

**Table S1.** NCBI login numbers for transcription factors in *Santalum album*

Genes	NCBI login numbers
SaMYC1	MZ297933
SaMYC3	MZ297935
SaMYC4	MZ297937
SaMYC5	MZ297938
SabHLH1	MZ297934
SabHLH2	MZ297936
SabHLH3	MZ297939
SabHLH4	MZ297940

**Table S2.** Premier information in *Santalum album*

Premier names	Premier lists (5'→3')	Usages
SaMYC1-ORF-F	ATGGCTACTTCACTCCGACATCA	ORF
SaMYC1-ORF-R	TCAGAACTTGTGGACAACACCAT	ORF
SaMYC3-ORF-F	ATGAACCTGTGGAGTGACGACAA	ORF
SaMYC3-ORF-R	CTACCGGGTTTCCGATAATTTGGAA	ORF
SaMYC4-ORF-F	ATGGCTTCGCTGCCGCCACCGCC	ORF
SaMYC4-ORF-R	TCATTCATGCGGAATTATTTGGTTT	ORF
SaMYC5-ORF-F	ATGGAAGATGTGCTTGCTCTCCTCT	ORF
SaMYC5-ORF-R	TTACTCTTCAAATCGTTTAATAAGA	ORF
SabHLH1-ORF-F	ATGGAGTTCAACAATGAGCATGGCT	ORF
SabHLH1-ORF-R	CTACAGGCACCTCCCGCCATACCT	ORF
SabHLH2-ORF-F	ATGGGAGAGTTAAGCACCGAGAGCA	ORF
SabHLH2-ORF-R	TCATCTATACAAGCATCCTCTGTAA	ORF
SabHLH3-ORF-F	ATGGCGAATAACCCCTTCTGAAGGT	ORF
SabHLH3-ORF-R	CTACGGAGGAGGATTAGTTTCGGGCT	ORF
SabHLH4-ORF-F	ATGCTGTCCCAGGATAACACCAATT	ORF
SabHLH4-ORF-R	TTAGGCAACGGGGGACGGAGTACA	ORF
YFP-SaMYC1-F	CTCAAGCTTCGAATTCATGGCTACTTCACTCCGACATCAG	SaMYC1-YFP vector
YFP-SaMYC1-R	CTCACCATCAGGATCCTGAACCTTGTGGACAACACCATGA	SaMYC1-YFP vector
YFP-SaMYC3-F	CTCAAGCTTCGAATTCATGAACCTGTGGAGTGACGACA	SaMYC3-YFP vector
YFP-SaMYC3-R	CTCACCATCAGGATCCTCCGGGTTTCCGATAATTTGGA	SaMYC3-YFP vector
YFP-SaMYC4-F	CTCAAGCTTCGAATTCATGGCTTCGCTGCCGCCACCGCC	SaMYC4-YFP vector
YFP-SaMYC4-R	CTCACCATCAGGATCCTTTCATGCGGAATTATTTGGTTT	SaMYC4-YFP vector
YFP-SaMYC5-F	CTCAAGCTTCGAATTCATGGAAGATGTGCTTGCTCTCCTCT	SaMYC5-YFP vector
YFP-SaMYC5-R	CTCACCATCAGGATCCTCTCTTCAAATCGTTTAATAAGA	SaMYC5-YFP vector
YFP-SabHLH1-F	CTCAAGCTTCGAATTCATGGAGTTCAACAATGAGCATGGC	SabHLH2-YFP vector
YFP-SabHLH1-R	CTCACCATCAGGATCCTCAGGCACCTCCCGCCATAC	SabHLH2-YFP vector
YFP-SabHLH2-F	CTCAAGCTTCGAATTCATGGGAGAGTTAAGCACCGAGA	SabHLH2-YFP vector
YFP-SabHLH2-R	CTCACCATCAGGATCCTTCTATACAAGCATCCTCTGTAAG	SabHLH2-YFP vector
YFP-SabHLH3-F	CTCAAGCTTCGAATTCATGGCGAATAACCCCTTCTGAAG	SabHLH3-YFP vector
YFP-SabHLH3-R	CTCACCATCAGGATCCTCGGAGGAGGATTAGTTTCG	SabHLH3-YFP vector
YFP-SabHLH4-F	CTCAAGCTTCGAATTCATGCTGTCCCAGGATAACACCAAT	SabHLH4-YFP vector
YFP-SabHLH4-R	CTCACCATCAGGATCCTGGCAACGGGGGACG	SabHLH4-YFP vector
62S-SaMYC1-F	TCTAGAACTAGTGGATCCATGGCTACTTCACTCCGACATCA	SaMYC1-62-SK vector

