

Sequences referred to in the present application

Table 2: Assignment of SEQ ID NOs.

SEQ ID NO:	type of sequence	description
1	nucleotide sequence	Gene sequence* 1,3- β -D-glucan synthase I of <i>S. commune</i> strain Lu15531
2	amino acid sequence	translation of SEQ ID NO: 5
3	nucleotide sequence	Gene sequence* 1,3- β -D-glucan synthase II of <i>S. commune</i> strain Lu15531
4	amino acid sequence	translation of SEQ ID NO: 7
5	nucleotide sequence	cDNA 1,3- β -D-glucan synthase I of <i>S. commune</i> strain Lu15531
6	amino acid sequence	polypeptide sequence 1,3- β -D-glucan synthase I of <i>S. commune</i> strain Lu15531
7	nucleotide sequence	cDNA 1,3- β -D-glucan synthase II of <i>S. commune</i> strain Lu15531
8	amino acid sequence	polypeptide sequence 1,3- β -D-glucan synthase II of <i>S. commune</i> strain Lu15531
9	nucleotide sequence	Gene sequence* 1,3- β -D-glucan synthase I of <i>S. commune</i> strain Lu15634
10	amino acid sequence	translation of SEQ ID NO: 13
11	nucleotide sequence	Gene sequence* 1,3- β -D-glucan synthase II of <i>S. commune</i> strain Lu15634
12	amino acid sequence	translation of SEQ ID NO: 15
13	nucleotide sequence	cDNA 1,3- β -D-glucan synthase I of <i>S. commune</i> strain Lu15634
14	amino acid sequence	polypeptide sequence 1,3- β -D-glucan synthase I of <i>S. commune</i> strain Lu15634
15	nucleotide sequence	cDNA 1,3- β -D-glucan synthase II of <i>S. commune</i> strain Lu15634
16	amino acid sequence	polypeptide sequence 1,3- β -D-glucan synthase II of <i>S. commune</i> strain Lu15634
17	nucleotide sequence	<i>tef1</i> promoter from <i>S. commune</i>
18	nucleotide sequence	<i>tef1</i> terminator from <i>S. commune</i>
19	nucleotide sequence	Ura_forw (NotI) primer
20	nucleotide sequence	Ura_rev (XbaI) primer
21	nucleotide sequence	TefP_forw (XbaI) primer
22	nucleotide sequence	TefP_rev (SpeI) primer
23	nucleotide sequence	TefT_forw (Sall) primer
24	nucleotide sequence	TefT_rev (Sall) primer

25	nucleotide sequence	TefT_forw (EcoRV) primer
26	nucleotide sequence	TefT_rev (ApaI) primer
27	nucleotide sequence	GS1_forw (SpeI) primer
28	nucleotide sequence	GS1_rev (Sall) primer
29	nucleotide sequence	Fusion TefP_GS1_forw (XbaI) primer
30	nucleotide sequence	Fusion TefP_GS1_rev (Sall) primer
31	nucleotide sequence	GS2_forw (SpeI) primer
32	nucleotide sequence	GS2_rev (EcoRV) primer
33	nucleotide sequence	<i>ura</i> gene (<i>S. commune</i>)
34	amino acid sequence	Ura protein

*Gene sequence includes introns and flanking regions. In the gene sequences below (for SEQ ID NOs. 1, 3, 9 and 11), predicted exons are shown in capital letters, introns are shown in lower case letters.

