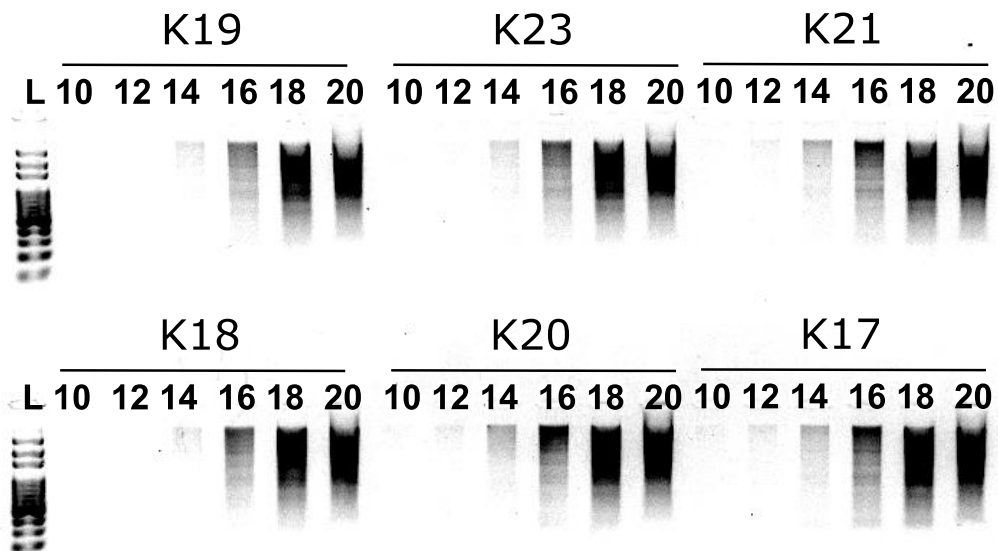
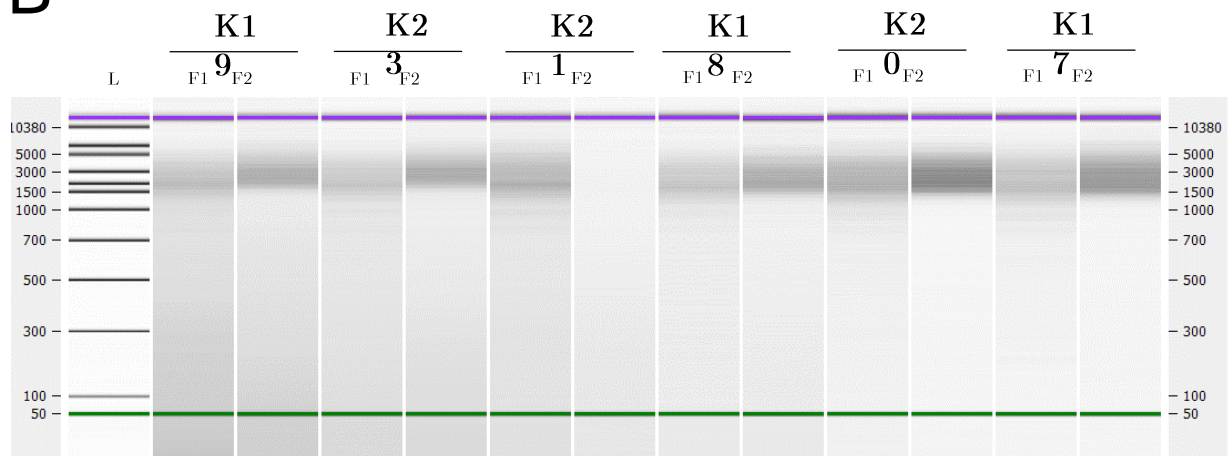


