



黄瓜性别分化之 ACS基因家族分析

ACS gene family analysis of sex differentiation in Cucumber

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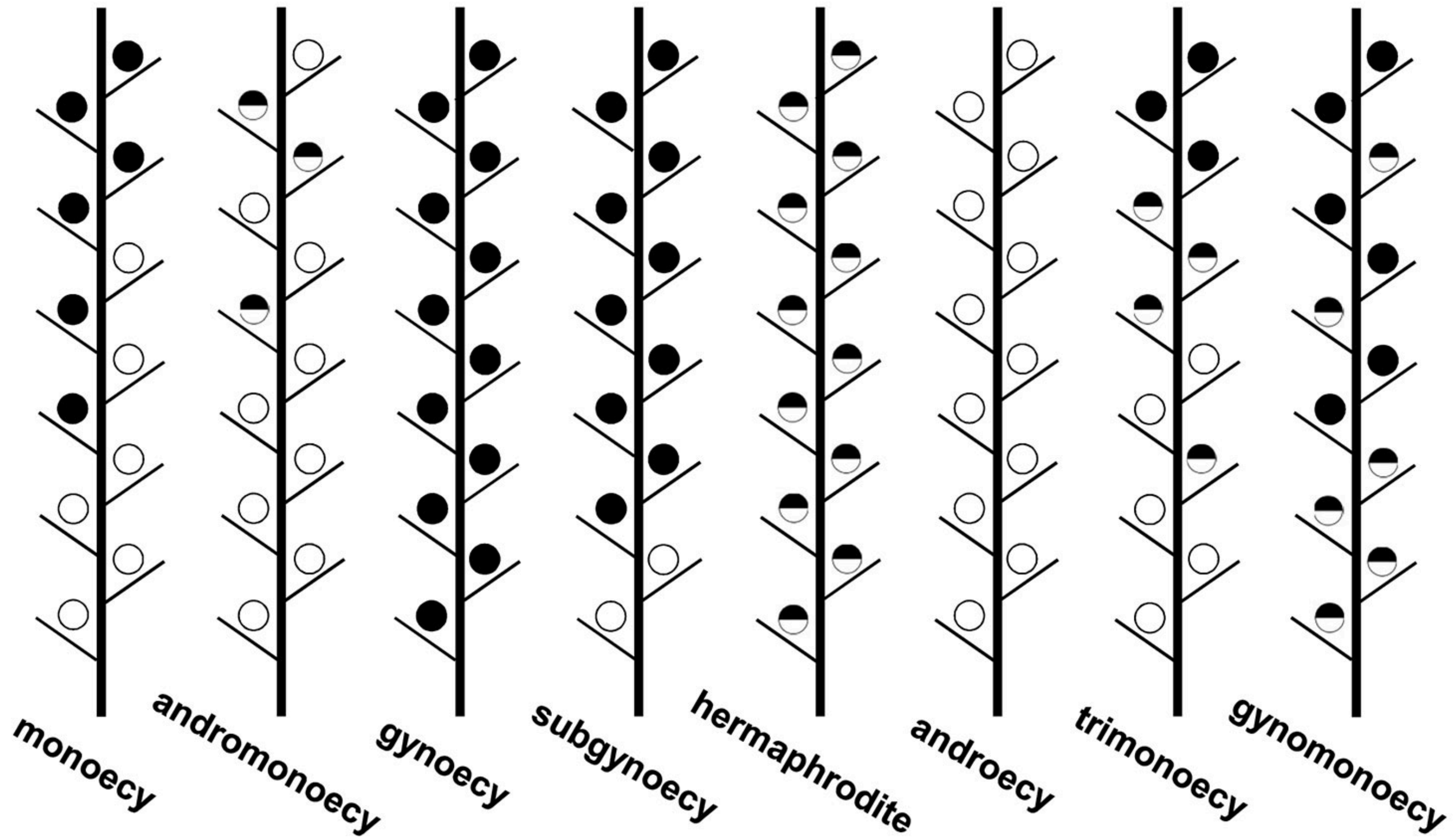
染色体定位

基因结构分析

同源性分析

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黄瓜的性型



雌雄株 雄全株 纯雌株 强雌株 完全株 纯雄株 雌雄全株 雌全株

最为常见

生产需要

外因:

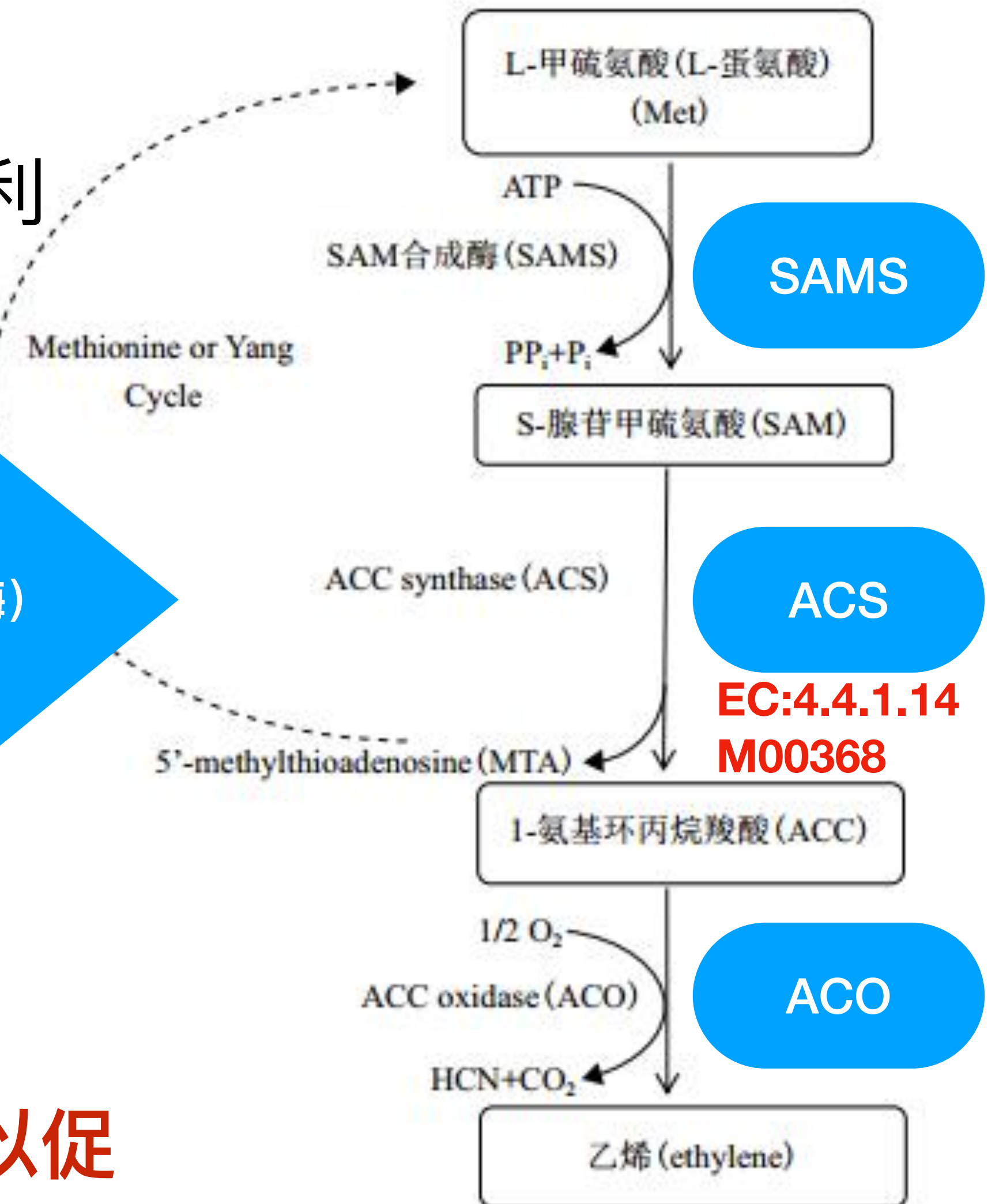
温度、光照; 湿度; 矿质营养; 植物生长调节剂-乙烯利

本质: 影响内源激素乙烯的平衡

内因:

