

Supplemental Table S4. Oligonucleotides used in this study.

Oligoname ¹	Length (b)	Sequence(5'-3')
orf19.7459.V5	25	CATAAATAGACTGAATAAAGATCTC
orf19.7459.V3	25	AATAATGAAAGTAACAAATAATCTC
orf19.7459.5	120	CGGTTCCCTTCAAAACATTAGCTTGAAAATAATAAAACTATTCTATAAGAATCATATTTATACACCTATAATAAT ACCTTAATTAATTTTACCAAAAGGAAGCTTCGTACGCTGCAGGTC
orf19.7459.3	120	TACATAAAACTATTTTTTTTATTATTTTGAACAAAAAACAACACTATTAAATATAAAACATTTAGGGGGTGATA AACGTCAAATCTATTCCTTTGGTCTGATATCATCGATGAATTCGAG
SUN41.V5	25	TTTCCAATATACTAACATCAATAAC
SUN41.V3	25	AAAGCATATTGATATAATTAGAAAG
SUN41.5	120	TTCTTTTAGTCGTTCCTTTTTTTATAATTCACCTGTTTGTCATATAGTCTCAACTGTACATTCGTTTTTCAACTACT GTTCAATTTATTTTAATTATCAGAAGCTTCGTACGCTGCAGGTC
SUN41.3	120	AAAAACACTAACTTGAAAACAAACACTATTCTTTTTTAAAAAACAATATAAAGGAAGAAGAGAAAAAGGGG TATCTTGTAATTTTCTCAATCTCATCTGATATCATCGATGAATTCGAG
orf19.6090.V5	25	AATGTACAGCCAACTACATTTAGCA
orf19.6090.V3	25	CATTCGCTTCTTGTTGATTGTCGTG
orf19.6090.5	120	TTTTTCTTTTTTTGTTCTCATCTCATCACAAATGAAACATTTTTCTAAAAAAGATTCTTAAAGTTATAG CTTTTCTTTACATCTAATCGAATGAAGCTTCGTACGCTGCAGGTC
orf19.6090.3	120	AGTCAAAGGGGTGCCACAATCGGCAAGAAAAAATGGGTAACAAATCTTATGCTTAAACTACGGAAAC TTATTTAACTATTATACACTAGATTCTGATATCATCGATGAATTCGAG
orf19.2286.V5	25	TCAGTTATTGGTAGAGAAAACCGGA
orf19.2286.V3	25	CTGTGGGTACCGTTTCAGAACTAAC
orf19.2286.5	120	GTATAGCCATCATCATCCAAGGCTGAAAAAATGAGAACTAAATTTTTCACAACACACCACCACTTA TACTCATCACCAACAACAATAACCAGAAGCTTCGTACGCTGCAGGTC
orf19.2286.3	120	GAACTAACAATTAGGGTATGTGCTTTATAGACAGTATATTTATGTAAATGAAAATTAAAACGATACAATAA AAACGGAAAACTAGAGCACGTTCTGATATCATCGATGAATTCGAG
RHR2.V5	25	CGTGTAGGGCAGAAATTTTTTCTC
RHR2.V3	25	ATCTTGGTGTTATCTGCTACATTAC
RHR2.5	120	AATGATTTCCACATTCGTAAAAAATTGTAATCAGATTCACCTTCATCAGATTTCAACTAATCAATATACTCATTC ATACATTAATTACTACTACTACAGAAGCTTCGTACGCTGCAGGTC
RHR2.3	120	CCTATCCTGTATTGTACACTCTATAAAATTTAAACATGTTCTAAATAAAGACAACTTATCCTGTTATTCTAT TATACAATGTTAAGCTCTGACTCTGATATCATCGATGAATTCGAG

orf19.2527.V5	25	AGCTGCTGTTATGAATGAGAGTTTC
orf19.2527.V3	25	GCTATAATAAACAAACAAAGTATAC
orf19.2527.5	120	CCTTACACATTAACAGCATTATTTATACATTAACAAAGAAAATTTAACTTTACTCTATTAGCATGATATTCACA TACTAGATTCACTTAATGTAAATGAAGCTTCGTACGCTGCAGGTC
orf19.2527.3	120	ATATGGTTTAAATCTAACGCTTTCTTATGTTTCTTTTTATCTTTCTTTTTGTCCCTCTTTTTATCTTTTTGTCCCTT TTTAGATTCTTCTCCAGTCTGATATCATCGATGAATTCGAG
NPL3.V5	25	CACTGGTACAATTATATCACCGTCG
NPL3.V3	25	AAAATCCAATATAATGGCTTGGCCA
