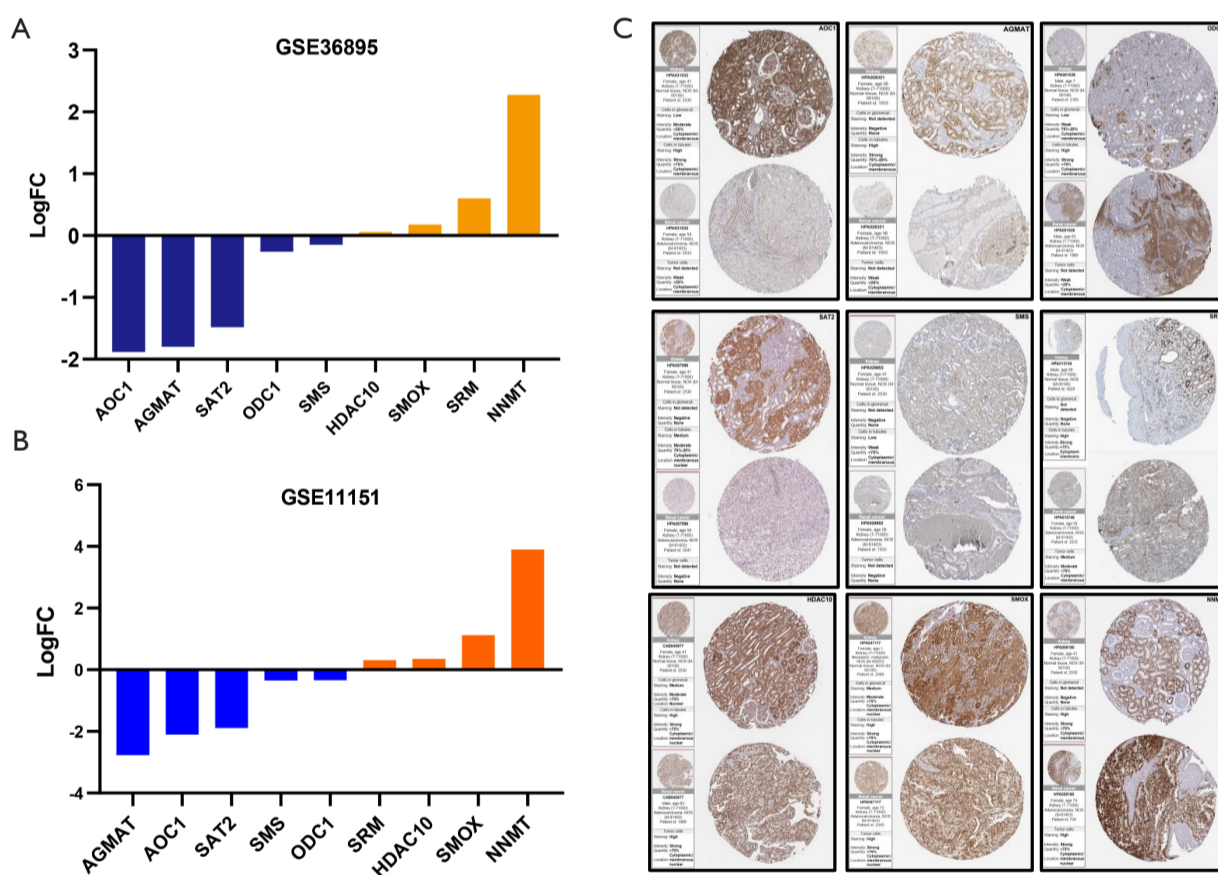


**Table S1** Polyamine metabolism-related genes

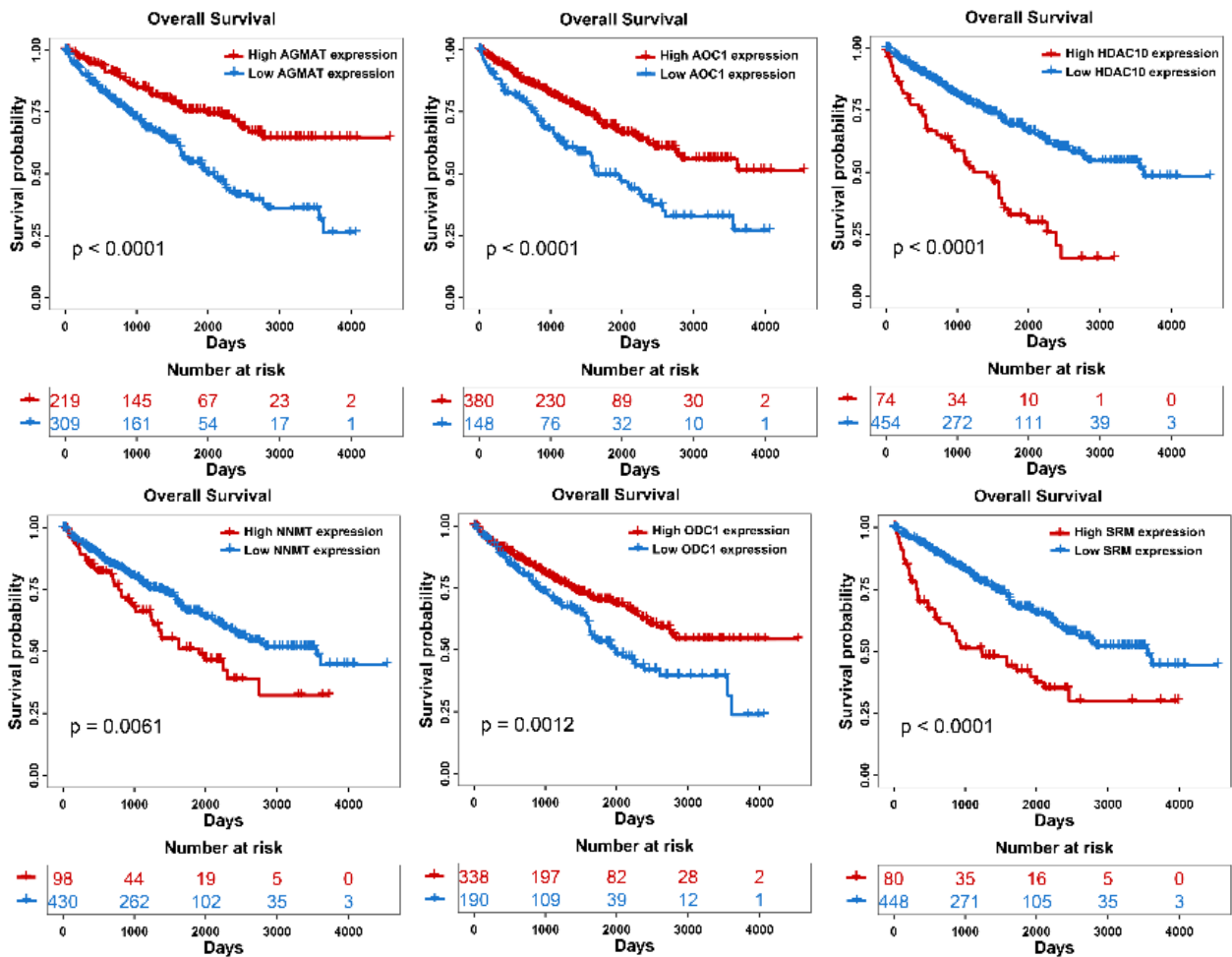
Symbol	Reference
HDAC6	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
SAT2	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
AZIN2	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
DHPS	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
PAOX	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
AOC1	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
AMD1	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
NNMT	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
OAZ1	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
OAZ2	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
ODC1	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
AZIN1	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
OAZ3	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
SMOX	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
SAT1	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
SMS	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
SRM	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
AGMAT	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>
HDAC10	<a href="https://www.gsea-msigdb.org/gsea/msigdb/index.jsp">https://www.gsea-msigdb.org/gsea/msigdb/index.jsp</a>



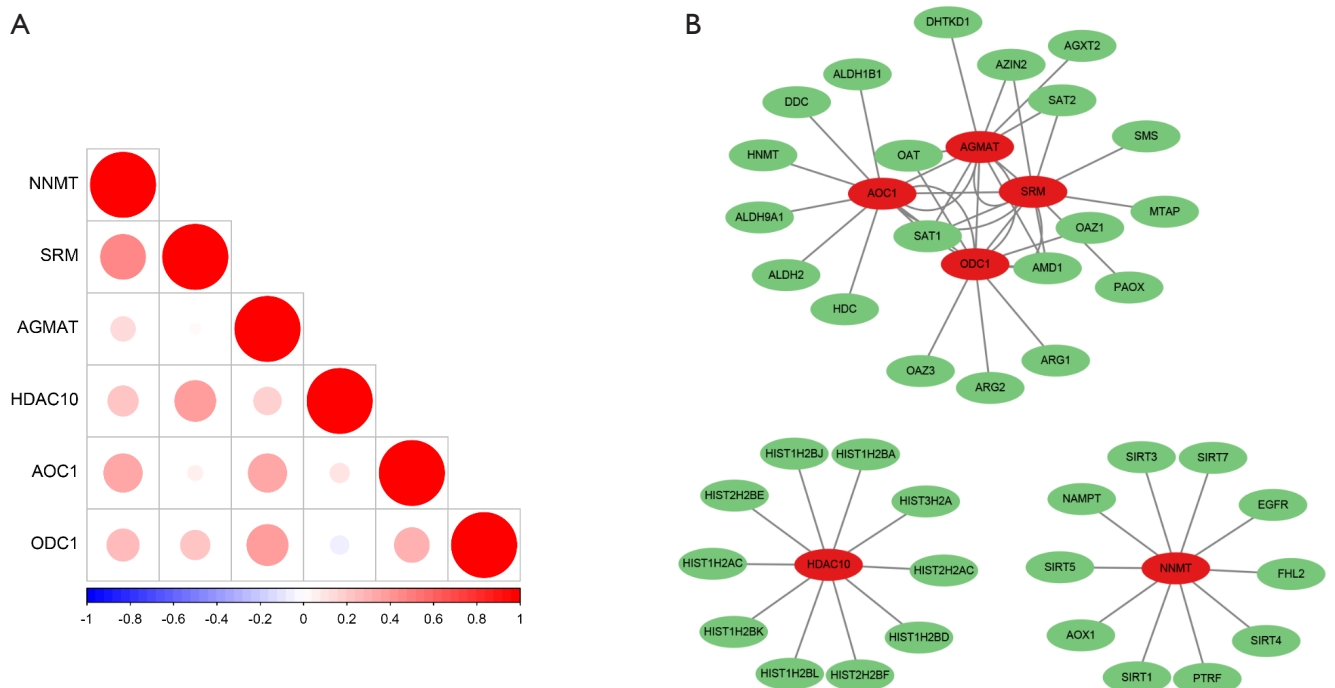
**Figure S1** Validation of expression. (A,B) Bar plots showing the log<sub>2</sub> (fold change) of the PMRGs in the GSE36895 and GSE11151 datasets. The orange and yellow color represent expression upregulation, while the blue color represents expression