S1 Table. A detailed reference description of the WES method: DNA mapping Analysis Pipeline

No.	Tools	Version (release)	Option	Reference (website)	Description
1	bbmap				
2	cutadapt	1.8.1	-	http://journal.embnet.org/index.php/embnetjournal/article/view/200	It finds and removes adapter sequences, primers, poly-A tails and other types of unwanted sequence from your high-troughput sequencing
3	sickle	1.33	-	https://github.com/najoshi/sickle	Sickle is a tool that uses sliding windows along with quality and length thresholds to determine when quality is sufficiently low to trim the 3'-end of reads and also determines when the quality is sufficiently high enough to trim the 5'-end of reads.
4	fastqc	0.10.1	-	http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc/	A quality control for high throughput sequence data
5	bwa	0.7.12	-	https://www.ncbi.nlm.nih.gov/pubmed/19451168	BWA is a software package for mapping low-divergent sequences against a large reference genome, such as the human genome
6	picard	1.98	MergeSamFiles.jar	https://github.com/broadinstitute/picard	Picard is a set of command line tools for manipulating high-throughput sequencing (HTS) data and formats such as SAM/BAM/CRAM and VCF
7-1	sentieon	201608	Realigner	https://web.stanford.edu/~chekh/Sentieon%20genomics%20Manual%20201606.01.pdf	
7-2	sentieon	201608	QualCal	https://web.stanford.edu/~chekh/Sentieon%20genomics%20Manual%20201606.01.pdf	
7-3	sentieon	201608	Haplotype	https://web.stanford.edu/~chekh/Sentieon%20genomics%20Manual%20201606.01.pdf	
8	qualimap	2.0.1	-	https://www.ncbi.nlm.nih.gov/pubmed/22914218	Evaluating next-generation sequencing alignment data

WES, whole exome-sequencing.