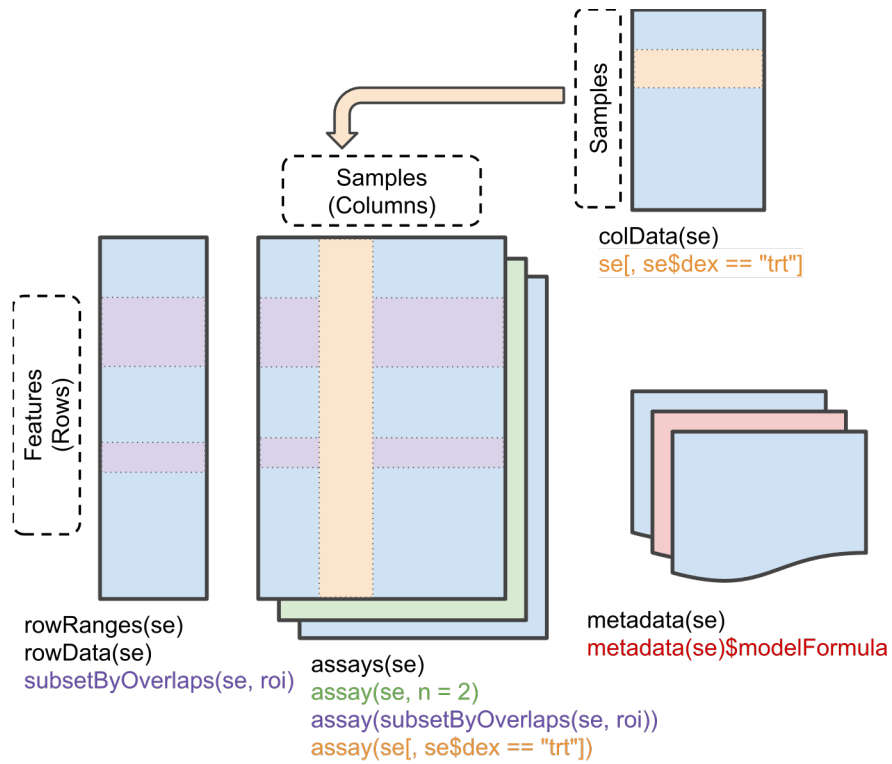
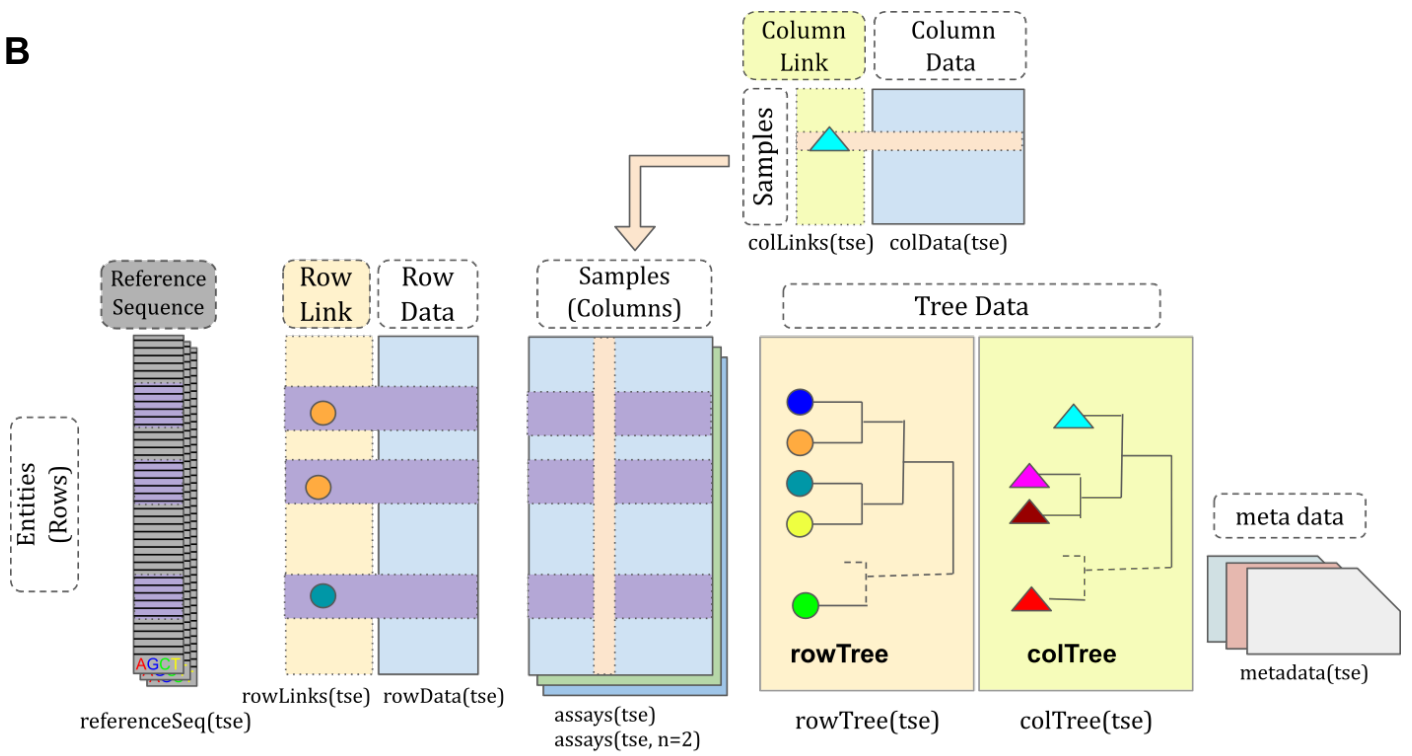
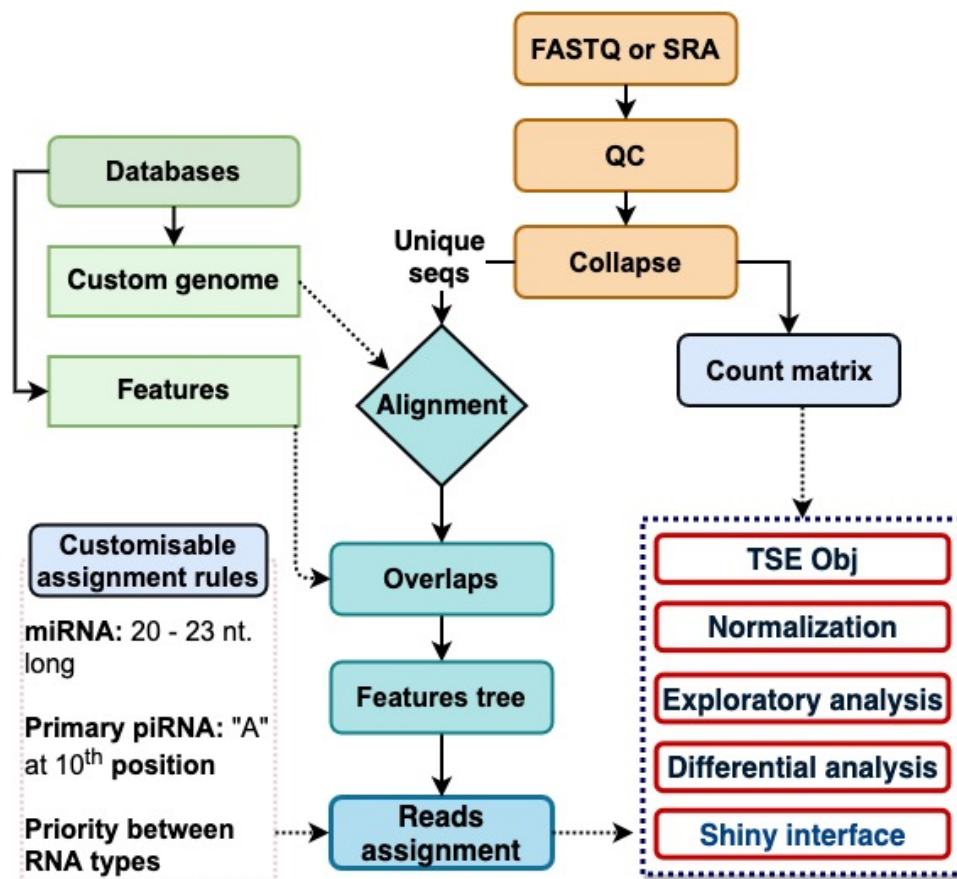


