

Bioinformatic Research on OsSPL9 in Rice

水稻OsSPL9 的生物信息学探究



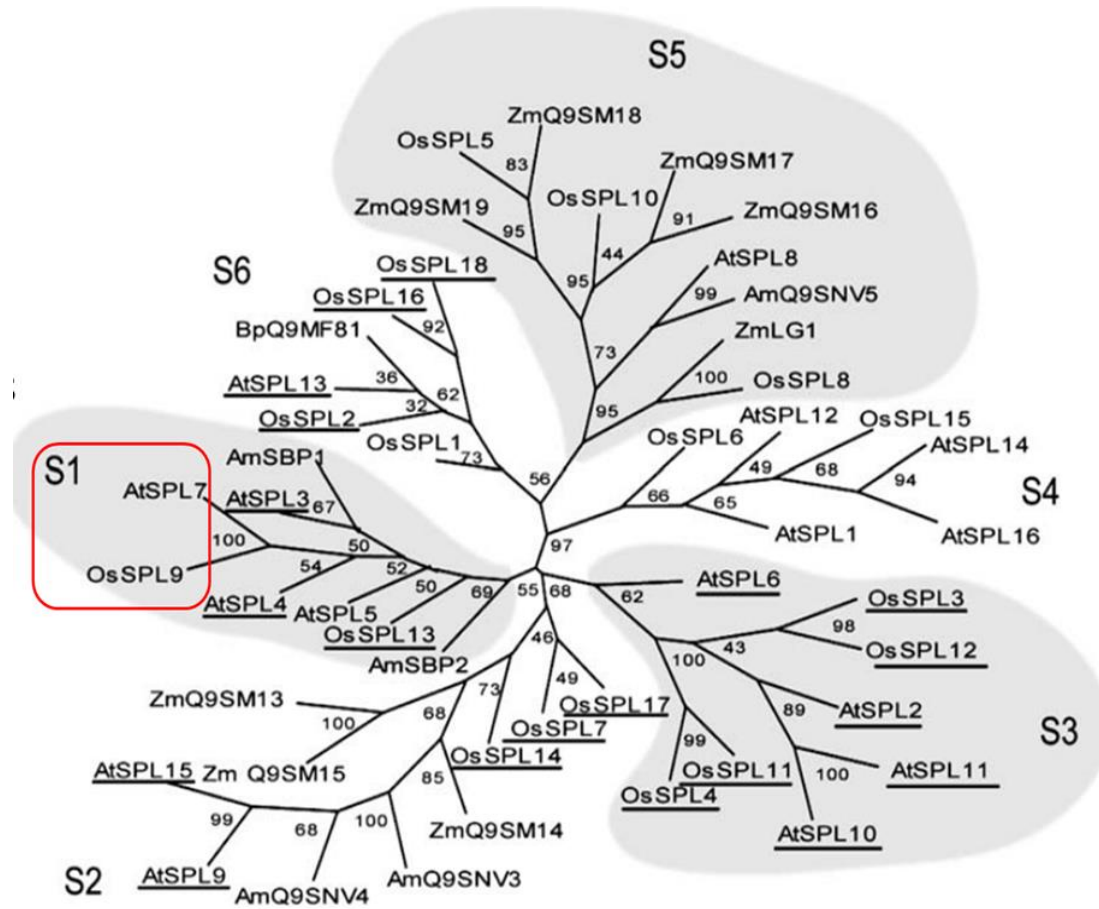
G01
姚升泽
王迪
石源
刘丹

背景介绍

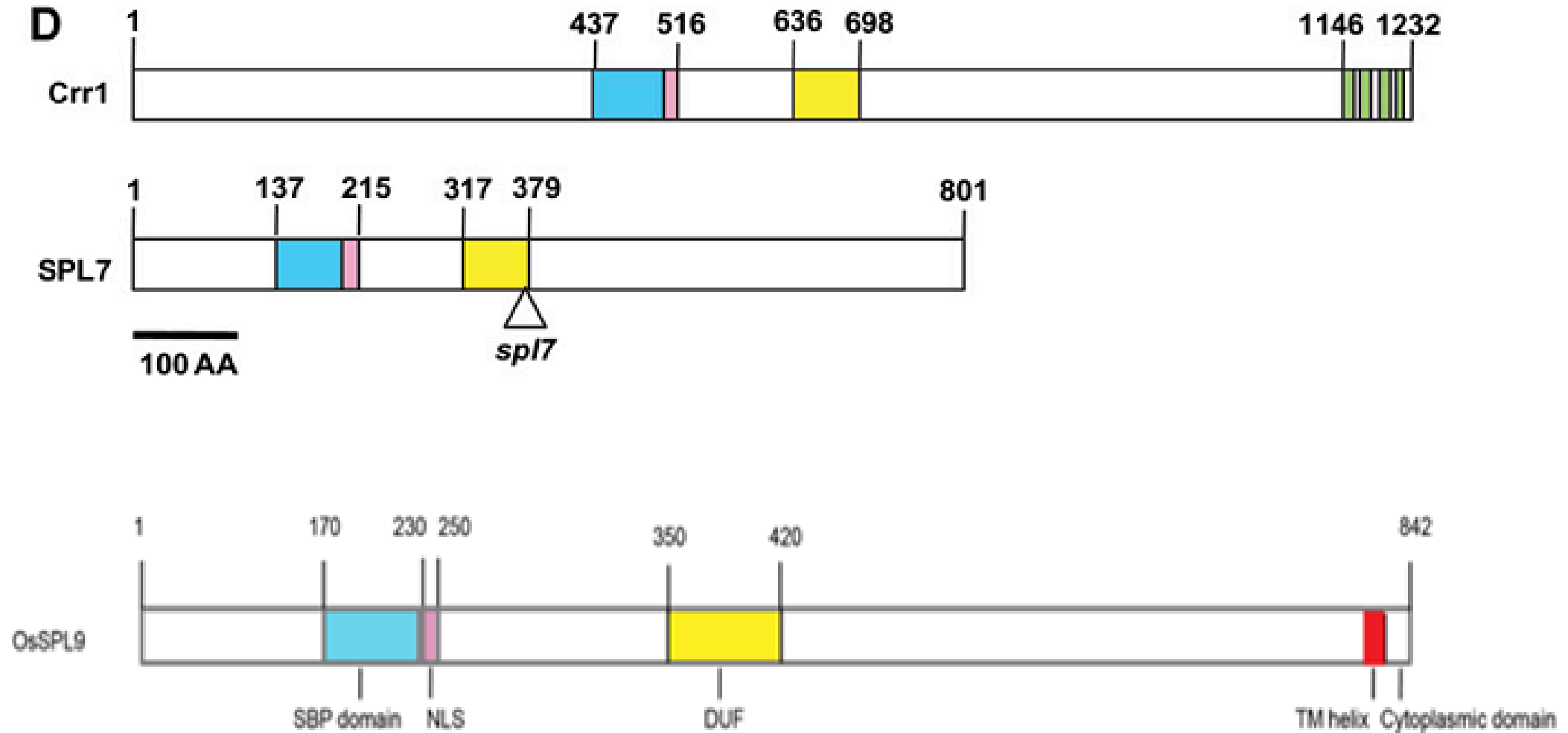
- **SPL9**过表达水稻对**RSV**抗性减弱
SPL9属于植物特有的转录因子**SBP**家族
- **SBP**家族专一性结合**DNA promoter**区域的**GTAC**

CRR1 含有植物特有的 DNA binding domain叫做**SBP domain**, 最早在 *Antirrhinum majus* 发现, 因为结合 the SQUAMOSA promoter, 称作 **Squamosa promoter binding protein**)