NPL3.5	120	TACCTTTTGTACTTTTGTGTTAGAAATTTAATTACTTGCAAGTATTGATGTTTTTTGATGGGTATTAAACAAAACG TTGGTCCTGTCAAAGTCGTGTGAAGCTTCGTACGCTGCAGGTC
NPL3.3	120	ATTGAATATAACAAATAAACACAACAACTGTAATCTTTTTCTTAATTCCTTTGGAAACACATCCTAAACGTA CTTGATTCTTAGCTGATGTAGATCTGATATCATCGATGAATTCGAG
orf19.7069.V5	25	GTATTAGGGATATTGTCAACTCATC
orf19.7069.V3	25	TCCTCTATAGGCTTTCATTTTGTAC
orf19.7069.5	120	TGGAAAAAGAGTAACAGGATCGAAAAAAGAAAAAATTTGAATTGTGTAATACATTAATAACAAT CAATCACCCAATTTTCACTCTTAAACAGAAGCTTCGTACGCTGCAGGTC
orf19.7069.3	120	AATTTCTTTTAAAAAATAGTATAAACTCTAATAAAGCTACGTGTAGAAATGTTTCATGTCTAAACTAATCCT GTCCCCCTGAACTGCTACCATCTGATATCATCGATGAATTCGAG
TYE7.V5	25	AAAAATAACAGGAAATGTCCCTTCG
TYE7.V3	25	ATCTATCTATCAAAGAATAAAAGAC
TYE7.5	120	GAAATTCGTTTTTCTTTTTTTTGTTTTCATTATTTATTATTCATTTATTTATTATAAACAGGTGTCAACGGTGT ACTAAGCAATTACAATTTCAATGAAGCTTCGTACGCTGCAGGTC
TYE7.3	120	TAAAGAATAATAATATAAAATAGCACTAATAATAAAAGGACCCAGAAGAAACGAAACAAATAATAAAAGA CTCTAAAAGAAGAATAAAAAAATATCTGATATCATCGATGAATTCGAG
FAA4.V5	25	CCCTCCTCGTTTTTCACTACCCGAC
FAA4.V3	25	TCACAAACAGGAATATAGATTGGTC
FAA4.5	120	TTTTAAATCATATTTATTTATTTTAACTTATCCTATTTATCCTATTTATTTATTTATCTAAATAAACCTATAAAC ACACATATAAACACATTTAATTGAAGCTTCGTACGCTGCAGGTC
FAA4.3	120	GAAATTCAAACCTTGATGTTATATAAATGAAACAAAATAAAATAAAATAAACAGAACTTACTACAACAA TTAATAACTTGACCTACTTAACCTTCTGATATCATCGATGAATTCGAG
QDR1.V5	25	TGGTTCCATATTAAGACATAAATCG
QDR1.V3	25	GTTATACTCTCTATAAGTATTTCTC
QDR1.5	120	CCACCCCCCTCCTTGTTTAAAGCTGAATACAATGTCATAGTATGTTTTGAATTATTTCCATTTTCGTAAATCAAAAA ACCATTTCTACAAAAAACCAATGAAGCTTCGTACGCTGCAGGTC
QDR1.3	120	GCTTGTAATAAATAAAAAAATGGGAAATCTATTATTGTTATTGTTGTGGTTGTGTCTTCAATGATAATAT

		TGATTATCGAAATTATCTCTATCTGATATCATCGATGAATTTCGAG
orf19.1964.V5	25	ATTGCTTATTCTTCATTCCAATTG
orf19.1964.V3	25	AAAGGGGCATATATAATTAATTGG
orf19.1964.5	120	TTTTTTAGTTTTTTCAGTTTTTATCAATAGTTTAAACCAATTCAACCTTTGTTTGATTTCTTTCTTTCACGAAAACCTTC
		ACCTTTATATCTACTGCAAAAGAAGCTTCGTACGCTGCAGGTC
orf19.1964.3	120	AAATATAAGGAAAAAAAAAAAAAACGGTCTATATATATAAGTTTTAAAAGTCTTCTATAAATGGGGAAGGGGAG
		GGGGAGGATATTCTTTTGTTTGCTCTGATATCATCGATGAATTTCGAG
HMX1.V5	25	ATCTTTTTGGGTATTTTCATCCCTTC
HMX1.V3	25	AAGAGAAGAGTACGATGAAGAGACC
HMX1.5	120	ATATCATTCAATAATTTTTTTTTTACATTTTTTTTTTAGGTTTTCTATACTATAGAATTAATCATTTACTAATCCAAT
		CATATATCATTACACATACAATGAAGCTTCGTACGCTGCAGGTC
HMX1.3	120	AGAGATGGAGCATACAGAAGATATTGCACAATAGAAAAGGCATATATTATCTAAATTAATGTACAGAAGTTTT
		CATAAGTGTTTTTATTTTTTTTATTCTGATATCATCGATGAATTTCGAG
MP65.V5	25	CTACAACCATTTTTCCCACTTGTTG
