

S4 Table. A detailed reference description of the WES method: annotation pipeline

No.	Tools	Version	Option	Reference (Web-site)	Description
1	snpeff	4.2	S.Table3-5	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3679285/	For annotating and predicting the effects of single nucleotide polymorphisms

WES, whole exome-sequencing.