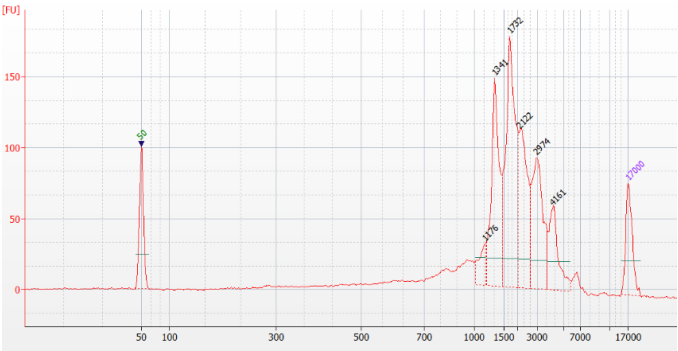
A



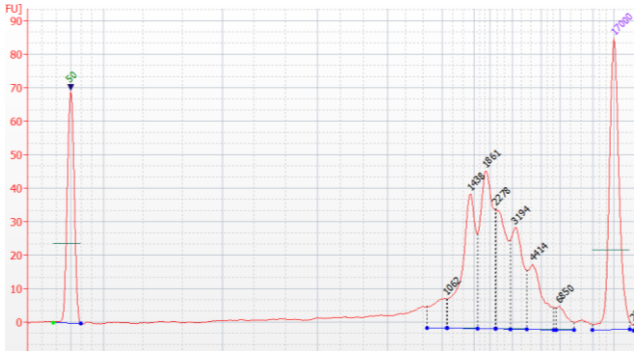
B



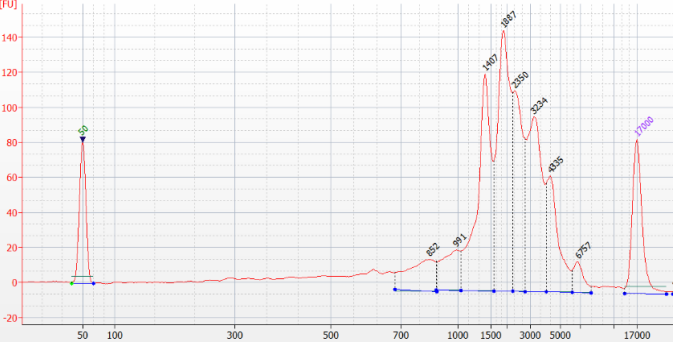
A Batch 1 (Target Capture)



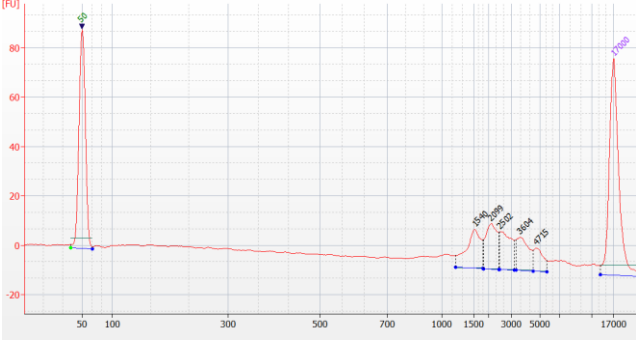
B Batch 1(Final)



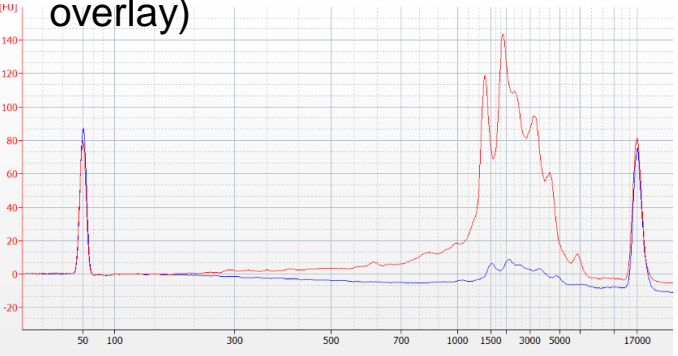
C Batch 2 (Target Capture)



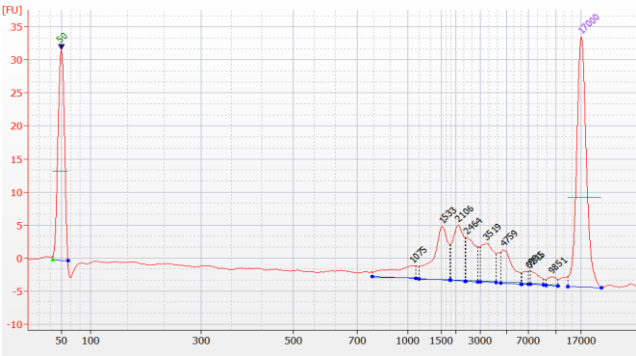
D Batch 2 (Final)