MP65.V3	25	TAACAAAGTAGGTAGTAGGTATCAC
MP65.5	120	ACTAAAACCAAAGTTATATTCTATCAGTCTTTCCTTACAATCCTTTAGAAGTAACTTTATTCGTTCTTTTTTATAT
		AAACATAATACCCAACCTTAATAGAAGCTTCGTACGCTGCAGGTC
MP65.3	120	AGGAAAGGAAAACGTGTTTGTAATTGTTATTTTTAAAAAAATAAAAAAGGATTCAACGGATATATAATGAAAAAT
		AAAACATAAAGCCAATTAATGTGCTCTGATATCATCGATGAATTTCGAG
HGT7.V5	25	ACTCTTACTAAAACATAGATTTTCAG
HGT7.V3	25	TCTAAATTCTATAACTATATTAAC
HGT7.5	120	AAGGTATAAATATGTAGTAGTTTTCCATCAATGCTCCGAGTTTAGTTTCATTTTTCTTTTGGGCTTTTTCTACAT
		CATCCTCACACAATTTCAAATGAAGCTTCGTACGCTGCAGGTC
HGT7.3	120	TTTTTTCATTTTGTAATTCATTGCTAAACATTAAATCATTGGGAGAACAAATTAAACATAACCGCAACTTGT
		GCATTTATTTTTCTTAAATCATCTGATATCATCGATGAATTTCGAG
RBT5.V5	25	TATTTTCTTTGCGAACCAAATTTGG
RBT5.V3	25	GCGGCGGCGGTGGCGGCTCAAGTGC
RBT5.5	120	ATGGAAAATTAGGGTATAAATACATAGGCATTTTCCATGACTTCCGTTGTTCTGAATTCTAATTCTTCACTAACT
		ATCACTAATAACTAATACTACAAGAAGCTTCGTACGCTGCAGGTC
RBT5.3	120	CTTGTATAGCTATCGCAAATTACATTAAACGTAAATACTCTAGTTGCAATAAGATCATATATTAGTTATGTATTA
		TCAGCAATACTATAATTCAACTCTGATATCATCGATGAATTTCGAG
CLG1.V5	25	ACTCAGTTTGTAAGACAGGGAGAAG
CLG1.V3	25	CAAAAGCGTTAGCGGAAAGACAAAC
CLG1.5	120	AATTTTTTTTTGTCTTTTTTTTTTTTTTAGGTTGTTCTTCAGTCCACTGACCCATCACCTATACCTCCTACCTCCTCCG
		ACCCAACCCACCCTTTTACAGAAGCTTCGTACGCTGCAGGTC

CLG1.3	120	ACAAAGATTAAAAAATCAAAAAATCAAAAAAACTTGACTCTAAAAATTAAAGGATGAACACAAT GTCTTGGACTGACCAATATTATTCTCTGATATCATCGATGAATTCGAG
HGT6.V5	25	TAGAAAAGAAAGCCCGAGACTGTAG
HGT6.V3	25	GTAACATACATATTAATATTATTGTC
HGT6.5	120	TTAAATGGGCACTTCCTGTCCCAATTTCTCATAAAGAAAACCTGGTTCTTGAAAATTTGATTTTTCTTTTGCAT CAAGTTAATTTATTCAAAGCAAAGAAGCTTCGTACGCTGCAGGTC
HGT6.3	120	TTAAATTTTTCAATTTTATTTCTGAACTATGGGTATTCTTTAAATGCCAGCAAATAAAATGAAAACAAGTACAG CATTAAATGACAAAGAGTTGATCTGATATCATCGATGAATTCGAG
orf19.7107.V5	25	CAGTCAAGCACTGAAGGAAGTTCGG
orf19.7107.V3	25	GATGTGTTGTCAACTTCCATGGCCG
orf19.7107.5	120	TCCTGCATATTAGCTTCTTCTCCAACTACTTCACAAAAGATAATTTTTTTTTTTTGAGATGCCTTTACAACATC TTCTTTTCCAACTATCCAACAGAAGCTTCGTACGCTGCAGGTC
orf19.7107.3	120	CTTGAGTTTGTTAGCAGCTAAATACCGCTGGTTTCTGGCAATCTTTTAGCTCTTTTGTTAGATAATGTCTGGGTT GTCATGGTCGAGGTTGGCTGTCTGATATCATCGATGAATTCGAG
CUP9.V5	25	TGAGAAACTCCATTCGTATATTCTC
CUP9.V3	25	AGATAACCTATAAACGAAAGAAACG
CUP9.5	120	TCCATATCTCTCTGATACACACAAACATACAGAATTCCAAGTTTTTTTTTACTATAAATAATCAATAGAATCTCC CTCTAAACTATTTTGTTATTTTAGAAGCTTCGTACGCTGCAGGTC
CUP9.3	120	AATGTAAAACGAATTGAAATAAAATATAAAACGAATTAAACAAAAAAGTACCCAAAATCTTTGTAAAAC AACCTTCTCTTCTCTTAATCTTCCTCTGATATCATCGATGAATTCGAG
