Article title: Identification of a Leafy Head Formation Related Gene in Chinese Cabbage(*Brassica rapa* L. ssp. *pekinensis*)

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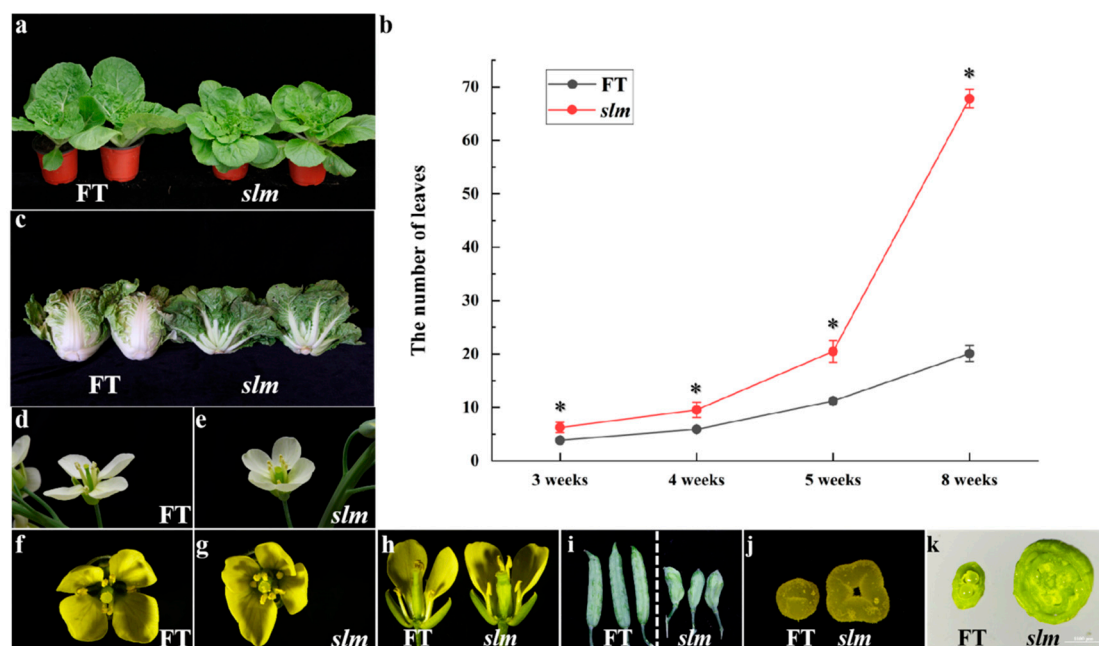
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Figure S1. Phenotype characterize of FT and *slm*.

