

Table S3. Alignment statistics of *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, against a *de novo* transcriptome assembly, performed with Trinity software using these same reads.

Statistics	Counts	Percentages
Total reads	204084574	-
Paired-end reads	204084574	100%
Uniquely aligned reads	30963937	15.2%
Reads aligned multiple times	165311208	81%
Total aligned reads	196275145	96.2%
Concordantly or discordantly unaligned reads	7374204	3.6%
Concordantly unaligned and discordantly aligned reads	435225	0.2%
Total concordantly unaligned reads	7809429	3.8%
Mates make up the pairs	14748408	-
Unaligned mates	3360270	22.8%*
Uniquely aligned mates	1263913	8.6%*
Mates aligned multiple times	10124225	68.7%*
Total aligned mates	11388138	2.8%**
Overall alignment rate		99.2%