orf19.6507.V5	25	CCCCTTCTAATCATCACTTCTTTTC
orf19.6507.V3	25	AAAACCAATGCAGTTGACGCAATTG
orf19.6507.5	120	TTATTCAAAGAAAACAATTATGTCTTCCACTGATAAAAGTACGTTTTAAACCCGAGATAGCTCTCGATGAATAC AATTATACTAACAATTGTCATATAGAAGCTTCGTACGCTGCAGGTC
orf19.6507.3	120	TATATATGAGGATGTGATGTGTTCTTGATAATGATTGTAATGTGTATATAAGATTTATAATCTATGTATTTACAT AAAAAGAAAAGACCCAAGTGTTCTGATATCATCGATGAATTCGAG
orf19.1287.V5	25	CCCCCCCCACTATATCCATACACAC
orf19.1287.V3	25	ACATCAATTCACAATATACACAATC
orf19.1287.5	120	TGATATTTATTATTTTAATTTAATTTTTTTTGCATATCAAATTATATTTATTTTCATTTCAATATTACTTTAT TAATTTATTTTATTTTGCATAGAAGCTTCGTACGCTGCAGGTC
orf19.1287.3	120	ATATTATTATTTAAAAATAACCCGAAAAATGAAATAAAACACAGACACACACAAATATATGTAACACTTGGGA TAAAACCCCTCTTGAGAATTCCTTCTGATATCATCGATGAATTCGAG
FLC1.V5	25	CATACACATAGAGACACATTATTGC
FLC1.V3	25	TCAAGATAAAAACCAATCAATTCCT
FLC1.5	120	CATTTATTAAAATTTCTATTTCTGTTTTTGTTCGTTTTTCGTTTTCGTTGTTTTTCATACTTAACTTATTGAA

FLC1.3	120	TTGCTTTATTACACAATTATCGAAGCTTCGTACGCTGCAGGTC TATACATATATAACAACAATTAGGAATTAAATCATAAACTCTATTAATACAATAATTAAAAAAAATAAAATG GAGGGGATGAGCTAAACTCACATTCTGATATCATCGATGAATTTCGAG
MUP1.V5	25	AAAAGTAACATAAAAGTCCCAGTCTC
MUP1.V3	25	CATTGGAAACATTGTCTGAATATAAC
MUP1.5	120	GTTTATTGTTTCATTTCCTTTTGGTTTCCCCTTTCTCCTGAGAAGGCTTATCACTTTTATCAATTACACCCATAC TAATACCTTACACAACCTTCAAGGAAGCTTCGTACGCTGCAGGTC
MUP1.3	120	TACCCTCCCAAATTAAAAGTGATACTAAACTAATAGAATATATAATTAACAATACGAGAAAAATTGAACTGA AAAGCGTCTAATTTTTTTTTTTTTCTGATATCATCGATGAATTTCGAG
PTR2.V5	25	CTGACTCCATAGGTTTTTTTTTTGGG
PTR2.V3	25	TTTACGCGCTATTTAGAAGGGGAGG
PTR2.5	120	TTTTTTTCTTTCTTGTTTCTTACTTGGATAATAGTTGTTTTGCAATTTAAGTATTCTCTTCATTTTTTTTTCTTATTC TCCATCTTTGTTAATTTGCAGAAGCTTCGTACGCTGCAGGTC
PTR2.3	120	AACCAAGCTCGCGTCAGGCAATCTACAAACGCTCTAACCGGTATTCGTCTAACGTATCGTATTTTCGTAAATAAC TATATGTATATGTATACAGCTCTCTGATATCATCGATGAATTTCGAG
MET3.V5	25	ATCATCAAGTATACGTAATCTCCCC
MET3.V3	25	ACTATAATAATAATTTACAAATGCC
MET3.5	120	TTTAGTTGTTCTTTTTTTCTTTCTATTCTTCAACTTCCAAGTGTTGTCACCTTCTTCTTGTTAACTATATTTAAAAG TAAATACCCTCCCCAGAAAACGAAGCTTCGTACGCTGCAGGTC
MET3.3	120	ATACATAAAAGCTTTCCACATAAACGCTAATAAAATAGGATACACACACATAATCCATCAATCAATAAAAT CCAATATTTTCTTCTTTTTCAAGTTCTGATATCATCGATGAATTTCGAG
CAN1.V5	25	ATAGATATATATTTGCTATTGTTTC
CAN1.V3	25	AGAGTTTGATAATCACTTTGCACCC
CAN1.5	120	AGGTTTTTTTTGTTCACTTTATATTCTCCTTTTTTTATCAAATCTTCTCCTCTTCCAGTTTCCAATTAACTCTAAA TATATCATATATCTCCTCAATGAAGCTTCGTACGCTGCAGGTC
