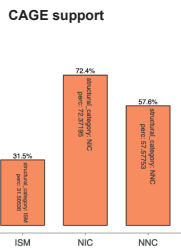
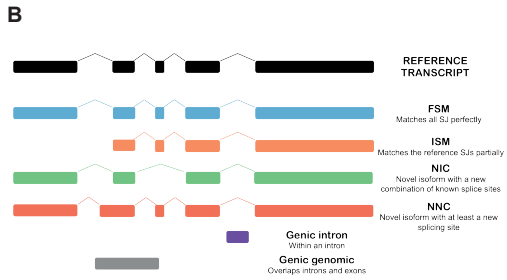
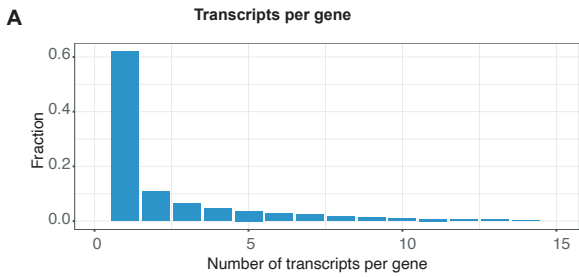
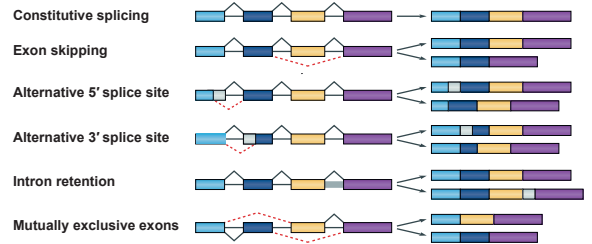


# Supplementary Figure 1



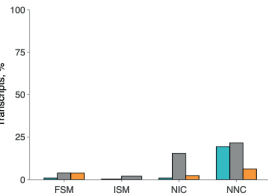
## Alternative splicing event definitions in SplAdder



## SQANTI3 report

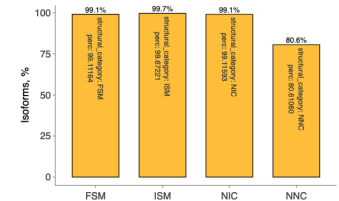
### Features of bad quality

Quality Control Attributes Across Structural Categories



### Features of good quality

All Canonical Junctions



## SQANTI transcripts

Gene Classification	Genes, count	Transcript Classification	Isoforms, count
Annotated Genes	24022	FSM	41311
Novel Genes	26680	ISM	10079
		NIC	30369
		NNC	29119
		Genic	5913
		Genic Antisense	9243
		Fusion	891
		Intergenic	21252
		Genic Intron	1257

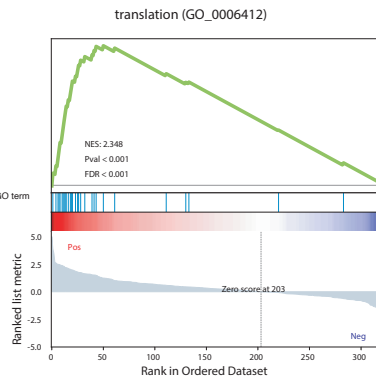
## SQANTI transcripts after CAGE filtering

Gene Classification	Genes, count	Transcript Classification	Isoforms, count
Annotated Genes	14017	FSM	25235
Novel Genes	3152	ISM	3781
		NIC	22995
		NNC	19878
		Genic	1041
		Genic Antisense	856
		Fusion	549
		Intergenic	2131
		Genic Intron	551