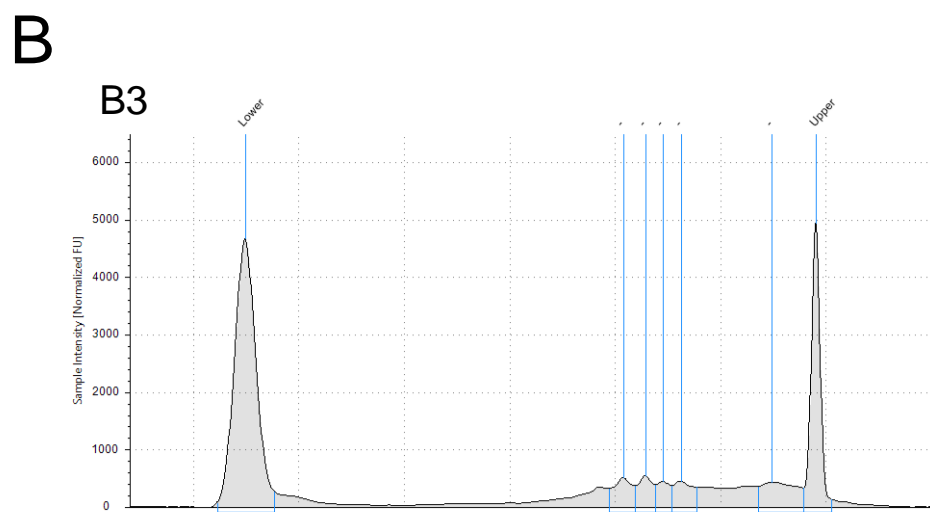
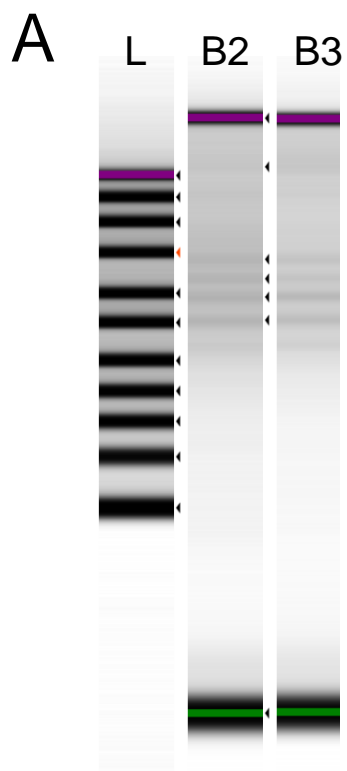


