

(a)

Partial Cyp51 sequence -----FVAFVILSVVLNVANQILLKNPNEPPVVFHFLFPLIGSTVEYGDPPRRFFKKMRA 54  
Cyp51 sequence by WGS **MGVVFQQAIEPLQEAFAQQLGIASQGVVAFVAFVILSVVLNVANQILLKNPNEPPVVFHFLFPLIGSTVEYGDPPRRFFKKMRA 81**

KYGDVFTFILLGKKTTCVCGTKGNDFILNGKLRVNAEEITYVLTTPVFGDRDVVYDCPNAKLMQKQKFMKASLTDDAFRSY 135  
KYGDVFTFILLGKKTTCVCGTKGNDFILNGKLRVNAEEITYVLTTPVFGDRDVVYDCPNAKLMQKQKFMKASLTDDAFRSY 162

VPITGEVQNYFKNNPNFKGNSGTMNVAKAMAQITITFASHSLQGKEIRDQFDETLADLYHDLDMGFPTINFLHWAPLPW 216  
VPITGEVQNYFKNNPNFKGNSGTMNVAKAMAQITITFASHSLQGKEIRDQFDETLADLYHDLDMGFPTINFLHWAPLPW 243

NKKRDHAQRTVAKIYMNTIKKRREEGRTEGLDVMRSLMNSTYKSGVKVPDHEIAHMMIALLMAGQHSSSSTSAWIMLRLAQ 297  
NKKRDHAQRTVAKIYMNTIKKRREEGRTEGLDVMRSLMNSTYKSGVKVPDHEIAHMMIALLMAGQHSSSSTSAWIMLRLAQ 324

NPHIMEELYQEQRVRLGADLPLQYEDLAKLPLNQAIIKETLRMHAPIHSIMRAVKSMPMPVPGSKWV IPTSHTLLAAPGLS 378  
NPHIMEELYQEQRVRLGADLPLQYEDLAKLPLNQAIIKETLRMHAPIHSIMRAVKSMPMPVPGSKWV IPTSHTLLAAPGLS 405

ASDPQYFPNPDLDWPHRWEQDSPNAPTIVRQIEEEDDEKIDYGYGLVSKGAGSPYLPFGAGRHRICIGEHFANVQLQTVAN 459  
ASDPQYFPNPDLDWPHRWEQDSPNAPTIVRQIEEEDDEKIDYGYGLVSKGAGSPYLPFGAGRHRICIGEHFANVQLQTVAN 486

IVRMFKFRNVDSNTIGTDYQSLFSRPLEPC----- 491  
IVRMFKFRNVDSNTIGTDYQSLFSRPLEPC**NIHWELRDEA** 528

(b)

Partial Fks1 sequence -----MSGYADGGRCQYDDGYGRPNDDQEQYYQQDQYYDSNGYNGQQGGDGYDESQYINADPNPNYHQDGGYDGHQYQDEYYNDG 85  
Fks1 sequence by WGS -----MSGYADGGRCQYDDGYGRPNDDQEQYYQQDQYYDSNGYNGQQGGDGYDESQYINADPNPNYHQDGGYDGHQYQDEYYNDG 85

AYHDQDYNQGGAGLRHGSHEDETFSDFTTRGGDMDYHGGDERYNSYNDGQMGSRGYPSSQIYANRSGGASTPNYGM DY 170

GNALPAGQRSREPYPAWTSDSQIPLSKEEIEDIFIDLTSKFGQRDSMRNMYDHFMTLLDSRASRMTPNQALLSLHADYIGGDNA 255

NYRKWYFAAHLDDAVGFAANMKKGLRRSRKIKKKKNDDEEGQTEAELQGMEDDLSLAAEYRWKTRNMRMSQHDRVQIALYLL 340

-----RFMPECLCFIKCADDYLNSPACQNLVEPVEEFTYLNVIITPLYQYIRDQCYELDGVYVREKDHQNTIGYDDCNO 77  
**CWGEANQVRFMPECLCFIKCADDYLNSPACQNLVEPVEEFTYLNVIITPLYQYIRDQCYELDGVYVREKDHQNTIGYDDCNO 425**