62S-SaMYC1-R	GACGGTATCGATAAGCTTTCAGAACTTGTGGACAACACCAT	SaMYC1-62-SK vector
62S-SaMYC3-F	TCTAGAACTAGTGGATCCATGAACCTGTGGAGTGACGACAA	SaMYC3-62-SK vector
62S-SaMYC3-R	GACGGTATCGATAAGCTTCTACCGGGTTCCGATAATTTGGAA	SaMYC3-62-SK vector
62S-SaMYC4-F	TCTAGAACTAGTGGATCCATGGCTTCGCTGCCGCCACCGCC	SaMYC4-62-SK vector
62S-SaMYC4-R	GACGGTATCGATAAGCTTTCATTCATGCGGAATTATTTGGTTT	SaMYC4-62-SK vector
62S-SaMYC5-F	TCTAGAACTAGTGGATCCATGGAAGATGTGCTTGTCTCCTCCT	SaMYC5-62-SK vector
62S-SaMYC5-R	GACGGTATCGATAAGCTTTTACTCTTCAAATCGTTTAATAAGA	SaMYC5-62-SK vector
62S-SabHLH1-F	TCTAGAACTAGTGGATCCATGGAGTTCAACAATGAGCATGGCT	SabHLH1-62-SK vector
62S-SabHLH1-R	GACGGTATCGATAAGCTTCTACAGGCACCTCCCGCCATACCCT	SabHLH1-62-SK vector
62S-SabHLH2-F	TCTAGAACTAGTGGATCCATGGGAGAGTTAAGCACCGAGAGCA	SabHLH2-62-SK vector
62S-SabHLH2-R	GACGGTATCGATAAGCTTTCATCTATAACAAGCATCCTCTGTAA	SabHLH2-62-SK vector
62S-SabHLH3-F	TCTAGAACTAGTGGATCCATGGCGAATAACCCCTTCTGAAGGT	SabHLH3-62-SK vector
62S-SabHLH3-R	GACGGTATCGATAAGCTTCTACGGAGGAGGATTAGTTTCGGGC T	SabHLH3-62-SK vector
62S-SabHLH4-F	TCTAGAACTAGTGGATCCATGCTGTCCCAGGATAACACCAATT	SabHLH4-62-SK vector
62S-SabHLH4-R	GACGGTATCGATAAGCTTTTAGGCAACGGGGGGACGGAGTACA	SabHLH4-62-SK vector
GAD-SaMYC1-F	GAGGCCAGTGAATTCATGGCTACTTCACTCCGACATCAG	SaMYC1-pGADT7 vector
GAD-SaMYC1-R	GAGCTCGATGGATCCCGAACTTGTGGACAACACCATGAAG	SaMYC1-pGADT7 vector
GAD-SaMYC3-F	GGAGGCCAGTGAATTCATGAACCTGTGGAGTGACGA	SaMYC3-pGADT7 vector
GAD-SaMYC3-R	CGAGCTCGATGGATCCCCCGGGTTTCCGATAAATTGG	SaMYC3-pGADT7 vector
GAD-SaMYC4-F	GGAGGCCAGTGAATTCATGGCTTCGCTGCCGCCACCGCC	SaMYC4-pGADT7 vector
GAD-SaMYC4-R	CGAGCTCGATGGATCCCTTCATGCGGAATTATTTGGTTT	SaMYC4-pGADT7 vector
GAD-SaMYC5-F	GGAGGCCAGTGAATTCATGGAAGATGTGCTTGTCTCCTCCT	SaMYC5-pGADT7 vector
GAD-SaMYC5-R	CGAGCTCGATGGATCCCCTCTTCAAATCGTTTAATAAGA	SaMYC5-pGADT7 vector
GAD-SabHLH1-F	GAGGCCAGTGAATTCATGGAGTTCAACAATGAGCATGG	SabHLH1-pGADT7 vector
GAD-SabHLH1-R	GAGCTCGATGGATCCCCAGGCACCTCCCGCCATACCCTG	SabHLH1-pGADT7 vector
GAD-SabHLH2-F	GGAGGCCAGTGAATTCATGGGAGAGTTAAGCACCGAGA	SabHLH2-pGADT7 vector
GAD-SabHLH2-R	CGAGCTCGATGTTCTATAACAAGCATCCTCTGTAAAG	SabHLH2-pGADT7 vector
GAD-SabHLH3-F	GGAGGCCAGTGAATTCATGGCGAATAACCCCTTCTGAA	SabHLH3-pGADT7 vector
GAD-SabHLH3-R	CGAGCTCGATGGATCCCCGGAGGAGGATTAGTTTCGG	SabHLH3-pGADT7 vector
GAD-SabHLH4-F	GGAGGCCAGTGAATTCATGCTGTCCCAGGATAACACCAA	SabHLH4-pGADT7 vector
GAD-SabHLH4-R	CGAGCTCGATGGATCCCCGCAACGGGGGGACG	SabHLH4-pGADT7 vector

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**Table S3.** The cluster multiple sequence alignment of SabHLHs in *Santalum album*