5

SEQ ID NO : 1

Gene sequence 1,3- β -D-glucan synthase I of *S. commune* strain Lu15531

DNA

S. commune

10 CCCGTCCCTCAAGGCCGTTCTTTCGCTGGCGACCGACCCGGTGTTGCGGAGAA
 CCTGTTGTTTCTGACGATCATCAGCCCTTTCTTCTCGTCGCTCTTTAGCTCTCCC
 TAGACCGTCTTTTACTCTACTCTTCGACGCACGCCATGTCCGGCCCAGGATATG
 GCAGGAATCCATTCGACAATCCCCGCCCAACAGAGGTCCCTATGGCCAGCAG
 CCAGGTTTCCCGGGGGCCCGGCCCTCGGCCTTACGACTCGGACGCGGACATGA
 15 GCCAGACCTATGGCAGCACAACCAGGCTCGCCGGCAGTGCCGGTTACAGCGA
 CAGAAACGgtgcgacgtcgctaccgtacttctcgatcgctgattcacataccatgcagGCAGCTTCGAC
 GGCGACCGCTCCTACGCGCCCTCAATTGACTCGCGCGCCAGCGTGCCCGAGCAT
 ATCGCCCTTCGCAGACCCGGGTATCGGCTCTAATGAGCCGTATCCCGCTTGGT
 CGGTGCAACGCCAGATTCCCATGTCCACGGAGGAGATTGAGGACATCTTCCTC
 20 GACCTCACCCAAAAGTTTGGCTTCCAGCGCGACTCCATGCGGAATACGgtgctga
 ataagcagcccactcgaccgcggaacagcacaattgacctgtcaccagTTCGACTTCATGATGCAC
 CTCCTCGATTCCCGTGCCTCGCGCATGACGCCCAACCAAGCTCTGCTCACGCTT
 CACGCCGACTACATTGGTGGCCAGCATGCCAATTACCGGAAGTGGTATTTCCGC
 GCACAGCTCAACCTCGATGACGCGGTGCGGCAAACCAATAACCCCGGTATCCA
 25 GCGCTTGAAGACCATCAAGGGCGCTACGAAGACCAAGTCGCTCGACAGCGCAC
 TCAACCGCTGGCGCAACGCGATGAACAACATGAGCCAGTACGATCGCCTCCGG
 CAAATTGCGCTCTACCTCCTCTGCTGGGGTGAAGCAGGCAACATCCGTCTGGC
 GCCCGAGTGCTTGTGCTTCATCTTCAAGTGCGCGGACGACTACTACAGAAGTCC
 CGAGTGTCAGAACCGGATGGACCCCGTGCCGGAAGGGCTGTACCTGCAGACG
 30 GTCATCAAGCCGCTCTATCGCTTCTACGTGATCAGGCGTACGAAGTCGTTGAT
 GGAAGCAAGTGAAGCGCGAGAAGGACCACGACCAGATTATCGGTTATGACGA
 CGTCAACCAGTTATTCTGGTATCCGGAAGGTTTGGCTAAGATCGTCATGTCGGA
 CAACgtgctgatgatcttatcggttaaaattcgctccgctcacatcttccagACACGACTTGTAGATGTAC
 CTCCGGCGCAGCGGTTTCATGAAGTTCGCCAAGATCGAGTGGAACCGCGTCTTC
 35 TTCAAGACGTACTTTGAGAAGCGCTCTACTGCCATCTCCTGGTCAACTTCAAC
 CGTATATGGATCCTCCACGTCTCGATGTACTTCTTCTACACGGCATTCAACTCTC
 CACGAGTCTACGCGCCGACGGCAAACCTCGACCCCTCCCCTGAGATGACCTGG
 TCCGCGACTGCCCTTGGAGGCGCTGTGTCCACCATGATCATGATCCTTGCCACT
 ATCGCGGAGTACACCTACATCCCCACGACATGGAACAATGCGTCGCACCTCAC

