Ultra-dense SNP genetic map construction and identification of *SiDt* gene controlling the determinate growth habit in *Sesamum indicum* L.

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Supplementary Fig. S1. QDt1 location for determinate growth habit on LG8 of the ultra-dense SNP map.

Supplementary Fig. S2. Amplification and screening of *Si*Dt 27-1 in F_2 population of the cross between Yuzhi DS899 and Ningbohei. M: DL 2,000 marker with the partial DNA bands of 250 bp and 100 bp; Lane 1-20: 92 bp amplicon of *Si*Dt 27-1 in *dt1* genotype individuals of F_2 population. Lane 21, 22, 28, 29, 31, 35 and 37: 97 bp amplicon of *Si*Dt 27-1 in *Dt* genotype individuals; Lane 23-27, 30, 32-34, 36, 38-40: amplicons of 92 bp and 97 bp in heterozygotic genotype (*Dt*/*dt1*).

Supplementary Fig. S3. Protein homology comparison of 3D structure between the SiDt and Sidt1 proteins. The SNP site of S79N is located at the junction region between different domains. Homology modelling shows that the 3D structures of SiDt (left) and Sidt1 (right) are same.

Supplementary Fig. S4. Phylogenetic analysis of *SiDt* homologues in sesame. Seven homologues of *Sis00046-1*, *Sis00076-1*, *Sis00121-1*, *Sis00157-1*, *Sis00157-2*, *Sis00154-1* and *Sis00141-1* are detected in the Yuzhi 11 genome (PRJNA315784) (version 2). Compared with SiDt, the protein identity of the 7 homologues ranges from 29%- 78%. The phylogenetic tree is constructed using MEGA 5.2 program according to the neighbor-joining (NJ) method. The line unit indicates the bootstrap value of 0.05.

Supplementary Fig. S5. Diversity analysis of *SiDt* among the sesame germplasm resources. Thirty core sesame germplasm are applied for the diversity analysis. A total of 18 SNP sites are detected in *SiDt* sequences among 5 accessions, i.e., M10, M11, M18, M19 and M29 as listed in Supplementary Table S10 online. Asterisks above the nucleotide sequences indicate the SNP sites of *SiDt* (*Sidt*) in Yuzhi 11, YuzhiDS899 and the 30 germplasm. The arrowhead indicates the SNP G397A site between Yuzhi 11 and Yuzhi DS899. The SNPs presented in more than 2 accessions are shaded in black. The

SNPs presented in one specific accession are shaded in grey. Bases in frame are exon sequences of *SiDt*.

Supplementary Table S1. Genome sequencing information of two parents and 120 F_2 progeny in this study. Yuzhi DS899 as parent 1 is determinate (*dt1* type), JS012 as parent 2 is indeterminate (the wild type). A total of 120 F_2 progeny are randomly chosen from the F_2 population of the cross between Yuzhi DS899 and JS012.

Supplementary Table S2. Genotyping matrix information of bin and SNP markers in the F_2 progeny. The information of 3,101 bins and 30,494 SNP markers are listed for linkage mapping.

Supplementary Table S3. Bin marker information of the ultra-density SNP genetic linkage map in sesame. 3,041 bin markers containing 30,193 SNP markers are located in the SNP linkage map.

Supplementary Table S4. Characteristics of the three phenotypes of determinacy growth habit in sesame. The determinacy trait of the five accessions are investigated at Sanya (109°50' E and 18°25' N), Pingyu (113°62' E and 32°97' N) and Yuanyang (113°97' E and 35°05' N) experimental stations in 2013. The average height trait data listed in the table are investigated at Yuanyang experimental station in 2013. Photoperiodic treatments of SD (12h light/12h dark) and LD (15h light/9h dark) are performed in growing chamber under the day/night temperature of 28℃/24℃ with 70±1% relative humidity.

Supplementary Table S5. Location of QDt1 associated with the determinate growth habit in sesame using winQTLCart and QTLNetwork.

