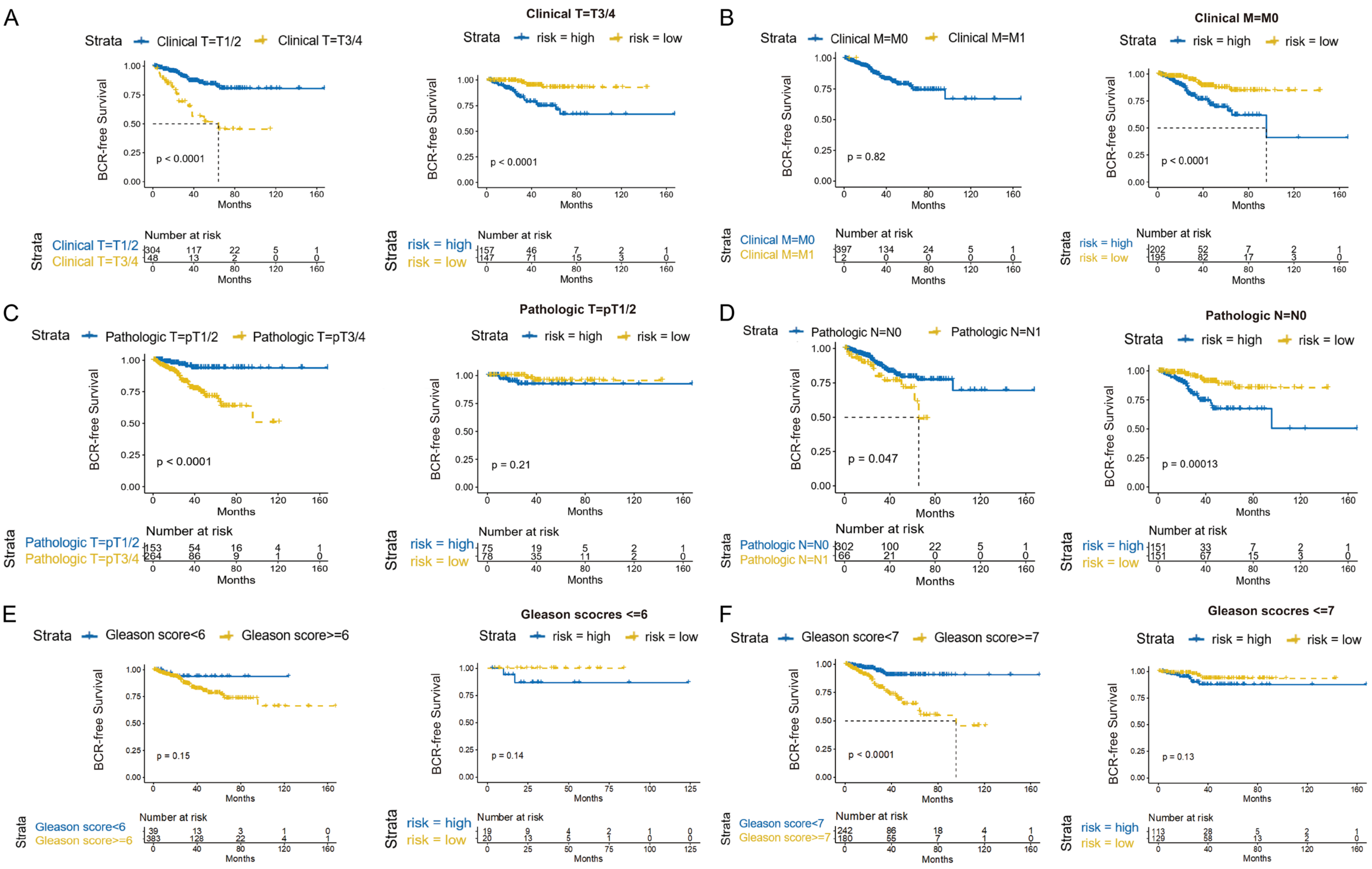
Supplementary Table 1. List of the genes in three commercial panels for PCa risk-stratification