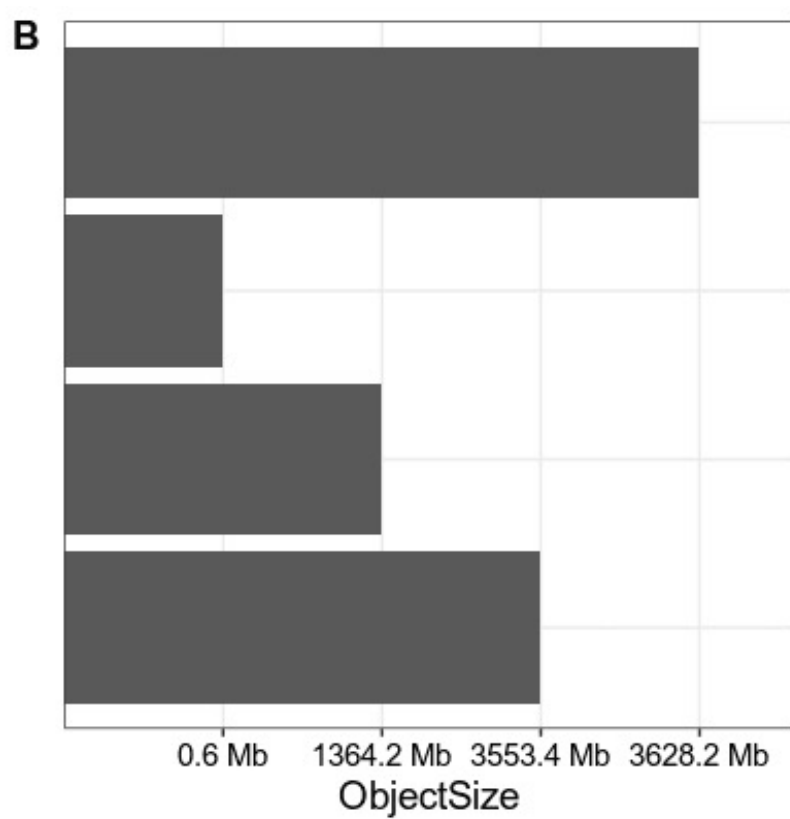
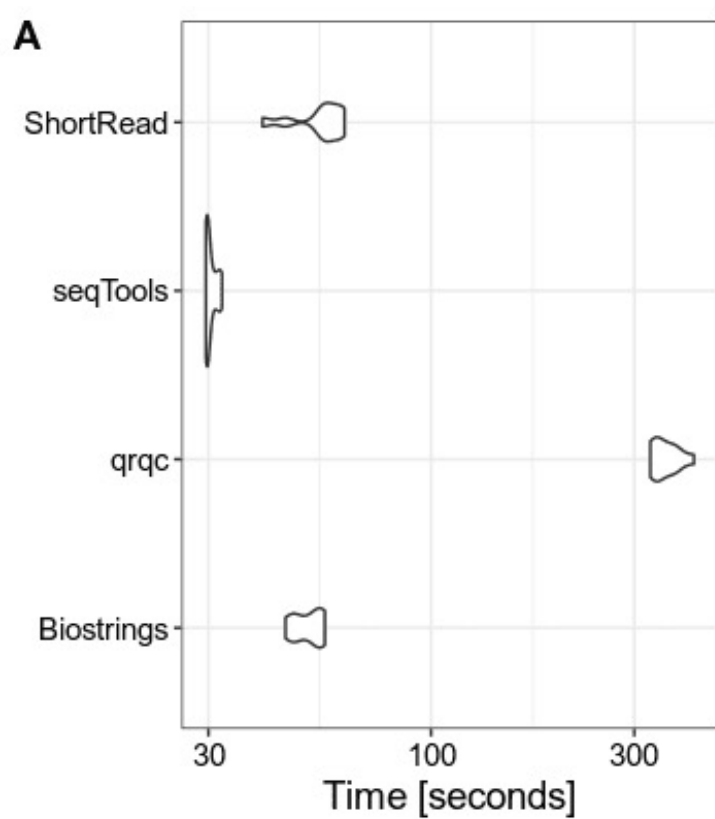
**A**



**B**



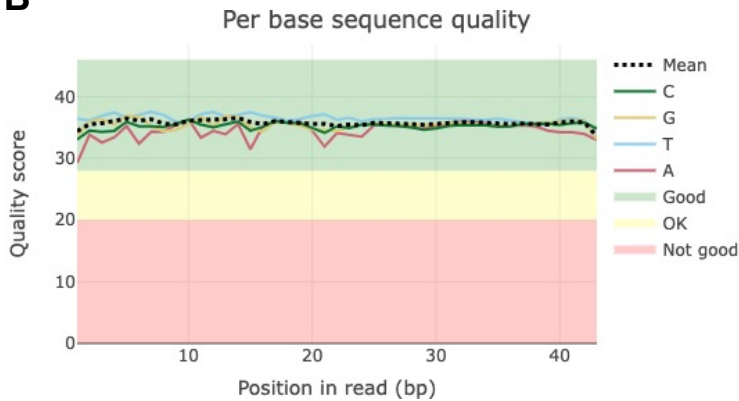




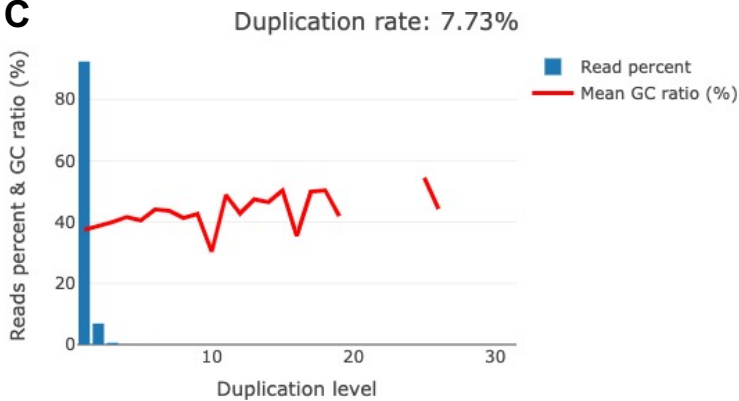
A

SRR13129036	
General	
Sequencing	single-end (43 cycles)
Mean length before filtering	43
Mean length after filtering	30
Duplication rate	7.73% (may be overestimated since this is SE data)
Before QC	
Total reads	11451376
Total bases	492409168
Q20 bases	463828448 (94.1957%)
Q30 bases	436401257 (88.6257%)
GC content	52.99%
After QC	
Total reads	11102724
Total bases	340958795
Q20 bases	324750375 (95.2462%)
Q30 bases	307362232 (90.1464%)
GC content	53.66%
Filtering	
Reads passed filters	11102724 (96.96%)
Reads with low quality	126063 (1.1%)
Reads with too many N	1 (0%)
Reads too short	222588 (1.94%)
Reads too long	0 (96.96%)