(**a**) Phenotype characterize of FT and *slm* at rosette stage. (**b**) The leaves number of FT and *slm*. * represents significantly different based on the Student's *t*-test (P<0.05). (**c**) Phenotype characterize of FT and *slm* at heading stage. (**d**) Flower of FT. (**e**) Flower of *slm*. (**f**) Vertical view image of flower of FT. (**g**) Vertical view image of flower of *slm*. (**h**) Internal structure of flower of FT and *slm*. (**i**) Pod of FT and *slm*. (**j**) Stigma of FT and *slm*. (**k**) Transversal anatomical drawing of pistil of FT and *slm*. Scale is shown at the bottom.
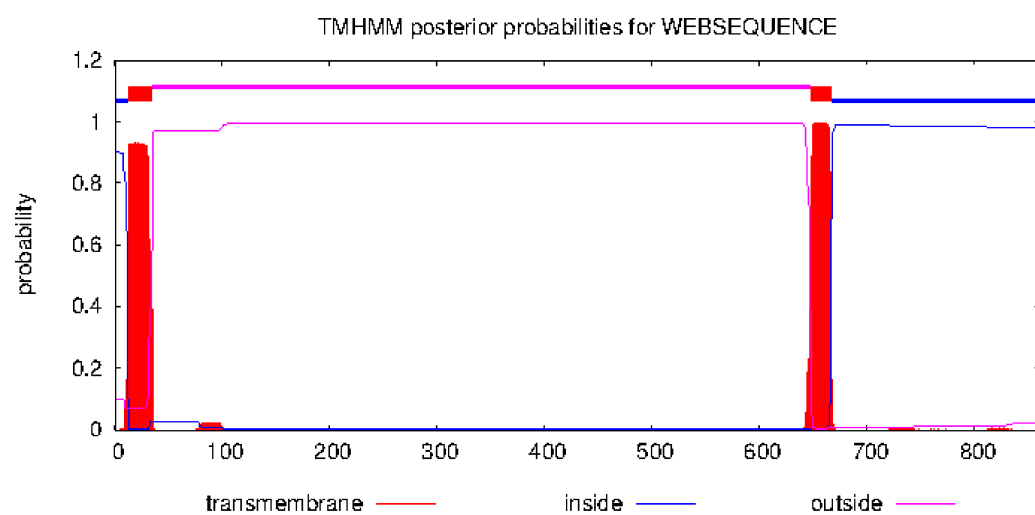
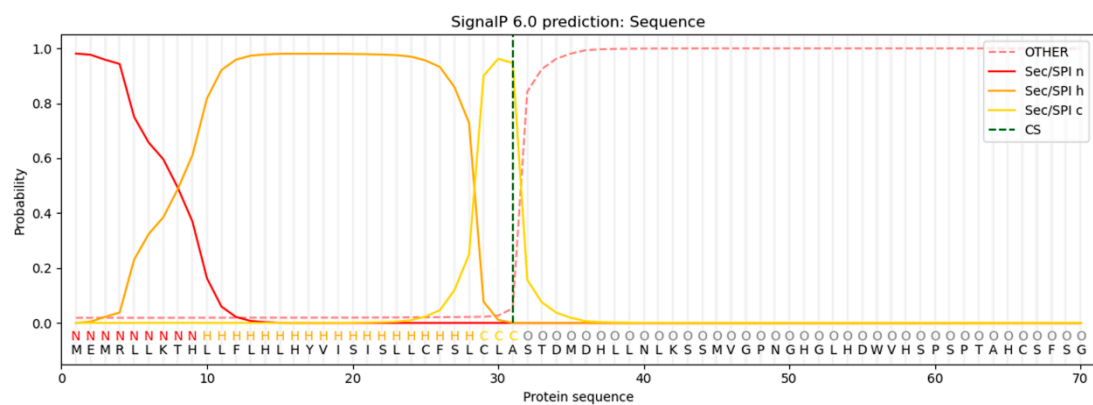**Figure S2.** Prediction of transmembrane helices by TMHMM-2.0.

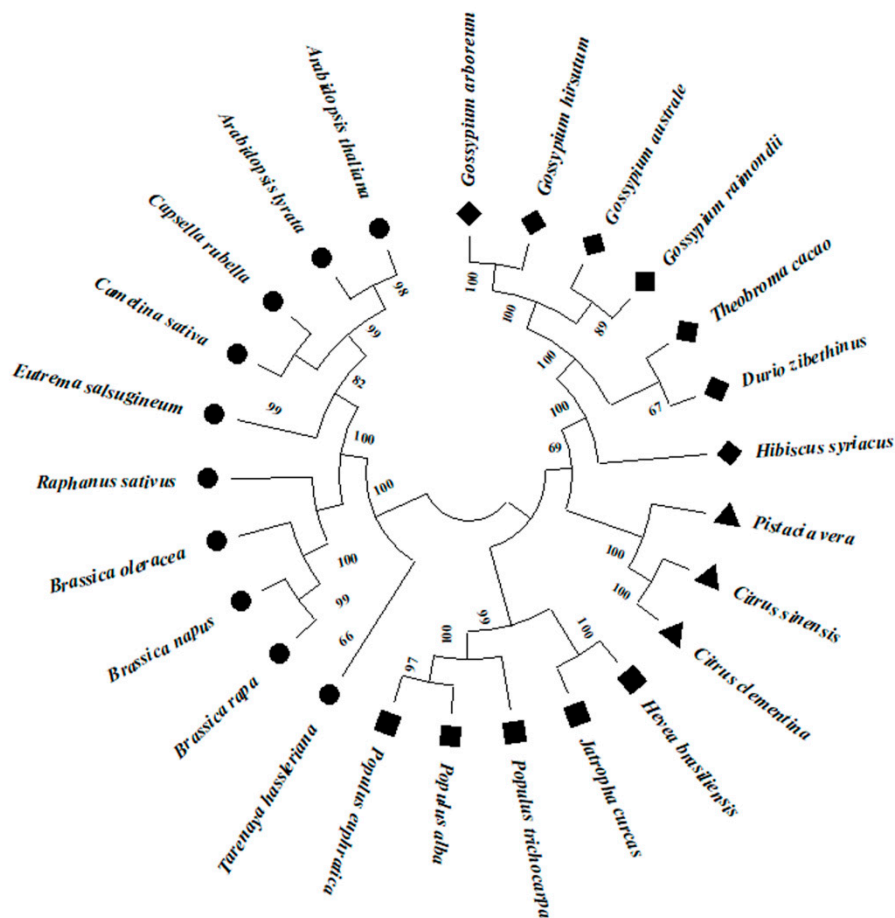**Figure S3.** Prediction of signal peptides by SignalP-6.0.