CACGCGGCTCATTTTCCTCCTGGTCATCCTCGCGCTCACTGCTGGCCCAACATT
CTATATCGCCATGATAGACGGACGCACGGACATCGGCCAAGTACCACTCATCGT
GGCCATAGTGCAGTTCTTCATCTCCGTCGTCGCCACCCTCGCTTTGCTACCAT
CCCTTCTGGTCGCATGTTCCGGCGACCGTGTGGCTGGCAAGTCAAGAAAGCACA
5 TGGCATCGCAGACGTTACAGCGTCGTACCCGTCCATGAAGCGGTCATCTCGC
GTAGCGAGTATCATGCTGTGGCTTTTGGTCTTTGGCTGCAAATACGTCGAGTCT
TACTTCTTCTTGACGTCCTCCTTCTCCAGCCCGATCGCGGTTCATGGCGCGTACG
AAGGTACAGGGCTGCAACGACCGTATCTTCGGCAGCCAGCTGTGCACGAATCA
GGTCCCGTTTCGCGCTGGCAATCATGTACGTGATGGACCTGGTACTGTTCTTCT
10 GGACACGTACCTGTGGTACATCATCTGGCTGGTGATCTTCTCGATGGTGCGCG
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TGCCGAAGCGTATTTACGCAAAGCTGCTGGCGACGGCCGAGATGGAGGTCAAG
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15 CATCGAGCACGTCCAGCGCTTGCTTTACCACCAGGTTGATGGTCCCGATGGCC
GCCGCACCCTCAGGGCACCGCGCTTCTTCACCAGCCAGCGAACTGCGAAGCCA
GGCCTGTTCTTCCCTCCTGGTGGCGAGGCTGAGCGCCGCATCTCGTTCTTTGC
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CCTTCACCGTGCTCGTTCCCCATTACTCCGAGAAGATTCTGCTCAGTCTGCGCG
20 AGATTATCCGCGAGGAGGACCAGAACACCCGCGTTACCTTACTGGAGTACCTCA
AGCAGCTCCACCCTGTCTGAATGGGACAATTTCTGTCAAGGACACCAAGATCTTGG
CGGAAGAGTCGGGAGACGTCCAGGACGAGAAGCGCGCGCGCACGGACGACTT
GCCGTTCTATTGCATCGGGTTCAAGACCTCGTCACCAGAGTACACCCTGCGTAC
GCGTATCTGGGCCTCACTGCGCGCACAGACGCTGTACCGCACGGTCTCCGGTA
25 TGATGAACTACTCCAAGGCGATTAAGCTCCTCTATCGCGTCGAGAACCCGGATG
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ATGTCTCGCCGCAAGTTCAAGTTCTGTCATCTCGATGCAGCGGTACTCCAAGTTC
AACAAGGAGGAGCAGGAGAACGCCGAGTTCTTCTGCGCGCGTACCCGGATTT
GCAGATCGCGTACCTCGATGAAGAGCCCGGTCCCAGCAAGAGCGACGAGGTT
30 GGTGTTTTTCGACACTCATCGACGGACACTCCGAGGTGGACGAGAAGACGGGC
CGCCGCAAGCCCAAGTTCCGCATCGAGCTGCCCGGTAACCCCATCCTCGGTGA
CGGGAAGTCGGATAACCAGAACCACGCCATCGTCTTCTACCGCGGCGAGTACA
TTCAGGTCAATTGACGCTAACCCAGGACAATTACCTGGAAGAGTGTCTCAAGATCC
GTAATGTCTTGGGCGAGTTTGAGGAATACTCCGTGTGCGAGCCAGAGCCCGTAC
35 GCGCAGTGGGGCCACAAGGAGTTCAACAAGTGCCCCGTGCTATCCTGGGTTC
CCGCGAGTACATCTTCTCGGAGAACATCGGTATCCTCGGTGACATCGCTGCCG
GCAAGGAACAGACGTTCCGTACCATACGGCGCGTGCCTTGCGTGGATCGGC
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CGTGGTGGCGTGTCAAAAGCGCAGAAGGGCTTGCATCTTAACGAGGATATCTTC
40 GCTGGTATGACCGCCGTGTCCCGCGGAGGGCGCATCAAGCACATGGAGTACTA
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CTGGGCACGCAATTGCCTATCGACCGGTTCTTGACGTTCTACTACGCGCACGCT
GGTTTCCATGTCAACAACATCCTGGTCATCTACTCCATCCAGGTCTTCATGGTCA
45 CCCgtaagtgcaggccctcatgaccgccgagcaagcagcttaacggatgtgcagTGCTGTACCTGGGC
ACATTGAACAAGCAGCTGTTTCATCTGCAAGGTCAACTCCAATGGCCAGGTTCTT
AGTGGACAAGCTGGGTGCTACAACCTCATCCCGGTCTTCGAGTGGATTCGCCG
GAGTATCATCTCCATCTTCTTGGTGTTCCTTCATCGCCTTCTTGCCGTTGTTCTTG
CAAGgtatgttcacttctcatgtgccatttgaatcgctcactcgtagacagAGCTTTGCGAACGCGGA
50 ACAGGAAAGGCGTTGCTGCGTCTCGGGAAGCACTTCCTGTCACTGTCGCCCAT

CTTCTGAAGTGTCTCCACCCAAATCTACTCGCAGGCGCTCTTGAACAACATGAG
 TTTCGGTGGTGC GCGCTACATCGCTACAGGACGCGGTTTCGCGACGAGTCGGA
 TACCCTTCAACATCCTCTACTCGCGTTTCGCGCCGCGGAGCATCTACATGGGCA
 TCGTAATCTGCTGCTCTTGCTGTACGCGACGATGGCCATTTGGATCCCACACC
 5 TGATCTACTTCTGGTTCTCCGTCTCTCCCTCTGCATCGCGCCATTTCATGTTCAA
 TCCGCATCAATTCTCGTACGCTGACTTCATCATCGACTACCGGGAGTTCTTGCG
 CTGGATGTCGCGCGGTAAGTCTCGCGGACGAAGGCGAGTAGCTGGTACGGATATT
 GCCGTCTGTGCGGTACCGCGATTACTGGGTACAAGAAGAAGAACTGGGACAC
 CCGTCGGAGAAGCTGTGCGGGCGATGTGCCGCGTGCGCCGTGGAGGAACGTCA
 10 TCTTCTCGGAGATCCTTTGGCCCATCGGCGCGTGCATCATCTTCATCGTCGCGT
 ACATGTTTCGTCAAATCGTTCCCTGACGAGCAGGGCAACGCGCCGCGGAGCCCG
 CTGGTCCGCATTCTGCTCATCGCGGTTGGCCCTACTGTGTGGAACGCGGCGGT
 GCTCATCACGCTGTTCTTCTGTCGCTCTTCTGGGCCCGATGATGGATGGCTG
 GGTCAAGTTCGGCTCAGTCATGGCGGCACTTGCGCATGGTCTAGCGCTCATAG
 15 GCATGCTCACGTTCTTCGAGTTCTTCgtacgtccttcggtgtgtgtgagtgcttgcacacccg
 ccttcagTGGTTCCTCGAGCTCTGGGATGCCTCGCACGCCGTGCTCGGCGTCATC
 GCCATTATTGCCGTTTACGCGCGGGATCCAGAAGATCCTCATTGCCGTCTTCTG
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 GTATGGACGCGGGGCTGGGTACCTCGGCCATGTCCCAGCCGGCGCGCGAGTTC
 20 ATCGTGAAGATCGTGGAGATGTGCGTGTGGACGTCGGACTTCCTGCTTGCGCA
 CCTGTTGCTCATCATCTTGACGGTGCCGCTACTGCTGCCGTTCTTCAACTCGAT
 CCATTTCGACGATGCTTTgtgagtgattgtagtcgttggtcacggatgattgctgactcgctgcagTCTG
 GTTGCGCCCTTCGAAGCAGATTAGGCAACCTCTGTTCTCCACTAAGCAGAAGCG
 GCAACGGCGATGGATTgtaagttccttgattgctctggtaccgaccttcgctcacctgtctcagGTCATG
 25 AAGTATACCGTGGTATATCTCGTGGTGGTGGCTTTCCTCGTTGCGCTCATCGCT
 CTGCGtacgtttctgtcgcgctcacctctattttcactaacgtttcctccagCCGCGCTCTTCCGCGAGA
 GCATCCACTTCAACTGCGAGATCTGCCAGAGTATATAGTCATATAACGACGTCTA
 TCGTATCGCCGGACGAGAGCCCCGTGCGCTACACACTGACATGGAATTGCTGT
 GTATACAATCGATCTTCTGACCGCGTCGGGGGCGTTGCCGTCTTCTACTATCA
 30 ACTTGCTTGTGTATCAACATTTCTTCTCTCCAAGCCTACATTGACATAGAGTAATA
 GCCCATGTTCATACAACAATCGCATAGCATTGCATATACCAT