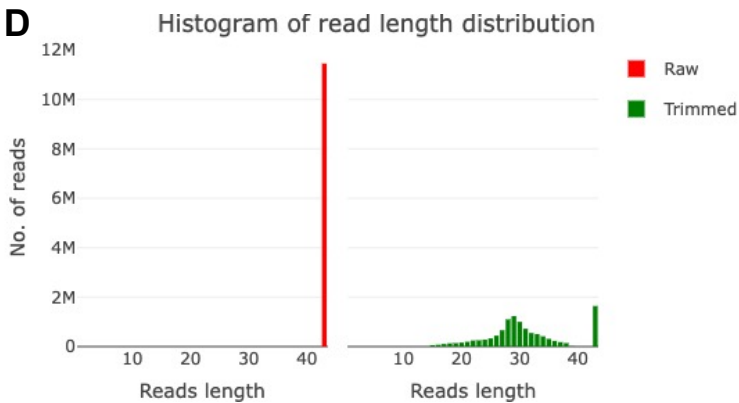
B

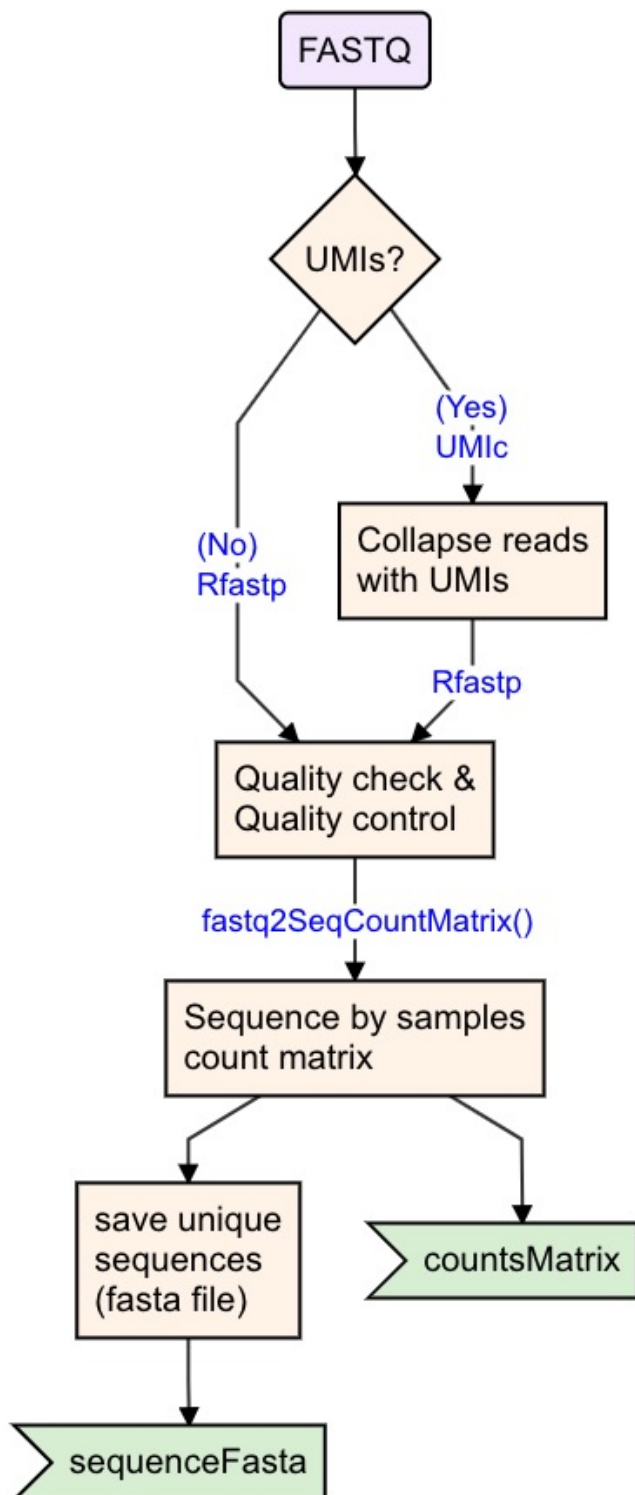


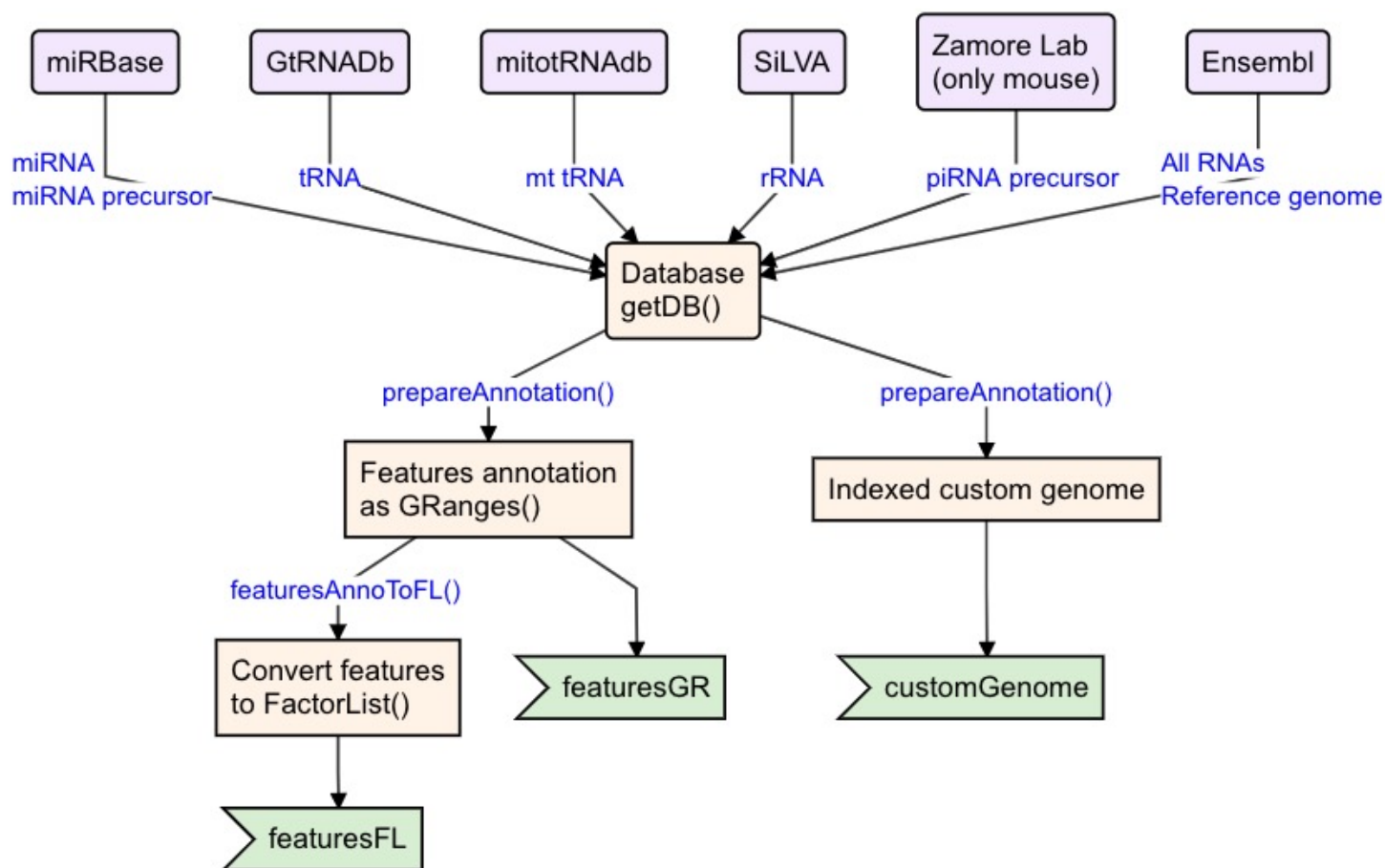
C

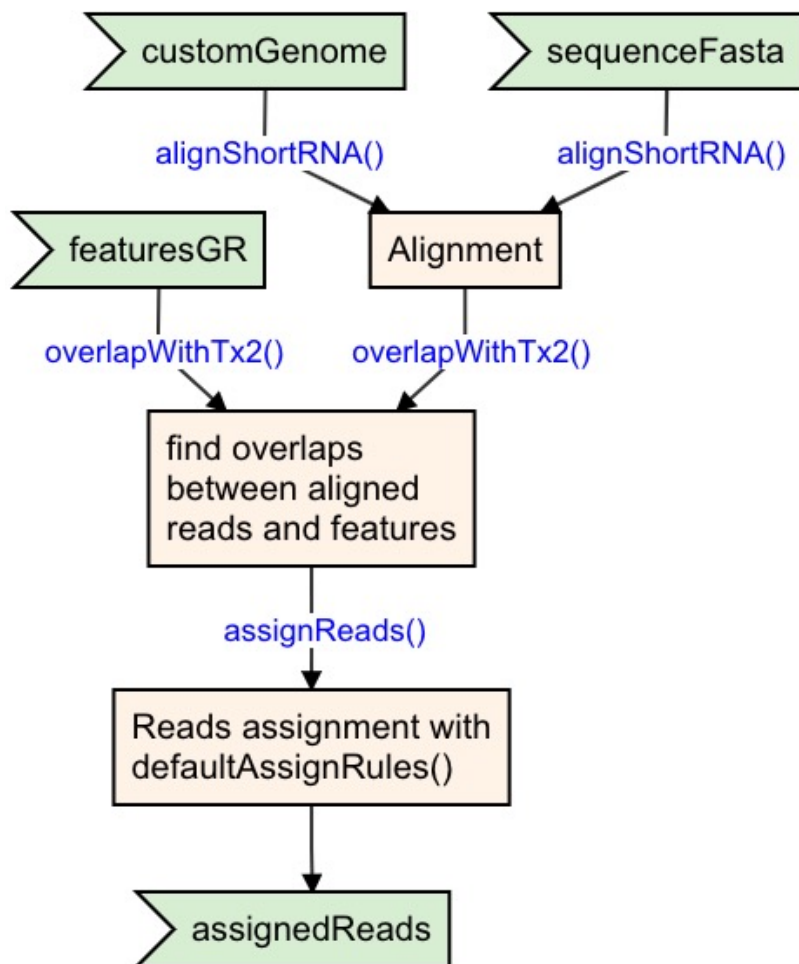


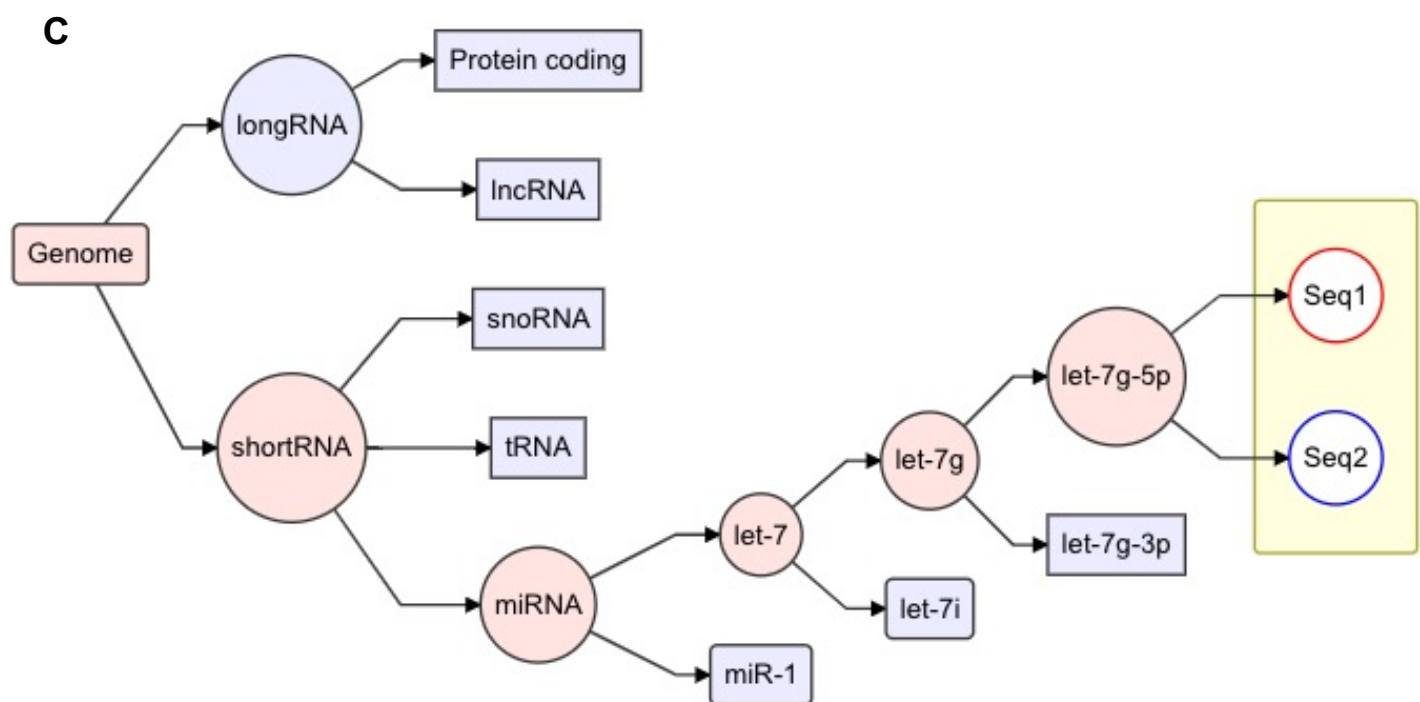
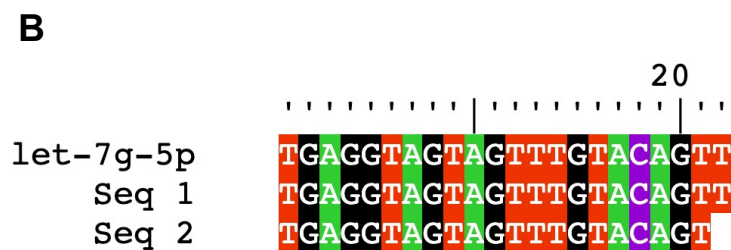
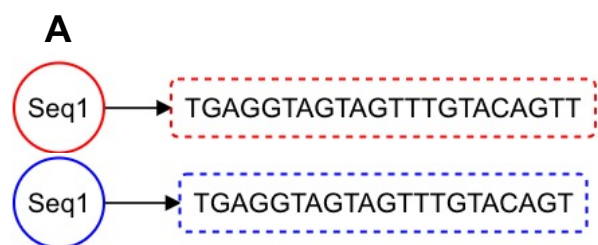
D





