

Supplementary Table S2 The amount of sequencing data of different tissues.

<b>Sample</b>	<b>Raw reads</b>	<b>Raw bases</b>	<b>Clean reads</b>	<b>Clean bases</b>	<b>Q20 rate</b>	<b>Q30 rate</b>	<b>GC content</b>
YRBR1	40,058,032	6,008,704,800	40,058,016	5,917,689,124	99%	97%	45%
YRBR2	40,007,520	6,001,128,000	40,007,420	5,859,369,150	99%	96%	46%
YRBR3	40,017,912	6,002,686,800	40,017,906	5,836,993,448	99%	98%	47%
YRBS1	40,056,210	6,008,431,500	40,056,210	5,857,305,880	99%	97%	46%
YRBS2	40,003,568	6,000,535,200	40,003,564	5,827,549,522	99%	98%	46%
YRBS3	40,064,952	6,009,742,800	40,064,948	5,853,806,962	99%	98%	46%