Figure S13

A

Annotation (%)	Cerebellum				Cortex				FrontalCortex				Hippocampus				Hypothalamus				Esophagus				Kidney			
	Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level	
	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP
RefSeq	90.7	49.0	95.5	60.7	87.9	54.4	93.3	60.3	90.8	52.5	94.5	60.6	92.0	58.5	94.0	60.7	88.2	54.9	94.7	60.8	90.1	52.1	89.6	58.2	87.6	53.4	93.7	61.0
GENCODE (manual)	84.2	63.3	94.0	94.7	87.1	65.5	91.8	94.0	84.7	67.7	92.0	94.4	85.3	67.3	92.5	94.7	89.1	66.0	93.2	95.0	84.5	64.9	88.7	91.3	82.7	66.4	92.4	95.3
GENCODE (automatic)	94.0	31.2	94.7	23.4	84.1	33.4	96.1	24.5	88.0	34.1	96.7	22.5	94.1	33.9	95.1	25.6	92.4	35.6	96.5	24.5	89.4	32.4	96.8	24.7	86.1	35.3	96.2	23.6
PacBio (MCF7)	82.8	47.0	89.9	59.9	86.3	43.2	91.6	59.3	84.1	46.0	90.0	57.2	87.2	39.7	90.5	59.2	84.4	37.6	90.3	59.2	85.0	37.9	91.3	58.1	79.1	48.3	91.1	59.7
EST	.	.	77.7	78.2	.	.	76.2	78.0	.	.	77.0	78.1	.	.	76.6	78.3	.	.	77.1	78.5	.	.	74.0	76.0	.	.	76.5	78.9
RefSeq + GENCODE + PacBio + EST	.	.	80.9	95.3	.	.	79.2	94.7	.	.	80.1	95.1	.	.	79.7	95.3	.	.	80.3	95.6	.	.	79.4	92.0	.	.	79.5	95.8

Annotation (%)	Liver				Lung				Ovary				Pancreas				Prostate				Testis				Whole Blood			
	Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level	
	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP
RefSeq	90.3	51.5	92.4	60.7	91.2	49.6	95.9	58.9	88.8	49.6	93.8	60.5	90.9	50.9	94.0	59.2	91.3	49.2	95.6	59.9	93.7	50.3	98.2	57.6	93.0	45.4	95.9	56.9
GENCODE (manual)	83.4	67.4	91.0	94.7	81.4	64.2	94.6	92.0	86.4	64.2	92.2	94.2	84.5	67.3	92.3	92.2	86.3	63.7	94.1	93.5	88.7	64.4	97.6	90.8	89.7	59.4	94.8	89.3
GENCODE (automatic)	86.1	43.2	96.8	24.8	89.4	31.2	97.1	23.9	94.3	38.1	96.7	24.6	92.1	43.1	96.7	24.3	92.7	37.1	97.2	22.2	94.5	31.5	97.5	22.4	91.3	29.8	96.9	23.4
PacBio (MCF7)	82.7	40.1	91.1	60.0	83.1	39.0	91.4	58.1	83.8	38.8	89.2	59.5	84.9	41.7	91.4	58.8	84.0	37.7	90.4	58.7	84.6	38.3	89.1	56.9	88.3	36.0	91.5	57.1
EST	.	.	75.7	78.7	.	.	78.2	76.0	.	.	76.6	78.2	.	.	76.6	76.4	.	.	77.8	77.2	.	.	80.1	74.4	.	.	78.6	73.8
RefSeq + GENCODE + PacBio + EST	.	.	78.5	95.3	.	.	81.7	92.7	.	.	79.4	94.8	.	.	79.5	92.7	.	.	81.0	94.1	.	.	83.9	91.5	.	.	81.8	90.1

Annotation (%)	ESCA				HNSC				LIHC				LUAD				LUSC			
	Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level		Base level		Intron level	
	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP	SN	SP
RefSeq	91.1	45.2	96.4	56.8	88.6	51.9	98.1	59.9	91.4	51.4	98.4	58.5	87.7	46.9	96.3	59.7	89.4	50.8	97.6	59.6
GENCODE (manual)	88.0	60.6	96.5	90.2	89.2	57.0	98.0	95.0	88.3	55.9	97.7	92.2	86.9	52.1	98.6	94.9	89.1	54.8	97.8	94.6
GENCODE (automatic)	92.8	30.7	97.6	23.4	91.4	33.8	97.2	23.9	89.5	33.7	97.6	23.6	87.6	30.2	97.4	23.8	90.7	34.4	95.9	23.1
PacBio (MCF7)	82.6	35.2	92.0	57.1	80.2	39.1	90.1	57.8	84.8	41.3	91.7	57.3	85.0	35.3	91.2	57.6	82.0	38.3	89.9	56.3
EST	.	.	79.6	74.3	.	.	80.4	77.9	.	.	80.3	75.7	.	.	80.8	77.7	.	.	81.2	74.7
RefSeq + GENCODE + PacBio + EST	.	.	83.8	91.2	.	.	84.9	95.8	.	.	84.0	93.0	.	.	84.4	95.7	.	.	83.7	94.4