SEQ ID NO: 2

35 Translation of SEQ ID NO: 5

amino acid

S. commune

MSGPGYGRNPFDPNPPNRPYPYGGQPGFPGPGRPYDSADMSQTYGSTTRLAG
 SAGYSDRNGSFDGDRSYAPSIDSRASVPSISPFADPGIGSNEPYPAWSVERQIPMS
 40 TEEIEDIFDLTQKFGFQRDSMRNTFDFMMHLLDSRASRMTPNQALLTLHADYIGGQ
 HANYRKWYFAAQLNLDDAVGQTNNPQIRLKTIKGATKTKSLDSALNRWRNAMNN
 MSQYDRLRQIALYLLCWGEAGNIRLAPECLCFIFKCADDYYRSPECQNRMDPVPEG
 LYLQTVIKPLYRFLRDQAYEVVDGKQVKREKDHDQIIGYDDVNQLFWYPEGLAKIVM
 SDNTRLVDVPPAQRFMKFAKIEWNRVFFKTYFEKRSTAHLLVNFNRIWILHVS MYFF
 45 YTAFN SPRVYAPHGKLDPSPEMTWSATALGGAVSTMIMILATIAEYTYIPTTWNNAS
 HLTTTRLIFLLVILALTAGPTFYIAMIDGRDIDIGQVPLIVAIVQFFISVVATLAFATIPSGRM
 FGDRVAGKSRKHMASQTFTASYPMSMKRSSRVASIMLWLLVFGCKYVESYFFLTSSF
 SSPIAVMARTKVQGCNDRIFGSQLCTNQVPFALAIMYVMDLVLF LD TYLWYIWLVI
 FSMVRAFKLGISIWTPWSEIFTRMPKRIYAKLLATAEME VKYKPKVLVSQIWNNAVIISM
 50 YREHLLSIEHVQRLLYHQVDGPDGRRTL RAPPFFTSQRTAKPGLFFPPGGEAERRIS

FFASSLTTALPEPLPIDAMPTFTVLVPHYSEKILLSLREIIREEDQNTRVTLLEYLKQLH
PVEWDNFKVDTKILAEESGDVQDEKRARTDDLFPYCIGFKTSSPEYTLRTRIWASLR
AQTLYRTVSGMMNYSKAIKLLYRVENPDVVHAFGGNTERLERELERMSRRKFKFVI
5 SMQRYSKFNKEEQENAEFLRAYPDLQIAYLDEEPGPSKSDEVRLFSTLIDGHSEVD
EKTGRRKPKFRIELPGNPILGDGKSDNQNHAI VFYRGEYIQVIDANQDNYLEECLKIR
NVLGEFEEYSVSSQSPYAQWGHKEFNKCPVAILGSREYIFSENIGILGDIAAGKEQTF
GTITARALAWIGGKLHYGHPDFLNATFMTTRGGVSKAQKGLHLNEDIFAGMTAVSR
GGRIKHMEYYQCGKGRDLGFGTILNFQTKIGTGMGEQLLSREYYYLGTLQPIDRFLT
10 FYYAHAGFHVNNILVIYSIQVFMVTLTYLGTLNKQLFICKVNSNGQVLSGQAGCYNLI
PVFEWIRRSIISIFLVFFIAFLPLFLQELCERGTGKALLRLGKHFLSLSPIFEVFSTQIYS
QALLNNMSFGGARYIATGRGFATSRIPFNILYSRFAPPSIYMGMRNLLLLLYATMAIW
IPHLIYFWFSVLSLCIAPFMFNPHQFSYADFIIDYREFLRWMSRGNRSRTKASSWYGY
CRLSRTAITGYKKKKLGHHPSEKLSGDVPRAPWRNVIFSEILWPIGACIIFIVAYMFVKS
FPDEQGNAPPSPLVRILLIAVGPTVWNAAVLITLFFLSLFLGPMMDGWVKFGSVMMAA
15 LAHGLALIGMLTFFEFFWFLELWDASHAVLGVIHIAVQRGIQKILIAVFLTREYKHDET
NRAWWTGKWYGRGLGTSAMSQPAREFIVKIVEMSLWTSDFLLAHLIIIITVPLLLP
FFNSIHSTMLFWLRPSKQIRQPLFSTKQKRQRRWIVMKYTVVYLVVVAFLVALIALPA
LFRESIHFNCEICQSI

