Supplementary Table 1. Library quality for saturation mutagenesis

	Ser	Val	Cys	Ile	Asn	Pro	Ala	Gly	Thr	Xxx	Others	Sum
1st 80	6	9	1	2	2	3	6	4	5	4	38	80
2nd 80	3	7	1	3	2	3	3	7	3	4	44	80
Sum	9	16	2	5	4	6	9	11	8	8	82	160

We used saturation mutagenesis at S484 to determine the quality of the library. We screened 160 mutants; 92% coverage of full diversity (The plasmids of 20 different clones from the library were first purified, digested, and run on the agarose gel. All clones contained inserts of the correct size.). After the screening, the number of occurrences was counted based on the product profile, and the representatives were sequenced. 'Others' indicates the clones whose *in vivo* productivity was not detected. As shown in the above table, the substitutions were well distributed for the relatively smaller sized residues listed above, and roughly half of all clones corresponded to those residues. The other half of the clones should correspond to the relatively larger, aromatic, and charged (10 other) residues (not listed). We did not sequence the last substitution notated by 'Xxx' in the table, because *in vivo* productivity was very low. The number 80 is a simply the number that we can screen using GC-MS in a day and that gives sufficient coverage as indicated in the table. Interestingly, charged residues such as K, R, D, and E were rarely found from screening for any residues. The hydrophilic property of these residues should not be suitable for hydrophobic active site.

Supplementary Table 2. β-bisabolene synthase construction

Clones Generation	Mutations	Product Distributions (%)							Yield*[1] (times)
		1	**2**	**3**	**4**	**5**	**6**	**7**	
WT	WT	3.3	26.1	36.1	16.4	6.1	5.6	**3.3**	1
1	M447H	12.2	2.0	21.4	9.9	5.4	1.0	**48.3**	9.1
2	A336V, M447H	18.5	0.4	3.9	3.9	1.9	0.1	**71.2**	13.0
3-1 (BBA)	A336V, M447H, I562T	6.4	0.5	4.4	7.1	1.8	0.3	**79.4**	3.5
3-2	A336V, M447H, I562V	15.5	0.3	2.4	3.9	1.4	0.2	**76.4**	6.4
Predicted Clones	Mutations*[2]	Predicted Product Distributions (%)							
		1	**2**	**3**	**4**	**5**	**6**	**7**	
2	A336V, ***M447H***	16.7	0.5	5.7	2.5	2.2	0.2	**72.2**	
3-1	A336V, ***M447H***, I562T	8.8	0.3	3.1	2.4	1.5	0.2	**83.9**	
3-2	A336V, ***M447H***, I562V	8.3	0.2	1.7	1.0	0.7	0.1	**88.1**	
3-1	***A336V***, ***M447H***, I562T	9.7	0.3	2.1	3.7	1.3	0.1	**82.9**	
3-2	***A336V***, ***M447H***, I562V	9.3	0.1	1.2	1.5	0.6	0.0	**87.3**	

ND means "Production is not detected"

WT = wild type, **BBA** =β-bisabolene(**7**) synthase,

E-β-farnesene(**1**), sibirene(**2**) , γ-humulene(**3**), longifolene(**4**), α-longipinene(**5**), α-ylangene(**6**), and *Z,E*-α-farnesene (**8**)

Each product distribution was normalized to total of **1-7** product distribution as 100%

All product distributions were determined from triplicates, and standard deviations were lower than 2 %.

*[1] The yield is the *in vivo* productivity of a particular compound by each mutant over that by the wild type enzyme.

*[2]The starting product distribution used was represented as bold and italic

Supplementary Table 3. Sibirene synthase construction.

