

Supplementary Materials

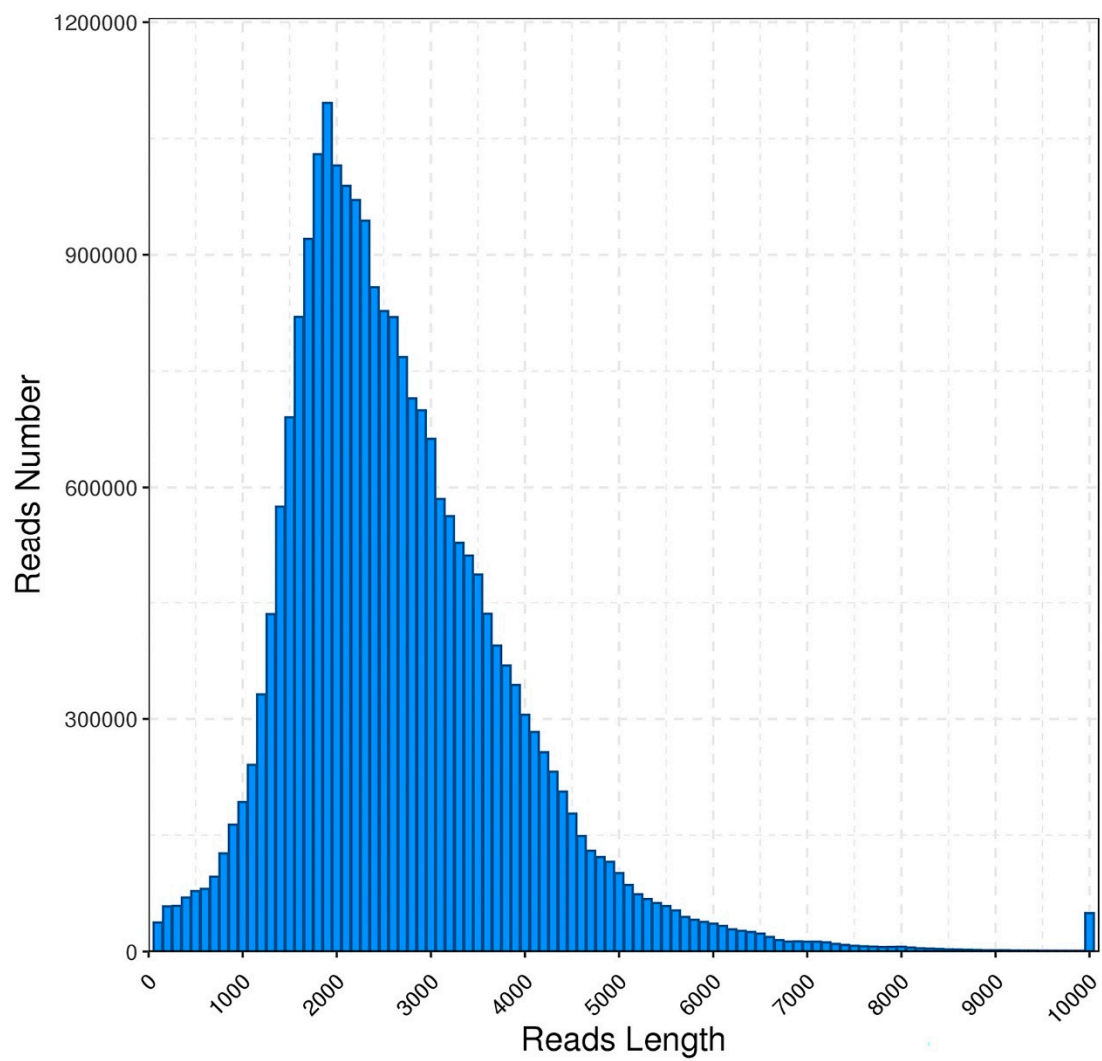


Figure S1: length distribution of subreads from SMRT sequencing