Supplementary Table S6. Annotation of all the genes in the QDt1 interval of Yuzhi DS899. Twenty five putative genes are detected in the physical distance corresponding to the QDt1 interval using BLASTP program. DS899s00170.026 and DS899s00170.027 listed in the table are adjacent genes to the QDt1 interval. *'F' refers to forward direction and 'R' refers to reverse direction. KEGG refers to Kyoto Encyclopedia of Genes and Genomes.

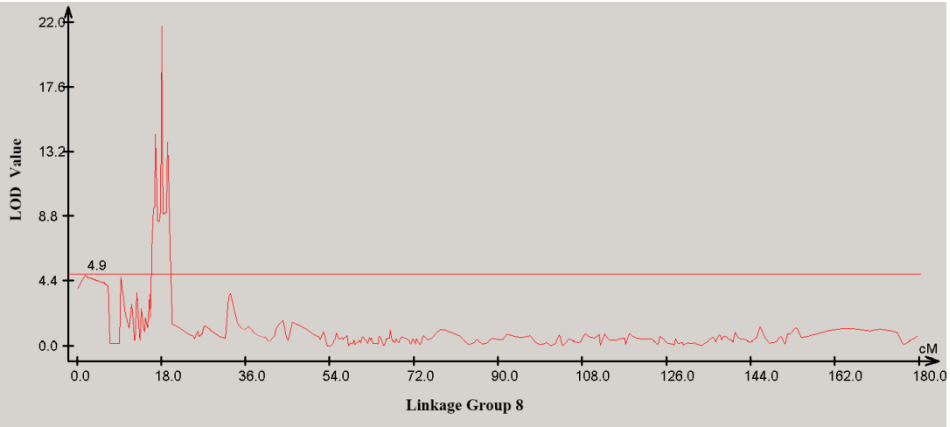
Supplementary Table S7. Genotypic variation and validation of the candidate SNP/InDel sites in sesame. Nine SNPs and 5 InDels are detected in the QDt1 interval. The *Si*Dt27-15 SNP and the *Si*Dt27-16 InDel listed in the table are detected at the adjacent flanking region of the QDt1 window. A total of 400 progeny of two F_2 populations of 'Yuzhi DS899 × JS012' and 'Yuzhi DS899 × Ningbohei' are used for screening target SNP/InDel marker.

Supplementary Table S8. Primer information of *SiDt* alleles for gene amplification and for real time PCR in sesame. *β-Tubulin* in sesame (*SiTUB*, JP631640) is used as the endogenous reference gene for qPCR.

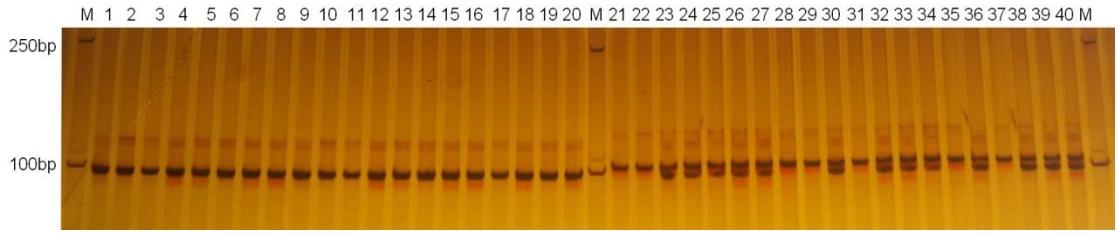
Supplementary Table S9. Global screening of *SiDt* homologues in the Yuzhi 11 genome. Seven homologues are detected using BLASTP, with the cutoff of E value ⩽1E-20 and the coverage of ⩾ 50%.

Supplementary T**able S10.** *SiDt* gene diversity analysis in sesame germplasm resources using PCR amplification. *SiDt* sequences in 30 sesame germplasm resources (M1-M30) are compared using DNAMAN software, in addition to the parents of the mapping population in the study.

Supplementary Table S11. Diversity analysis of *SiDt* gene in sesame germplasm resources using public genome re-sequencing data. The public genome data of 715 accessionss are collected from PRJEB8078 in NCBI dataset.