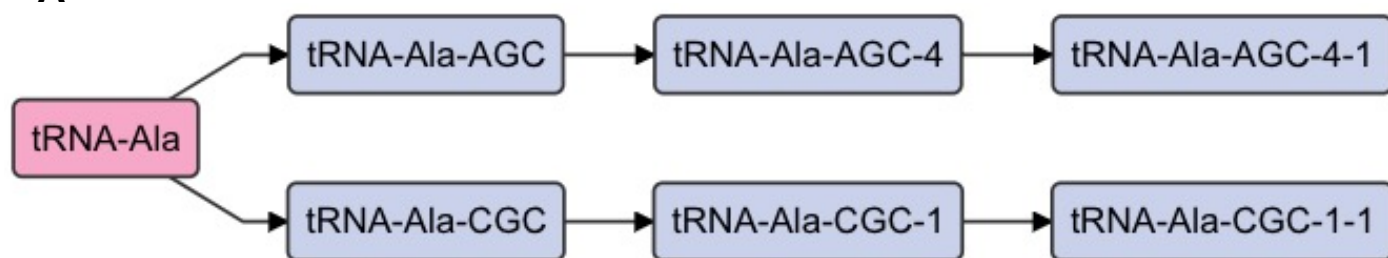




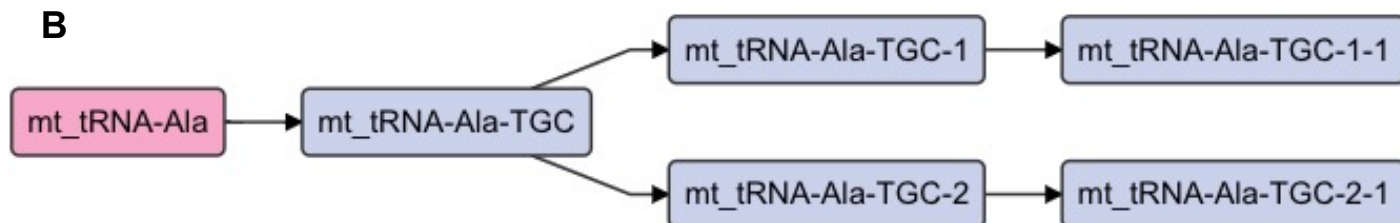




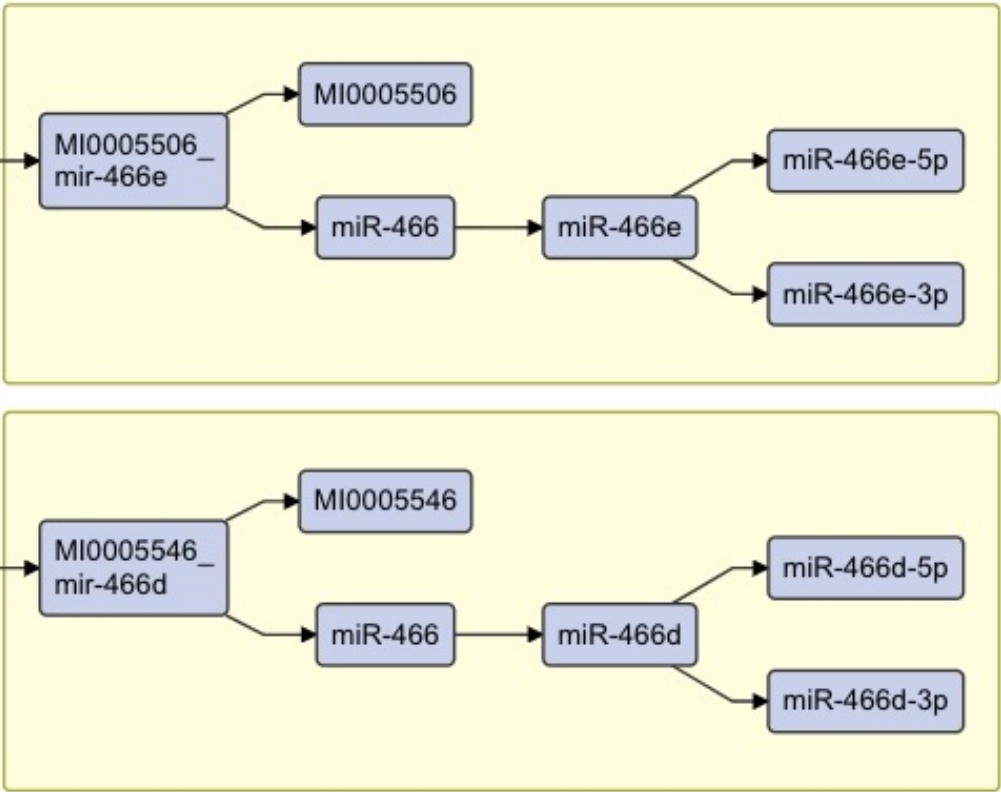
**A**



**B**



miRNAcluster\_  
2:10465287-10518279+



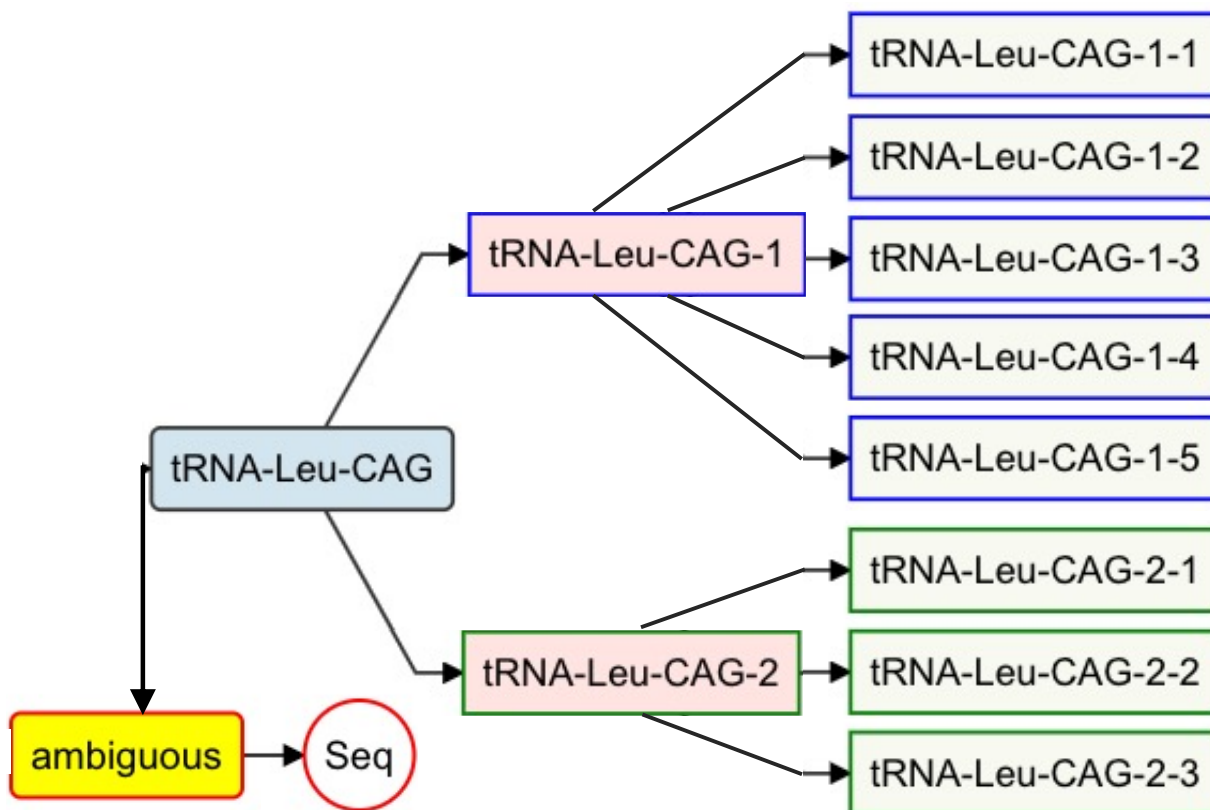
**A**

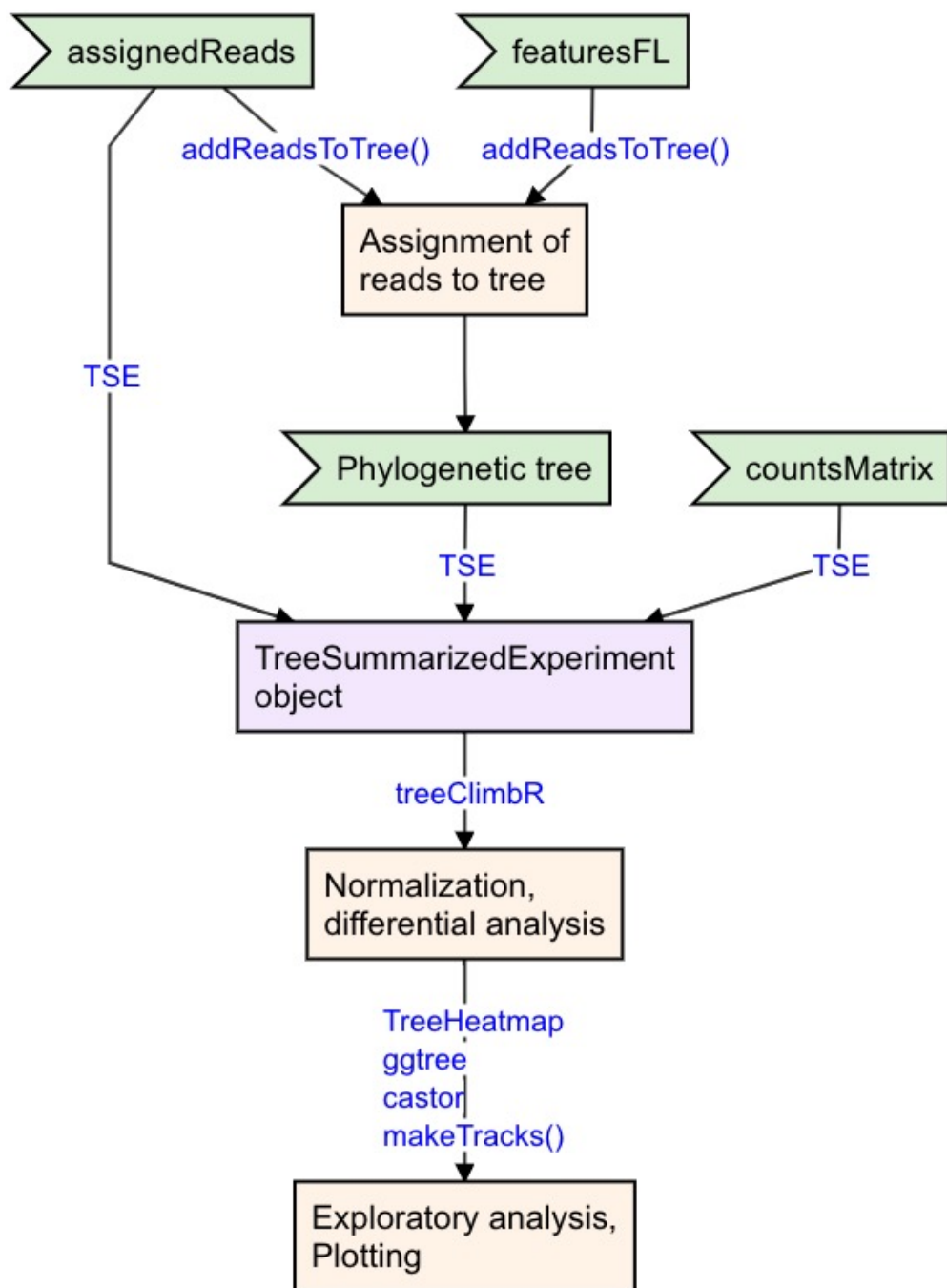
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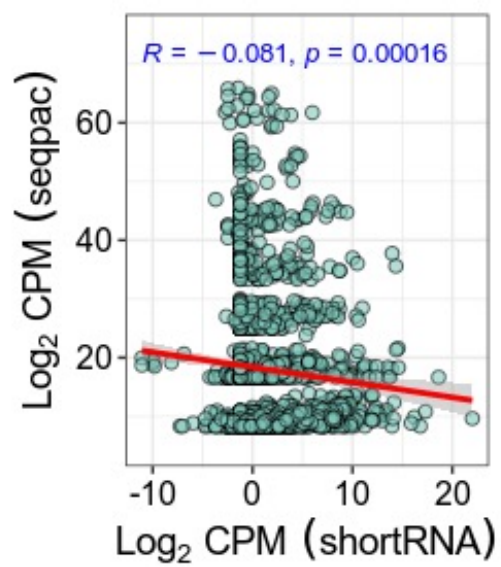
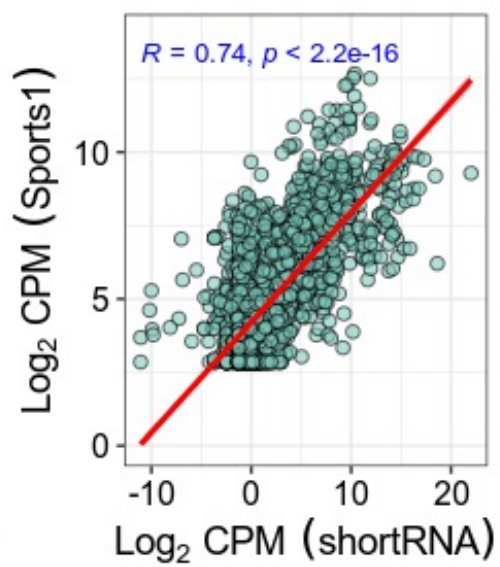
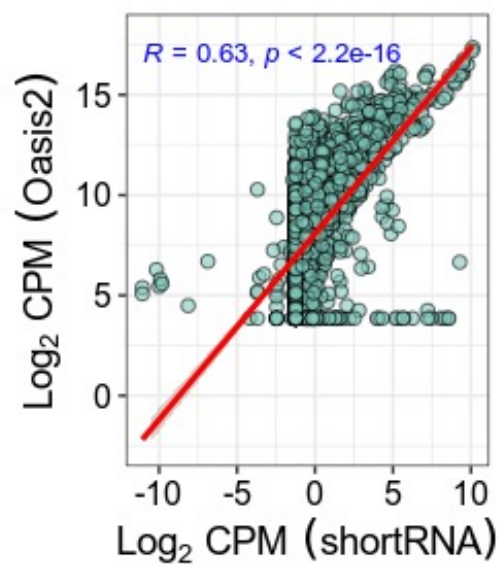
**B**