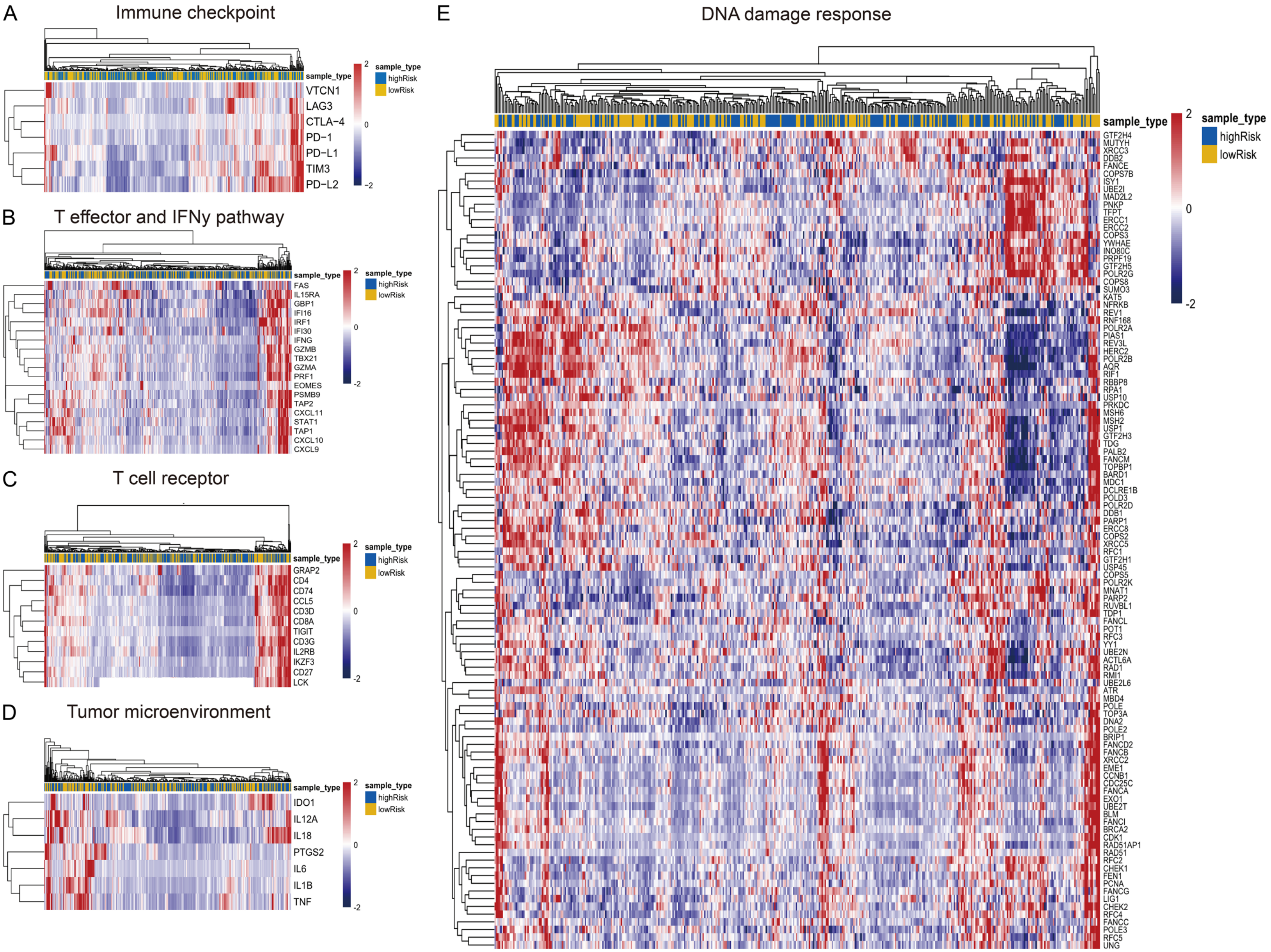
Test	Biomarkers	Genes	Ref
OncotypeDx	17 genes	*BGN, COL1A1, SFRP4, FLNC, GSN, TPM2, GSTM2, GAM13C, KLK2, AZGP1, SRD5A2, TPX2, ARF1, ATP5E, CLTC, GPS1, PGK1*	[1-3]
Decipher	22 genes	*LASP1, IQGAP3, NFIB, S1PR4, THBS2, ANO7, PCDH7, MYBPC1, EPPK1, TSBP, PBX1, NUSAP1, ZWILCH, UBE2C, CANK2N1, RABGAP1, PCAT-32, GLYATL1P4/PCAT-80, TNFRSF19*	[4-7]
Prolaris	46 genes	*FOXM1, CDC20, CDKN3, CDC2, KIF11, KIAA0101, NUSAP1, CENPF, ASPM, BUB1B, RRM2, DLGAP5, BIRC5, KIF20A, PLK1, TOP2A, TK1, PBK, ASF1B, C18orf24, RAD54L, PTTG1, CDCA3, MCM10, PRC1, DTL, CEP55, RAD51, CENPM, CDCA8, ORC6L, RPL38, UBA52, PSMC1, RPL4, RPL37, RPS29, SLC25A3, CLTC, TXNL1, PSMA1, RPL8, MMADHC, RPL13A, LOC728658, PPP2CA, MRFAP1*	[8-12]