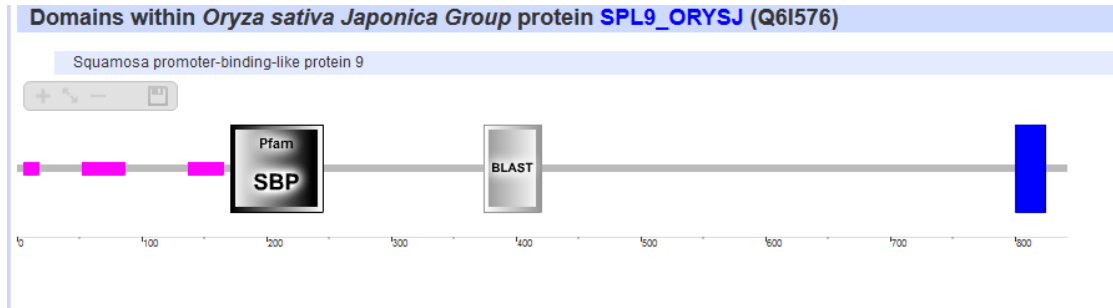
Background



蛋白序列分析



结构域寻找



DISCOVERED MOTIFS

Logo	E-value	Sites	Width	More	Submit/Download
1.	1.4e+000	2	7	I	=>
2.	1.3e+001	3	8	I	=>

Stopped because requested number of motifs (2) found.