Figure S4. The phylogenetic evolutionary tree of CLV1.

The phylogenetic evolutionary tree of CLV1 was constructed in 25 species by MEGA-X with Clustal W and neighbor joining method based on 1,000 bootstrap replications. The species name and accession numbers of the 25 CLV1 homologs were as follows: *Brassica rapa* (XP_009106236.1); *Brassica napus* (XP_013717912.1); *Brassica oleracea* var. *Oleracea* (XP_013591703.1); *Raphanus sativus* (XP_018445747.1); *Eutrema salsugineum* (XP_006390268.1); *Camelina sativa* (XP_010428620.1); *Capsella rubella* (XP_006300675.1); *Arabidopsis lyrata* subsp. *Lyrata* (XP_020891600.1); *Arabidopsis thaliana* (NP_177710.1); *Tarenaya hassleriana* (XP_010536408.1); *Populus alba* (TKS03250.1); *Theobroma cacao* (EOY15070.1); *Gossypium arboreum* (XP_017623398.1); *Gossypium australe* (KAA3484481.1); *Gossypium hirsutum* (XP_016741841.1); *Gossypium raimondii* (XP_012478138.1); *Durio zibethinus* (XP_022772630.1); *Hibiscus syriacus* (KAE8659851.1); *Hevea brasiliensis* (XP_021692733.1); *Jatropha curcas* (XP_012073772.1); *Citrus sinensis* (XP_006473681.1); *Citrus clementina* (XP_006435205.1); *Populus trichocarpa* (XP_002307734.1); *Pistacia vera* (XP_031283197.1); *Populus euphratica* (XP_011045060.1).

Table S1. Primer sequences of Kompetitive allele specific PCR.

SNP location	Allele primer -F1	Allele primer -F2	Common primer
A07: 2690 5702	GAAGGTCGGAGTCAACGG ATTCCGGTTTAATCAGTTTA AAATCTCTAA	GAAGGTGACCAAGTTCATG CTCCGGTTTAATCAGTTTAA AATCTCTAG	AGGGAGATGA AGCTCTGAGG AAT
A07: 2757 1059	GAAGGTCGGAGTCAACGG ATTTTTTGCTCTCTCACTTTC CCC	GAAGGTGACCAAGTTCATG CTAGTTTTGCTCTCTCACTT TCCCT	GGAAACTGGT TGTCTGAATGT CTC
A07: 2792 1459	GAAGGTCGGAGTCAACGG ATTTGTGGTATTTGTAGGTG AATAAGAAA	GAAGGTGACCAAGTTCATG CTTGTGGTATTTGTAGGTGA ATAAGAAG	CACTGCTTGTT GAGCGACCA
A07: 2827 8890	GAAGGTCGGAGTCAACGG ATTAGAAGAAGAGGATGTC CTGGAAA	GAAGGTGACCAAGTTCATG CTAGAAGAAGAGGATGTCC TGGAAG	TCCTCTGAGAT TTGTTCAATAT ATGTTC

Table S2. Primer sequences used for clone sequencing.

Marker	Forward sequence (5′-3′)	Reverse sequence (5′-3′)
BrCLV1-1	TCGTGATCGTCTTCTTTCCTCT	ATTCGCCAAAAACGGTAGTG
BrCLV1-2	TACATTTCTTTAAGATTCTTGAGGC	CATCTATTAACGGTCAGTTCAGATC
BrCLV1-3	TCTCGTGCTTCTTCTTGTTCAT	GAGAGATCCCAGAGAGTTACGG
BrCLV1-4	CAAAATTCAAAACCAAAACAAAC	GAACAAGAAGAAGCACGAGAGA
BrCLV1-5	GCCATCATCAATAAGCATACAA	TGCATAGAGACGTTAAGTCCAAT

Table S3. Primer sequences for qRT-PCR.

