**RNA-seq Total Expression GLP**

1. Run full Event Analysis (including transcriptome reduction)
2. Run RSEM on reduced transcriptome (SE and PE separately) and output transcript-level TPM values
3. Sum SE and PE TPM values for each transcript
4. For splicing/DE analyses:
   1. Use tappAS feature analysis/DE with summed RSEM TPM values to analyzed transcripts
   2. If tappAS methods are not favored, use summed RSEM TPM values in outside splice/DE analysis

NOTE: Both (a) and (b) assume the TPM values for the transcripts are the TPM value for any feature within the transcript and TPM values are summed across transcripts that share a particular feature (e.g. A common fragment TPM value is equal to the sum of TPM values of all transcripts that share that particular fragment)