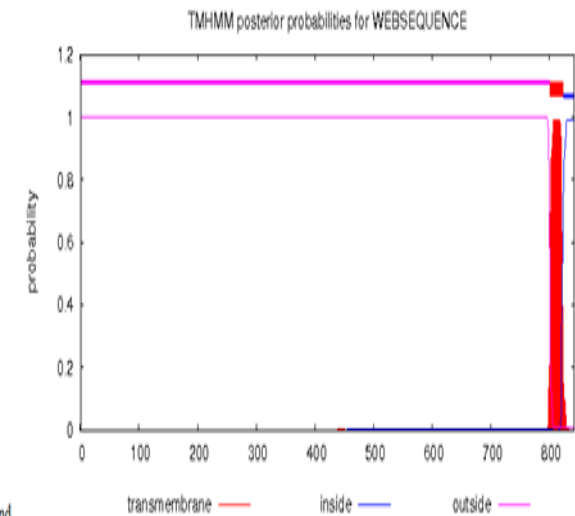
MOTIF LOCATIONS

Only Motif Sites Motif Sites+Scanned Sites All Sequences

Name p-value Motif Location

1. spl9	2.89e-13	
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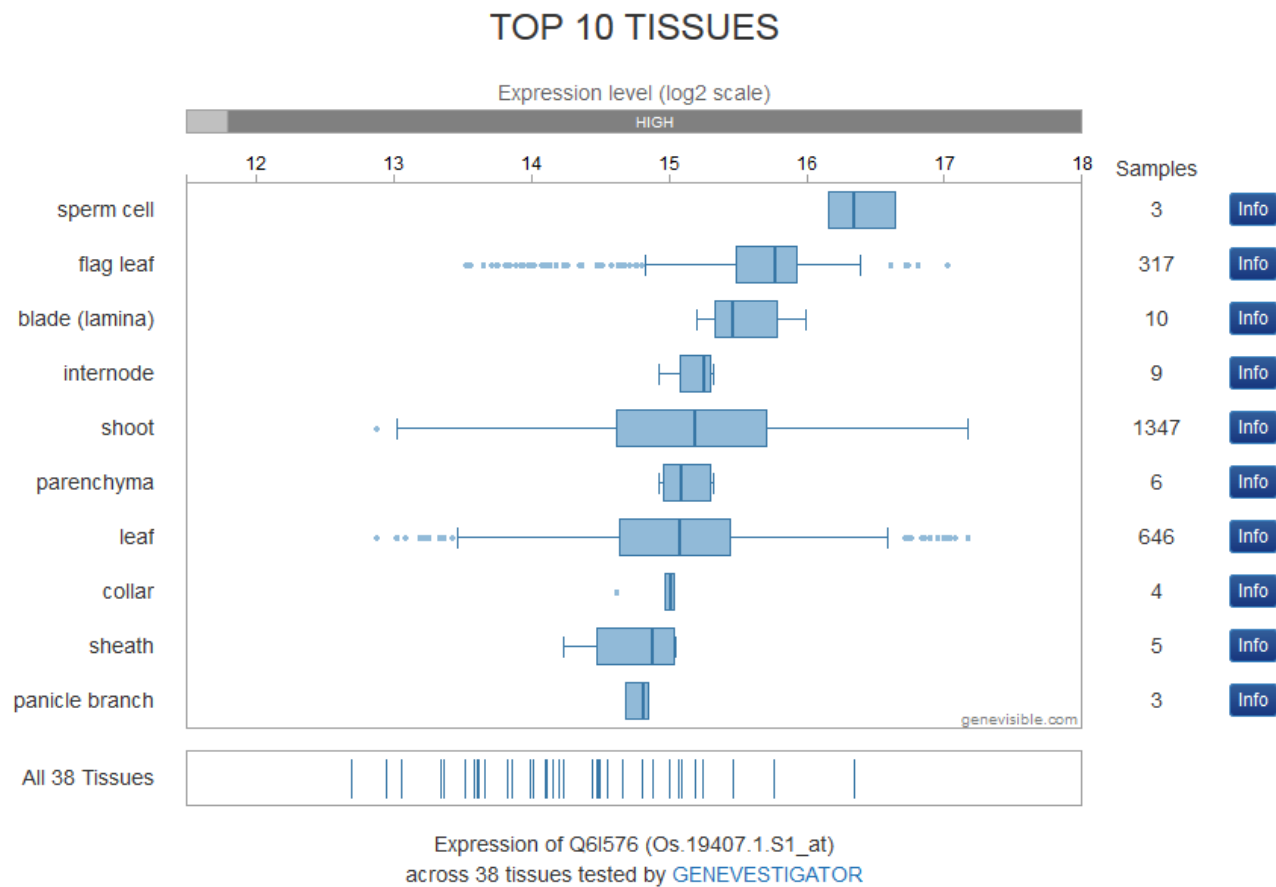
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# WEBSEQUENCE Number of predicted TMs: 1
# WEBSEQUENCE Exp number of AAs in TMs: 21.49698
# WEBSEQUENCE Exp number, first 60 AAs: 0.0004
# WEBSEQUENCE Total prob of N-in: 0.00006
WEBSEQUENCE TM00M2.0 outside 1 800
WEBSEQUENCE TM00M2.0 TMhelix 801 823
WEBSEQUENCE TM00M2.0 inside 824 842
```



ppmotif: computing colormap... ppmotif: 5 colors found




plot in postscript, script for making the plot in gnuplot, data for plot

表达分析



Display log₂-fold change



Log ₂ -fold change	Species	Gene name	Comparison	Experimental variables	Experiment name
		<u>SPL9</u>	<u>'IR24; Xanthomonas oryzae PXO99A-2' vs 'IR24; mock'</u>	ecotype, infect	<u>Transcription profiling by array of rice infected with different strains of Xanthomonas oryzae</u>
		<u>SPL9</u>	<u>'IR24; Xanthomonas oryzae PXO99A' vs 'IR24; mock'</u>	ecotype, infect	<u>Transcription profiling by array of rice infected with different strains of Xanthomonas oryzae</u>
		<u>SPL9</u>	<u>'IR24; Xanthomonas oryzae PXO99AME1' vs 'IR24; mock'</u>	ecotype, infect	<u>Transcription profiling by array of rice infected with different strains of Xanthomonas oryzae</u>

PSI-BLAST

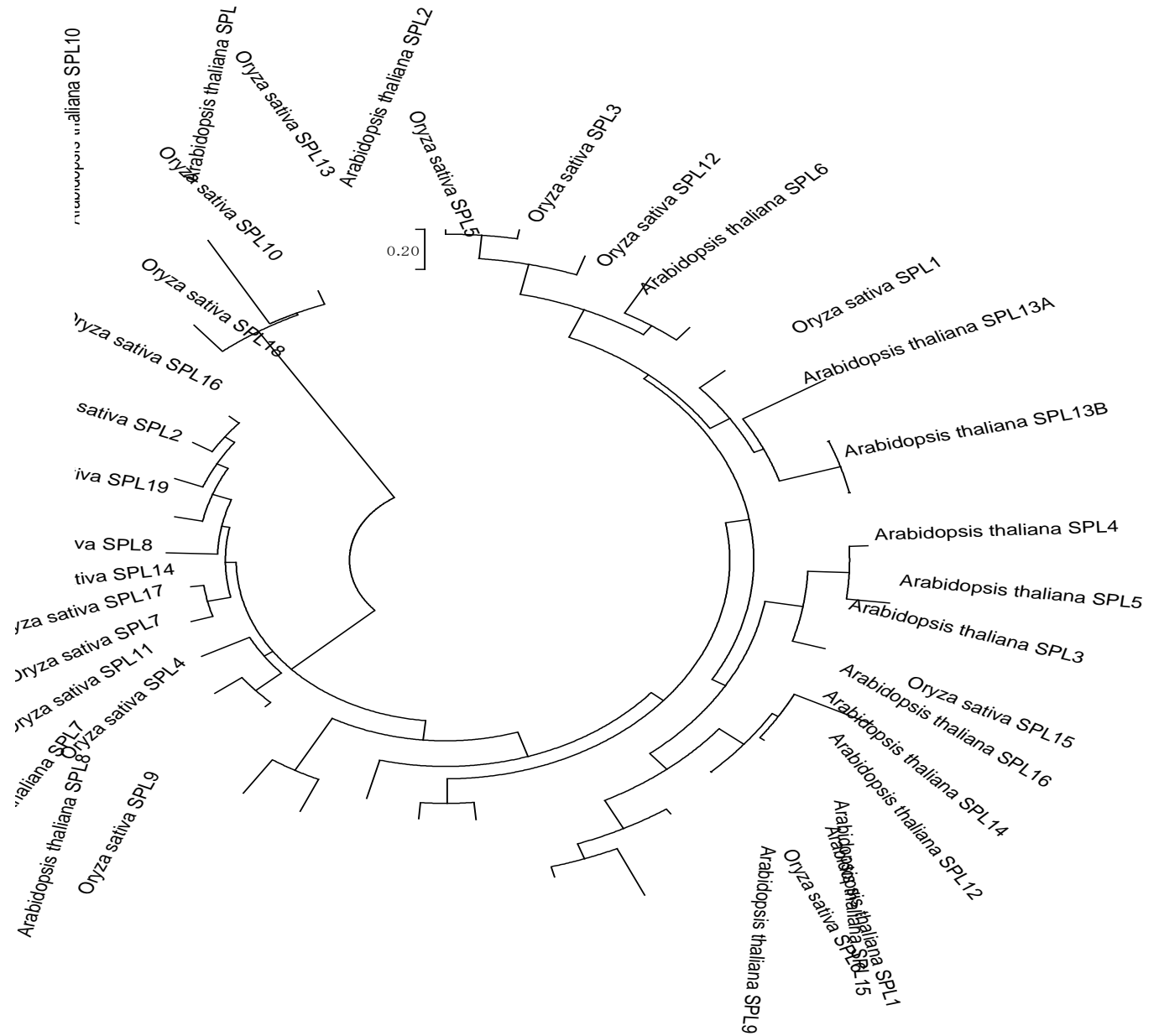
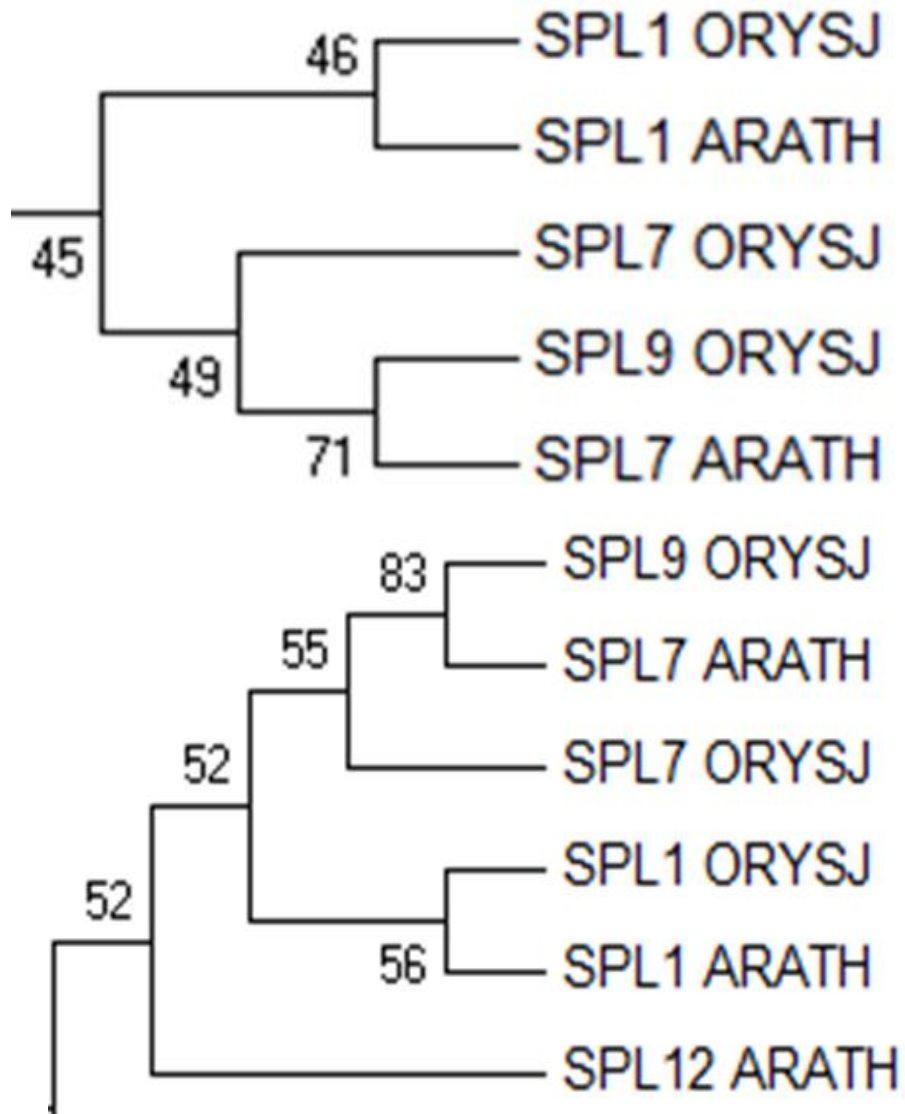
Japanese rice

Description	Max score	Total score	Query cover	E value	Ident	Accession	Select for PSI blast	Used to build PSSM
RecName: Full=Squamosa promoter-binding-like protein 9	1404	1404	99%	0.0	100%	Q8I576.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 1	663	663	64%	0.0	23%	Q9L GU7.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 6	549	549	63%	0.0	25%	Q75LH6.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 15	376	538	60%	1e-115	28%	Q6Z8M8.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 11	212	212	18%	9e-63	34%	Q653Z5.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 12	183	183	12%	9e-51	38%	Q5Z818.