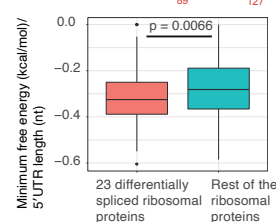
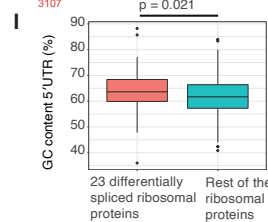
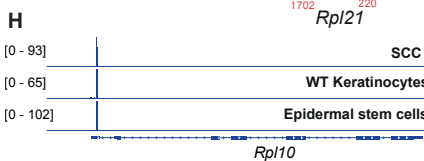
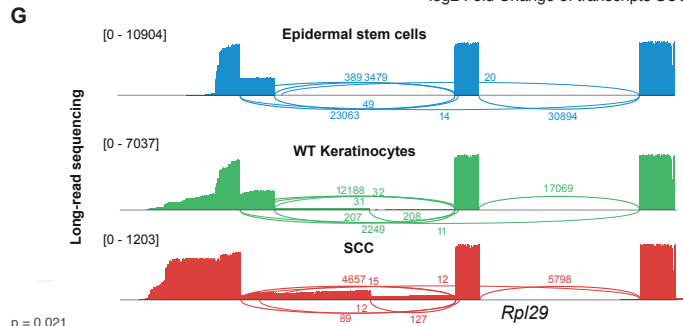
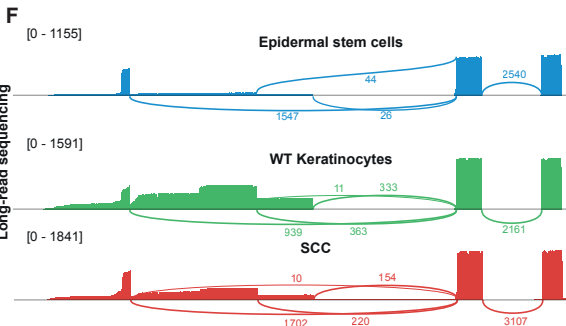
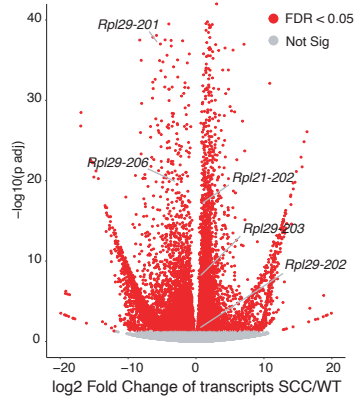
## C GO terms for significant alternative splicing events in EpSC



