

Table S3 Genome location, characteristics and sequence identity of *Sly* copies in the FGSC 2489 genome

Sly copy	<i>Sly1-1</i>	<i>Sly1-2</i>	<i>Sly1-3</i>	<i>Sly1-4</i>	
LG	VI	II	V	I	
Start	309012	1151460	1020794	3791908	
End	320545	1155073	1033091	3803673	
Strand	+	+	-	-	
Length of region (bp)	11534	3614	12298	11763	
TSD1	TACCA	TACCA	TACCA	TACCA	
TSD2	TATCA	—	TATTA	TAGCT	
TIR1 Length	110	110	110	110	
TIR2 Length	113	—	113	113	
% similarity to <i>Sly1</i>	Query coverage	—	31%	94%	91%
	Identity		100%	67%	72%
Gene(s) contained	NCU09968, NCU09969	NCU16528	None	None	
Small RNAs produced	Yes	Yes	No	No	
BLASTX hits	—	NCU09968	NCU09968, NCU09969	NCU09968, NCU09969	
GC %	51.6	48.3	29.4	29.8	