

Table 3 Reference genome comparison results

Map to genome	CK1		CK2		T1		T2	
	Number of reads	Percentage	Number of reads	Percentage	Number of reads	Percentage	Number of reads	Percentage
Total clean reads	50 898 872	100%	47 053 916	100%	56 962 334	100%	55 148 520	100%
Total mapped reads	42 751 411	83.99%	43 799 711	93.08%	47 686 172	83.72%	50 399 573	91.39%
Total unmapped reads	8 147 461	16.01%	3 254 205	6.92%	9 276 162	16.28%	4 748 947	8.61%
Uniquely mapped reads	40 975 578	80.50%	41 882 143	89.01%	45 917 037	80.61%	48 383 173	87.73%
Reads map to “+”	21 520 911	40.24%	20 955 767	44.54%	22 969 364	40.32%	20 415 139	44.40%
Reads map to “-”	21 499 452	40.20%	20 926 376	44.47%	22 947 673	40.29%	20 386 904	44.34%
Non-splice reads	27 388 205	51.21%	28 745 384	61.09%	28 292 569	49.67%	27 376 856	59.54%
Splice reads	15 632 158	29.23%	13 136 759	27.92%	17 624 468	30.94%	13 425 187	29.20%