CAN1.3	120	CTTTACAAGTAAATGGTATCTTTATTATTATGCAAATGTGTAATTAAATTTTTTAAAAAACAGTCTAAACTTATA GAATTATATATAAAAAAACGTTCTGATATCATCGATGAATTTCGAG
GNP1.V5	25	ATAGATGCGATAATTTCTCTTCTCC
GNP1.V3	25	AACATCTAATGTAGTTCATTAATCC
GNP1.5	120	AAGTTCTCCTTCTTTTAAGCATTAATTTTTTTTTTTTTTTTTCATTTCCATTTGATTAGTCTTTTTGTTTGTTTGTAC CCTCAAATATATTTGATACCGAAGCTTCGTACGCTGCAGGTC
GNP1.3	120	ACCTTACAACTGGTTCTACTTTACAACCTTGATTCTAAAATCATCAATTTACATGAACATTTAAGAAGAAAAA AAACACAACAATCAAACCTATATCTGATATCATCGATGAATTTCGAG
FRE10.V5	25	AAGAATTTTTTCAGCCATTCCCATCC
FRE10.V3	25	ACCAAACAATTTTGGTAAGAAAAAC

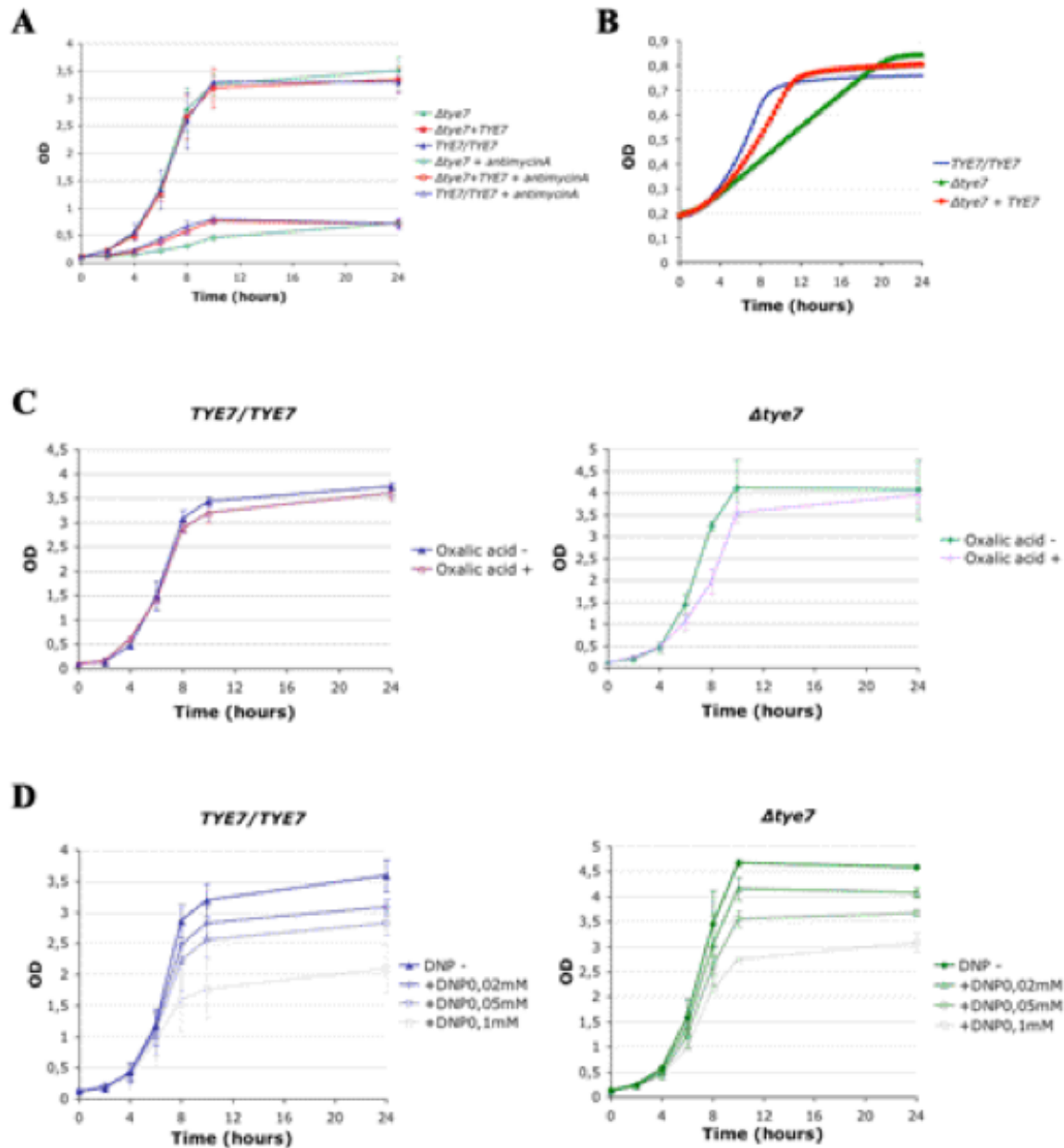
FRE10.5	120	AAGTAAAAAATAGAATAATAGATTGTAATATTTTCTTGACAAGAATTTCAAAC TAAGGGGAACAAAGAAGGAA AAAAAAAAAAGAATATAGATACAATGAAGCTTCGTACGCTGCAGGTC
FRE10.3	120	ATGAAAATAAAAAAAAAAAGCAAAGTGATGAATCAATAGTTGCAACTATAACAGGGTTTATGTTATAACCACAC TTTTTCTTCTTCTATTTTTAAATTCTGATATCATCGATGAATTCGAG
orf19.1691.V5	25	AATTTTACTACTAACTTCTTCCGTG
orf19.1691.V3	25	TGGCAGTAGTTGTTCCCTTCTTGACG
orf19.1691.5	120	ATTTTGGAGATACATCAGTGGTTTCCATTTCCTATCACTAGTATAGATTGTTTATCAATTGTGAAAAGTCCAGCT ATTCTCTGTTAACCTCTACTTACCGAAGCTTCGTACGCTGCAGGTC
orf19.1691.3	120	TAGAAATTAATAAGAGAGACAACGAACCTTCTCTATTGATCCAATTGATATAACATATTTATTATAAAACCAGTT TATATAAAGAGCTTTTCCTAATTCTGATATCATCGATGAATTCGAG
ALP1.V5	25	TGCCATTTTCGGAGGGGGCAATTACT
ALP1.V3	25	GTTAGTCATTACGTATTGCCACCGC
ALP1.5	120	TAGTTTATATATATATAAATATGATTATTTCTTGAAAAACACGTTGTTTTTGT TTTTATAATACTATCGAGTTTTT ATTCATTTTTTTTTCTTCAAATAGAAGCTTCGTACGCTGCAGGTC
ALP1.3	120	ATGTAAACGCTTCTTTTTTCTAAATTCGTGATAGTCATTATATATTTTGAAGCATAACTGCTTATTCTATTCTAT GATAAAAGTACGTAATCCCGTCTGATATCATCGATGAATTCGAG
orf19.3483.V5	25	TCCCTTTCACTTTCATAGTGTTGTC
orf19.3483.V3	25	TTCTCACTCACATAATATACAAGAG
orf19.3483.5	120	CTTCCCCCTCCGTCCCTCCCTTAGATTTTACTCCACATTAAAAAATTAAAATTATTGTGATATTTTACAACCAAC AAAAAATTCATTAACCAATATCAGAAGCTTCGTACGCTGCAGGTC
orf19.3483.3	120	AATAATAATTTAATTCTCTTAAC TAATAGGATATATCTATACAAACAAAATAATTCAATCCACTCTAATTATTAT CTCTATACTTTAATCAAAC TATCTGATATCATCGATGAATTCGAG
YWP1.V5	25	TCCCATTTTCAATTTCTTCTATATC
YWP1.V3	25	TGAAGGAATAATTGAAATATGAATC
YWP1.5	120	CTAATTAATCATCTTCATATCAAATATCATTAATCTTTTGATCAATTAATTCACACTCGCTTTAATTAATTTATCA AATCCAAGAAATAATAATAATAGAAGCTTCGTACGCTGCAGGTC
YWP1.3	120	ATGATTGTAGAAAGTTAATAACGTGGGGGGTGGGGGTATATTGTCTTATGCGAAATAGTTGATTGTGAATCAAA GTGTGAATGGAGAATGTAAACTCTGATATCATCGATGAATTCGAG
HXT5.V5	25	CTATCAACACTGTGAGTTTCTGCAG
