Table S1 Collected primers and their coverage and specificity

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Primer | Sequence (5' - 3') | Number | Forward (F)/  Reverse (R) | Coverage (%) | Specificity (%) | Reference |
| ndoB1.1.f | CGATGAAGAACTTTTCCA | 1 | F | 0.001 | 99.952 | [1] |
| ndoB2.1.r | CAGCCCAGTTGGAGCTGCTG | 1 | R | 0.001 | 99.952 |
| P1.1.f | TGYCGSCAYCGNGGNA | 2 | F | 0.288 | 87.654 |
| P2.1.r | CCANCCRTGRTANGARCA | 2 | R | 0.005 | 99.734 |
| P1.2.f | TGYCGNCAYAGRGGNA | 3 | F | 0.228 | 88.962 |
| P2.2.r | CCANCCRTGRTARCTRCA | 3 | R | 0.093 | 95.013 |
| P1.1.f | TGYCGSCAYCGNGGNA | 4 | F | 0.288 | 87.654 |
| P2.2.r | CCANCCRTGRTARCTRCA | 4 | R | 0.005 | 99.734 |
| P1.2.f | TGYCGNCAYAGRGGNA | 5 | F | 0.228 | 88.962 |
| P2.1.r | CCANCCRTGRTANGARCA | 5 | R | 0.093 | 95.013 |
| DP1,Rieske\_f | TGYMGNCAYMGNGG | 6 | F | 0.367 | 83.563 | [2, 3] |
| DP2,Rieske\_r | CCANCCRTGRTANSWRCA | 6 | R | 0.301 | 84.241 |
| nahAc1 | GTTTGCAGCTATCACGGCTGGGGCTTCGGC | 7 | F | 0.009 | 99.952 | [4] |
| nahAc3 | TTCGACAATGGCGTAGGTCCAGACCTCGGT | 7 | R | 0.002 | 99.952 |
| nahAcfor | TGGCGATGAAGAACTTTTCC | 8 | F | 0.001 | 99.952 | [5-8] |
| nahAcrev | AACGTACGCTGAACCGAGTC | 8 | R | 0.000 | 100.000 |
| P8073 | TTCGAGCTGGAATGTGAGC | 9 | F | 0.001 | 100.000 |
| P9047 | AATAACCGGCGATTCCAAAC | 9 | R | 0.001 | 100.000 |
| 2NT-F | TTTGTGTGCGGYTACCACGGNTGGGG | 10 | F | 0.004 | 100.000 | [9] |
| 2NT-R | TGTCACCTACAAAGTTTTCCGCAAAARSCTTCCAGTT | 10 | R | 0.001 | 100.000 |
| NAH-F | CAAAARCACCTGATTYATGG | 11 | F | 0.003 | 99.952 | [10-12] |
| NAH-R | AYRCGRGSGACTTCTTTCAA | 11 | R | 0.016 | 99.806 |
| nagAc-like-F | GGCTGTTTTGATGCAGA | 12 | F | 0.005 | 99.855 | [13] |
| nagAc-like-R | GGGCCTACAAGTTCCA | 12 | R | 0.005 | 99.855 |
| nagAc-like-F | GGCTGTTTTGATGCAGA | 13 | F | 0.005 | 99.855 |
| nagAc-like-P | CCAGGCTGCATCACCCAGATA | 13 | R | 0.005 | 99.855 |
| nahAF | CCCYGGCGACTATGT | 14 | F | 0.008 | 99.806 | [14, 15] |
| nahARev | TGCGTCCAACCMACG | 14 | R | 0.012 | 99.855 |
| nahAc-1F | AAGAGCTGTACGGCGAGTC | 15 | F | 0.008 | 99.952 | [16] |
| nahAc-1R | CCTGATCGAAGCAACCATAG | 15 | R | 0.007 | 100.000 |
| nahAc-3F | GACGCTGCTTGGTACCTAGA | 16 | F | 0.007 | 99.952 |
| nahAc-3R | TCCAGTTGGCCTTGATCA | 16 | R | 0.013 | 99.637 |
