

Processing overview

- For transcriptome quantification in transcriptome – eXpress on Bowtie alignments, GENCODE V29
- For genome-space quantification – mapping with STAR, quantification on GENCODE V29 using Stringtie
- Also ran Stringtie on a BAM file from HA
- Comparisons at the gene level only

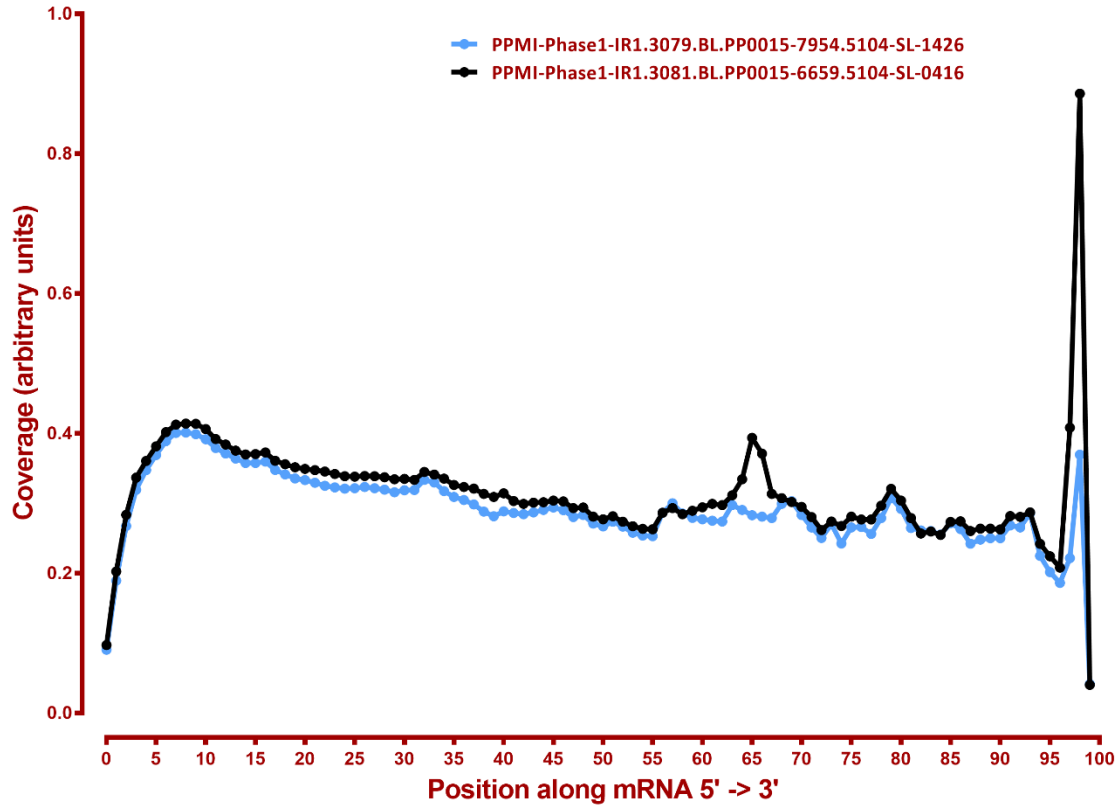
Dataset stats

Species	Assay	Read Type + Length	Mapping	#	Complexity	Unique	Unique Splices	Multi	Multi Splices	Mapped fraction	Raw fragments
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	PPMI-Phase1-IR1.3079.BL.PP0015-7954.5104-SL-1426	0.57	126,069,424	11,695,048	19,625,647	4,882,855	0.90	90,309,488
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	PPMI-Phase1-IR1.3081.BL.PP0015-6659.5104-SL-0416	0.47	158,084,633	16,313,948	57,041,454	9,546,858	0.96	126,003,919

