

**Supplemental Table S2. Quality statistics of sequencing data.**

<b>Samples</b>	<b>Clean reads</b>	<b>Clean bases</b>	<b>GC Content</b>	<b>%≥Q30</b>
CU2-1	28,991,341	8,675,803,280	44.51%	94.59%
CU2-2	22,702,220	6,795,752,998	44.54%	94.14%
CU2-3	27,669,102	8,281,888,480	44.60%	94.48%
OE-WOX1-1	23,851,005	7,138,208,530	44.42%	94.65%
OE-WOX1-2	27,925,911	8,353,871,898	44.07%	93.67%
OE-WOX1-3	26,212,388	7,844,843,546	43.78%	94.29%