| nahAc-6F | TGATCAAGGCCAACTGGA | 17 | F | 0.013 | 99.637 |
| nahAc-6R | AGCGACGCGAAGATAGACTC | 17 | R | 0.005 | 99.952 |
| nahAc-7F | ACTTGGTTCCGGAGTTGATG | 18 | F | 0.005 | 99.952 |
| nahAc-7R | CAGGTCAGCATGCTGTTGTT | 18 | R | 0.003 | 99.952 |
| Nah-for | TGCMVNTAYCAYGGYTGG | 19 | F | 0.365 | 80.537 | [17] |
| Nah-rev1 | CCCGGTARWANCCDCKRTA | 19 | R | 0.002 | 99.564 |
| Nah-for | TGCMVNTAYCAYGGYTGG | 20 | F | 0.365 | 80.537 |
| Nah-rev2 | CRGGTGYCTTCCAGTTG | 20 | R | 0.009 | 99.855 |
| Nid-for | TCCRMTGCCCDTACCACGG | 21 | F | 0.022 | 98.959 |
| Nid-rev1 | GAASGAYARRTTSGGGAACA | 21 | R | 0.015 | 99.903 |
| Nid-for | TCCRMTGCCCDTACCACGG | 22 | F | 0.022 | 98.959 |
| Nid-rev2 | GCGSCKRKCTTCCAGTTCG | 22 | R | 0.024 | 99.831 |
| NahAc-forward | CAGAGCGTYCCRTTYGAAAA | 23 | F | 0.011 | 99.952 | [18, 19] |
| NahAc-reverse | TCGAAGCAACCRTARATGAA | 23 | R | 0.011 | 99.952 |
| NahAc-forward | CAGAGCGTYCCRTTYGAAAA | 24 | F | 0.011 | 99.952 |
| NahAc-probe | TGGGGTTGAAAGAAGTCGCTCG | 24 | R | 0.011 | 99.952 |
| nidA-forward | TTCCCGAGTACGAGGGATAC | 25 | F | 0.005 | 100.000 |
| nidA-reverse | TCACGTTGATGAACGACAAA | 25 | R | 0.005 | 100.000 |
| nidA-forward | TTCCCGAGTACGAGGGATAC | 26 | F | 0.005 | 100.000 |
| nidA-probe | TCCTACCCGTCGCCGGTACA | 26 | R | 0.005 | 100.000 |
| NAPH-1F | TGGCTTTTCYTSACBCATG | 27 | F | 0.000 | 100.000 | [20] |
| NAPH-1R | DGRCATSTCTTTTTCBAC | 27 | R | 0.007 | 99.952 |
| NAPH-2F | TATCACGGCTGG | 28 | F | 0.111 | 95.449 |
| NAPH-2R | ATSTCTTTTTCBAC | 28 | R | 0.007 | 99.903 |
| FRT5A | TYRARGCYAACTGGAA | 29 | F | 0.035 | 98.523 | [21] |
| FRT3B | CATGTCTTTTTCKACVATGGC | 29 | R | 0.006 | 99.952 |
| FRT6A | TACCACGTBGGTTGGAC | 30 | F | 0.013 | 99.782 |
| FRT4B | GWHDCYGTYTCCATRTTGTC | 30 | R | 0.003 | 99.952 |
| PAH-RHDαGN F | GAGATGCATACCACGTKGGTTGGA | 31 | F | 0.003 | 99.952 | [22-24] |
| PAH-RHDαGN R | AGCTGTTGTTCGGGAAGAYWGTGCMGTT | 31 | R | 0.000 | 100.000 |
| Cyc372F | CGATGAGTTGGATAGAGATTCG | 32 | F | 0.001 | 100.000 | [25] |
| Cyc854R | GGTTCTCCAAGGTTCTCTG | 32 | R | 0.001 | 100.000 |
| RieskeF | TGYCGBCAYCGBGGSAWG | 33 | F | 0.119 | 96.926 | [26] |
| RieskeR | CCAGCCGTGRTARSTGCA | 33 | R | 0.095 | 95.740 |
| ARHD1F | TTYRYNTGYANNTAYCAYGGNTGGG | 34 | F | 0.067 | 98.765 | [27] |
