Supplementary Table 1. Bioinformatics pipeline to analyze raw sequences from RNA-seq of HIV/HCV-infected and HIV-monoinfected patients.

1. Filtering step
Settings employed to eliminate adapters and low quality reads.
- Software:
Trimmomatic
- Version:
0.33
- Code:
java -jar PATH-TO-TRIMMOMATIC/trimmomatic-0.33.jar SE -threads 10 -phred33 PATH-TO-SAMPLES/"sample".fastq.gz "sample"/"sample"_filtered.fastq ILLUMINACLIP:all_PE.fa:2:30:10 SLIDINGWINDOW:4:15 MINLEN:50

2. Mapping Step
Settings employed for mapping the filtered counts.
- Software:
Tophat2
- Version:
2.0.14
- Human genome:
GRCh38
- Code:
mkdir -p "sample"; qsub -V -b y -j y -cwd -N TOPHATALIGNMENT -q all.q -pe openmp 10 tophat2 -p 10 -o 026C -G ../../REFERENCES/GRCh38_refseq.gtf --transcriptome-index ../../REFERENCES/ ../../REFERENCES/hg38.fullAnalysisSet.fa ../02-preprocessing/"sample"/"sample"_filtered.fastq.gz

3. Count step
Settings employed to obtain the number of counts per gene and sample
- Software:
HTSeq
- Version:
0.6.1
- Code:
#!/bin/bash
#$ -V
#$ -b y
#$ -j y
#$ -cwd
#$ -N HTSEQCOUNT
#$ -q all.q
#$ -t 1-100
set -e
set -x
infile=../samples_id.txt
in=$(awk "NR==$SGE_TASK_ID" $infile)
mkdir -p $in
htseq-count -f bam ../04-tophat/$in/"$in"_accepted_hits.bam ../../REFERENCES/GRCh38_refseq.gtf > $in/"$in"_htseqCount.txt