Supplementary Online Information

MUFFINN: cancer gene discovery via network analysis of somatic mutation data

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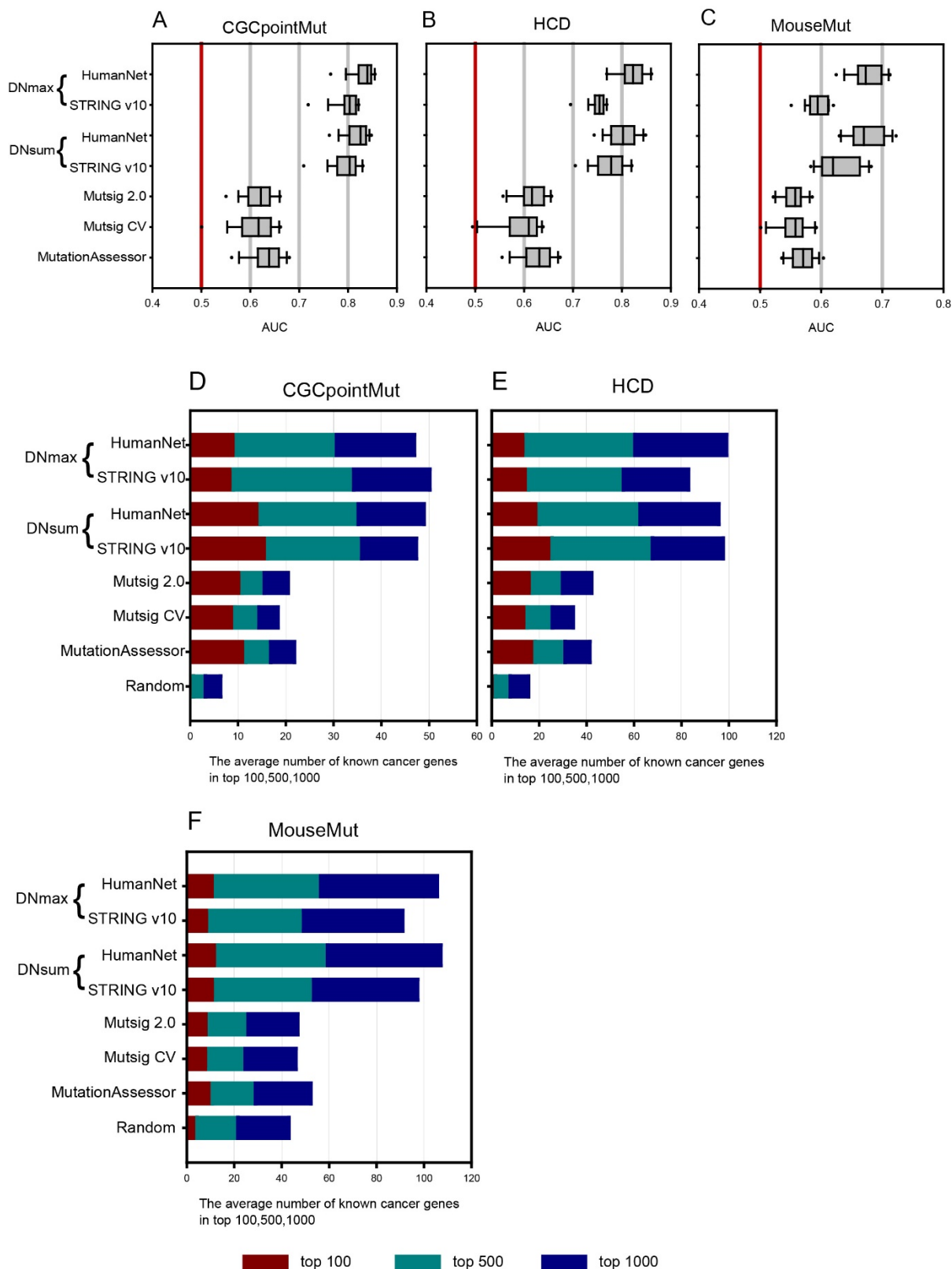
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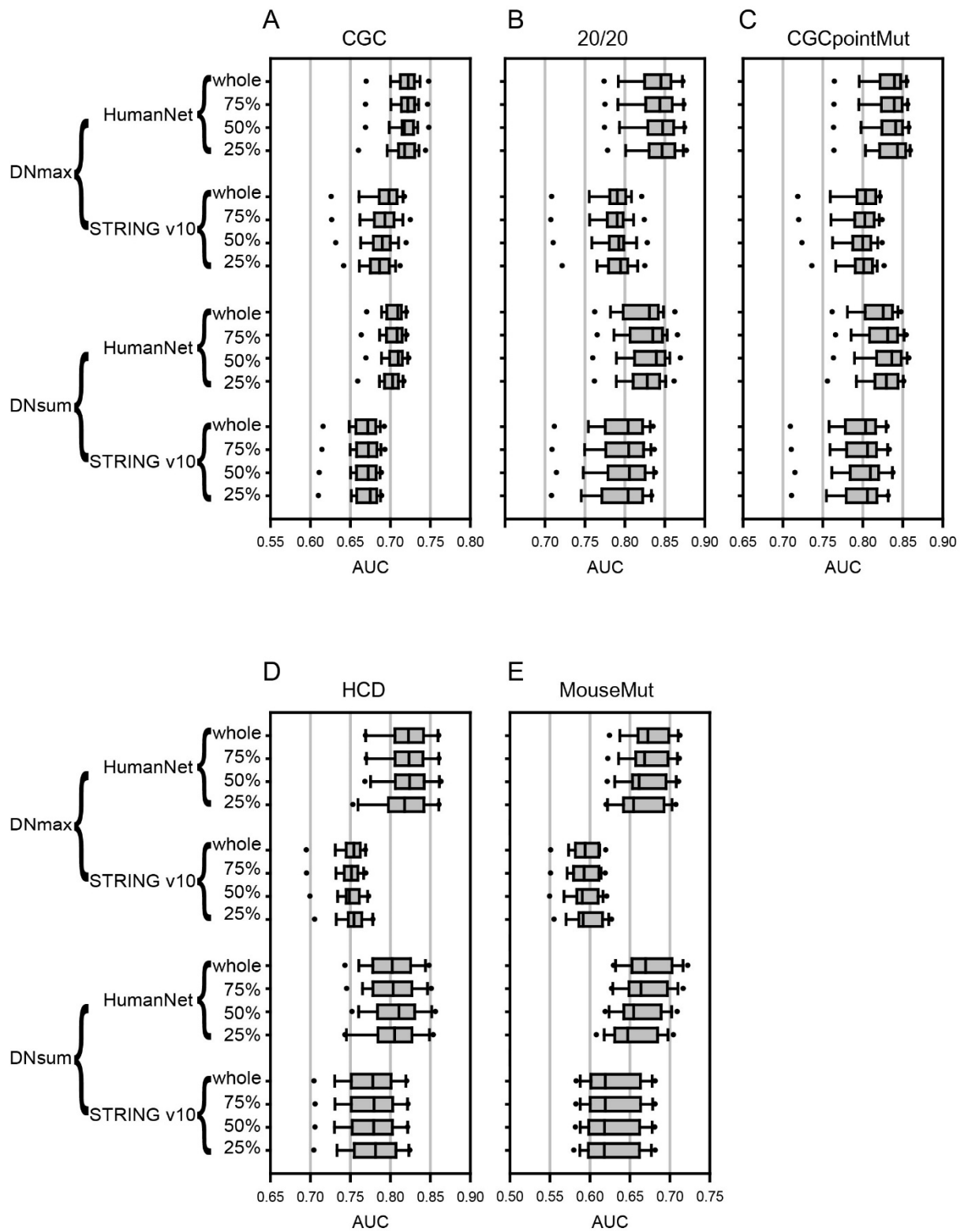
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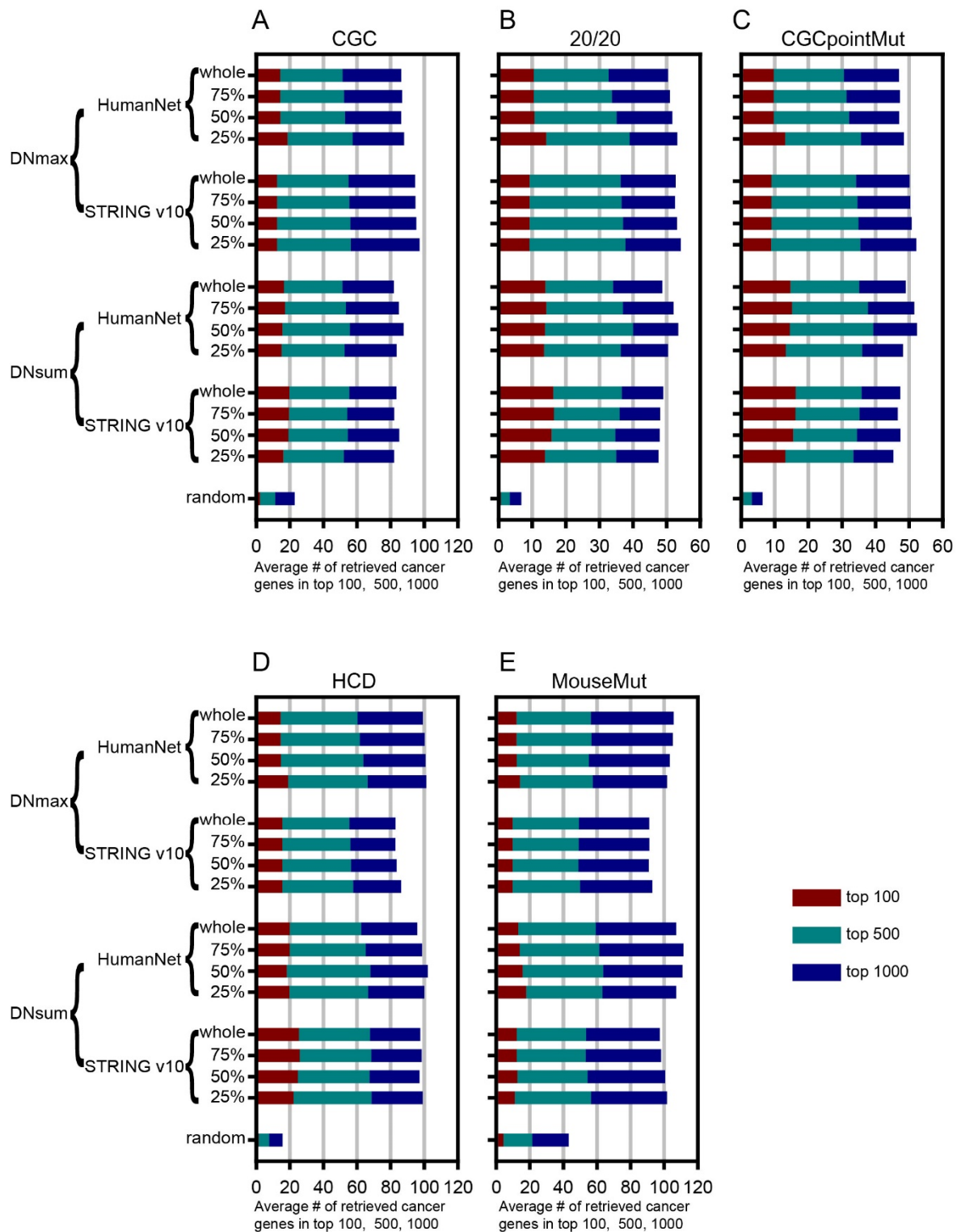
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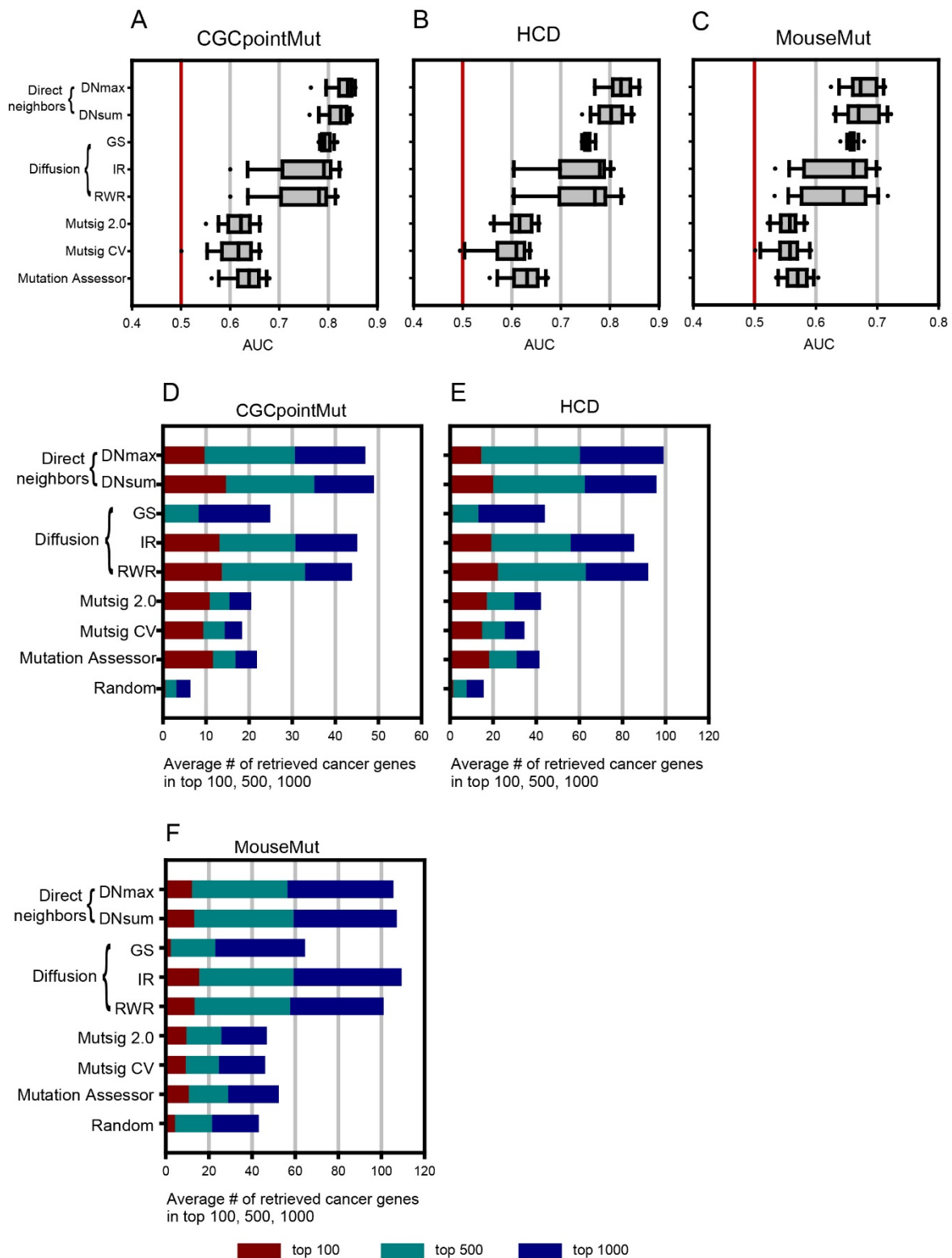