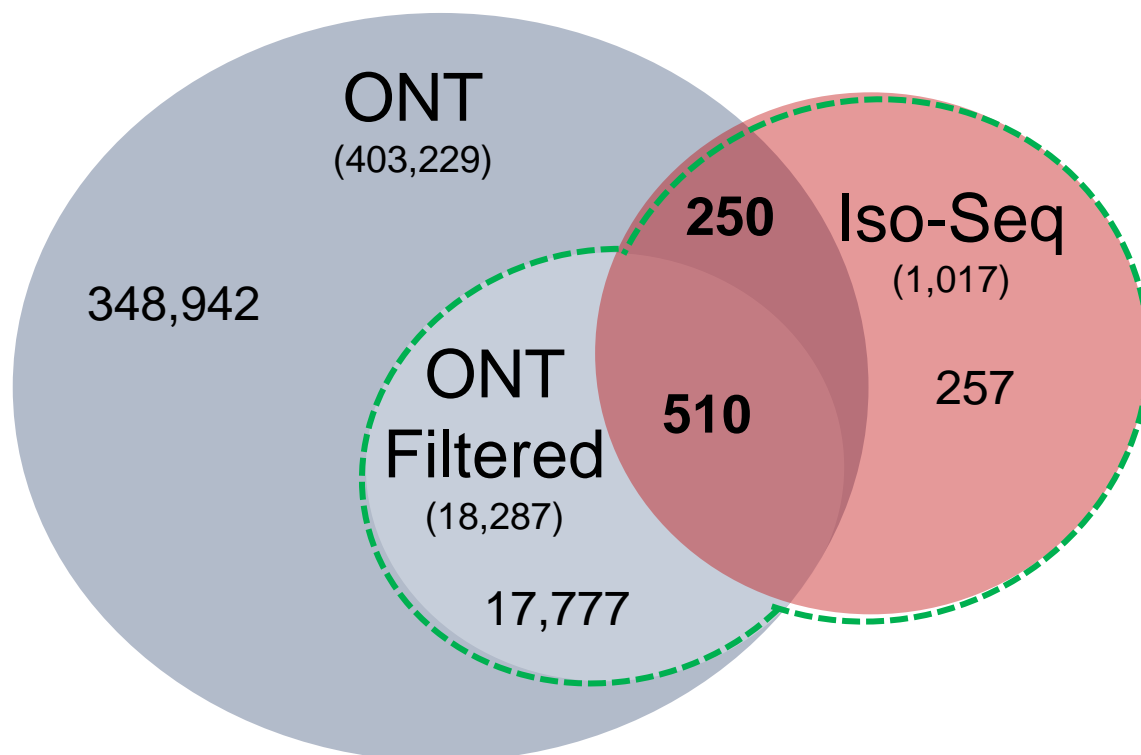
E Batch 2 (Target Capture & Final