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 2	171	171	15%	3e-47	37%	Q0JG1.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 7	168	168	11%	1e-46	43%	Q7XT42.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 16	170	170	11%	2e-46	45%	Q8YZE8.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 4	162	162	20%	5e-46	29%	Q8H509.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 3	168	168	23%	9e-46	27%	A3A228.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Putative squamosa promoter-binding-like protein 19	161	161	11%	2e-44	41%	Q2R3Y1.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 18	162	162	10%	1e-43	47%	Q0J0K1.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 8; AltName: Full=OsLG1; AltName: Full=Protein LIGULELESS 1	159	159	9%	6e-43	47%	Q7XPY1.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 14	158	158	9%	1e-42	49%	Q7EXZ2.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 17	152	152	8%	5e-41	48%	A3C057.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 13	146	146	10%	8e-41	42%	Q8Z461.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 10	147	147	8%	5e-39	52%	Q0DAE8.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 5	147	147	10%	1e-38	53%	Q0E3F8.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

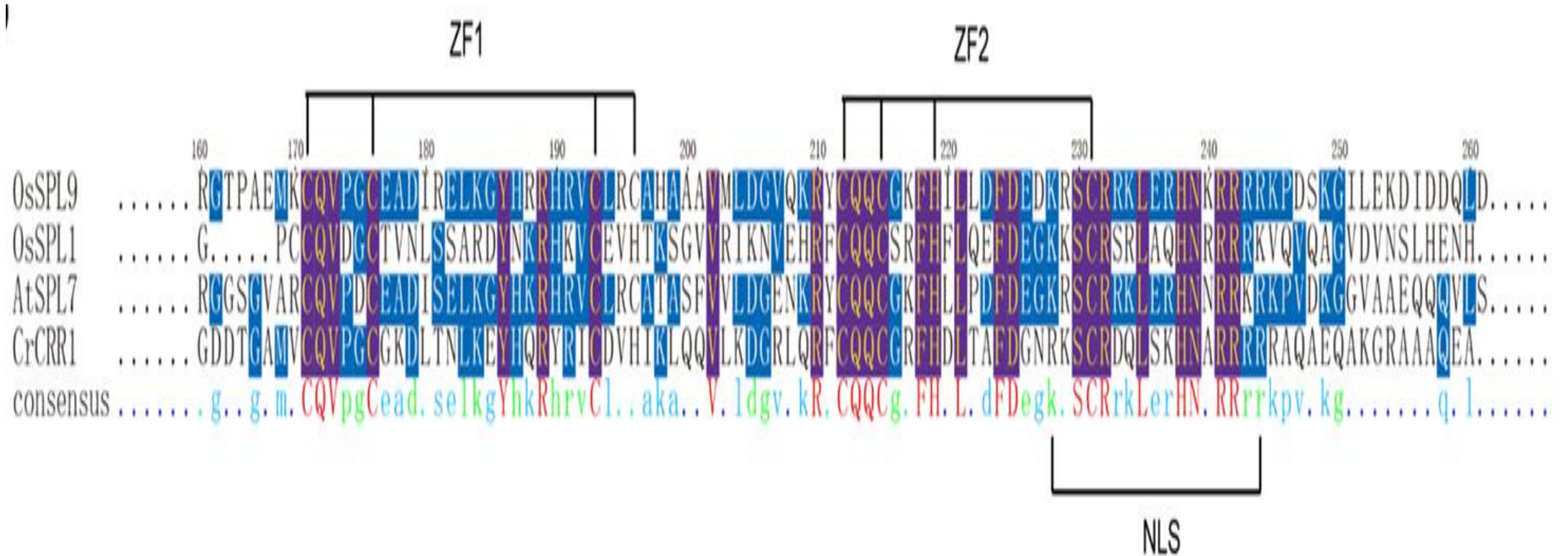
Arabidopsis thaliana

Description	Max score	Total score	Query cover	E value	Ident	Accession	Select for PSI blast	Used to build PSSM
RecName: Full=Squamosa promoter-binding-like protein 7	1015	1015	96%	0.0	37%	Q8S9G8.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 1	513	513	70%	9e-170	24%	Q8SMX9.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 14; AltName: Full=Protein FUMONISIN B1-RESISTANT 6; AltName: Full=SPL1-related prot	367	532	62%	2e-112	24%	Q8RY95.3	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 12	361	540	59%	2e-111	23%	Q9S7P5.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 16; AltName: Full=SPL1-related protein 3	351	507	59%	4e-107	23%	Q700C2.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 9	238	238	22%	2e-71	34%	Q700W2.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 15	170	170	16%	4e-47	31%	Q9M2Q6.