遗传特性: *F/f*、*M/m*、*A/a*

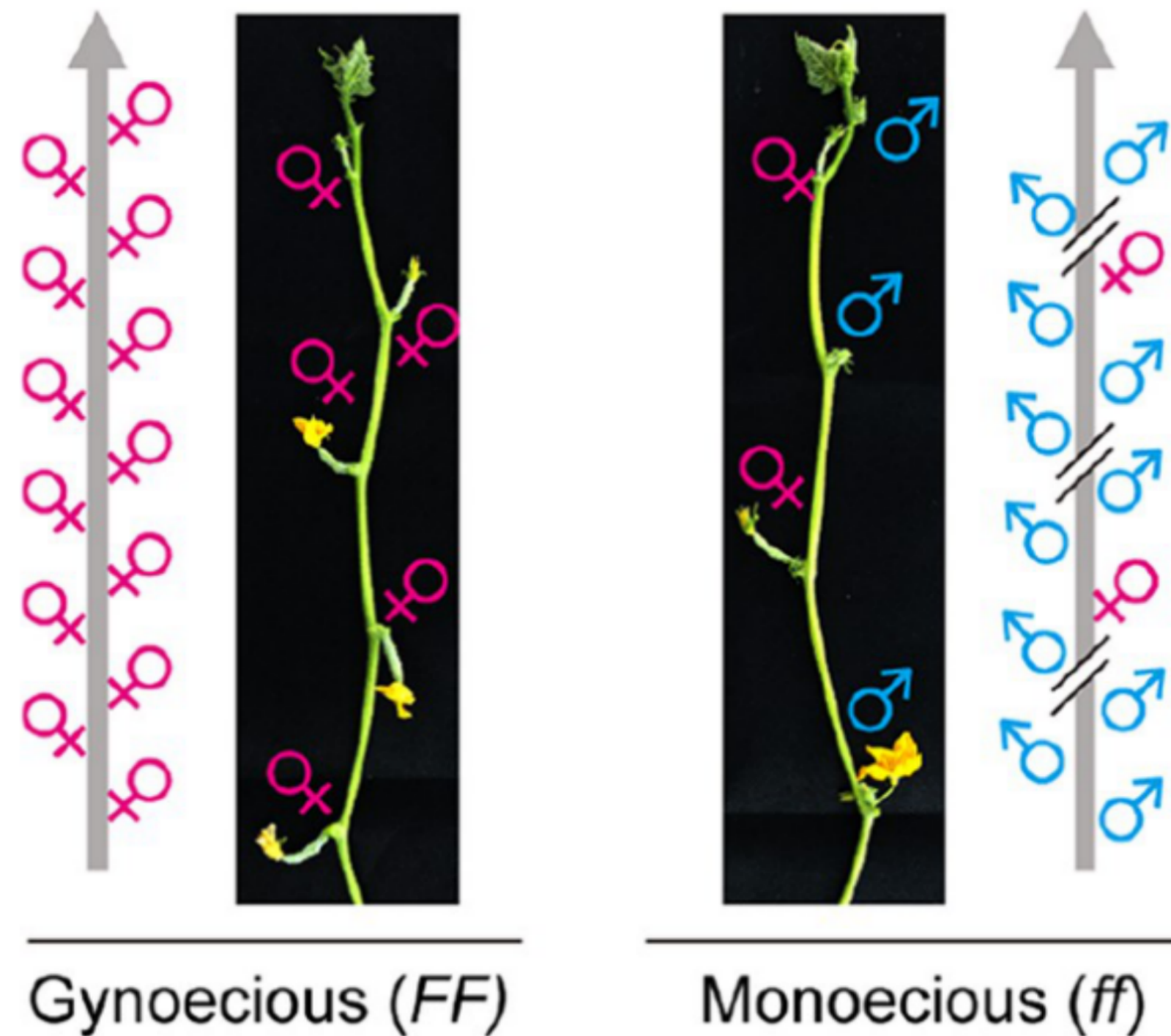
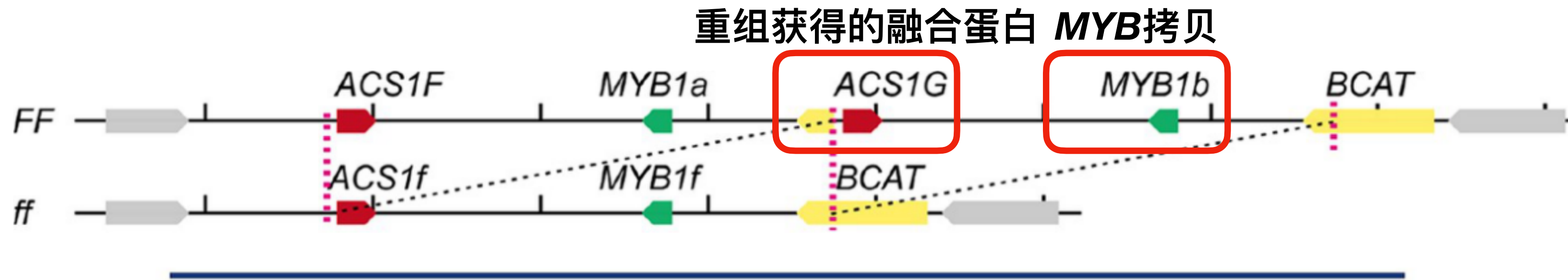
编码控制乙烯合成关键酶 (ACC合成酶)

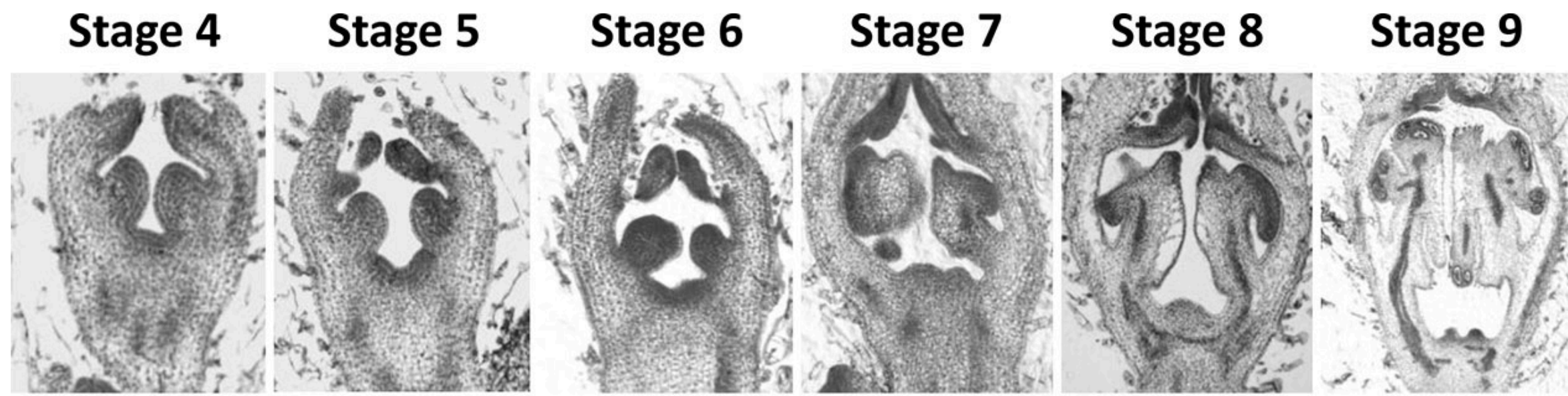


乙烯与黄瓜雌花的形成密切相关:

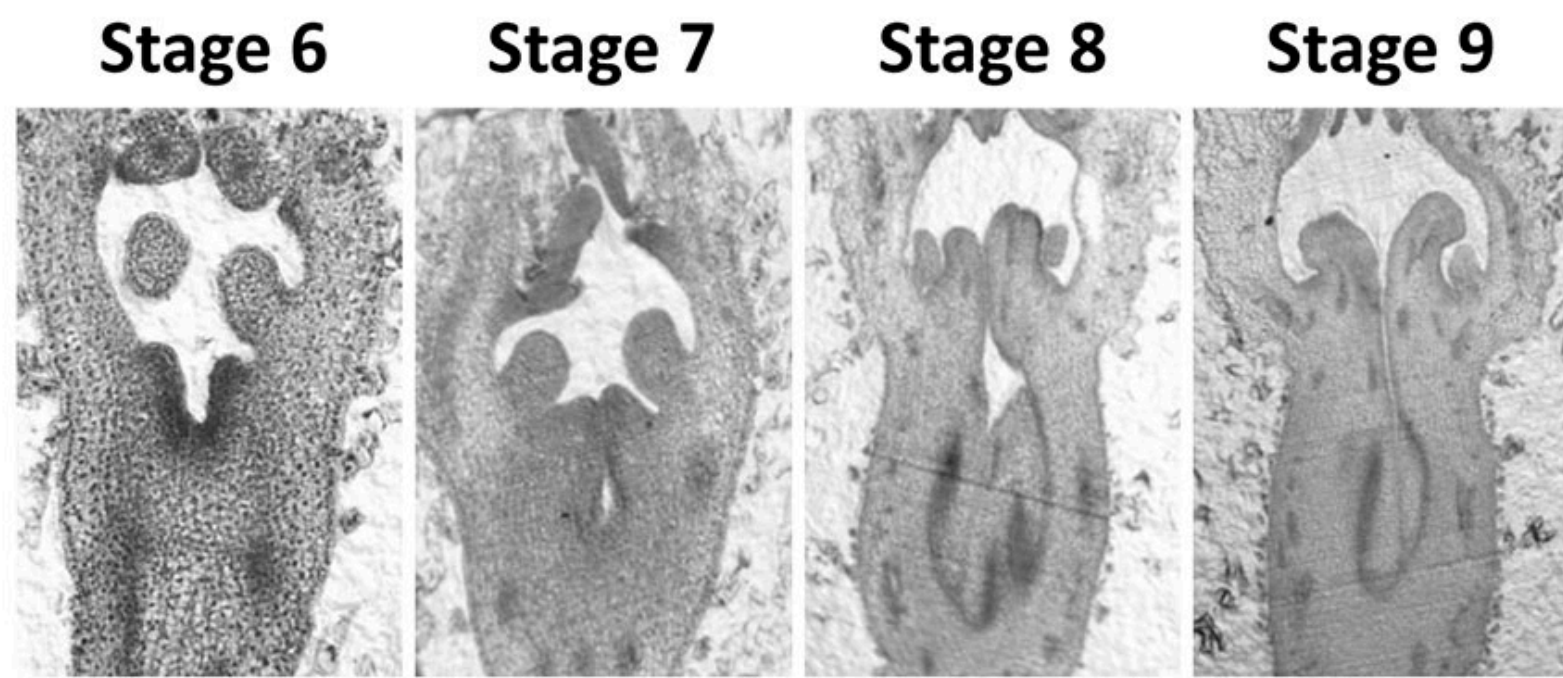
发育中的花同时具有雄性和雌性的花原基, 乙烯可以促进雌性花的产生, 抑制雄性花原基的发育