HXT5.V3	25	TCTAATTAATTAACATACATAATAC
HXT5.5	120	AATACCCATGATTTCCCTTCACGTTGGTTTTTTCTTTTTTCACTTTTGGAGTACTTTTTTGTTC AATCTTCAGA TCTACAATAAACTATCTACCAGAAGCTTCGTACGCTGCAGGTC
HXT5.3	120	ATATAACTGAATACGGACATATACAAAAGAACCGGGGGAGAGAATAAAAAAGAAAAAGCAGCCCCAATCCGT GTAATCAAATCAACACTCCCCCTTCTGATATCATCGATGAATTCGAG
PTC8.V5	25	TATTTTAATTCCCTCCGCCTACCTG

PTC8.V3	25	ATGAATAGTATTACTTTTTCCCCTTC
PTC8.5	120	ATATATACATCCTTTTTCCCATACCAATATAAATTTATTCAACATTTGGTAAATTTTTTTTTTTTCAACTATACACT ACTACTAAATAAAACAATCAACGAAGCTTCGTACGCTGCAGGTC
PTC8.3	120	ATATTATATGTATAAGTATGTGAATAACTTTTTAATGCAAAATGAAAAAAAAAAAAAAAAAACCTCTCGAATG TAAAAAAAAAAACCACTACTACTGTCTGATATCATCGATGAATTCGAG
orf19.4792.V5	25	TAATATTTCTCACTATACTTTCTTG
orf19.4792.V3	25	ATATGTATATATTATGTTAATCTCA
orf19.4792.5	120	TTCATACTTGGATTTTCGTTTTGTAAAAGGAATAGAGAACCCTGTCTTGATAATTGATACTAAACAAACAAATT GGAGGGCAAGAGTTGTATATAACGGAAGCTTCGTACGCTGCAGGTC
orf19.4792.3	120	AATGCACGTAAATAATTTGTTTTTAATCCCTTAATCCTACAAAACAAAAACAGAAAGCAAATCCAAAA ACCAATTGGAACCTCAACTATGCTTCTGATATCATCGATGAATTCGAG
SIM1.V5	25	TGCTTTTCATTTAGCAACTAGTTTC
SIM1.V3	25	CTATTGGTACAACAATCAATAAACC
SIM1.5	120	GTTATTCTATCATATTTTCACATTCCTTTGATTTCCAAATCATCCAAATATTATTTTATAGCAACAATTAAAAGA AAAATAACTGATATCCTTTTCATTGAAGCTTCGTACGCTGCAGGTC
SIM1.3	120	ATATATTAATTTCTGTATAGTAGCATTATTAATCATGTCAATAATTACCAAGATTGTAATAGTTGTCCAACCTGG ATATCAGATAACTGTGATTCTTCTGATATCATCGATGAATTCGAG
orf19.5525.V5	25	CAAAGTGCAGTTCGTTCCGAACGGA
orf19.5525.V3	25	CAAAGTAATAAGAATTCGATACGTG
orf19.5525.5	120	AGCGGGGGATCCTTACTTCGGCATATTTTTTTTTTTCAGTTTTTTTCTCCCTAATTAATACAACAACCTTCAAGTATCA CCAATCCTTATATAATCAAAATGAAGCTTCGTACGCTGCAGGTC
orf19.5525.3	120	TCTACTTTGACATTAGATCCGTTGTTTTTTGAAGATTCTAATGCAGCAGCCACAATTGCTAAATGATGGAATGCT TTTCTCGGTGGTACTTTGACCTCTGATATCATCGATGAATTCGAG
orf19.7328.V5	25	CACTCTCTCCACCGAAATCAAACCC
orf19.7328.V3	25	AACAAACTACTACTACTCGCTACCA
orf19.7328.5	120	TTCAATTGAAATTTTCACTCTCTTTTGATTTCTTCATTTTCTTTCTAAATCATCATATTTTAATACGAAGCCTC CCCCCTCCCCCATTCATATGAAGCTTCGTACGCTGCAGGTC
orf19.7328.3	120	AATTTCCACTATGTACGACGACATAATATTGTACATTATCATTCGTATATATCTCACACGACTGCTGCTATTATA TACATAATTTTCAACTTTTTTCTGATATCATCGATGAATTCGAG
orf19.7445.V5	25	TCTTCATCAACTTATTCATTCATCT
orf19.7445.V3	25	AAACCAAACCAAATCAAATCAATTG
orf19.7445.5	120	CCTTATTTATAAGAATAATTATATTCAATTAATACATTTAGAGGAGAGATCAATAGATAAAGAACAAAAGAAA GTATTCAAACACGTTTTTCAAATGAAGCTTCGTACGCTGCAGGTC
