Table S2. Sanger validation of 31 rare InDels (Zhen et al. 2019). Genotype concordance of 98.4% (123/125) was achieved. Of 15 Indel PTVs assessed, 15 (100%) were confirmed.

Chr	Hg19	Consequence	Gene	Indel	#A	#C
chr18	21743019	UTR3	OSBPL1A	DATCTC	10	10
chr19	6381765	inframe_deletion	GTF2F1	DCCTCGAAGG	5	5
chr1	52305910	inframe_deletion	NRD1	DGTT	5	5
chr3	169496829	inframe_deletion	MYNN	DAAG	5	4
chr17	52991153	inframe_deletion	TOM1L1	DAAA	4	4
chr9	136272148	inframe_deletion	REXO4	DCTT	4	4
chr1	114376976	inframe_insertion	PTPN22	IGATGTTCCACCCCATTCCAGT	3	2
chr10	**75158004**	**frameshift_variant**	**ANXA7**	**DCT**	**4**	**4**
chr11	57798976	inframe_deletion	OR6Q1	DGCCTCACCCTTGCTA	4	4
chr11	**85437157**	**frameshift_variant**	**SYTL2**	**IC**	**2**	**2**
chr13	43462477	inframe_insertion	EPSTI1	IGAAGCC	3	3
chr12	**58165828**	**frameshift_variant**	**METTL1**	**IA**	**3**	**3**
chr3	**46008479**	**frameshift_variant**	**FYCO1**	**DCT**	**3**	**3**
chr11	35489704	intron	PAMR1	DT	7	7
chr15	89015823	intron	MRPS11	DACA	5	5
chr2	189943080	intron	COL5A2	DTC	4	4
chr20	52786117	intron	CYP24A1	DGAC	5	5

chr22	37331652	intron	CSF2RB	ICCTCCGTGGTGTCTT	5	5
chr17	32583190	intron	CCL2	DA	5	5
chr11	118626067	intron	DDX6	IA	2	2
chr2	68622798	intron	PLEK	DTC	3	3
chr4	7006432	intron	TBC1D14	IT	4	4
chr6	51776569	intron	PKHD1	DAG	4	4
chr7	133827772	intron	LRGUK	DTT	4	4
chr10	32977938	intron	C10orf68	DTTTATT	4	4
chr12	7302316	intron	CLSTN3	ITG	4	4
chr15	67457558	intron	SMAD3	DTG	2	2
chr6	152751116	intron	SYNE1	DTAAT	4	4
chr19	**46177411**	**splice_donor**	**GIPR**	**DCCTGCTCATCTTGAGTTTGTTCAGGTGGGA**	**3**	**3**
chr2	100175331	splice	AFF3	IAGT	3	3
chr4	89039419	splice	ABCG2	DAAAAGTG	2	2

Bold_red: detected as PTVs;

#A: number of assessed Indels;

#C: number of confirmed Indels.