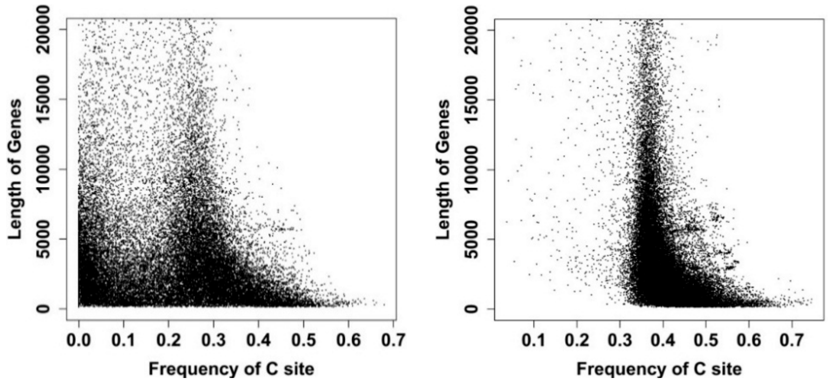
Supplementary Information

Figure S1. Correlation between the frequency of C sites and the length of a gene. The *x*-axis indicates the frequencies of C sites, and the *y*-axis indicates the length of the gene. (**A**) The distribution of the frequencies of mC sites; (**B**) The distribution of the frequencies of the whole genome C sites.



(**A**) (**B**)

Figure S2. Methylation level analysis on gene bodies and their up- and down-stream sequences. All coding genes were divided into seven transcription elements, and the methylation level was analyzed over these regions. The vertical green lines indicate transcription start site (TSS).

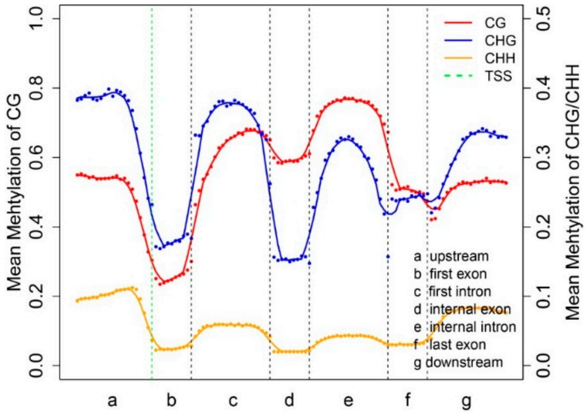


Figure S3. Correlation analysis between the two transcriptomes. The *x*-axis indicates the expression values for one transcriptome, and the *y*-axis indicates the expression values for the other transcriptome. All the values were log2 transformed.

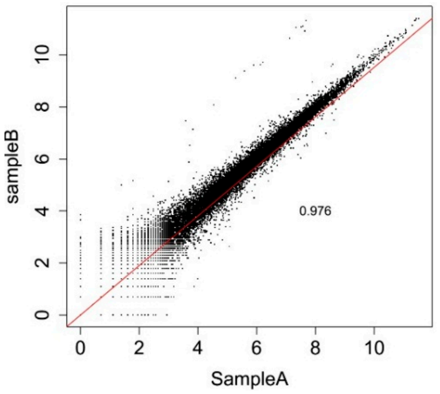


Table S1. Quality controls of mRNA transcriptome data.

Samples	Total Raw Reads	Total Clean Reads	Total Clean Nucleotides	Q20 Percentage	GC Percentage
Birch_xylem_A	27,278,632	25,647,400	2,308,266,000	98.26%	45.75%
Birch_xylem_B	28,703,868	26,811,962	2,413,076,580	98.17%	45.91%

Q20 percentage: Percentage of the bases that the quality was not lower than 20 after filteration. GC percentage: Percentage of G and C bases account fortotal bases.