11 | 3.19E-09 | 9210/650/655/656/6357/6362/10563/4283/2022/10220/2885/3605/3570/4282/7042/7048/8600 |
| GO (MF) | GO:0046934 | phosphatidylinositol-4,5-bisphosphate 3-kinase activity | 10/127 | 4.37E-11 | 3.53E-09 | 1956/2069/8817/2252/2254/2263/2264/2885/5154/5781 |
| GO (MF) | GO:0052813 | phosphatidylinositol bisphosphate kinase activity | 10/127 | 7.14E-11 | 3.87E-09 | 1956/2069/8817/2252/2254/2263/2264/2885/5154/5781 |
| GO (MF) | GO:0004879 | RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding | 9/127 | 8.39E-11 | 3.87E-09 | 2100/2103/3172/3174/190/5465/5916/6257/7421 |
| GO (MF) | GO:0098531 | transcription factor activity, direct ligand regulated sequence-specific DNA binding | 9/127 | 8.39E-11 | 3.87E-09 | 2100/2103/3172/3174/190/5465/5916/6257/7421 |
| GO (MF) | GO:0035004 | phosphatidylinositol 3-kinase activity | 10/127 | 1.53E-10 | 6.18E-09 | 1956/2069/8817/2252/2254/2263/2264/2885/5154/5781 |
| GO (MF) | GO:0008528 | G-protein coupled peptide receptor activity | 12/127 | 3.24E-10 | 1.15E-08 | 553/1236/10803/1240/1524/10800/57105/1910/2149/2740/6751/7253 |
| GO (MF) | GO:0001653 | peptide receptor activity | 12/127 | 3.55E-10 | 1.15E-08 | 553/1236/10803/1240/1524/10800/57105/1910/2149/2740/6751/7253 |
| GO (MF) | GO:0003707 | steroid hormone receptor activity | 9/127 | 7.16E-10 | 2.10E-08 | 2100/2103/3172/3174/190/5465/5916/6257/7421 |
| GO (MF) | GO:0005125 | cytokine activity | 14/127 | 1.76E-09 | 4.75E-08 | 9210/650/655/656/6357/6362/10563/4283/10220/3605/4282/10135/7042/8600 |
| GO (MF) | GO:0005160 | transforming growth factor beta receptor binding | 8/127 | 4.42E-09 | 1.10E-07 | 9210/650/655/656/2022/10220/7042/7048 |
| GO (MF) | GO:0016303 | 1-phosphatidylinositol-3-kinase activity | 7/127 | 3.75E-08 | 8.66E-07 | 8817/2252/2254/2263/2264/2885/5781 |
| GO (MF) | GO:0052742 | phosphatidylinositol kinase activity | 7/127 | 1.28E-07 | 2.76E-06 | 8817/2252/2254/2263/2264/2885/5781 |
| GO (MF) | GO:0004896 | cytokine receptor activity | 8/127 | 4.51E-07 | 9.11E-06 | 1236/10803/1240/1524/2057/3595/3570/4352 |
| GO (MF) | GO:0070851 | growth factor receptor binding | 9/127 | 6.06E-07 | 1.15E-05 | 2069/11082/8817/2252/2254/2885/3570/5154/7039 |
| GO (MF) | GO:0005031 | tumor necrosis factor-activated receptor activity | 5/127 | 9.99E-07 | 1.70E-05 | 355/8793/7293/943/3604 |