downregulation. (C) Immunohistochemistry diagrams from the HPA database showing the protein expression levels of PMRGs in tumor and normal tissues (URL: AGMAT, <https://www.proteinatlas.org/ENSG00000116771-AGMAT/pathology/renal+cancer#img>, <https://www.proteinatlas.org/ENSG00000116771-AGMAT/tissue/kidney#img>; AOC1, <https://www.proteinatlas.org/ENSG0000002726-AOC1/tissue/kidney#img>, <https://www.proteinatlas.org/ENSG0000002726-AOC1/pathology/renal+cancer#img>; ODC1, <https://www.proteinatlas.org/ENSG00000115758-ODC1/pathology/renal+cancer#img>, <https://www.proteinatlas.org/ENSG00000115758-ODC1/tissue/kidney#img>; SAT2, <https://www.proteinatlas.org/ENSG00000141504-SAT2/tissue/kidney#img>, <https://www.proteinatlas.org/ENSG00000141504-SAT2/pathology/renal+cancer#img>; SMS, <https://www.proteinatlas.org/ENSG00000102172-SMS/tissue/kidney#img>, <https://www.proteinatlas.org/ENSG00000102172-SMS/pathology/renal+cancer#img>; SRM, <https://www.proteinatlas.org/ENSG00000116649-SRM/tissue/kidney#img>, <https://www.proteinatlas.org/ENSG00000116649-SRM/pathology/renal+cancer#img>; HDAC10, <https://www.proteinatlas.org/ENSG00000100429-HDAC10/tissue/kidney#img>, <https://www.proteinatlas.org/ENSG00000100429-HDAC10/pathology/renal+cancer#img>; SMOX, <https://www.proteinatlas.org/ENSG00000088826-SMOX/tissue/kidney#img>, <https://www.proteinatlas.org/ENSG00000088826-SMOX/pathology/renal+cancer#img>; NNMT, <https://www.proteinatlas.org/ENSG00000166741-NNMT/tissue/kidney#img>, <https://www.proteinatlas.org/ENSG00000166741-NNMT/pathology/renal+cancer#img>). PMRG, polyamine metabolism-related gene; HPA, Human Protein Atlas.