Clones Generation	Mutations	Product Distributions (%)							Yield*[1] (times)
		1	**2**	**3**	**4**	**5**	**6**	**7**	
WT	WT	3.3	**26.1**	36.1	16.4	6.1	5.6	3.3	1
1	M447F	2.7	**46.4**	23.5	20.7	1.3	3.3	2.1	2.2
2	F312Q, M447F	3.7	**79.4**	10.3	4.0	0.4	1.6	0.6	2.3
3 (SIB)	F312Q, M339A, M447F	3.3	**80.7**	11.1	3.4	0.3	1.1	ND	2.7
3	F312Q, M339L, M447F	6.0	**75.4**	19.5	6.3	0.5	0.7	ND	0.9
Predicted Clones	Mutations*[2]	Product Distributions (%)							
		1	**2**	**3**	**4**	**5**	**6**	**7**	
2	F312Q, ***M447F***	1.8	**73.3**	11.2	11.2	0.3	1.8	0.5	
3-1	F312Q, M339L, ***M447F***	5.1	**77.7**	9.9	4.8	0.1	2.2	0.3	
3-2	***F312Q***, M339L, ***M447F***	9.9	**77.8**	8.4	1.6	0.1	1.8	0.3	

ND means "Production is not detected"

WT = wild type, **SIB** = sibirene(**2**) synthase,

E-β-farnesene(**1**),γ-humulene(**3**), longifolene(**4**), α-longipinene(**5**), α-ylangene(**6**), β-bisabolene(**7**), and *Z,E*-α-farnesene (**8**)

Each product distribution was normalized to total of **1-7** product distribution as 100%

All product distributions were determined from triplicates, and standard deviations were lower than 2 %.

*[1] The yield is the *in vivo* productivity of a particular compound by each mutant over that by the wild type enzyme.

*[2]The starting product distribution used was represented as bold and italic

Supplementary Table 4. γ-humulene synthase construction.

Clones Generation	Mutations	Product Distributions (%)							Yield*[1] (times)
		1	**2**	**3**	**4**	**5**	**6**	**7**	
WT	WT	3.3	26.1	**36.1**	16.4	6.1	5.6	3.3	1
1	S484C	1.6	1.6	**13.7**	59.6	16.3	3.6	3.6	0.37
2	M339N, S484C	4.0	0.8	**73.1**	7.9	7.8	6.4	ND	0.36
3 (HUM)	M339N, S484C, M565I	2.9	0.6	**77.8**	4.7	6.3	7.8	ND	0.64
Predicted Clones	Mutations*[2]	Product Distributions (%)							
		1	**2**	**3**	**4**	**5**	**6**	**7**	
2	M339N, ***S484C***	27.6	1.7	27.3	20.1	0.0	22.2	1.0	
3-1	M339N, ***S484C***, M565I	19.8	1.8	32.4	16.0	0.0	28.6	1.4	
3-2	***M339N***, ***S484C***, M565I	2.6	0.7	76.8	5.6	7.0	7.3	0.0	

ND means "Production is not detected"

WT = wild type, **HUM** = γ-humulene(**3**) synthase,

E-β-farnesene(**1**), sibirene(**2**) , longifolene(**4**), α-longipinene(**5**), α-ylangene(**6**), β-bisabolene(**7**), and *Z,E*-α-farnesene (**8**)

Each product distribution was normalized to total of **1-7** product distribution as 100%

All product distributions were determined from triplicates, and standard deviations were lower than 2 %.

*[1] The yield is the *in vivo* productivity of a particular compound by each mutant over that by the wild type enzyme.

*[2]The starting product distribution used was represented as bold and italic

Supplementary Table 5. Longifolene synthase construction

Clones Generation	Mutations	Product Distributions (%)							Yield*[1] (times)
		1	**2**	**3**	**4**	**5**	**6**	**7**	
WT	WT	3.3	26.1	36.1	**16.4**	6.1	5.6	3.3	1
1	S484C	1.6	1.6	13.7	**59.6**	16.3	3.6	3.6	2.6
2	S484C, I562V	1.4	1.2	13.1	**62.6**	14.5	3.8	3.5	2.7
3 (LFN)	A336S, S484C, I562V	1.6	1.3	9.3	**64.7**	15.0	3.9	4.2	1.9
Predicted Clones	Mutations*[2]	Product Distributions (%)							
		1	**2**	**3**	**4**	**5**	**6**	**7**	
2	***S484C***, I562V	2.0	1.5	10.3	**58.8**	13.1	3.1	11.2	
3-1	A336S, ***S484C***, I562V	1.3	1.3	8.0	**62.2**	13.9	2.3	10.9	
3-2	***A336S***, ***S484C***, I562V	0.9	1.1	10.2	**66.3**	15.4	2.8	3.4	