Marker	Forward sequence (5′-3′)	Reverse sequence (5′-3′)
Actin	ATCTACGAGGGTTATGCT	CCACTGAGGACGATGTTT
BrCLV1-qRT	CGGTGCTGCTTCTGAGTGTATG	CGTGTTCCTCACCCACCTAACTA

Table S4. Quality statistics of raw data.

Sample	Reads Number	Total Bases(bp)	N(%)	GC(%)	Q20(%)	Q30(%)
slm	52,570,348	7,885,552,200	0.0005	38.35	97.18	92.65
Mutant-phenotype DNA mixed pool	141,247,084	21,187,062,600	0.0002	38.18	96.54	91.00

Table S5. Statistics of high quality (HQ) data.

Sample	HQ reads_number	HQ reads%	HQ Bases(bp)	HQ Bases%
slm	51,983,342	98.88	7,717,466,695	97.87
Mutant-phenotype DNA mixed pool	139,638,760	98.86	20,722,467,565	97.81

Sample	HQ reads_number	HQ reads%	HQ Bases(bp)	HQ Bases%

Table S6. Statistics of sequence alignment reference genome.

Sample		Mapped_reads	Mapping_rate
FT		94,719,968	98.00%
slm		51,983,342	98.50%
Mutant-phenotype mixed pool	DNA	139,638,760	98.80%

Table S7. Genotype results of four candidate SNPs (SNP A07: 26905702, SNP A07:27571059, SNP A07: 27921459, SNP A07:28278890).

	Phenotype	Genotype: SNP A07: 26905702	Genotype: SNP A07: 27571059	Genotype: SNP A07: 27921459	Genotype: SNP A07: 28278890
FT	wild-type	C/C	C/C	C/C	C/C
slm	mutant	T/T	T/T	T/T	T/T
F$_1$	wild-type	T/C	T/C	T/C	T/C
s1	mutant	T/T	T/T	T/T	T/T
s2	mutant	T/T	T/C	T/C	T/C
s3	mutant	T/T	T/T	T/T	T/T
s4	mutant	T/T	T/T	T/T	T/T
s5	mutant	T/T	T/T	T/T	T/T
s6	mutant	T/T	T/T	T/C	T/C
s7	mutant	T/T	T/T	T/T	T/T
s8	mutant	T/T	T/T	T/T	T/T
s9	mutant	T/T	T/T	T/T	T/T
s10	mutant	T/T	T/T	T/T	T/T
s11	mutant	T/T	T/T	T/T	T/T
s12	mutant	T/T	T/T	T/T	T/T
s13	mutant	T/T	T/T	T/T	T/T
s14	mutant	T/T	T/T	T/T	T/T
s15	mutant	T/T	T/T	T/T	T/T
s16	mutant	T/T	T/T	T/T	T/T
s17	mutant	T/T	T/T	T/T	T/T
s18	mutant	T/T	T/T	T/T	T/T
s19	mutant	T/T	T/T	T/T	T/T
s20	mutant	T/T	T/T	T/T	T/T
s21	mutant	T/T	T/T	T/T	T/T
s22	mutant	T/T	T/T	T/C	T/C
s23	mutant	T/T	T/T	T/T	T/T
s24	mutant	T/T	T/T	T/T	T/T
s25	mutant	T/T	T/T	T/T	T/T
s26	mutant	T/T	T/T	T/T	T/T
s27	mutant	T/T	T/T	T/T	T/T
s28	mutant	T/T	T/T	T/T	T/T
s29	mutant	T/T	T/T	T/T	T/T
s30	mutant	T/T	T/T	T/T	T/T
s31	mutant	T/T	T/T	T/T	T/T
s32	mutant	T/T	T/T	T/T	T/T
s33	mutant	T/T	T/T	T/T	T/T
s34	mutant	T/T	T/T	T/T	T/T
s35	mutant	T/T	T/T	T/T	T/T
s36	mutant	T/T	T/T	T/T	T/T
s37	mutant	T/T	T/T	T/T	T/T