Read distribution QC

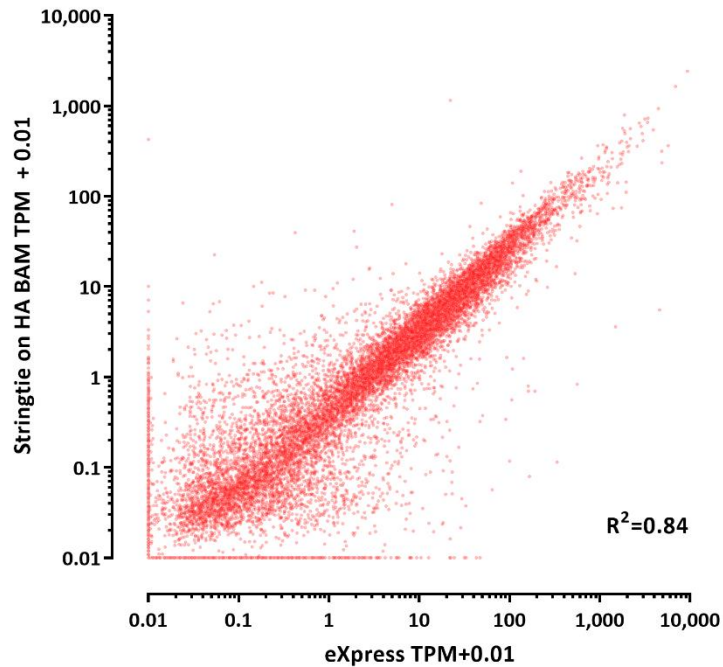
#	Exonic:	Intergenic:	Intronic:
PPMI-Phase1-IR1.3079.BL.PP0015-7954.5104-SL-1426	0.448452	0.05425346	0.497295
PPMI-Phase1-IR1.3081.BL.PP0015-6659.5104-SL-0416	0.506405	0.03840683	0.455188

Coverage of genes; >1000bp

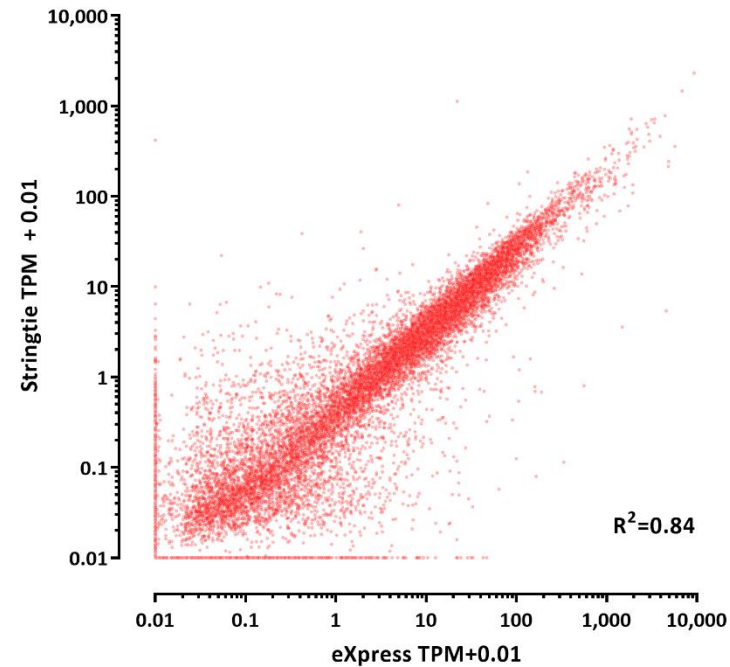


eXpress vs Stringtie, reprocessing , protein coding genes only (n=19,908)

