Supplemental File 1

Supplemental Table 1
Tools used for comparing WES versus RNA-Seq data.

Method/tool	Purpose	URL
FASTQC	Check quality of WES and RNA-Seq reads	http://www.bioinformatics.babraham.ac.uk/projects/fastqc/
BWA	Map WES reads to the reference genome	http://bio-bwa.sourceforge.net/
Picard	Mark duplicate WES reads	http://broadinstitute.github.io/picard/
GATK	Perform local realignment and recalibration of WES reads	https://www.broadinstitute.org/gatk/
MuTect	Detect SNVs in WES and RNA-Seq	http://www.broadinstitute.org/cancer/cga/mutect
Samtools	Generate mpileup files for WES and RNA-Seq	http://samtools.sourceforge.net/
VarScan2	Generate read counts for WES and RNA-Seq	http://varscan.sourceforge.net/
TopHat2	Map RNA-Seq reads to the human reference transcriptome and genome	http://ccb.jhu.edu/software/tophat/index.shtml
Cufflinks	Calculate FPKM gene expression levels for RNA-Seq	https://github.com/cole-trapnell-lab/cufflinks
Bedtools	Intersect RNA-Seq SNVs with WES capture kit	https://github.com/arq5x/bedtools2
Oncotator	Annotations for strand analysis of WES SNVs	http://www.broadinstitute.org/oncotator/
R	Perform the analysis for SNV comparisons	http://www.r-project.org/

This table summarizes the computational tools used in our WES versus RNA-Seq comparative analysis. We include each tool used in our analysis, our use for the tool, and the URL link to the website. Further details including citations for all tools listed above are in the main methods section of the text.