

Supplementary Table 5. Versions and options of software used in RNA-Seq

Process	Software	Version	Option
Pre-processing of raw reads	Trimmomatic	0.39	PhredScore \geq 21, > 50 bp
Read mapping to reference	BWA	0.7.17-r1198	mem
Mapping filter and MarkDuplicate	Bamtools	2.4.1	filter
	Samtools	1.11	sort, fixmate, markdup
Variant calling	GATK	4.2.0.0	HaplotypeCaller, GenotypeGVCFs
Gene information addition	SnEff	5.0e	
Significant variant selection	GATK	4.2.0.0	SelectVariants, VariantFiltration