

Table S5. Statistical results of alignment information with reference genome sequence

Samples	Samples ID	Total reads	Mapped reads	Mapped Reads(+)	Mapped Reads(-)
ML1	S07	5442275	2812972(51.69%)	2016065(37.04%)	796907(14.64%)
ML1	S08	7039688	3025250(42.97%)	2139088(30.39%)	886162(12.59%)
ML1	S09	6707220	3514381(52.40%)	2490399(37.13%)	1023982(15.27%)
CMS1	S10	7350251	3769811(51.29%)	2612210(35.54%)	1157601(15.75%)
CMS1	S11	10572690	5663494(53.57%)	4000370(37.84%)	1663124(15.73%)
CMS1	S12	7339089	3852452(52.49%)	2640131(35.97%)	1212321(16.52%)
ML2	S01	3567922	999775(28.02%)	696390(19.52%)	303385(8.50%)
ML2	S02	3999590	1164923(29.13%)	815905(20.40%)	349018(8.73%)
ML2	S03	3878672	1057913(27.28%)	726391(18.73%)	331522(8.55%)
CMS2	S04	3203022	1446936(45.17%)	1010935(31.56%)	436001(13.61%)
CMS2	S05	3898282	1665137(42.71%)	1155461(29.64%)	509676(13.07%)
CMS2	S06	3785218	1641336(43.36%)	1148022(30.33%)	493314(13.03%)