ND means "Production is not detected"

WT = wild type, **LFN** = longifolene(**4**) synthase,

E-β-farnesene(**1**), sibirene(**2**) , γ-humulene(**3**), α-longipinene(**5**), α-ylangene(**6**), β-bisabolene(**7**), and *Z,E*-α-farnesene (**8**)

Each product distribution was normalized to total of **1-7** product distribution as 100%

All product distributions were determined from triplicates, and standard deviations were lower than 2 %.

*[1] The yield is the *in vivo* productivity of a particular compound by each mutant over that by the wild type enzyme.

*[2]The starting product distribution used was represented as bold and italic

Supplementary Table 6. α-longipinene synthase construction

Clone Generation	Mutations	Product Distributions (%)							Yield*[1] (times)
		1	**2**	**3**	**4**	**5**	**6**	**7**	
WT	WT	3.3	26.1	36.1	16.4	**6.1**	5.6	3.3	1
1	S484C	1.6	1.6	13.7	59.6	**16.3**	3.6	3.6	2.6
2-1	T445C, S484C	2.5	2.0	19.2	35.0	**36.0**	4.0	1.3	5.9
2-2	S484C, I562L	8.0	1.1	8.3	42.2	**34.5**	3.0	2.9	8.5
3	T445C, S484C, I562L	6.7	1.1	13.8	19.1	**54.8**	2.5	2.1	6.9
4-1	A336C, T445C, S484C, I562L	9.4	1.2	11.5	18.5	**53.7**	2.0	3.5	14.7
4-2	T445C, S484C, I562L, M565L	5.3	0.7	12.2	13.6	**63.0**	3.3	1.9	10.7
5 (ALP)	A336C, T445C, S484C, I562L, M565L	4.4	0.5	9.7	13.6	**66.3**	2.6	2.9	11.7
Predicted clone	Mutations*[2]	Predicted Product Distributions (%)							
		1	**2**	**3**	**4**	**5**	**6**	**7**	
2-1	T445C, ***S484C***	3.1	3.4	17.1	39.4	**28.9**	6.5	1.6	
2-2	***S484C***, I562L	1.7	1.1	18.1	43.7	**28.1**	4.1	3.2	
3	T445C, ***S484C***, I562L	2.9	2.0	19.5	25.0	**42.9**	6.4	1.2	
4-1	A336C, T445C, ***S484C***, I562L	1.4	1.6	15.6	21.0	**54.7**	4.7	1.0	
4-2	T445C, ***S484C***, I562L, M565L	1.7	0.9	19.2	20.8	**50.3**	6.1	1.0	
5	A336C, T445C, ***S484C***, I562L, M565L	0.8	0.7	14.9	16.8	**61.8**	4.3	0.8	

ND means “Production is not detected”

WT = wild type, **ALP** = α-longipinene(**5**) synthase,

E-β-farnesene(**1**), sibirene(**2**) , γ-humulene(**3**), longifolene(**4**), α-ylangene(**6**), β-bisabolene(**7**), and *Z,E*-α-farnesene (**8**)

Each product distribution was normalized to total of **1-7** product distribution as 100%

All product distributions were determined from triplicates, and standard deviations were lower than 2 %.

*[1] The yield is the *in vivo* productivity of a particular compound by each mutant over that by the wild type enzyme.