SEQ ID NO: 3

Gene sequence 1,3- β -D-glucan synthase II of *S. commune* strain Lu15531

DNA

S. commune

25 CTGTCCAAAGAAGAGATCGAGGACATCTTCCTCGATCTGACGCAGAAGTTTGGC
TTTCAGCGGGATTCCATGCGGAACATGgtacgtggcgtatgcccgtgctgaggcctaa
acgttttccgccagTTCGACTTCACCATGCAGCTGCTTGACAGCCGAGCGTCTCGTATG
ACCCCCAACCAGGCGCTCCTCACCTCCACGCCGACTACATTGGTGGCCAGCA
TGCGAACTACCGGAAGTGGTACTTCGCGGCGCAGCTCGACCTTGACGACGCCG
30 TGGGACAAACTCAGAATCCGGGTCTCAACCGCCTCAAGTCCACTCGCGGATCG
GGCAAGCGACCACGCCATGAAAAGTCGCTGAACACGGCATTGGAGCGCTGGC
GGCAAGCCATGAACAACATGTCGCAGTATGACCGCTTACGCCAGATCGCGCTC
TACCTGCTCTGCTGGGGCGAAGCGGCGCAAGTGCGATTTCATGCCCCGAGTGCTT
GTGCTTCATCTTCAAGTGCGCCGACGACTATTATCGTTGCGCCGAGTGCCAGAA
35 CAGGATGGAGCCGGTACCGGAGGGTCTCTACCTGAGGACGGTTCGTAAAGCCG
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CGGCGGGGAACGGGATCACGACCAAATCATTGGTTACGATGACGTGAATCAGCT
GTTCTGGTACCCGGAGGGCATTGCCCCGTATCGTCCTGTCGGACAAGGtaagcacctc
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40 CAGCGCTTCATGAAGTTCGACCGTATCGAGTGGAATCGCGTCTTCTTCAAGACG
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TCGTGCACATCGCTCTCTACTTCTTCTACACCGCATACTCCCCACGATCTA
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45 CACATCCCCACGACATGGAACAACACCTCGCATCTGACTCGCCGCCTCGCCTTC
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GAGAGCAACGGGAGCGGGCGGCTCTTTGGCCTTGATTCTCGGCATCGTCCAGTT
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50 TCACGGCCAGCTACCCGTCGTTGCCCAAGCACCAGCGGTTTCGCATCACTCCTG

ATGTGGTTCCTCATCTTCGGGTGCAAGTTGACGGAGAGTTACTTCTTCCTGACG
TTGTCCTTCCGCGACCCCTATTCGCGTCATGGTCGGCATGAAGATCCAGAACTGC
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CACGATCATGTACATCATGGACCTCGTCTTGTTCTTCCTCGACACCTTCCTTTGG
5 TATGTCATCTGGAACCTCGGTTTTAGTATCGCACGCTCTTTCGTA CTCTCGGCCTTT
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20 GTCCTTGCGCGCGCAGACCCTCTACCGCACGGTCTCCGGCATGATGAACTATG
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25 TACCTGGAGGAAGAGCCTCCTCGCAAGGAGGGTGGCGATCCACGCATCTTCTC
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35 GTCTCCAAGGCGCAGAAGGGTCTCCATCTCAACGAGGATATTTACGCCGGTATG
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CAAGGGTCTGTGACCTCGGTTTTGGCACCATCTTGAAGTTCCAGACCAAGATCGG
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40 TCAACAACATGCTGGTTATCCTATCCGTGCAGGTCTTCATCGTTACCAgtacgttgatt
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45 acctgctcaagggccttgcgctgatcatcatctcagAACTCGTCGAGCGCGGTACCTGGAGTGCC
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50 ATGCTGCTCTACGTGACGTTGACGATCTGGACGCCATGGGTCAATTACTTCTGG

