		Naive	**0 division**	**2 divisions**
Unique	Isoforms	**10,527**	**12,602**	**11,109**
	Genes	**5,644**	**5,902**	**5,499**
Gene classification	Annotated	4,751	5,582	5,162
	Novel	893	320	337
Characterization of transcripts based on splice junctions	FSM (Full Splice Match)	5,552	7,324	6,550
	ISM (Incomplete Splice Match)	1,112	1,978	1,878
	NIC (Novel In Catalog)	1,824	1,761	1,407
	NNC (Novel Not in Catalog)	921	1,047	793
	Genic / Genomic	98	73	55
	Antisense	343	156	156
	Fusion	15	8	6
	Intergenic	662	253	264
	Genic Intron	0	2	0
Splice junction classification	Known canonical	44,857 (97.47%)	53,239 (97.6%)	48,206 (98.05%)
	Known non-canonical	37 (0.08%)	29 (0.05%)	32 (0.07%)
	Novel canonical	879 (1.91%)	1,020 (1.87%)	709 (1.44%)
	Novel non-canonical	247 (0.54%)	261 (0.48%)	217 (0.44%)

Table S1. Summary of Pacbio long read sequencing analysis.