

Supplemental Table S1. Illumina alignment summary for RNA-seq samples.

Sample ID	Sex	# of reads	# of aligned reads	alignment %
mule3703CG	Male	62554362	39578210	63.27%
mule3710CG	Male	31610658	5996733	18.97%
mule3713CG	Female	31240756	22727279	72.75%
mule3561CG	Female	30312343	20198937	66.64%
mule3669CG	Female	19344761	9290943	48.03%
mule3680CG	Female	22625558	12714609	56.20%
mule4107CG	Female	27623537	18732426	67.81%
hinny3702	Male	52769690	39578210	63.27%
hinny4108	Male	32205536	19693181	61.15%
horse3654CG	Male	32411158	13874727	42.81%
horse3879CG	Female	68433090	46383671	67.78%
horse4061CG	Female	32083321	20602456	64.22%
horse4102CG	Female	29369756	15893689	54.12%
horse4105CG	Female	30068132	19694290	65.50%
horse4119CG	Female	29078593	19406166	66.74%
donkey3879	Male	45936028	33142526	72.15%
donkey3643CG	Male	31915778	21914722	68.66%
donkey3694CG	Male	22987558	7462943	32.47%
donkey3693CG	Female	28752411	20634904	71.77%