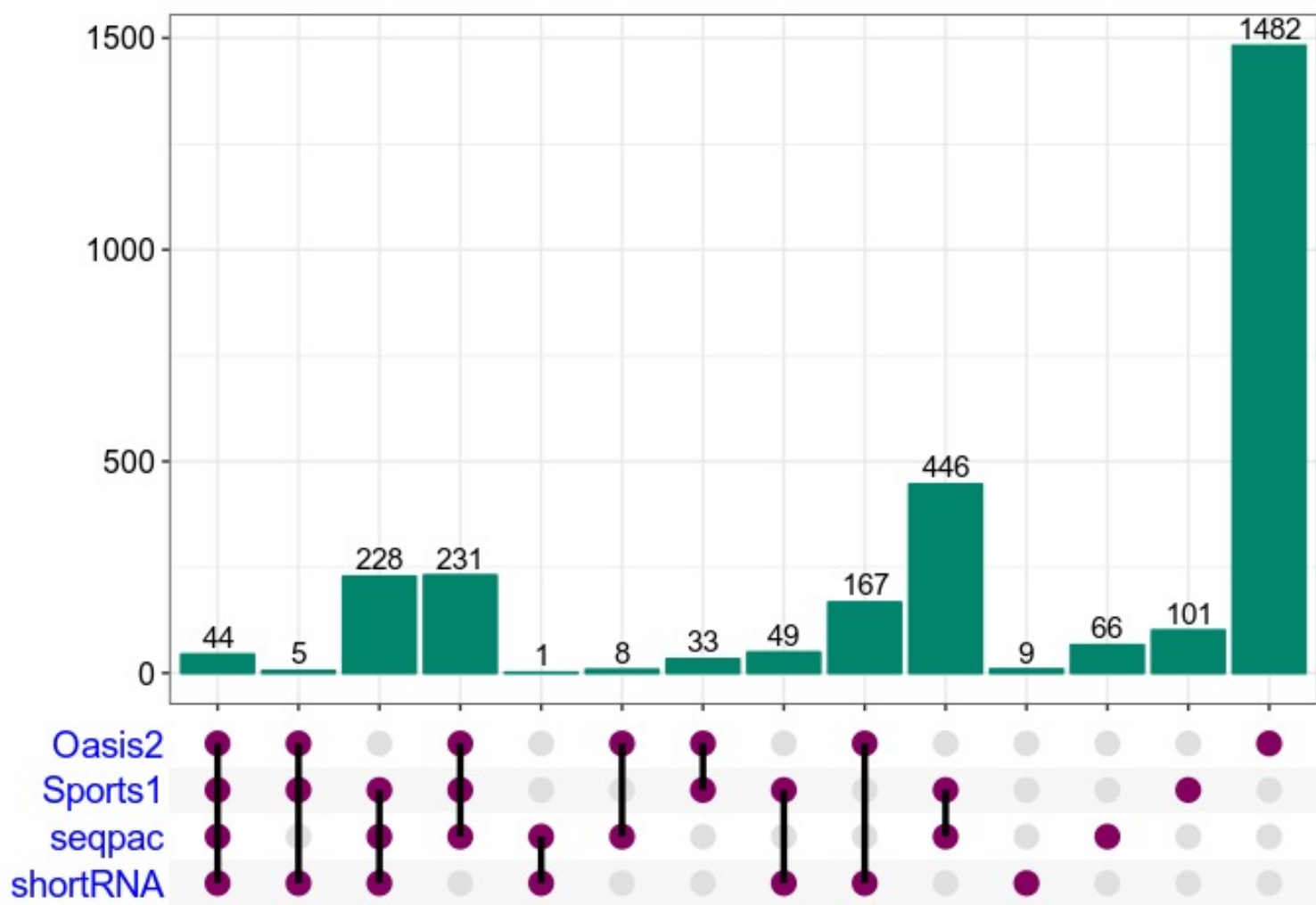
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	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAAT				
tRNA-Leu-CAG-1-1	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA				
tRNA-Leu-CAG-1-2	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA				
tRNA-Leu-CAG-1-3	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA				
tRNA-Leu-CAG-1-4	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA				
tRNA-Leu-CAG-1-5	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA				
tRNA-Leu-CAG-2-1	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTTCTGACA				
tRNA-Leu-CAG-2-2	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTTCTGACA				
tRNA-Leu-CAG-2-3	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTTCTGACA				