1.	SaMYC1	1800kb	g11854.t1
<p>ATGGCTACTTCACTCCGACATCAGGAGGAAGTGCCACAAAACCTAAAAAATCAGCTTGCTGTTGTAGTTAGAAGCATTCAATGGAGCT  ATGCAGTCTTCTGGTCCACTTCAAGTAGACAACCAGGGGTGTGGAATGGGGAGATGGGTACTACAATGGGGATATTAAGACGAGGAA  AACAGTTCAGGCTGTGGAGCTTAACGCGGTCCAAATGAATTCGCAGCGAAGCGAGCAGTTGAGAGAACTCTACGAGTCCCTTGTGTG  GGTGAAACCAGCCCACAAGCTCGGAGGCCAACGGCTGCATTGTCCCCTGAAGACCTAACCGATACTGAATGGTTTTACTTGGTTTGCAT  GTCCTTTGTATTTAACATTGGCCAAGGTTTGCCGGGAAGAGCATTGGCCAATGGTCAACCCATCTGGGTCTGTAACGCTCCCTTTCGAGA  TAGTAAAGTATTACGCCGTTCTCTGCTAGCTAAGAGTGCCGCTATTAGACTGTTGTATGCTTTCCATTTTTAAAGGAGTGCTGGAGCT  GGGTGTGACTGAGCAAGTCGCGGAGGATCCTGGTCTCATTAGGGCATAAAAACTACTTTGTTGGAGAATCCATACCTCTCAAGTACTG  ATGACAATCCAGCTTTCATTGACCTGGATTATAAGATTTGAACAGCATTCTTAGCCCAGTTTCTGAATGCGAGGAAGTCAAAACTGATT  CTCCTAATCAGACCACAGATTGGATTGAACCCATTCAACAAAGAGAGGAGTCTTTATGGTTGAAGGGATCAATGGGGGTGCTTCTTCT  CAAGTACAAAGTTGGCATTTTATGGACGATGATTCGCTGCTGATAACCATAATCCCTGAACCTCTGGCGATTGTGTATCTCAAACTTT  GTAAATCCTGAAAAAATTATCACTGCTACAAATCAGAAGAGACTGACCCCACTGGATCTTCGGAGCAATGACGTACATTATCAGGGAG  TTCTTGGAGCCCTTCTGAAGAGTTCTACCAATTGGTCTTAGGACCACACTTCAGAAATTGTAACAAGGAGTCTAGTTTGTAGTTGGA  GAAAAGGATTGGTAAATTTCCAGAAGCCGAGAAATGGAGCCTGCCAGAAATTACTGAAGAAGGTATTGTTTCAGGTGGCCCAAATGC  ATGGTGGCATTTCCTGAAGTCTGTGAAGATGATGGCATTAAAGGATGAACCTTGGAGACCAGAGGCTGATAAAAAATAGAATGTGTTG  CACGGAGAAAAATAAACGAAAAGCTTATTATTCTCAGATCGTTGGTCCCCTCGATTAACAAGGTTGACAGGGTTTCTACACTTGATGACA  CTATAGAGTACCTGAAAAGAGCTTAAGAAAAAGTTGATGACTTGGAATTTTTAGAGAACAATAACATCTCCAGATACCATAGAGAG  AACATCAGATAATCGTGGAATGGCAAAATCGGTAGTGAAGGAGGCCATCGATAAATAAGAGGAAGGCTGTGAATGCAATGAGAT  TTCTGAGATTGACTTGATTTAATGAAAGATGGTGAACAGATGATTGAATATAAGCATCATTGAGAAGGATGTGCTGATTGAAATCA  GGTGCCCATGGAGGGAGTGCTTGTGTTTCGAGATCATGGATACGCTAAGCAATCTACATTGGATACTCACTCGGTACAATCATCTAAT  GTTGATGGAATTTTACACTGACCATTAATCTAAGCACTTGAAGGGTTCACCTGCTAATGTAACAGTGAGGATGCTCAGAGAACTACT  TCATGGTGTGTCCACAAGTTCTGA</p>			
2.	SabHLH1	999kb	g17775.t1
<p>ATGGAGTTCAACAATGAGCATGGCTTCTTTGAAGAGTTACTTCCCTGAGAAGAGACAATGCTAGCTGGGTGAAACCATCCCCACCAC  AGGAATGTCTGAATCTGCCCAATCCCAGCAGTTTCGAGGACTTCTACGAATACCCAAATGAGATCACTTCCCTCATTTCTACTTCTCC  TTCCCTGGAGTCCCTTCTGCTCCGTTCTCGAGCAGGGCCTGTTGAGTACCCAGCAGTGAGCTCTGCTGCCCGTTTGGGGACGGTTT  CTCGGCGATGGAAGTTACCGATATGCCCCGTTCCCCGGGCAGGGGTGGAGGACGATTCGGGCGGGGTCGAGCCGGGACTGGACCG  GAGGGGGGCTTGAGATGTTGACGCATGTAAAGTGGAGCCGGTCAGGGATCCGAAACCGCGGTTTTCGACATCGGGTCTGCCTCG  ATCGGAAGAGCAACCGAGGGAAGAAGGTGGAGGGGCAGCAGTCAAGAATCTTATGGCGGAGAGGCGGCGGAGGAAGCGGCTGAAT  GATCGGCTCTCGATGCTCCGATCCGTCGTTCCAAAAATAAGTAAGATGGACAGGACATCTATCCTTGGGGACCCATAGATTACATGA  AGGAGTTGCTAGAGAAAATCAACAATCTGCAAGAAGAATCAGATGTGGACTCCAAGCAGCTGGACTTGATGGGTATATTCAAGGACA  TAAAGCCCAATGAAATCTAGTCAGAAACTCACCAAGTTTCGATGCGGAAAGGAGGAACCTCGGATACCCGGATCGAGATTGTGTCAC  CGGAAGCCTGGATTGTTGCTGTCTACTATGACGACGCTCGAGGCATTAGGCCTTGAAATCGAGCAGTGTGTCATAAGCTGCTTTAACG  ATTTTGGCTCCATGCTTCGTGCTCAGAGGATTCGGAGCAAAGAACAGTAATAAGCTGTGAAGACATAAAGCAAGCGTTATTTAGGAA  TGCAGGGTATGGCGGGAGGTGCCTGTAG</p>			
3.	SaMYC3	2022kb	g7080.t1
<p>ATGAACCTGTGGAGTGACGACAACGCGTCGATGATGGAAGCTTTCATGAGCTCTGAACTCTCCTCCTACGGGTGGGCCCCCTCAGTCCTC  CTCGTCCGTCGCCTCCACCTCCACCCCGCTCCTCCTCCTCCTCCTCCGCTACCGACGGCTCCTCCTCCGACCACCGCCGGCGTGGG  ACAGTCTCAAGCTCCTCCCATGGCGTTCTTCAACCAGGATACCTTGACAGCAGCGGCTCCAGACCCCTATCGAGGGCGCCCGGAGAGCT  GGACCTACGCCATCTTCTGGCAGTCTCGGTTGATTTCTCCGGCGCCGCCCTGTTGGGGTGGGGCGATGGCTACTACAAGGGGGAGGAG  AACAAGTGCGGTGGCGGGGGGAAGCGCCGAAGGCTAAGCAACCCCGCCACCGCCCGGAGCAGGAGCACCGCAAGAAGGTCCTCCG  CGAGCTCAACTCCCTCATCTCCGGCGCTCCGCATCGGCTGCCGCCGTCGACGATAACCGTCGACGAGGAGGTACCGACACCGAGTGG  TTCTTCTCGTCTCCATGACGAGTCTTCGCCAGCGGGATGGGTCTCCCGGTGAGGCCTTCTTACCTCCAACCCCGTCTGGCTCGCC</p>			