| ARHD2R | AANTKYTCNGCNGSNRMYTTCCA | 34 | R | 0.131 | 98.983 |
| ARHD1F | TTYRYNTGYANNTAYCAYGGNTGGG | 35 | F | 0.067 | 98.765 |
| ARHD1R | CCCANCCRTGRTANNTRCANRYRAA | 35 | R | 0.067 | 98.765 |
| Dxn1F | TGYASNTAYCAYGGVTGG | 36 | F | 0.253 | 87.122 | [28] |
| Dxn2R | TBVGGNCCVYKNGGVTGCC | 36 | R | 0.111 | 98.088 |
| AJ025 | TAYATGGGBGARGAYCCVGT | 37 | F | 0.040 | 99.903 | [29] |
| AJ026 | GCRAAYTTCCARTTRCABGG | 37 | R | 0.019 | 99.879 |
| BPDOXF | ATHCCNTGTAAYTGGAARTTYGC | 38 | F | 0.017 | 99.976 | [30] |
| BPDOXR | CCARTTYTCNCCRTCRTCYTGYTC | 38 | R | 0.029 | 99.758 |
| todC1F | GCGAGATAGAAGCGCTCTTT | 39 | F | 0.000 | 100.000 | [31] |
| todC1R | GTATTGATACCTGGGAGGAAG | 39 | R | 0.001 | 100.000 |
| adoF1 | GTGTTCCTGAACCAGTGCCGSCACCG | 40 | F | 0.004 | 99.976 | [32, 33] |
| adoB1 | TGGTACATGTCRCTGCARAACTGCTC | 40 | R | 0.010 | 99.927 |
| BPH1-F | GGACGTGATGCTCGAYCGC | 41 | F | 0.005 | 99.976 | [10] |
| BPH1-R | TGTTSGGYACGTTMAGGCCCAT | 41 | R | 0.001 | 100.000 |
| BPH2-F | GACGCCCGCCCCTATATGGA | 42 | F | 0.004 | 100.000 |
| BPH2-R | AGCCGACGTTGCCAGGAAAAT | 42 | R | 0.002 | 100.000 |
| BPH3-F | CCGGGAGAACGGCAGGATC | 43 | F | 0.000 | 100.000 |
| BPH3-R | TGCTCCGCTGCGAACTTCC | 43 | R | 0.003 | 100.000 |
| TOD-F | ACCGATGARGAYCTGTACC | 44 | F | 0.001 | 100.000 |
| TOD-R | CTTCGGTCMAGTAGCTGGTG | 44 | R | 0.001 | 100.000 |
| TOL-F | TGAGGCTGAAACTTTACGTAGA | 45 | F | 0.000 | 100.000 |
| TOL-R | CTCACCTGGAGTTGCGTAC | 45 | R | 0.000 | 100.000 |
| TODC1-F | CAGTGCCGCCAYCGTGGYATG | 46 | F | 0.002 | 99.879 | [34, 35] |
| TODC1-R | GCCACTTCCATGYCCRCCCCA | 46 | R | 0.001 | 100.000 |
| TBMD-F | GCCTGACCATGGATGC(C/G)TACTGG | 47 | F | 0.000 | 100.000 |
| TBMD-R | CGCCAGAACCACTTGTC(A/G)(A/G)TCCA | 47 | R | 0.000 | 100.000 |
| TMOA-F | CGAAACCGGCTT(C/T)ACCAA(C/T)ATG | 48 | F | 0.000 | 100.000 |
| TMOA-R | ACCGGGATATTT(C/T)TCTTC(C/G)AGCCA | 48 | R | 0.000 | 100.000 |
| bphAf371-B | GGCTTTCACCTGCASYTAYCAYGG | 49 | F | 0.004 | 99.976 | [36, 37] |
| bphAr1153-2 | CCAGTTCTCGCCRTCRTCYTGHTC | 49 | R | 0.020 | 99.879 |
| bphAf668-3 | GTTCCGTGTAACTGGAARTWYGC | 50 | F | 0.000 | 100.000 |
| bphAr1153-2 | CCAGTTCTCGCCRTCRTCYTGHTC | 50 | R | 0.020 | 99.879 |
| ditAf543 | GGCGATGCSAAGTGGTAYTWCGAC | 51 | F | 0.005 | 99.927 | [36] |
| ditA1186 | CCACGTGTCMGAGTCRTCCTGYTC | 51 | R | 0.001 | 100.000 |