overlay)



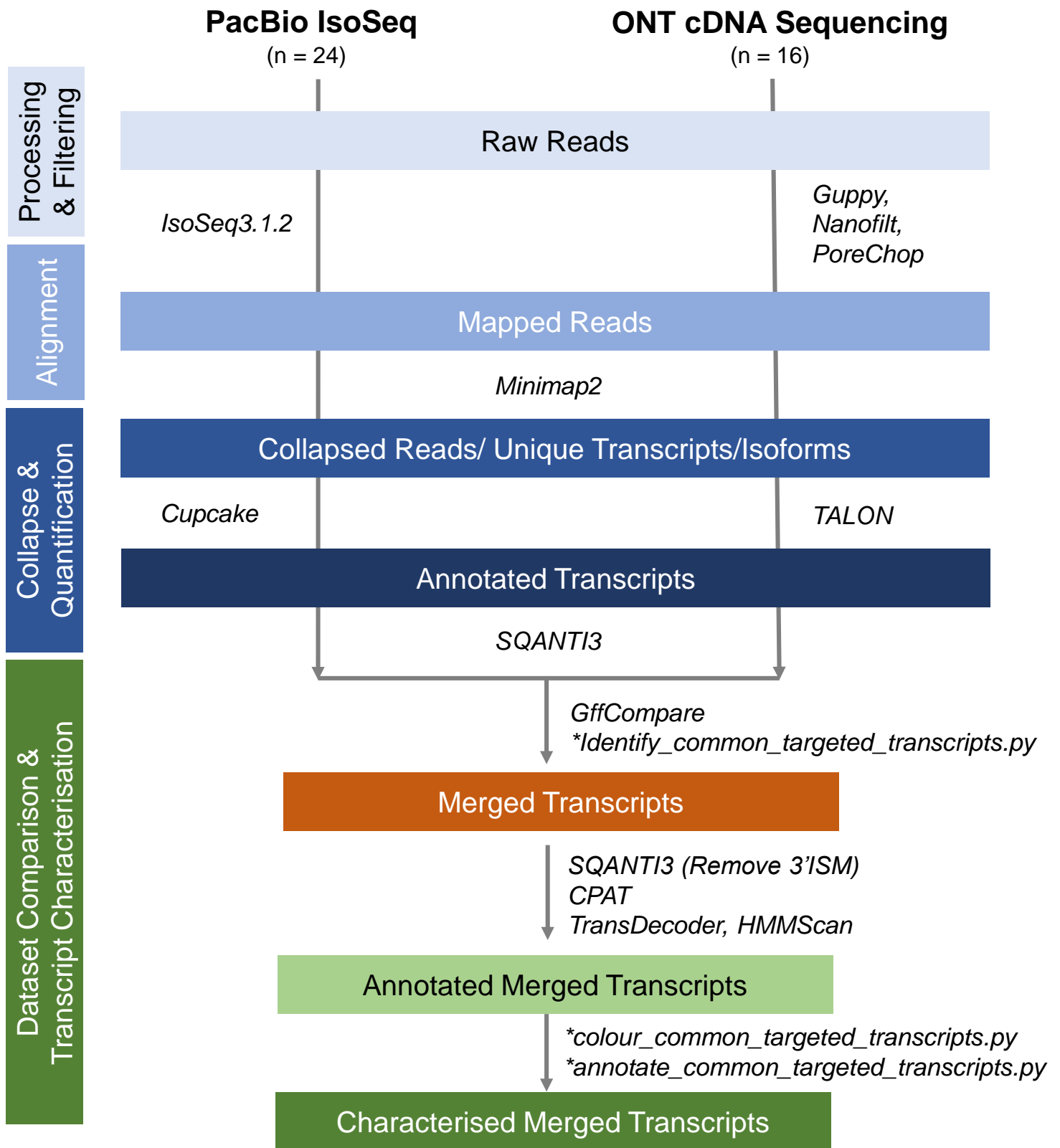
F Batch 3 (Final)



