

Table S4. Quality assessment of a *de novo* transcriptome assembly, using gVolante website with BUSCO v2.0.1 option. The transcriptome was performed with Trinity software, using *Casuarina glauca* nodulated by nitrogen-fixing *Frankia casuarinae* Thr (NOD⁺) and non-nodulated plants supplied with KNO₃ (KNO₃⁺) reads, from samples grown at 0, 200, 400, and 600 mM NaCl.

Completeness assessment	Values
Total number of core genes queried	1440
Number of core genes detected	
Complete	1366 (94.86%)
Complete + Partial	1412 (98.06%)
Number of missing core genes	28 (1.94%)
Average number of orthologs per core genes	1.92
% of detected core genes that have more than 1 ortholog	60.54
Scores in BUSCO format	C:94.8%[S:37.4%,D:57.4%], F:3.2%,M:2.0%
Length statistics and composition	Values
Number of sequences	181484
Total length (nt)	289780263
Longest sequence (nt)	17867
Shortest sequence (nt)	183
Mean sequence length (nt)	1597
Median sequence length (nt)	1036
N50 sequence length (nt)	2792
L50 sequence count	34704
Number of sequences > 1K (nt)	92205 (50.8%)
Number of sequences > 10K (nt)	170 (0.1%)
Number of sequences > 100K (nt)	0
Number of sequences > 1M (nt)	0
Number of sequences > 10M (nt)	0
Base composition (%)	A: 30.98
T: 27.94	
G: 19.24	
C: 21.85	
N: 0.00	
Other: 0.00	
GC-content (%)	41.09
Number of non-ACGTN (nt)	0