| BEDemF | CAYGGVTGGGCBTAYGAYA | 52 | F | 0.013 | 99.637 | [38] |
| BEDeR | GTTYTCDCCRTCRTCYTGCT | 52 | R | 0.017 | 99.927 |
| BEDemF | CAYGGVTGGGCBTAYGAYA | 53 | F | 0.013 | 99.637 |
| BEDmR | GGAASGARCASGTDGGRAA | 53 | R | 0.011 | 99.952 |
| Forwardprimer1 | GGCTGGGCCTACGACANCGC | 54 | F | 0.005 | 99.879 | [39] |
| Reverseprimer2 | ADVCCSCGBGCCGCBTCHTCG | 54 | R | 0.009 | 99.879 |
| Forwardprimer1 | GGCTGGGCCTACGACANCGC | 55 | F | 0.005 | 99.879 |
| Reverseprimer3 | CRTCGTCCTGMTCRAAVACRCC | 55 | R | 0.018 | 99.903 |
| Forwardprimer1 | GGCTGGGCCTACGACANCGC | 56 | F | 0.005 | 99.879 |
| Reverseprimer4 | TTGAGSGYVKCCCAGYBVGG | 56 | R | 0.004 | 99.976 |
| MGED-F11 | ATGGGTGAGGACCCSGT | 57 | F | 0.004 | 99.952 | [40] |
| CSYH-R10 | CCAGCCGTGGTAGCTGCA | 57 | R | 0.023 | 99.250 |
| FLNQ-F3 | AACCAGTGCCGICACCGIGG | 58 | F | 0.000 | 100.000 |
| CSYH-R10 | CCAGCCGTGGTAGCTGCA | 58 | R | 0.023 | 99.250 |
| BPHD-f3 | AACTGGAARTTYGCIGCVGA | 59 | F | 0.077 | 99.806 | [41] |
| BPHD-r1 | ACCCAGTTYTCICCRTCGTC | 59 | R | 0.014 | 99.952 |
| NidAf | ATGACCACCGAAACAACCGGAACAGC | 60 | F | 0.003 | 100.000 | [42] |
| NidAr | TCAAGCACGCCCGCCGAATGCGGGAG | 60 | R | 0.004 | 100.000 |
| NidBf | ATGAACGCGGTTGCGGTCGATCGGGA | 61 | F | 0.000 | 100.000 |
| NidBr | CTACAGGACTACCGACAGGTTCTTGA | 61 | R | 0.000 | 100.000 |
| NidA1f | TCCAGAAAGGGTCCAACCATATG | 62 | F | 0.000 | 100.000 |
| NidA1r | GCCTGGGCAGAAGCTTCATCA | 62 | R | 0.000 | 100.000 |
| NidB1f | TGGTCGAGGAGTTCGGTGTGATG | 63 | F | 0.000 | 100.000 |
| NidB1r | GGTGGTGAACGGAGCTGGCCCTA | 63 | R | 0.000 | 100.000 |
| pdo1-f | GTTCTACCTCGACCTCATTGCG | 64 | F | 0.005 | 100.000 | [43] |
| pdo1-r | CTGACCCATGTATTCCAGCC | 64 | R | 0.004 | 100.000 |
| NidA-forward | TTCCCGAGTACGAGGGATAC | 67 | F | 0.024 | 100.000 | [44] |
| NidA-reverse | TCACGTTGATGAACGACAA | 67 | R | 0.005 | 100.000 |
| NidA-forward | TTCCCGAGTACGAGGGATAC | 68 | F | 0.005 | 100.000 |
| NidA-probe | TCCTACCCGTCGCCGGTACA | 68 | R | 0.005 | 100.000 |
| PAH-RHDαGP F | CGGCGCCGACAAYTTYGTNGG | 69 | F | 0.008 | 99.976 | [23] |
| PAH-RHDαGP R | GGGGAACACGGTGCCRTGDATRAA | 69 | R | 0.008 | 99.976 |
| NMR331f | TGCCCKTACCACGGYTGG | 70 | F | 0.079 | 96.805 | [45] |
| NMR1134r | CTCGGCGTCGTCCTGYTC | 70 | R | 0.018 | 99.903 |