**Table S2** Basic information of prognosis-related polyamine metabolism-related genes

Gene	Complete name	Nature	Function	Pathways	Bibliographic references	Separated risky and protective characteristics
NNMT	Nicotinamide N-Methyltransferase	Protein coding	GO:MF: enables nicotinamide N-methyltransferase activity, methyltransferase activity, transferase activity, enables pyridine N-methyltransferase activity; CC: cytoplasm; BP: involved_in nicotinamide metabolic process	KEGG: nicotinate and nicotinamide metabolism Other: PP2A/MEK/ERK/c-Jun/ABCA1 pathway, ROS and cell cycle, P13K/AKT	PMID: GO:8182091, 21823666, 23455543, 26571212, 23455543, 31043742, 30044909, 8182091, 35988817, 36977555, 34642500	Risk: kidney cancer (our research), breast cancer (promote metastasis), colorectal cancer (drug resistance), gastric cancer (progression)
SRM	Spermidine Synthase	Protein coding	GO:MF: enables protein binding, catalytic activity, enables spermidine synthase activity, enables identical protein binding; CC: located_in cytosol; BP: involved_in polyamine metabolic process, polyamine biosynthetic process, involved_in spermidine biosynthetic process, involved_in cellular response to leukemia inhibitory factor	KEGG: cysteine and methionine metabolism, arginine and proline metabolism, Beta alanine metabolism, Glutathione metabolism	PMID: GO: 21044950, 17585781, 17585781, 27189574	Risk: kidney cancer (Our research); protective: colorectal cancer (inhibit tumor growth)
HDAC10	Histone Deacetylase 10	Protein coding	GO:MF: enables histone deacetylase activity, enables protein binding, enables deacetylase activity, enables enzyme binding, enables protein lysine deacetylase activity, enables histone deacetylase binding; CC: part_of histone deacetylase complex, located_in nucleus, located_in cytoplasm; BP: involved_in negative regulation of transcription by RNA polymerase II, involved_in chromatin organization, involved_in regulation of DNA-templated transcription, involved_in macroautophagy	TGF- $\beta$ pathway, cell cycle related pathway, WNT/ $\beta$ -catenin	PMID: GO: 11861901, 11726666, 11677242, 11739383, 17172643, 28516954, 23801752, 28073598, 26240284, 33481338	Risk: kidney cancer (our research), ovarian cancer (deletion of HDAC10 increase the drug sensitivity), non-small cell lung carcinoma (correlate to poor prognosis)
AGMAT	Agmatinase	Protein coding	GO: MF: enables agmatinase activity, hydrolase activity, enables metal ion binding; CC: located_in mitochondrion; BP: involved_in putrescine biosynthetic process from arginine, using agmatinase, involved_in spermidine biosynthetic process	KEGG: arginine and proline metabolism; other: P13K/AKT	PMID: GO: 21873635, 11914032, 31699997, 36680755	Risk: lung cancer (promote tumorigenesis), colorectal cancer (promote tumor progression) protective: kidney cancer (our research)
AOC1	Amine Oxidase Copper Containing 1	Protein coding	GO:MF: enables copper ion binding, enables calcium ion binding, enables protein binding, enables primary amine oxidase activity, enables heparin binding; CC: located_in extracellular space, located_in extracellular exosome; BP: involved_in amine metabolic process, involved_in putrescine metabolic process, involved_in cellular response to copper ion starvation	KEGG: arginine and proline metabolism, Histidine metabolism, Tryptophan metabolism; other: ferroptosis, AKT, EMT, STAT3	PMID: GO: 12072962, 12072962, 32296183, 8144586, 12072962, 9399025, 21082674, 21873635, 8144586, 9399025, 35922412, 32210620, 34777591	Protective: kidney cancer (our research), prostate cancer (inhibit proliferation); risk: colorectal cancer (promote tumor progression), gastric cancer (promote tumor progression), hepatocellular carcinoma
ODC1	Ornithine Decarboxylase 1	Protein coding	GO:MF: catalytic activity, enables ornithine decarboxylase activity, enables protein binding; CC: is_active_in cellular_component, located_in cytoplasm; BP: involved_in response to virus, involved_in polyamine metabolic process, involved_in cell population proliferation	KEGG: arginine and proline metabolism, glutathione metabolism; other: AKT/GSK3 $\beta$ / $\beta$ -catenin	PMID: GO: 25416956, 2317811, 17407445, 16548883, 35242701, 31239700	Protective: kidney cancer (our research); risk: neuroblastoma (tumor progression), hepatocellular carcinoma (promote proliferation)