GGTCCGGAACGCCTCTCCGGTTCGACCTGCGAGCGCGCGACAGGGGATGGGCTTCGGCCTTCGGACGATGGTGTGCATCCCCGTGGT  
GAACGGGGTCGTGAACTGGGGTCCACGGAGTTGATTCTCCAGACGCCAGATCTGATGAACAAGGTTAGGGTTCTGTCAATTCAGTA  
GTTCCGAGATCAGCTCGTGGCCAATTCATGGCGATCAGCGCGAGAACGAACCCCACTCCGCAATCTGGGTTCCCGACCAACCCACCTCC  
TCCCTCCTCCGCCGTGAAATTAGGGATTCTGTAAGCGCCGACCACCACCAATCCCACTCCCAATCACAATTCCAATCCCAGTT  
CGAGTACCCTAACCGATCTAAACCCTAACCTAGTTCTTCAAATGTAAAATCCACACCTACCCGGCGCGGTTGGTAACGACCCCGCG  
CCGGCGCCACTGCAGACGAAAGCTTCTCAGAGGGAGATAAATTCGCCGAATTCGGGTACGAGGGAAGCGCGCGCGGGAGTG  
AGGACCGCGGGTGCAAGCCGAGTCGGGAGAAATCTGAATTCGGGGAGAGTAAGAGGAGCTCGTGAATGGGAATGGGAGTTTA  
TTCTCCGGCCACCCTCAGCTCGTAGCCGAGGAGAATTGTCGGAAGGGCGGTCTCCGGCGTCGCGAGGTAGCAACGAGGAGGGAATG  
CTGTCTTCTCCGGGATGGTGAATCCACCGCGCGCGCGCGGATTTCGGACCAGTCCGATCTCGAGGCCTCGGTTGTGGTCAGAGAAAC  
TGACAGTAGCAGAGTGGTGGATCCCCGAGAAACGCCCCGGAACGGGGACGAAAGCCCGCAACGGGAGGGAGGAGCCGTTGAACC  
ACGTCGAGGCGGAGCGGCAGCGCGCGAGAAGCTTAACCAGAGATTCTACGCGCTCCGCGCCGTCGTCCCCAACGTCTCGAAGATGG  
ACAAGGCGTCCCTCCTGGGCGACGCCATCGCGTACATTAACGAGCTCCGCACCAAGGTCCAGACCGCGGTCTCCGAGAAGGAAGAGTT  
GCAGAAAGAGGTGGCGGGGTGAAGAAGGAGAAAGCAGTTCCTCCCCGAACAACACCCCCCTAAATCGTCGGACCATTGGCGGGGA  
GAAGTTGGTGGACATTGAAATCGACGTGAAGATCATCGGTTGGGACGCGATGATCAGAATACAATGTAGTAAGAGGAATCATCCGGC  
GGCGAAGTTGATGGCGCGGTTGAAAGAGCTGGATTGGATGTTACCATTGCGAGCGTTTCTGTAGTGAAAGATTTGATGATACAGCAA  
GCAACATTGAAGATGGGGAGCCGATTTACACGCAGGAACAGCTCAAAATGGCCTTATCTTCAAATTATCGGAAACCCGGTAG