| GO (MF) | GO:0005035 | death receptor activity | 5/127 | 9.99E-07 | 1.70E-05 | 355/8793/7293/943/3604 |
|  |  |  |  |  |  |  |
| GO (CC) | GO:0009897 | external side of plasma membrane | 11/127 | 7.95E-07 | 0.000169381 | 567/811/1236/4283/2022/355/3595/3605/55576/7048/3604 |
| GO (CC) | GO:0098552 | side of membrane | 13/127 | 1.04E-05 | 0.001106934 | 567/811/1236/4283/1540/2022/355/3595/3605/3845/55576/7048/3604 |
| GO (CC) | GO:0043235 | receptor complex | 10/127 | 9.38E-05 | 0.005692421 | 93/567/650/917/1956/2022/3570/7048/7253/7421 |
| GO (CC) | GO:0031983 | vesicle lumen | 6/127 | 0.0001069 | 0.005692421 | 213/811/1956/3082/5154/7042 |
| GO (CC) | GO:0005769 | early endosome | 9/127 | 0.00027277 | 0.011620023 | 208/567/22943/1956/2149/5604/5879/6272/5987 |
| GO (CC) | GO:0005838 | proteasome regulatory particle | 3/127 | 0.000419633 | 0.01393991 | 5701/5717/5710 |
| GO (CC) | GO:0031093 | platelet alpha granule lumen | 4/127 | 0.000617639 | 0.01393991 | 213/3082/5154/7042 |
| GO (CC) | GO:0022624 | proteasome accessory complex | 3/127 | 0.000628776 | 0.01393991 | 5701/5717/5710 |
| GO (CC) | GO:0045121 | membrane raft | 8/127 | 0.000679348 | 0.01393991 | 867/1910/1956/2149/355/5045/3845/7048 |
| GO (CC) | GO:0098857 | membrane microdomain | 8/127 | 0.000695923 | 0.01393991 | 867/1910/1956/2149/355/5045/3845/7048 |
| GO (CC) | GO:0098589 | membrane region | 9/127 | 0.000769382 | 0.01393991 | 867/1910/1956/2149/355/5045/3845/6272/7048 |
| GO (CC) | GO:0030141 | secretory granule | 9/127 | 0.000785347 | 0.01393991 | 213/551/811/998/1755/3082/5154/7042/7200 |
| GO (CC) | GO:0060205 | cytoplasmic membrane-bounded vesicle lumen | 5/127 | 0.000901039 | 0.014763173 | 213/811/3082/5154/7042 |
| GO (CC) | GO:0098802 | plasma membrane receptor complex | 6/127 | 0.001215014 | 0.018485571 | 567/650/917/2022/3570/7048 |
| GO (CC) | GO:0044297 | cell body | 10/127 | 0.001716061 | 0.024368073 | 998/1524/2173/4137/4352/6276/6272/6654/6750/7042 |
| GO (CC) | GO:0031091 | platelet alpha granule | 4/127 | 0.001879241 | 0.025017396 | 213/3082/5154/7042 |
| GO (CC) | GO:0043025 | neuronal cell body | 9/127 | 0.002411803 | 0.030218475 | 998/1524/2173/4352/6276/6272/6654/6750/7042 |
| GO (CC) | GO:0008540 | proteasome regulatory particle, base subcomplex | 2/127 | 0.003132058 | 0.036433064 | 5701/5710 |
| GO (CC) | GO:0034774 | secretory granule lumen | 4/127 | 0.003249898 | 0.036433064 | 213/3082/5154/7042 |