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 10 CATGCTCGACCCGGTCTTCCCCCTCTTCGGTTCCGTTATGGCCTTCATCGCGCA
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 CGCTCATCGCGCTTCgtgagtaccctgtctatctttgtacgtgagcgtcgctgaccctttccagCCCTC
 GTCTTCCGACACACTCTAAAGGTCGAGTGCTCCCTTTGCGACAGCTTGTAATAT
 CGGACTCGTATATATCTAGACTTCTCCGCACCATGTGTAGCTGACGCTTGGGTA
 25 TACTTCGCGGTGCCGAGCTAATTGTGCGACGGACATTCTCCATCGTTGAGTGCAG
 CGACATCGGGTGGTTTACGACACGGACACTTTTCATTGTACCCTCTACGAATGC
 AAGAACTCTCTTACGACCAGTACCTATGTGCTAAGCCGTCGCCTGTTTCAGGATC
 ATACATACATACGTTTCTAGATACCTTACAGTTAGGCCTATTACAGGGAGAGTCTG
 CATAAAA
 30

SEQ ID NO: 4

Translation of SEQ ID NO: 7

amino acid

35 *S. commune*
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5 AHPGFQINNMLVILSVQVFIVTMVFLGTLKSSVTICKYTSSGQYIGGQSGCYNLVPVF
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10 LDGKQPPSGLVRIAVVSIGPIVWNAAILLTFLVSLFLGPMLDPVFPLFGSVMAFIAHF
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SEQ ID NO: 5cDNA 1,3- β -D-glucan synthase I of *S. commune* strain Lu15531

DNA

S. commune

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25 ACTCATCGACGGACACTCCGAGGTGGACGAGAAGACGGGGCCCGCCGAAGCCC
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SEQ ID NO: 6

polypeptide sequence 1,3- β -D-glucan synthase I of *S. commune* strain Lu15531
amino acid

S. commune

25

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5 LFRESIHFNCEICQSI

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SEQ ID NO: 7cDNA 1,3- β -D-glucan synthase II of *S. commune* strain Lu15531

DNA

S. commune

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5 CCTCGTCTTCCGACACACTCTAAAGGTCGAGTGCTCCCTTTGCGACAGCTTGTA
A

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SEQ ID NO: 8polypeptide sequence 1,3- β -D-glucan synthase II of *S. commune* strain Lu15531

15 amino acid

S. commune

MRNMFDFTMQLLDSRASRMTPNQALLTLHADIYGGQHANYRKWYFAAQLDLDDAV
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SEQ ID NO: 9Gene sequence 1,3- β -D-glucan synthase I of *S. commune* strain Lu15634

50 DNA

S. commune

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15

SEQ ID NO: 10

translation of SEQ ID NO: 13

amino acid

S. commune

20

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50

SEQ ID NO: 11Gene sequence 1,3- β -D-glucan synthase II of *S. commune* strain Lu15634

DNA

5 *S. commune*

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SEQ ID NO: 12

translation of SEQ ID NO: 15

15 amino acid

S. commune

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VIYFWVSILSLCIA PFLFNPHQFVFSDFLIDYREYLRWMSRGNRSRSHNNNSWIGYCRL
SRTMITGYKKKKLGH PSEKLSGDVPRAGWRAVLFSEIIFPACMAILFIIAYMFVKSFPL
DGKQPPSGLVRIAVVSIGPIVWNAAILLTFLVSLFLGPM LDPVFPFLFGSVMAFIAHFL
45 GTIGMIGFFEFLWFLESWEASHAVLGLIAVISIQRAIHKILIAVFLSREFKHDETNRW
WTGRWYGRGLGTHAMSQPA REFVVKIIELSLWSSDLILGHILLFMLTPAVLIPYFDR
HAMMLFWLRPSKQIRAPLYSIKQKRQRWRWIIMKYGT VYVTVIAIFVALIALPLVFRHTL
KVECSLCDSL

50

SEQ ID NO: 13cDNA 1,3- β -D-glucan synthase I of *S. commune* strain Lu15634

DNA

S. commune

5 ATGTCCGGTCCAGGATATGGCAGGAATCCATTGACAATCCCCCGCCCAACAG
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5 CGGTGGGAACACGGAACGTCTTGAACGCGAGCTTGAGCGCATGTCTCGCCGCA
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50 CAAGCAGAAGCGGCAACGGCGATGGATTGTCATGAAGTATACCGTGGTATATCT

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5 **SEQ ID NO: 14**

polypeptide sequence 1,3- β -D-glucan synthase I of *S. commune* strain Lu15634
amino acid

S. commune

MSGPGYGRNPFDPNPPNRPYPYGGQPGFPGPRPYDSADMSQTYGSTTRLAG
10 SAGYSRNGSFDGDRSYAPSIDSRASVPSISPFADPGIGSNEPYPAWSVERQIPMS
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15 SDNTRLVDVPPAQRFMKFAKIEWNRVFFKTYFEKRSTAHLLVNFNRIWILHVS MYFF
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20 FSMVRAFKLGISIWTPWSEIFTRMPKRIYAKLLATAEME VKYKPKVLVSQIWNNAVIISM
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35 FPDEQGNAPPSPLVRILLIAVGPTVWNAAVLITLFFLSLFLGPMMDGWVKFGSVMAA
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40

