

Figure S1: Analysis of Small RNA sequencing data

Genotype	Input reads	rRNA reads (2 mismatches)	Reads perfectly matching to the genome (non-rRNA)	Genome Collapsed Reads	Genome unique mapping reads	Transposon mapping reads (Unique)	Normalized transposon reads (Unique)
Control	10526656	541800	8100473	1410100	414166	560892	560892
Hop GLKD	9197807	5388073	788928	239139	113138	71373	261225

Normalization factor

3.66

Genome collapsed reads mapping to coding portion of the genome	Transposon mapping reads (Unique)	Normalized transposon reads (Unique)
220763	560892	560892
100429	71373	157021

Normalization factor

2.2

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