

Table S1a. Classification of sequence reads. Classification and abundance of high-throughput sequence reads obtained from ribo-depleted and dual-depleted cDNA libraries derived from symptomatic and non-symptomatic grapevine leaves, when mapped to virus/viroid database.

Category of sequence reads	Reads from ribo-depleted cDNA library		Reads from dual-depleted cDNA library	
	Symptoms	No Symptoms	Symptoms	No Symptoms
Total reads	34,504,862	76,668,556	1,865,157	3,345,220
Total hits to virus/viroid database	53,988	16,268	3,232	2,539
Unmapped reads	34,465,910	76,652,288	1,862,331	3,342,861

Table S1b. Sequence reads summary for host subtraction and assembly approach.

Category of sequence reads	Reads from ribo-depleted cDNA library		Reads from double depleted cDNA library	
	Symptoms	No Symptoms	Symptoms	No Symptoms
Total reads	34,504,862	76,668,556	1,865,157	3,345,220
Reads mapped to <i>Vitis</i> genome	11,938,839	34,459,395	597,216	1,350,283
Reads not mapped to <i>Vitis</i> genome (used in assembly)	22,566,023	42,209,161	1,267,941	1,994,937
# of Scaffolds assembled from non-<i>Vitis</i> reads	20,066		436	