SEQ ID NO: 15

cDNA 1,3- β -D-glucan synthase II of *S. commune* strain Lu15634

DNA

45 *S. commune*

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SEQ ID NO: 1650 polypeptide sequence 1,3- β -D-glucan synthase II of *S. commune* strain Lu15634

amino acid

S. commune

MPRPGGTS AEGGYASSPSMETTPSDPFGTANGAPRRYYDNDSEEGPGRRD TYA
 SDSSNQGLTDPGYDQNGAYDPYPTGDTSDGDVYGQRYGPSAESLGTHKFGHS
 5 DSSTPTFVDYSASSGGRDSYPAWTAERNIPLSKEEIEDIFDLTQKFGFQRDSMRN
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 20 SKFNKEEHENAEFLLRAYPDLQIAYLEEEPPRKEGGDPRIFSALVDGHS DIIPETGKR
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 EEYDVSSQSPYAQWSVKEFKRSPVAIVGAREYIFSEHIGILGDLAAGKEQTFGT LTA
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 30 DGKQPPSGLVRIAVV SIGPIVWNAAILLTLFLVSLFLGPM LDPVFPLFGSVMAFIAHFL
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 KVECSLCDSL

35

SEQ ID NO: 17*tef1* promoter

DNA

40 *S. commune*

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 TCTCGTCTCTCACTCTTCCCCCCTCCACCACTACCAAGTAAGTTCAAACCTTCCTC
 50 TCATCGCCTTTGCACACATCGCCTACGCCCCATCTCTCTCCATCTGCCTCGCGA

ACGGCGCCCCCATCGTCGCTTTCCCGCGCGAGATCTTGTGCGATCTAGTTTACT
GACAATCTCACCTAGAAAACATCAAA

5 **SEQ ID NO: 18**

tef1 terminator

DNA

S. commune

ATCCAAGTCCGGTGGCAAGGTCACCAAGTCCGCCGAGAAGGCCGCCAAGAAGA
10 AGTAAATGTAGATGTACATATGTATTTTCTCATTCCGTTTCCTTCCTCTTGTTGTT
GTTTCACTGGTCCTCTCGTGCTCGCTCGCATCGCATACAGCCATTGTTGTCACC
ACTATAACTTCACGCATTCTGTATTTTCATGCCAGGCGACGGGGTGTTCCCTGCCA
GGCCTGTGCTTGTGTTGTAACGCTAATGAAAAGTCACGAGTAGTGGACGAACGAC
GATGTATTTCTATGTGCTGTAGCGATTATCCATTTTCGAGTTCGCCATCGAGCTCT
15 CTTCAAACCTAGGTGCGACGTTGTGAATGCAGTAGCAAGTGCAGAGTATTGCAG
ACTCGTCCATTGATGATAACTTCAAGCTACGTCAGAGCCAGATGCTACTGAACC
CGGGCC

