

Table S3: Primers used in this study

Name	Plasmid	Sequence (5' to 3')	Specific Restriction Site
BGO480	pBG363	GCGCGCAAGCTTCGAGGTATGTAGGTCACAGAACG	Hind III
BGO481	pBG363	GCGCGCCC GCGGCCCTCTTCTTCGTCCACGTGC	Sac II
BGO482	pBG363	CACTGTTTTTACCACAGTCGGATCCGCGCACTAGTCATATAAACTTGTAATTATTACCCG	Spe I
BGO483	pBG363	CGGGTAATAATTACAAGTTTATATGACTAGTGCGCGGATCCGACTGTGGTAAAAACAGTG	BamH I
BGO493	pBG364	CCACCTCAGCCTAGTACTCAGGCTAACTTTACTACGCATTTATC	Sca I
BGO494	pBG364	GATAAATCGGTAGTAAAGTTAGCCTGAGTACTAGGCTGAGGTGG	Sca I
BGO495	pBG365	CTGTTGAAGTGAATGCTGCGTCTGAATTCCAAG	Bsm I
BGO496	pBG365	CTTGGAATTCAGACGCAGCATTCACTTCAACAG	Bsm I
BGO497	pBG366	CTCTGGGATTTTGCCGGCCGAAGACTCTGCG	Nae I
BGO498	pBG366	CGCAGAGTCTTCGGCCGGCAAAATCCCAGGAG	Nae I
BGO499	pBG367	GCGTTGTGGGAGCAGGTGCTGCTAACTTTGGTGTTTTC	AlwN I
BGO500	pBG367	GAAAACACCAAAGTTAGCAGCACCTGCTCCCACAACGC	AlwN I
BGO501	pBG368	GAAGGTCGTGATAACGCTGGCGTCTTCATATCCTGGGATTC	BsaH I
BGO502	pBG368	GAATCCCAGGATATGAAGACGCCAGCGTTATCACGACCTTC	BsaH I
BGO503	pBG369	CTTGTCATTTGAAGCAAAGTGCACCTATGAGATCTATG	ApaL I
BGO504	pBG369	CATAGATCTCATAGGTGCATTTGCTTCAAATGACAAG	ApaL I
BGO505	pBG370	CAAGGACCTCCATTTGCCGCCTCGGCCAGTGACAGAAC	Bgl I
BGO506	pBG370	GTTCTGTCACTGGCCGAGGCGGCAAATGGAGGTCTTG	Bgl I
BGO507	pBG371	CAGAACACACCACGCACAAGGCTCAGCTGTCAGGGATGTTG	Pvu II
BGO508	pBG371	CAACATCCC TGACAGCTGAGCCTTGTGCGTGGTGTGTTCTG	Pvu II
BGO509	pBG372	GTTGAATTTTACCTGCCTCGGGTGAATTTGTTATTAC	Ava I
BGO510	pBG372	GTAATAACAAATTCACCCGAGGCAGGTGAAAATTC AAC	Ava I
BGO511	pBG373	GAAAGATTTCTTGCTTTGCCGGCGCATCAGGTGAGTTTC	Nae I
BGO541	pBG373	GAAACTCACCTGATGCGCCGGCAAAGCAAGAAATCTTTC	Nae I
BGO542	pBG374	CACTATCGTGGCTGGCCAGCCAAAAGTTTGCTAC	Eae I
BGO543	pBG374	GTAGCAAAC TTTTGCTGGCCAGCCACGATAGTG	Eae I
BGO544	pBG375	CATTAGTGGTCATAACGCCGGCATTACTGCTTTGACAG	Nae I
BGO545	pBG375	CTGTCAAAGCAGTAATGCCGGCGTTATGACCACTAATG	Nae I
BGO546	pBG376	CCACTAATCAGTGGATCCTATGCTGGTAGGATTATGG	BamH I
BGO547	pBG376	CCATAATCCTACCAGCATAGGATCCACTGATTAGTGG	BamH I
BGO548	pBG377	GTATTTCTTGGGATGCCACTTTGGCAGTGAACGGTATTAC	Bgl I
BGO549	pBG377	GTAATACCGTTC ACTGCCAAAGTGGCATCCCAAGAAATAC	Bgl I
BGO550	pBG378	CAGTTGGTTTGGAAAGCCGGCAATACTATT CAGGTATTC	Nae I
BGO551	pBG378	GAATACCTGAATAGTATTGCCGGCTTCCAAACCAACTG	Nae I
BGO552	pBG379	CGCCATCTGAAACAGCGATCGCTGCTGGAG	Pvu I
BGO553	pBG379	CTCCAGCAGCGATCGCTGTTTTCAGATGGCG	Pvu I
BGO554	pBG380	GAGATGTTATGGGCGCCATATTGCTATATGATTTAC	BsaH I
BGO555	pBG380	GTAAATCATATAGCAATATGGCGCCATAACATCTC	BsaH
BGO556	pBG381	GGGCTTTCCACACTAGTGCAATCAACGCCATTTC	Spe I
BGO557	pBG381	GAAATGGCGTTGATTGCACTAGTGTGAAAAGCC	Spe I
BGO558	pBG382	GAAAAGGGAGCAAACGCAGCGGCAATTGCAGCGGCCTTAGTTGCCACT	Mfe I
BGO559	pBG382	CAGTGGCAACTAAGGCCGCTGCAATTGCCGCTGCGTTTGTCTCCCTTTTCGGGACTTCTATTAGTGATGGG	Mfe I
BGO563	pBG383	CCTTAAACTTCTATGAATGAGTTCATGACGAGGTTTTAAAAACC	BspH I
BGO564	pBG384	GGTTTTTAAAACTCTGTCATGACCTCATT CATAGAAGTTTAAGG	BspH I
BGO565	pBG003, pBG403-423	CCATCTCCAAAATCGGATCTGCTGTTGGTGGTGGTGGTCTGGTTCCGCGTGGATCCATG TCATCTATCTTTGAAGG	BamH I
BGO566	pBG003, pBG403-423	CCGTCATCACCGAAAACGCGGAGGCAGATCGTCAGTCAGTCACGATGAATTAAGCTTTCA CTCGAGGACAACATTCACC	Hind III
BGO599	pBG443	GTCATCTATCTTTTGAAGGAAATTATACCACCTCAGGCTGCTGCTGCTACCTTAAAC TTCTATGAACTTGGACATGACGAGG	XhoI
BGO600	pBG443	CCTCGTCATGTCCAAGTTCATAGAAAGTTAAGGTAGCAGCAGCAGCAGCCTGAGGTGGTA TAATTTCTTCAAAGAGATAGATGA	XhoI
BGO675	pBG606-607	CATGCCATGGCGATGTCATCTATCTTTTGAAGGAAA	Nco I
BGO676	pBG606-607	CGCGGATCCTCACTCGAGGACAACATTCACCTTT	BamH I