

## Supplementary Note 1. Sample STAR command

```
~/STAR --genomeDir ~/reference_indices/hs37/star_genome \  
--readFilesIn ~/sample_1.fastq ~/sample_2.fastq \  
--runThreadN 8 \  
--outFilterMultimapScoreRange 1 \  
--outFilterMultimapNmax 20 \  
--outFilterMismatchNmax 10 \  
--alignIntronMax 500000 \  
--alignMatesGapMax 1000000 \  
--sjdbScore 2 \  
--alignSJDBoverhangMin 1 \  
--genomeLoad NoSharedMemory \  
--limitBAMsortRAM 0 \  
--outFilterMatchNminOverLread 0.33 \  
--outFilterScoreMinOverLread 0.33 \  
--sjdbOverhang 100 \  
--outSAMstrandField intronMotif \  
--outSAMattributes NH HI NM MD AS XS \  
--outSAMunmapped Within \  
--outSAMtype BAM SortedByCoordinate \  
--outSAMheaderHD @HD VN:1.4 \  
--twopassMode Basic \  
--twopass1readsN -1 \  
> ~/star_output.log
```

## Supplementary Note 2. Reference files used in RNA-VACAY

**repeat\_masker\_hg19.no\_chr.bed** – a BED file generated from the RepeatMasker track found in the UCSC Genome Browser

**pon.no\_header.vcf** – a VCF of variants found in GTEx samples (not included)

**00-common\_all.vcf.gz** – a VCF of common variants from the dbSNP database (hg19)

**pcawg8.snps.indels.svs.phased.tcga.v2.controlled.vcf.gz** – a VCF of germline variants found in TCGA samples (not included)

**pcawg8.snps.indels.svs.phased.icgc.v2.controlled.vcf** – a VCF of germline variants found in ICGC samples (not included)

**pcawg\_normal.vcf** – a VCF of variants found in normal PCAWG samples (not included)

**publication\_hotspots.vcf** – a VCF of known cancer hotspots (hg19)

**TABLE1\_hg19.txt** – a TXT with a list of known RNA editing sites from REDportal

**02\_cds.regions.bed** – a BED file with CDS regions (hg19)

## Supplementary Note 3. Sample RNA-VACAY commands

### **PCAWG manifests and metadata:**

```
python rna-vacay.py -pc ~/manifests/sample_manifest.tsv -pm  
~/metadata/sample_metadata.tsv > rna_vacay_output.log
```

### **User-generated or previously downloaded aligned RNA-seq reads:**

```
python rna-vacay.py -bm ~/manifests/sample_manifest.tsv >  
rna_vacay_output.log
```