纯雌性型决定基因 F/f

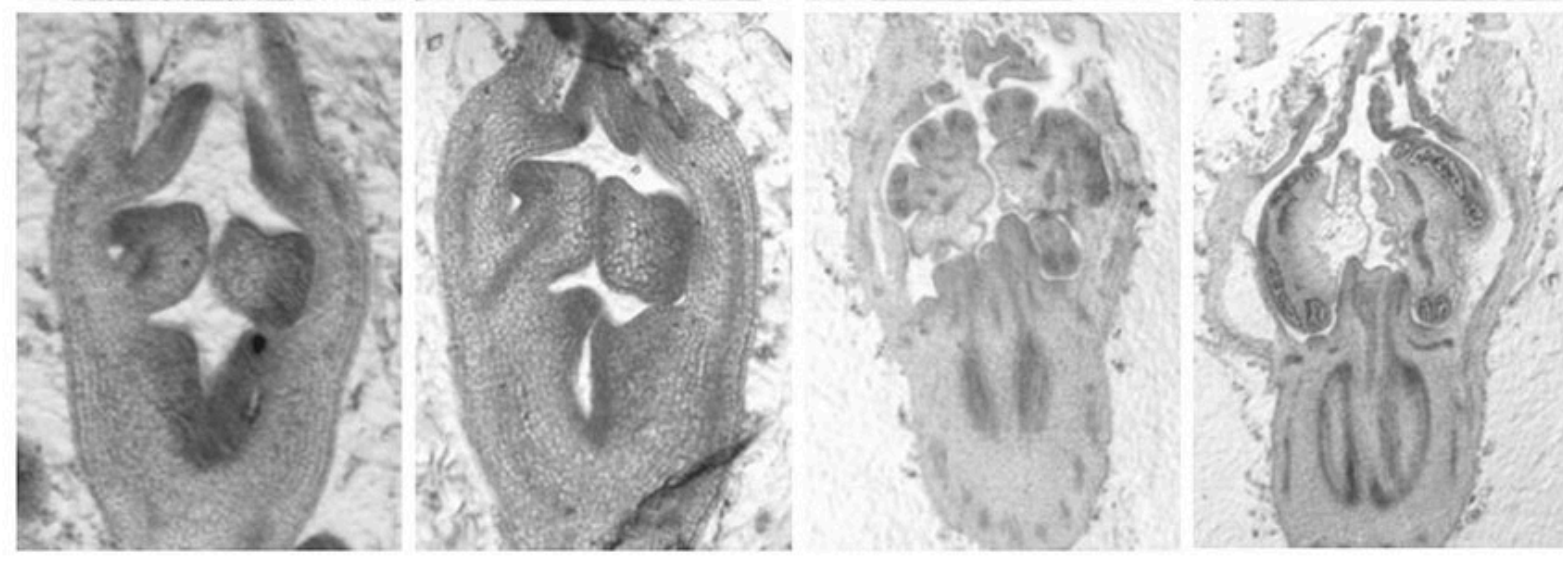




male flower



female flower

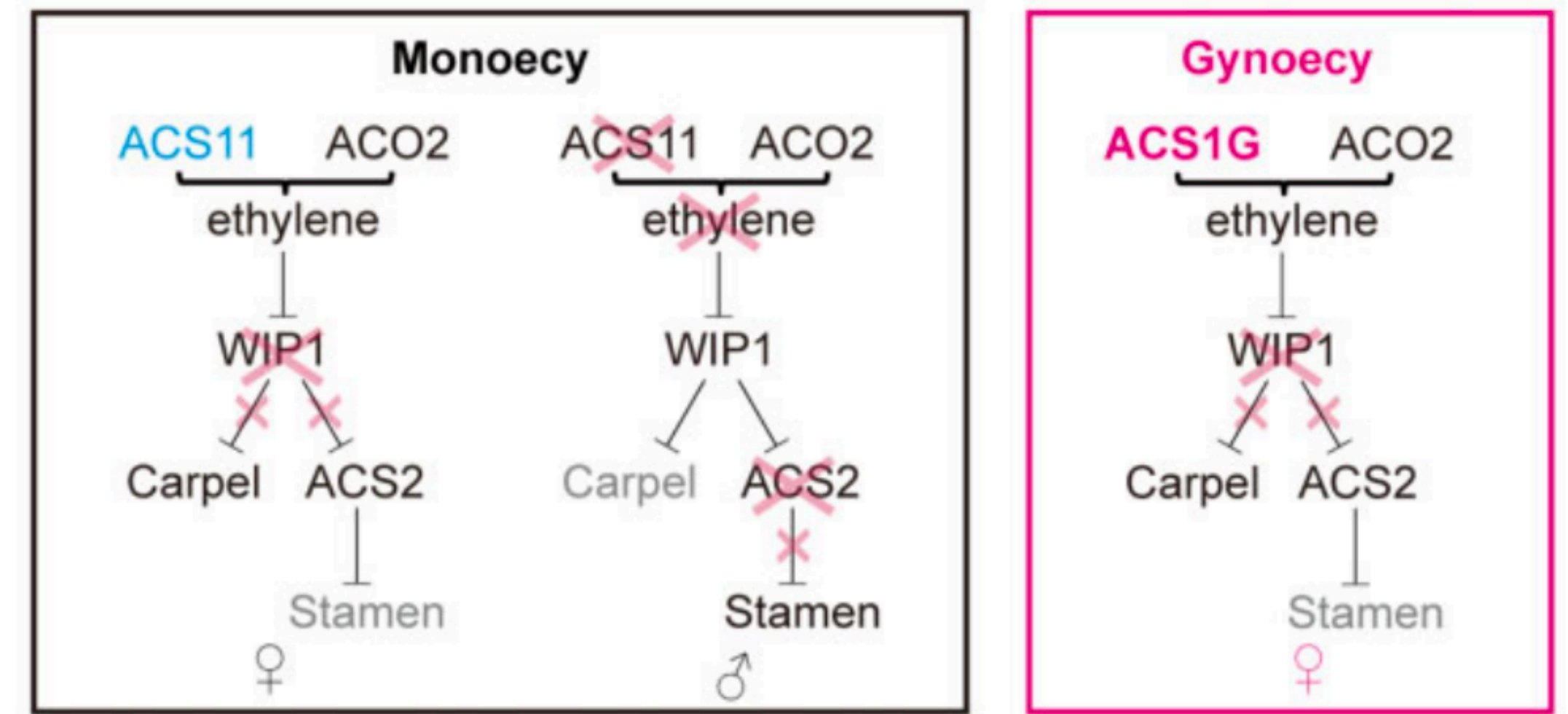


bisexual flower



雌雄花, *ff* 植株

纯雌花, *F* 植株



ACS1G在所有的花原基发育时都表达

基因家族成员鉴定

- 1、利用已报道的CsACS1序列从Pfam数据库中搜索HMM profile，下载相似度最高的Aminotransferase class I / II 【Pfam: PF00155】，或者从swissprot里拟南芥的ACS成员的Pfam交叉链接进入
- 2、获得hmm结构模式后，下载黄瓜蛋白数据库，利用hmmsearch搜索

```
[zhengyingying@login1 02_tree]$ cat Aminotran_1_2_work
ls pep/ | while read i
do
hmmsearch Aminotran_1_2.hmm pep/${i} > Aminotran_1_2/${i}
done
```


Query: Aminotran_1_2 [M=363]

Accession: PF00155.24

Description: Aminotransferase class I and II

Scores for complete sequences (score includes all domains):

--- full sequence ---			--- best 1 domain ---			-#dom-		Sequence	Description
E-value	score	bias	E-value	score	bias	exp	N		
1.8e-108	363.5	0.0	2e-108	363.3	0.0	1.0	1	Csa6G006800.1	Y
1.4e-105	354.0	0.0	1.6e-105	353.7	0.0	1.0	1	Csa6G496450.1	Y
2.6e-103	346.5	0.0	3e-103	346.3	0.0	1.0	1	Csa4G049610.1	Y_1
8.9e-99	331.6	0.0	1e-98	331.4	0.0	1.0	1	Csa4G099220.1	Y
9.2e-99	331.5	0.0	1e-98	331.4	0.0	1.0	1	Csa4G049610.2	Y_2
6.6e-98	328.7	0.0	7.7e-98	328.5	0.0	1.0	1	Csa3G889160.1	
2e-95	320.5	0.0	2.3e-95	320.3	0.0	1.0	1	Csa1G580750.1	Y
2.1e-95	320.5	0.0	2.7e-95	320.1	0.0	1.1	1	Csa2G382520.1	
6.2e-91	305.8	0.0	7e-91	305.6	0.0	1.0	1	Csa2G353460.1	Y
7e-89	299.0	0.0	8e-89	298.8	0.0	1.0	1	Csa1G096620.1	
6.2e-83	279.5	0.0	7.2e-83	279.2	0.0	1.0	1	Csa3G177920.1	Y
3e-77	260.8	0.0	3.4e-77	260.6	0.0	1.0	1	Csa4G329570.1	
3.5e-73	247.4	0.0	5.5e-73	246.7	0.0	1.3	1	Csa5G157380.1	Y
1.9e-72	245.0	0.0	2.2e-72	244.8	0.0	1.0	1	Csa4G000870.1	
3.8e-64	217.7	0.0	5.2e-64	217.2	0.0	1.2	1	Csa4G371570.1	
3.8e-64	217.7	0.0	5.2e-64	217.2	0.0	1.2	1	Csa4G371570.2	
1.1e-55	189.8	0.0	1.3e-55	189.6	0.0	1.0	1	Csa4G629470.1	
1.2e-55	189.7	0.0	1.4e-55	189.4	0.0	1.0	1	Csa1G000720.1	
4.4e-55	187.8	0.0	5.4e-55	187.5	0.0	1.0	1	Csa6G155030.1	
5.6e-53	180.9	0.0	6.9e-53	180.6	0.0	1.0	1	Csa7G405990.1	
5.6e-53	180.9	0.0	6.9e-53	180.6	0.0	1.0	1	Csa7G405990.2	
9.4e-49	167.0	0.0	1.1e-48	166.8	0.0	1.0	1	Csa7G435520.1	
2e-48	165.9	0.0	2.3e-48	165.7	0.0	1.0	1	Csa4G629470.2	