LFWYPEGIERIVMEDKTRLDVPPAERYLKLKDVVWKKCFKTYKETRSHWHLVNFNRIWIHLTMFWFYTSNAPSLVLGSA 162  
LFWYPEGIERIVMEDKTRLDVPPAERYLKLKDVVWKKCFKTYKETRSHWHLVNFNRIWIHLTMFWFYTSNAPSLVLGSA 610

KQRENNQPPASKQWSVVAIGGAIALIQLATLAEWAYYPRRWAGAQHLTKRLLFLIVFVINVAPSVYIFGFKEPILKENIAKI 247  
KQRENNQPPASKQWSVVAIGGAIALIQLATLAEWAYYPRRWAGAQHLTKRLLFLIVFVINVAPSVYIFGFKEPILKENIAKI 595

LGIVQFFIALATFLFSSVMPGLGGLFGSYLTKNSRRYVASQTFATASYPRLRGNDMAMSYGLWLIVFGIKFGVSYAYLTL SFRDPIR 332  
LGIVQFFIALATFLFSSVMPGLGGLFGSYLTKNSRRYVASQTFATASYPRLRGNDMAMSYGLWLIVFGIKFGVSYAYLTL SFRDPIR 680

YLSIMDIQCHGDALFGKVLCEQPSILLGLMAFTDLLFFLDYLYFVLANLTF SFARSFYLGSLLWTPWRNVYARLPKR IYSKI 417  
YLSIMDIQCHGDALFGKVLCEQPSILLGLMAFTDLLFFLDYLYFVLANLTF SFARSFYLGSLLWTPWRNVYARLPKR IYSKI 765

LATTDMEIKYKPKVLSQIWNAAIIVISMYREHLLAIDHVQKLLYHQVPSQEGKRTLRAPTFFVSDQEDHSFKTEFFPAHSEADRRLL 502  
LATTDMEIKYKPKVLSQIWNAAIIVISMYREHLLAIDHVQKLLYHQVPSQEGKRTLRAPTFFVSDQEDHSFKTEFFPAHSEADRRLL 850

SFFAQSLSTPIPEPLPVDNMPFTVLIPHYSEKILLSLREIIREDEPYSRVTLLEYLQKLPHEWDCFKVDTKILADETSQFNGD 587  
SFFAQSLSTPIPEPLPVDNMPFTVLIPHYSEKILLSLREIIREDEPYSRVTLLEYLQKLPHEWDCFKVDTKILADETSQFNGD 935

YEKNEKDSAKSKIDDLPFYCFIKGSSAPEYTLRTRIWASLRSQTLYRTVSGFMNYSRAIKLLYRVENPEVQMFGGNSDKLEREL 672  
YEKNEKDSAKSKIDDLPFYCFIKGSSAPEYTLRTRIWASLRSQTLYRTVSGFMNYSRAIKLLYRVENPEVQMFGGNSDKLEREL 1020

ERMARRKFKLCISMQRYAKFKKEEMENAEFLRAYPDLOIAYLDEEPPLEVEEPRISYALIDGHSEIMENGMRRPKFR IQLSGN 757  
ERMARRKFKLCISMQRYAKFKKEEMENAEFLRAYPDLOIAYLDEEPPLEVEEPRISYALIDGHSEIMENGMRRPKFR IQLSGN 1105

PVLDGKSDNQNSHLIFYRGEYIQLIDANQDNYLEELKIRSVLAEEFEMKVENVSPYTPGVKNPMTSPVAILGAREYIFSENI 842  
PVLDGKSDNQNSHLIFYRGEYIQLIDANQDNYLEELKIRSVLAEEFEMKVENVSPYTPGVKNPMTSPVAILGAREYIFSENI 1190

ILGDVAAGKEQTFGLFARTLAQIGGKLYHGHPDILNGIFMTTRGGVSKAQKGLHLNEDIYAGMNAVLRGGR IKHCEYYQCGKGR 927  
ILGDVAAGKEQTFGLFARTLAQIGGKLYHGHPDILNGIFMTTRGGVSKAQKGLHLNEDIYAGMNAVLRGGR IKHCEYYQCGKGR 1275