**C**

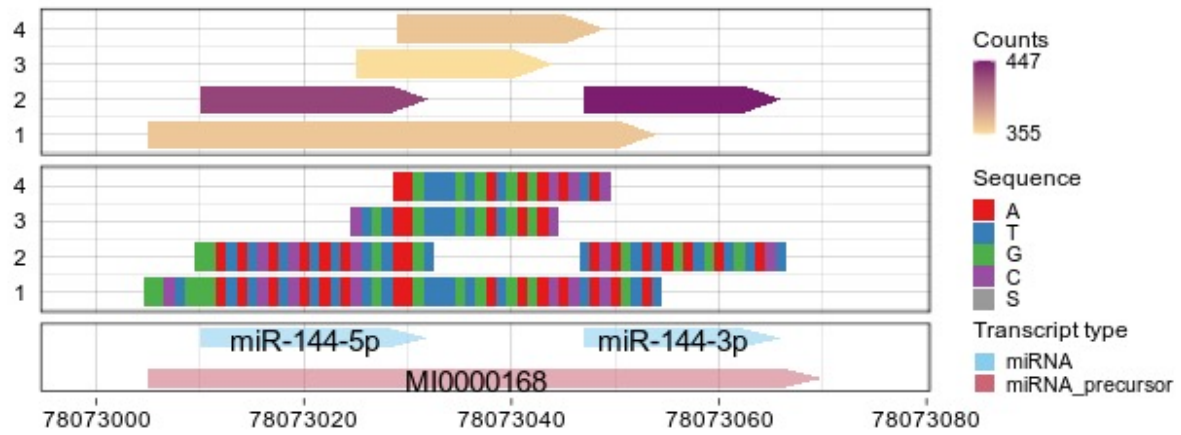


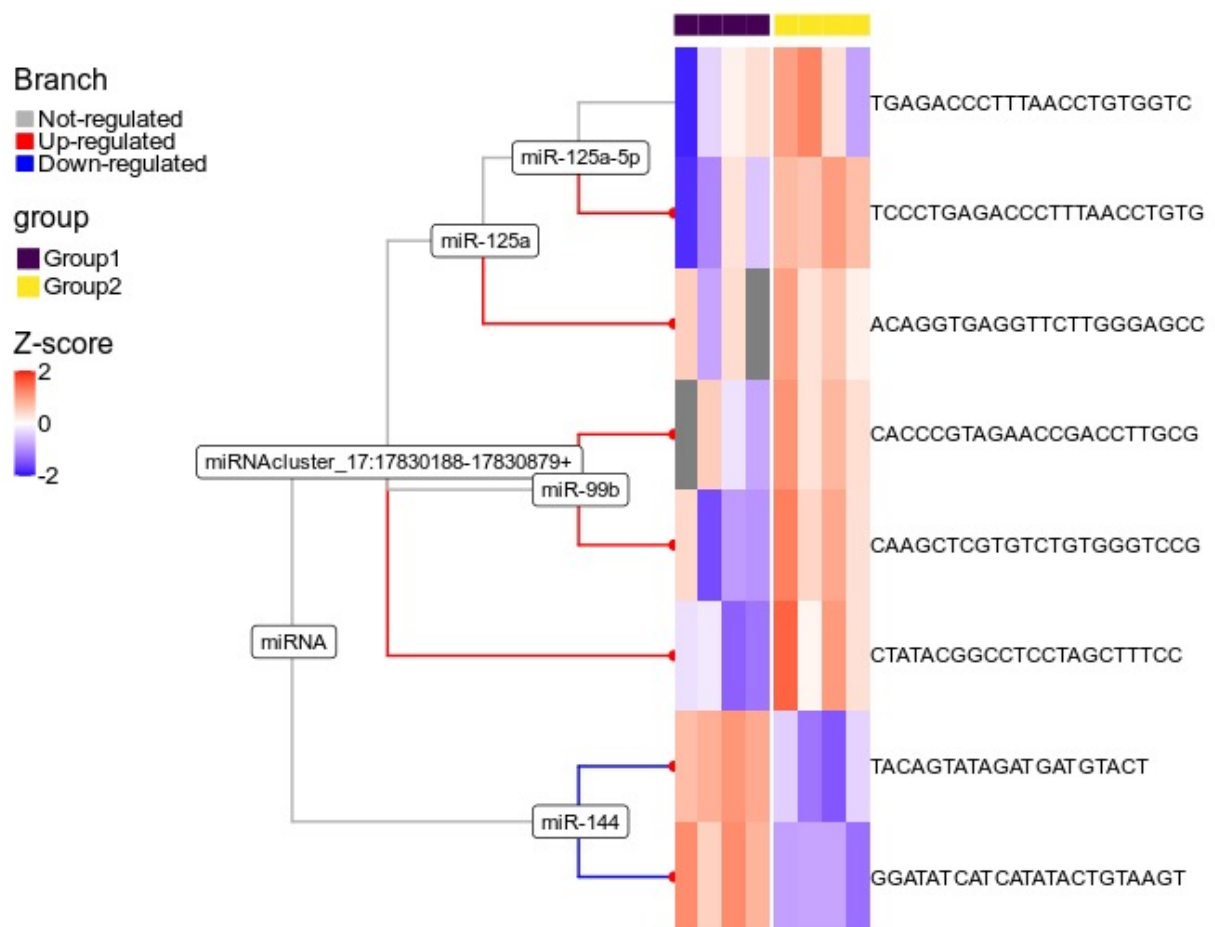




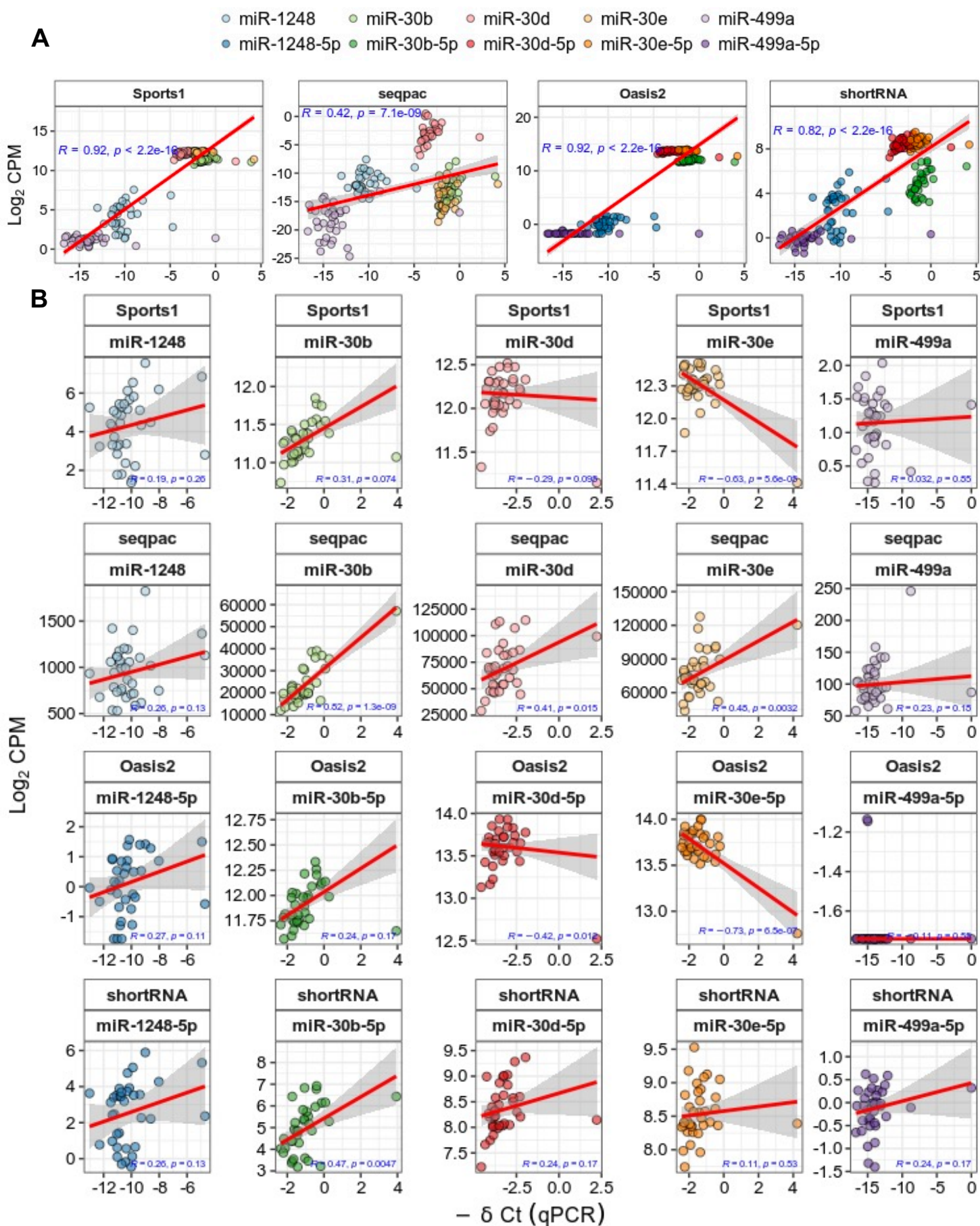