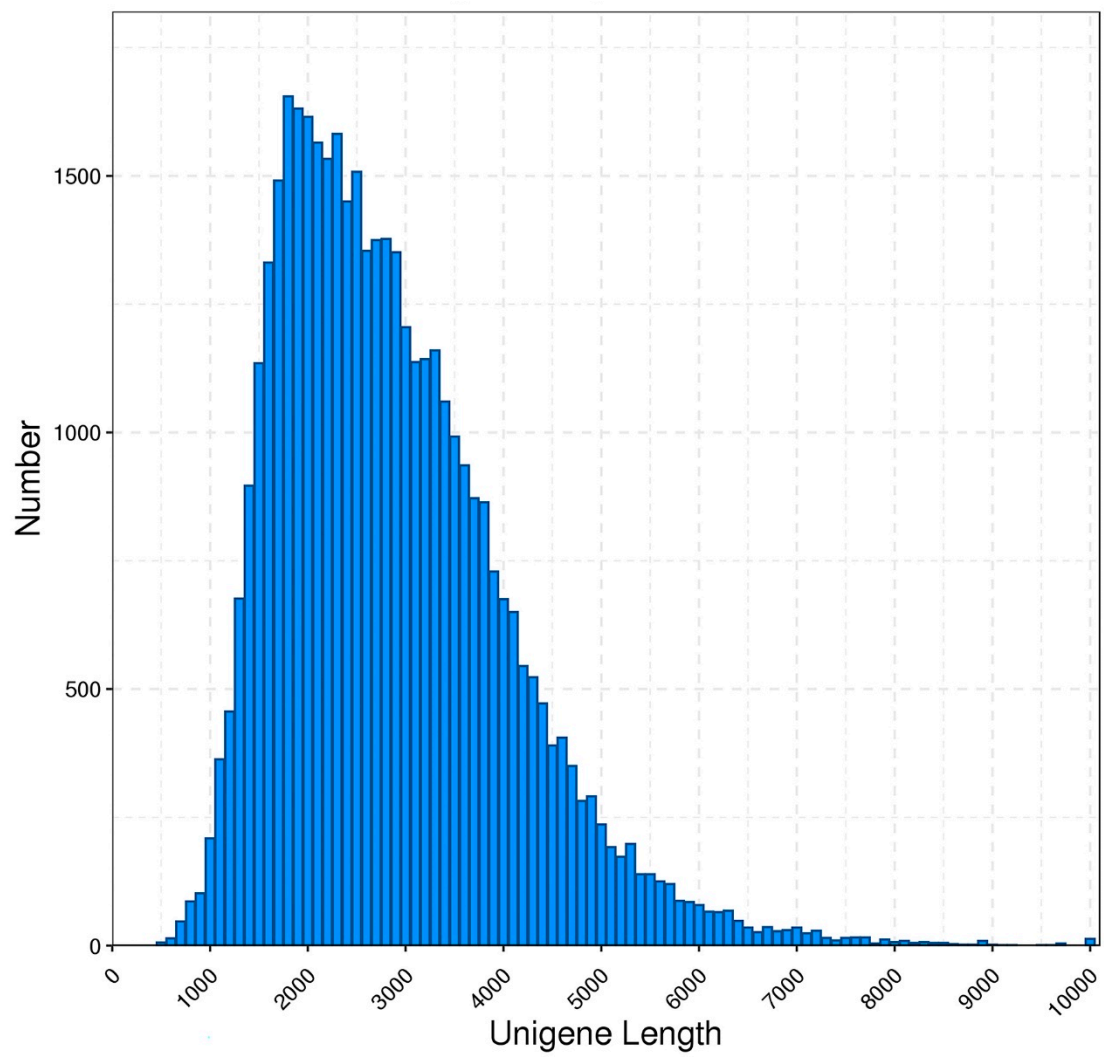


Figure S2: length distribution of unigenes. The X-axis represents length (bp), the Y-axis represents the number of genes

