

Supplemental Table S1 – Total number of trimmed reads and percent alignment to chloroplast and mitochondria genomes.

		Chloroplast				Mitochondria			
		Aligned reads				Aligned reads			
		forward		reverse		forward		reverse	
Leaves	Endo	244480	(17.7%)	223941	(18.1%)	804478	(58.2%)	634143	(51.3%)
	Exo	18279	(1.4%)	16957	(1.4%)	87100	(6.7%)	151996	(12.9%)
Stem	Endo	216685	(12.0%)	198996	(12.4%)	1449544	(80.2%)	1214015	(75.7%)
	Exo	34722	(2.3%)	33616	(2.4%)	426106	(28.1%)	375094	(26.8%)
Root	Endo	868	(0.1%)	1186	(0.1%)	108640	(10.5%)	24483	(2.5%)
	Exo	1719	(0.2%)	1895	(0.2%)	5645	(0.6%)	3820	(0.5%)
bulk soil		1040	(0.4%)	1049	(0.5%)	406	(0.2%)	238	(0.1%)

Supplemental Table S2 – Total number of filtered, merged, and non-chimeric sequences by DADA2 denoise software.

		input sequences	filtered sequences	percentage of input passed the filter	merged	percentage of merged sequences	non-chimeric sequences	percentage of input non-chimeric
Leaves	Endo	1667666	646315	38.8%	588565	35.3%	535149	32.1%
	Exo	1385405	541294	39.1%	478064	34.5%	470594	34.0%
Stem	Endo	2017452	796841	39.5%	751176	37.2%	685153	34.0%
	Exo	1727798	730743	42.3%	689366	39.9%	651548	37.7%
Root	Endo	1236001	447073	36.2%	343321	27.8%	323264	26.2%
	Exo	1060996	369250	34.8%	241843	22.8%	234588	22.1%
bulk soil		277222	94275	34.0%	63738	23.0%	59994	21.6%
Total		9372540	3625791		3156073		2960290	