| pah-rhdα-396F | ATTGCGCTTAYCAYGGBTGG | 71 | F | 0.000 | 100.000 | [46] |
| pah-rhdα-696R | ATAGGTGTCTCCAACRAARTT | 71 | R | 0.000 | 100.000 |
| Cyc372F | CGATGAGTTGGATAGAGATTCG | 72 | F | 0.001 | 100.000 | [47] |
| Cyc854R | GGTTCTCCAAGGTTCTCTG | 72 | R | 0.001 | 100.000 |
| NP45F | GGAGGTTTATGGTGGCTTAC | 73 | F | 0.000 | 100.000 |
| NP560R | GATAAATTCTGGCACGATCAGC | 73 | R | 0.000 | 100.000 |
| RP007-296F | GCTTCGCCTGCAATTATCATG | 74 | F | 0.002 | 100.000 |
| RP007-770R | ACGTCATATAGCGCACCGATC | 74 | R | 0.002 | 100.000 |
| nagAc108F | CTGGCTTTTTYTSACYCATG | 75 | F | 0.004 | 99.952 |
| nagAc858R | CCGRACATCRCCGATTTC | 75 | R | 0.003 | 99.855 |
| pPAH-F | GGYAAYGCNAAAGAATTCGTNTGYYWSHTAYCAY | 76 | F | 0.002 | 99.879 | [8] |
| pPAH-NR700 | CCAGAATTCNGTNGTRTTHGCATCRATSGGRTKCCA | 76 | R | 0.000 | 100.000 |
| RHD-1\_F | GAGACTGCAGAGAAGGAAGCCCTATCATGTTAAATATTGAAAGTCTG | 77 | F | 0.000 | 100.000 | [48] |
| RHD-1\_R | CTCTCCATGGTTACAACATGAAGTTGAGATTTTTACC | 77 | R | 0.000 | 100.000 |
| RHD-2\_F | GAGACTGCAGAGAAGAAGGAGTTGATATGACAAACGTGAGTTCGTTA | 78 | F | 0.000 | 100.000 |
| RHD-2\_R | CTCTCCATGGTTAAAATAAAGTGTTCATGTTGCTATC | 78 | R | 0.000 | 100.000 |
| RHD-3\_F | GAGACTGCAGAGAAGAAGAGAGTGAAATGGTCGATGTAAATAGTCTG | 79 | F | 0.000 | 100.000 |
| RHD-3\_R | CTCTCCATGGCTACATCGGGAAGTTATGGTTCTTGCC | 79 | R | 0.000 | 100.000 |
| RHD-4\_F | GAGACTGCAGAGAAGAAGGAGTTGGCATGAATAAGCTTGAAGGCTTG | 80 | F | 0.000 | 100.000 |
| RHD-4\_R | CTCTCCATGGTTAAAAAAATGTGTTCATGTTGCTGTC | 80 | R | 0.000 | 100.000 |
| RHD-5\_F | GAGACTGCAGAGAAGAAAGGTGAATAATGACAAGCTTTAACTATCAG | 81 | F | 0.000 | 100.000 |
| RHD-5\_R | CTCTCCATGGTCAGAAAAACATGTTCAGATTTTTATC | 81 | R | 0.000 | 100.000 |
| RHD-6\_F | GAGACTGCAGAGAAGAAGATACTGCAATGAAAATTGAAAAATTCAAG | 82 | F | 0.000 | 100.000 |
| RHD-6\_R | CTCTCCATGGCTACAAATATATGTTGAGGTTTTTGCT | 82 | R | 0.000 | 100.000 |
| RHD-7\_F | GAGACTGCAGAGAAGAAATTACACATATGACTTCGCTGAAGCCAACC | 83 | F | 0.000 | 100.000 |
| RHD-7\_R | CTCTCCATGGTTAGAGAATGCTGGCCATATTGGGCAT | 83 | R | 0.000 | 100.000 |
| RHD-8\_F | GAGACTGCAGAGAAGAAAGGCGGTGCATGGGTGATTTCGACGCGTTA | 84 | F | 0.000 | 100.000 |
| RHD-8\_R | CTCTCCATGGTTACAGGATAAACAACAAATTTTTTCC | 84 | R | 0.000 | 100.000 |
| Phn-RHDf2 | TTCRYBTGCAAYTATCAYGGYTGG | 85 | F | 0.005 | 99.952 | [49] |