Supplementary Fig. S1. QDt1 location for determinate growth habit on LG8 of the ultra-dense SNP map. LOD refers to the Logistic Organ Dysfunction score. To determine the locus associated with the determinate trait locus, the LOD value is set at 4.9 using 1,000 permutations.



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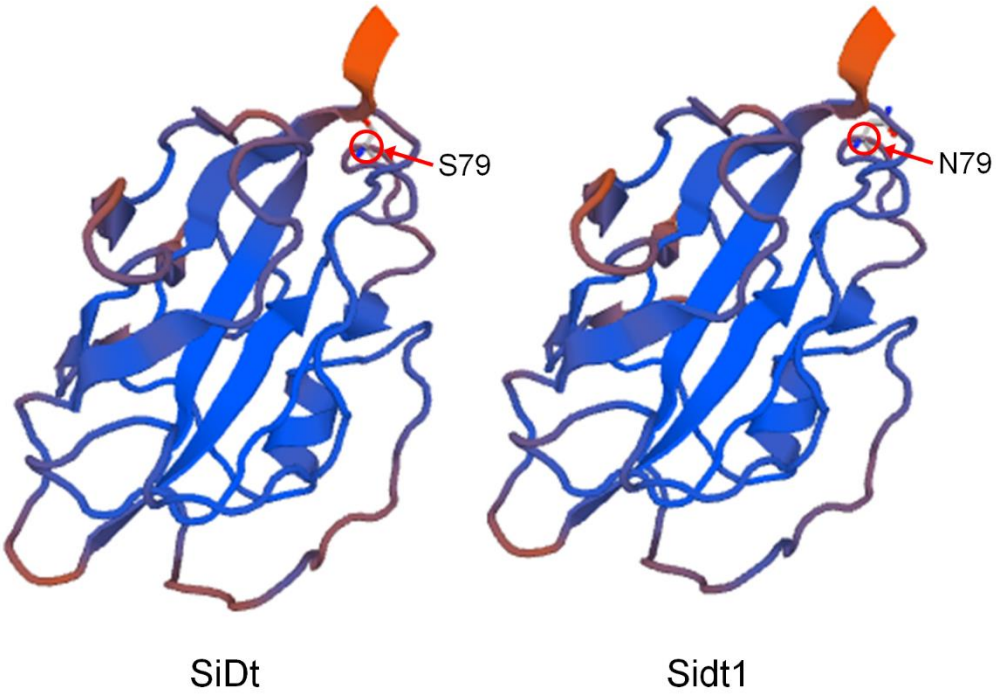

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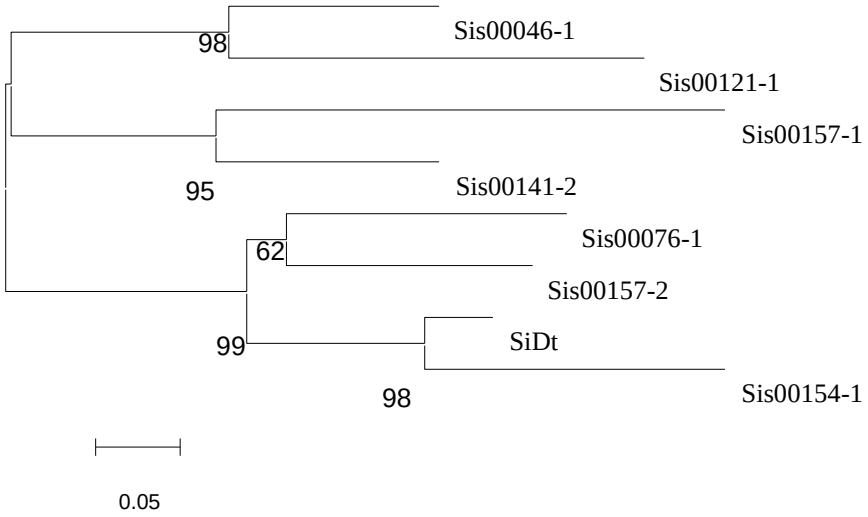