*[2]The starting product distribution used was represented as bold and italic

Supplementary Table 7. α-ylangene synthase construction

Clones Generation	Mutations	Product Distributions (%)							Yield*[1] (times)
		1	**2**	**3**	**4**	**5**	**6**	**7**	
WT	WT	3.3	26.1	36.1	16.4	6.1	**5.6**	3.3	1
1	Y566F	2.6	1.4	56.4	4.2	20.1	**11.0**	4.2	2.1
2 (AYG)	S484A, Y566F	3.0	0.5	55.6	3.7	17.2	**12.7**	7.3	2.0
Predicted Clones	Mutations*[2]	Predicted Product Distributions (%)							
		1	**2**	**3**	**4**	**5**	**6**	**7**	
2	S484A, ***Y566F***	2.9	0.6	58.7	3.6	17.4	**9.8**	6.9	

ND means "Production is not detected"

WT = wild type, **AYG** =α-ylangene(**6**)synthase,

E-β-farnesene(**1**), sibirene(**2**) , γ-humulene(**3**), longifolene(**4**), α-longipinene(**5**), β-bisabolene(**7**), and *Z,E*-α-farnesene (**8**)

Each product distribution was normalized to total of **1**-**7** product distribution as 100%

All product distributions were determined from triplicates, and standard deviations were lower than 2 %.

*[1] The yield is the *in vivo* productivity of a particular compound by each mutant over that by the wild type enzyme.

*[2]The starting product distribution used was represented as bold and italic

Supplementary Table 8. Primers used for saturation and site-directed mutagenesis

Name	Sequences(5'→3')
HUM-W312SatF	CGTAAATGCTATGTGGAANNNTACTTCTGGATGGCCGCG
HUM-W312SatR	CGCGGCCATCCAGAAGTANNNTTCCACATAGCATTTACG
HUM-W315SatF	TATGTGGAATTTTACTTCNNNATGGCCGCGGCAATTTCA
HUM-W315SatR	TGAAATTGCCGCGGCCATNNNGAAGTAAAATTCCACATA
HUM-A336SatF	GTGGCATTCACTAAAATTNNNATCTTGATGACAATGTTA
HUM-A336SatR	TAACATTGTCATCAAGATNNNAATTTTAGTGAATGCCAC
HUM-M339SatF	ACTAAAATTGCGATCTTGNNNACAATGTTAGATGACTTA
HUM-M339SatR	TAAGTCATCTAACATTGTNNNCAAGATCGCAATTTTAGT
HUM-T340SatF	AAAATTGCGATCTTGATGNNNATGTTAGATGACTTATAC
HUM-T340SatR	GTATAAGTCATCTAACATNNNCATCAAGATCGCAATTTT
HUM-Y419SatF	GAACGCTATCTGGAAGCGNNNTTGCAGGATGCCGAATGG
HUM-Y419SatR	CCATTCGGCATCCTGCAANNNCGCTTCCAGATAGCGTTC
HUM-T445SatF	AACAATGGCACCCCCAACNNNGGTATGTGTGTACTTAAT
HUM-T445SatR	ATTAAGTACACACATACCNNNGTTGGGGGTGCCATTGTT
HUM-G446SatF	AATGGCACCCCCAACACCNNNATGTGTGTACTTAATCTG
HUM-G446SatR	CAGATTAAGTACACACATNNNGGTGTTGGGGGTGCCATT
HUM-M447SatF	GGCACCCCCAACACCGGTNNNTGTGTACTTAATCTGATC
HUM-M447SatR	GATCAGATTAAGTACACANNNACCGGTGTTGGGGGTGCC
HUM-L450SatF	AACACCGGTATGTGTGTANNNAATCTGATCCCGTTGCTG
HUM-L450SatR	CAGCAACGGGATCAGATTNNNTACACACATACCGGTGTT
HUM-S484SatF	CATCTGATTGAACTGGCTNNNCGACTGGTCGATGATGCG
HUM-S484SatR	CGCATCATCGACCAGTCGNNNAGCCAGTTCAATCAGATG
HUM-V487SatF	GAACTGGCTAGCCGACTGNNNGATGATGCGAGAGATTTT
HUM-V487SatR	AAAATCTCTCGCATCATCNNNCAGTCGGCTAGCCAGTTC
HUM-L558SatF	AAATACTCATTCCACGTCNNNGCGCGGTCGATTCAGTTT
HUM-L558SatR	AAACTGAATCGACCGCGCNNNGACGTGGAATGAGTATTT
HUM-I562SatF	CACGTCCTGGCGCGGTCGNNNCAGTTTATGTATAACCAG
HUM-I562SatR	CTGGTTATACATAAACTGNNNCGACCGCGCCAGGACGTG
HUM-M565SatF	GCGCGGTCGATTCAGTTTNNNTATAACCAGGGGGACGGG
HUM-M565SatR	CCCGTCCCCCTGGTTATANNNAAACTGAATCGACCGCGC
HUM-Y566SatF	CGGTCGATTCAGTTTATGNNNAACCAGGGGGACGGGTTT
HUM-Y566SatR	AAACCCGTCCCCCTGGTTNNNCATAAACTGAATCGACCG
HUM-D570SatF	TTTATGTATAACCAGGGGNNNGGGTTTTCGATTTCGAAC
HUM-D570SatR	GTTCGAAATCGAAAACCCNNNCCCCTGGTTATACATAAA
HUM-F572SatF	TATAACCAGGGGGACGGGNNNTCGATTTCGAACAAAGTT
HUM-F572SatR	AACTTTGTTCGAAATCGANNNCCCGTCCCCCTGGTTATA

