

S2 Table. A detailed reference description of the WES method: statistics analysis

No.	Tools	Version	Option	Reference (website)	Description
1	bedtools	2.17.0	coverage	http://bedtools.readthedocs.io/en/latest/content/tools/coverage.html	Computes both the depth and breadth of coverage of features
2	samtools	1.2	stats	https://www.ncbi.nlm.nih.gov/pubmed/19505943	Collects statistics from BAM files and outputs in a text format.

WES, whole exome-sequencing.