

Table SA. Stability of hybrids formed by binding of Probe A to mycobacterial 16S rRNA gene amplicons

Sequence of Probe A Compared to Target Sequences *	Species	T _m
5' - GCTTTCCACCACA A GACATGCATCC C GTGGTCCTATCCG-3'	<i>M. tuberculosis</i>	73
5' - GCTTTCCACCACA G GACATGCATCC C GTGGTCCTATCCG-3'	<i>M. asiaticum</i>	71
5' - GCTTTCCACCACAC A CCATGC A GCATGTGGTCCTATCCG-3'	<i>M. branderi</i>	70
5' - GCTTTCCACCACA A GACATGCATCC C ATGGTCCTATCCG-3'	<i>M. celatum</i>	70
5' - GCTTTCCACCACA G GACATGA A TCC C GTGGTCCTATCCG-3'	<i>M. marinum</i>	69
5' - GCTTTCCACCACAC A CCATGC G ACATGTGGTCCTATCCG-3'	<i>M. shimoidei</i>	68
5' - GCTTTCCACCACA G GCATGC G CGTGGTCCTATCCG-3'	<i>M. chubuense</i>	68
5' - GCTTTCCACCACA G AACATGCATCC C ATGGTCCTATCCG-3'	<i>M. terrae</i>	67
5' - GCTTTCCACCACA A GGCATGC G CC A AGTGGTCCTATCCG-3'	<i>M. kansasii</i>	67
5' - GCTTTCCACCACA G AAGACATGC G TCT T GAGGTCCTATCCG-3'	<i>M. avium</i>	65
5' - GCTTTCCACCACA A GGCATGC G CT T CGTGGTC A TATCCG-3'	<i>M. sherisii</i>	65
5' - GCTTTCCACCACAC G ACATGCATC G CGT A GTCCAT T CG-3'	<i>M. aurum</i>	64
5' - GCTTTCCACCACAC A CCATGA A GC G CGTGGTCCTATCCG-3'	<i>M. senegalense</i>	64
5' - GCTTTCC C ACA A AGGCATGC G CT T GAGGTCCTATCCG-3'	<i>M. haemophilum</i>	64
5' - GCTTTCCACCACAC A CCAT T CGATGC G CGGTCCTATCCG-3'	<i>M. triviale</i>	63
5' - GCTTTCCACC T AA A GACATGC G CT A AAAGGTCCTATCCG-3'	<i>M. intracellulare</i>	62
5' - GCTTTCCACC C CA A GGCATGC G CT C GGGTCCTATCCG-3'	<i>M. szulgai</i>	62
5' - GCTTTCCACCACAC A CCATGA A GC G CGGTCCTATCCG-3'	<i>M. engbaekii</i>	61
5' - GCTTTCCACCACA G GCATGA A T G CGTGGTCCTAT T CG-3'	<i>M. tokaiense</i>	61
5' - GCTTTCCACC A AA A GGCATGC G CC A AAAGGTCCTATCCG-3'	<i>M. lentiflavum</i>	60
5' - GCTTTCCACCACAC A CCATGA A GC G CGTGGTC A TAT T CG-3'	<i>M. fortuitum</i>	58
5' - GCTTTCCACC C CA A GGCATGC G CT C GGGGTCCTAT T CG-3'	<i>M. malmoense</i>	58
5' - A CTTTCCACCAC C CCACATGC G C A GA A TGGTCCTATCCG-3'	<i>M. xenopi</i>	57
5' - GCTTT G CACC A CT C ACCATGA A GT G TGTGGTCCTATCCG-3'	<i>M. abscessus</i>	57
5' - GCTTTCCACCACA A CCATGC A GG C ATGA T CCAT T CG-3'	<i>M. rhodesiae</i>	54
5' - GCTTTCCACCACAC C CCATGA A G A GC G CGGTC A TAT T CG-3'	<i>M. diernhoferi</i>	52
5' - GCTTTCCACCACA A CCATGA A GG C ATGA T CCAT T CG-3'	<i>M. aichiense</i>	48

* Those nucleotides in each target sequence that are not complementary to the corresponding nucleotide in Probe A are indicated by black letters.