**Figure S2** The survival curve of the prognosis-related genes.



**Figure S3** The cross-talk of PMRGs. (A) Diagram showing the coexpression relationship of PMRGs. (B) Network diagram showing the proteins potentially interacting with PMRGs. PMRG, polyamine metabolism-related gene.

**Table S3** Protein–protein interaction network of polyamine metabolism–related genes

PMRGs	Interaction protein
SRM	AGMAT
SRM	AMD1
SRM	AOC1
SRM	AZIN2
SRM	MTAP
SRM	ODC1
SRM	PAOX
SRM	SAT1
SRM	SAT2
SRM	SMS
AGMAT	AGXT2
AGMAT	AMD1
AGMAT	AOC1
AGMAT	AZIN2
AGMAT	DHTKD1
AGMAT	OAT
AGMAT	ODC1
AGMAT	SAT1
AGMAT	SAT2
AGMAT	SRM
AOC1	ODC1
AOC1	HDC
AOC1	HNMT
AOC1	SRM
AOC1	SAT1
AOC1	DDC
AOC1	AGMAT
AOC1	ALDH1B1
AOC1	ALDH2
AOC1	ALDH9A1
HDAC10	HIST1H2BD
HDAC10	HIST1H2BL
HDAC10	HIST1H2BA
HDAC10	HIST2H2BF

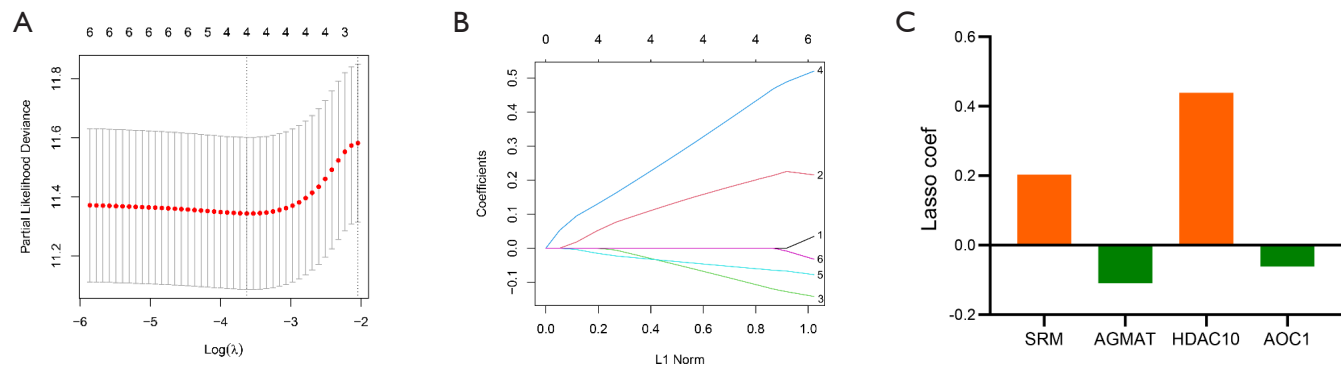
**Table S3** (continued)