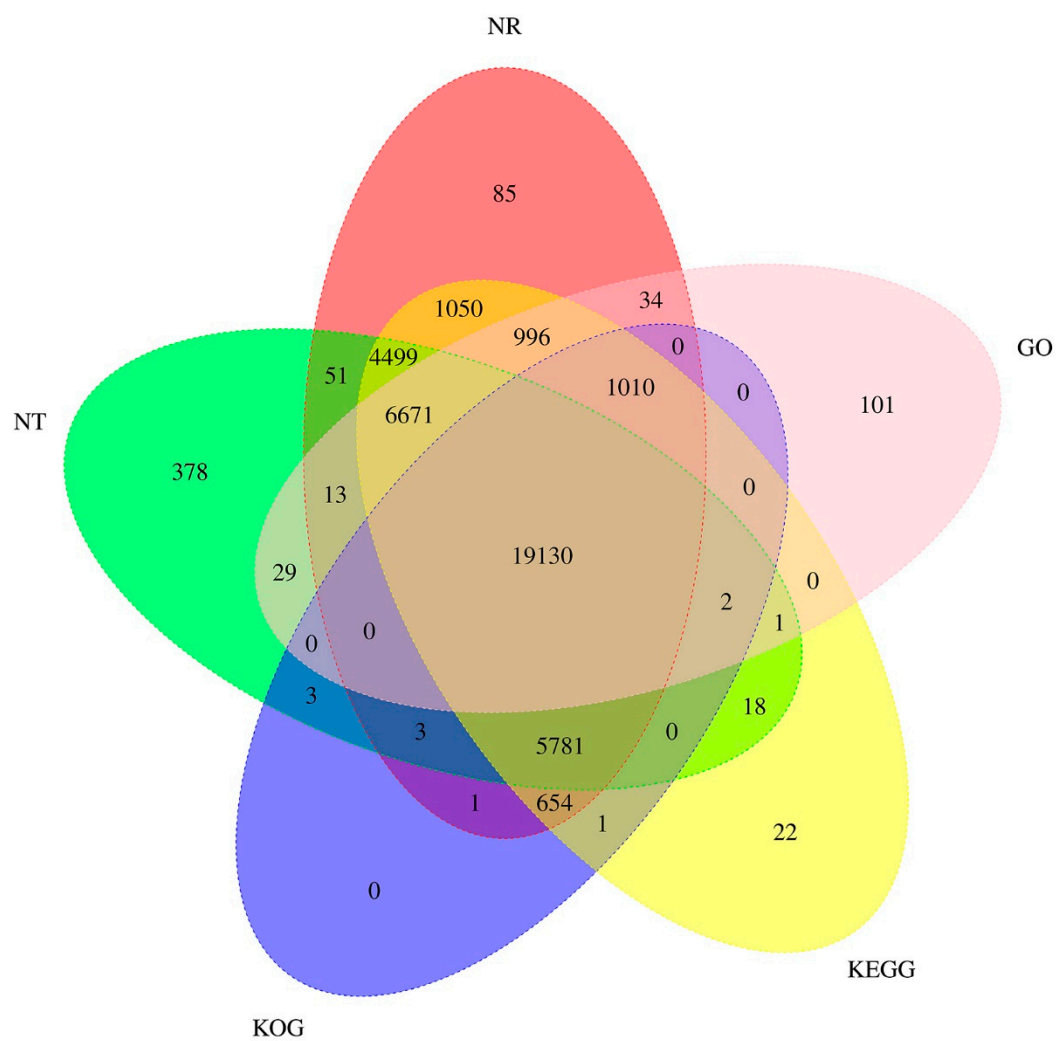


Figure S3: Venn diagram of unigene annotation.

The sum of the numbers in each large circle represents the number of unigenes for the database annotation, and the overlapping parts of the circles represent unigenes annotation results that are common among databases