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Supplementary Figure S5. Distribution of AUC for 18 type and the pan-cancer sample (red triangular dots) by MUFFINN using direct neighbours on HumanNet based on cancer ge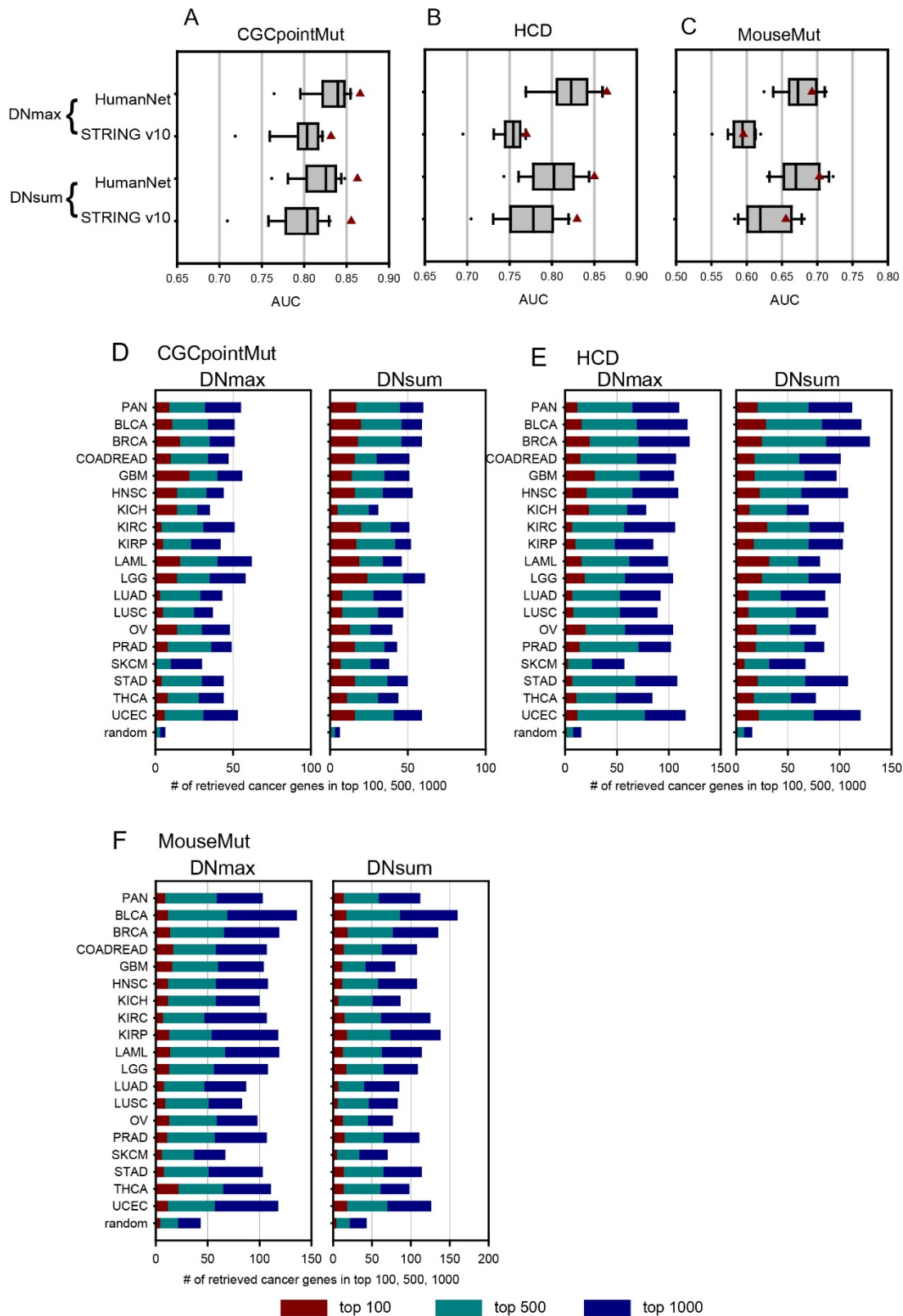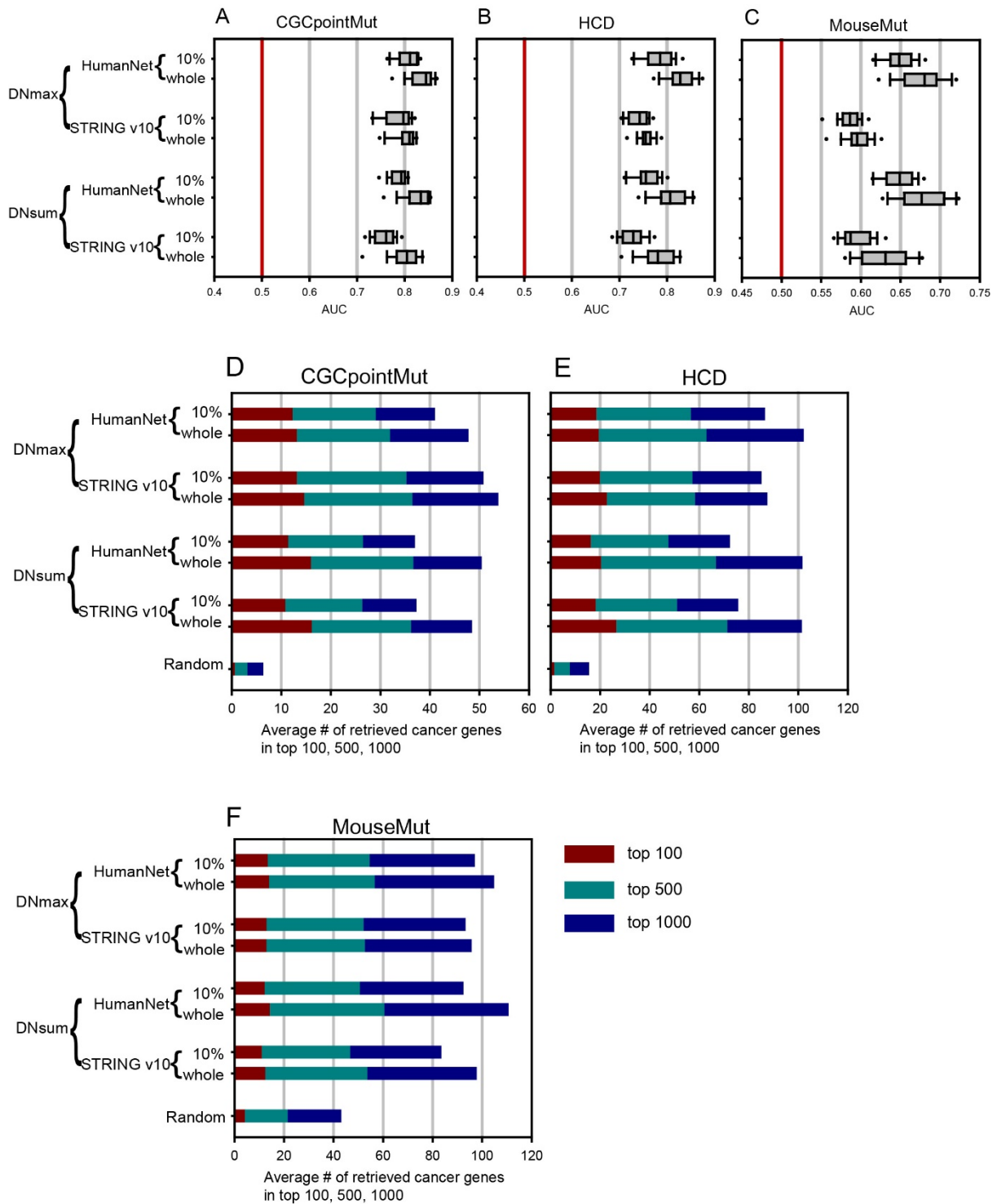nes annotated by (A) CGCpointMut, (B) HCD, and (C) MouseMut. The number of retrieved known cancer genes in top 100, 500, 1000 candidates for the pan-cancer and 18 type samples by MUFFINN using direct neighbours on HumanNet based on cancer genes annotated by (D) CGCpointMut, (E) HCD, and (F) MouseMut.