**Table S3** (continued)

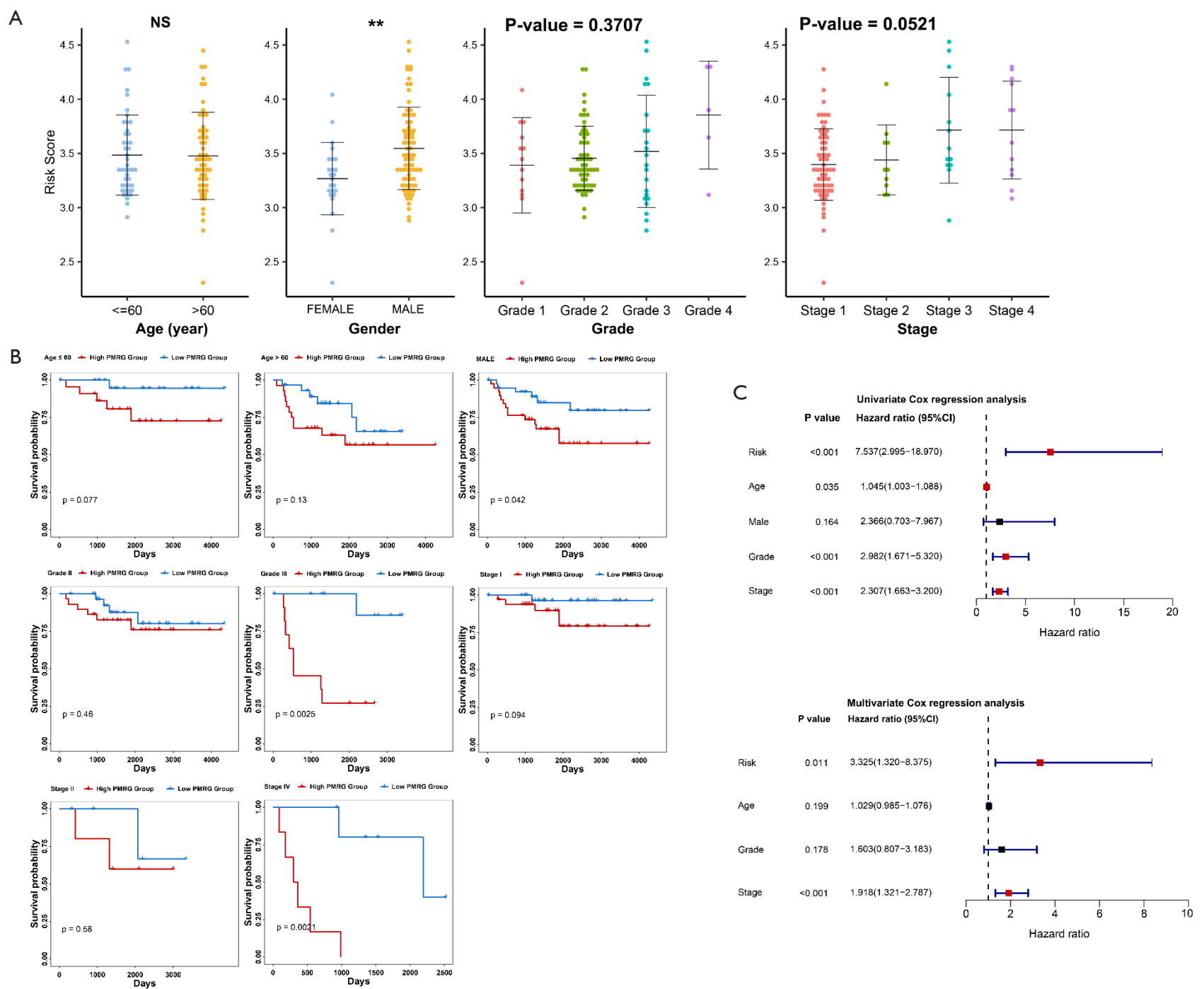
PMRGs	Interaction protein
HDAC10	HIST1H2BJ
HDAC10	HIST1H2AC
HDAC10	HIST1H2BK
HDAC10	HIST3H2A
HDAC10	HIST2H2AC
HDAC10	HIST2H2BE
NNMT	SIRT4
NNMT	SIRT1
NNMT	SIRT7
NNMT	PTRF
NNMT	SIRT3
NNMT	SIRT5
NNMT	AOX1
NNMT	EGFR
NNMT	FHL2
NNMT	NAMPT
ODC1	SAT1
ODC1	SRM
ODC1	AGMAT
ODC1	AMD1
ODC1	AOC1
ODC1	ARG1
ODC1	ARG2
ODC1	OAT
ODC1	OAZ1
ODC1	OAZ3

**Table S4** Potential pathways of coexpressed polyamine metabolism-related genes obtained from the single-cell sequence datasets

