

Table S1. Statistics of transcriptome sequencing quality analysis of the wt and *rpl1001Δ* strains

Sample	Raw reads	Clean reads	Clean bases (G)	Error rate	Q20%	Q30%	GC pct
wt-1	47703748	46447832	7.0	0.0	98.3	94.6	41.4
wt-2	46164428	45173776	6.8	0.0	98.5	95.1	41.4
wt-3	45435808	44388600	6.7	0.0	98.1	94.1	41.2
<i>rpl1001</i> -1	46569660	45398452	6.8	0.0	98.6	95.5	41.7
<i>rpl1001</i> -2	45874544	44824696	6.7	0.0	98.4	94.9	41.5
<i>rpl1001</i> -3	47331844	46056410	6.9	0.0	98.3	94.8	41.5