

Table S1 Primers Used

Name	Purpose	Sequence	Rd-start	Rd-stop	NP-start	NP-stop
F_Rd_A.E10	test tract 106	<u>C</u> GTTTCTTTATTCTTATTTGGTGC	805,155	805,178	871,522	871,545
R_Rd_A.E10	test tract 106	GAAAGTACAAATAG <u>A</u> GC <u>G</u> AA	805,496	805,477	871,863	871,844
F_NP_A.E10	test tract 106	<u>T</u> GTTTCTTTATTCTTATTTGG <u>A</u> GC	805,155	805,178	871,522	871,545
R_NP_A.E10	test tract 106	GAAAGTACAAATAG <u>C</u> GC <u>A</u> AA	805,496	805,477	871,863	871,844
F_Rd_B.E10	test tract 106	AAG <u>C</u> CG <u>C</u> AAAGAATTACAAGA	831,046	831,066	896,435	896,455
R_Rd_B.E10	test tract 106	TGG <u>C</u> GCAGTTT <u>C</u> ATCATA	831,517	831,500	896,906	896,889
F_NP_B.E10	test tract 106	AAG <u>T</u> CG <u>T</u> AAAGAATTACAAGA	831,046	831,066	896,435	896,455
R_NP_B.E10	test tract 106	TGGTGCAGTTT <u>C</u> GCATA	831,517	831,500	896,906	896,889
F_Rd_comM	test tract 143	GGCGGA <u>A</u> GTGTTTCGCTGCCT	1,181,122	1,181,141	1,214,974	1,214,993
F_NP_comM	test tract 143	GGCGGA <u>A</u> TCCTTTCGCTGCCT	1,181,122	1,181,141	1,214,974	1,214,993
R-comM	test tract 143	GCAGGGCGTAAACCGTGGCAT	1,186,049	1,186,030	1,219,901	1,219,881
F-murE-Rd	test tract 143	ACGC <u>G</u> CAATGGTGGAAGGCTAC	1,199,339	1,199,360	1,233,187	1,233,208
F-murE-NP	test tract 143	ACGC <u>A</u> CAATGGTGGAAGGCTAC	1,199,339	1,199,360	1,233,187	1,233,208
R-murE	test tract 143	AACAAGCGCAAGCGCACCT	1,201,362	1,201,343	1,235,210	1,235,191
F-xylFlank	test tract 143	AGTCTGCGTGGACATCATCGGA	1,173,109	1,173,130	1,210,948	1,210,969
R-xylFlank	test tract 143	CCAGCAAGCGTCGCGTGGTTA	1,178,735	1,178,715	1,212,587	1,212,567
F-xylG-Rd	test tract 143	TGCCGTGTTTCTCCGATCTTCAGG	1,175,579	1,175,603	0	0
R-xylG-Rd	test tract 143	ACAGCAGGTGCAATTAGATGCCG	1,176,249	1,176,227	0	0
<i>comM</i> _F	<i>comMΔ::spc</i>	GCGGTAAGTTTTTCGGGTAA	1,182,091	1,182,111	NA	NA
<i>comM</i> _R	<i>comMΔ::spc</i>	CCACACCAAGTCCCAAAA	1,185,779	1,185,799	NA	NA
<i>comM</i> _EcoRI_F	<i>pSU20-comM</i>	<u>GGAATTC</u> CCTGAAGATACGGGCATTG	1,182,399	1,182,418	NA	NA
<i>comM</i> _EcoRI_R	<i>pSU20-comM</i>	<u>GGAATTC</u> GGAGGAAAATAATGACATCAAAT	1,185,284	1,185,307	NA	NA

For test primers, bold underlined bases indicate variants between the recipient and donor genomes (RR722 and RR3131). Genome coordinates of primer sequences are provided for both genomes. For cloning primers, bold underlined GAATTC indicates the *EcoRI* restriction site.