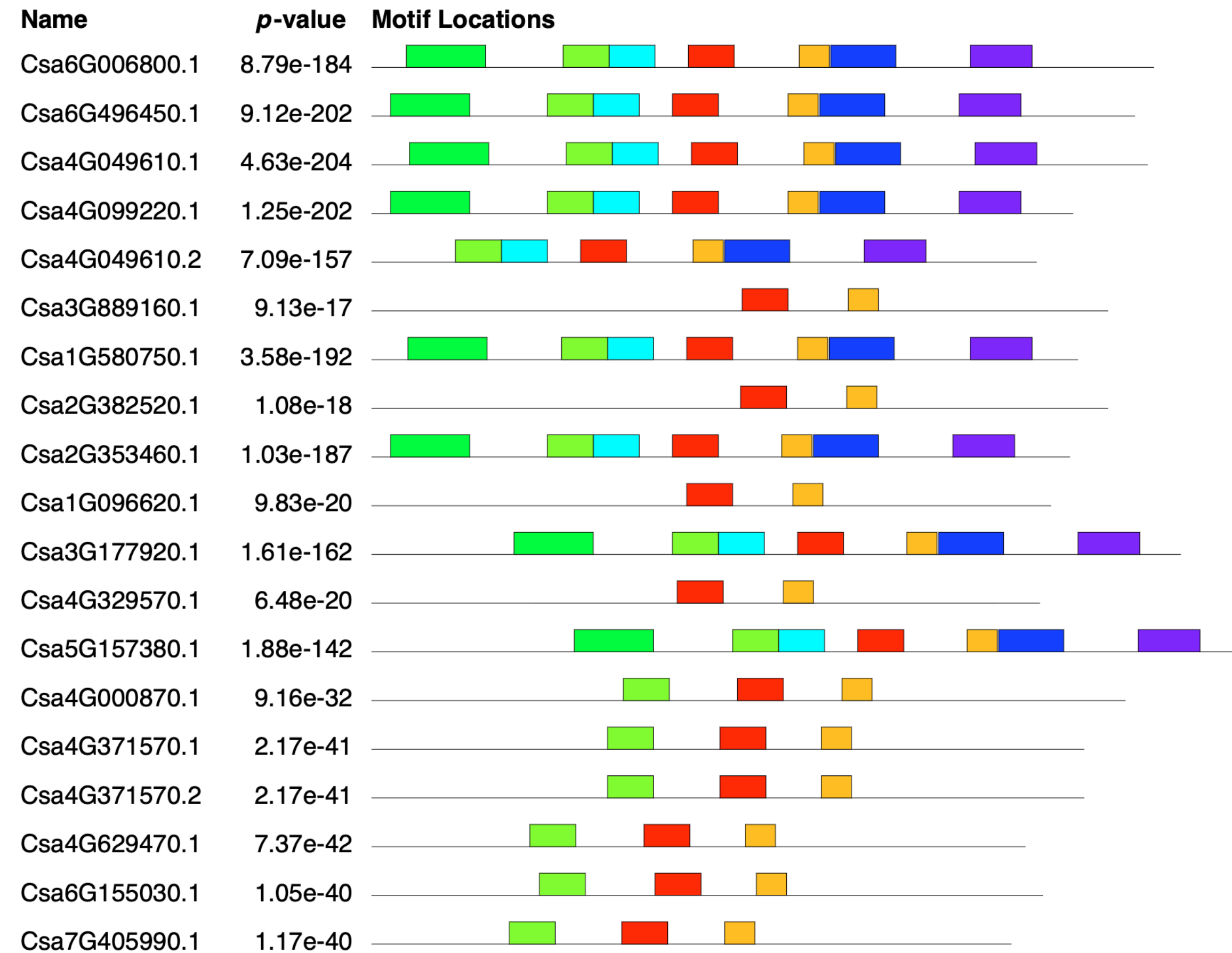
■ ■ ■

0.0084	15.8	0.0	0.016	14.9	0.0	1.4	1	Csa6G483410.1	
0.0099	15.6	0.0	0.016	14.9	0.0	1.3	1	Csa1G537330.1	
----- inclusion threshold -----									
0.033	13.9	0.0	0.048	13.3	0.0	1.2	1	Csa3G611340.1	
0.08	12.6	0.0	0.12	12.0	0.0	1.3	1	Csa7G067490.1	

初筛：48条

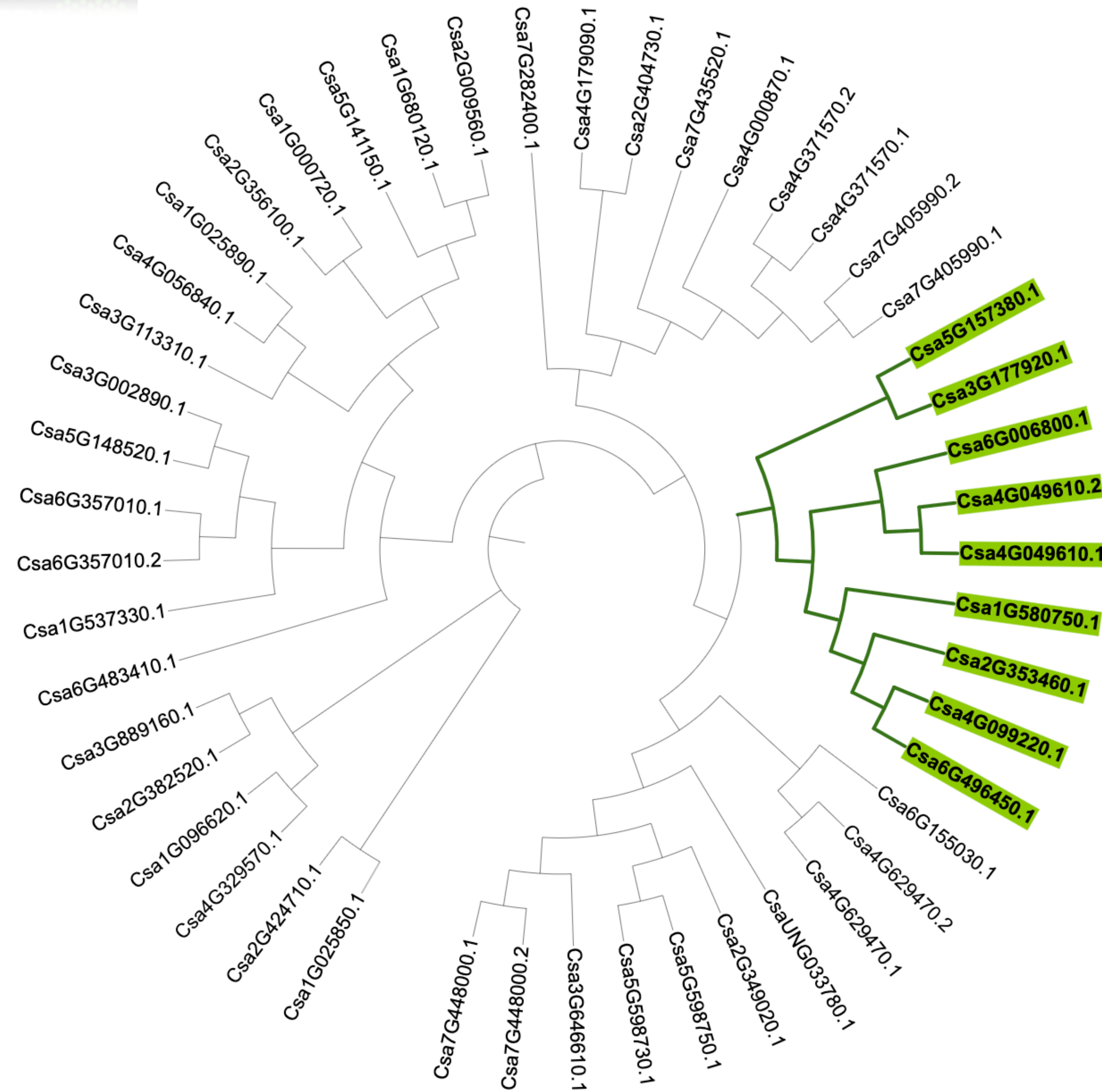


精筛：Motif预测得到8条基因序列




(依据：依赖PLP的7个保守结构域)

By 郑盈盈



No.	Name	研究情况
Csa6G496450	CsACS1	纯雌花基因F/f
Csa1G580750	CsACS2	两性花基因M/m
Csa2G353460	CsACS11	纯雄花基因A/a
Csa3G177920	CsACS8	
Csa4G049610	CsACS6	
Csa4G099220	CsACS5	
Csa5G157380	CsACS9	
Csa6G006800	CsACS4	

染色体定位

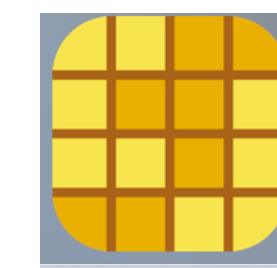


Cucumber (Chinese Long) genome v2 | v2
Search | Batch Query | Genome Browser | Pathway | Download