orf19.7445.3	120	TGGGAAAATAATCTGTGAATTAATGAAGGAAACAGATTGAAAGAATCAGCATTCTTTCTATGCAATGAAAAAA AAAACGGGTATTGTATAATTACTTCTGATATCATCGATGAATTCGAG

Arg.V5	27	CTGGTGAATGTGTTAGAAAAGCTGAAG
Arg.V3	28	GATTGTTGTTGTTGTTGTTGGGATGGCC
His.V5	27	CTACAATGCCCCAAAATCCATCCAAGC
His.V3	26	GGAACAGCAAATAACAAACGGTCTGG
ClpU-R	26	ATTACTATTTACAATCAAAGGTGGTC
ClpU-L	26	ATACTACTGAAAATTTCTGACTTTC
Arg1-S	26	GCTACCGATATGAGAATTTTCGTTCG
Arg2-S	26	GTAGCCAACATATCCATAGTTAAAGC
His2-S	25	CGAGTACCAATATATCGGTTGCACC
His5-S	25	CTTGTGCCTTGGGTGTTGCTGATGC
TYE7-F	20	GGAATTCGCTTTTGAAACCA
TYE7-R	21	CGGTCAACTTCTTTCTTGGTG
TEF3-F	20	GATCACAATTGGGTCCAAGG
TEF3-R	20	AGCAGCGGCAATCTTGTTAC
ACT1-F	20	GGAAGCTGCTGGTATTGACC
ACT1-R	20	AGCAATACCTGGGAACATGG
ADH5-F	20	TTACCGTCAAGGGCTCATTC
ADH5-R	20	GCAATTCTGACAATGGAGCA
HXK2-F	20	AAAATTGGGCATTGAAACCA
HXK2-R	20	TCTTTTGGCAAATAGCAGCA
PFK1-F	20	TGAACAAGCCAGTGCTGTTT
PFK1-R	20	GGCACTGGTGTGAAACCTT
PGK1-F	20	GATGGGTTTGGACTGTGGTC
PGK1-R	20	GTACCGTTGGCGAATTTTTC

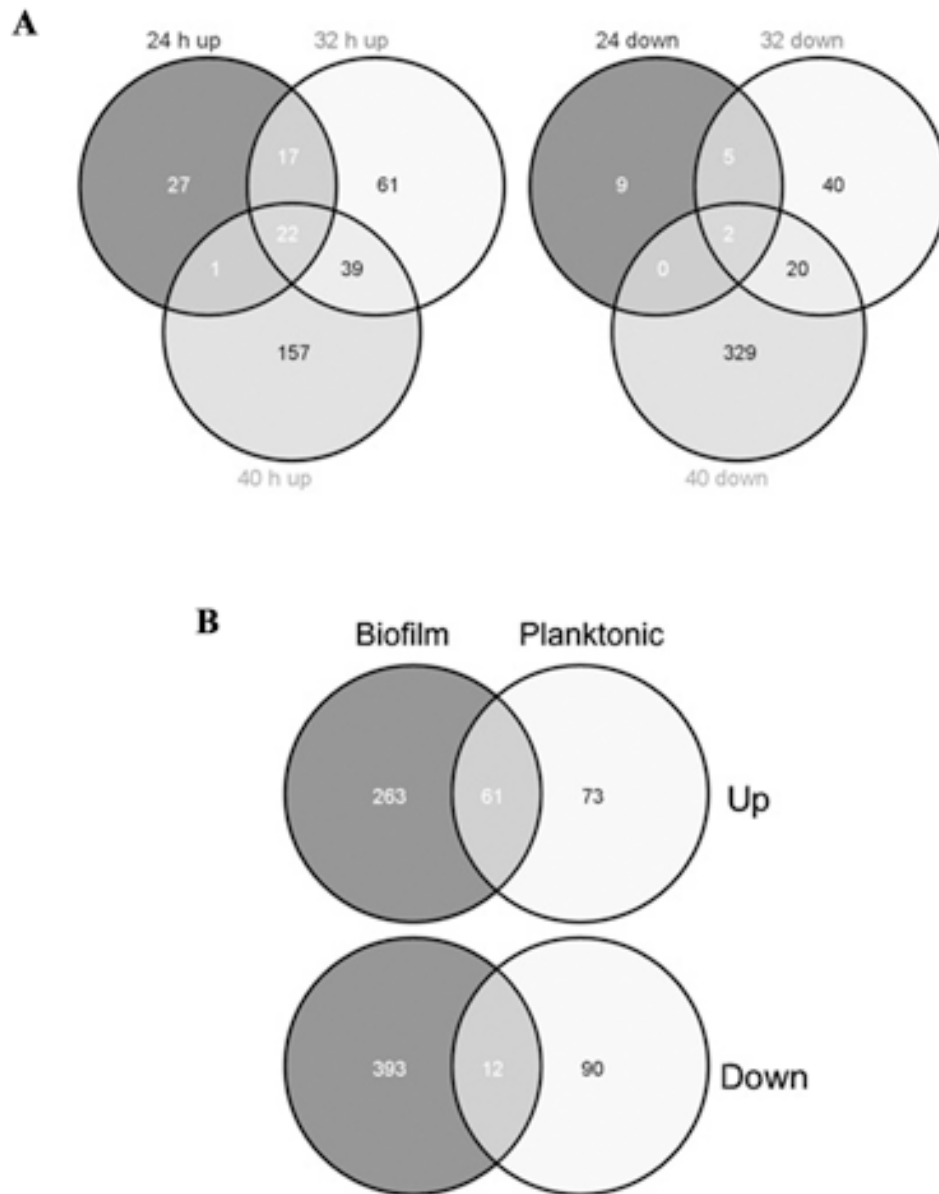
¹Nomenclature: .V5/.V3: Oligonucleotides used for validation of gene replacement by PCR; .5/.3.: Oligonucleotides used for amplification of gene replacement cassettes; -R/-L: Oligonucleotides used to verify Clp10 derivatives integration at the *RPS1* locus; -R/-F: Oligonucleotides used for qRT-PCR; -S: Oligonucleotides used for the preparation of probes used in Southern blot experiments

Supplemental Figure 1



Supplemental Figure S1. A. Representative growth curves of the deleted (Δ tye7), complemented (Δ tye7+TYE7) and wild-type (TYE7/TYE7) strains in Erlenmeyer flasks in SD 0.4% glucose at 37°C in normoxia and agitation, without and with antimycin A (10 mg.l⁻¹). **B.** Representative growth curves of the wild-type (TYE7/TYE7), knock-out (Δ tye7), and complemented (Δ tye7+TYE7) strains in 96-well microtiter plates in SD 0.4% glucose at 37°C with shaking. **C.** Representative growth curves of the wild-type (TYE7/TYE7, left graph) and deleted (Δ tye7, right graph) strains in Erlenmeyer flasks in SD 0.4% glucose at 37°C in normoxia and agitation, without and with oxalate (10 mM). Differences in doubling times for each strain according to oxalate were not significant (p -values = 0.63 and 0.23 for TYE7/TYE7 and Δ tye7, respectively [Student's t -test]). **D.