s38	mutant	T/T	T/T	T/T	T/T
s39	mutant	T/T	T/T	T/T	T/T
s40	mutant	T/T	T/T	T/T	T/T
s41	mutant	T/T	T/T	T/T	T/T
s42	mutant	T/T	T/T	T/T	T/T
s43	mutant	T/T	T/T	T/T	T/T
s44	mutant	T/T	T/T	T/T	T/T
s45	mutant	T/T	T/T	T/T	T/T
s46	mutant	T/T	T/T	T/T	T/T
s47	mutant	T/T	T/T	T/T	T/T
s48	mutant	T/T	T/T	T/T	T/T
s49	mutant	T/T	T/T	T/T	T/T
s50	mutant	T/T	T/T	T/T	T/T
s51	mutant	T/T	T/T	T/T	T/T
s52	mutant	T/T	T/T	T/T	T/T
s53	mutant	T/T	T/T	T/T	T/T
s54	mutant	T/T	T/T	T/T	T/T
s55	mutant	T/T	T/T	T/T	T/T
s56	mutant	T/T	T/T	T/T	T/T
s57	mutant	T/T	T/T	T/T	T/T
s58	mutant	T/T	T/T	T/T	T/T
s59	mutant	T/T	T/T	T/T	T/T
s60	mutant	T/T	T/T	T/T	T/T
s61	mutant	T/T	T/T	T/T	T/T
s62	mutant	T/T	T/T	T/T	T/T
s63	mutant	T/T	T/T	T/T	T/T
s64	mutant	T/T	T/T	T/T	T/T
s65	mutant	T/T	T/T	T/T	T/C
s66	mutant	T/T	T/T	T/C	T/C
s67	mutant	T/T	T/T	T/T	T/T
s68	mutant	T/T	T/T	T/T	T/T
s69	mutant	T/T	T/T	T/T	T/C
s70	mutant	T/T	T/T	T/T	T/T
s71	mutant	T/T	T/T	T/T	T/T
s72	mutant	T/T	T/T	T/T	T/T
s73	mutant	T/T	T/T	T/T	T/T
s74	mutant	T/T	T/T	T/T	T/C
s75	mutant	T/T	T/T	T/T	T/T
s76	mutant	T/T	T/T	T/T	T/T
s77	mutant	T/T	T/T	T/T	T/T
s78	mutant	T/T	T/T	T/T	T/T
s79	mutant	T/T	T/T	T/T	T/T
s80	mutant	T/T	T/T	T/T	T/T
s81	mutant	T/T	T/T	T/T	T/T

s82	mutant	T/T	T/T	T/T	T/T
s83	mutant	T/T	T/T	T/T	T/T
s84	mutant	T/T	T/T	T/T	T/T
s85	mutant	T/T	T/T	T/T	T/T
s86	mutant	T/T	T/T	T/T	T/T
s87	mutant	T/T	T/T	T/T	T/T
s88	mutant	T/T	T/T	T/T	T/T
s89	mutant	T/T	T/T	T/T	T/T
s90	mutant	T/T	T/T	T/T	T/T
s91	mutant	T/T	T/T	T/T	T/T
s92	mutant	T/T	T/C	T/C	T/C
s93	mutant	T/T	T/T	T/T	T/T
s94	mutant	T/T	T/T	T/T	T/T
s95	mutant	T/T	T/C	T/C	T/C
s96	mutant	T/T	T/T	T/T	T/T
s97	mutant	T/T	T/T	T/T	T/T
s98	mutant	T/T	T/T	T/T	T/T
s99	mutant	T/T	T/T	T/T	T/C
F1	wild-type	T/C	T/C	T/C	T/C
F2	wild-type	C/C	C/C	C/C	C/C
F3	wild-type	T/C	T/C	T/C	T/C
F4	wild-type	C/C	C/C	C/C	T/C
F5	wild-type	T/C	T/C	C/C	T/C
F6	wild-type	T/C	T/C	T/C	T/C
F7	wild-type	C/C	T/C	C/C	T/C
F8	wild-type	T/C	T/C	T/C	T/C
F9	wild-type	T/C	T/C	T/C	T/C
F10	wild-type	C/C	C/C	C/C	T/C
F11	wild-type	C/C	C/C	C/C	C/C
F12	wild-type	T/C	T/C	T/C	T/C
F13	wild-type	C/C	C/C	C/C	C/C
F14	wild-type	T/C	T/C	T/C	T/C
F15	wild-type	T/C	T/C	T/C	T/C
F16	wild-type	T/C	T/C	T/C	T/C
F17	wild-type	C/C	C/C	T/C	T/C
F18	wild-type	T/C	T/C	T/C	T/C
F19	wild-type	T/C	T/C	T/C	T/C
F20	wild-type	T/C	T/C	C/C	C/C
F21	wild-type	T/C	T/C	T/C	T/C
F22	wild-type	T/C	T/C	T/C	T/C
F23	wild-type	T/C	T/C	C/C	C/C
F24	wild-type	T/C	T/C	T/C	T/C
F25	wild-type	T/C	T/C	T/C	T/C
F26	wild-type	T/C	T/C	T/C	T/C