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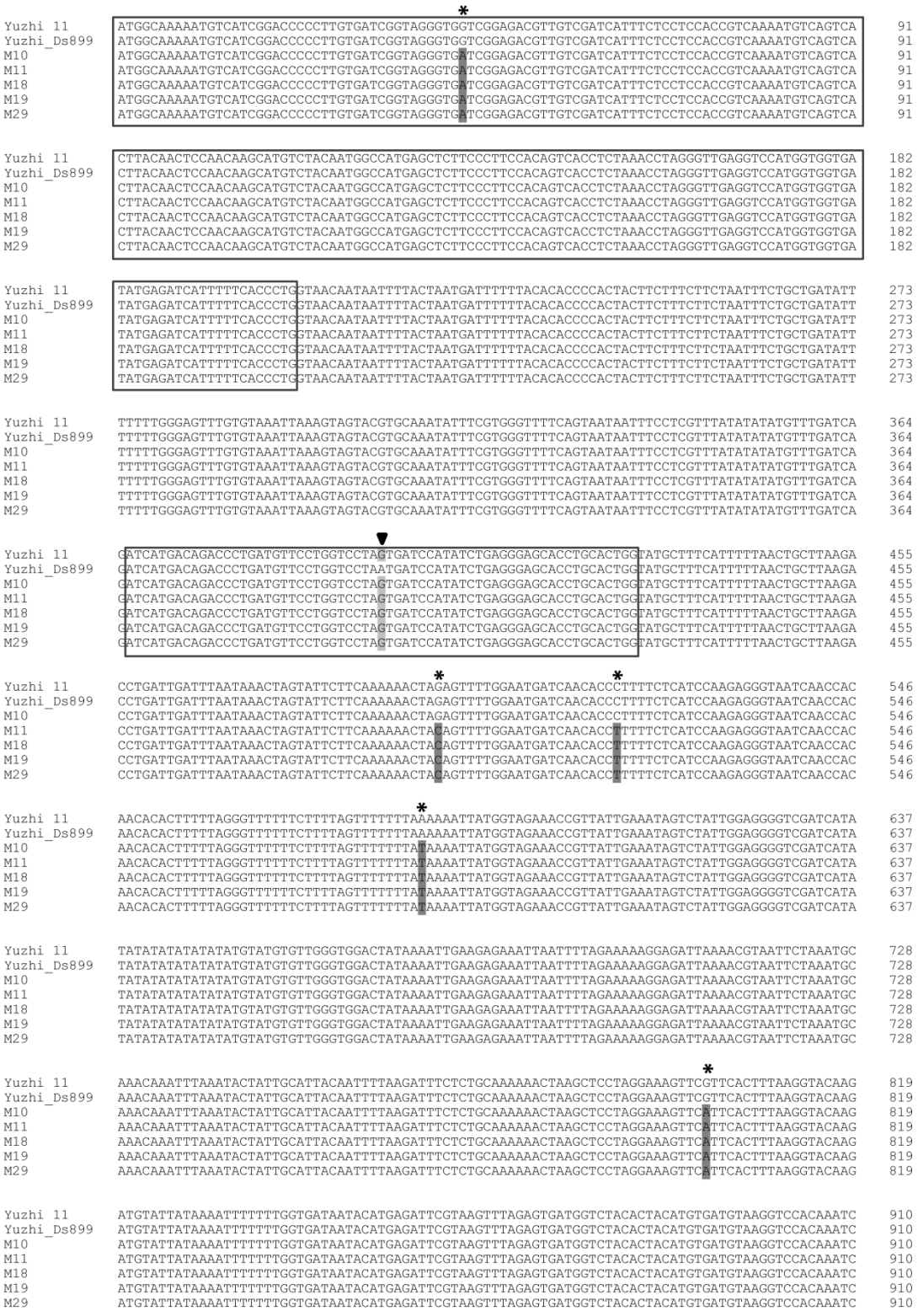
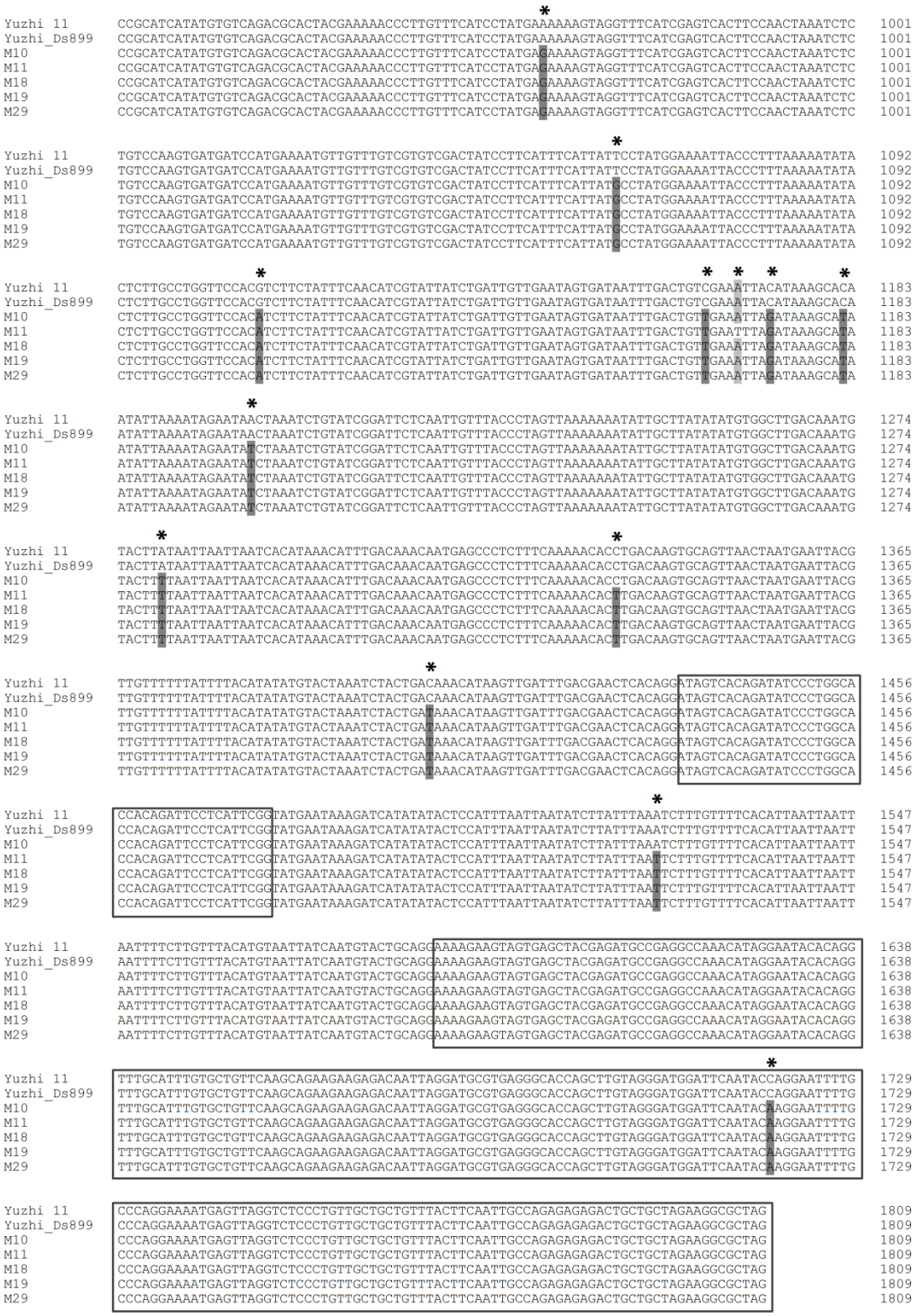
Supplementary Fig. S5-1



Supplementary Fig. S5-2



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