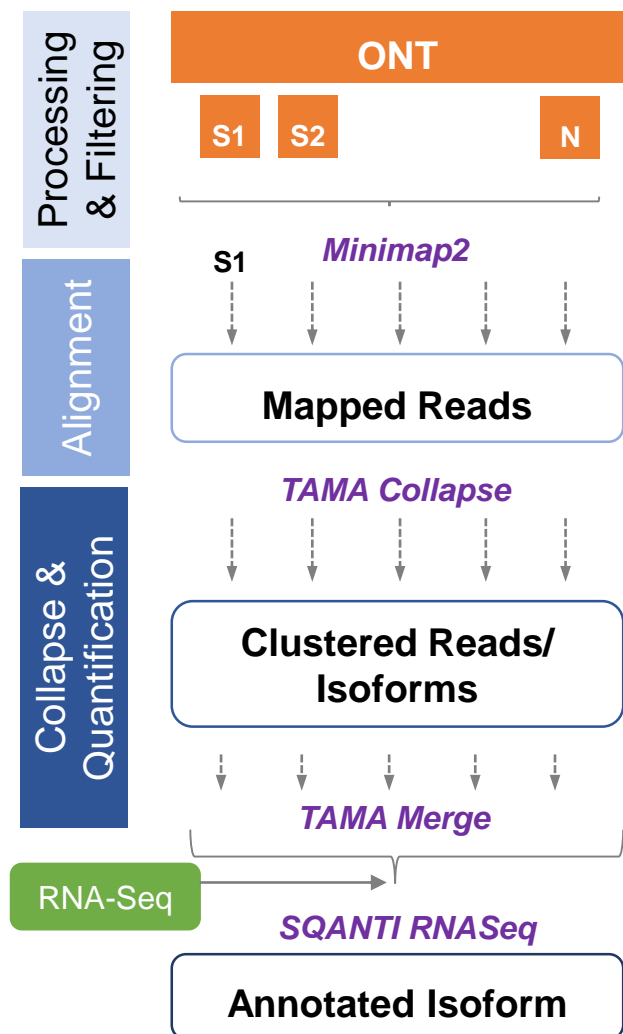




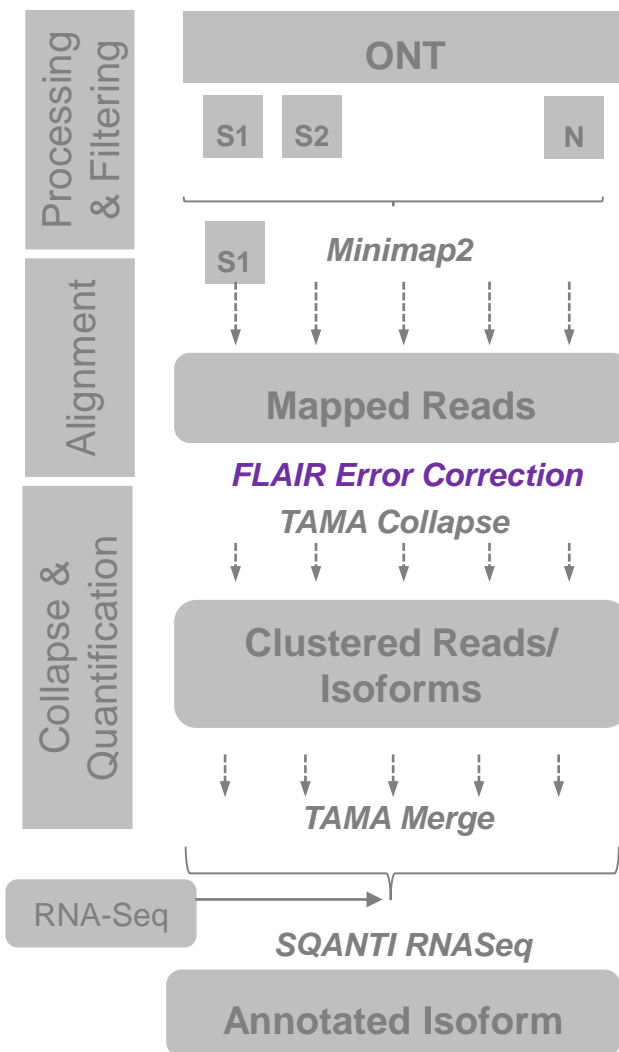
— — Transcripts retained for annotation (18,794)

