PacBio long-read sequencing (LRS) data has a low false discovery rate relative to short-read sequencing (SRS) data.

	Deletions >50 bp			Insertions >50 bp		
	LRS	SRS Manta	SRS Pindel	LRS	SRS Manta	SRS Pindel
Initial call set	6,971	5,827	62,119	6,821	1,212	1,348
Not in segmental duplication	5,893	5,055	54,328	6,254	1,151	1,165
Not in NA12878 control	2,476	2,745	50,275	3,171	488	1,096
Overlaps RefSeq coding exon	39	225	1,186	16	2	9
Gene linked to disease in OMIM	3	46	231	3	0	0

Table S1. Filtering structural variants calls from LRS and SRS data. The same filters and control datasets were used to prioritize LRS and SRS call sets of deletions and insertions greater than 50 bp and less than 50 kb. The control data set for NA12878 is a combination of LRS and SRS variant calls.

Merker, J.D. et al., 2017. Long-read genome sequencing identifies causal structural variation in a Mendelian disease. *Genetics in Medicine*, ePub Ahead of Print.