

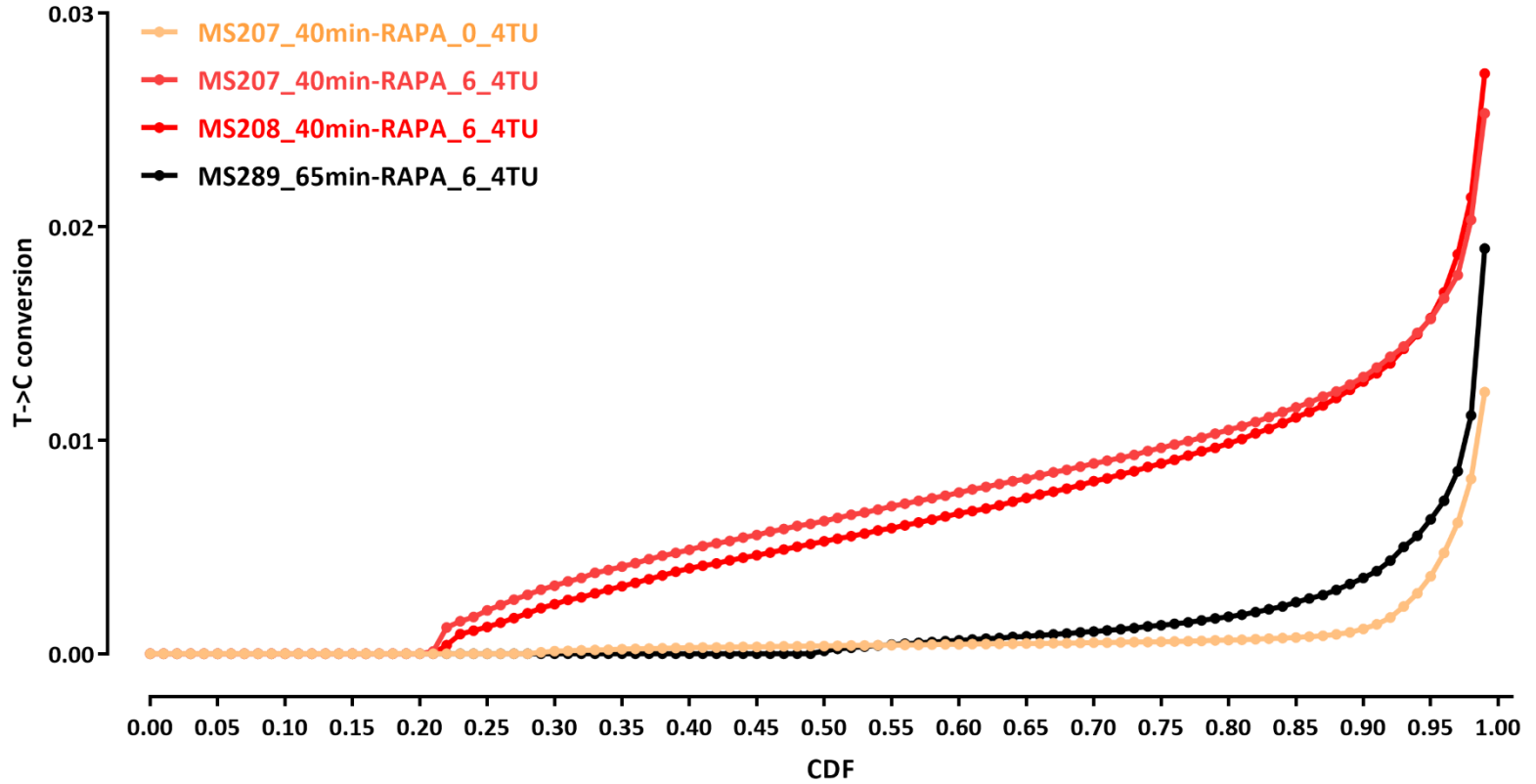
Processing notes

- Used slamdunk (the only available package for processing SLAM-seq data)
- Most slamdunk analysis examples use 3'UTRs (which is because QuantSeq is used to make libraries; we do not have UTRs for all genes so I used the whole transcripts and worked in transcriptome space)

Mapping stats

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
2020-06-20-SLAMseq_exp200525_MS207_40min-RAPA_0_4TU	2x150	slamdunk-0.4.3, transcriptome	S.cerevisiae	8,315,938	0.31	10,899,429		722,766		0.70
2020-06-20-SLAMseq_exp200525_MS207_40min-RAPA_0_4TU	2x150	slamdunk-0.4.3, transcriptome	S.pombe	8,315,938	0.41	3,434,487		340,592		0.23
2020-06-20-SLAMseq_exp200525_MS207_40min-RAPA_6_4TU	2x150	slamdunk-0.4.3, transcriptome	S.cerevisiae	7,125,563	0.33	9,219,195		660,782		0.69
2020-06-20-SLAMseq_exp200525_MS207_40min-RAPA_6_4TU	2x150	slamdunk-0.4.3, transcriptome	S.pombe	7,125,563	0.44	2,948,949		298,475		0.23
2020-06-20-SLAMseq_exp200525_MS208_40min-RAPA_6_4TU	2x150	slamdunk-0.4.3, transcriptome	S.cerevisiae	8,406,072	0.31	9,980,146		671,343		0.63
2020-06-20-SLAMseq_exp200525_MS208_40min-RAPA_6_4TU	2x150	slamdunk-0.4.3, transcriptome	S.pombe	8,406,072	0.38	4,527,549		436,228		0.30
2020-06-20-SLAMseq_exp200525_MS289_65min-RAPA_6_4TU	2x150	slamdunk-0.4.3, transcriptome	S.cerevisiae	9,734,142	0.38	2,100,550		197,921		0.12
2020-06-20-SLAMseq_exp200525_MS289_65min-RAPA_6_4TU	2x150	slamdunk-0.4.3, transcriptome	S.pombe	9,734,142	0.25	14,086,713		1,380,369		0.79

S_cerevisiae



S_pombe