HUM-Y573SatF	AACCAGGGGGACGGGTTTNNNATTTCGAACAAAGTTATT
HUM-Y573SatR	AATAACTTTGTTCGAAATNNNAAACCCGTCCCCCTGGTT
HUM-M565I/V/L-F	GCGCGGTCGATTCAGTTTVTTTATAACCAGGGGGACGGG
HUM-M565I/V/L-R	CCCGTCCCCCTGGTTATAAABAAACTGAATCGACCGCGC
HUM-A336CF	GTGGCATTCACTAAAATTTGCATCTTGATGACAATGTTA
HUM-A336CR	TAACATTGTCATCAAGATGCAAATTTTAGTGAATGCCAC
HUM-T445CF	CTGAACAATGGCACCCCCAACTGCGGTATGTGTGTACTTAATCTG
HUM-T445CR	CAGATTAAGTACACACATACCGCAGTTGGGGGTGCCATTGTTCAG

All primers were purchased from OPERON.

Supplementary Table 9. Primers used for γ-humulene synthase gene synthesis

Name	Forward Sequence (5'→3')
HUMNcoIF	CATGCCATGGCTCAAATCAGCGAATCAGTGT
HUM-F-01	CTCCAAGCACCGACCTTAAAAGCACGGAATCTTCT
HUM-F-02	ATTACCAGCAACCGCCACGGTAACATGTGGGAAGA
HUM-F-03	TGACCGCATTCAGAGCTTAAACAGCCCATATGGCG
HUM-F-04	CACCCGCTTATCAGGAACGTAGCGAAAAATTGATT
HUM-F-05	GAAGAAATTAAGCTCCTGTTTCTGTCCGATATGGA
HUM-F-06	CGATAGTTGCAATGATTCGGATCGCGACTTGATCA
HUM-F-07	AACGCCTGGAGATCGTAGATACGGTTGAGTGTCTG
HUM-F-08	GGCATTGATCGTCATTTCCAACCTGAAATTAAGCT
HUM-F-09	GGCGCTGGATTACGTGTACCGTTGCTGGAATGAGC
HUM-F-10	GTGGCATCGGAGAAGGTAGCCGTGATAGCTTAAAA
HUM-F-11	AAGGACCTGAATGCGACCGCCTTGGGCTTTCGGGC
HUM-F-12	TTTACGCTTACACCGTTATAATGTAAGCTCAGGAG
HUM-F-13	TGCTGGAGAACTTCCGTGATGACAATGGTCAATTC
HUM-F-14	TTTTGCGGTTCTACTGTGGAGGAGGAAGGCGCGGA
HUM-F-15	GGCCTACAATAAACATGTACGTTGCATGCTGTCCC
HUM-F-16	TGTCCCGCGCTTCCAATATTTTATTCCCGGGCGAG
HUM-F-17	AAAGTGATGGAAGAAGCGAAGGCGTTTACGACCAA
HUM-F-18	CTATCTTAAGAAAGTCCTGGCGGGTCGTGAAGCAA
HUM-F-19	CTCATGTCGACGAGAGTCTCCTTGGAGAGGTCAAG
HUM-F-20	TATGCACTAGAATTTCCGTGGCATTGTTCCGTGCA
HUM-F-21	GCGCTGGGAGGCACGTTCTTTTATCGAAATTTTCG
HUM-F-22	GTCAGATTGATAGTGAACTGAAAAGCAACCTCTCT
HUM-F-23	AAAAAAATGCTCGAACTCGCAAAACTTGATTTTAA
HUM-F-24	CATACTCCAGTGTACGCATCAAAAAGAGCTCCAGA
HUM-F-25	TCATTAGTCGATGGTTCGCCGATTCAAGTATCGCA
HUM-F-26	AGTCTGAACTTTTACCGTAAATGCTATGTGGAATT
HUM-F-27	TTACTTCTGGATGGCCGCGGCAATTTCAGAACCAG
HUM-F-28	AATTTAGTGGCTCTCGCGTGGCATTCACTAAAATT
HUM-F-29	GCGATCTTGATGACAATGTTAGATGACTTATACGA
HUM-F-30	CACGCATGGGACGCTGGATCAATTGAAAATATTTA
HUM-F-31	CCGAAGGTGTGCGCAGGTGGGACGTGTCGCTGGTG
HUM-F-32	GAGGGCCTGCCGGATTTCATGAAAATTGCCTTTGA
HUM-F-33	GTTCTGGTTAAAGACCTCCAACGAACTGATTGCGG
HUM-F-34	AGGCGGTTAAGGCCCAAGGCCAGGATATGGCGGCC
HUM-F-35	TATATCCGCAAAAACGCTTGGGAACGCTATCTGGA