Table SB. Stability of hybrids formed by binding of Probe B to mycobacterial 16S rRNA gene amplicons

Sequence of Probe B Compared to Target Sequences *	Species	T _m
5' - GCTTTCCACCACAA G ACATGCATCCCGTGGTCCTATCCG - 3'	<i>M. tuberculosis</i>	77
5' - GCTTTCCACCACA GG ACATGCATCCCGTGGTCCTATCCG - 3'	<i>M. asiaticum</i>	76
5' - GCTTTCCACCACAA G ACATGCATCC A TGGTCCTATCCG - 3'	<i>M. celatum</i>	74
5' - GCTTTCCACCACA G CACATGCAT G CCGTGGTCCTATCCG - 3'	<i>M. chubuense</i>	73
5' - GCTTTCCACCACA GG ACATG AA TCCCGTGGTCCTATCCG - 3'	<i>M. marinum</i>	73
5' - GCTTTCCACCACA G CACATG AA T G CCGTGGTCCTAT T CG - 3'	<i>M. tokaiense</i>	73
5' - GCTTTCCACCACA GA ACATGCATCC A TGGTCCTATCCG - 3'	<i>M. terrae</i>	72
5' - GCTTTCCACCACA C ACCATGC A GCATGTGGTCCTATCCG - 3'	<i>M. branderi</i>	67
5' - GCTTTCCACCACA C ACCATGC G ACATGTGGTCCTATCCG - 3'	<i>M. shimoidei</i>	66
5' - GCTTTCCACCACA C ACCATG AA GC G CGTGGTCCTATCCG - 3'	<i>M. senegalense</i>	66
5' - GCTTTCCACCACAA GG CATGC G CC AA GTGGTCCTATCCG - 3'	<i>M. kansasii</i>	65
5' - GCTTTCCACCACAA GG CATGC G CC T CGTGGTC A TATCCG - 3'	<i>M. sherisii</i>	63
5' - GCTTTCCACCACA C ACCATG AA GC G CGCGGTCCATCCG - 3'	<i>M. engbaekii</i>	63
5' - GCTTTCCACCACA C ACCAT T CGATG C GCGGTCCATCCG - 3'	<i>M. triviale</i>	63
5' - GCTTTCCACCACA C GCATGCAT C GCGT A GTCCAT T CG - 3'	<i>M. aurum</i>	62
5' - GCTTTCCACCAG AA GACATGC G T T T G AGGTCCATCCG - 3'	<i>M. avium</i>	61
5' - GCTTTCCACCACA C ACCATG AA GC G CGTGGTC A TAT T CG - 3'	<i>M. fortuitum</i>	60
5' - GCTTTCCACC CC AA GG CATGC G CC T CGGGTCCTATCCG - 3'	<i>M. szulgai</i>	60
5' - GCTTTCC CC CA AA GGCATGC G CC T T G AGGTCCATCCG - 3'	<i>M. haemophilum</i>	60
5' - GCTTTCCACCACA A CCATGC A GG CC ATG A TCCAT T CG - 3'	<i>M. rhodesiae</i>	59
5' - A CTTTCCACCAC CC CACATGC G C A GAATGGTCCTATCCG - 3'	<i>M. xenopi</i>	58
5' - GCTTTCCACC T AA AG ACATGC G CC T AA AG GTCCATCCG - 3'	<i>M. intracellulare</i>	58
5' - GCTTTCCACC AAA GGCATGC G CC AAA AGGTCCATCCG - 3'	<i>M. lentiflavum</i>	57
5' - GCTTTCCACC CC AA GG CATGC G CC T CGGGTCCTAT T CG - 3'	<i>M. malmoense</i>	57
5' - GCTTTCCACCACA A CCATG AA GG CC ATG A TCCAT T CG - 3'	<i>M. aichiense</i>	55
5' - GCTTT G CACCAC T CACCATG AA GT G TGTGGTCCTATCCG - 3'	<i>M. abscessus</i>	55
5' - GCTTTCCACCACA C CCATG AA G AG CGCGGT C A T AT T CG - 3'	<i>M. diernhoferi</i>	54

* Those nucleotides in each target sequence that are not complementary to the corresponding nucleotide in Probe B are indicated by black letters.