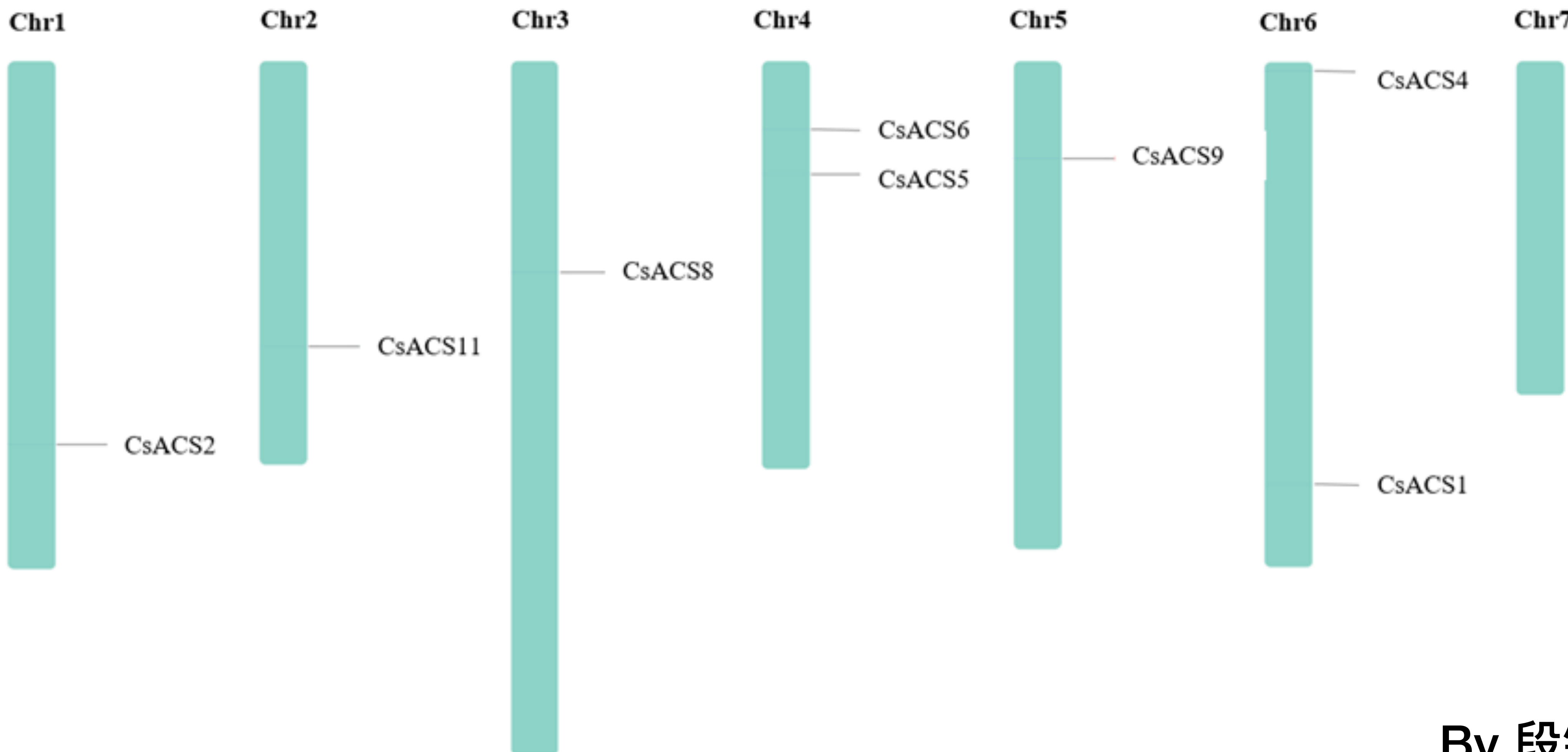
Cucumber (Gy14) genome v2 | v1
Search | Batch Query | Genome Browser | Pathway | Download

Cucumber (PI183967) genome
Search | Batch Query | Genome Browser | Pathway | Download

基因位置信息
染色体长度信息

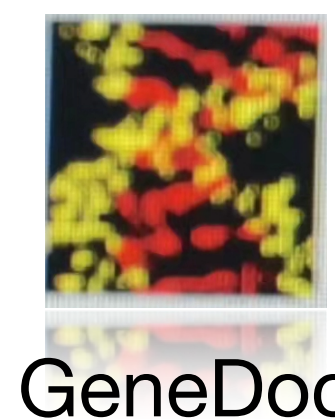
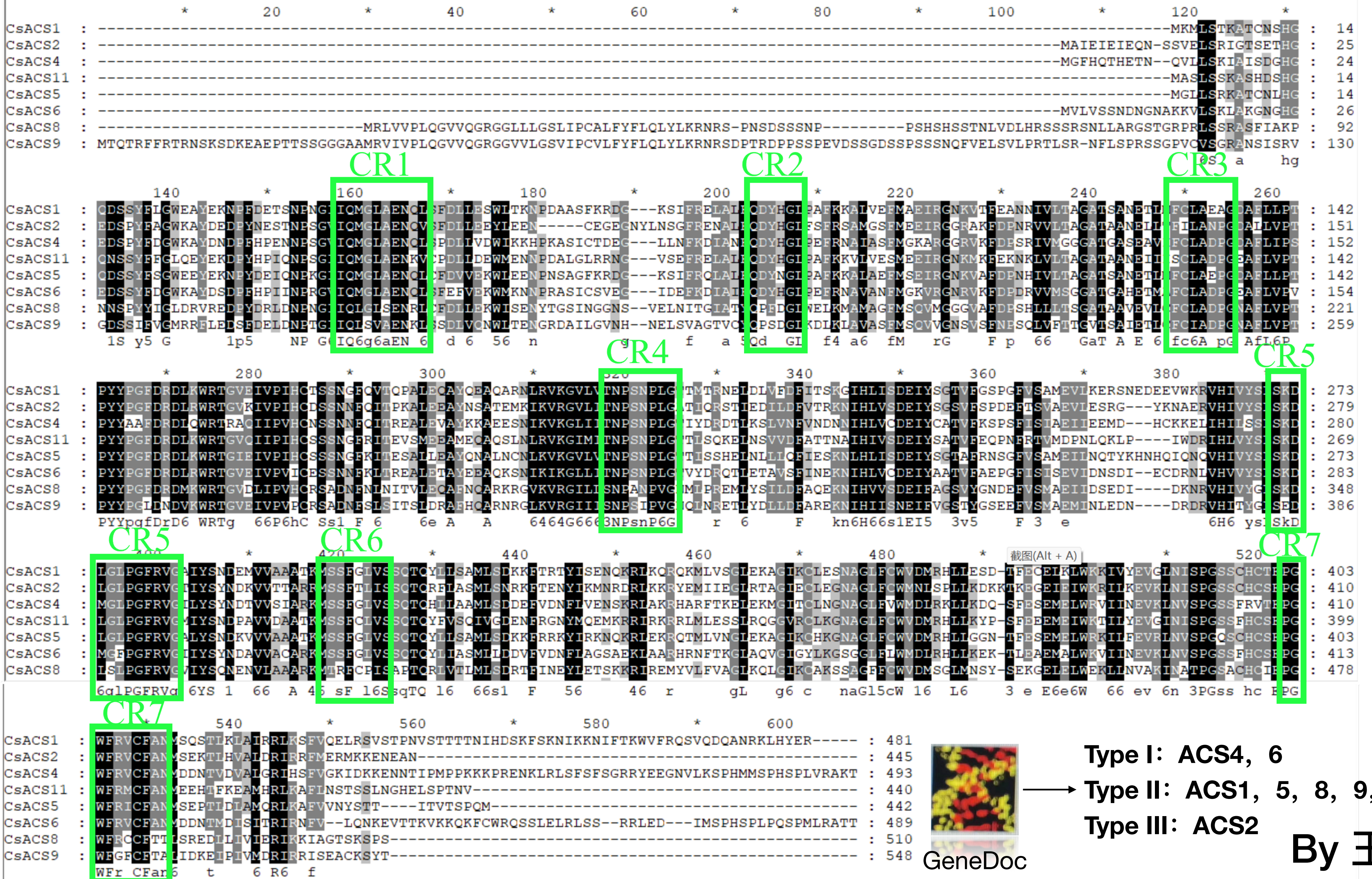