Supplementary Figure S6. Comparison of AUC distribution for 18 types by MUFFINN using direct neighbours between using whole patient and 10% samples based on cancer genes by (A) CGCpointMut, (B) HCD, and (C) MouseMut. Each box plot for 10% sample is based on 18 average AUC scores of 100 random sampling for each of 18 types, and that for whole sample is based on 18 AUC scores for each type. Comparison of the number of retrieved known cancer genes in top 100, 500, 1000 candidates for 18 types by MUFFINN using direct neighbours between using whole patient and 10% samples based on cancer genes by (D) CGCpointMut, (E) HCD, and (F) MouseMut. Each box plot for 10% sample is based on 18 average AUC scores of 100 random samples and that for whole sample is based on 18 AUC scores for each type.
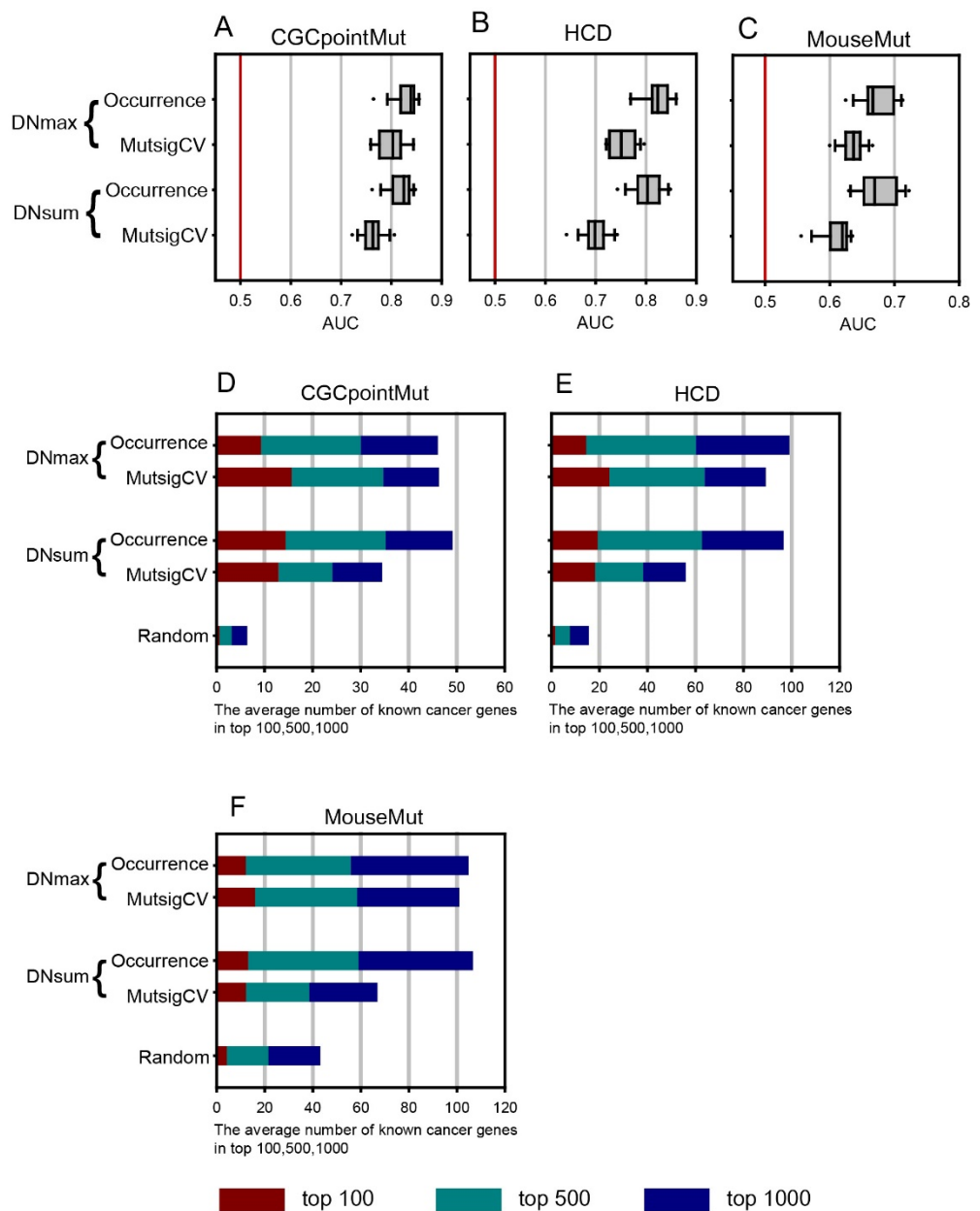
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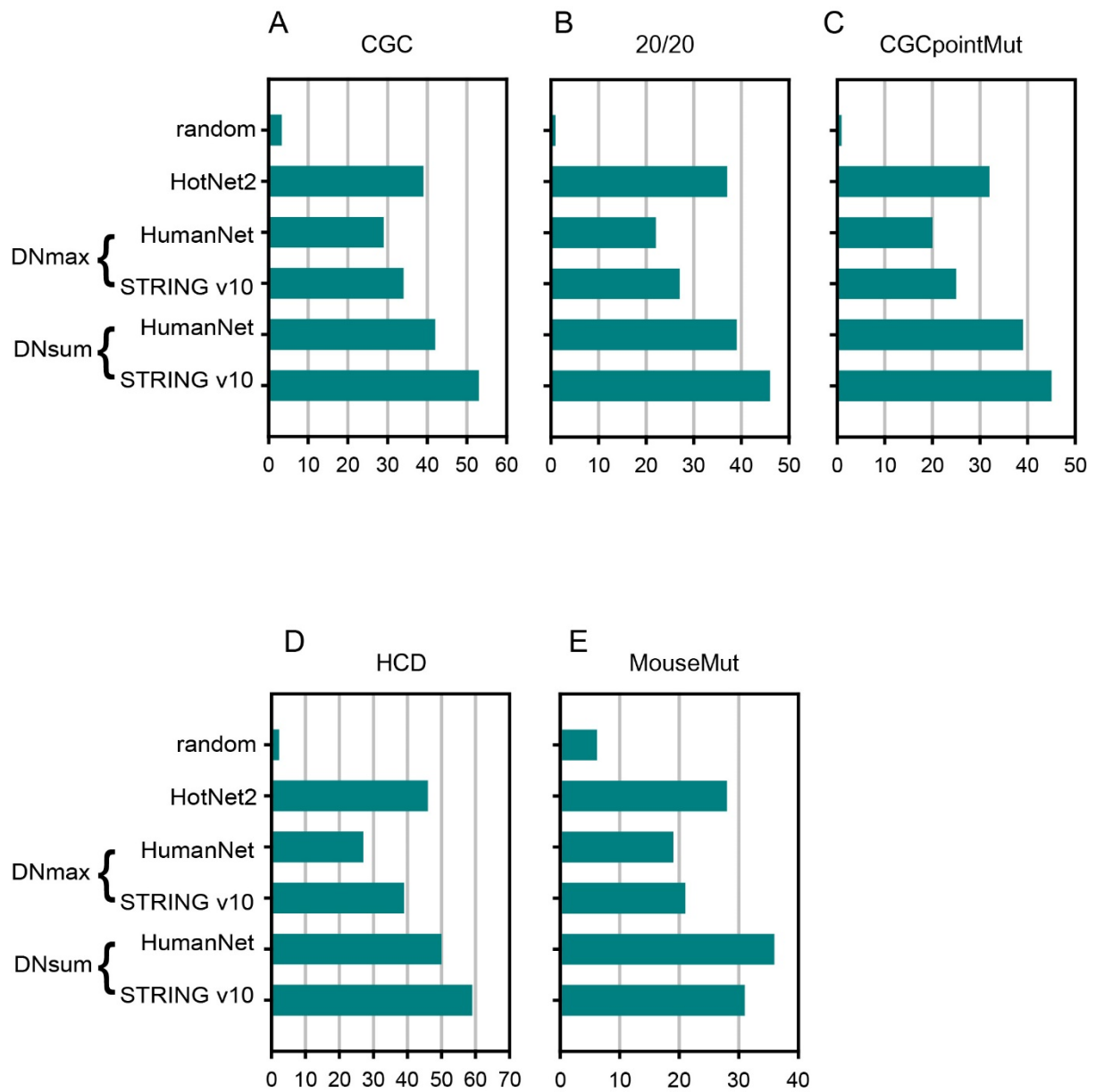
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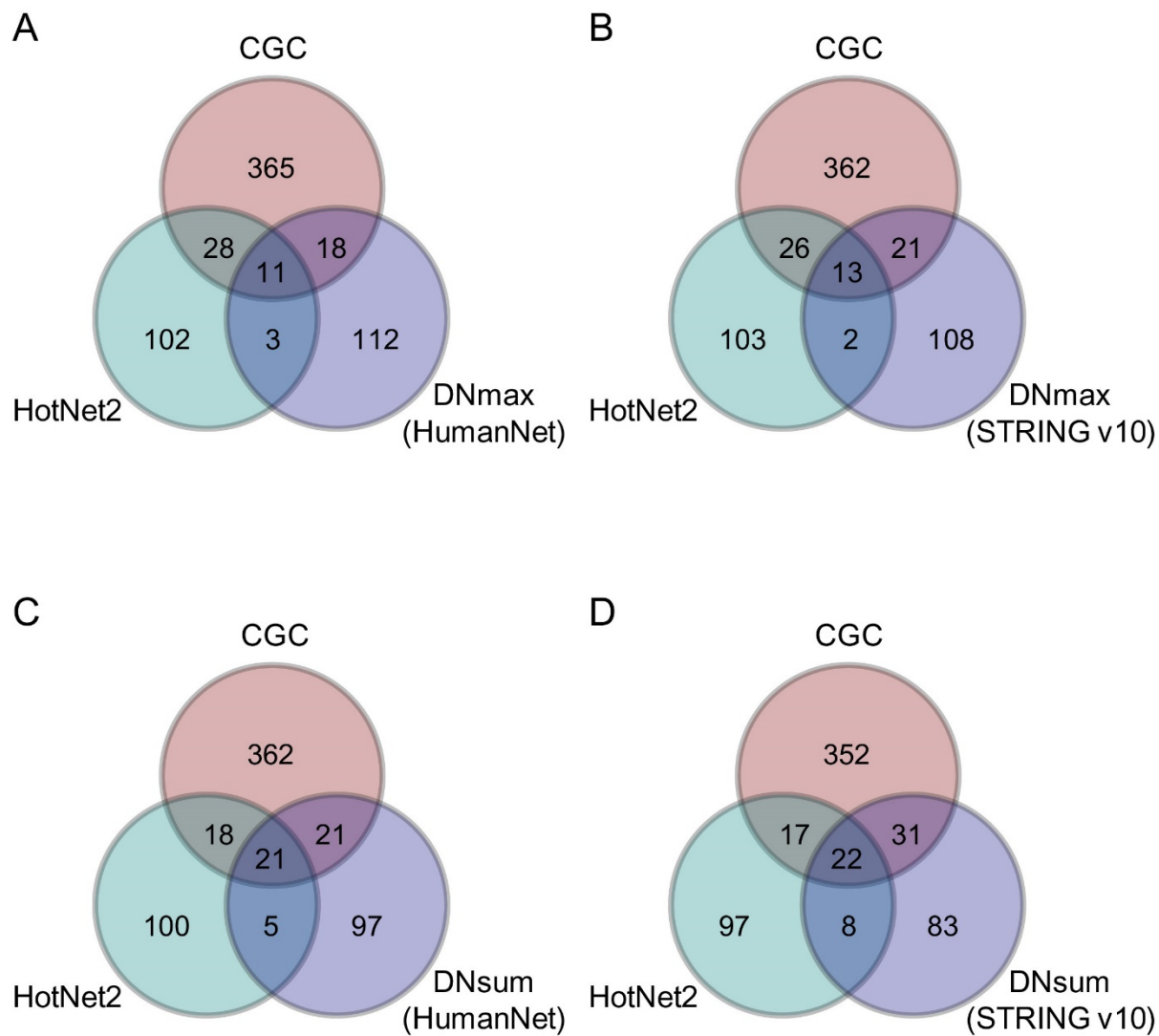
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Supplementary Table S1. 199 candidate cancer genes not identified by gene-centric methods but prioritised by MUFFINN.