Table SC Stability of hybrids formed by binding of Probe C to mycobacterial 16S rRNA gene amplicons

Sequence of Probe C Compared to Target Sequences *	Species	T _m
5' - GCTTTCCACCAAAAAGGCATGCGCC AAA AGGTCCTATCCG - 3'	<i>M. lentiflavum</i>	71
5' - GCTTTCC CCAC AAAAGGCATGCGCCT TG AGGTCCTATCCG - 3'	<i>M. haemophilum</i>	71
5' - GCTTTCCACCA CA AGGCATGCGCC AAG TGGTCCTATCCG - 3'	<i>M. kansasii</i>	66
5' - GCTTTCCACC CCA AGGCATGCGCCT CG GGGTCCTATCCG - 3'	<i>M. szulgai</i>	65
5' - GCTTTCCACCT TAAAG ACATGCGCCT AA AGGTCCTATCCG - 3'	<i>M. intracellulare</i>	64
5' - GCTTTCCACCA GAA AGACATGCG TCT TGAGGTCCTATCCG - 3'	<i>M. avium</i>	64
5' - GCTTTCCACCA CA AGGCATGCGCCT CG TGGTCATATCCG - 3'	<i>M. sherrisii</i>	63
5' - GCTTTCCACCA CCA AGGCATGCGCCT CG GGGTCCTAT TCG - 3'	<i>M. malmoense</i>	62
5' - GCTTTCCACCA CAC ACCATGCG AC AT GT GGGTCCTATCCG - 3'	<i>M. shimoidei</i>	55
5' - GCTTTCCACCA CAAG ACATGCAT CC ATGGTCCTATCCG - 3'	<i>M. celatum</i>	53
5' - GCTTTCCACCA CAG CACATGCAT GC CGTGGTCCTATCCG - 3'	<i>M. chubuense</i>	53
5' - GCTTTCCACCA CAAG ACATGCAT CC CGTGGTCCTATCCG - 3'	<i>M. tuberculosis</i>	53
5' - ACT TTTCCACCA CCC ACATGCG CAG AATGGTCCTATCCG - 3'	<i>M. xenopi</i>	52
5' - GCTTTCCACCA CAG ACATGCAT CC CGTGGTCCTATCCG - 3'	<i>M. asiaticum</i>	52
5' - GCTTTCCACCA CAC ACCATGC AG CAT GT GGGTCCTATCCG - 3'	<i>M. branderi</i>	51
5' - GCTTTCCACCA CAC ACCAT TC GATGC CG GGTCCTATCCG - 3'	<i>M. triviale</i>	51
5' - GCTTTCCACCA CAGA ACATGCAT CC ATGGTCCTATCCG - 3'	<i>M. terrae</i>	48
5' - GCTTT GC ACCA CTC ACCATGA AGTGTGT GGGTCCTATCCG - 3'	<i>M. abscessus</i>	—
5' - GCTTTCCACCA CAA CCCATGA AGGCC ATGATCCTAT TCG - 3'	<i>M. aichiense</i>	—
5' - GCTTTCCACCA CAC GACATGCAT CG CGTAGTCCTAT TCG - 3'	<i>M. aurum</i>	—
5' - GCTTTCCACCA CAC CCCATGA AGAG CGCGGGTCATAT TCG - 3'	<i>M. diernhoferi</i>	—
5' - GCTTTCCACCA CAC ACCATGA AG CGCGGGTCCTATCCG - 3'	<i>M. engbaekii</i>	—
5' - GCTTTCCACCA CAC ACCATGA AG CGCGTGGTCATAT TCG - 3'	<i>M. fortuitum</i>	—
5' - GCTTTCCACCA CAG ACATGAAT CC CGTGGTCCTATCCG - 3'	<i>M. marinum</i>	—
5' - GCTTTCCACCA CAA CCCATGC AGGCC ATGATCCTAT TCG - 3'	<i>M. rhodesiae</i>	—
5' - GCTTTCCACCA CAC ACCATGA AG CGCGTGGTCCTATCCG - 3'	<i>M. senegalense</i>	—
5' - GCTTTCCACCA CAG CACATGAAT GC CGTGGTCCTAT TCG - 3'	<i>M. tokaiense</i>	—

* Those nucleotides in each target sequence that are not complementary to the corresponding nucleotide in Probe C are indicated by black letters.