TBtools



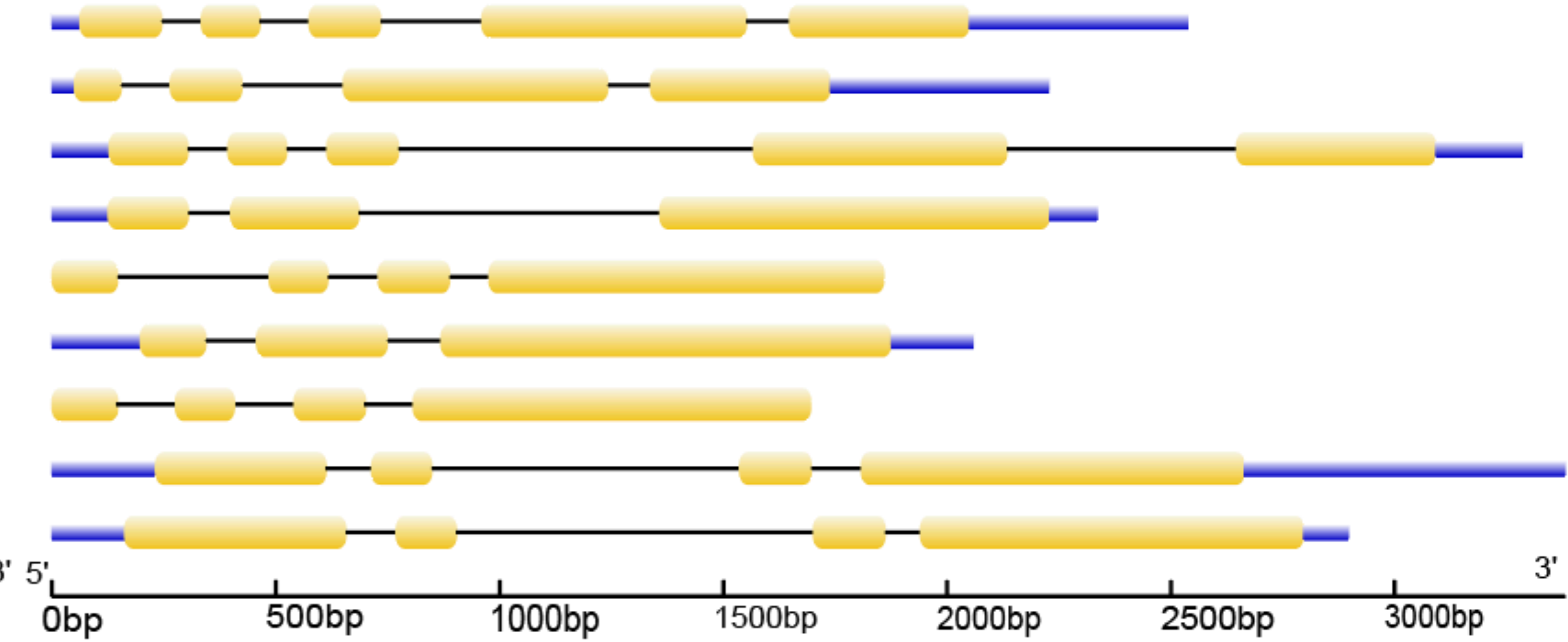
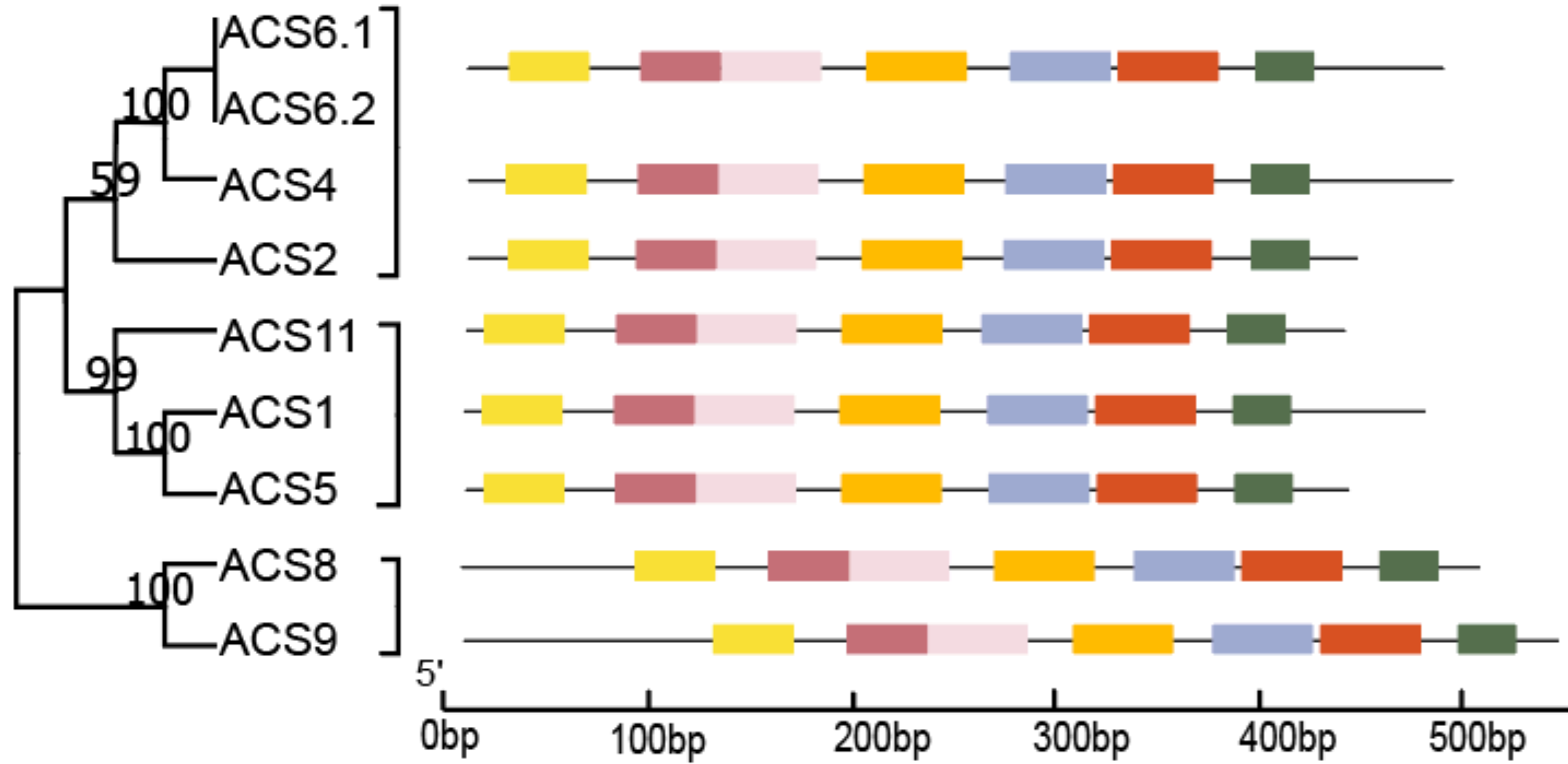
By 段铭奥

基因结构分析



Type I: ACS4, 6
Type II: ACS1, 5, 8, 9, 11
Type III: ACS2

By 王少骅



进化树分析

motif分布

内含子、外显子的分布结构

	Motif 1	LTAGATAANETLIFCLADPGDAFLVPTPYYPGFDRDLKWRTGVEIVPIHC
	Motif 2	RVHIVYSLSKDLGLPGFRVGAIYSYBEAVVAAARKMSSFGLVSSQTQYLL
	Motif 3	SNSHGZDSSYFDGWKAYEEDPYDEJQNPSGIIQMGLAENQ
	Motif 4	EVKLVNVPSSSCHCSEPGWFRVCFANMSE
	Motif 5	NJKVKGILITNPSNPLGTTJSRETLESLLDFITEKNIHLVSDEIYSGTVF
	Motif 6	SDKKFVDNYJRENKKRLKKRHKMFVKGLEKAGIKCLKGNAGLFCWVDMRH
	Motif 7	FREJALFQDYHGLPEFKKALAEFMSEIRGNKVKFDPNRIV



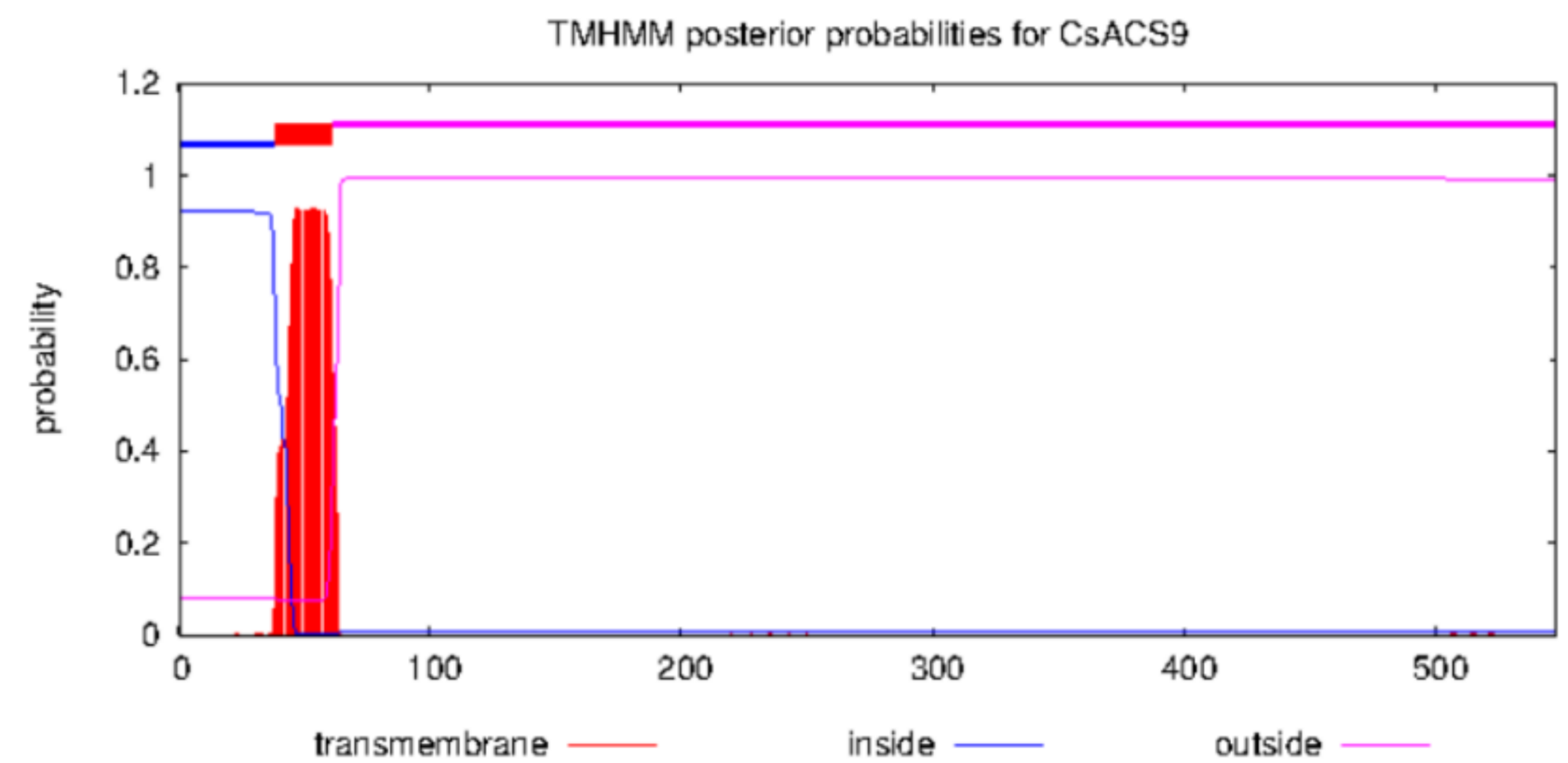
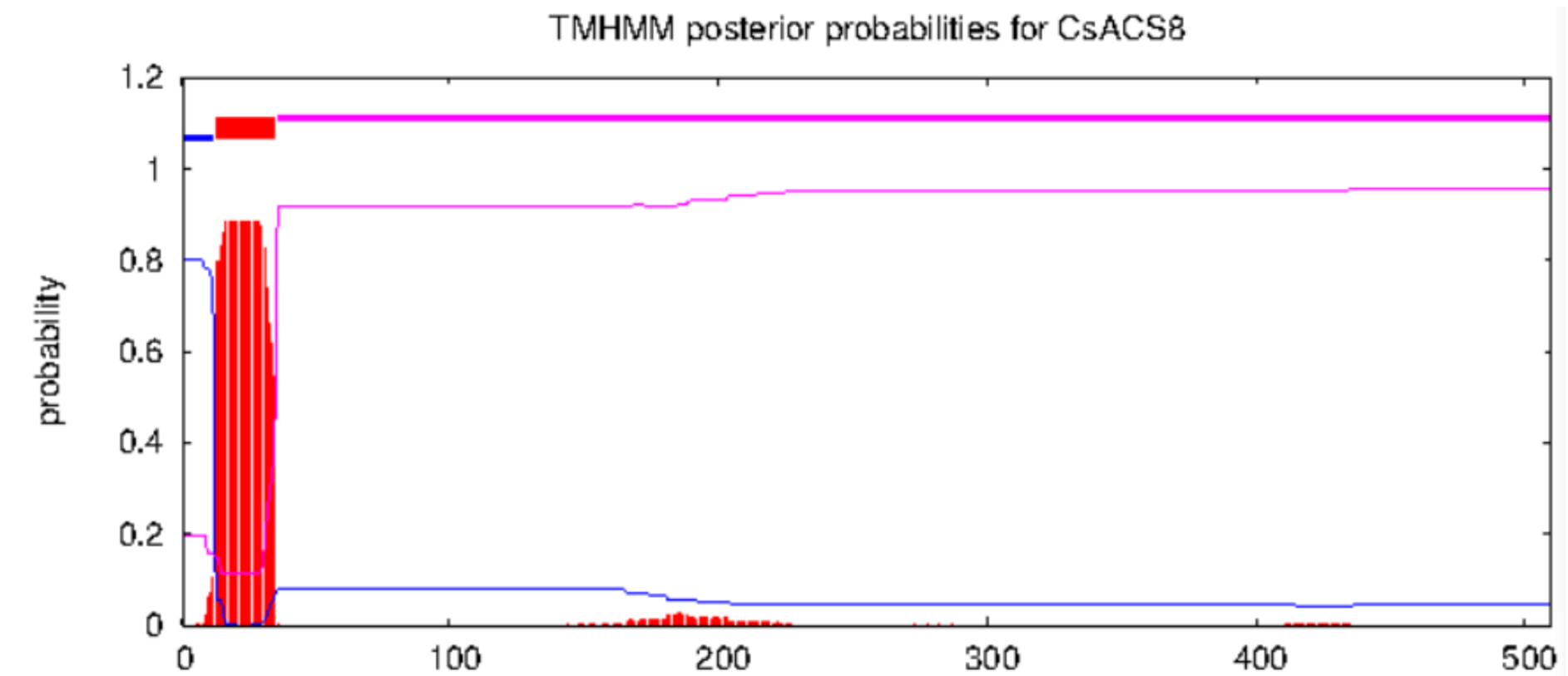
预测保守的7个motif信息

