

Table S2. The sequencing data mapping statistics and reference genome comparison

Items	Group		SEM
	C	H	
Valid reads	48375098.57	45209943.14	1071083.06
Mapped reads (%)	88.93	89.77	0.27
Unique mapped reads (%)	61.1	60.54	0.22
Multi mapped reads (%)	27.83	29.23	0.35
PE mapped reads (%)	82.72	84.14	0.45

Note: C: control group, H: intensive MR feeding group.