## D Significant alternative splicing events in SCC

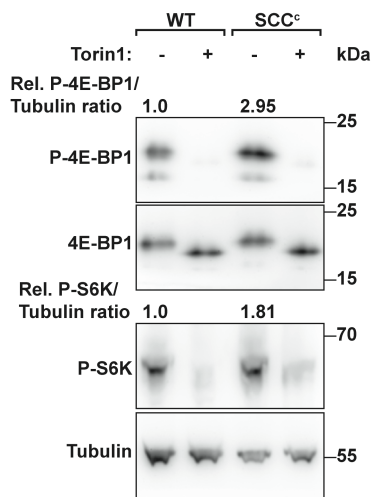


## E Short-read transcript changes in SCC vs. WT

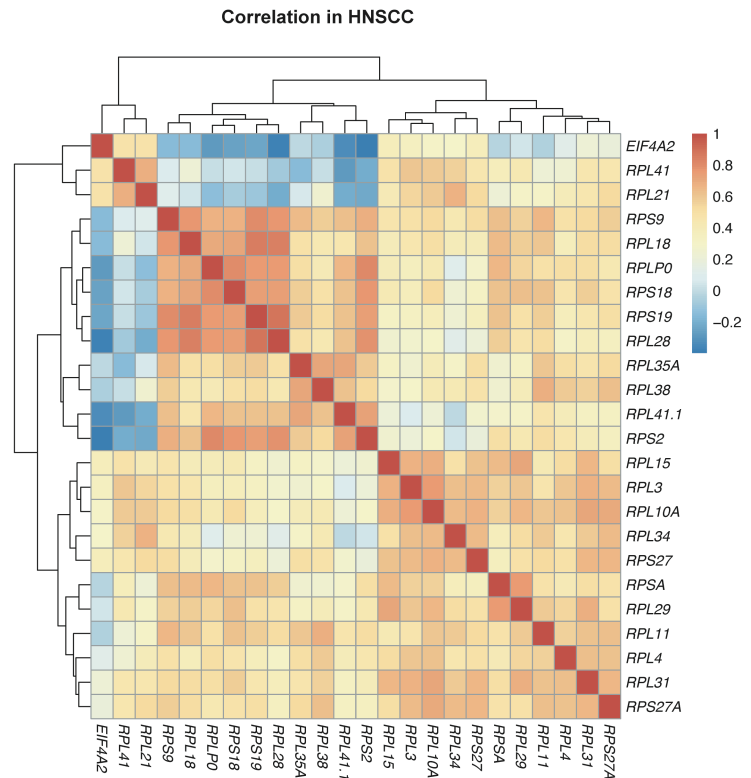


# Supplementary Figure 2

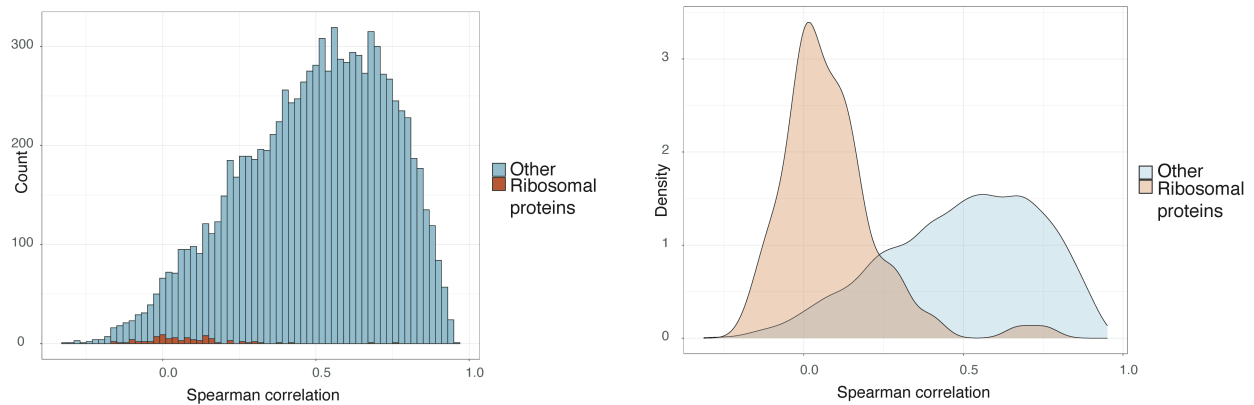
**A**



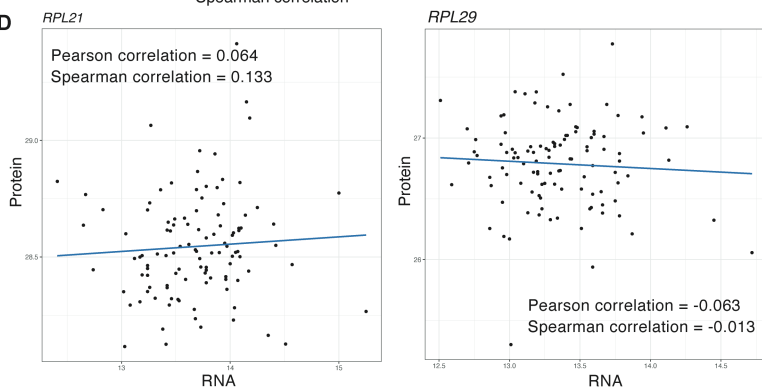
**B**



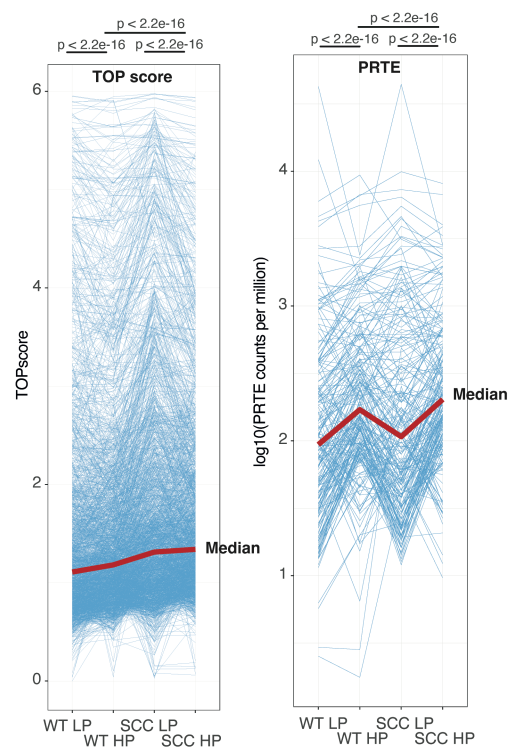