# Table S7. Reported prognostic models included in this study for comparison

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Name | Gene number | N (training set) | N (validation set) | N (total) | Reference |
| Sabatier 2011 | 7 | 35 | 366 | 401 | (17) |
| Hernandez 2010 | 9 | 185 | 135 | 320 | (18) |
| Kernagis 2012 | 16 | 242 | 53, 119 | 414 | (19) |
| Kang 2012 | 23 | 511 | 65, 285 | 861 | (20) |
| Konstantinopoulos 2010 | 60 | 61 | 70 | 131 | (6) |
| Crijns 2009 | 86 | 157 | 118 | 275 | (12) |
| Yoshihara 2012 | 126 | 260 | 131, 185, 119, 319, 40 | 1054 | (14) |
| TCGA 2011 | 193 | 215 | 255, 237, 169, 118 | 994 | (16) |
| Denkert 2009 | 300 | 80 | 118 | 198 | (1) |

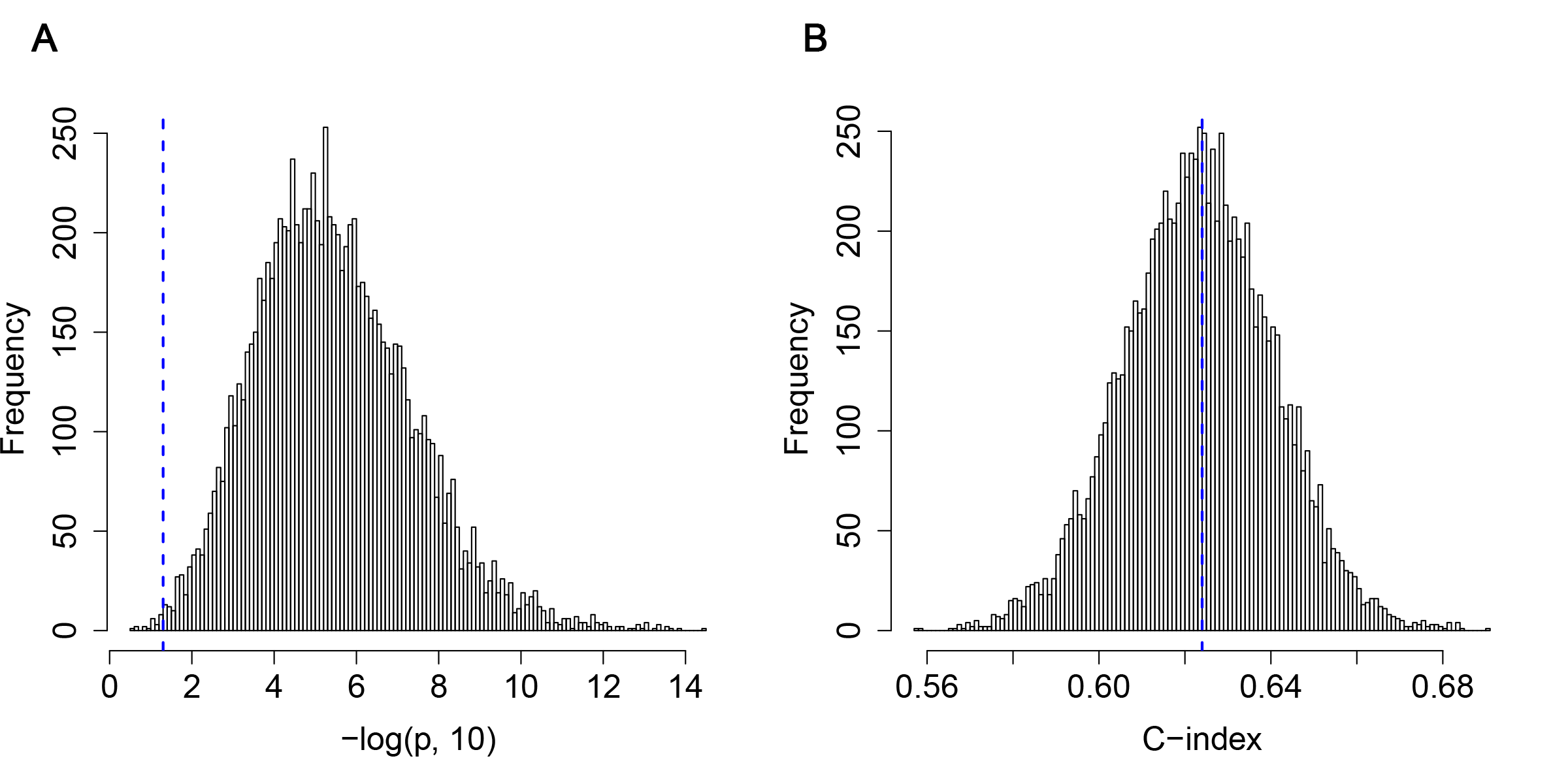


# Figure S1. Meta-analysis for IPSOV and overall survival in the six datasets.



# Figure S2. Subgroup and sensitivity analysis for IPSOV.

We estimate HRs between IPSOV and overall survival in different subgroups including age, histology type, stage, grade and debulking status in the combined dataset.



# Figure S3. Robustness test of IPSOV

**(A)** Histogram of –log10(*P*) values from the resampling datasets for 10,000 times. **(B)** Histogram of C-index values from the resampling datasets for 10,000 times.

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