| Phn-RHDR3 | CCYCKRTAVCWKGTYTCKCCRA | 85 | R | 0.005 | 99.952 |
| RHD-Beta-Grp1f | TTCASYTGCACYTATCACGGCTGG | 86 | F | 0.011 | 99.952 |
| RHD-Beta-Grp1r | CCKCKRTARGASGTYTCRCCAA | 86 | R | 0.000 | 100.000 |
| dxnA1/dfdA1-F | TACAAVGGGCTGRTTTTCGG | 87 | F | 0.015 | 99.927 | [50] |
| dxnA1/dfdA1-R | GARAAVTTVGGGAACAC | 87 | R | 0.016 | 99.903 |
| dbfA1-F | GGCGACGACTAYCACGTGCT | 88 | F | 0.001 | 100.000 |
| dbfA1-R | TCGAAGTTCTCGCCRTCRTC | 88 | R | 0.001 | 99.976 |
| carAa-F | TGCCTNCAYCGHGGBGT | 89 | F | 0.032 | 91.866 |
| carAa-R | TTSAGHACRCCBGGSAGCCA | 89 | R | 0.000 | 99.927 |
| ARHDf | TTY RYI TGY AII TAY CAY GGI TGG G | 90 | F | 0.000 | 100.000 | [51] |
| ARHDr | AAI TKY TCIGCI GSI RMY TTC CA | 90 | R | 0.000 | 100.000 |
| A13-gc | ATGTTCGGCCAGCACATGACG | 91 | F | 0.003 | 100.000 | [52] |
| A1r | GTCAAGAGCGGCAGCAGGAC | 91 | R | 0.000 | 100.000 |
| phnA1f | GGGTGGACTAGCTGGAA | 92 | F | 0.001 | 100.000 | [53] |
| phnA1r | TTCGCATGAATAGCGATGG | 92 | R | 0.001 | 100.000 |
| Agroup-f | CAGAAAGATGGTTCGGTCAAAG | 93 | F | 0.000 | 100.000 |
| Agroup-r | GTATTCCCTGCTTCAACTGATG | 93 | R | 0.000 | 100.000 |
| Bgroup-f | GGATTTGTCTACGGTTGTTTCG | 94 | F | 0.000 | 100.000 |
| Bgroup-r | GAGGTACCACGCAAATTCTC | 94 | R | 0.000 | 100.000 |
| Cgroup-f | CTTCGTRTTCGGATGCATG | 95 | F | 0.000 | 99.976 |
| Cgroup-r | CATGAAGCTATYCAGATACCAG | 95 | R | 0.000 | 100.000 |
| Dgroup-f | AACCCTCACCTGCTCCTAC | 96 | F | 0.000 | 100.000 |
| Dgroup-r | TAAAGTAGGCGCTYTGCTCC | 96 | R | 0.000 | 100.000 |
| phnAcf | CCYAGCTTGAATGACTATCTTG | 97 | F | 0.001 | 100.000 |
| phnAcr | AGTTYAAYAATGATCGACTTGG | 97 | R | 0.001 | 100.000 |
| nahAcf | TATCACGGCTGGGRCTTC | 98 | F | 0.014 | 99.588 |
| nahAcr | GAASCCATGGAAGCTCTC | 98 | R | 0.011 | 99.952 |
| NAH-306F | AAGGGCTTCGTGTGCAACTAYCAYGGNTG | 99 | F | 0.000 | 100.000 | [54] |
| NAH-621F | CGTGGGCGACGCCTAYCAYRTNGG | 99 | R | 0.000 | 100.000 |
| NAH-627F | GACGCCTACCACGTGGGNTGGRMNCA | 100 | F | 0.002 | 99.927 |
| NAH-612R | TGGTAGGCGTCGCCCRYRAARTTYTC | 100 | R | 0.000 | 99.976 |
| NAH-633R | GGCGTGGGTCCAGCCNAYRTGRTA | 101 | F | 0.001 | 99.976 |
| NAH-1110R | TGTTCATCTGGGTCACGGTCNHCATRTTNTC | 101 | R | 0.000 | 100.000 |
| P1&2F | AACGGYGAACTGCARAGC | 102 | F | 0.014 | 99.806 | [55] |
