

**Table S2.** Quantification of basic quality metrics *de novo* transcriptome assembly of *Casuarina glauca*. Samples of *C. glauca* nodulated by nitrogen-fixing *Frankia casuarinae* Thr (NOD<sup>+</sup>) and non-nodulated plants supplied with KNO<sub>3</sub> (KNO<sub>3</sub><sup>+</sup>), grown at 0, 200, 400, and 600 mM NaCl, were combined to perform a *de novo* transcriptome assembly using Trinity software.

Metrics	Values
Total assembled contigs	181484
Smallest contig	183
Largest contig	17867
Total assembled bases	289780263
Total assembled genes	86202
Average contig length	1597
Median contig length	1036
# Contig sequences under 200	7
# Contig sequences over 1k	92205
# Contig sequences over 10k	170
# Contig sequences with ORF	76648
% Mean ORF	40
N90	727
N70	1904
N50	2792
N40	3260
N30	3805
N20	4520
N10	5729
% GC	41