

**Table S3. Confirmed functional alternative splicing in predicted dataset.**

GENE	DESCRIPTION	EXON ID*	RSPR	P <sub>RSPR</sub>	REFERENCES
GRIN1	Glutamate receptor, ionotropic, N-methyl D-aspartate 1	19712	8.92	7.72×10 <sup>-25</sup>	[1]
		19695	8.46	1.40×10 <sup>-13</sup>	
SYK	Spleen tyrosine kinase	86312	4.68	7.10×10 <sup>-16</sup>	[2]
DGKH	Diacylglycerol kinase, eta	18868	3.71	4.03×10 <sup>-4</sup>	[3]
WT1	Wilms tumor 1	79366	3.73	1.25×10 <sup>-4</sup>	[4]
LRP8 (ApoER2)	Low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	102438	6.08	3.32×10 <sup>-4</sup>	[5]

\*An exon is identified by EXON ID defined in ASAPII

#### References:

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2. Wang L, Duke L, Zhang PS, Arlinghaus RB, Symmans WF, et al. (2003) Alternative splicing disrupts a nuclear localization signal in spleen tyrosine kinase that is required for invasion suppression in breast cancer. *Cancer Res* 63: 4724-4730.
3. Murakami T, Sakane F, Imai S, Houkin K, Kanoh H (2003) Identification and characterization of two splice variants of human diacylglycerol kinase eta. *J Biol Chem* 278: 34364-34372.
4. Richard DJ, Schumacher V, Royer-Pokora B, Roberts SG (2001) Par4 is a coactivator for a splice isoform-specific transcriptional activation domain in WT1. *Genes Dev* 15: 328-339.
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