Gene symbol	Supportive cancer type (Key type is marked by underline)	DNmax score (for the key type)	DNsum score (for the key type)	Class	Evidence/Implication	Ref.
TTN	COADREAD,KIRC,LGG,THCA,UCEC	0.9995	1.0000	5		
NEB	BLCA,COADREAD,GBM,KIRP,PRAD,UCEC	0.9991	0.8105	4	Nebulin(protein) was also strongly expressed in the pancreatic juice of pancreatic cancer patients.	[1]
MAEA	KICH	0.9738	0.3842	5		
ISM2	KICH	0.9710	0.3679	5		
CACNA1A	BLCA,COADREAD,GBM,HNSC,LUAD,SKCM,STAD	0.9707	0.3339	4	It was identified as novel tumor suppressor candidates methylated in lung tumors.	[2]
SNED1	KICH,KIRP,STAD	0.9596	0.4316	4	High expression of SNED1 correlates with poor outcome for ER(-)/PR(-) breast cancer patient.	[3]
OBSCN	BLCA,KIRP,LUSC,PRAD,STAD,UCEC	0.9495	0.8506	2	A germline nucleotide variant of OBSCN could be involved in cancer predisposition.	[4]
MYOM2	BRCA,COADREAD,KIRP,LUSC,PRAD,STAD,UCEC	0.9431	0.1309	4	Downregulated in breast cancer	[5]
ANK1	COADREAD,HNSC,LUSC,STAD,UCEC	0.9370	0.1858	3	Mapped to deleted region in colorectal cancer	[6]
ANKRD1	BRCA,HNSC,KIRP,LUSC,PRAD,STAD	0.9199	0.0817	4	High expression of ANKRD1 in ovarian carcinoma is associated with poor survival.	[7]
MYBPC3	BLCA,BRCA,COADREAD,HNSC,STAD	0.9104	0.0822	5		
ANKRD23	BLCA,COADREAD,HNSC,LUAD,LUSC	0.8990	0.0603	5		
IGF1R	BRCA,UCEC	0.8984	0.2164	4	miR-133a functions as a tumor suppressor in gastric cancer by repressing IGF1R	[8]
VBP1	KIRC	0.8954	0.0774	4	Differentially expressed in the uveal melanoma cell lines	[9]