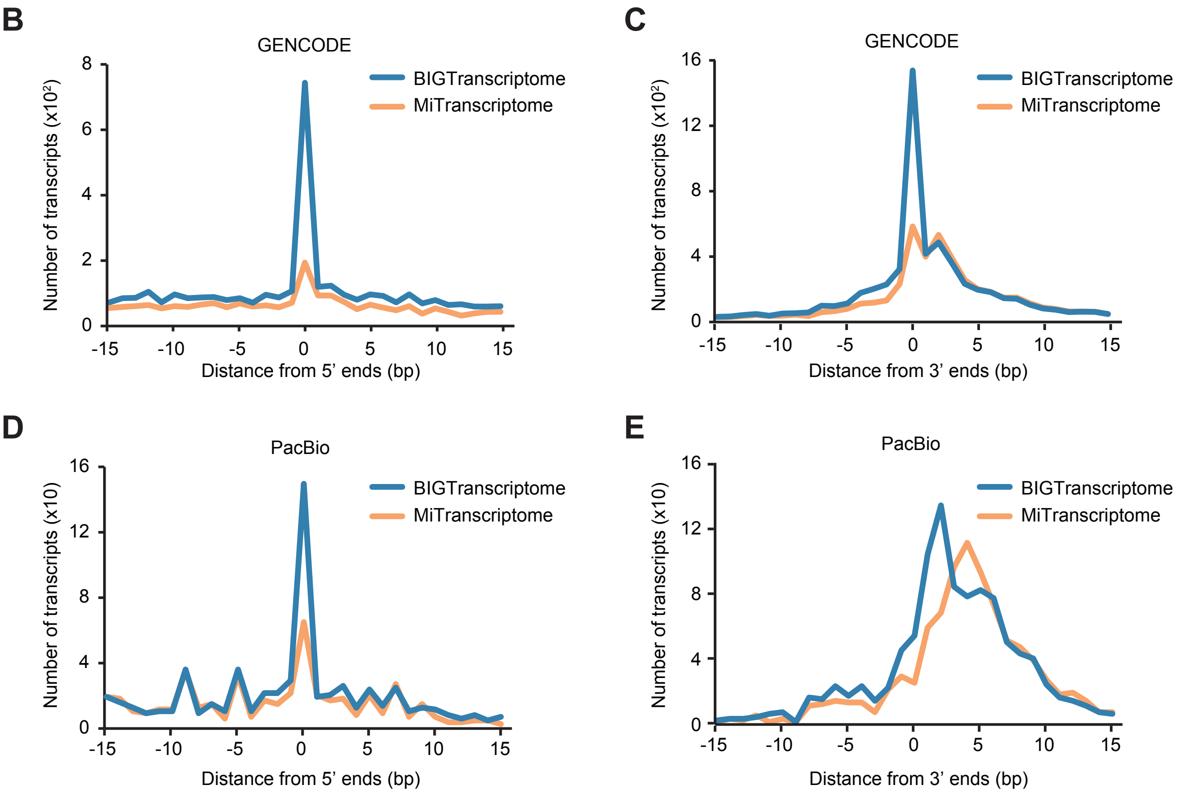

Figure S13. Accuracies of BIGTranscriptome-TS and boundary comparisons of BIGTranscriptome (A) Shown are the accuracies of BIGTranscriptome-TS (19 tissues and cancer) at the base and intron levels compared with those of four different sets of annotations (RefSeq, manual and automatic GENCODE, PacBio, and EST) and a combined set of annotations. SN: sensitivity and SP: specificity. (B-C) Shown are the relative distances from the ends of GENCODE transcripts with the same splicing pattern to the ends of BIGTranscriptome isoforms (blue) versus to the ends of MiTranscriptome isoforms (orange). (B) for the 5’ end and (C) for the 3’ end. (D-E) Shown are the relative distances from the ends of the PacBio (MCF7) transcripts with the same splicing pattern to the ends of BIGTranscriptome isoforms versus to the ends of MiTranscriptome (orange). (D) for the 5’ end and (E) for the 3’ end.