HUM-F-36	AGCGTATTTGCAGGATGCCGAATGGATCGCCACCG
HUM-F-37	GTCACGTTCCGACATTCGATGAATATCTGAACAAT
HUM-F-38	GGCACCCCCAACACCGGTATGTGTGTACTTAATCT
HUM-F-39	GATCCCGTTGCTGCTTATGGGCGAACACTTGCCGA
HUM-F-40	TCGATATTCTTGAACAGATCTTTCTGCCGAGCCGG
HUM-F-41	TTCCACCATCTGATTGAACTGGCTAGCCGACTGGT
HUM-F-42	CGATGATGCGAGAGATTTTCAAGCCGAAAAAGATC
HUM-F-43	ATGGTGATTTATCCTGCATCGAATGCTACCTGAAA
HUM-F-44	GACCATCCGGAATCAACAGTTGAAGACGCCCTGAA
HUM-F-45	TCACGTCAACGGCCTGCTGGGGAATTGTTTGCTGG
HUM-F-46	AAATGAATTGGAAATTTCTGAAAAAACAGGACTCG
HUM-F-47	GTACCTCTGTCGTGTAAAAAATACTCATTCCACGT
HUM-F-48	CCTGGCGCGGTCGATTCAGTTTATGTATAACCAGG
HUM-F-49	GGGACGGGTTTTCGATTTCGAACAAAGTTATTAAA
HUM-F-50	GACCAGGTCCAGAAAGTTCTAATCGTTCCGGTTCC