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 6	166	166	11%	4e-45	43%	Q94JW8.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 4	157	157	10%	1e-44	53%	Q8S7A9.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 13A	163	163	15%	3e-44	37%	B9DI20.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 2	164	164	23%	4e-44	30%	Q8S840.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 3	150	150	9%	1e-42	50%	P93015.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 8	155	155	10%	5e-42	48%	Q8GXL3.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 10	156	156	22%	9e-42	27%	Q8S9L0.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 5	149	149	10%	1e-41	49%	Q8S758.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
RecName: Full=Squamosa promoter-binding-like protein 11	153	153	11%	1e-40	36%	Q9FZK0.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

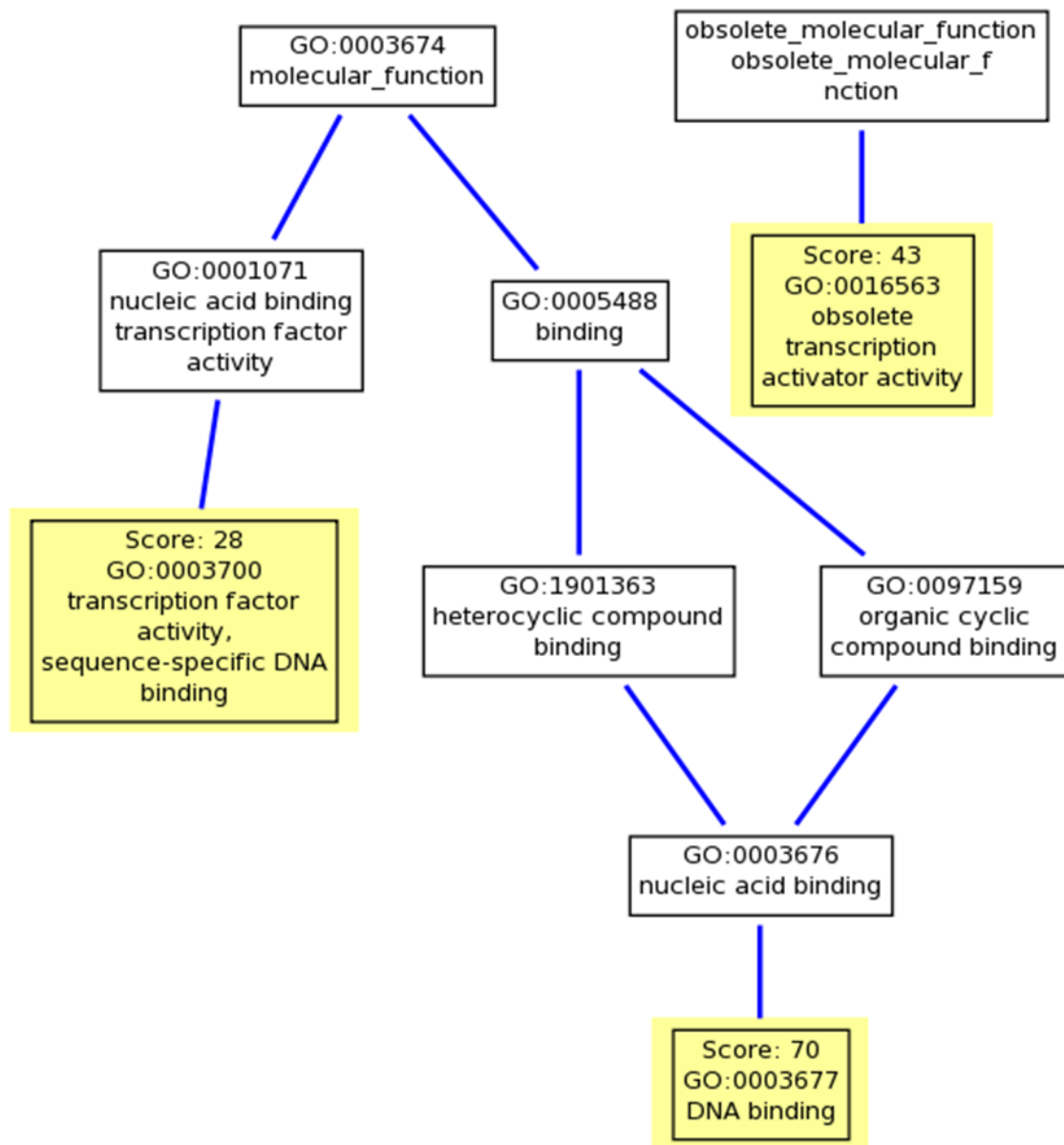
进化树构建与分析



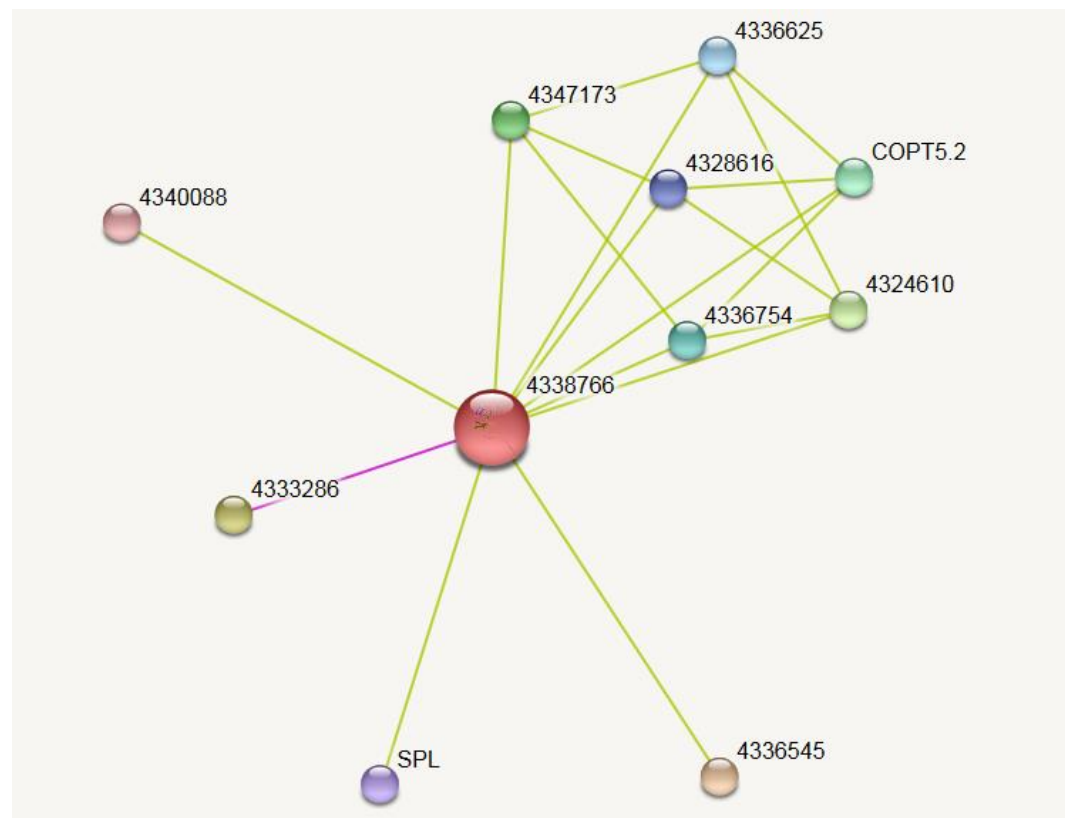
保守结构域分析



GO分析

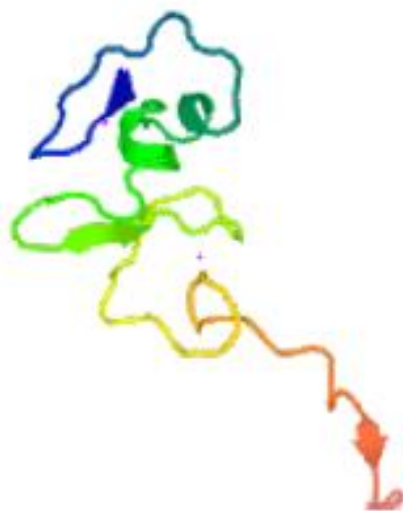
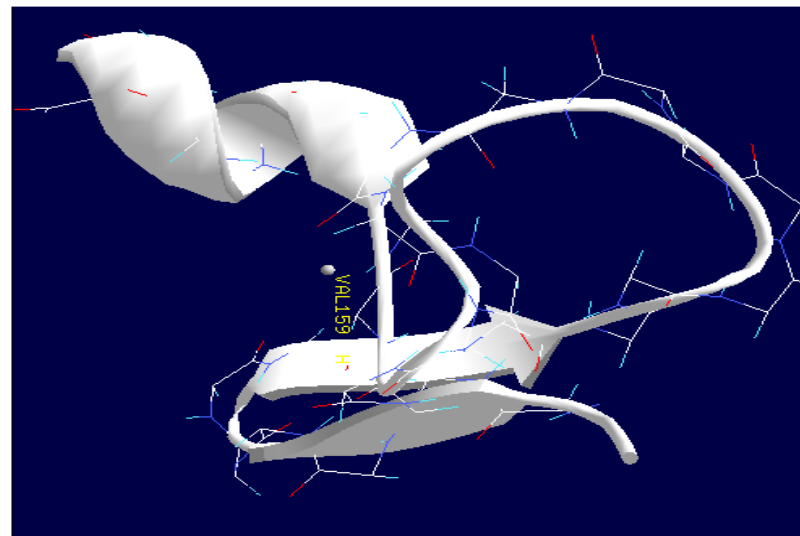


互作蛋白预测

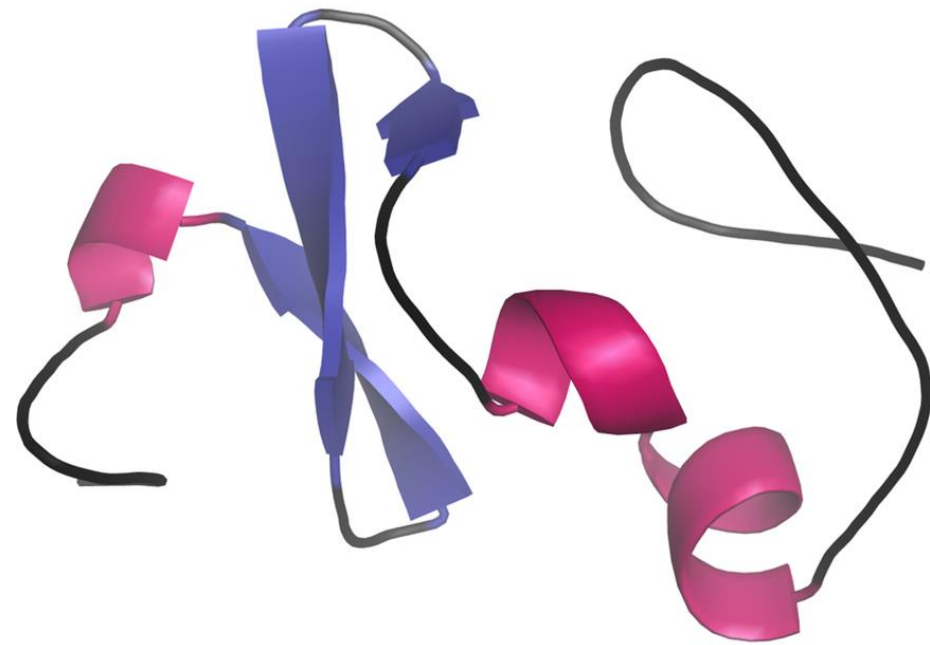


●	4336545	<i>transposon protein, putative, unclassified, expressed; May be involved in the transport of nicotianamine- chelated metals (By s...</i>	●	0.824
●	4333286	<i>KIN, antigenic determinant of recA protein, putative, expressed (430 aa)</i>	●	0.775
●	4324610	<i>ctr copper transporter family protein, putative, expressed; Involved in the transport of copper, in cooperation with SWEET11 an...</i>	●	0.620
●	4347173	<i>ctr copper transporter family protein, putative, expressed; Involved in the transport of copper (By similarity) (149 aa)</i>	●	0.563
●	COPT5.2	<i>ctr copper transporter family protein, putative; Involved in the transport of copper (By similarity) (176 aa)</i>	●	0.563
●	4336754	<i>ferric-chelate reductase, putative, expressed (574 aa)</i>	●	0.563
●	4336625	<i>copper-transporting ATPase 3, putative, expressed (849 aa)</i>	●	0.547
●	4328616	<i>copper-transporting ATPase, putative, expressed (978 aa)</i>	●	0.547