Supplementary Table 2. The AUC values of the 8-gene signature and three commercial panels for predicting 1-, 2- and 3-year BFS

Panel	1 year-AUC	*p* value	2 year-AUC	*p* value	3 year-AUC	*p* value
8-gene vs. Decipher	0.737 vs. 0.612	0.226	0.760 vs. 0.619	0.074	0.737 vs. 0.702	0.563
8-gene vs. OncotypeDx	0.737 vs. 0.712	0.776	0.760 vs. 0.698	0.347	0.737 vs. 0.761	0.651
8-gene vs. Prolaris	0.737 vs. 0.718	0.820	0.760 vs. 0.726	0.616	0.737 vs. 0.784	0.376



Supplementary Figure 1. Performance evaluation of the 8-gene signature in the subgroups stratified according to TNM status or Gleason score in the TCGA cohort. Kaplan-Meier BFS analyses of the 8-gene predicative model in the subgroup with clinical stage T1-2 PCa (A), clinical stage M0 PCa (B), pathologic stage T1-2 PCa (C), pathologic stage N0 PCa (D), or a Gleason score of ≤6 (E) or 7 (F). BFS: biochemical recurrence-free survival; TCGA: The Cancer Genome Atlas Project; PCa: prostate cancer.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PD−1
PD−L1
TIM3
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sample_type
highRisk
lowRisk
B
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sample_type
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IL15RA
GBP1
IFI16
IRF1
IFI30
IFNG
GZMB
TBX21
GZMA
PRF1