Name	Reverse sequence (5'→3')
hum-R-1	AAGGTCGGTGCTTGGAGACACTGATTCGCTGATTT
hum-R-2	TGGCGGTTGCTGGTAATAGAAGATTCCGTGCTTTT
hum-R-3	AGCTCTGAATGCGGTCATCTTCCCACATGTTACCG
hum-R-4	TTCCTGATAAGCGGGTGCGCCATATGGGCTGTTTA
hum-R-5	AGGAGCTTAATTTCTTCAATCAATTTTTCGCTACG
hum-R-6	AATCATTGCAACTATCGTCCATATCGGACAGAAAC
hum-R-7	TACGATCTCCAGGCGTTTGATCAAGTCGCGATCCG
hum-R-8	AAATGACGATCAATGCCCAGACACTCAACCGTATC
hum-R-9	ACACGTAATCCAGCGCCAGCTTAATTTCAGGTTGG
hum-R-10	ACCTTCTCCGATGCCACGCTCATTCCAGCAACGGT
hum-R-11	GTCGCATTCAGGTCCTTTTTTAAGCTATCACGGCT
hum-R-12	AACGGTGTAAGCGTAAAGCCCGAAAGCCCAAGGCG
hum-R-13	ACGGAAGTTCTCCAGCACTCCTGAGCTTACATTAT
hum-R-14	ACAGTAGAACCGCAAAAGAATTGACCATTGTCATC
hum-R-15	CATGTTTATTGTAGGCCTCCGCGCCTTCCTCCTCC
hum-R-16	ATTGGAAGCGCGGGACAGGGACAGCATGCAACGTA
hum-R-17	GCTTCTTCCATCACTTTCTCGCCCGGGAATAAAAT
hum-R-18	GGACTTTCTTAAGATAGTTGGTCGTAAACGCCTTC
hum-R-19	ACTCTCGTCGACATGAGTTGCTTCACGACCCGCCA
hum-R-20	GGAAATTCTAGTGCATACTTGACCTCTCCAAGGAG
hum-R-21	AACGTGCCTCCCAGCGCTGCACGGAACAATGCCAC
hum-R-22	TTCACTATCAATCTGACCGAAAATTTCGATAAAAG

hum-R-23	AGTTCGAGCATTTTTTTAGAGAGGTTGCTTTTCAG
hum-R-24	GCGTACACTGGAGTATGTTAAAATCAAGTTTTGCG
hum-R-25	GAACCATCGACTAATGATCTGGAGCTCTTTTTGAT
hum-R-26	CGGTAAAAGTTCAGACTTGCGATACTTGAATCGGC
hum-R-27	CGGCCATCCAGAAGTAAAATTCCACATAGCATTTA
hum-R-28	GCGAGAGCCACTAAATTCTGGTTCTGAAATTGCCG
hum-R-29	ATTGTCATCAAGATCGCAATTTTAGTGAATGCCAC
hum-R-30	CCAGCGTCCCATGCGTGTCGTATAAGTCATCTAAC
hum-R-31	CCTGCGCACACCTTCGGTAAATATTTTCAATTGAT
hum-R-32	AAATCCGGCAGGCCCTCCACCAGCGACACGTCCCA
hum-R-33	AGGTCTTTAACCAGAACTCAAAGGCAATTTTCATG
hum-R-34	TTGGGCCTTAACCGCCTCCGCAATCAGTTCGTTGG
hum-R-35	GCGTTTTTGCGGATATAGGCCGCCATATCCTGGCC
hum-R-36	CATCCTGCAAATACGCTTCCAGATAGCGTTCCCAA
hum-R-37	GAATGTCGGAACGTGACCGGTGGCGATCCATTCGG
hum-R-38	CCGGTGTTGGGGGTGCCATTGTTCAGATATTCATC
hum-R-39	TAAGCAGCAACGGGATCAGATTAAGTACACACATA
hum-R-40	CTGTTCAAGAATATCGATCGGCAAGTGTTCGCCCA
hum-R-41	TCAATCAGATGGTGGAACCGGCTCGGCAGAAAGAT
hum-R-42	AATCTCTCGCATCATCGACCAGTCGGCTAGCCAGT
hum-R-43	GCAGGATAAATCACCATGATCTTTTTCGGCTTGAA
hum-R-44	GTTGATTCCGGATGGTCTTTCAGGTAGCATTCGAT
hum-R-45	GCAGGCCGTTGACGTGATTCAGGGCGTCTTCAACT
hum-R-46	AAATTTCCAATTCATTTCCAGCAAACAATTCCCCA
hum-R-47	TTACACGACAGAGGTACCGAGTCCTGTTTTTTCAG
hum-R-48	GAATCGACCGCGCCAGGACGTGGAATGAGTATTTT
hum-R-49	AATCGAAAACCCGTCCCCCTGGTTATACATAAACT
hum-R-50	ACTTTCTGGACCTGGTCTTTAATAACTTTGTTCGA
humXbaIR	GCTCTAGATTATATAGGAACCGGAACGATTAGA

All primers were purchased from OPERON.