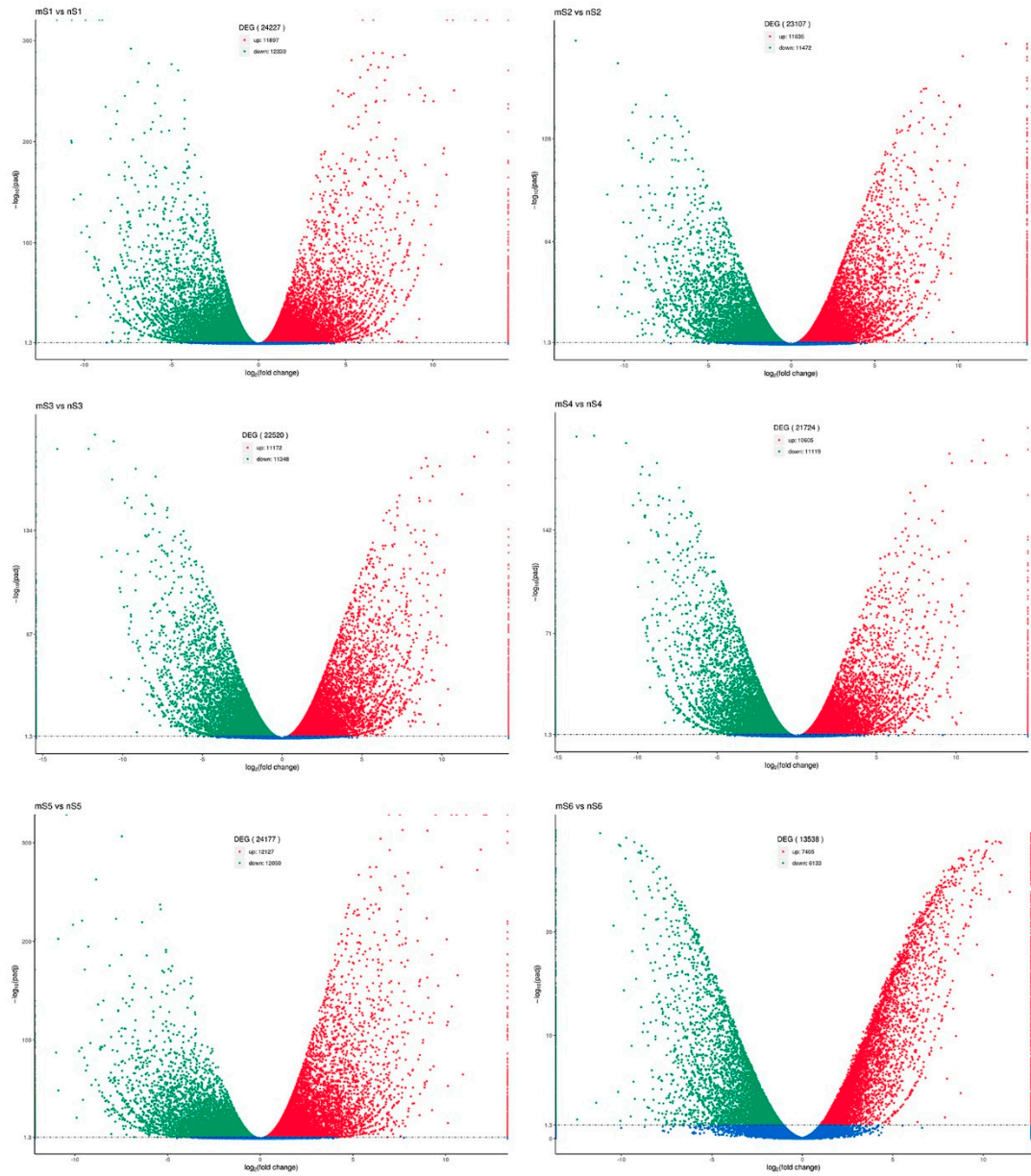


Figure S4: DEGs at each stage.

DEGs were then screened by comparing the genes expressed in two types of materials at the same developmental stage. Corrected p -value of 0.05 and \log_2 (Fold change) of 1.5 were set as the threshold for significantly differential expression, values are means of three biological replicates

Table S1: specific primers used for qRT-PCR verification

No.	Name	Forward	Reverse	Tm	size
1	<i>CoSEP3.1</i>	CTGTGCTTTGCGATGCTGAA	GTCTCGAGCTCCTTGCTGTT	59	277
2	<i>CoAGL6</i>	GACGCTGAAGTGGCTCTCAT	CTAGTTGTGCAAGCGCTCC	59	293
3	<i>CoAP3</i>	CCAGAAGGCTCTTGGGATCG	TCGTTCGCGTACAATCGTCA	59	202
4	<i>CoSEP3.2</i>	ATCTTGGCCCCCTAAACAGC	TGTCGGCTGTAACCCACATC	59	238
5	<i>CoGAPDH</i>	GATAGTGTTACGGTCAATGGA	GCAGCAGCCTTATCCTTATCAG	59	188

Table S2: total reads of each sample and mapped reads against the reference sequence.

Sample.name	Total.reads	Total.mapped
mS1_1	31615594	18664014(59.03%)
mS1_2	31717608	18426428(58.10%)
mS1_3	31953620	18399504(57.58%)
mS2_1	31982686	19011318(59.44%)
mS2_2	34913448	21028004(60.23%)
mS2_3	33963842	20802142(61.25%)
mS3_1	31861874	19243838(60.40%)
mS3_2	32809414	19596368(59.73%)
mS3_3	35707546	21333306(59.74%)
mS4_1	32277182	18527666(57.40%)
mS4_2	33129180	19602880(59.17%)
mS4_3	33479692	19572580(58.46%)
mS5_1	33153162	19452166(58.67%)
mS5_2	34858064	20148052(57.80%)
mS5_3	34317570	20668328(60.23%)
mS6_1	34134634	20454666(59.92%)
mS6_2	32625540	19897846(60.99%)
mS6_3	32432544	19280460(59.45%)
nS1_1	33421522	20117422(60.19%)
nS1_2	32821080	20233020(61.65%)
nS1_3	33321724	20340710(61.04%)
nS2_1	32678562	19412806(59.41%)
nS2_2	30681976	18543326(60.44%)
nS2_3	32560624	19585152(60.15%)
nS3_1	30996634	17949892(57.91%)
nS3_2	31601274	18358150(58.09%)
nS3_3	29809620	17895290(60.03%)
nS4_1	33929032	19999706(58.95%)
nS4_2	31422302	18846174(59.98%)
nS4_3	34191026	20273568(59.29%)
nS5_1	33503308	20051740(59.85%)
nS5_2	32200108	18693640(58.05%)
nS5_3	30052086	18640506(62.03%)
nS6_1	30634964	16591566(54.16%)
nS6_2	30259884	15687506(51.84%)
nS6_3	30808730	18035174(58.54%)

Total reads represent clean data of sequencing reads after quality control; Total mapped represent the number of clean reads that can be matched to the reference sequence.