

Supplementary Table S1. Summary of the assembly statistics presented as per sample number of read pairs generated by the sequencing facility as well as the number of read pairs that remained after the data had been filtered and trimmed. The number of transcripts assembled by trinity and the sequences deemed as good by transrate is presented together with the fraction of complete, fragmented and missing BUSCO genes found in each transrate curated assembly.

Sample number	Number of read pairs (M)	Number of filtered and trimmed read pairs (M)	Number of transcripts	Transrate good transcripts	BUSCO complete (%)	Fragmented (%)	Missing (%)
104	12,9	11,1	53770	40187	32,1	14,5	53,4
107	14,4	12,3	62769	48272	44,8	13,9	41,3
110	13,3	11,2	58828	44532	41,7	14,2	44,1
112	13,0	11,0	62712	46786	39,5	14,3	46,2
116	13,2	11,2	59632	44024	42,1	13,5	44,4
122	13,8	11,9	63022	45472	41,9	14,5	43,6
124	14,5	12,4	60811	43539	38,2	14,4	47,4
126	13,9	12,1	57467	42527	44,2	13,6	42,2
127	14,0	12,2	64140	46860	40,0	13,8	46,2
128	14,0	12,2	58481	43774	44,5	12,8	42,7