Supplemental Table S3. Mapping Statistics of RNA-Seq Reads to the Reference

Sample	Total	Mapped	Uniq	Multiple	Reads	Reads
	Reads	Reads	Mapped	Map	Map to	Map to '-'
			Reads	Reads	<b>'+'</b>	
CU2-1	57,98	56,569,885	54,801,854	1,768,031	29,503,106	29,498,494
	2,682	(97.56%)	(94.51%)	(3.05%)	(50.88%)	(50.87%)
CU2-2	45,40	44,284,167	42,905,121	1,379,046	23,100,641	23,091,572
	4,440	(97.53%)	(94.50%)	(3.04%)	(50.88%)	(50.86%)
CU2-3	55,33	53,749,568	51,994,374	1,755,194	28,130,955	28,121,964
	8,204	(97.13%)	(93.96%)	(3.17%)	(50.83%)	(50.82%)
OE-W	47,70	46,031,123	44,372,956	1,658,167	24,255,733	24,227,618
OX1-1	2,010	(96.50%)	(93.02%)	(3.48%)	(50.85%)	(50.79%)
OE-W	55,85	53,502,525	51,699,603	1,802,922	28,057,550	27,999,475
OX1-2	1,822	(95.79%)	(92.57%)	(3.23%)	(50.24%)	(50.13%)
OE-W	52,42	50,000,183	48,381,724	1,618,459	26,130,025	26,081,092
OX1-3	4,776	(95.38%)	(92.29%)	(3.09%)	(49.84%)	(49.75%)

Genome.