

Table S1. Quantification of basic quality and completeness metrics of *Limonium de novo* transcriptome assembly. Samples of apomictic (*L. multiflorum*), facultative apomictic (*L. dodartii*), sexual (*L. ovalifolium*, *L. auricolifolium*) in S1, S2, S1/S2, S3/S4 and S4 stages were combined to perform a *de novo* transcriptome assembly using Trinity software's.

Basic Metrics	Values
Total trinity unigenes	162520
Total trinity transcripts (isoforms)	315983
Percent GC (%)	42.94
Contig N10	4592
Contig N20	3604
Contig N30	2998
Contig N40	2528
Contig N50	2128
Completeness	
Total number of core genes queried	2326
Number of core genes detected	
Complete	2090 (89.85%)
Complete + Partial	2159 (92.82%)
Number of missing core genes	167 (7.18%)
Average number of orthologs per core gene	2.93
% of detected core genes that have more than 1 ortholog	70.81
Scores in BUSCO format	C:89.8% [S:26.2%, D:63.6%], F:3.0%, M:7.2%