PPMI-Phase1-IR1.3079.BL.PP0015-7954.5104-SL-1426 HA

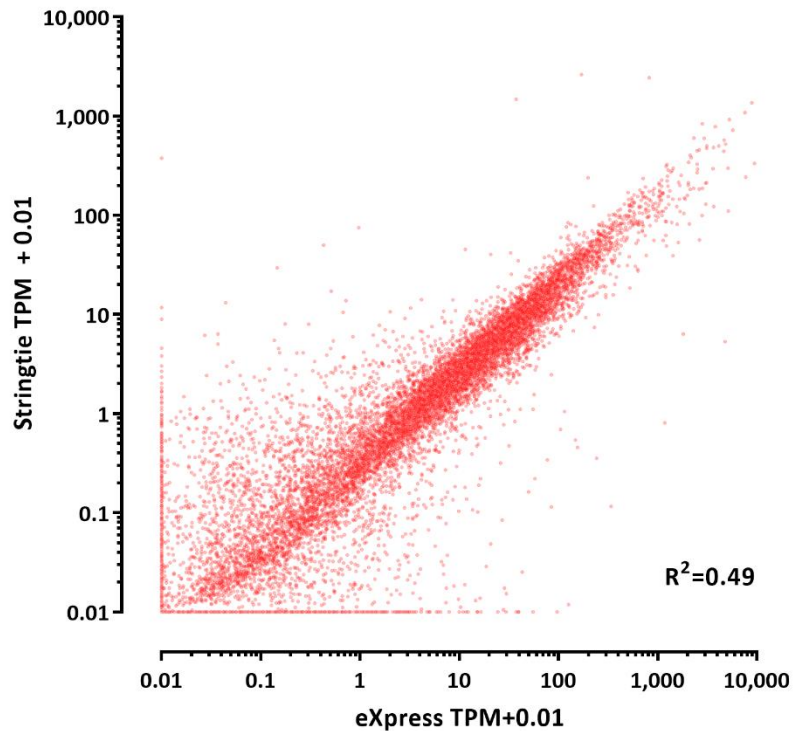


PPMI-Phase1-IR1.3079.BL.PP0015-7954.5104-SL-1426



eXpress vs Stringtie, reprocessing, protein coding genes only (n=19,908)

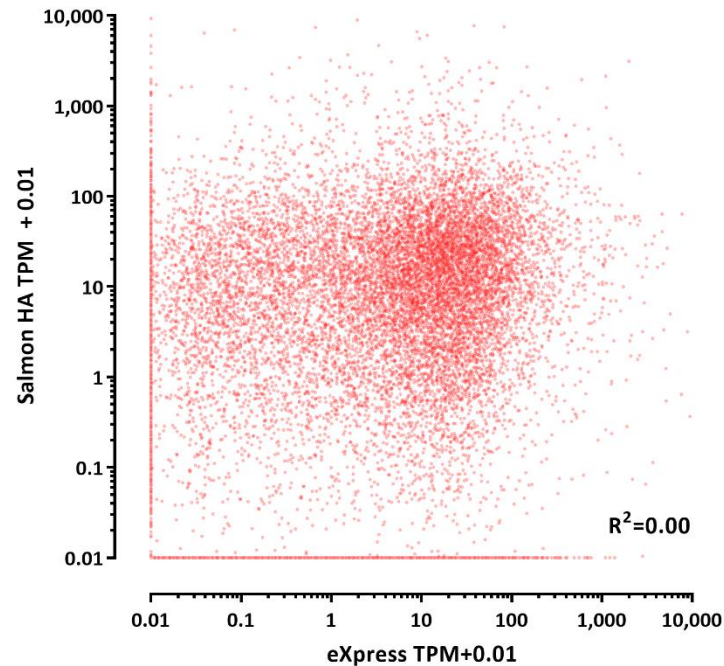
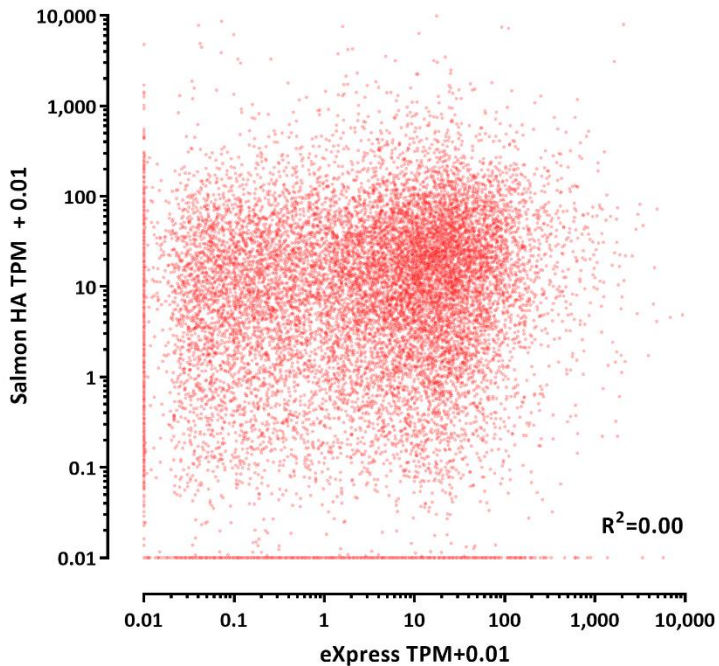
PPMI-Phase1-IR1.3081.BL.PP0015-6659.5104-SL-0416



eXpress vs Salmon, protein coding genes only (n=17,726)