Gene	Cancer Types	Score 1	Score 2	Level	Description	Ref
DNMT3L	LAML	0.8954	0.1886	4	DNA methylation profile at DNMT3L promoter is a promising biomarker for cervical cancer.	[10]
MAPK1	THCA	0.8924	0.2236	4	Tumor-suppressive role of miR-378 might be achieved by the direct interaction with MAPK1.	[11]
MAP2K2	THCA	0.8872	0.1207	1	Newly added to CGC	[12]
RBX1	KIRC	0.8840	0.0779	4	Aberrant expression of RBX1 is correlated to gastric cancer patient survival time.	[13]
COQ7	BRCA	0.8610	0.0648	5		
MYOM1	BLCA,COADREAD,KIR`P,LUAD,LUSC,PRAD,STAD	0.8373	0.1385	3	One of the targets of the viral DNA integration for the hepatitis B virus (HBV)-related hepatocellular carcinomas (HCCs).	[14]
PRG4	COADREAD,KIRP,LUAD,LUSC,STAD,UCEC	0.8258	0.1136	5		
HIST3H3	LAML	0.8188	0.1007	5		
PPP2R2A	THCA	0.8178	0.1272	3	Somatic deletion of PPP2R2A plays an important role in prostate cancer susceptibility.	[15]
REST	BLCA,COADREAD,KIRP,PRAD,STAD,UCEC	0.8143	0.1072	1	REST acts as a tumor suppressor and plays an oncogenic role based on the type of cancer.	[16]
NCL	LAML	0.8129	0.1052	4	NCL regulates the expression of a specific subset of miRNAs which are causally involved in breast cancer initiation, progression, and drug resistance.	[17]
MYH6	BLCA,COADREAD,LUSC,UCEC	0.8090	0.1457	5		
PPM1K	COADREAD,KIRP,LAML,THCA,UCEC	0.8077	0.2561	5		
USP33	KIRC	0.8068	0.1538	4	USP33 suppresses tumor by mediating the inhibitory function of	[18]

