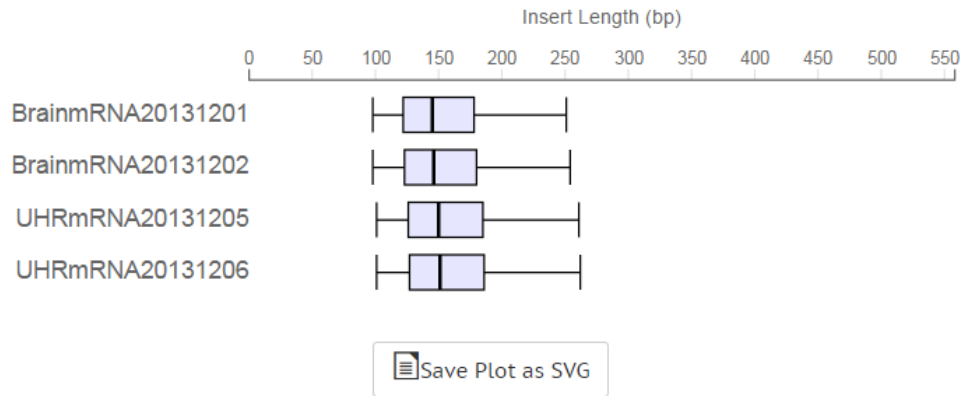


RNA-Seq Alignment on <https://basespace.illumina.com>

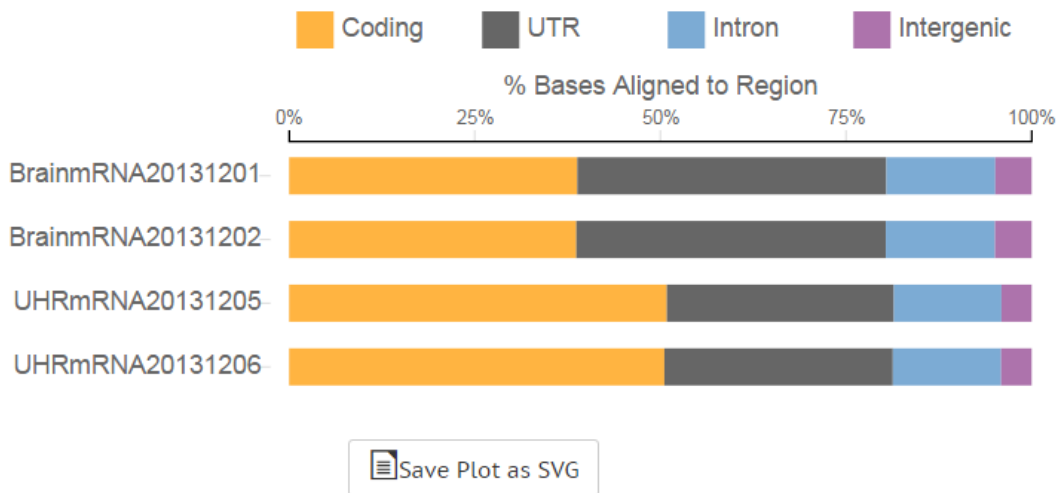
De-multiplexed read sequences were then aligned to the reference sequence using STAR (<https://www.ncbi.nlm.nih.gov/pubmed/23104886>) aligner.

Raw counts and FPKM normalized counts can be downloaded from this app as well as the following figures:

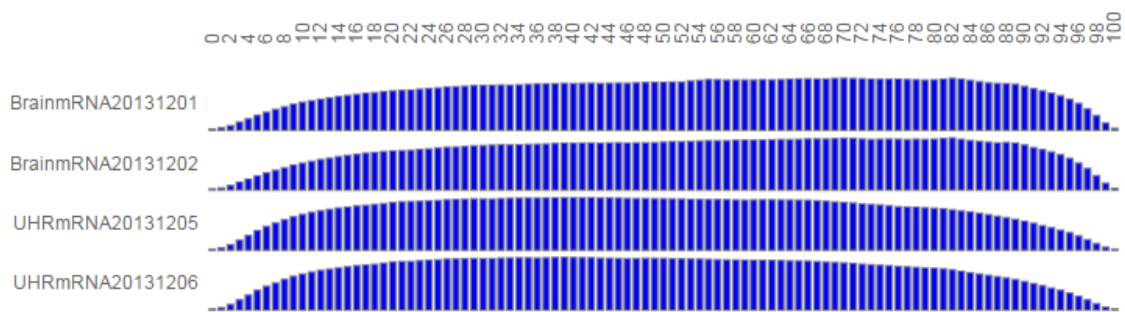
Insert Length Distribution *i*



Alignment Distribution *i*

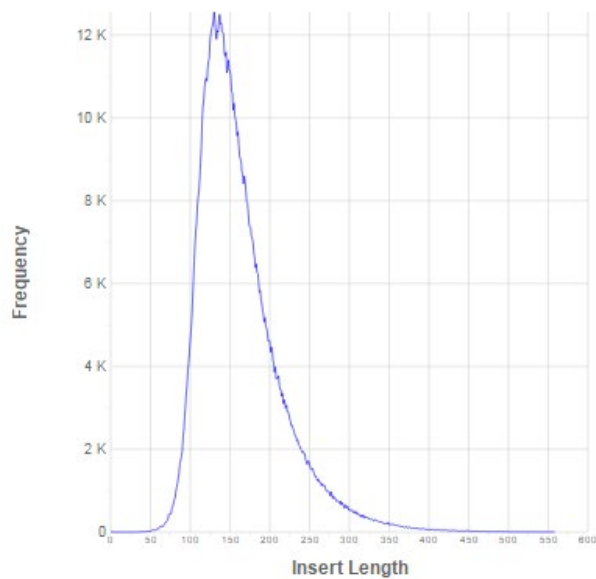


Transcript Coverage ⁱ



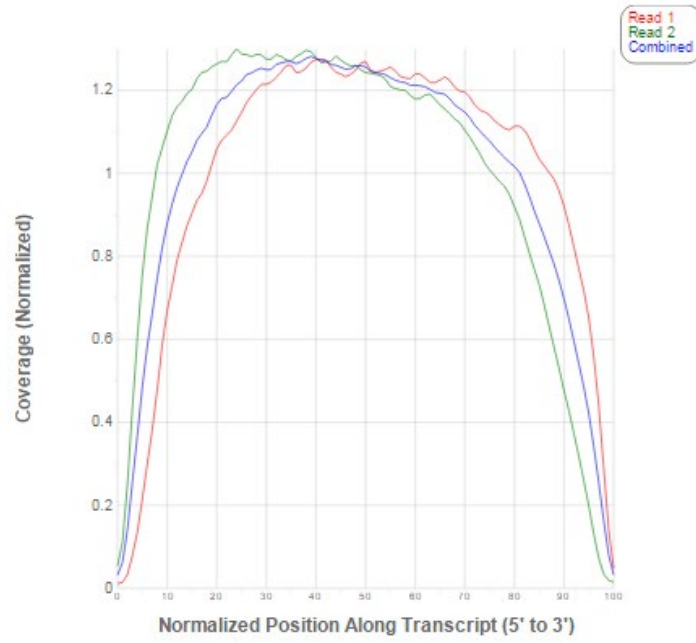
 Save Plot as SVG

Insert Length Distribution ⁱ



 Save Plot as SVG  Export Data as CSV

Transcript Coverage i



[Save Plot as SVG](#) [Export Data as CSV](#)

Cufflinks Assembly & DE on <https://basespace.illumina.com>

Assembly and differential expression was estimated using Cufflinks (<http://cole-trapnell-lab.github.io/cufflinks/>)

Normalized differential expression spreadsheets as well as the following figures generated:

Assembly ⁱ

	Control	Comparison	Merged
Gene Count	55,711	53,707	70,894
Transcript Count	107,397	107,458	142,136
Link to gene models	GTF result	GTF result	GTF result
Relation to reference transcripts			
Equal (=)	55,627	56,421	57,691
Potentially novel (j)	21,179	22,502	36,814
Unknown, intergenic (u)	28,558	26,339	44,247
Overlap with opposite-strand exon (x)	1,711	1,873	2,798
Other	322	323	586