| P1&2R | CGTCCAACCVACGTGGTC | 102 | R | 0.011 | 99.927 |
| P4F | CCGGAGACTTCCTGACGAC | 103 | F | 0.001 | 100.000 |
| P4R | GCASACGAAYCGACGGGT | 103 | R | 0.001 | 100.000 |
| P5F | TGGACCTACAGCAACACG | 104 | F | 0.003 | 99.976 |
| P5R | CCAGCGAGCCGAAGATCA | 104 | R | 0.003 | 99.976 |
| P6AF | CGAGTCGGAGTTGGCCAAG | 105 | F | 0.005 | 100.000 |
| P6AR | CTGTACACCCAGCCGTGGT | 105 | R | 0.006 | 99.976 |
| P6BF | TGGCGAACTCGTGTCGGCAC | 106 | F | 0.005 | 100.000 |
| P6BR | CGTCCAGRCAACCGAADAYC | 106 | R | 0.002 | 100.000 |
| P7AaF | ACCTACATGGGCGAAGACC | 107 | F | 0.005 | 99.976 |
| P7AaR | GTARGTGCAGGTGAAGGCCT | 107 | R | 0.003 | 99.952 |
| P7AbF | TGGTCGCTCTTGGCTGTTAC | 108 | F | 0.001 | 100.000 |
| P7AbR | GCTTGCCGGCGATGTCGTA | 108 | R | 0.002 | 100.000 |
| P7AcF | TAYCTGACCACCTACATGG | 109 | F | 0.002 | 99.976 |
| P7AcR | CCRCGATGCCGACATTG | 109 | R | 0.001 | 100.000 |
| P7BF | CACBTGCAGCTAYCACG | 110 | F | 0.005 | 100.000 |
| P7BR | CATGTGGTCCATGTAGAAC | 110 | R | 0.004 | 100.000 |
| A1a\_F(bphA1a) | CCTATTTCGGCGAACTCG | 111 | F | 0.001 | 100.000 | [56] |
| A1a\_R(bphA1a) | GAARTAGCGCTGRTTGTG | 111 | R | 0.001 | 100.000 |
| A1b\_F(bphA1b) | ACGKATCGGYCGYGARCCG | 112 | F | 0.001 | 100.000 |
| A1b\_R(bphA1b) | GTCGCGSGTTTCGGCCAC | 112 | R | 0.001 | 100.000 |
| A1c\_F(bphA1c) | GGWYGCCGGGTTCCSTAC | 113 | F | 0.001 | 99.952 |
| A1c\_R(bphA1c) | RTGGTCGGCATCCTCGGC | 113 | R | 0.001 | 99.952 |
| A1d\_F(bphA1d) | CCRACKGCGGTSGAYTAC | 114 | F | 0.001 | 99.976 |
| A1d\_R(bphA1d) | GCATAGCCGAAATAGGTC | 114 | R | 0.001 | 99.952 |
| A1e\_F(bphA1e) | AAYGARGTTCCSAAGGCG | 115 | F | 0.001 | 100.000 |
| A1e\_R(bphA1e) | ATATTCCCARCGGGGMAG | 115 | R | 0.000 | 100.000 |
| A1f\_F(bphA1f) | TGCCAYGATCCCGAAGCG | 116 | F | 0.003 | 100.000 |
| A1f\_R(bphA1f) | VGCCCAATCKGGBGCATC | 116 | R | 0.001 | 100.000 |
| X\_F(xylX) | GGYMGGATTGCCGAYTTGC | 117 | F | 0.001 | 100.000 |
| X\_R(xylX) | GGCMACCGCCGGGCTGC | 117 | R | 0.001 | 100.000 |
| QH-11\_F | CGGTCGCATCATCGGTCTT | 118 | F | 0.000 | 100.000 | [57] |
| QH-11\_F | CCCTTGCTCTGCTTGGTGTA | 118 | R | 0.000 | 100.000 |
| JDC-11\_F | STTYAAYATGTGCCTSCAYC | 119 | F | 0.012 | 100.000 | [58] |
| JDC-11\_R | CCCARTTCTCVACRTCRTC | 119 | R | 0.020 | 100.000 |
| F1f(fadA1) | GGCGTTTGACAAGAGTCGGCTAG | 120 | F | 0.000 | 100.000 | [59] |