●	SPL	<i>decarboxylase, putative, expressed; Cleaves phosphorylated sphingoid bases (PSBs), such as sphingosine-1-phosphate, into f...</i>	●	0.547
●	4340088	<i>cytochrome c oxidase subunit 5B, mitochondrial precursor, putative, expressed (154 aa)</i>	●	0.534

结构预测



<input type="checkbox"/>	Metal binding	231	Zinc 2. {ECO:0000250}.
<input type="checkbox"/>	Metal binding	219	Zinc 2. {ECO:0000250}.
<input type="checkbox"/>	Metal binding	215	Zinc 2. {ECO:0000250}.
<input type="checkbox"/>	Metal binding	212	Zinc 2. {ECO:0000250}.
<input type="checkbox"/>	Metal binding	196	Zinc 1. {ECO:0000250}.
<input type="checkbox"/>	Metal binding	193	Zinc 1. {ECO:0000250}.
<input type="checkbox"/>	Metal binding	176	Zinc 1. {ECO:0000250}.
<input type="checkbox"/>	Metal binding	171	Zinc 1. {ECO:0000250}.
<input type="checkbox"/>	Motif	228 - 244	Bipartite nuclear localization signal.
<input type="checkbox"/>	Zinc finger	168 - 245	SBP-type. {ECO:0000255 PROSITE-



- The solution structure of the SBP zinc finger has been solved [[PMID: 15001351](#)]. The first four Cys or His coordinate one zinc ion and the last four coordinate the other. It can be viewed as two structural subdomains, each subdomain containing a single zinc-binding pocket. The N-terminal subdomain consists of two short alpha helices whereas the C-terminal one contains a three-stranded antiparallel beta-sheet.

OsSPL9的启动子分析

+ ABRE

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
ABRE	Hordeum vulgare	201	+	9	CCTACGTGGC	cis-acting element involved in the abscisic acid responsiveness
ABRE	Oryza sativa	944	-	9	GCCGCGTGGC	cis-acting element involved in the abscisic acid responsiveness
ABRE	Arabidopsis thaliana	554	-	6	TACGTG	cis-acting element involved in the abscisic acid responsiveness

+ CGTCA-motif

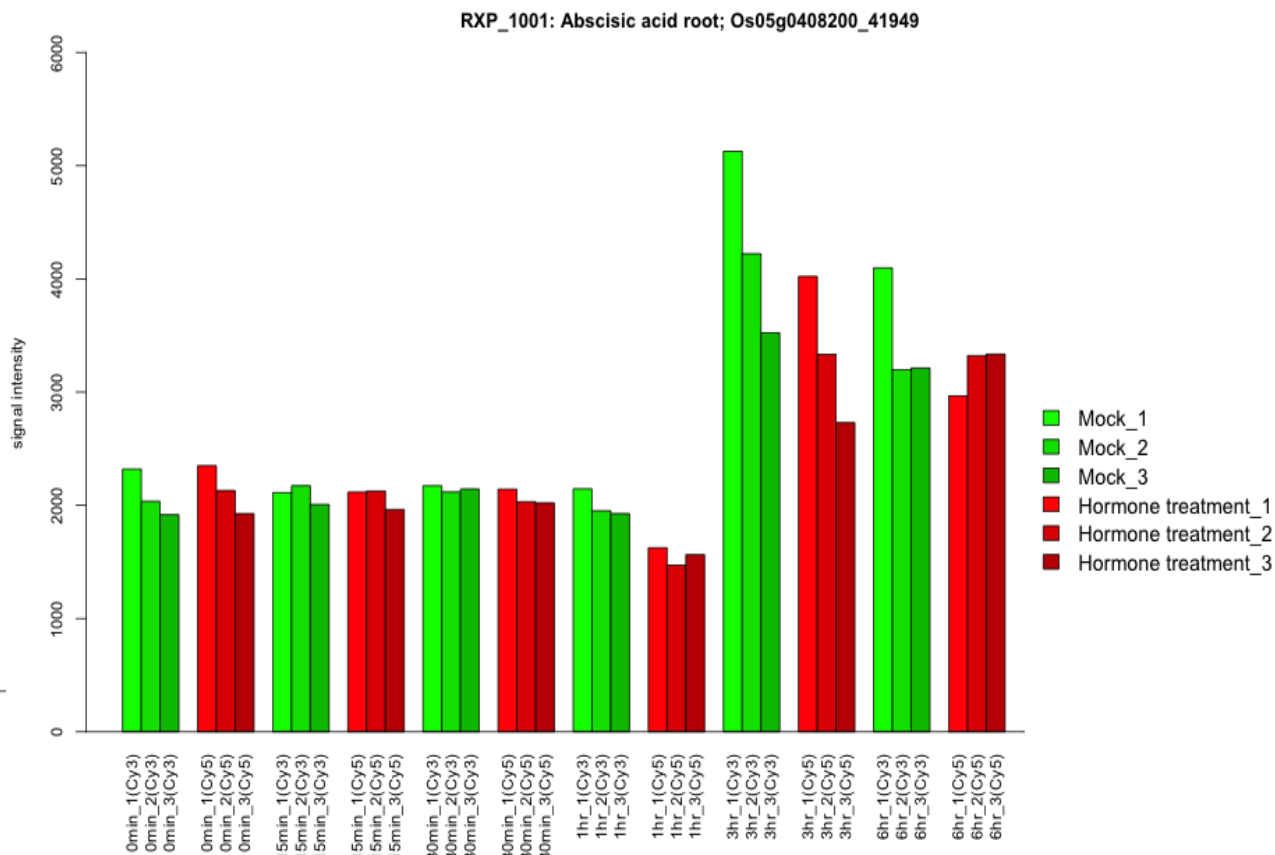
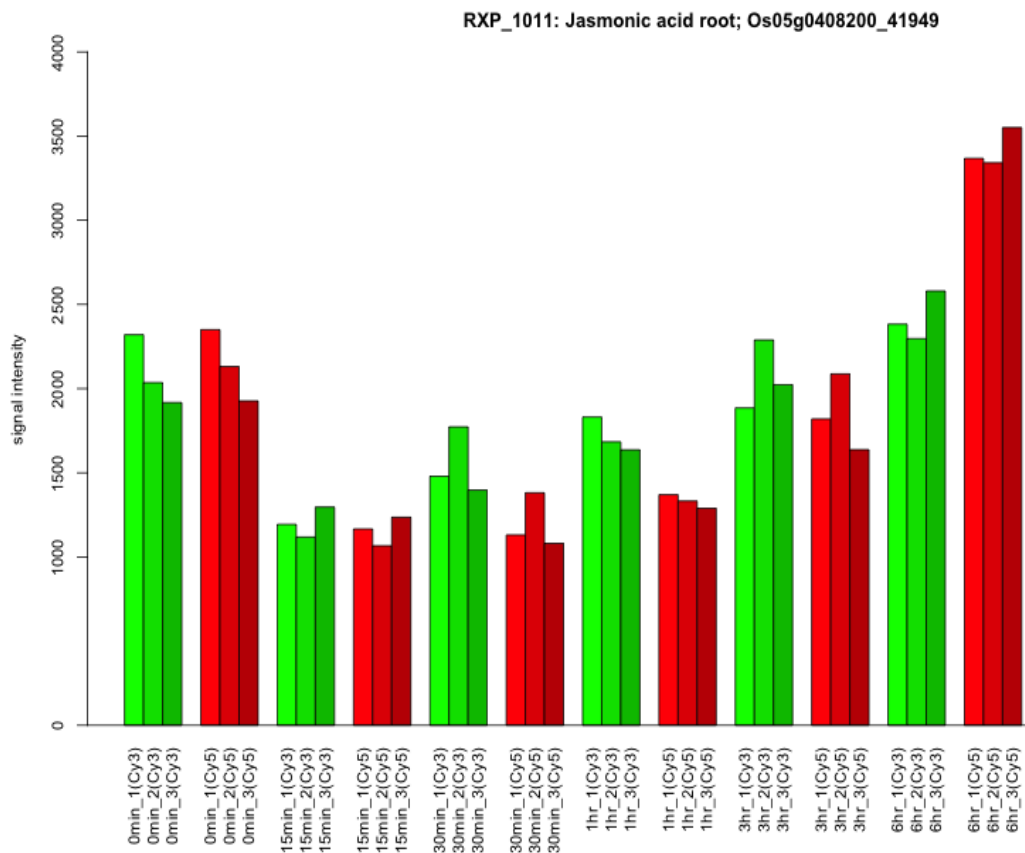
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CGTCA-motif	Hordeum vulgare	739	+	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
CGTCA-motif	Hordeum vulgare	1213	-	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
CGTCA-motif	Hordeum vulgare	851	-	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
