

S1 Table. Results of the mapping parameters tested for distinguishing between reads from *L. maculans* and *L. biglobosa*.

^a. Reads of the two samples from *in vitro* cultures of either *L. maculans* (isolate JN2) or *L. biglobosa* (isolate G12-14) were mapped independently on the genomes of *L. maculans* (isolate JN3) and *L. biglobosa* isolate G12-14)

^b. Reads of the two samples from *in vitro* cultures of either *L. maculans* (isolate JN2) or *L. biglobosa* (isolate G12-14) were both mapped on one artificial genome created by the concatenation of the *L. maculans* (isolate JN3) and *L. biglobosa* (isolate G12-14) genomes.

Reference mapping genome	RNAseq samples used	Number of mismatch allowed	% of reads mapped on <i>L. maculans</i> (JN3) genome	% of reads mapped on <i>L. biglobosa</i> (G12-14) genome
^a . JN3 or G12-14 genomes	<i>In vitro</i> culture of <i>L. maculans</i> (JN2)	0	96.62	0.46
		1	97.27	0.97
		2	97.42	1.63
	<i>In vitro</i> culture of <i>L. biglobosa</i> (G12-14)	0	0.76	95.13
		1	1.54	95.59
		2	2.66	95.69
^b . JN3 and G12-14 concatenated genomes	<i>In vitro</i> culture of <i>L. maculans</i> (JN2)	0	96.7	0.04
		1	97.32	0.06
		2	97.45	0.08
	<i>In vitro</i> culture of <i>L. biglobosa</i> (G12-14)	0	0.10	95.15
		1	0.11	95.58
		2	0.12	95.67