

Supplementary Table 1. Summary of RNA-seq reads mapping of Sijihua and Beihua.

Sample	Total pairs	Uniquely mapped pairs	Mapped ratio
Beihua-WB_1	19,011,300	16,587,532	87.25%
Beihua-WB_2	19,867,853	17,329,283	87.22%
Beihua-WB_3	20,821,749	18,201,062	87.41%
Beihua-GF_1	19,440,581	17,062,764	87.77%
Beihua-GF_2	19,378,840	17,022,163	87.84%
Beihua-GF_3	19,610,884	17,254,536	87.98%

Sample	Total pairs	Uniquely mapped pairs	Mapped ratio
Sijihua-WB_1	20,155,910	17,786,113	88.24%
Sijihua-WB_2	20,702,201	18,592,886	89.81%
Sijihua-WB_3	19,997,260	17,157,451	85.80%
Sijihua-GF_1	19,146,871	17,200,272	89.83%
Sijihua-GF_2	18,875,064	16,701,638	88.49%
Sijihua-GF_3	20,650,767	17,633,993	85.39%