| F1r(fadA1) | TGTGCGGCGGTGCGGGTAT | 120 | R | 0.004 | 100.000 |
| Nf(nidA) | TCCAGAAAGGGTCCAACCATATG | 121 | F | 0.000 | 100.000 |
| Nr(nidA) | GCCTGGGCAGAAGCTTCATCA | 121 | R | 0.000 | 100.000 |
| F2f(fadA2) | TCAAGTGGCGCATCAAGTCC | 122 | F | 0.000 | 100.000 |
| F2R(fadA2) | GACAGGTTGGGGAACAGGGT | 122 | R | 0.000 | 100.000 |
| Pf(phnA1) | CATGAGCGGCGACACCAC | 123 | F | 0.001 | 100.000 |
| Pr(phnA1) | ATTTGGACCGGCTCTGGC | 123 | R | 0.000 | 100.000 |
| EnidA3-F(nidA3) | ACATATGGCGCCTGATGCGACGACAATG | 124 | F | 0.000 | 100.000 | [60] |
| EnidB3-R(nidA3) | CAAGCTTTTAGATCCAGAATGACAGGTT | 124 | R | 0.000 | 100.000 |
| touA-F | AAGACCTATCCSGARTACGT | 125 | F | 0.000 | 100.000 | [61] |
| touA-R | GGCTGG ATCWGRCCTGCSAGGAA | 125 | R | 0.000 | 100.000 |
| catA-F | GTCACCTACGACGAATACAACGGCCTCAAG | 126 | F | 0.000 | 100.000 |
| catA-R | AAGTAGAGCTGGGTGGTGAT | 126 | R | 0.000 | 100.000 |
| Ac114F | CTGGCWWTTYCTCACYCAT | 127 | F | 0.004 | 99.952 | [47] |
| Ac596R | CRGGTGYCTTCCAGTTG | 127 | R | 0.009 | 99.855 |
| Ab248F | CGTGACASAGAACATCAAAACATA | 128 | F | 0.000 | 100.000 |
| Ac893R | AGTTGAGGTGSSWGCGATA | 128 | R | 0.007 | 99.952 |
| Ab248F | CGTGACASAGAACATCAAAACATA | 129 | F | 0.000 | 100.000 |
| Ac1095R | TTGTCAYTGTCGTCGSYTTC | 129 | R | 0.003 | 99.952 |
| Ac307F | TATCACGGCTGGKSYTTCGGCT | 130 | F | 0.011 | 99.903 |
| Ac893R | AGTTGAGGTGSSWGCGATA | 130 | R | 0.007 | 99.952 |
| Ac307F | TATCACGGCTGGKSYTTCGGCT | 131 | F | 0.011 | 99.903 |
| Ac1095R | TTGTCAYTGTCGTCGSYTTC | 131 | R | 0.003 | 99.952 |
| Nah-for | TGCMVNTAYCAYGGYTGG | 132 | F | 0.365 | 80.537 | [12] |
| Ac596R | CRGGTGYCTTCCAGTTG | 132 | R | 0.009 | 99.855 | [47] |
| P8420 | CTCCACCTTGCCAATTTCAT | 133 | F | 0.002 | 100.000 | [62] |
| P9047 | AATAACCGGCGATTCCAAAC | 133 | R | 0.001 | 100.000 | [5-8] |
| BPH4-F | AAGGCCGGCGACTTCATGAC | 134 | F | 0.001 | 100.000 | [10] |
| BPH1-R | TGTTSGGYACGTTMAGGCCCAT | 134 | R | 0.001 | 100.000 |
| BPH4-F | AAGGCCGGCGACTTCATGAC | 135 | F | 0.001 | 100.000 |
| BPH2-R | AGCCGACGTTGCCAGGAAAAT | 135 | R | 0.002 | 100.000 |
| BPH4-F | AAGGCCGGCGACTTCATGAC | 136 | F | 0.001 | 100.000 |
| BPH3-R | TGCTCCGCTGCGAACTTCC | 136 | R | 0.003 | 100.000 |

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