**C**



**D**



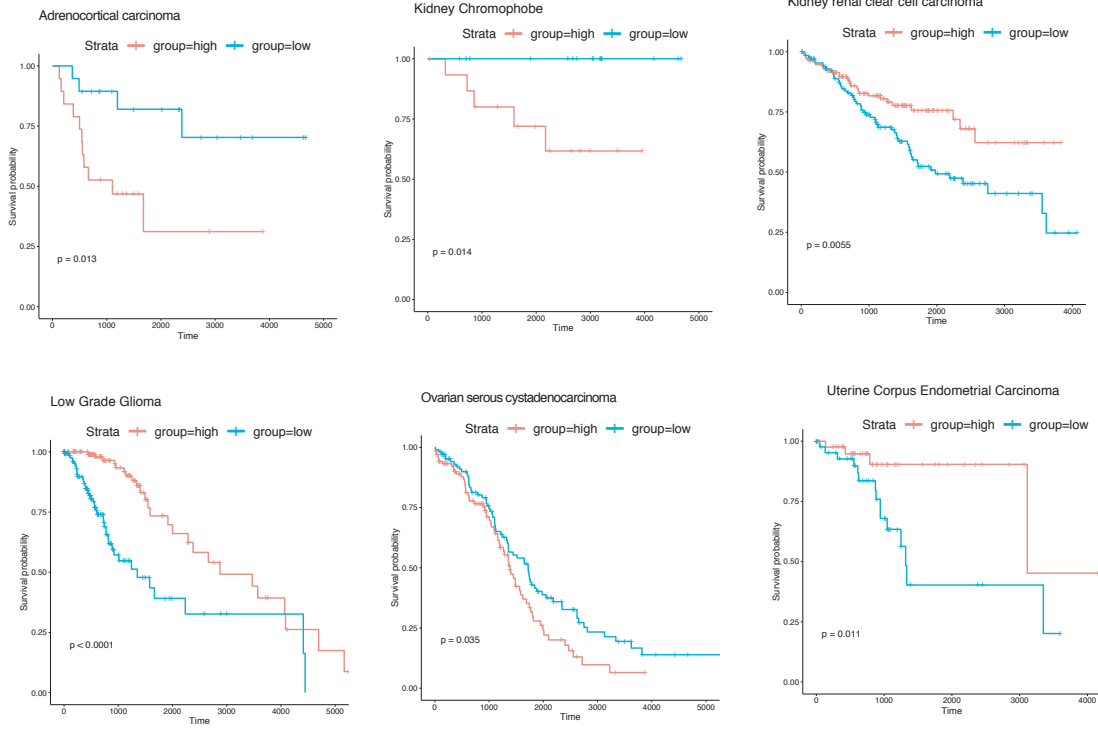
**E** Parallel coordinate plots for TOP and PRTE scores



# Supplementary Figure 3

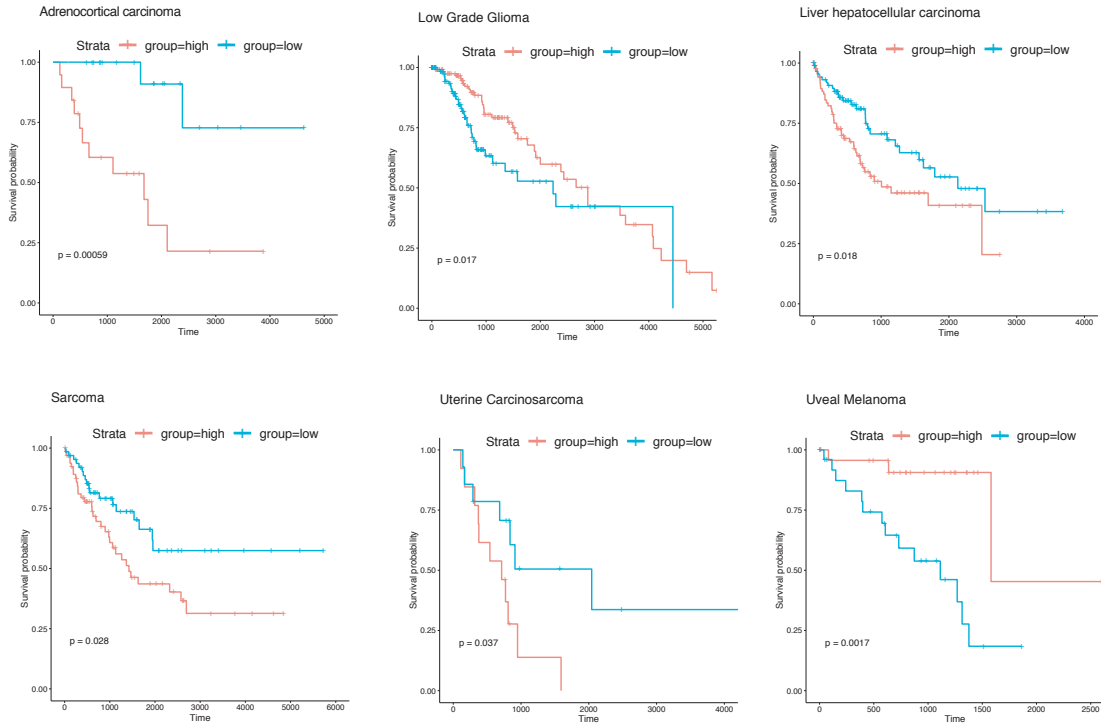
**A**

## RPL21 levels and survival in human cancer



**B**

## RPL29 levels and survival in human cancer



# Supplementary Figure 4

