

Table S12. Summary of RNA-seq alignment statistics for AC-containing and AC-lost strains, with reads mapped to the SS20_T2T reference genome.

Strain	Total reads	Mapped reads	Percentage
1695SS11-7S32-1	54,572,474	53,326,810	97.72%
1695SS11-7S32-2	53,136,784	51,974,766	97.81%
1695SS11-7S32-3	52,192,799	51,220,926	98.14%
1695SS11-7S32L-1	49,006,618	47,910,115	97.76%
1695SS11-7S32L-2	50,619,992	49,442,771	97.67%
1695SS11-7S32L-3	50,731,213	49,635,407	97.84%
1695SS11-7S45-1	46,758,650	45,914,907	98.20%
1695SS11-7S45-2	46,471,359	45,588,514	98.10%
1695SS11-7S45-3	54,743,371	53,513,194	97.75%
1695SS11-7S45L-1	55,745,612	54,319,876	97.44%
1695SS11-7S45L-2	60,065,619	58,446,315	97.30%
1695SS11-7S45L-3	53,268,335	51,818,897	97.28%