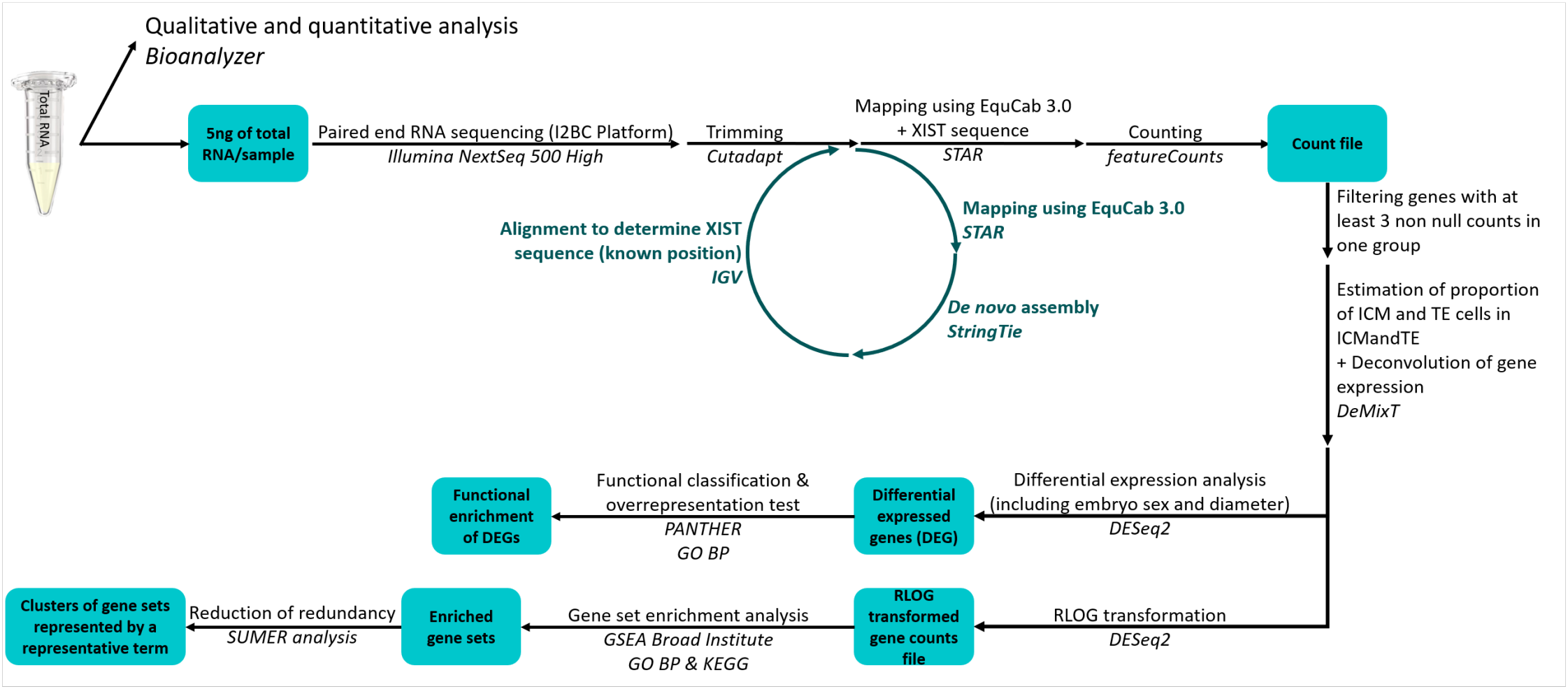
Qualitative and quantitative analysis
Bioanalyzer
Total RNA
5ng of total RNA/sample
Paired end RNA sequencing (I2BC Platform)
Illumina NextSeq 500 High
Trimming
Cutadapt
Mapping using EquCab 3.0
+ XIST sequence
STAR
Counting
featureCounts
Count file
Mapping using EquCab 3.0
STAR
De novo assembly
StringTie
Alignment to determine XIST sequence (known position)
IGV
Filtering genes with at least 3 non null counts in one group
Estimation of proportion of ICM and TE cells in ICMandTE
+ Deconvolution of gene expression
DeMixT
Differential expression analysis
(including embryo sex and diameter)
DESeq2
Differential expressed genes (DEG)
Functional classification & overrepresentation test
PANTHER
GO BP
Functional enrichment of DEGs
RLOG transformation
DESeq2
RLOG transformed gene counts file
Gene set enrichment analysis
GSEA Broad Institute
GO BP & KEGG
Enriched gene sets
Reduction of redundancy
SUMER analysis
Clusters of gene sets represented by a representative term