CGTCA-motif	Hordeum vulgare	790	-	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
CGTCA-motif	Hordeum vulgare	1207	+	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness



Sp1

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Sp1	Oryza sativa	822	-	6	GGGCGG	light responsive element
Sp1	Zea mays	881	+	5.5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	977	+	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	984	+	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1060	+	5.5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1132	+	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1133	+	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1202	+	5.5	CC(G/A)CCC	light responsive element
Sp1	Oryza sativa	1284	-	6	GGGCGG	light responsive element
Sp1	Zea mays	1322	+	5	CC(G/A)CCC	light responsive element
Sp1	Oryza sativa	1447	+	6	GGGCGG	light responsive element
Sp1	Zea mays	1451	-	5.5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1455	-	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1456	-	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1457	-	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1458	-	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1459	-	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1460	-	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1461	-	5	CC(G/A)CCC	light responsive element
Sp1	Zea mays	1485	-	5.5	CC(G/A)CCC	light responsive element

不同激素处理的表达量

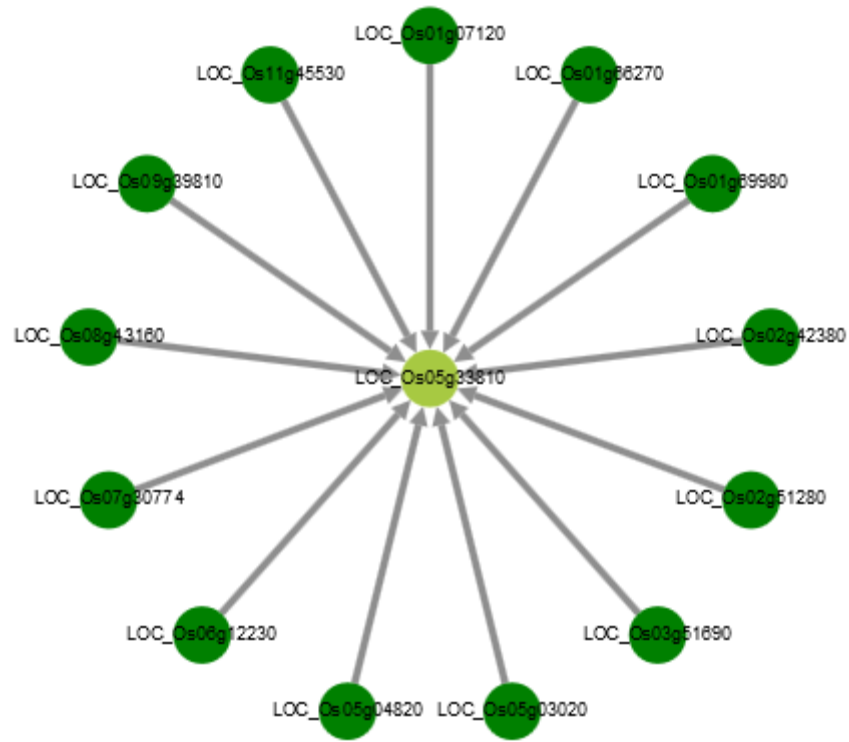


- Mock_1
- Mock_2
- Mock_3
- Hormone treatment_1
- Hormone treatment_2
- Hormone treatment_3

调控网络

Plant Transcriptional Regulatory Map

346 regulations(346 unique regulations) are found.



Upstream Regulator

TF	Target
LOC_Os05g33810	ChrUn.fgenes.h.gene.81
LOC_Os05g33810	LOC_Os01g02120
LOC_Os05g33810	LOC_Os01g03144
LOC_Os05g33810	LOC_Os01g03640
LOC_Os05g33810	LOC_Os01g04910
LOC_Os05g33810	LOC_Os01g07070
LOC_Os05g33810	LOC_Os01g07810
LOC_Os05g33810	LOC_Os01g08860
LOC_Os05g33810	LOC_Os01g10440
LOC_Os05g33810	LOC_Os01g11054

Target Gene

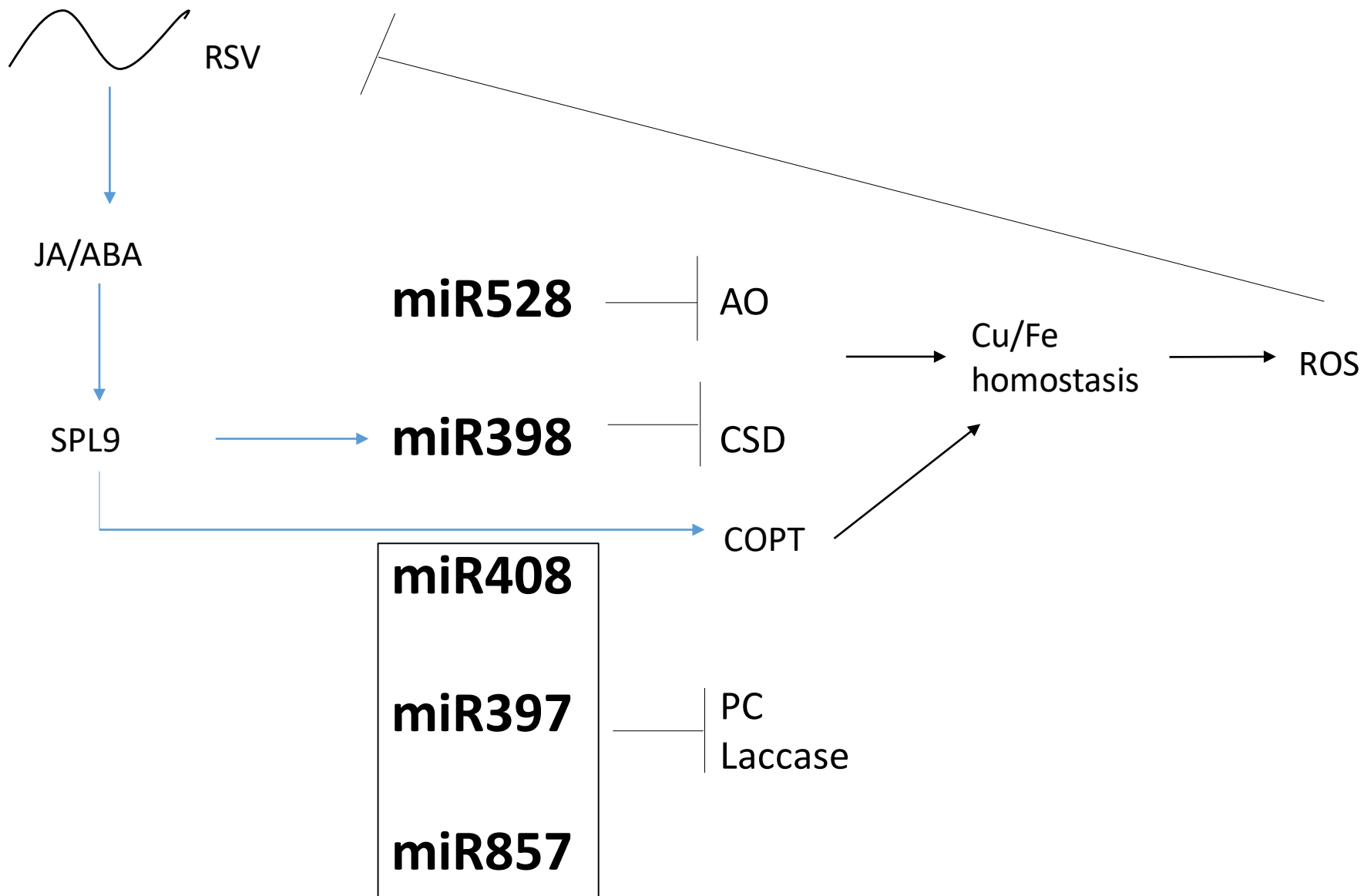
SPL9可能的调控基因

tgctcacatttattgtatcttactaaaccacttttataaatacatgacagcattgacttttgaacatatattatctta
