

Supplementary table1 Primer sequences for RT-qPCR

Gene ID	Forward primer (5'-3')	Reverse primer (5'-3')
Cluster-13447.0	AGCTGGTGTGACGGTAATCG	AAGACTCCACCCCCCAACTCT
Cluster-769.6797	GAAATGCCTGACAAGGTGCG	AACCGCTCAGGCAGGTAAAG
Cluster- 769.34168	TCCCCGACGACAACATCAAG	CCCATAGCTCTTCAGCTCGG
Cluster-769.37917	GGGAACCTAAGGTGACGGTG	TCGCCTTCTCATCTCCTCCA
Cluster-769.46875	TTGCTGTGACAAAGCCAACG	CCTATCTTCTGGGGCAAGGC
Cluster-769.56890	GGACATGAGCTTCAGTGCCT	GATCTCCATTGCCACCGCTA
Cluster-769.48503	ACCATAGCCGTTTGGTCCAG	GTGGGGCCAAACTGTGTTTC
Cluster-769.2256	GCGAAGGCATCGAATTGGTC	GGCGGTGGGTTTTGTTTACC
CnGAPDH	GGGAATCCTTGGTTACACTGAG	ACCCCATTCGTTGTCATACC

Supplementary table 2 Transcriptome analysis of *C. nitidissima* stamens in three stages

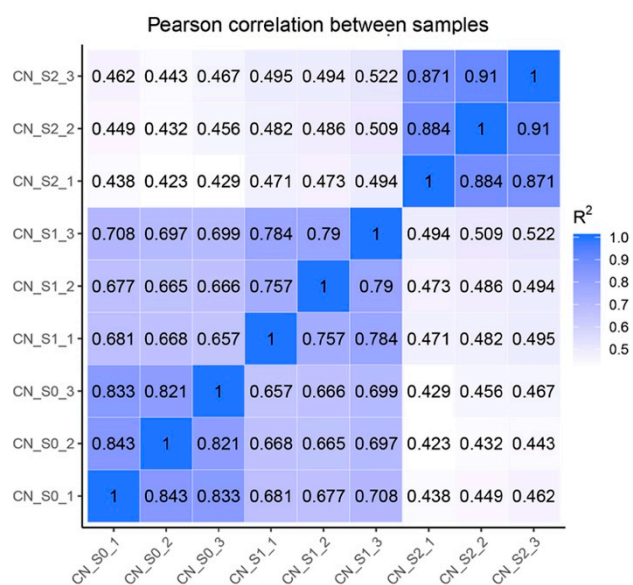
sample	raw reads	clean reads	error rate	Q20	Q30	GC_pct
S0	22534958	21624002	0.03	96.54	90.98	44.62
S1	23788150	23129446	0.03	96.26	90.40	44.11
S2	22366701	21563033	0.03	96.71	91.41	44.85

Supplementary table 3 Summary for the transcriptome assembly of *C. nitidissima* stamens

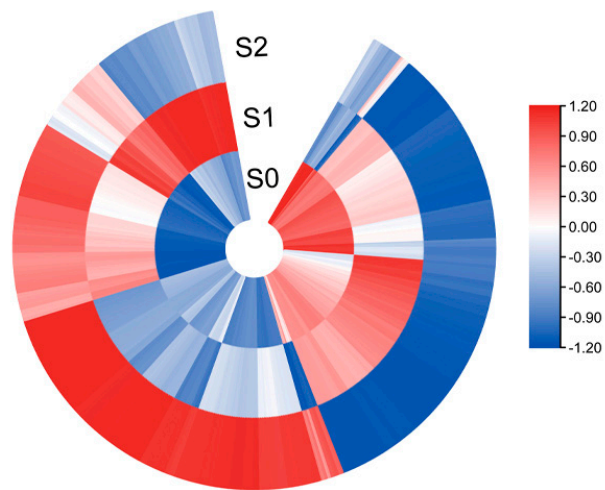
Type	Mean length	Median length	Max length	N50	N90	Total
transcripts	1297	941	11340	1879	586	205172
unigenes	1124	702	11340	1752	468	78997

Supplementary table 4 Unigenes annotation

Database	Number of Unigenes	Percentage
Total Unigenes	78997	100
Annotated in SwissProt	26284	33.27
Annotated in PFAM	27307	34.56
Annotated in NT	52766	66.79
Annotated in NR	40252	50.95
Annotated in KOG	6600	8.35
Annotated in KO	12135	15.36
Annotated in GO	27304	34.56
Annotated in at least one Database	58120	73.57
Annotated in all Databases	3952	5



Supplementary Fig. 1 Clustering heat map of samples.



Supplementary Fig. 2 A heat map showing DEGs enriched in “oxidoreductase activity” during the S0–S2 stages.