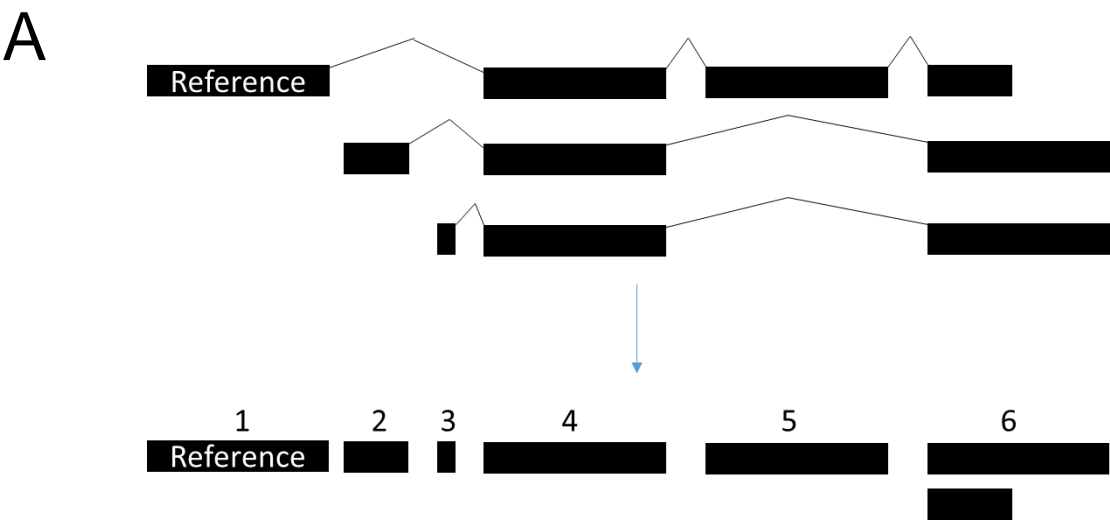


A



B





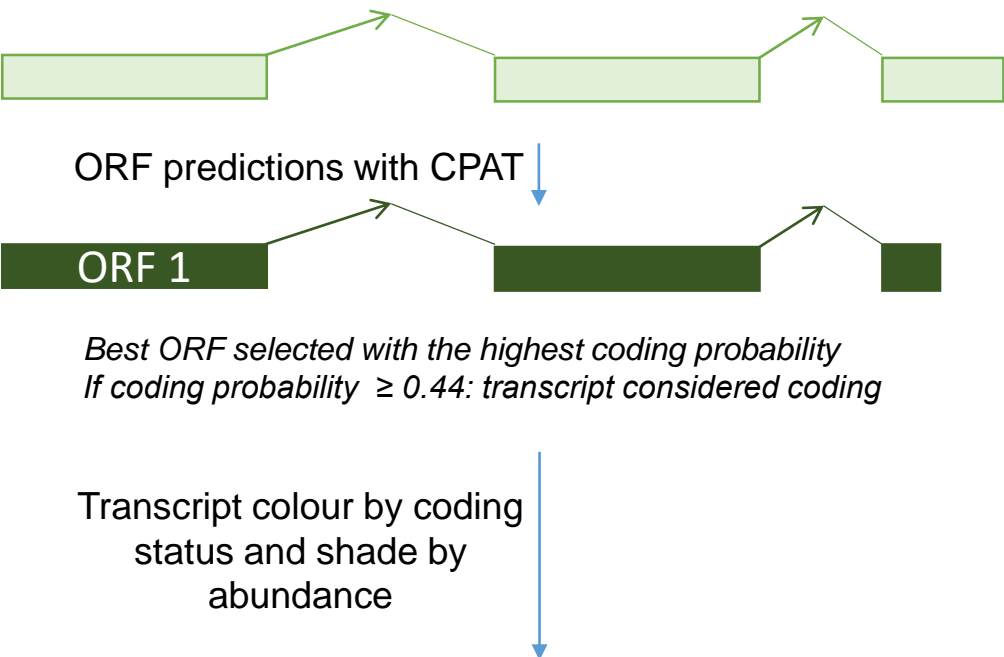
B

↔ Wobble allowed (10bp)

↔ IR threshold (100bp)

Reference	Classifications
	Match
	Truncated A5, A3
	Extended A5, A3
	Intron Retention
	Novel Exon
	Alternative Promoter
	Alternative Terminator

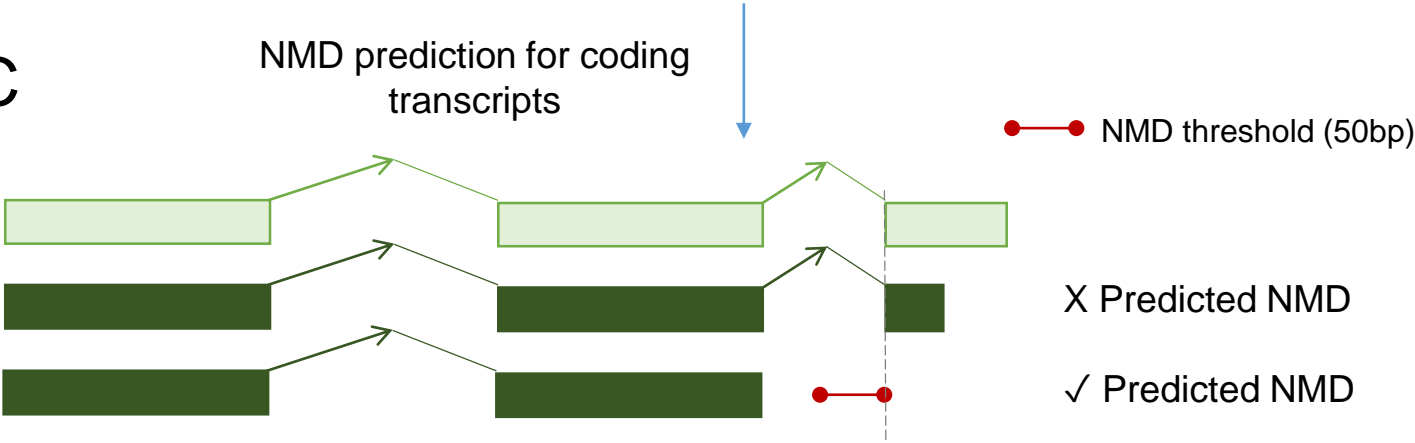
A



B

		Coding Status		
		Coding	Non-coding	No ORF
Abundance (FL Reads)	≤ 25			
	$25 < FL \leq 50$			
	$50 < FL \leq 100$			
	$100 < FL \leq 250$			
	≥ 500			

C



Transcript is predicted for NMD if distance between ORF end and last exon-exon junction is more than 50bp