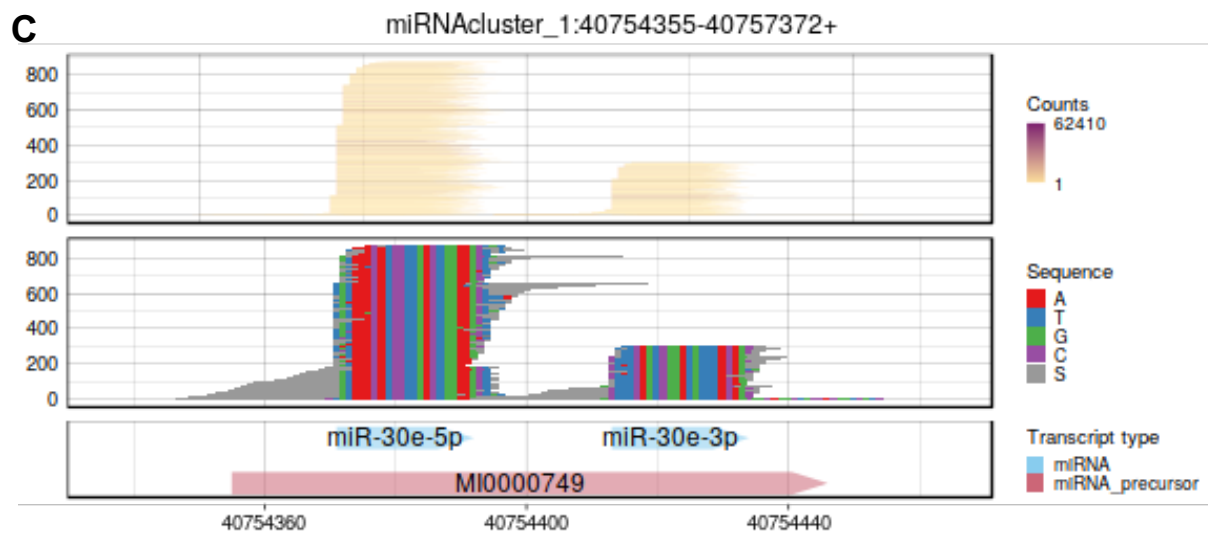
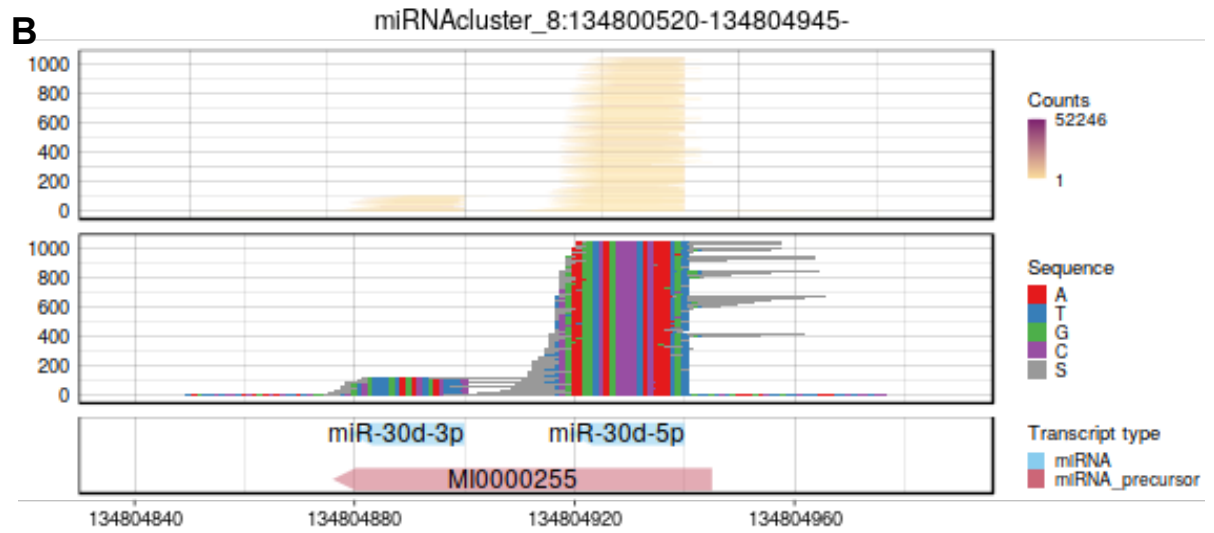
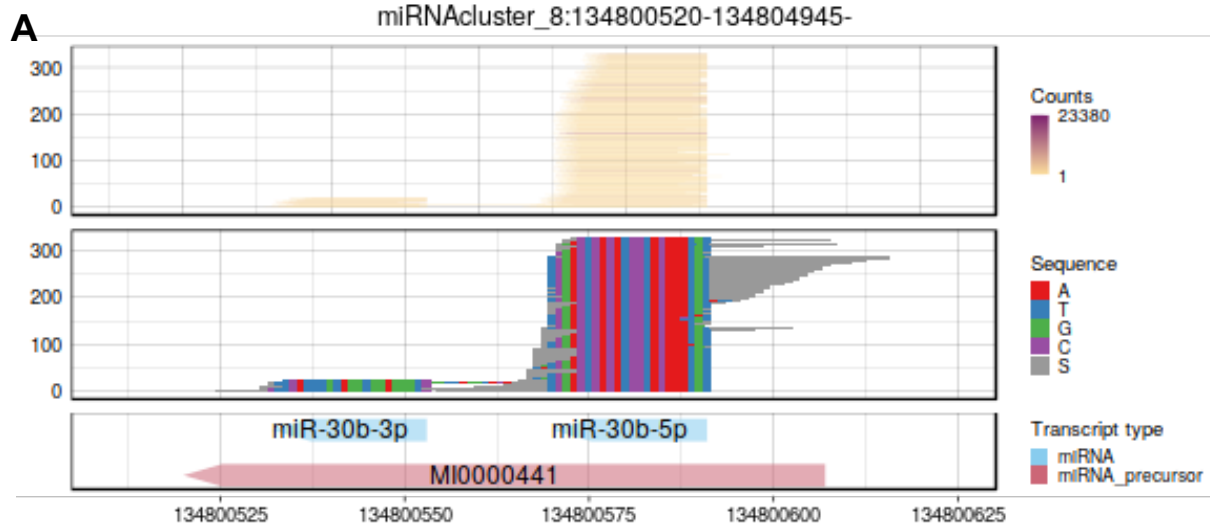
# miRNAcluster\_11:78073005-78073241+