Gene Browser ⁱ

Filters

q Value: 0 - 1

|log₂(Ratio)|: 0 - 21.31

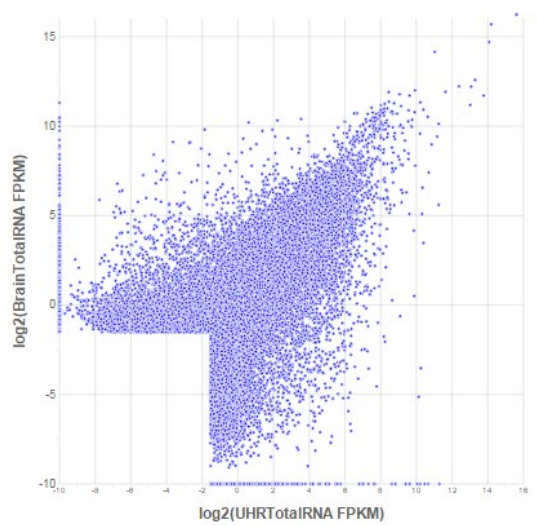
log₂(UHRTotalRNA FPKM): -10 - 17.12

log₂(BrainTotalRNA FPKM): -10 - 16.261

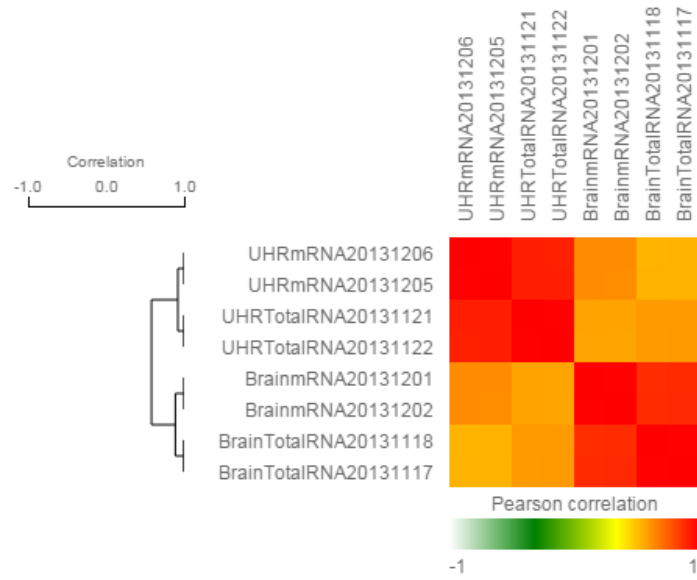
Significant
Choose a value... ▼

Status
OK ▼

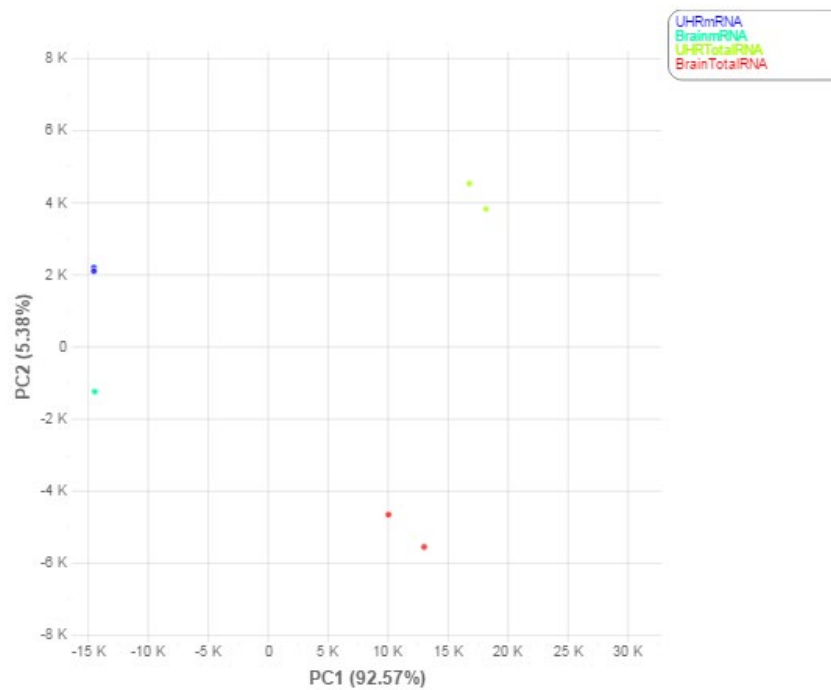
Gene

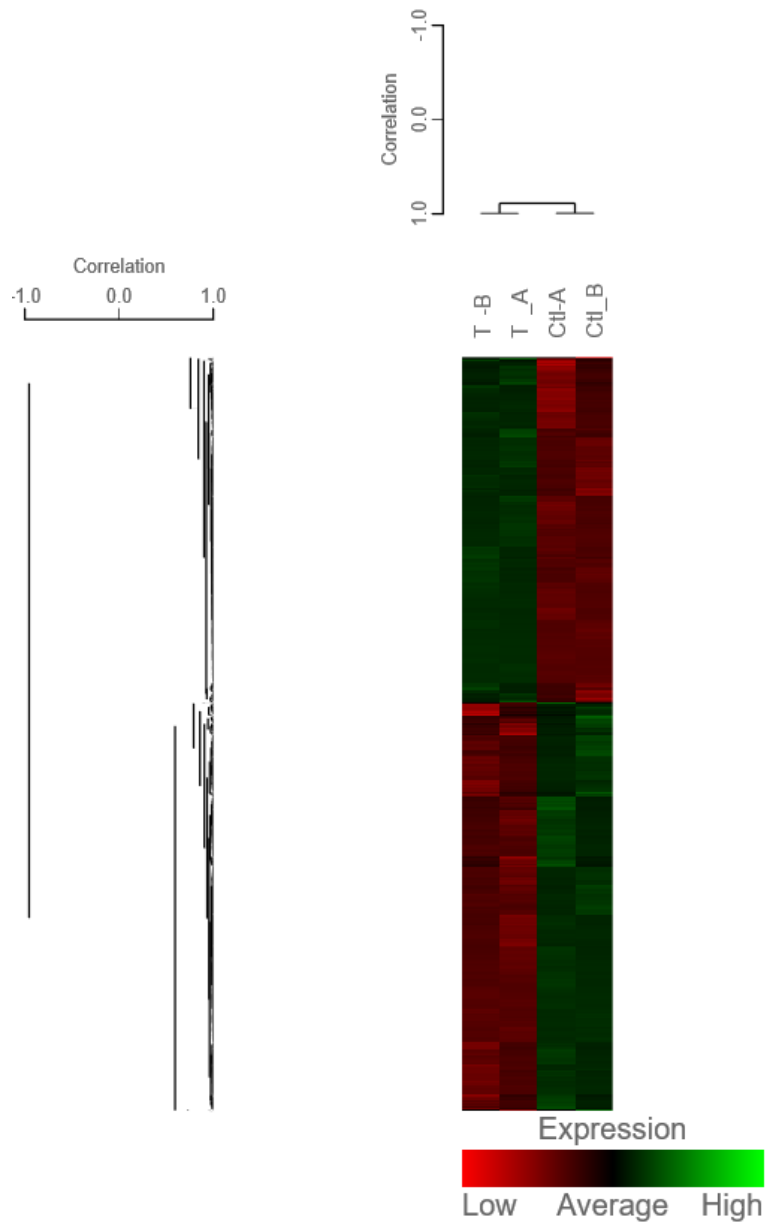


Sample Correlation i



PCA Plot i





Tertiary Analysis Resources

VisR <https://visrsoftware.github.io/>

BioGPS <http://biogps.org/#goto=welcome>

Gene Ontology Consortium <http://www.geneontology.org/>

Morpheus <https://github.com/visrsoftware>

Correlation Engine Trial Domain: <https://ubc.ussc.informatics.illumina.com>

(free with @brc.ubc.ca email or ask for guest account credentials)