4. SabHLH2 1302kb g31888.t1

ATGGGAGAGTTAAGCACCGAGAGCACTTCTCTTGCTATTTCTTCTCTTCGGCTCACAACTGGTGGGATCTCCATTCAACCTCATGG  
AACCTAGTGTCATACCCATAACCCCTTGGAACTCTTTGAACCCTAGTTCCAATTCCTCCACTTGTGAGGAGGATGTTTCGATCTCCACA  
TCGTTACCAACGGTTCCAATCACTCCGGCGTGAGCGTCGATTCTCTCACCAGTTCGGTGAATCCCATGAGTTGATTGGAGAAATCGT  
GTCCGATAATCATATGTGGAACCATGTTCTCTTAAGCAGCGGTGGTGGCGATCATGGGATGATGTTCCAGTTACCTCAGAAACAATACT  
GGGAGTTCTTAACACCAATTACTTTGACAAAACGCACCACTTGAATGGATTCATCCACAGCGACATAACAAGCAATGAAAATGAAAG  
CAACAATAGTAAGAATCTCTTAATTTGGTCAGCAATTGGTCCATTGCTCCTCCATGCCCCACAAGCCGACCATCTCGATCCCCAACCGT  
ACGATAATCAGGGTCTGTTTTTGCACTCCGGCGACACAAAATCGATCCGCAGGGATGACAGCAGTGGTGGTTTATTACAGAGGTTGCAG  
GCAGCGCGCCGTCATTGGATGCGAATTATGGTGTAGTGAAAGTTGTTACTATGGTGGTGGCCTTGAAGACAATAATAATGGGAGAA  
AATTATGTGATGTTATATCATTTAGTGGTAGTAGCAATGGTGTGAAGCCCAGCTGCCAGAAATCCTGAATTTATCAGCTGGGTGGAGG  
AAGCAAGGTCTCTTTACTTCTAATTCCCAGTGAAAAACAGTGGAAGAAGACAGATCATCAACAATGAAGTAAAGAAGAGAAGATCA  
AACAGCAATAGTTTCAGAGACGCTCCCCAAAAAGCAAAAGCATGAAAGCAGTGCAGTTTCATCGGTAAAGATCATGGCACCAAAAAGTC  
AAGCTTGGGGACAAGATCAGTGCTCTTCAGCAAATTTGTGTCACCATTGGAAAGACAGACACAGCGTCTGTGTTATTAGAAGCAATCG  
GATACATAAGGTTTCTACAAGAGCAAGTGACGCTGCTTAGCAATCCTTACATGAAGACTATGCCATGCAAGGATCCATGGGGAGCTCT  
GGACAGAAAAGAGCAAGGAGATGCAGAATTGGACCTTCAGAGTAGAGGTCTTTGTTAGTTCCAACTCTTGACCCCTCAAACGTAT  
CATGAGAATGGGGTTGGATCAGATTATTGGACACCCACTTACAGAGGATGCTTGATATAGATGA

5. SaMYC4 2151bp g13570.t1

ATGGCTTCGCTGCCGCCACCGCCCGCCGCACTGAGCACTCGATTGCAGTCCATGTTACAGACCGCAGTCCAATCCGTGCAGTGGACTTA  
CAGTCTCTTTTGGCAGTTTGTCCGCAACAAGGGATTCTGGTGTGGGGGATGGGTACTACAATGGGGCAATAAAGACGAGGAAGACG  
GTGCAACCGGTGGAGGTGAGCACGGAGGAGGCGTCGCTGCAGCGGAGCCAGCAACTCCGAGAGCTCTACGACTCGTTATCGGCCGA  
GACACGAACTCGCAGCAGCCGCTCGCCGCCCTCCGCCTCGTTGTCGCCGAGGACTTGACCGAGTCGGAGTGGTTCTATCTCATGTG  
TGCTCCTTCTCTTTCTCCCGCATCGGGTTGCCGGGAAAGCATATTCAAAGAGGCAGCATGTGTGGCTTACGGGAGCAAACGAGG  
TTGACAGCAAAGTGTCTTCTAGAGCTATTCTTGCTAAGAGTGCTCGCATACAGACTGTGATGTGCATTCTCTATTAGACGGGTCTGTTG  
AGCTTGGCACACAGACAAGGTGCAAGAGGACCACGGATTGATCCGCCGAGTGAAAAGCGTCTTACGAACCACAGCAATGATCCCC  
CTCCTCCCAAGCCGGCCCTCTCCGAGCACTCCACTTCCAATCCCGTCTCTCTGCCCGCCCTCCACCCACATTGTACGCAGGTGCCG  
CAGCAGCAGACCCGGACGGAGAAGAAGAAGAAGAGAGACGACGATGACGACGATGATGATGACGACGAAGACGACGGAGGAGG  
AGGAGGAGGAGGAGGAGCCGAGTCGGAATCAGAAGCCGGGAACGGGCAGAAACAATGGATTCTCGGTACGGCATGTGGAGGCCA  
TGGGGGTGGGGACGGCCGAGCCGAGCGAGCTCATGCAGCTCGAGATGTCGGAGGATATTCGGATTGGCTCGCCCGATGACGGGTCTGA  
ACAACCTCGACTGCGACTTCCACTTGCTCGCGTGCTCAGTCGGAGACCCGACGGCGGAGGCGGATCTTACGCGCCGGGTGACTC  
GTACAGGGCTGAGTCGAGCCGAGGTGGCCGACGGTGCCGAAATGGGTATTACTGCGATGATTAAACCGCCACCTTCAGGTGGAGA