F27	wild-type	T/C	T/C	T/C	T/C
F28	wild-type	T/C	T/C	T/C	T/T
F29	wild-type	T/C	T/C	T/C	T/C
F30	wild-type	T/C	T/C	T/C	T/C
F31	wild-type	C/C	C/C	C/C	C/C
F32	wild-type	C/C	C/C	C/C	C/C
F33	wild-type	C/C	C/C	C/C	C/C
F34	wild-type	T/C	C/C	C/C	T/C
F35	wild-type	C/C	C/C	C/C	C/C
F36	wild-type	C/C	C/C	C/C	C/C
F37	wild-type	T/C	T/T	T/T	T/T
F38	wild-type	T/C	T/C	T/C	T/C
F39	wild-type	T/C	T/C	T/C	T/C
F40	wild-type	T/C	T/C	T/C	T/C
F41	wild-type	C/C	C/C	C/C	C/C
F42	wild-type	C/C	C/C	C/C	C/C
F43	wild-type	T/C	T/C	T/C	T/C
F44	wild-type	C/C	C/C	C/C	C/C
F45	wild-type	T/C	T/C	T/C	T/C
F46	wild-type	C/C	C/C	C/C	C/C
F47	wild-type	T/C	T/C	T/C	T/C
F48	wild-type	T/C	T/C	T/C	T/C
F49	wild-type	T/C	T/C	T/C	T/C
F50	wild-type	T/C	T/C	T/C	T/C
F51	wild-type	T/C	T/C	T/C	T/C
F52	wild-type	C/C	C/C	C/C	C/C
F53	wild-type	C/C	C/C	C/C	C/C
F54	wild-type	T/C	T/C	T/C	T/C
F55	wild-type	T/C	T/C	T/C	T/C
F56	wild-type	T/C	T/C	T/C	T/C
F57	wild-type	T/C	T/C	T/C	T/C
F58	wild-type	T/C	T/C	T/C	T/C
F59	wild-type	T/C	T/C	T/T	T/T
F60	wild-type	T/C	T/C	T/C	T/C
F61	wild-type	T/C	T/C	T/C	T/C
F62	wild-type	T/C	T/C	T/C	T/C
F63	wild-type	C/C	C/C	C/C	C/C
F64	wild-type	C/C	T/C	T/C	T/C
F65	wild-type	T/C	T/C	T/C	T/C
F66	wild-type	T/C	T/C	T/C	T/C
F67	wild-type	T/C	T/C	T/C	T/C
F68	wild-type	C/C	C/C	C/C	C/C
F69	wild-type	T/C	T/C	T/C	T/C
F70	wild-type	C/C	T/C	T/C	T/C

F71	wild-type	T/C	T/C	T/C	T/C
F72	wild-type	T/C	T/C	T/C	T/C
F73	wild-type	T/C	T/C	T/C	T/C
F74	wild-type	T/C	T/C	T/C	T/C
F75	wild-type	C/C	C/C	C/C	C/C
F76	wild-type	T/C	T/C	T/C	T/C
F77	wild-type	C/C	C/C	C/C	C/C
F78	wild-type	T/C	T/C	T/C	T/C
F79	wild-type	T/C	C/C	C/C	C/C
F80	wild-type	T/C	T/C	T/C	T/C
F81	wild-type	T/C	T/C	T/C	T/C
F82	wild-type	T/C	T/C	C/C	C/C
F83	wild-type	T/C	T/C	T/C	T/C
F84	wild-type	T/C	T/C	T/C	T/C
F85	wild-type	T/C	T/C	T/C	T/C
F86	wild-type	C/C	C/C	T/C	T/C
F87	wild-type	T/C	T/C	T/C	T/C
F88	wild-type	C/C	C/C	C/C	C/C
F89	wild-type	C/C	C/C	C/C	C/C
F90	wild-type	T/C	T/C	T/C	T/C

Table S8. Prediction of transmembrane helices by TMHMM-2.0.

Prediction	Start	end
inside	1	12
TMhelix	13	35
outside	36	647
TMhelix	648	666
inside	667	861

Table S9. Prediction of signal peptides and the location of their cleavage sites in proteins by SignalP-6.0.

Protein type	Other	Signal Peptide (Sec/SPI)	cleavage sites (Probability)
Likelihood	0.0212	0.9787	between position 31 and 32(0.946839)