

Supplementary Code 1. Custom code used for TPM calculations.

This code was used to estimate expression of all Trinity assembled transcripts using quasi-mapping of Salmon in samples from TCGA or GTEx. Executable lines are marked with '>'. The bash script assumes the Salmon transcriptome index was generated prior to executing and is provided as first Argument. The bam or fastq file name is provided as second Argument.

```
> salmon index -t flattened_transcriptome.fasta -i ./transcriptome_index
```

Salmon version 0.8.2

SAMtools version 1.3.1

Python version 3.5.2

TCGA paired-end RNA-seq was downloaded through GDC portal as bam files. GTEx paired-end RNA-seq was downloaded with the SRA toolkit as fastq files. Hence, TCGA files were first converted to fastq files. Here, the following programs were used from github.com/A-N-Other/pedestal: deinterleave (commit 169dd81) and interleavei (commit 800e78f). They are available under the permissive MIT license and we encourage code re-use and comment.

```
#####
```

```
##### Step 1
```

```
### file input & directory and test if file exists
```

```
> indexfile=$1
```

```
> bamname=$2 #collects string of input file from 1st argument (*.bam)
```

```
> fullfilename="${bamname##*/}"
```

```
> indirectory="${bamname%/*}"
```

```
> subdirectory="${indirectory##*/}"
```

```
> filename="${fullfilename%_gdc_realn_rehead.bam}"
```

```
#> filename="${fullfilename%_1.fastq.gz}" # for GTEx fastq files
```

```
> if [ -s ./countFiles/"$subdirectory"/"$filename".counts.gz ]; then
```

```
exit 3; fi
```

```
#####
```

```
#####
```

```
##### Step 2
```

```
### separate first and second read of every pair with deinterleave script
```

```
> samtools fastq -n "$bamname" | interleave -u -
```

```
| deinterleave ~/Scratch/tcgarecycle/fastq.files/"$filename"_1.fq
```

```
~/Scratch/tcgarecycle/fastq.files/"$filename"_2.fq
```

```
#####
```

#####

Step 3

Expression estimate with Salmon quasi-mapping

```
> ~/bin/salmon-0.8.2/bin/salmon quant \  
    -p 8 -i "$indexfile" \  
    -l IU --seqBias --gcBias \  
    -1 ~/Scratch/tcgarecycle/fastq.files/"$filename"_1.fq \  
    -2 ~/Scratch/tcgarecycle/fastq.files/"$filename"_2.fq \  
    -o ./countFiles/"$subdirectory"/"$filename".tmpdirectory  
  
> mv ./countFiles/"$subdirectory"/"$filename".tmpdirectory/quant.sf \  
    ./countFiles/"$subdirectory"/"$filename".counts  
> mv ./countFiles/"$subdirectory"/"$filename".tmpdirectory/aux_info/ambig_info.tsv  
\  
    ./countFiles/"$subdirectory"/"$filename".ambig_info.tsv
```



Supplementary Table 1. Primers used in this study

5' RACE PCR primers

Primer name	Sequence (5' – 3')	Target
GSP1	TTTGTGCACATAAGGATCCTCC	Human <i>ACE2</i>
GSP2	TTTGTCCCAGCCTGCTTC	Human <i>ACE2</i>

RT-qPCR primers

Primer name	Sequence (5' – 3')	Target
<i>ACE2</i> Forward	GTAACGGACCCAGGAAAT	Human <i>ACE2</i>
<i>MIRb-ACE2</i> Forward	TACAAGTGCTTCATTGAGG	Human <i>MIRb-ACE2</i>
Human <i>ACE2</i> Common Reverse	CCATTGTACCTTTGTGC	Human <i>ACE2</i> and <i>MIRb-ACE2</i>
Vervet <i>Ace2</i> Forward	CTAACTGATCCAGGAAAT	Vervet <i>Ace2</i>
Vervet <i>MIRb-Ace2</i> Forward	CACAAATGCTTCATTGAGG	Vervet <i>MIRb-Ace2</i>
Vervet <i>Ace2</i> Common Reverse	CCATTGTACCTTTGTGC	Vervet <i>Ace2</i> and <i>MIRb-Ace2</i>
Rabbit <i>Ace2</i> Forward	CTAACTGAGCCAGGAGAT	Rabbit <i>Ace2</i>
Rabbit <i>MIRb-Ace2</i> Forward	TACAAGTGTTTCATTTAGA	Rabbit <i>MIRb-Ace2</i>
Rabbit <i>Ace2</i> Common Reverse	CCATTGTTACTTTTGTGC	Rabbit <i>Ace2</i> and <i>MIRb-Ace2</i>
Dog <i>Ace2</i> Forward	CTAACTGAGCCAAGTGAC	Dog <i>Ace2</i>
Dog <i>MIRb-Ace2</i> Forward	TACAAATGTTTCATTGAGG	Dog <i>MIRb-Ace2</i>
Dog <i>Ace2</i> Common Reverse	CCATCGTTACCTTTGTGC	Dog <i>Ace2</i> and <i>MIRb-Ace2</i>
Mouse <i>Ace2</i> Forward	ACTTCTCTAACATGTAAG	Mouse <i>Ace2</i>
Mouse <i>MIRb-Ace2</i> Forward	TACAAGTTGTGTATGTTCT	Mouse <i>MIRb-Ace2</i>
Mouse <i>Ace2</i> Common Reverse	GTCTCTTGCTACTTACAC	Mouse <i>Ace2</i> and <i>MIRb-Ace2</i>
<i>CXCL10</i> Forward	TGCCATTCTGATTTGCTGCC	Human <i>CXCL10</i>
<i>CXCL10</i> Reverse	TGCAGGTACAGCGTACAGTT	Human <i>CXCL10</i>
<i>CD274</i> Forward	TACAGCTGAATTGGTCATCCCA	Human <i>CD274</i>
<i>CD274</i> Reverse	TCAGTGCTACACCAAGGCAT	Human <i>CD274</i>
<i>HPRT</i> Forward	TGACACTGGCAAACAATGCA	<i>HPRT</i> (all species)
<i>HPRT</i> Reverse	GGTCCTTTTACCAGCAAGCT	<i>HPRT</i> (all species)