6.	SaMYC5	1542bp	g18261.t1
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7.	SabHLH3	927kb	g13803.t1
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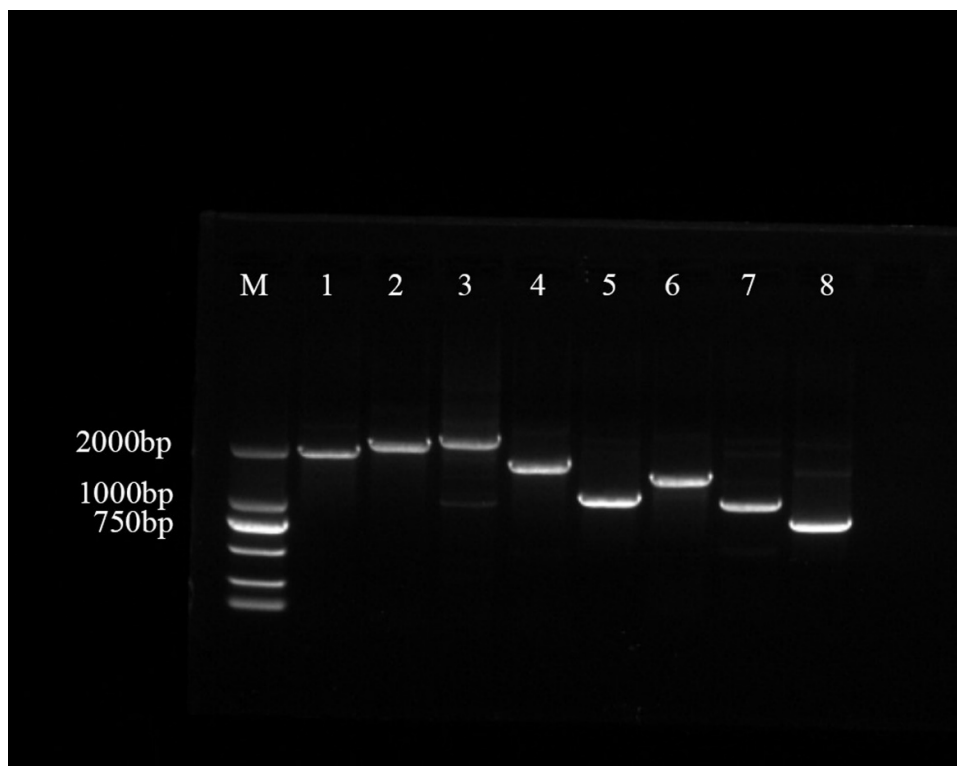
8.	SabHLH4	708kb	g2451.t1
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ATGCTGTCCCAGGATAACACCAATTGGCTGTTGATTACGGATTGATCGAGGATATCGCTGCACCAGACGGGAATTTCCCTGCTCCGGC  
TTCGGGCTTCACTGGCCATTACAGGCCCGGAATGATCCTCCTTATCTCGGTGTTGATGTCGATGGCTCACTCGGGGATTAGATTGTCC  
CAAAGAAACAGGCTCAAAAAAGAGGGGGAGATCTGAACCATCTGGCCCTTCTAGTTCCAAAGCATGTAGGGAGAAGCTGCGGAGGGA  
TAGGCTAAACGACAAGTTTTTGGAGCTGGGTCTATTCTGGACCCTGGAAGGCCTCTAAAAACAGACAAGGCTGCTGTTTTGGTTGATG  
CGGTAAAAATGGTGACTCAGTTACGGGGTGAAGCCCACAAGCTAAAGGACTCCAATTACAGATCTCCAACAGAAGATTAAGGAGTTGAA  
GGCTGAGAAGAATGAGCTGCGTGATGAGAAGCATCGATTGAAGACTGAGAAGGAAAAGCTAGAGCAACAGATGAAAGGCATGAATG  
CTCAACCCAGTACCTCCCCCACCTGCCATTCCCCTGTCATATACTGCTCAAGGTCAACCCGGCGGAAACAAGTTGGTGCCTTTCATT  
GGTTACCCGGGAGTCGCTATGTGGCAGTTCATGCCACCCGCTGCGGTAGACACCTCTCAGGATCATGTACTCCGTCCCCCGTTGCCTA  
A