Table SD. Stability of hybrids formed by binding of Probe D to mycobacterial 16S rRNA gene amplicons

Sequence of Probe D Compared to Target Sequences *	Species	T _m
5' - GCTTTCCACCACACACCATGAAGCGCGTGGTCCTAT CCG -3'	<i>M. senegalense</i>	77
5' - GCTTTCCACCACACACCATGAAGCGCGTGGTC A TATTCG-3'	<i>M. fortuitum</i>	75
5' - GCTTTCCACCACACACCATGAAGCGCG C GGTCCTAT CCG -3'	<i>M. engbaekii</i>	73
5' - GCTTTCCACCACACACCATG CAGC ATGTGGTCCTAT CCG -3'	<i>M. branderi</i>	66
5' - GCTTTCCACCACAC CCC ATGAAG AGCG CGGTC A TATTCG-3'	<i>M. diernhoferi</i>	66
5' - GCTTTCCACCACAG C ACATGAAT GC CGTGGTCCTATTCG-3'	<i>M. tokaiense</i>	66
5' - GCTTTCCACCACACACCAT TCG ATGCGCGGGTCCTAT CCG -3'	<i>M. triviale</i>	66
5' - GCTTTCCACCACACACCATG CGA CTGTGGTCCTAT CCG -3'	<i>M. shimoidei</i>	64
5' - GCTTT G CACCAC T CACCATGAAG TGT GTGGTCCTAT CCG -3'	<i>M. abscessus</i>	64
5' - GCTTTCCACCACAC G ACATG CA T CG CGT AG TCCTATTCG-3'	<i>M. aurum</i>	63
5' - GCTTTCCACCACAG C ACATG CA T GC CGTGGTCCTAT CCG -3'	<i>M. chubuense</i>	61
5' - GCTTTCCACCACA A CCCATGAAG GC CA TGA TCCTATTCG-3'	<i>M. aichiense</i>	60
5' - GCTTTCCACCACAG G ACATGAAT CC CGTGGTCCTAT CCG -3'	<i>M. marinum</i>	59
5' - GCTTTCCACCACA A AGACATG CA T CC CGTGGTCCTAT CCG -3'	<i>M. tuberculosis</i>	58
5' - GCTTTCCACCACA A GGCATG CGC CA AG TGGTCCTAT CCG -3'	<i>M. kansasii</i>	56
5' - GCTTTCCACCACA A GGACATG CA T CC CGTGGTCCTAT CCG -3'	<i>M. asiaticum</i>	56
5' - GCTTTCCACCACA A CCCATG CGA GC ATGA TCCTATTCG-3'	<i>M. rhodesiae</i>	56
5' - GCTTTCCACCACA G AACATG CA T CC ATGGTCCTAT CCG -3'	<i>M. terrae</i>	52
5' - GCTTTCCACCACA A AGACATG CA T CC ATGGTCCTAT CCG -3'	<i>M. celatum</i>	51
5' - GCTTTCC CCACA AAGGCATG CGC CT TG AGGTCCTAT CCG -3'	<i>M. haemophilum</i>	51
5' - GCTTTCCACCACA A GGCATG CGC CT CG TGGTC A TAT CCG -3'	<i>M. sherisii</i>	50
5' - GCTTTCCACC CCA AAGGCATG CGC CT CG GGTCCTATTCG-3'	<i>M. malmoense</i>	50
5' - A CTTTCCACCAC CC CACATG CGC AG AA TGGTCCTAT CCG -3'	<i>M. xenopi</i>	49
5' - GCTTTCCACCAG AA GACATG CGT CT TG AGGTCCTAT CCG -3'	<i>M. avium</i>	—
5' - GCTTTCCACC TAA AGACATG CGC CT AAA AGGTCCTAT CCG -3'	<i>M. intracellulare</i>	—
5' - GCTTTCCACC AAA AAGGCATG CGC CA AAA AGGTCCTAT CCG -3'	<i>M. lentiflavum</i>	—
5' - GCTTTCCACC CCA AAGGCATG CGC CT CG GGTCCTAT CCG -3'	<i>M. szulgai</i>	—

* Those nucleotides in each target sequence that are not complementary to the corresponding nucleotide in Probe D are indicated by black letters.