					Slit-Robo signaling on for colorectal cancer cell migration.	
CSF2RB	LAML	0.8038	0.1515	2	CSF2RB rs16997517 was directly related to pollen allergies in controls and to reduced squamous cell cervical cancer risk.	[19]
AEBP1	BLCA,LUSC,PRAD,STAD,UCEC	0.7942	0.1861	4	Its promoters are densely methylated in the rat prostate cancer cell lines.	[20]
YWHAB	THCA	0.7938	0.1668	1	It is known to play a key role in cellular proliferation and oncogenic transformation and has been reported to be involved in the development of breast cancer.	[21]
MCC	COADREAD	0.7818	0.1433	1	MCC mutations can drive colon carcinogenesis in the mouse and in vitro experiments.	[22]
CYCS	KICH	0.7790	0.3876	5		
MAP1B	BLCA,KIRP,LUSC,PRAD	0.7782	0.1990	5		
FLT4	LAML	0.7754	0.1433	1	Newly added to CGC	[12]
MYH7	BLCA,COADREAD,LUSC,STAD,UCEC	0.7709	0.2417	5		
CCT3	KIRC	0.7558	0.0743	4	Its expression is significantly elevated in hepatocellular carcinoma.	[23]
CAB39	KIRC	0.7549	0.0691	4	Known to play a critical role in regulating a biochemical balance between rapid proliferation and invasion in the presence of metabolic stress in microenvironment in glioblastoma.	[24]
UBE2I	GBM,HNSC,KICH,LAML,LGG,OV	0.7544	0.0888	4	Showed distinct expression patterns in histological types of epithelial ovarian cancer.	[25]

TCAP	COADREAD,LUAD,LUSC,STAD,<u>UCEC</u>	0.7346	0.0520	3	Belongs to amplicon on chromosome 17q21 which is frequently amplified in breast tumor.	[26]
PPM1B	COADREAD,KIRP,LAML,PRAD,<u>UCEC</u>	0.7313	0.2854	5		
ARHGEF7	<u>LAML</u>	0.7296	0.1368	4	Arhgef7 protein is a positively regulate Hippo pathway of which inactivation contribute to cancer.	[27]
ZBTB18	<u>LAML</u>	0.7269	0.1891	5		
CAPN3	COADREAD,KIRP,STAD,<u>UCEC</u>	0.7111	0.1160	4	Activated Capn3 leads to the overexpression of E2F3, which in turn could be responsible for urothelial tumor cell proliferation.	[28]
LIF	<u>LAML</u>	0.7102	0.1308	1	It is known to play an important role in inducing cancer cachexia.	[29]
HIF1A	BLCA,<u>BRCA</u>,GBM,HNSC,LGG,OV	0.7102	0.0754	2	Polymorphism in HIF1A contribute to the risk of digestive tract cancer	[30]
GRB2	<u>GBM</u>,KIRP,LAML,THCA	0.7091	0.1829	4	Key molecule in intracellular signal transduction and a therapeutic target for solid tumor invasions and metastasis	[31]
UBE3A	BRCA,<u>HNSC</u>,LGG,OV	0.7049	0.0829	4	UBE3A plays an important role in negating the consequences of p53 activation on ERK pathway which are often deregulated in cancer	[32]
IRS2	<u>BRCA</u>	0.7012	0.0815	4	Contribute to tumor progression in Pten(+/-) mice by stimulating both Myc and DNA synthesis	[33]
IL3	<u>LAML</u>	0.6827	0.1426	3	IL3/IgH fusion is identified in cutaneous lymphoma cell	[34]
MDH1	<u>LGG</u>	0.6810	0.1011	5		
PPM1L	BLCA,KIRP,<u>LAML</u>,PRAD,STAD,THCA	0.6802	0.1949	4	The 3'UTR of PPM1L transcript was down-	[35]

					regulated more than two-folds in tumors compared to matched mucosa.	
LIN7C	GBM	0.6799	0.0680	5		
NR1I2	BRCA	0.6797	0.0885	2	Common polymorphisms of regulator gene NR1I2 could be implicated in lymphoma risk.	[36]
SPTBN4	BLCA,COADREAD,KIRP,UCEC	0.6786	0.2689	5		
TRDMT1	LAML	0.6773	0.2000	4	Aberrant tRNA post-translational modification including methylation has been implicated in cancer, and TRDMT1 methylates tRNA.	[37]
WISP2	LAML	0.6687	0.1895	1	WISP-2 is relevant to tumorigenesis and malignant transformation, particularly in breast cancer, colorectal cancer and hepatocarcinoma.	[38]
CASK	GBM	0.6630	0.1061	4	CASK overexpression is associated with an unfavorable prognosis in colorectal cancer.	[39]
APBA2	GBM	0.6630	0.0781	4	Aberrant APBA2 methylation predict peritoneal micrometastasis for gastric cancer patients.	[40]
MYH3	BLCA,STAD,UCEC	0.6582	0.2644	5		
IDH3G	LGG	0.6521	0.0951	5		
IDH3A	LGG	0.6382	0.0971	4	Differentially expressed (down regulated) by chromosomal aneuploidy affect in colorectal cancer cells.	[41]
USP7	BRCA,PRAD	0.6343	0.0979	4	Plays an important role in the regulation of lung cancer development	[42]
ACTN1	BLCA,COADREAD,KIRP,STAD,UCEC	0.6291	0.1478	4	Is known as tumor specific splice variant in many type of cancer	[43]

CALM1	BRCA,COADREAD,KIRP,UCEC	0.6277	0.6050	4	Differentially Expressed in non-small cell lung cancer	[44]
MYH4	BLCA,COADREAD,STAD,UCEC	0.6269	0.2019	5		
HDAC1	LAML	0.6224	0.3091	1	Regulates cell proliferation in human myeloid leukemia cell	[45]
MYH8	BLCA,COADREAD,STAD,UCEC	0.6159	0.1917	5		
FHL2	BLCA,COADREAD,STAD,UCEC	0.6126	0.1222	4	Interacts with a variety of transcription factors known to be involved in tumor development and expression in deregulated in cancer.	[46]
PTPN6	LAML	0.6069	0.1488	4	Both the PTPN6 transcripts and proteins were overexpressed in ovarian epithelial carcinoma cell lines	[47]
APEX1	BLCA,GBM,HNSC	0.6058	0.0853	2	Germline variants in APEX1 increases the risk of cancer development by contributing apurinic/apyrimidinic site accumulation in DNA.	[48]
NRF1	BLCA,STAD,UCEC	0.6052	0.0737	4	Regulate NOR1 promoter which is a candidate tumor suppressor gene.	[49]
ATR	BLCA,BRCA,GBM,OV	0.5998	0.2001	1	Newly added to CGC	[12]
TP53BP2	HNSC,OV	0.5977	0.0757	5		
GALNT11	KICH	0.5972	0.3700	5		
HOXA5	COADREAD	0.5928	0.0747	4	miR-1271 regulates non-small-cell lung cancer cell proliferation and invasion, via the down-regulation of HOXA5.	[50]
TRIM63	BLCA,COADREAD,STAD,UCEC	0.5926	0.0656	5		
ING1	BRCA,HNSC	0.5918	0.0860	4	Recently reported as a validated target of a miRNA let-7b which suppresses gastric cancer malignancy	[51]

