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2 **TABLE 1S. Primers list**

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Target gene	Primer name	Sequence
<i>lacZ</i>	<i>lacZ</i> .CATBAD.A1.500-5	CTCACTCGCAATCAAATTCAG
	<i>lacZ</i> .CATBAD.B1.500-3	CTCAGGTCAAATTCAGACGGC
	<i>lacZ</i> .A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTCCGCTCACAATTCCACACAAC
	<i>lacZ</i> .B2.CATBAD.L-5	TTCTCCATACCCGTTTTTTTGGATCAATTTACACAGGAAACAGC
	<i>lacZ</i> .ext-5	CATTGGGTCACCAGCAAATC
	<i>lacZ</i> .CATBAD.ext-3	CCAGATAACTGCCGTCCTC
<i>Sequence^a</i>	<i>lacZ</i> ATG+100-3	GGGGGATGTGCTGCAAGGCGATTAAG
<i>flu</i>	<i>flu</i> .CATBAD.A1.500-5	GCCTGGGTATTGAAAACCTATGG
	<i>flu</i> .CATBAD.B1.500-3	CATATCCGGGGAGATAACTTG
	<i>flu</i> .A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTTCATGCATTCGTCCTCTCTG
	<i>flu</i> .B2.CAT.BAD.Lrbs-5	GTTTTTTTTGGATGGAGTGAAACGATGATCAGCAGAGTGACAGAAGCTC
	<i>flu</i> .ext-5	TCCGCTGGACATGCGTATGGAC
	<i>flu</i> .CATBAD.ext-3	TGCCGCGGGAGGTGGAAACTTGCTG
<i>Sequence^a</i>	<i>flu</i> ATG+100-3	GAACAGGCAGAGTGGCAGCTTC
<i>ftsL</i>	<i>ftsL</i> .CATBAD.A1.500-5	GCCTGGGTATTGAAAACCTATGG
	<i>ftsL</i> .CATBAD.B1.500-3	CATATCCGGGGAGATAACTTG
	<i>ftsL</i> .A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTTCATGCATTCGTCCTCTCTG
	<i>ftsL</i> .B2.CAT.BAD.Lrbs-5	GTTTTTTTTGGATGGAGTGAAACGATGATCAGCAGAGTGACAGAAGCTC
	<i>ftsL</i> .ext-5	TCCGCTGGACATGCGTATGGAC
	<i>ftsL</i> .CATBAD.ext-3	TGCCGCGGGAGGTGGAAACTTGCTG
<i>Sequence^a</i>	<i>ftsL</i> ATG+100-3	GAACAGGCAGAGTGGCAGCTTC
<i>ccdB</i>	<i>ccdB</i> .SPECBAD.A1.500-5	CTAAAATTGAGGATTTTAATG

	<i>ccdB</i> . SPECBAD.B1.500-3	GATCCGGGACGTAATGGAGC
	<i>ccdB</i> .A2. SPECBAD.L-3	CTTGGTGCCAGCCAATGAGAATCCCTCATAGCACACCTCTTTTTGAC
	<i>ccdB</i> .B2. SPEC.BAD.Lrbs-	GTTTTTTTGGATGGAGTGAAACGATGCAGTTTAAGGTTTACAC
	<i>ccdB</i> .ext-5	AGTTTTTGAAAATTGTGATG
	<i>ccdB</i> . SPECBAD.ext-3	GTGTGGCCAGCAGCATCTTG
<i>Sequence^a</i>	<i>pCcdB</i> -3	CTGACAGCAGACGTGCACTGGC
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<i>tray</i>	<i>traY</i> .CATBAD.A1.500-5	GATGATATCAGAAATATAATC
	<i>traY</i> .CATBAD.B1.500-3	CATCATGTACATGACAGCAC
	<i>traY</i> .A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTCTTTGGATAGCGGTGAAGATG
	<i>traY</i> .B2.CAT.BAD.Lrbs-5	TTCTCCATACCCGTTTTTTTTGGATCAGGGCAGGGAATATCTATG
	<i>traY</i> .ext-5	CTCATGTTTCGTCATAAAGAC
	<i>traY</i> .CATBAD.ext-3	CATACCCACAGCAATAAATAC
<i>Sequence^a</i>	<i>traY</i> ATG+100-3	CAGAACAGCAGCCGGGATCACTGCG
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<i>ypjA</i>	<i>ypjA</i> .500-5	GTAAACTGAACCGACTGGGGC
	<i>ypjA</i> .500-3	CAGTCAATTTTCTGGTGGAAAAG
	<i>ypjA</i> .GBL-3	GATTTTGAGACACAACGTGGCTTTCATAAATTTTCATCCTCTGAAAAG
	<i>ypjA</i> .GBL-5	CTTCACGAGGCAGACCTCAGCGCCTGACCATCAACGAAAAAGCCAC
	<i>ypjA</i> .EXT-5	GGTCCGGACTGAAAAAACTG
	<i>ypjA</i> .EXT-3	GAAACTGTTATTAAGGAAC
	<i>ypjA</i> .B1.CATBAD-500-3	GCCCTTGAACTTTTACTATC
	<i>ypjA</i> .A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTTGAATACTGAGTAGCGTTTAAG
	<i>ypjA</i> .B2.CATBAD.L-5	TTCTCCATACCCGTTTTTTTTGGATCTTTTCAGAGGATGAAATTTATG
	<i>ypjA</i> .ext.CATBAD-3	GACTTATTTATCGTTGTACC
<i>Sequence^a</i>	<i>ypjA</i> .ATG+100	CTACAGTCTCATCGTTTACCACAC
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<i>ydhQ</i>	<i>ydhQ</i> .500-5	GAAGACCAGATTAAGAAAATC
	<i>ydhQ</i> .500-3	GGGCTTATGGTGGGTGTCTGTATGGC
	<i>ydhQ</i> .GBL-3	GATTTTGAGACACAACGTGGCTTTCATGATTTATTCCTTTGCTGC
	<i>ydhQ</i> .GBL-5	CTTCACGAGGCAGACCTCAGCGCCTAAAAATACAGGCGCAACCCGTG