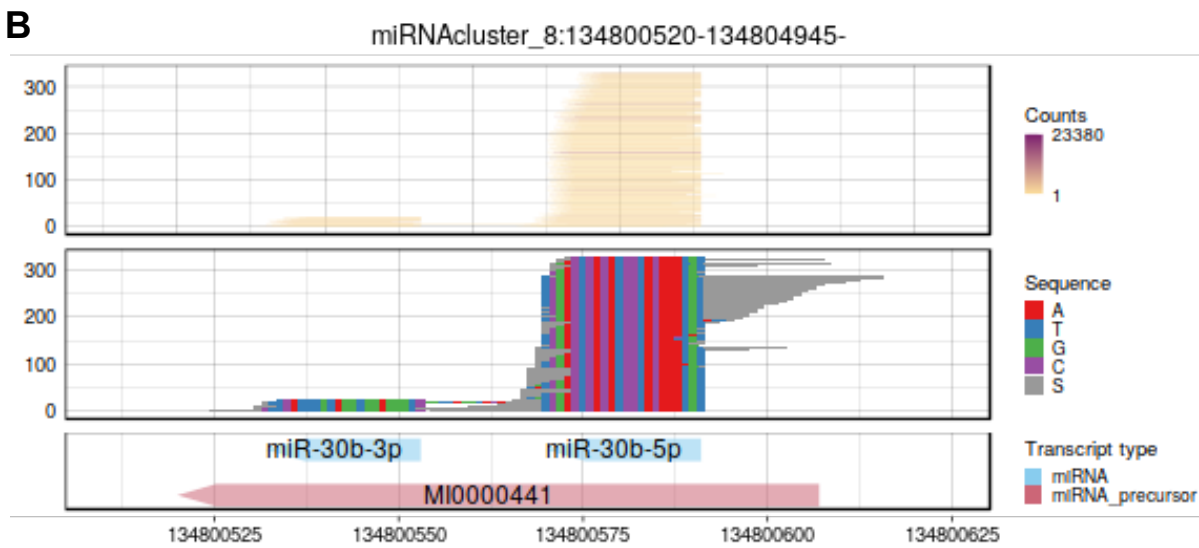
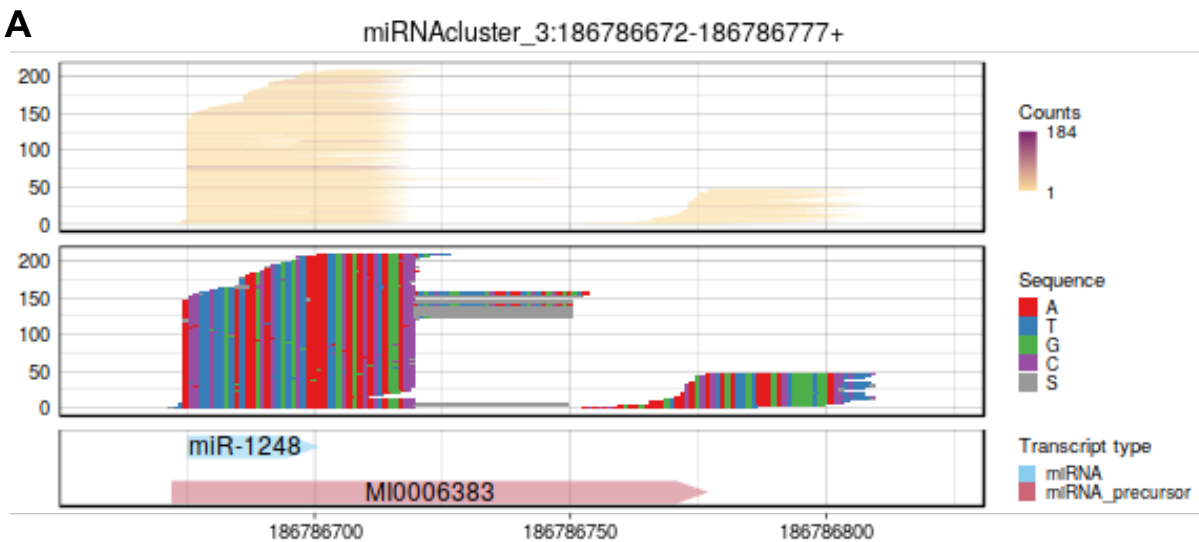






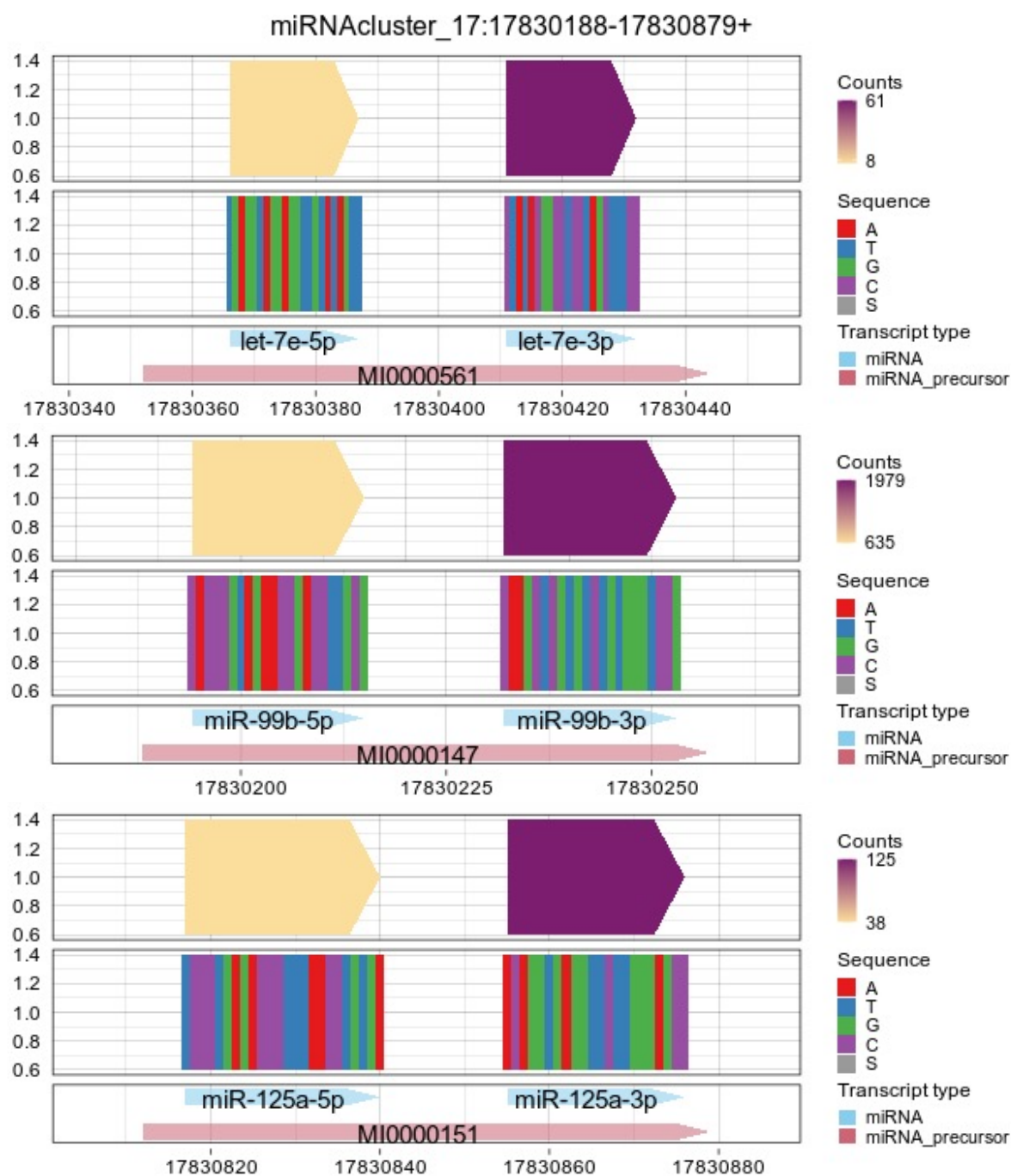










**A****B**