DLGFGSILNFTTKIGTGMEQMLSREYYLGTQLPLDRFLSFYYAHAGFHIINMFMILSVQMFMLTLNLGALRHETIPCNYNRD 1012  
DLGFGSILNFTTKIGTGMEQMLSREYYLGTQLPLDRFLSFYYAHAGFHIINMFMILSVQMFMLTLNLGALRHETIPCNYNRD 1360

VPI TDALLPTGCANTDALTDWYRCVFSIFFVAFLAFIPLVVQEMTERGFWRRAATRLAKQLFSFLFFEVFVQIYANSVQQDLS 1097  
VPI TDALLPTGCANTDALTDWYRCVFSIFFVAFLAFIPLVVQEMTERGFWRRAATRLAKQLFSFLFFEVFVQIYANSVQQDLS 1445

FGGARYIGTGRGFATARIPFGVLYSRFAGPSIYFGARLF----- 1136  
FGGARYIGTGRGFATARIPFGVLYSRFAGPSIYFGARLF**LMLLFTTVMQQAALTYFWITILALII SFPLFNPHQFAWDDFIDY** 1530

-----RDFLRWL SRGNSRSHASWIAFCRLSRTRI TGYKRKTLGDPGKLSADVPRAALTNLFYGEILVPLFLVAVTYIPYLI NAQTGV 1615

-----TDQDAEATHSLIRLAI IAFAPIAVNAGTLGVLFMACFMGPVLSMCCCKFGSVLAGI AHGVAVVMLLIFFEAMFLLEGFNPARTL 1700

-----AGMI AVVAVQRFVFKLIVSLAL TRELKTQDANI AFWTGKWYSMGWHSVSPAREFLCKITELSMFAADFI LGHFLFVMLPVI LI 1785

-----PKVDLSHSIMLFWLLPSRQIRPPIYSMKQTKLRRRRVFRFAI LYFVMLVVFVGLIVGPPVAGSKIPTDSI IGLDKYKLIQVPDQN 1870

-----NNNTSEPTGAPSGSADDTAQTDEEDDSLKFLVI 1905

**Figure S1.** (a) Amino acid sequence alignment of published partial sequence of Cyp51 (MH120874.1) of *L. prolificans* and Cyp51 homologous protein sequence (Accession number: PKS10573.1) from *L. prolificans* strain JHH-5317 whole genome sequence data (NLAX01000008.1). (b) Amino acid sequence alignment of published partial sequence of Fks1 (EU337013.1) and Fks1 homologous protein sequence (Accession number: PKS10859.1) from *L. prolificans* strain JHH-5317 whole genome sequence data. One hundred percent conserved residues are written in black.

**Table S1.** List of oligos used in this study

Primers	Sequence	Purpose
CYP51-F1	TCGACCTTACCCTATATAGGATGAGCT	
CYP51-R1	CCGTGATCCACGCCATGTCT	PCR and Sequencing for CYP51 gene
CYP51-S1	TAATGATAGGGACGTAGCTGCG	
CYP51-S2	GAGCCGTTTGATGAATTCCAC	
UTR-F1	TGGAGAGGCTCAATGGCCTGT	
UTR-R1	CTTGCTAGCATCCAGGGTGACT	PCR and Sequencing for CYP51 gene 5' UTR
UTR-S1	TACAGTGACATCCCGGATAGC	
UTR-S2	TGCTCAACGTCCATACTTGC	
FKS1-F1	GCCTTTCAAGTGTCAAGAACCGACT	
FKS1-R1	GCGATGAAGAATTGAACTATGCCAAGT	
FKS1-F2	CAAGGAACCGATTTTGAAGGAGAACAT	
FKS1-R2	CCGATCTTGGTTCGTGAAGTTGAGAAT	
FKS1-F3	GTGATCTCGGATTCGGCTCCAT	PCR and Sequencing for FKS1 gene
FKS1-R3	CTGGTCCGATTATCATTGACCGTCAT	
FKS1-S1	ATAGCGCTTGGTTCCGGTGTC	
FKS1-S2	GAATGATCCTCTTGGGAGACG	
FKS1-S3	CAAATCGCTTACCTGGATGAGG	
FKS1-S4	AAGGATTCAACTTCGCGAGG	