	<i>ydhQ</i> .EXT-5	ACGTATTGGATACAGAGAAG
	<i>ydhQ</i> .EXT-3	ACTATCCGCGTAGGTTATCG
	<i>ydhQ</i> .B1.CATBAD-500-3	CCTGGATACACCAACAATTC
	<i>ydhQ</i> OK A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTGTGCCTTTATTGCTACCTAAG
	<i>ydhQ</i> .B2.CATBAD.L-5	TTCTCCATAACCCGTTTTTTTTGGATCAGCAAAGGAATAAATCATGGG
	<i>ydhQ</i> .ext.CATBAD-3	GATTAATCTCACAATTGCTG
<i>Sequence^a</i>	<i>ydhQ</i> .ATG+100	CCGTGACCACGGTATTTTCGGCTC
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<i>ycgH</i>	<i>ycgH</i> .500-5	CTTAATGCCCTTGTTTGGCTGGCG
	<i>ycgH</i> .500-3	CGCGTAAAGGTGCAAAAGTG
	<i>ycgH</i> .GBL-3	GATTTTGAGACACAACGTGGCTTTCATAGATTAACCATCCATTC
	<i>ycgH</i> .GBL-5	CTTCACGAGGCAGACCTCAGCGCCTGATCCCGCCGTTAGCTAAAAAAC
	<i>ycgH</i> .EXT-5	CGGGCTGGGAGAAGTGCTTG
	<i>ycgH</i> .EXT-3	GGTGTTGGTGCAGTAACAGAAAAAGG
	<i>ycgH</i> .B1.CATBAD-500-3	CTGAATATGCCCCACCCGAC
	<i>ycgH</i> .A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTATTGGATTAACAAACATTCC
	<i>ycgH</i> .B2.CATBAD.L-5	TTCTCCATAACCCGTTTTTTTTGGATGAATGGATGGTTAATCTATG
	<i>ycgH</i> .ext.CATBAD-3	CAAGACGGGTGTTATTTACC
<i>Sequence^a</i>	<i>ycgH</i> .ATG+100	CAATCGGCGATTCTTCATCAGTC
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<i>ycgV</i>	<i>ycgV</i> .500-5	CAATATGCTGGCAAGATGAAAATG
	<i>ycgV</i> .500-3	GCTGGTGAATAACAAATTAC
	<i>ycgV</i> .GBL-3	GATTTTGAGACACAACGTGGCTTTCATACCACTCCTATATAGTACCC
	<i>ycgV</i> .GBL-5	CTTCACGAGGCAGACCTCAGCGCCTAAGTGCGGGATAGACAAGCCC
	<i>ycgV</i> .EXT-5	CATTAGCAGTGATATAACGTAAG
	<i>ycgV</i> .EXT-3	GTATGCGGCGTGGCAGCATTC
	<i>ycgV</i> .B1.CATBAD-500-3	GGGTATAGTCACCAATTAAG
	<i>ycgV</i> .A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTCTATGGGTCTATGGATTTTGTC
	<i>ycgV</i> .B2.CATBAD.L-5	TTCTCCATAACCCGTTTTTTTTGGATGTACTATATAGGAGTGGTATG
	<i>ycgV</i> .ext.CATBAD-3	CGTTCGAGTTTTCAATGGTG

