

Table S2. Summary of sequenced 51-bp reads from NGS of *C. difficile*

	RNA-seq		TAP+		TAP-	
	Number of reads	% of reads	Number of reads	% of reads	Number of reads	% of reads
Total*	37,139,449	100%	75,557,518	100%	38,125,969	100%
Filter**	33,596,273	90%	70,790,096	93%	35,002,829	91%
Remaining***	3,543,176	10%	4,767,422	6.3%	3,123,140	8.2%
Genome coverage****	42x		57x		37x	

NGS, next generation sequencing. For 5'-end RNA-seq analysis: TAP+, RNA treated with Tobacco acid pyrophosphatase, TAP-, RNA not treated with Tobacco acid pyrophosphatase. ***All reads after removal of adapter derived sequences; ** reads corresponding to rRNA sequences; *** reads after removal of rRNA sequences; **** genome coverage for 51-bp reads corresponding to 4,290,252-bp *C. difficile* 630 genome.**