ACS8和ACS9两个成员具有跨膜结构

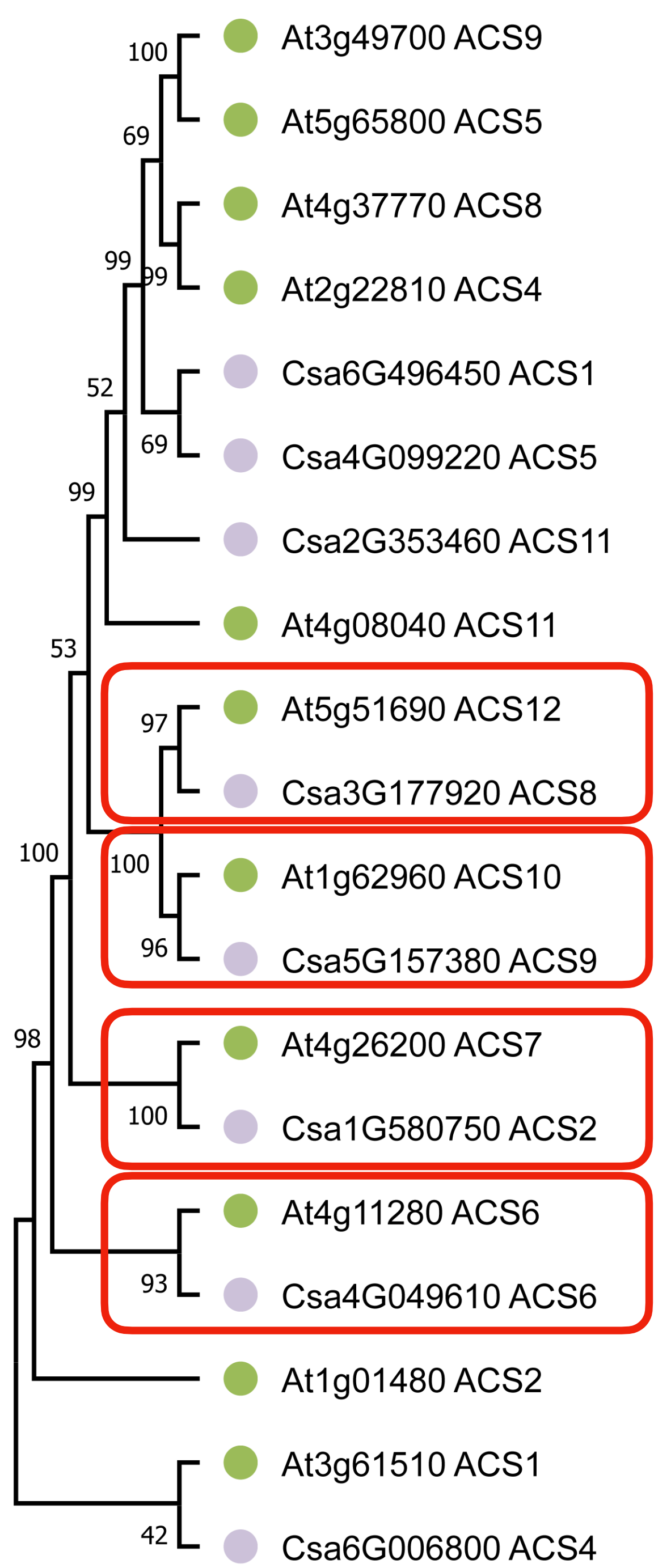


TMHMM - 2.0
Prediction of transmembrane helices in proteins

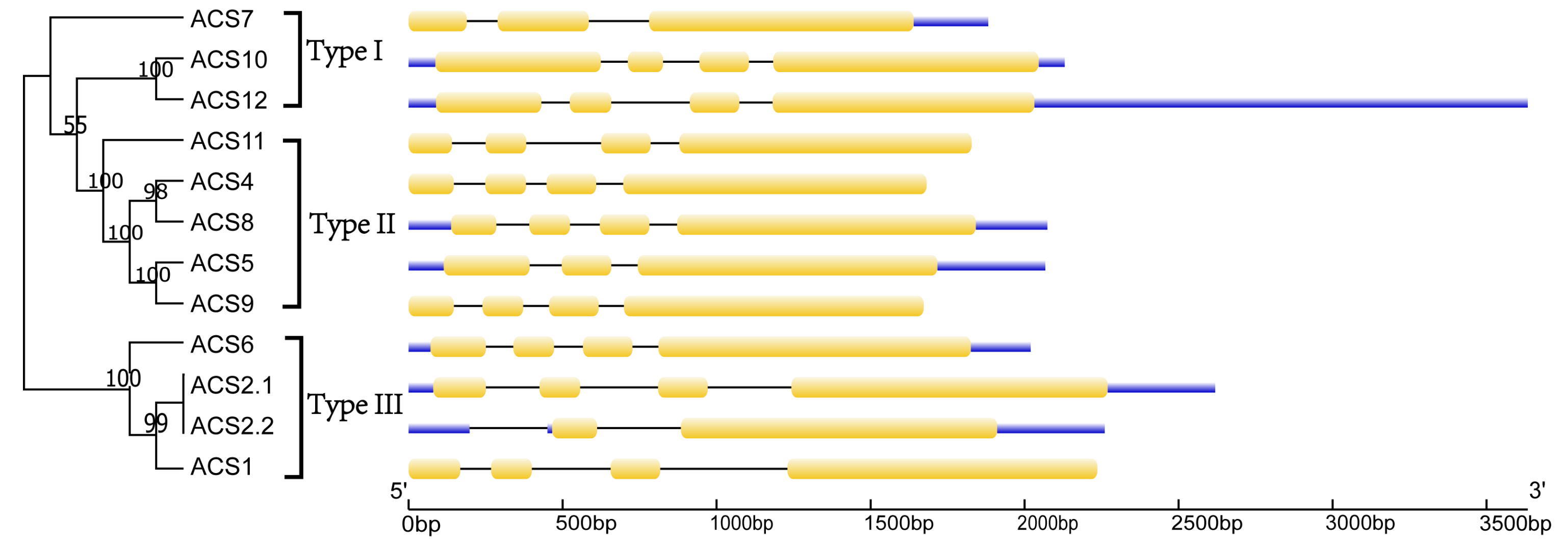
Prediction of transmembrane helices in proteins