PPM1A	STAD	0.5912	0.2530	4	Loss of PPM1A expression enhances invasion and epithelial-to-mesenchymal transition in cancer.	[52]
ELK1	THCA	0.5898	0.1847	4	Binding of Est1 to CIP2A promoter is required for expression of CIP2A which has been identified as proto-oncogene in various types of human cancer.	[53]
PIN1	BLCA,BRCA,OV	0.5868	0.0917	4	Prevalently over-expressed in kinds of breast cancer cell lines and tissues.	[54]
MYH2	BLCA,COADREAD,STAD	0.5830	0.2302	5		
CHEK1	HNSC,OV	0.5822	0.0848	4	CHEK1 protein levels were significantly associated with higher tumor stage, higher mitotic index, pleomorphism and lymphovascular invasion.	[55]
EFEMP2	BLCA,GBM,OV	0.5818	0.0733	2	SNP in the EFEMP2 gene was associated with increased risk in breast cancer.	[56]
PRMT1	BRCA,HNSC	0.5817	0.0926	4	Overexpressed in Non-Small Cell Lung Carcinomas and are involved in proliferation in lung cancer	[57]
SREK1	LAML	0.5811	0.1085	5		
XYLB	COADREAD,KIRP,STAD	0.5808	0.0903	5		
SH3BP2	LAML	0.5801	0.1309	5		
SIRT1	BLCA,BRCA,OV	0.5795	0.1070	1	SIRT1 could act as either a tumor suppressor or tumor promoter depending on its targets in specific signaling pathways or in specific cancers.	[58]
RPS6	LAML	0.5781	0.1102	4	Reduced Rps6 phosphorylation and activation of p53 results	[59]

					in selective elimination of leukemia cells.	
NOP2	LAML	0.5757	0.2351	5		
ARHGEF4	COADREAD	0.5744	0.0736	4	Inactivation of ARHGEF4 can promote tumorigenesis.	[60]
GK	BLCA,COADREAD,STAD	0.5710	0.1078	5		
GK2	STAD	0.5710	0.0849	5		
EPS8	GBM	0.5700	0.0745	4	Overexpressed in >60% of human breast cancer sample and knock down of Eps8 inhibits breast cancer cell migrations	[61]
GK5	BLCA,COADREAD,STAD	0.5682	0.0593	5		
E4F1	HNSC	0.5678	0.0739	5		
MRI1	LGG	0.5662	0.0996	5		
C1QBP	LGG	0.5657	0.1086	4	Critical for prostate cancer cell proliferation and may be a novel marker of clinical progression in prostate cancer.	[62]
CAT	BRCA	0.5639	0.0692	2	SNPs of CAT have limited associations with the risk of prostate cancer in Chinese populations.	[63]
COL4A5	GBM	0.5638	0.1568	5		
FGGY	BLCA,UCEC	0.5616	0.0735	5		
AK2	LGG	0.5614	0.1044	4	AK2 deficiency enhances cell proliferation and induces tumor formation.	[64]
CKS1B	THCA	0.5614	0.1263	4	Frequently overexpressed in different tumor subtypes.	[65]
STK4	HNSC	0.5604	0.0660	4	miR-18a acts as an oncomiR targeting STK4 in prostate cancer.	[66]

Gene	Cancer types				Description	Ref
SUV39H1	LAML	0.5601	0.2080	4	Pin1-mediated reduction of SUV39H1 stability contributes to convey oncogenic signals for aggressiveness of human breast cancer.	[67]
ILKAP	LAML	0.5600	0.1858	3	Frequently observed allelic loss at chromosome 2q37 regions contains ILKAP	[68]
MYH13	BLCA,COADREAD,STAD,UCEC	0.5593	0.1567	5		
YWHAZ	KIRP,THCA,UCEC	0.5586	0.2410	4	YWHAZ knock-down significantly affected cell proliferation and migration in the prostate cancer cells.	[69]
TGFBR1	UCEC	0.5584	0.2971	3	Tgfbr1 haploinsufficiency was associated with early onset adenocarcinoma and increased tumor cell proliferation.	[70]
MYH1	BLCA,COADREAD	0.5580	0.1696	5		
DCC	HNSC	0.5575	0.2794	4	Known as putative candidate tumor suppressor and inactivated by promoter hypermethylation in cancer	[71]
TP53BP1	BLCA,GBM	0.5575	0.1184	2	TP53BP1 rs2602141 A/C was associated with cancer risk in Asians.	[72]
YWHAQ	THCA	0.5558	0.1408	5		
EMILIN1	BLCA,UCEC	0.5537	0.0923	5		
DDB2	COADREAD,STAD	0.5535	0.0751	4	Overexpressing DDB2 in human ovarian cancer cells suppressed its capability to recapitulate tumors in athymic nude mice	[73]
PLK1	LAML	0.5512	0.1433	1	known as oncoprotein in leukemia	[74]
ANKRD2	HNSC,STAD	0.5492	0.0604	5		
DMBT1	GBM	0.5491	0.1243	3	DMBT1 expression is frequently lost in lung	[75]

					cancer due to gene deletion, suggesting that inactivation of DMBT1 may play an important role in lung tumorigenesis.	
MUC4	KIRP	0.5479	0.8303	4	MUC4 is an important tumor marker overexpressed in lung cancer and uniquely expressed in pancreatic ductal adenocarcinoma.	[76]
MYBPC1	BLCA,UCEC	0.5447	0.0877	4	MYBPC1 mRNA expression were highly correlated between CUB (contralateral unaffected breasts) and matched tumor samples.	[77]
HIBADH	LGG	0.5440	0.1011	5		
PARP1	BRCA,HNSC	0.5420	0.1853	4	PARP1 expression was correlated to clinicopathological variables, outcome and expression of other key DNA repair proteins expression in breast cancer.	[78]
ERCC3	BLCA,OV	0.5298	0.0756	5		
S100B	OV	0.5294	0.0743	4	S100B promotes glioma growth.	[79]
SSTR3	OV	0.5268	0.0701	4	The expression of SSTR3 protein was significantly lower in gastric cancer compared with normal mucosa.	[80]
ACADSB	LGG	0.5266	0.1058	5		
IRS1	BRCA	0.5255	0.1031	4	miR200c plays crucial roles in prostate cancer by post-transcriptional regulation of IRS1.	[81]
SYNE1	BLCA,BRCA,COADREAD,KIRC,STAD,UCEC	0.5247	0.9554	5		
PPM1G	LAML	0.5242	0.1970	4	PPM1G downregulate USP7S which plays a major role in regulating genome stability and cancer prevention by controlling the key	[82]

					proteins involved in the DNA damage response.	
FIZ1	LAML	0.5214	0.1357	5		
PCYT1A	LGG	0.5194	0.1108	5		
KAT2B	HNSC	0.5181	0.0996	4	KAT2 proteins are differentially expressed in pancreatic cancer	[83]
SHPK	BLCA,STAD	0.5144	0.0583	5		
TP63	BRCA	0.5135	0.0707	2	rs10937405-G allele and rs4488809-G allele in TP63 might be risk-conferring factors for the development of lung cancer, especially for East Asian populations.	[84]
FN1	KIRC,KIRP	0.5125	0.2101	3	FN1 is a novel fusion partner of ALK in myofibroblastic tumor.	[85]
CD82	BRCA,HNSC	0.5116	0.0686	4	Upregulation of CD82 in gastric cancer cells resulted in the inhibition of gastric cancer migration and invasion.	[86]
EIF2AK2	LAML	0.5032	0.1033	4	Generally considered to have a tumor suppressor function, and some clinical data show a correlation between suppressed or inactivated EIF2AK2 and a poor prognosis for several cancers.	[87]
PHF17	KIRC	0.5015	0.0967	5		
MUC16	LUSC	0.4815	0.9759	4	MUC16-carboxy terminal mediated enrichment of cancer stem cells is partly responsible for tumorigenic, metastatic and drug-resistant properties of pancreatic cancer cells.	[88]
HUWE1	KIRP	0.4732	0.7558	4	Huwe1/Mcl-1 complex has a significant role in increasing the stability of Mcl-1 in breast cancer cells and	[89]