<i>Sequence^a</i>	<i>ycgV</i> .ATG+100	CTTCCTGTATCAGCAGCTATCAG
<i>yfaL</i>	<i>yfaL</i> .500-5	GGTCAGACAAGGTGTCCGGG
	<i>yfaL</i> .500-3	TGCAGGAAACCGTGGAAGAGCACGC
	<i>yfaL</i> .GBL-3	GATTTTGAGACACAACGTGGCTTTCATATTAATCTAACCATCATTTTC
	<i>yfaL</i> .GBL-5	CTTCACGAGGCAGACCTCAGCGCCTAATCACTGTCTAGTCGGCACGG
	<i>yfaL</i> .EXT-5	CATAACTTTGTGGATAACTCAGG
	<i>yfaL</i> .EXT-3	CAGGTGGCAAACTGCACGCACTGGA
	<i>yfaL</i> .B1.CATBAD-500-3	CGTTAGTGACACGTAAATCG
	<i>yfaL</i> .A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTCTATAAGACGGCGTATTTAATC
	<i>yfaL</i> .B2.CATBAD.L-5	TTCTCCATAACCGTTTTTTTTGGATATGATGGTTAGATTAATATG
	<i>yfaL</i> .ext.CATBAD-3	CATTATTAATGGTATAAATTG
<i>Sequence^a</i>	<i>yfaL</i> .ATG+100	CAACTCGCTTTGACATCATATC
<i>ydeKU</i>	<i>ydeUK</i> .500-5	AGTTTAGGCATTACCACTCC
	<i>ydeUK</i> .500-3	CTGTTAGTTTTTTGAGTATAG
	<i>ydeUK</i> .GBL-3	GATTTTGAGACACAACGTGGCTTTCATATTAATCTAACCATCATTTTC
	<i>ydeUK</i> .GBL-5	CTTCACGAGGCAGACCTCAGCGCCTAATCACTGTCTAGTCGGCACGG
	<i>ydeUK</i> .EXT-5	CATAACTTTGTGGATAACTCAGG
	<i>ydeUK</i> .EXT-3	CAGGTGGCAAACTGCACGCACTGGA
	<i>ydeUK</i> .B1.CATBAD-500-3	GTGACCCTTCTGTTTAATATTC
	<i>ydeUK</i> .A2.CATBAD.L	CAGGGCGGGGCGTAAGAATCCCTGCTCAATACAGCCACGAAAGAGATGAG
	<i>ydeUK</i> .B2.CATBAD.L-5	TTCTCCATAACCGTTTTTTTTGGATGTATATGGAGCGTTTATATG
	<i>ydeUK</i> .ext.CATBAD-3	GTCAGAACAGAGTCCTCTCCC
<i>Sequence^a</i>	<i>ydeUK</i> .ATG+100	GTTGTCAGTCCAGAGGATTTACG
<i>yeeJ</i>	<i>yeeJ</i> .500-5	GTTCAATTAATTAACAACCTTG
	<i>yeeJ</i> .500-3	CTCGATTAACGTTTCAGCAGCAATC
	<i>yeeJ</i> .GBL-3	GATTTTGAGACACAACGTGGCTTTCATGCTTACCTCCCTGAAC
	<i>yeeJ</i> .GBL-5	CTTCACGAGGCAGACCTCAGCGCCTGATTTTCCGTTATAAATTTCTTAAAGAG
	<i>yeeJ</i> .EXT-5	GCATCACGCTAATGATACAGACTCG

	<i>yeeJ</i> .EXT-3	GTCTACCGTTTATCCTTACCAC
	<i>yeeJ</i> .B1.CATBAD-500-3	CGCTTGCTCGCTGTTTCATATC
	<i>yeeJ</i> .JOK.A2.CATBAD.L-3	CAGGGCGGGGCGTAAGAATCCCTGCTCATAAATGCGCCCTTTCTAGCAC
	<i>yeeJ</i> .B2.CATBAD.L-5	TTCTCCATACCCGTTTTTTTTGGATGCTCGTTCAGGGAAGGTAAGC
	<i>yeeJ</i> .ext.CATBAD-3	CATTGCGCCTGAAGCCTGAGAAG
<i>Sequence^a</i>	<i>yeeJ</i> .ATG+100	AGCCATAGGGAACGCAAGTTGAG
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RExBAD	<i>cat-ara</i> .A1.500-5	CATTAACGCCGGGCAAGGGGAAG
<i>cassette</i>		
	<i>cat-ara</i> .B1.500-3	CACCGCTCTGCATTCCGGCAG
	<i>cat-ara</i> .A2. <i>catL</i> -3	GAAGTGATCTTCCGTCACAGCCCTATGCTACTCCGTCAAGCCGTC
	<i>cat-ara</i> .B2. <i>catLnp</i> -5	GAGTGGCAGGGCGGGGCGTAAGAATCCCTGCTTCGTCCATTTG
	K7.CAT- <i>araC</i> - <i>pBAD</i> -5	GCTTGCATAATGTGCCTGTC
	K7.CAT- <i>araC</i> - <i>pBAD</i> -3	CTCTCACCGGTAGCGCAGTC
<i>Sequence^b</i>	<i>paraB</i> -300-5	GTCCATATTGCATCAGACATTG

1 ^a primers used to sequence the junction between the end of the pBAD promoter and the ATG codon of target

2 genes.

3 ^b primer used to verify the integrity of the pBAD promoter region.