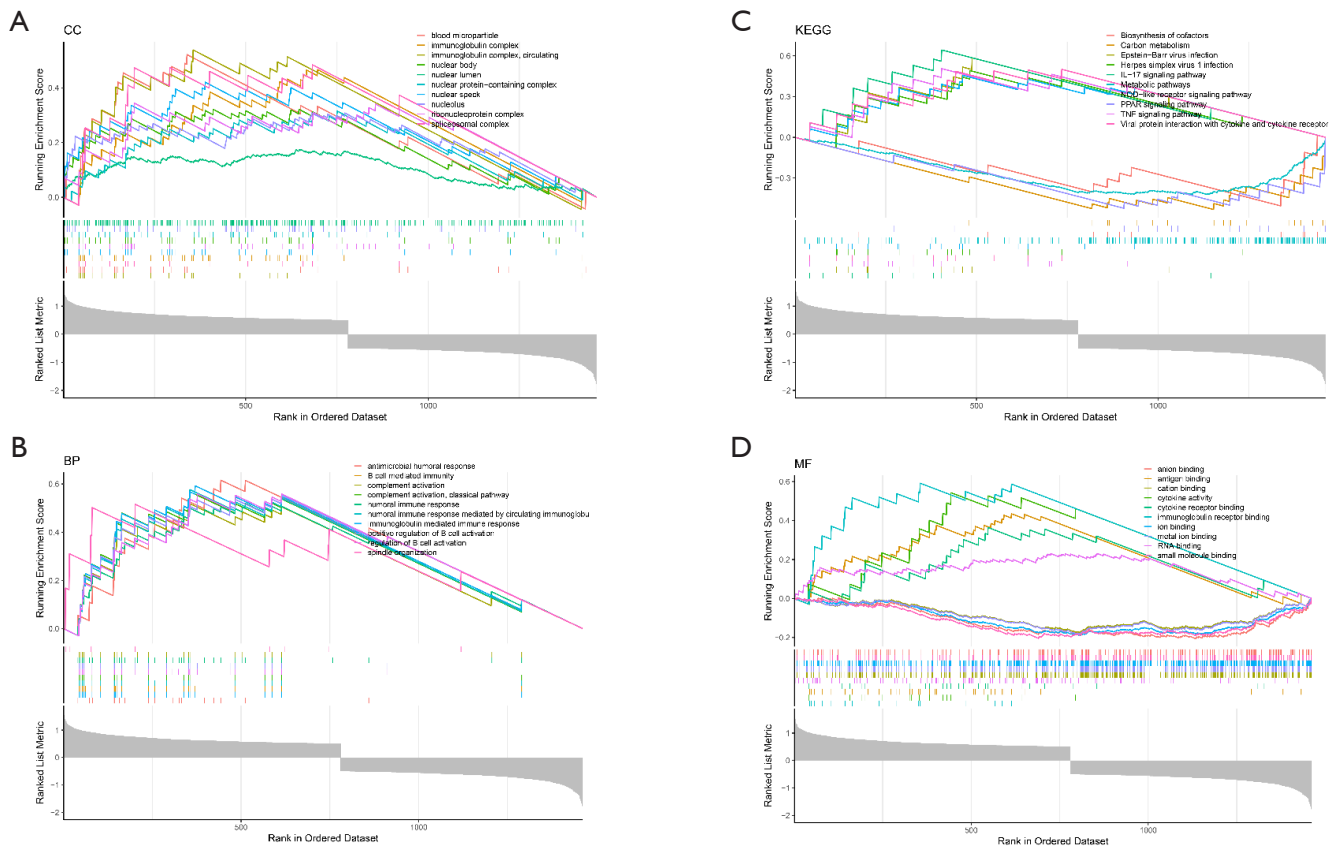
Category	Term	Count	P value	Genes	Fold.Enrichment	Bonferroni	Benjamini	FDR	Type
KEGG_PATHWAY	hsa01100: Metabolic pathways	45	2.69E-18	<i>DDC, ECHS1, ACY1, SHMT1, QPRT, AK4, GPPD3, GLYAT, ACAT1, CYP17A1, GCSH, LDHD, ASPDH, ACADM, DHRS4L2, HADH, ACAA1, PCK1, HAO2, PCK2, MIOX, PCYT2, HGD, AGXT2, DCXR, AKR1A1, FMO1, BBOX1, PRODH2, GCAT, ASS1, AGMAT, QDPR, GATM, ALDH6A1, TST, PSAT1, ADI1, CRYL1, SUCLG1, IDNK, ALDOB, B4GALT7, FBP1, HPD</i>	3.67012987	3.53E-16	3.53E-16	3.09E-16	AGMAT-GSE159115
KEGG_PATHWAY	hsa01200: Carbon metabolism	11	1.66E-08	<i>GCSH, ALDH6A1, ECHS1, PSAT1, SHMT1, SUCLG1, IDNK, ALDOB, FBP1, HAO2, ACAT1</i>	12.01391304	2.17E-06	1.09E-06	9.53E-07	AGMAT-GSE159115
KEGG_PATHWAY	hsa00280: Valine, leucine and isoleucine degradation	7	1.73E-06	<i>ALDH6A1, ECHS1, AGXT2, ACADM, HADH, ACAA1, ACAT1</i>	18.31666667	0.000227	7.57E-05	6.65E-05	AGMAT-GSE159115
KEGG_PATHWAY	hsa00260: Glycine, serine and threonine metabolism	6	1.35E-05	<i>GCSH, GATM, PSAT1, AGXT2, SHMT1, GCAT</i>	18.84	0.001761043	0.000441	0.000387	AGMAT-GSE159115
KEGG_PATHWAY	hsa00071: Fatty acid degradation	6	1.93E-05	<i>ECHS1, ECI2, ACADM, HADH, ACAA1, ACAT1</i>	17.5255814	0.002529086	0.000506	0.000445	AGMAT-GSE159115
KEGG_PATHWAY	hsa00620: Pyruvate metabolism	5	0.000476	<i>LDHD, AKR1A1, PCK1, PCK2, ACAT1</i>	13.36170213	0.06044207	0.010388495	0.009119671	AGMAT-GSE159115
KEGG_PATHWAY	hsa01212: Fatty acid metabolism	5	0.000994	<i>ECHS1, ACADM, HADH, ACAA1, ACAT1</i>	11.01754386	0.122125909	0.017546536	0.015403448	AGMAT-GSE159115
KEGG_PATHWAY	hsa01240: Biosynthesis of cofactors	7	0.001202221	<i>PSAT1, SHMT1, QPRT, ASPDH, AKR1A1, AK4, HPD</i>	5.746405229	0.145796351	0.017546536	0.015403448	AGMAT-GSE159115
KEGG_PATHWAY	hsa04978: Mineral absorption	5	0.001205487	<i>SLC34A3, SLC34A1, MT1G, MT1H, MT1HL1</i>	10.46666667	0.146162245	0.017546536	0.015403448	AGMAT-GSE159115
KEGG_PATHWAY	hsa00630: Glyoxylate and dicarboxylate metabolism	4	0.00160403	<i>GCSH, SHMT1, HAO2, ACAT1</i>	16.74666667	0.189656172	0.021012794	0.018446346	AGMAT-GSE159115
KEGG_PATHWAY	hsa00010: Glycolysis/Gluconeogenesis	5	0.001818862	<i>AKR1A1, ALDOB, PCK1, FBP1, PCK2</i>	9.373134328	0.212181766	0.021660994	0.019015376	AGMAT-GSE159115
KEGG_PATHWAY	hsa03320: PPAR signaling pathway	5	0.002752677	<i>FABP1, ACADM, PCK1, ACAA1, PCK2</i>	8.373333333	0.303089283	0.027738519	0.024350609	AGMAT-GSE159115
KEGG_PATHWAY	hsa01230: Biosynthesis of amino acids	5	0.002752677	<i>ACY1, PSAT1, SHMT1, ALDOB, ASS1</i>	8.373333333	0.303089283	0.027738519	0.024350609	AGMAT-GSE159115
KEGG_PATHWAY	hsa00380: Tryptophan metabolism	4	0.004242343	<i>DDC, ECHS1, HADH, ACAT1</i>	11.96190476	0.427034141	0.039696212	0.03484782	AGMAT-GSE159115
KEGG_PATHWAY	hsa01100: Metabolic pathways	43	2.44E-20	<i>GPI, ACAA2, GAL3ST1, QPRT, ACSM2A, FTCD, KHK, GCSH, ANPEP, ASPDH, DHRS4L2, ACAA1, PCK1, HAO2, PCK2, MPST, MIOX, FAHD1, PKLR, BHMT2, SORD, BBOX1, CMBL, FAH, PRODH2, AGMAT, DHRS4, GSTZ1, ALDH3A2, QDPR, GATM, ALDH6A1, BHMT, TST, GSTA2, GSTA1, RGN, CRYL1, ALPI, ALDOB, FBP1, NIT2, ACOT4</i>	4.070640074	2.09E-18	2.09E-18	1.80E-18	AGMAT-GSE171306
KEGG_PATHWAY	hsa00010: Glycolysis/Gluconeogenesis	7	5.14E-06	<i>ALDH3A2, GPI, PKLR, ALDOB, PCK1, FBP1, PCK2</i>	15.23134328	0.000442	0.000221	0.00019	AGMAT-GSE171306
KEGG_PATHWAY	hsa01200: Carbon metabolism	8	1.06E-05	<i>GCSH, GPI, ALDH6A1, PKLR, RGN, ALDOB, FBP1, HAO2</i>	10.14161491	0.000914	0.000305	0.000262	AGMAT-GSE171306
KEGG_PATHWAY	hsa00030: Pentose phosphate pathway	4	0.001032771	<i>GPI, RGN, ALDOB, FBP1</i>	19.43809524	0.085030171	0.022204573	0.01910626	AGMAT-GSE171306