**Table S4.** Yeast one-hybrid experimental genes synthesis sequences in *Santalum album*

Transformation lists name	Lists (genes 5'→3')
<i>pAbAi-SSy1G-box-F</i>	AATATAGAGTAACGTGCTAAGACTATAATATAGAGTAACGT GCTAAGACTATAATATAGAGTAACGTGCTAAGACTAT
<i>pAbAi-SSy1G-box-R</i>	ATAGTCTTAGCACGTTACTCTATATTATAGTCTTAGCACGTT ACTCTATATTATAGTCTTAGCACGTTACTCTATATT
<i>pAbAi-mSSy1G-box-F</i>	AATATAGAGTCCAACGCTAAGACTATAATATAGAGTCCAAC GCTAAGACTATAATATAGAGTCCAACGCTAAGACTAT
<i>pAbAi-mSSy1G-box-R</i>	ATAGTCTTAGCGTTGGACTCTATATTATAGTCTTAGCGTTGGACTCTATATTATAGT CTTAGCGTTGG ACTCTATATT
<i>pAbAi-CYP1G-box-F</i>	TTGATAGATATACGTGCACCTATAAGTTGATAGATATACGTGCACCTATAA GTTGATAGATATACGTGCACCTATAAG
<i>pAbAi-CYP1G-box-R</i>	CTTATAGGTGCACGTATATCTATCAACTTATAGGTGCACGTATATCTATCAACTTAT AGGTGCACGTATATCTATCAA
<i>pAbAi-CYP2G-box-F</i>	GTGTCCGAGCCACGTTACGGTTTGGGGTGTCCGAGCCACGTTACGGTTTGGGGTGT CCGAGCCACGTTACGGTTTGGG
<i>pAbAi-CYP2G-box-R</i>	CCCAAACCGTAACGTGGCTCGGACACCCCAAACCGTAACGTGGCTCGGACACCCC AAACCGTAACGTGGCTCGGACAC
<i>pAbAi-CYP3G-box-F</i>	TAATTTGAAGCACGTGAATTTGGCATTAAATTTGAAGCACGTGAATTTGGCATTAAAT TGAAGCACGTGAATTTGGCAT
<i>pAbAi-CYP3G-box-R</i>	ATGCCAAATTCACGTGCTTCAAATTAATGCCAAATTCACGTGCTTCAAATTAATGC CAAATTCACGTGCTTCAAATTA
<i>pAbAi-CYP4G-box-F</i>	TCCCACCCACGTAGCTTCGCCCACGTTTGAATCATCCCACCCACGTAGCTTCGCC CACGTTTGAATCATCCCACCCACGTAGCTTCGCCCACGTTTGAATCA
<i>pAbAi-CYP4G-box-R</i>	TGATTCCAAACGTGGGCGAAGCTACGTGGGTGGGATGATTCCAAACGTGGGCGAA GCTACGTGGGTGGGATGATTCCAAACGTGGGCGAAGCTACGTGGGTGGGA
<i>pAbAi-mCYP3G-box-F</i>	AATTTGAAGTCAACGAATTTGGCATTAAATTTGAAGTCAACG AATTTGGCATTAAATTTGAAGTCAACGAATTTGGCAT
<i>pAbAi-mCYP3G-box-R</i>	ATGCCAAATTCGTTGACTTCAAATTAATGCCAAATTCGTTGACTTCAAATTAATGCC AAATTCGTTGACTTCAAATTA
<i>pAbAi-mCYP4G-box-F</i>	TCCCACCATTTAAGCTTCGCCTTAATCTGGAATCATCCCACCATTTAAGCTTCGCCT TAATCTGGAATCATCCCACCATTTAAGCTTCGCCTTAATCTGGAATCA
<i>pAbAi-mCYP4G-box-R</i>	TGATTCCAGATTAAGGCGAAGCTTAAATGGTGGGATGATTCCAGATTAAGGCGAA GCTTAAATGGTGGGATGATTCCAGATTAAGGCGAAGCTTAAATGGTGGGA