同源性分析



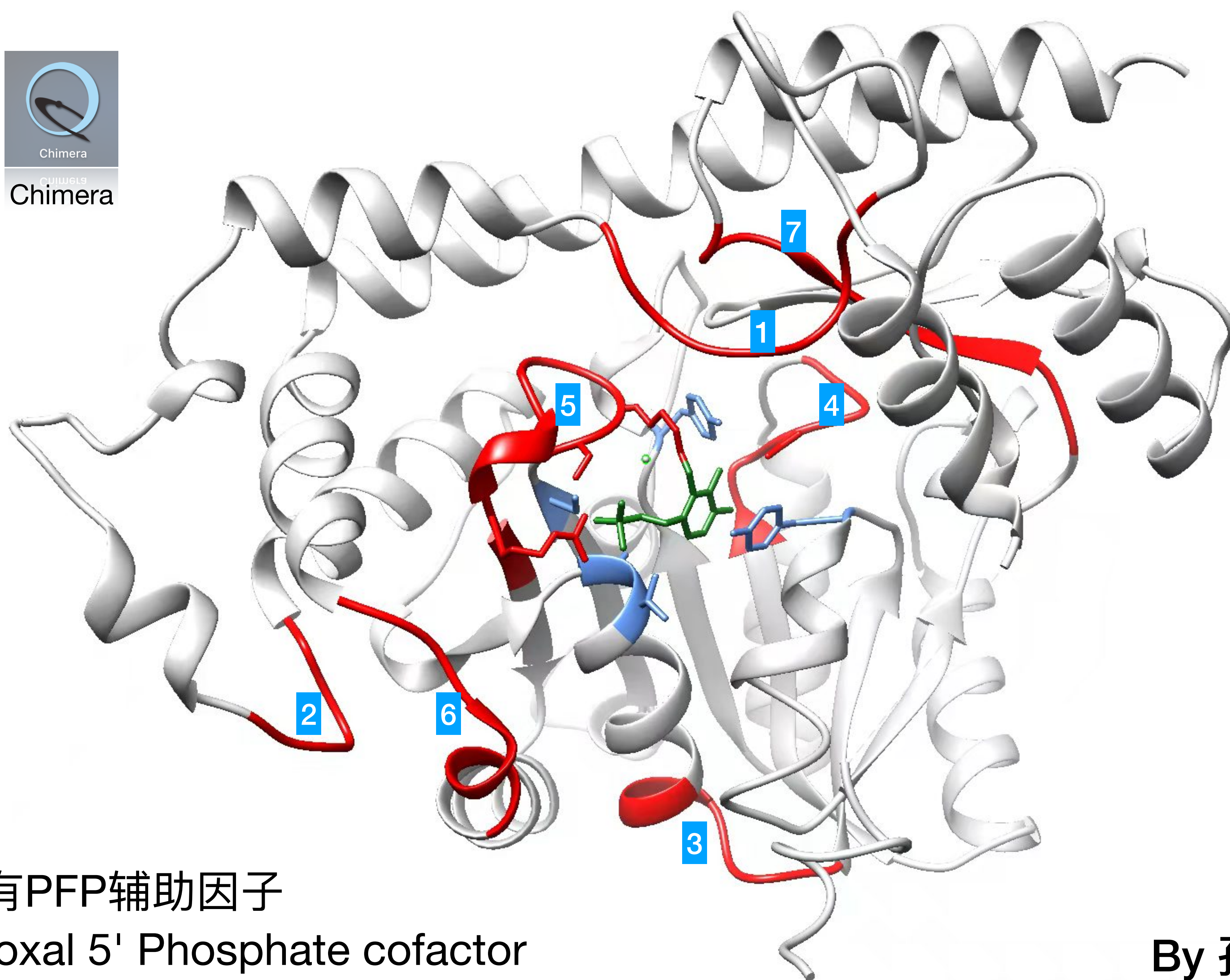
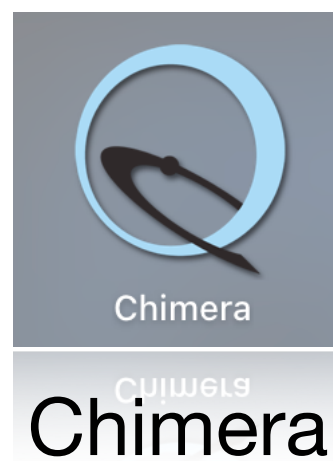
拟南芥ACS家族进化树、内外显子结构分析及分类



拟南芥	黄瓜
At5g51690 ACS12	Csa3G177920 ACS8
At1g62960 ACS10	Csa5G157380 ACS9
At4g26200 ACS7	Csa1G580750 ACS2
At4g11280 ACS6	Csa4G049610 ACS6

可能互为直系同源基因

蛋白质结构分析



携带有PFP辅助因子
Pyridoxal 5' Phosphate cofactor

By 孙凯悦

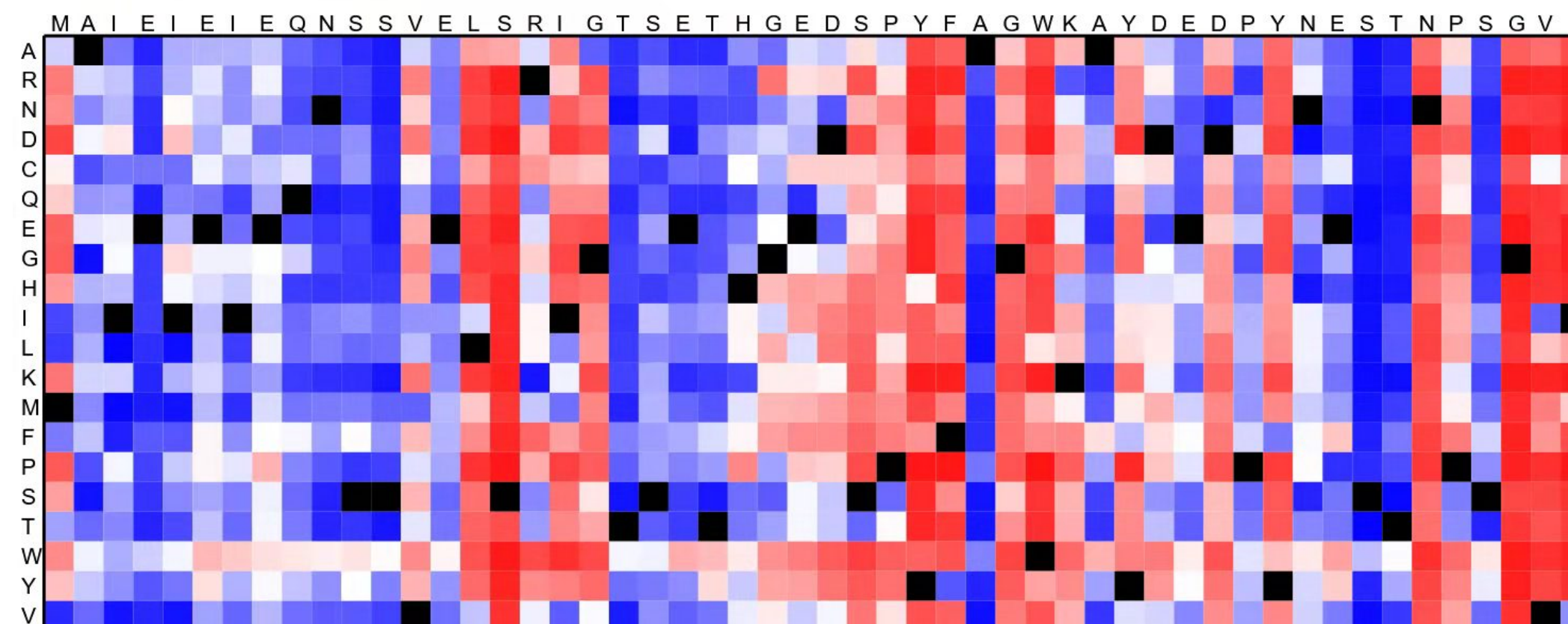
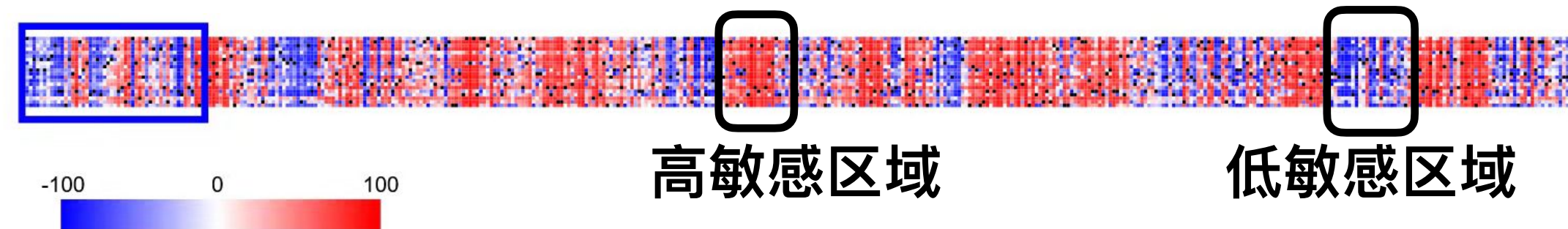
保守残基的突变影响催化活性


Uniprot近缘物种基因的突变敏感性信息

Mutagenesis

Feature key	Position(s)	Description
Mutagenesis ⁱ	46	A → V: Reduced activity. 1 Publication
Mutagenesis ⁱ	47	E → D or Q: Decreased catalytic activity and reaction specificity. 1 Publication
Mutagenesis ⁱ	85	Y → A: Strongly reduced catalytic activity. 1 Publication
Mutagenesis ⁱ	230	D → N: Loss of catalytic activity. 1 Publication
Mutagenesis ⁱ	233	Y → A: Decreased affinity for the substrate. 1 Publication
Mutagenesis ⁱ	273	K → A: Loss of catalytic activity. 2 Publications
Mutagenesis ⁱ	407	R → K: Strongly decreased catalytic activity. 1 Publication

PredictProtein





敬请老师和各位同学批评指正！