20 **SEQ ID NO: 19**

Ura_forw (NotI) primer

DNA

artificial

ATAAGAATGCGGCCGCTCCAGCTCGACCTTGCGCCG

25

SEQ ID NO: 20

Ura_rev (XbaI) primer

DNA

artificial

30 CTAGTCTAGAGGATCCGACGTGGAGGAGCC

SEQ ID NO: 21

TefP_forw (XbaI) primer

35 DNA

artificial

CTAGTCTAGAATCGCCATTGTAAGCCGCAG

40 **SEQ ID NO: 22**

TefP_rev (SpeI) primer

DNA

artificial

CTAGACTAGTTTTGATGTTTTCTAGGTGAG

45

SEQ ID NO: 23

TefT_forw (Sall) primer

DNA

50 artificial

ACGCGTCGACCAAGTCCGGTGGCAAGGTCA

SEQ ID NO: 24

5 TefT_rev (Sall) primer
DNA

artificial

CCGACGTCGACGGGTTCAGTAGCATCTGGCT

10

SEQ ID NO: 25

TefT_forw (EcoRV) primer
DNA

artificial

15 CATGGTGATATCCAAGTCCGGTGGCAAGGTCA

SEQ ID NO: 26

20 TefT_rev (ApaI) primer
DNA

artificial

CCGTATGGGCCCCGGGTTCAGTAGCATCTGGCT

25

SEQ ID NO: 27

GS1_forw (SpeI) primer
DNA

30 artificial

CTAGACTAGTCCCGTCCCTCAAGGCCGTTT

SEQ ID NO: 28

35 GS1_rev (Sall) primer
DNA

artificial

AATGGCCGACGTCGACATGGTATATGCAATGCTATG

40

SEQ ID NO: 29

Fusion TefP_GS1_forw (XbaI) primer
DNA

artificial

45 CTAGTCTAGAATCGCCATTGTAAGCCGCAG

SEQ ID NO: 30

50 Fusion TefP_GS1_rev (Sall) primer
DNA

artificial

AATGGCCGACGTCGACATGGTATATGCAATGCTATG

5 **SEQ ID NO: 31**

GS2_forw (SpeI) primer

DNA

artificial

CTAGACTAGTCTGTCCAAAGAAGAGATCGA

10

SEQ ID NO: 32

GS2_rev (EcoRV) primer

DNA

15 artificial

TACATGCGATATCTTTTATGCAGACTCTCCCTG

SEQ ID NO: 3320 *ura* gene

DNA

S. commune

TCCAGCTCGACCTTGCGCCGCTTGGAGTAACGTTTCAGCGTCTTCGTCTCCTCG

TCGCGCTCGTGTACGATGATGGGCTCAGCCATGGCAGGTATACAAGCTCAGAG

25 TCAATGGGGGACGAGGTCTCAAGCCGTGAAAGTCGTCTCGTCAACAACGTCAAG

TTCGAGACGGACCAGAGTTGGATTTCTGTGATTAGATCTACGCTCGATCACAGAA

TGATCAAAGAACAAAGCTTGCCAAAAGGGGATCTCCCATCAACTTCAACTTGCC

CCAAACCATCATGACCGCCGCTCATAAGCTCACATACGGTCAGCGCGCTGCAA

GGTTCACCAATCCCGCGGCGAAAGCCCTGCTGGAAACCATGGAGCGCAAGAAG

30 AGCAATCTATCCGTCAGCGTCGACGTCGTAAAATCCGCCGATCTGCTCGCTATT

GTCGATACCGTCGGGCCCTATATCTGTCTGATAAAGGCATTGCACTGTCTGCTTG

CGGTCTTGGGATGCTGCTTATACTCTATGAAGACCCATGTGGATGTTGTCTGAAG

ACTTCGACTCGTCGCTCGTCACCAAGCTTCAGGCTCTGGCCGAGAAGCATGATT

TCCTCATCTTTGAGGACAGAAAATTGCGCGACATAGGTCTGTCCGTCTGAATCTC

35 TATCGATGTCAACTCTGATGACTTGCACAGGCAACACCGTCGCTCTGCAGTACT

CTAGTGGCGTGCACAAAATTGCCAGCTGGTCGCACATCACGAACGCACACCCT

GTTCCAGGACCGTCAATCATCAGTGGCCTCGCATCGGTAGGACAACCCCTCGG

TCGCGGACTCCTCCTGCTCGCAGAGATGAGCACGAAGGGCTCACTTGCGACAG

GCGCGTACACTGAAGCCGCCGTCCAGATGGCAAGGGAGAACC GCGGCTTCGT

40 CATCGGGTTCATCGCCCAACGGCGGATGGATGGTATTGGCGCGCCTCCAGGG

GTGAATGTCGAGGACGAGGATTTTCTTGTCTTGACACCAGGTGTCGGACTCGAT

GTGAAGGGCGATGGGATGGGGCAGCAATACAGGACGCCGAAGCAAGTGGTAC

AGGAAGATGGGTGCGATGTAATCATCGTGGGTCGCGGGATTTATGGCAAGGAC

CCATCGAAGGTGGAAGAGATACGGAGGCAGGCAGAGCGTTACCAGGCTGCAG

45 GATGGGCGGCGTACATTGAGAGGGTCAACGCCTTGGTATAGCTAATCTGATCG

GTGTTGTCTTGTTAAGCGTCAGGCTCAATGGAACGCTTTGGACGAGCGGAGAGT

AACTTGAATTAGCAGTGTATACTTCGGGCAAATCAATCGTGATAAATACAAGAGC

ACGCTCACGCACGTCCAATCTCCCTCAAATCTCCATCTTTCTCGCCTCATTCAC

CTTCCTGAACCCAGCCGGCGACATCTCGAACAGACCATGCCACCCGACAGCG

50 CACGCAGCCTATTCGAGTAGTCCAGCATCCGGCTGAGCGGCGCCACCGCCTGC

ACCGCGCGCTTCATCTTCACGCCCGCCGCCTCCCTCGCCGCAGTGCCGCCAGA
GGGCGACACCCACTCCGGGGGACGTACACGCCGTCCGCAGGGTACGGCTCC
TCCACGTCGGATCC

5

SEQ ID NO: 34

Ura protein

amino acid

S. commune

10

MTAAHKLTYGQRAARFTNPAAKALLETMERKKSNLSVSVDVVKSAADLLAIVDTVGPY
ICLIKTHVDVVEDFDSSLVTKLQALAEKHDFLIFEDRKFDIGNTVALQYSSGVHKIAS
WSHITNAHPVPGPSIISGLASVGQPLGRGLLLAEMSTKGSLATGAYTEAAVQMARE
NRGFVIGFIAQRRMDGIGAPPGVNVEDEDFLVLTGPVGLDVKGDGMGQQYRTPKQ
VVQEDGCDVIIVGRGIYKDPKVEEIRRQAERYQAAGWAAYIERVNALV

15