KEGG_PATHWAY	hsa00051: Fructose and mannose metabolism	4	0.001368205	<i>SORD, ALDOB, FBP1, KHK</i>	17.67099567	0.111078369	0.023533126	0.020249434	AGMAT-GSE171306
KEGG_PATHWAY	hsa00071: Fatty acid degradation	4	0.002951134	<i>ALDH3A2, ACAA2, ECI2, ACAA1</i>	13.56146179	0.224442216	0.041233262	0.035479783	AGMAT-GSE171306
KEGG_PATHWAY	hsa00620: Pyruvate metabolism	4	0.003804647	<i>ALDH3A2, PKLR, PCK1, PCK2</i>	12.40729483	0.279509921	0.041233262	0.035479783	AGMAT-GSE171306
KEGG_PATHWAY	hsa00280: Valine, leucine and isoleucine degradation	4	0.004039094	<i>ALDH3A2, ALDH6A1, ACAA2, ACAA1</i>	12.14880952	0.29394739	0.041233262	0.035479783	AGMAT-GSE171306
KEGG_PATHWAY	hsa00330: Arginine and proline metabolism	4	0.004533961	<i>ALDH3A2, GATM, PRODH2, AGMAT</i>	11.66285714	0.323489499	0.041233262	0.035479783	AGMAT-GSE171306
KEGG_PATHWAY	hsa00270: Cysteine and methionine metabolism	4	0.004794565	<i>MPST, BHMT, TST, BHMT2</i>	11.43417367	0.338552238	0.041233262	0.035479783	AGMAT-GSE171306
KEGG_PATHWAY	hsa01100: Metabolic pathways	25	2.93E-05	<i>ACADVL, NNMT, GAL3ST1, CHPF, TECR, MGST1, ACSM2A, ENO1, FTCD, ACSM2B, KHK, ANPEP, UGT2A3, ASL, CYP2J2, HSD3B7, SDHA, HADHB, HADHA, GLUD1, NAT8, PKM, GSTA2, GSTA1, PFKP</i>	2.325131009	0.003946661	0.003954412	0.003749368	AOC1-GSE159115
KEGG_PATHWAY	hsa00480: Glutathione metabolism	5	0.000599	<i>NAT8, ANPEP, GSTA2, GSTA1, MGST1</i>	12.5638658	0.077673775	0.040416043	0.038320396	AOC1-GSE159115
KEGG_PATHWAY	hsa01100: Metabolic pathways	28	1.13E-09	<i>GAL3ST1, QPRT, ACSM2A, FTCD, KHK, ANPEP, ASPDH, PCK1, HAO2, PCK2, MPST, MIOX, FAHD1, PKLR, GPX3, SORD, BBOX1, PRODH2, AGMAT, ALDH3A2, ALDH6A1, BHMT, NAT8, TST, RGN, ALPI, ALDOB, ACOT4</i>	3.22687747	1.15E-07	1.15E-07	1.10E-07	AOC1-GSE171306
KEGG_PATHWAY	hsa00010: Glycolysis/Gluconeogenesis	5	0.000479	<i>ALDH3A2, PKLR, ALDOB, PCK1, PCK2</i>	13.24464633	0.047726595	0.024445687	0.023247369	AOC1-GSE171306
KEGG_PATHWAY	hsa05203: Viral carcinogenesis	8	0.000128	<i>HDAC10, ATF6B, IRF3, STAT3, IRF7, LTBR, ATF4, NFKB2</i>	6.811848144	0.020838773	0.021057612	0.021057612	HDAC10-GSE111360
KEGG_PATHWAY	hsa00010: Glycolysis/Gluconeogenesis	8	1.58E-07	<i>LDHA, PKM, TPI1, PGK1, ENO1, ALDOA, ENO2, PFKP</i>	18.74626866	2.65E-05	2.65E-05	2.61E-05	NNMT-GSE159115
KEGG_PATHWAY	hsa01230: Biosynthesis of amino acids	7	6.37E-06	<i>PKM, TPI1, PGK1, ENO1, ALDOA, ENO2, PFKP</i>	14.65333333	0.001063231	0.000532	0.000526	NNMT-GSE159115
KEGG_PATHWAY	hsa04066: HIF-1 signaling pathway	7	5.45E-05	<i>LDHA, INSR, PGK1, ENO1, ALDOA, ENO2, PFKP</i>	10.08256881	0.009064717	0.003035268	0.002998917	NNMT-GSE159115
KEGG_PATHWAY	hsa01200: Carbon metabolism	7	7.36E-05	<i>PKM, TPI1, PGK1, ENO1, ALDOA, ENO2, PFKP</i>	9.556521739	0.012222705	0.003074391	0.003037572	NNMT-GSE159115
KEGG_PATHWAY	hsa05230: Central carbon metabolism in cancer	5	0.000914	<i>LDHA, PKM, MYC, SLC16A3, PFKP</i>	11.21428571	0.141647748	0.030534177	0.030168498	NNMT-GSE159115
KEGG_PATHWAY	hsa04978: Mineral absorption	8	1.09E-07	<i>FXYD2, MT1M, MT1F, MT1G, MT1H, MT1X, ATP1B1, MT1E</i>	19.79151515	1.79E-05	1.79E-05	1.79E-05	NNMT-GSE171306
KEGG_PATHWAY	hsa05016: Huntington disease	11	1.28E-05	<i>UQCRB, UQCRQ, NDUFB2, AP2S1, CLTB, BAX, POLR2G, UQCR10, POLR2I, POLR2J, UQCRH</i>	5.754453415	0.001304039	0.001304882	0.001228124	SRM-GSE159115
KEGG_PATHWAY	hsa03010: Ribosome	7	0.000376	<i>RPLP1, RPLP0, RPL13A, RPS3A, MRPL34, MRPL12, RPL19</i>	7.092082403	0.037596885	0.01915734	0.018030437	SRM-GSE159115