** Representative growth curves of the wild-type (TYE7/TYE7, left graph) and deleted (Δ tye7, right graph) strains in Erlenmeyer flasks in SD 0.4% glucose at 37°C in normoxia and agitation, without and with increasing concentrations of DNP. Differences in doubling times for each strain according to DNP were not significant when DNP concentration was less than or equal to 0.05 mM (p -values = 0.29, 0.14, 0.60 and 0.37 04 [Student's t -test] for TYE7/TYE7 without DNP compared to TYE7/TYE7 with DNP 0.02 mM, DNP 0.05 mM, Δ tye7 without DNP compared to Δ tye7 with DNP 0.02 mM and DNP 0.05 mM, respectively, and are significant with DNP 0.1 mM for both strain (p -values = 0.04 [Student's t -test])).

Supplemental Figure S2



Supplemental Figure S2. Venn diagram showing overlaps between the significant sets of differentially expressed genes. A. Intersection between the sets of regulated genes arising from complemented (*Δtye7*+*TYE7*) versus deleted (*Δtye7*) strains comparisons in the biofilm in a microfermentor model at the three time points of growth. 24h up, genes up-regulated in the complemented versus deleted strain at 24 h growth of biofilm; 32h up, genes up-regulated in the complemented versus deleted strain at 32 h growth of biofilm; 40h up, genes up-regulated in the complemented versus deleted strain at 40 h growth of biofilm; 24h down, genes down-regulated in the complemented versus deleted strain at 24 h growth of biofilm; 32h down, genes down-regulated in the complemented versus deleted strain at 32 h growth of biofilm; and 40h down, genes down-regulated in the complemented versus deleted strain at 40 h growth of biofilm. **B.** Intersection between the sets of regulated genes arising from complemented (*Δtye7*+*TYE7*) versus deleted (*Δtye7*) strains comparisons at the three time points of growth in biofilm and in planktonic culture in exponential phase of growth. Up, intersection between the set of 324 genes up-regulated in the complemented versus deleted strain at any of the three time points of growth in biofilm and the set of 134 genes up-regulated in the complemented versus deleted strain in planktonic culture; Down, intersection between the set of 405 genes down-regulated in the complemented versus deleted strain at any of the three time points of growth in biofilm and the set of 102 genes down-regulated in the complemented versus deleted strain in planktonic culture.