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DDB2
FANCE
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COPS3
YWHAE
INO80C
PRPF19
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KAT5
NFRKB
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PIAS1
REV3L
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POLR2B
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RIF1
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RPA1
USP10
PRKDC
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MSH2
USP1
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PARP2
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TDP1
FANCL
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RFC3
YY1
UBE2N
ACTL6A
RAD1
RMI1
UBE2L6
ATR
MBD4
POLE
TOP3A
DNA2
POLE2
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FANCB
XRCC2
EME1
CCNB1
CDC25C
FANCA
EXO1
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BLM
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BRCA2
CDK1
RAD51AP1
RAD51
RFC2
CHEK1
FEN1
PCNA
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LIG1
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RFC5
UNG
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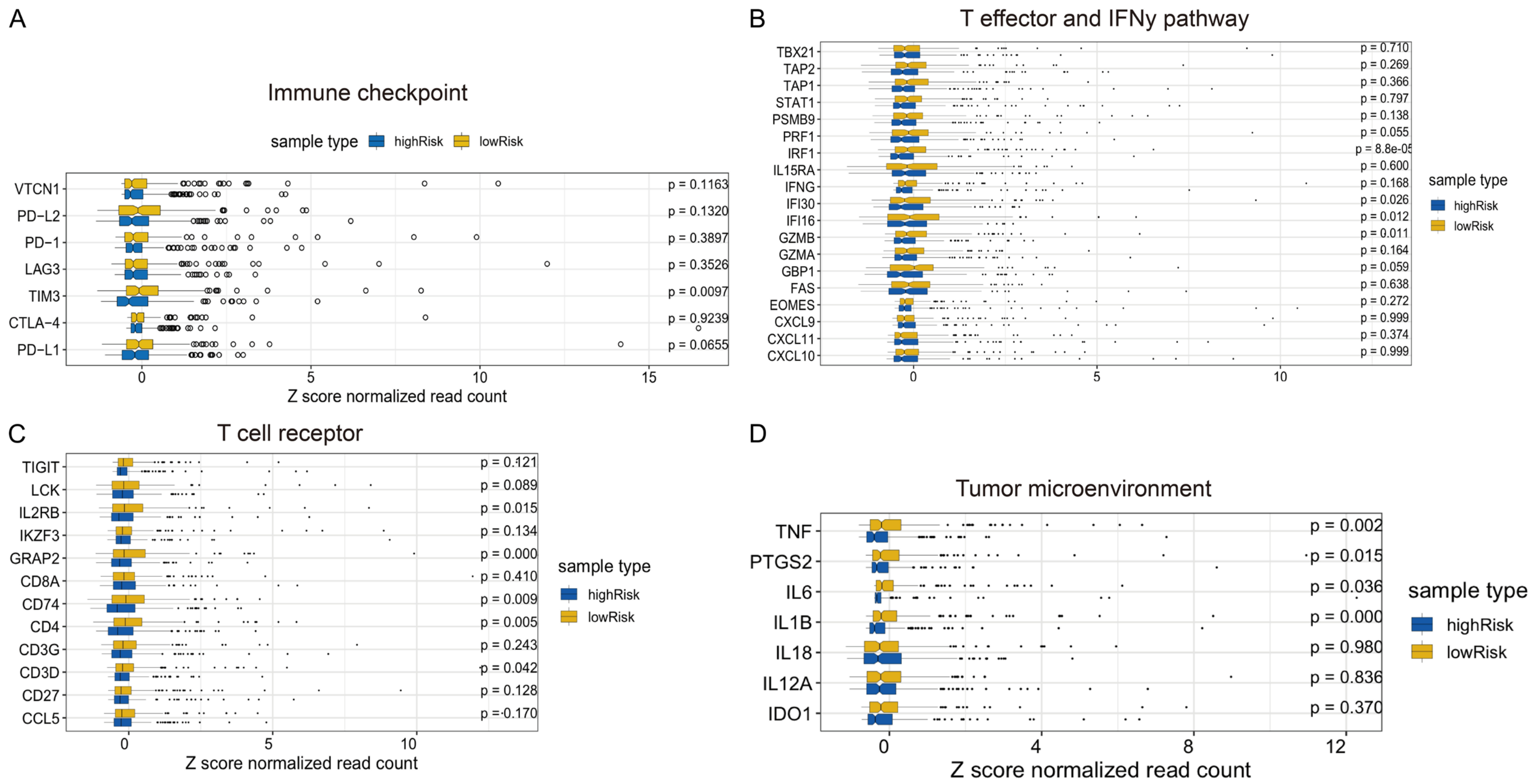
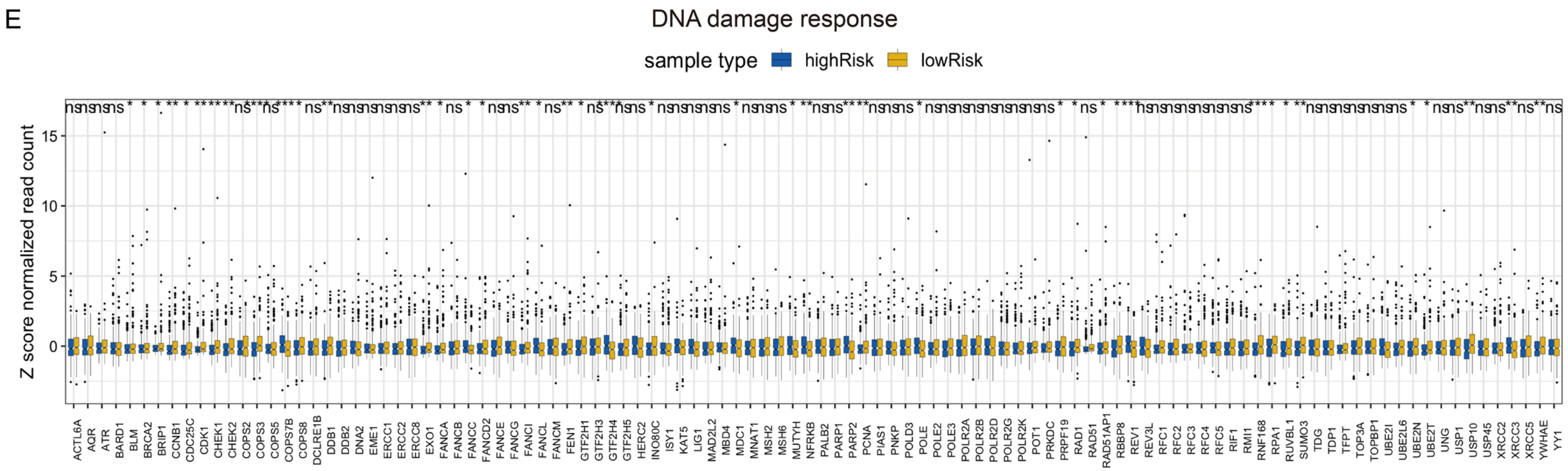
sample_type
highRisk
lowRisk

