TSVdb: a web-tool for TCGA splicing variants analysis Supplymentary material

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1 The clinical variable distribution

Table S1: The clinical variable distribution Varaible Cancer type n gender PAAD; GBM; COAD; UVM; ACC; READ; 27 THYM; KIRC; DLBC; STAD; LUSC; LAML; KICH; KIRP; BLCA; PCPG; THCA; LUAD; ESCA; LGG; SKCM; MESO; CHOL; LIHC; HNSC; SARC; BRCA PAAD; GBM; UCS; COAD; UVM; ACC; 33 race READ; OV; THYM; KIRC; DLBC; STAD; LUSC; LAML; CESC; KICH; KIRP; BLCA; PCPG; PRAD; THCA; LUAD; ESCA; LGG; SKCM; UCEC; MESO; BRCA; TGCT; CHOL; LIHC; HNSC; SARC pr_receptor BRCA 1 2 number_pack_years_smoked LUSC; LUAD location_in_lung LUSC 1 ACC; TGCT; HNSC laterality 3 STADh_pylori_infection 1 gleason_stage PRAD overall_survival PAAD; GBM; UCS; COAD; UVM; ACC; 33 READ; OV; THYM; KIRC; DLBC; STAD; LUSC; LAML; CESC; KICH; KIRP; BLCA; PCPG; PRAD; THCA; LUAD; ESCA; LGG; SKCM; UCEC; MESO; BRCA; TGCT; CHOL; LIHC; HNSC; SARC masaoka_stage THYM 1 family_history_of_cancer PAAD 1 fab_morphology LAML 1 er_receptor **BRCA** 1 $as bestos_exposure$ **MESO** 1 THYM tumor_tissue_site 1 pathological_stage PAAD; COAD; UVM; ACC; READ; KIRC; 21 STAD; LUSC; KICH; KIRP; BLCA; THCA; LUAD; ESCA; SKCM; MESO; BRCA; TGCT; CHOL; LIHC; HNSC grade CESC; UCEC; LIHC UCS; UVM; OV; DLBC; ESCA; UCEC; HNSC clinical_stage 7 tumor_site SKCM 1 smoking_history LUSC; CESC; ESCA 3 LIHC risk_factor 1 reflux_history STAD 1 microsatellite_instability COAD; READ; STAD 3 history_of_colon_polyps COAD; READ 2 **BRCA** her2_receptor 1 alcohol_consumption ESCA; HNSC 2 2 number_of_pregnancies CESC; UCEC 2 menopause_status CESC; UCEC 2 kras_mutation LUSC; LUAD 3 histological_type COAD; READ; THYM

2 The data download format

Table S2: The data download format

Attribute	Example	Description
sampleID	"TCGA-3L-AA1B-01A"	TCGA sample id.
clinical_[clinical type]	"Primary Solid Tumor"	Clinical variables.
os_time	348	Overall survival time (day).
os_event	0	Overall survival event
		(0=live, 1=death).
gene_[gene name]	100.1234	Gene expression normalized
		read count.
isoform_[isoform id]	100.2345	Isoform expression normal-
		ized read count.
$exon/junction_[location]$	0.1102	Exon/junction usage value.
		Exon/junction usage is
		calculated by dividing ex-
		on/junction quantification
		value to mean exon/junction
		quantification value of that
		person for a specific gene

3 The query dialogs for choosing the tumor type

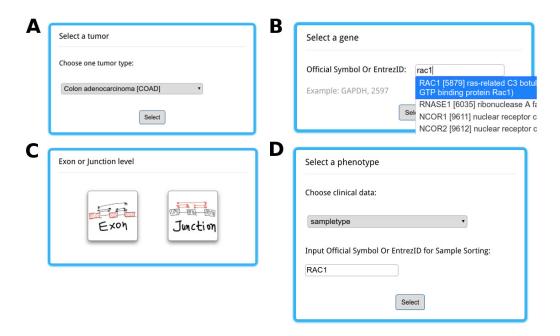


Figure S1: The query dialogs for choosing the tumor type (A), gene (B), exon/junction usage (C), phenotype and gene expression data that used to arrange samples in phenotype subgroups (D).

4 The procedures for calculating the RAC1 exon usage in colon adenocarcinoma

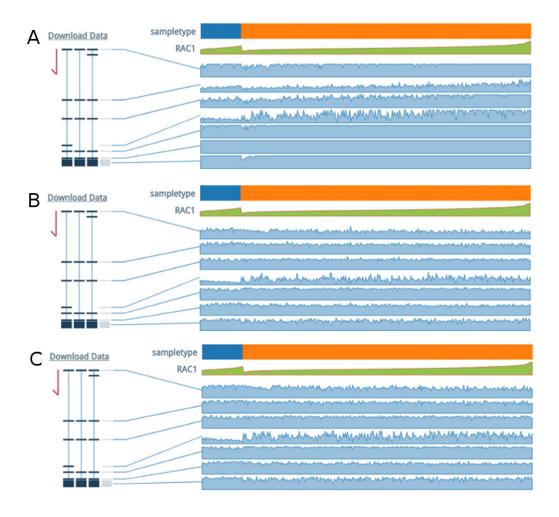


Figure S2: The procedures for calculating the RAC1 exon usage in colon adenocarcinoma. (A) Exon expression value (each peak represented for one sample value). (B) Exon usage value (the exon expression values were divided by gene expression). (C) The polished results of exon usage by diminishing the outlier effect.

5 The RAC1 junction usage in colon adenocarcinoma using TSVdb

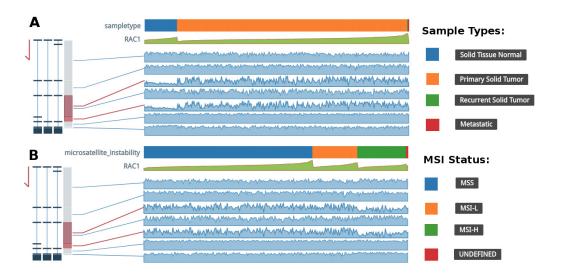


Figure S3: The RAC1 junction usage in colon adenocarcinoma using TSVdb. The different usage of junctions between sample types (A), and MSI status (B).

6 The Kaplan-Meier plots showing the associations for the RAC1 isoform uc003spw

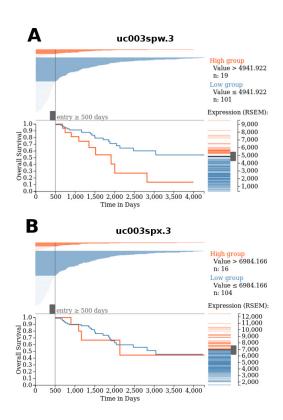


Figure S4: The Kaplan-Meier plots showing the associations for the RAC1 isoform uc003spw (A) and uc003spx.3(B) with patient overall survival after adjusting the onset.