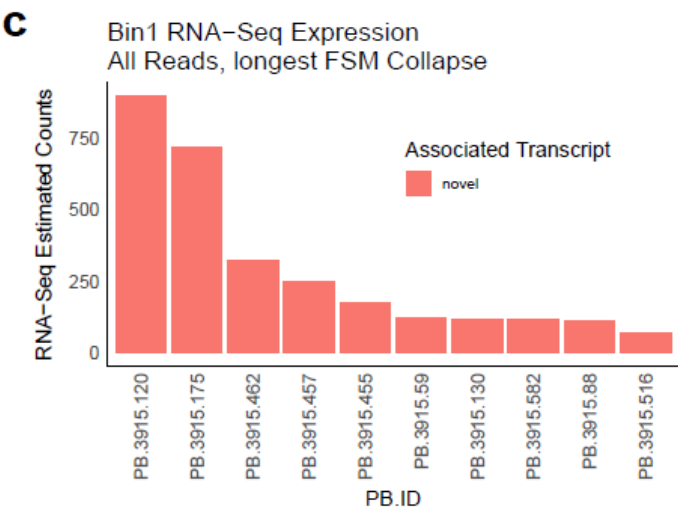
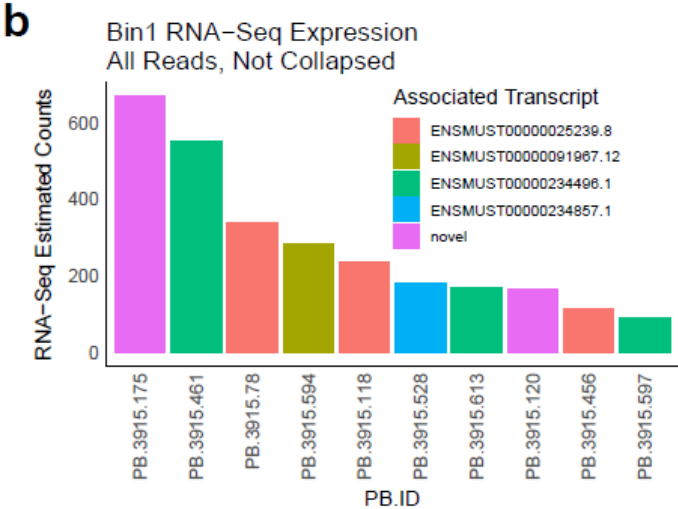
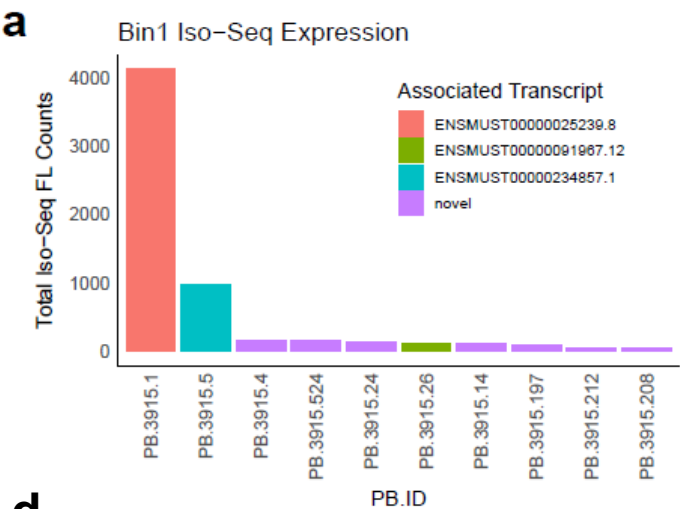







d

Gene	Associated Transcript	Length (bp)	Iso-Seq Mean Expression	RNA-Seq Expression	Structure
CLU	PB.2634.2 (FSM) ENSMUST00000022616.13	2175	2798	10.4, 13.4	
	PB.2634.365 (ISM) ENSMUST00000022616.13	1484	109	10568,NA	
	PB.2634.299 (NIC)	1688	5	38.6, 10477	



d

Gene	Associated Transcript	Length (bp)	Iso-Seq Mean Expression	RNA-Seq Expression	Structure
BIN1	PB.3915.1 (FSM) ENSMUST00000025239.8	2623	172	0, 0	
	PB.3915.120 (NIC)	7474	0.375	166.4, 898.6	
	PB.3915.175 (NIC)	1846	40.6	670.4, 718.4	

Reference Isoform				Label	Description
Known Genes	Known Isoforms			Full Splice Match (FSM)	Reference and query isoform have the same number of exons and matching internal junction. 5' and 3' end can differ by any amount
				Incomplete Splice Match (ISM)	Query isoform has fewer 5' exons than reference, but same 3' exons and internal junctions. 5' and 3' ends can differ by any amount
	Novel Isoforms			Novel In Catalogue (NIC)	Query isoform has different number and exon combination using a combination of known donor/acceptor splice sites
				Novel Not in Catalogue (NNC)	Query isoform has different combination of exons with ≥ 1 unannotated/novel donor or acceptor site
				Fusion	Query isoform incorporate exons from two or more genes
				Genic Intronic/Genomic	Query isoform is completely contained within annotated intron/overlaps with introns and exons
Novel Genes			Antisense	Query isoform overlaps with reference isoform but in opposite direction	
			Intergenic	Query isoform is in the intergenic region	