atTTTTAAAAATAAATAATTATTATTTATTTTGTGTGAGTTTTTTTATTGAAA GTAC TTTAAACATGATTATAT
TTTATGCATTTCTGTA AAAATATTCTAATAAGACGAACAATGGTATGTATTA AAAACGAGAGTATTTAACATTTAATC
T GTAC TATCATTCTCGACAATTTTTTTTCAA AATTGCGGAGTA GTAC TTCACATATTGGCATGGA GTAC ATCAGACGA
TACTA GTAC AGCATA CATGTCGTGGCGTTCAACTTGTGGAGATCTGATGCGATATAAATCGATCCTACGTCACATGAC
AGACTGGACCCCTGTCAA AATTATGGATTGGATGATTAATCACTGATAGGTA GTAC TAGTAGCAACTCAATCACACAAG
CGAAGTGAGAAGAAAAGGAACCTCTCCTGCATTAAGACAACGGCGACGGGTCACTGAAAGTGAAGCCTGTGGCGCAC
ACGACACGACCTCCTCAACGGATCTGTGGCTTACCCGTCGCCGTTAGAGCGTTTGTCCAACGCTTCTGCA GTAC AAGA
GTAC AGCTGAAAGCCATA GTAC ACTGATGATATTTGCAAGCCTGAA GTAC AAGCCGCCCTAACGATCTCCCCCATA
T GTAC TGCAGCTAACTT GTAC TACTACCAGTGCACCATGGCCGGG GTAC AAATATGCCACCCTCACCAATGGATGAT
CAGCAGCAGCCACAGCAA AATTGGTTGGGATAGGTAGGTGTTATGTTAGGTCGGTTTTTGGCTGTAGCAGCAGCA
GTGGAAGGGGCATGCAGAGGAGCAGGAGATTCAGTTTGAAGCTGGACTTCACTTTTGCCTCTCTCTCTGTGCTTGC
CTCTCCATT CCTGCTGCTAGGCTGTTCTGTGGAAGTTTGCAGAGTTTATATTATGGGTTTAAATCGTCCATGGCATCAGC
TTCTCAA AAGTCACCTTCTGTGCGGTGTCTACAGATATAACCACGATGTCGTGATGTCCTTATAGCAA AATTTGCCATTT
TTCTGTGGAAGGGAGGGAGGATATATATGGAATTTATGTTGCTTATATGGTC GTAC TT GTAC TAACATGGGATGATGCG
TT GTAC TCGACGTGCCTTGCAATGTGGAGTTAATCATGTCATGTCATCAA AAGAATTCACA GTAC TACTCTCTCCGTTA
TACATTTACGTTAACTTTTTCA GTGTCAA AATCTTTTAACCAAGTTTATAAAAAGTATAACAAGTTTATAAAAAGTAT
AGTAACAATTTTAAACAAAAATAATATATTATCATTATATTTAATGAAACTAATTTGTTGTCGTAGATGTTGTTATT
TTTTAAATTTAGTTAAACCTAAAAAATTGAATAGAAAAAATAAAAAC TACTTATAATATAAAAACGAAGAAAGTAGTTA
TTATTAATCACAGTTCTACATTTTTATTGTA AAGTTAAAGGCACC GTAC AAAAAATCATGCTAACTAGCCCATCATCC
TCGT GTAC AACCATTTTGCACACTTATCTTGTAACTCTGCAA AATTAACCAAGTCCCAAGATGCAGTTTGACTGGCATGT
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GGAAGGCAC TGTAC TCGGGGAGCCGGGGCAGTA GTAC AAGCT GTAC TCTTGGCTTCGGGCAAAGCCAGTGTA GTACGT
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CCCGTGGAAAAGAGTCTATAACGTGAGCGCTTTGCCTGCGTTTTGGCCAGGCAAACGCAGCCTCATCATTAAATCCG
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TTATTTCTCTTGCCAAAAGTCTCCTAAATGGCGCGGTGTAGGTATGTTCTCTCTCTCGATTACACAATTCGGTTGAT

miR528 promoter

miR398 promoter

调控模型假设



致谢

罗静初教授

李毅教授

吴建国、杨志蕊

我的组员

所有同学