

Table S1 Read mapping summary.

Reads mapping	HESCs	ESERs	FLERs	PBERs
Raw reads	124,622,688	117,854,028	45,861,338	59,418,706
Reads after filtering rRNAs	117,215,844	111,249,079	39,879,190	56,212,103
Mapped reads	49,560,369	42,813,442	12,830,921	14,361,541
Mapped to unique loci(/mapped)	37,880,552(76%)	31,153,327(72%)	8,922,516(70%)	9,319,730(65%)
Mapped to multi loci(2-10)	9,824,103(19.8%)	10,178,601(23.8%)	3,367,100(26.2%)	4,175,432(29%)
Mapped to introns	12,293,665(32.5%)	10,882,646(34.9%)	2,884,795(32.3%)	4,217,748(45.3%)
Mapped to exons	14,096,495(37.2%)	13,937,099(44.7%)	3,141,698(35.2%)	3,197,192(34.3%)
Mapped to intergenic regions	9,873,062(26.1%)	5,189,477(16.7%)	2,650,619(29.7%)	1,657,713(17.8%)
Mapped to intron-exon junctions	1,617,330(4.3%)	1,144,105(4.3%)	245,404(2.8%)	247,077(2.7%)