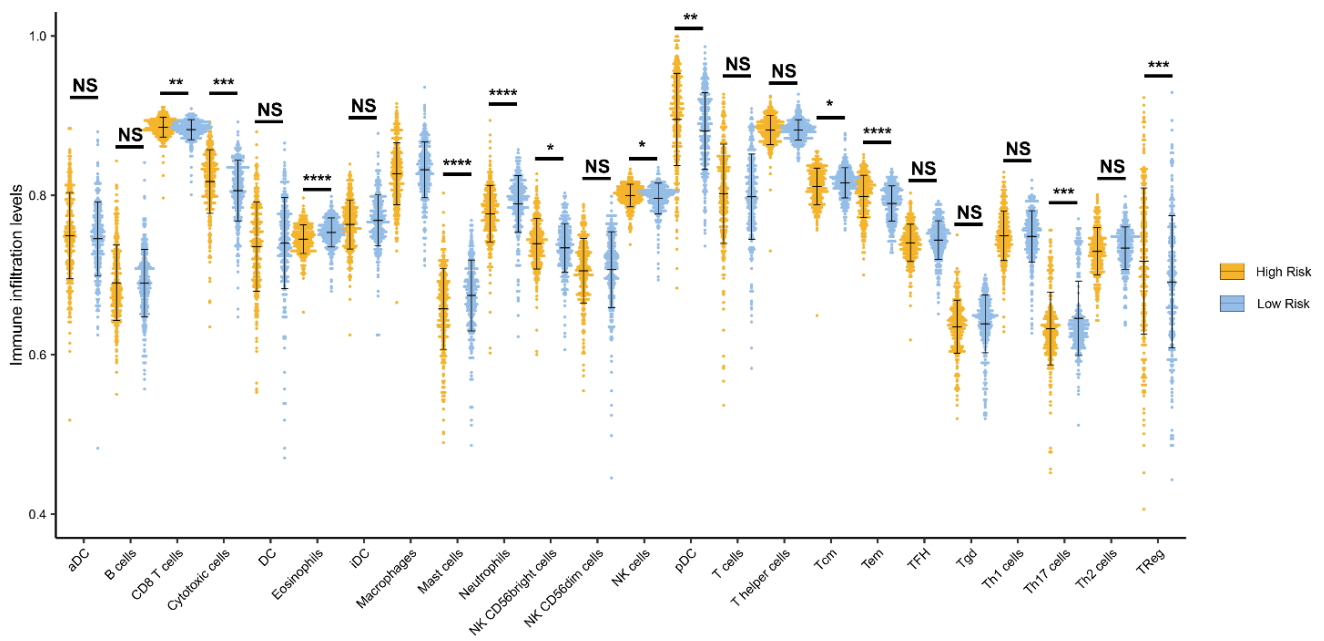
**Figure S4** Prognostic analysis and model construction. (A and B) The LASSO-Cox regression analysis progression. (C) Bar plot showing the coefficient of PMRGs for KIRC prognosis. The orange color represents the LASSO regression coefficient of the individual gene  $>0$ , while the green color represents the LASSO regression coefficient of the individual gene  $<0$ . PMRG, polyamine metabolism-related gene; KIRC, kidney renal clear cell; LASSO, least absolute shrinkage and selection operator.



**Figure S5** The model evaluation based on the E-MTAB-1980 dataset. (A) Dot plots showing the difference in the risk score in different clinical variables of the E-MTAB-1980 dataset. (B) The clinical variables were divided into different clinical subgroups, and then the survival curve was used to display the survival probability in the high and low PMRG risk groups. (C) Univariate and multivariate Cox regression analysis based on the PMRG risk signature and clinical variables (including age, gender, grade, and stage). NS, no significance; \*\*,  $P < 0.01$ . PMRG, polyamine metabolism-related gene.



**Figure S6 (A-D)** The function enrichment analysis results of DEGs in the high- and low-risk groups. DEG, differentially expressed gene.



**Figure S7** The dot plot for the immune infiltration levels of 24 immune cells in the high- and low-risk groups. NS, no significance; \*, P<0.05; \*\*, P<0.01; \*\*\*, P<0.001; \*\*\*\*, P<0.0001.