Supplementary Figure 2. mRNA expression profiles of different gene classifications between high-risk and low-risk groups in the TCGA cohort. The heat maps show mRNA expression profiles of different gene classifications between high-risk and low-risk groups, including common immune checkpoints (A), representative genes of IFNγ pathway, effector T cell (B), T cell receptor (C), and the tumor microenvironment (D), and DNA damage repair genes (E). TCGA: The Cancer Genome Atlas Project.





Supplementary Figure 3. Comparison of mRNA expression of different gene classifications between high-risk and low-risk groups in the TCGA cohort. The mRNA expression profiling analyses for common immune checkpoints (A), representative genes of IFNγ pathway, effector T cell (B), T cell receptor (C), and the tumor microenvironment (D), and DNA damage repair genes (E) between the two risk groups. *P<0.05, **P<0.01, ***P<0.001, and ****P<0.0001. TCGA: The Cancer Genome Atlas Project.

Supplementary Table 3. The differentially expressed DNA damage repair genes between the high-risk and low-risk groups in the TCGA cohort

Gene	*P* value	High-risk	Low-risk
BLM	0.029829042	-0.103942574	0.112135092
BRCA2	0.041661165	-0.097468548	0.105150798
BRIP1	0.019382566	-0.113383545	0.122320179
CCNB1	0.004667985	-0.134548703	0.145153527
CDC25C	0.030037404	-0.102600358	0.110687085
CDK1	0.005217301	-0.134560353	0.145166095
CHEK1	0.001822992	-0.148519804	0.160225799
CHEK2	0.001515887	-0.150122304	0.161954603
COPS3	1.22E-05	-0.205155828	0.221325745
COPS7B	0.000934291	0.154170673	-0.166322056
COPS8	0.024320428	-0.10586488	0.11420891
DDB1	0.005700649	-0.129984756	0.140229859
EXO1	0.004029355	-0.13711129	0.147918091
FANCA	0.028976696	-0.103627351	0.111795024
FANCC	0.013443946	0.113788324	-0.122756862
FANCD2	0.021192817	-0.10931184	0.117927551
FANCI	0.004434624	-0.135842843	0.146549669
FANCL	0.021431007	0.107706194	-0.116195352
FEN1	0.00713573	-0.127940837	0.138024844
GTF2H1	0.020075807	-0.109635925	0.11827718
GTF2H4	3.37E-06	0.214328168	-0.231221029
INO80C	0.017749556	-0.111841635	0.120656739
MDC1	0.042617574	0.095275714	-0.102785129
MUTYH	0.040772495	0.095478393	-0.103003784
NFRKB	0.002788265	0.138511415	-0.149428571
PARP2	0.00411484	0.134869937	-0.14550008
PCNA	0.002844698	-0.142599687	0.153839071
POLE	0.026184095	0.104749878	-0.113006026
PRPF19	0.029342079	-0.102880734	0.11098956
RAD1	0.046810852	-0.093702158	0.10108755
RAD51AP1	0.031127262	-0.102810912	0.110914235
RBBP8	0.024392086	-0.105786426	0.114124273
REV1	0.000253648	0.170397492	-0.183827837
RNF168	0.00072464	-0.158764688	0.171278161
RPA1	0.032319255	-0.100279107	0.108182879
RUVBL1	0.03174482	-0.101103648	0.109072408
SUMO3	0.005093212	-0.130476075	0.140759904
UBE2N	0.028733437	-0.103123008	0.11125093
UBE2T	0.026203703	-0.10546642	0.113779044
USP10	0.002250907	-0.142820558	0.154077351
XRCC3	0.005761013	0.129838086	-0.14007163
YWHAE	0.006637241	-0.127494558	0.13754339

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