					increased resistance to apoptosis.	
RYR2	BLCA,BRCA,COADREAD,HNSC,KIRP,PRAD,STAD,UCEC	0.4727	0.5499	4	RYR2 was the most prominent change in gene expression between the epithelial and mesenchymal-like states.	[90]
SP1	BLCA,COADREAD,HNSC,KIRP,UCEC	0.3908	0.7289	4	SP1 upregulates TINCR which contributes to the oncogenic potential of gastric cancer.	[91]
PKD1	KIRP	0.3835	0.6335	4	PDK1 is critical for Lin28A- and Lin28B-mediated cancer proliferation both in vitro and in vivo.	[92]
UBR4	KIRP	0.3660	0.6418	5		
RPA1	BLCA,BRCA,KIRP,STAD,UCEC	0.3527	0.6667	5		
DNAH5	COADREAD,STAD	0.3421	0.7936	3	DNAH5 is located in 5p amplification region which is related to tumor progression in urinary bladder cancer.	[93]
LRP1B	COADREAD	0.3397	0.8203	4	LRP1B inactivation results in changes to the tumor environment that confer cancer cells an increased growth and invasive capacity.	[94]
RYR3	UCEC	0.3355	0.5951	4	SNP in microRNA which targets RYR3 affects breast cancer risk.	[95]
SYNE2	BLCA	0.3277	0.6495	5		
ANK2	BLCA,KIRP	0.3186	0.5689	4	Silencing of ANK2 expression reduced the malignant phenotype of pancreatic cancer cells.	[96]
PLEC	BLCA	0.3156	0.6551	4	Plectin involved in critical molecular process (invadopodia) for cancer cell invasion and extravasation for metastasis.	[97]
LRP2	BLCA,BRCA,COADREAD,KIRC,LGG,UCEC	0.2926	0.8180	2	Common genetic variation within the lipoprotein-related protein 2 (megalin) gene could alter both	[98]

					risk of recurrence/progression and prostate-specific cancer mortality.	
BIRC6	BLCA,KIRP	0.2911	0.5548	4	Plays a role in prostate cancer progression and treatment resistance.	[99]
FAT4	BLCA	0.2864	0.8503	2	Nonsynonymous variants rs1014867 and rs1039808 of FAT4 contribute to esophageal cancer susceptibility.	[100]
USH2A	COADREAD,KIRC	0.2826	0.5910	5		
MRE11A	BLCA,COADREAD,GBM,HNSC,LGG,LUSC,PRAD,SKCM,STAD,THCA,UCEC	0.2771	0.9920	2	MRE11A is intermediate-risk breast cancer susceptibility genes.	[101]
APOB	UCEC	0.2633	0.5607	2	Polymorphism of APOB is associated with increased risk for development of gallbladder cancer.	[102]
TAF9	BLCA,COADREAD,KIRP,STAD	0.2512	0.8256	4	TAF9 is downregulated or deleted in 98% of high-grade serous ovarian cancers.	[103]
FLG	BLCA	0.2475	0.7849	3	Amplification of flg gene correlate with loss of heterozygosity at 17p.	[104]
HMCN1	BLCA,GBM,OV,UCEC	0.2348	0.7444	5		
DLG2	BLCA,BRCA,STAD	0.2345	0.6139	4	DLG2 has decreased expression in the tumor samples compared to their matched normal tissues.	[105]
MACF1	BRCA,KIRC,UCEC	0.2237	0.5865	5		
DYNC2H1	BLCA,COADREAD,KIRC,STAD	0.2122	0.6813	2	rs716274 SNP in the region of downstream of DYNC2H1 on chromosome 11q22.3 are associated with small-cell lung cancer survival.	[106]
ROBO1	KIRP	0.2063	0.5135	4	ROBO1 expression is significantly lost in primary and metastatic tumors.	[107]
YWHAG	BLCA,BRCA,COADREAD,KIRP,STAD	0.2033	0.8134	5		

DLG3	BLCA	0.2017	0.5169	4	DLG3 is down-regulated in glioblastoma.	[108]
LGALS1	BLCA,GBM,KIRP,LUAD,PRAD,SKCM,STAD	0.2009	0.8060	4	LGALS1 is significant prognostic factor, and could be potential therapeutic targets to improve pancreatic cancer survival.	[109]
SMAD9	COADREAD,KIRP,UCEC	0.1924	0.7917	4	Identified as a novel methylation marker is identified in gastric cancer.	[110]
CSMD1	STAD	0.1889	0.5156	4	Epigenetic silencing is contributing to the reduction in CSMD1 expression in squamous cancers.	[111]
PRKACA	BLCA,COADREAD,STAD	0.1858	0.8771	5		
DNAH3	BLCA	0.1840	0.5434	5		
DLG1	BLCA,KIRP	0.1831	0.5115	4	DLG1 is mislocalized during ocular carcinogenesis and its downregulation is involved in epithelial-mesenchymal transition in mouse.	[112]
DYNC1H1	BLCA,COADREAD,KIRC,STAD,THCA,UCEC	0.1814	0.9305	4	Protein levels of Dync1h1 were decreased in primary gallbladder cancer tissues.	[113]
CELSR3	BLCA	0.1806	0.5252	5		
DMD	STAD	0.1785	0.5903	5		
TAF9B	BRCA,STAD	0.1775	0.6007	5		
GPR98	BLCA	0.1697	0.5300	5		
PXDN	BRCA,COADREAD,STAD	0.1689	0.8652	4	The adhesion-promoting effects of HO-1 (promote growth and survival of neoplastic cells) were dependent on PXDN expression.	[114]
MSLN	BRCA,COADREAD,GBM,KIRP,LUSC,SKCM,STAD	0.1446	0.8006	4	MSLN is weak diagnostic classifiers, but may be useful in a	[115]

14

Gene	Cancers				Description	Ref
					diagnostic biomarker panel.	
SVEP1	BRCA,STAD	0.1386	0.6208	4	SVEP1 gene expression regulation may be involved in bone-cancer-microenvironment interactions.	[116]
SMARCA2	UCEC	0.1356	0.5294	4	Loss of SMARCA2 expression is a common feature among poorly differentiated tumors in clear cell renal cell carcinomas.	[117]
ATXN1	BLCA,HNSC,KIRP,LGG,UCEC	0.1320	0.7439	5		
PFDN5	BLCA,HNSC,UCEC	0.1309	0.9897	4	Showed significantly different expressions in peripheral blood cells of patients with hepatocellular carcinoma.	[118]
CUBN	HNSC	0.1233	0.5247	5		
DLG4	BRCA,STAD,UCEC	0.1166	0.6558	4	The results suggest that DLG4 may function as a tumor suppressor in the development of human papillomaviruses-associated cancers.	[119]
RFC1	BLCA,BRCA,UCEC	0.1142	0.5276	5		
PRKACB	BRCA,COADREAD,KIRP,UCEC	0.0954	0.6707	4	PRKACB is downregulated in non-small cell lung cancer (NSCLC) tissues and that upregulation of PRKACB may be an effective way to prevent the progression of NSCLC.	[120]
PKHD1L1	KIRC	0.0951	0.5220	3	Novel fusion transcript, SBF1-PKHD1L1 is identified in T-cell large granular lymphocyte leukemia.	[121]
DST	OV	0.0943	0.5420	5		
IGSF22	STAD	0.0754	0.5703	5		
DTNBP1	BRCA	0.0728	0.5595	5		

SLC30A1	HNSC,UCEC	0.0725	0.8546	5		
PTP4A3	KIRP	0.0725	0.5539	3	Deletion of PTP4A3 reduces the tumor-initiation ability in cancer in mice.	[122]
KLF17	BLCA,BRCA,COADREAD,HNSC,STAD	0.0671	0.6000	4	KLF17 may have an oncogenic role during endometrioid endometrial cancer progression via initiating epithelial-mesenchymal transition.	[123]
DROSHA	BRCA	0.0656	0.5625	4	Altered expression of Drosha may serve as markers for disrupted miRNA biogenesis in triple negative breast cancer.	[124]
CAMK1	COADREAD	0.0645	0.5498	5		
KLF7	BLCA,KIRP,STAD	0.0644	0.7994	4	Among diffuse type gastric cancers, signet ring cell carcinoma showed lower level of methylation for KLF7 compared to poorly differentiated carcinomas.	[125]
PPAPDC1B	COADREAD	0.0615	0.5276	3	PPAPDC1B is suggested to be a common driver in the 8p11-12 amplicon in cancer.	[126]

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