GTEx Quantifications

Flux Version

Flux Capacitor 1.2.3 (Flux Library: 1.20)

Read Mappings

Tophat mappings were employed, filtered for primary alignments (mapper comparison) by samtools

```
samtools view -bF 256 file.bam > filtered_file.bam
```

Annotation File

The quantifications are based on a modified Gencode (v12) annotation created at the Broad Institute:

http://www.broadinstitute.org/cancer/cga/tools/rnaseqc/examples/gencode.v12.annotation.patched_contigs.gtf.gz

Parameter File

```
ANNOTATION_FILE gencode.v12.annotation.patched_contigs_sorted.
gtf
COUNT_ELEMENTS [SPLICE_JUNCTIONS, INTRONS]
ANNOTATION_MAPPING AUTO
```

Command Line

```
flux-capacitor -p <parameter_file> -i <sample.bam> -o <output.gtf>
```