PPMI-Phase1-IR1.3079.BL.PP0015-7954.5104-SL-1426 eXpress vs. Salmon HA

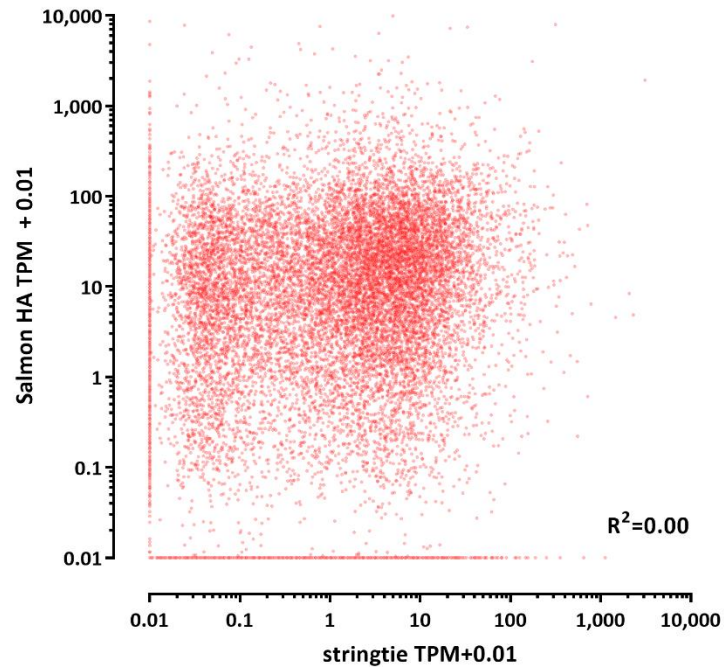
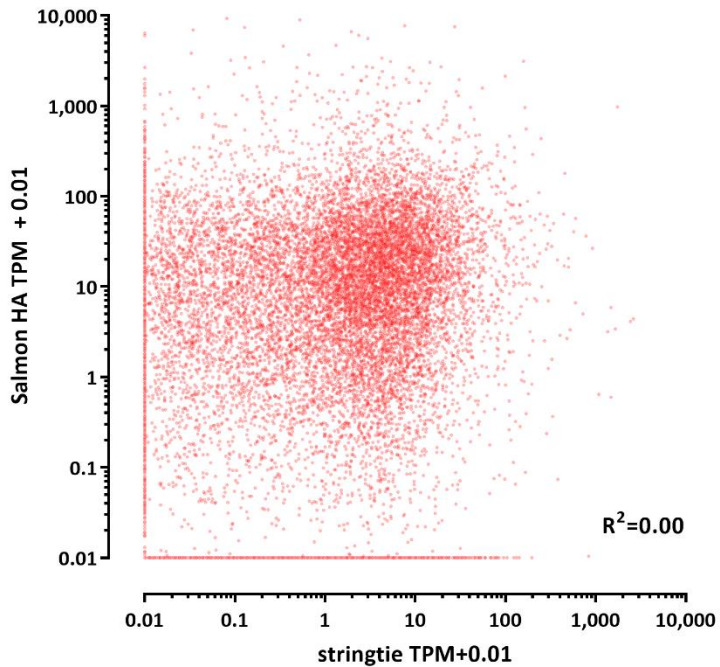
PPMI-Phase1-IR1.3081.BL.PP0015-6659.5104-SL-0416 eXpress vs. Salmon HA



stringtie vs Salmon, protein coding genes only (n=17,726)

PPMI-Phase1-IR1.3079.BL.PP0015-7954.5104-SL-1426 stringtie vs. Salmon HA

PPMI-Phase1-IR1.3081.BL.PP0015-6659.5104-SL-0416 stringtie vs. Salmon HA



stringtie vs Salmon, protein coding genes only (n=17,726)

PPMI-Phase1-IR1.3081.BL.PP0015-6659.5104-SL-0416 stringtie on HA vs. Salmon HA