Supplementary Figures



**Figure S1.** TF open reading frames (ORFs) were amplified by RT-PCR and then electrophoresed on a 0.1% agarose gel

a

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>PlantCARE_7091
+ GAGGAGCCTT AGGTGAGTGC AAATGCTTT AAGAGATGAA TAGGGGTGAG ATGGGTATTA GATTGAAAAA
- CTTCTGCTTA TCTCATCAGG TTACAGGAAA TTCTCTATTT ATTCCGACATC TAGCCATATAT CTACCTTTTT
+ GGAAATTTGAA CAGGAGACAA ATTTATCTAA TGTAAAGAG TAGGTTGAGA GAGAGAGAAA GTTGTAAATAT
- CTTTAACTTT GTCTCTCTGT TAAATGATAT ACATTTTTCG ATTCCTACTCT CTTCTCTTTT CAGACTTTTA
+ ATTTCTGTCA CATGTATGTT AAATAGGAAA AAGGATGCCC GGAAGTCCAC TAGCCCCACA AGCTGGCTGC
- TAAAGCAAGT GTACATACAA TTATCTCTTT TTCCCTAGCG CTTTCAGGTG ATCGGGGTGT TCGACCGAGC
+ CCACGAGACC AGTGTGTGAG AAATATCGAG CAATTTCTCA CTTTTATCT TATTATTTTT TTTTGAAG
- GGTGTGCTGG TCAACATCTC TTTTAGCTCT GTTAAAGAGT GAAAAATAGA ATAATAAAAA AAAACATTTT
+ TCTTAAATTA AAGTGAAGAG TTAAGTGTG TTTTCTTCTC TTTTCTCTCA TGATCTCTGG CGTGAGGCTG
- AGAATTAATY TTCACTTTTC AATTTACAC AACAAAGAG AAAAGGAGGT ACATGGAGAC SCATCTCGAC
+ GGGGAGCAGC TCACTGCTCT TATCTCTGTT AAATATATA GATTACAAAT AGTCAAAAT AGATTAAGT
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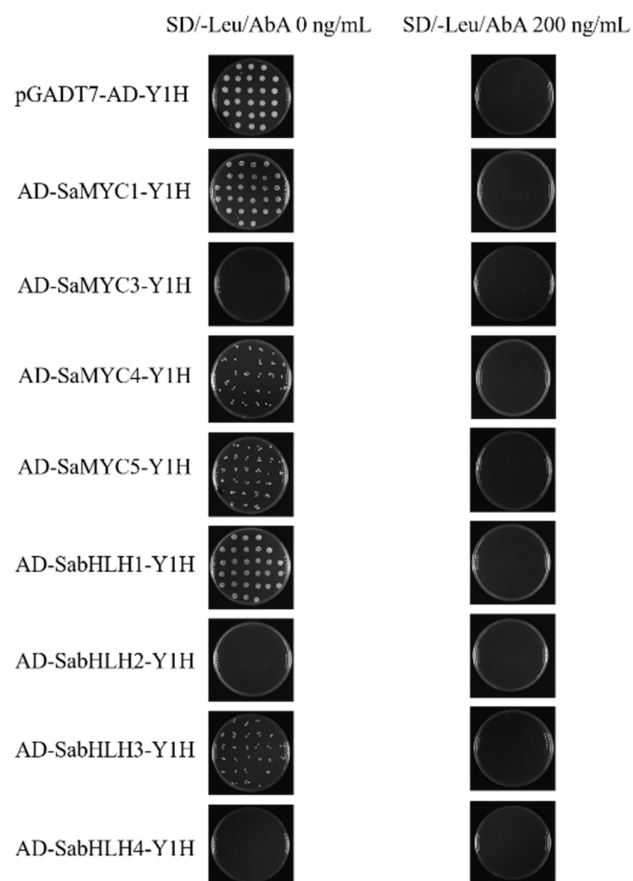
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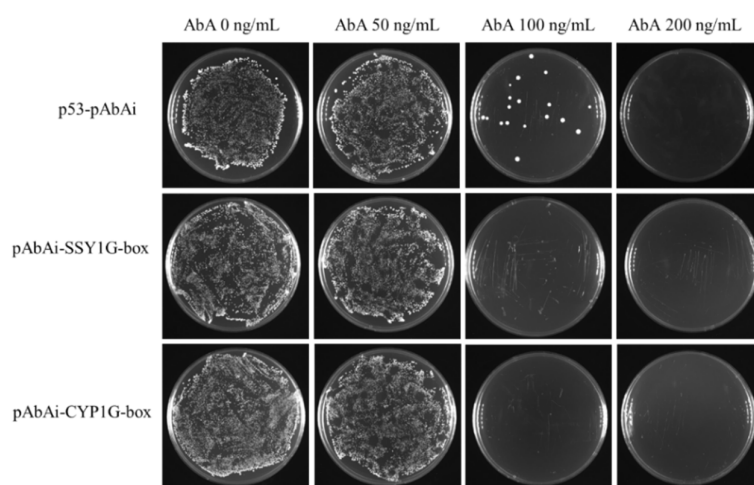
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Figure S2. Detection of G-box elements of *SaSsY* ((a) G-box marked blue) and *SaCYP736A167* ((b) G-box marked pink) promoter.

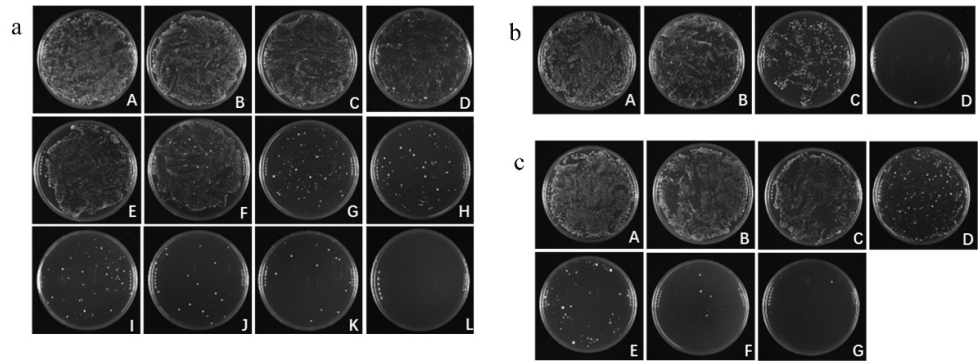




**Figure S3.** Transcription factor activity verification.



**Figure S4.** Screening of the inhibitory AbA concentrations of bait strain. Note: p53-AbAi was the positive control; pAbAi-SSy1G-box was the G-box element strain of *SaSSy*; pAbAi-CYP1G-box was the G-box element strain of *SaCYP736A67*; the SD/-Leu selection media with AbA concentration of 0 ng/mL, 50 ng/mL, 100 ng/mL, 200 ng/mL, respectively.



**Figure S5.** Screening AbA concentration of mutant G-box element bait strain. (a): Screening of the lowest inhibitory AbA concentration of mutant bait strain pAbAi-mSSy1G-box; (b): Screening of the lowest inhibitory AbA concentration of mutant bait strain CYP3G-box; (c): Screening of the lowest inhibitory AbA concentration of mutant bait strain pAbAi-mCYP3G-box. A-L: The SD/-Leu selection media with AbA concentration of 0 ng/mL, 50 ng/mL, 100 ng/mL, 200 ng/mL, 300 ng/mL, 400 ng/mL, 500 ng/mL, 600 ng/mL, 700 ng/mL, 800 ng/mL, 900 ng/mL, 1000 ng/mL, respectively.