Table S8. The sequence alignment results of the sample sequence data with the reference genome

Samples	Samples ID	Total reads	Mapped reads	Uniq mapped reads	Multiple mapped reads
ML1	S07	68,768,532	51,673,715 (75.14%)	51,673,715 (75.14%)	1,576,736 (2.29%)
ML1	S08	85,298,784	64,307,383 (75.39%)	64,307,383 (75.39%)	2,112,590 (2.48%)
ML1	S09	78,197,288	60,180,391 (76.96%)	60,180,391 (76.96%)	1,897,858 (2.43%)
CMS1	S10	73,943,440	52,303,161 (70.73%)	52,303,161 (70.73%)	1,475,020 (1.99%)
CMS1	S11	80,664,306	58,978,727 (73.12%)	58,978,727 (73.12%)	2,570,842 (3.19%)
CMS1	S12	74,097,366	53,966,421 (72.83%)	53,966,421 (72.83%)	2,369,705 (3.20%)
ML2	S01	83,770,774	77,887,958 (89.76%)	73,880,571 (85.14%)	4,007,387 (4.62%)
ML2	S02	77,257,468	69,431,461 (89.87%)	66,311,321 (85.83%)	3,120,140 (4.04%)
ML2	S03	75,009,460	64,617,111 (86.15%)	64,617,111 (86.15%)	3,058,521 (4.08%)
CMS2	S04	77,760,428	60,702,156 (78.06%)	60,702,156 (78.06%)	1,645,730 (2.12%)
CMS2	S05	69,712,214	52,983,713 (76.00%)	52,983,713 (76.00%)	1,455,110 (2.09%)
CMS2	S06	80,281,016	63,100,530 (78.60%)	63,100,530 (78.60%)	1,671,295 (2.08%)