

Gene Region #	Description	# of Samples	Aligned Length	Missing Data (%)	Taxon Coverage Density
1	ETS	109	691	7.6	0.92
2	ITS	107	677	9.3	0.91
3	matK	81	494	31.4	0.69
4	rpl16	107	1156	9.3	0.91
5	trnLF	100	1058	15.3	0.85
6	trnTL	112	578	5.1	0.95

Table 1: *Hesperolinon* gene regions sequenced so far...

Total number of taxa	118
Total length of matrix	4654
Taxon coverage density	0.87
Total % gaps	0.24
Partial decisiveness (fraction of triples)	0.98

Table 2: *Hesperolinon* data matrix stats so far...