

Supplementary Table 1. Targeted NGS primer pairs designed for amplifying conserved regions of 62 different equine pathogens.

Target	Forward	Reverse
AMPL1652307_1	ATGCAACTGAGGTTTTAACATCTCATTG	CTCCGATTGGCAAACGACCAACA
AMPL1652307_2	TTGTAAGTGGGTTTTAACATCTCATTG	CTCCGATTGGCAAACGACCAACA
AMPL1652307_3	TTGTAAGTGGGTTTTGACATCTCATTG	CTCCGATTGGCAAACGACCAACA
AMPL1652268	GGCAATAGTTCGATTGAATTAAGTAGAACTT	TGAATAGTAACCTCTTTCTTATCAGTACTCA
NeosH ITS_1.26453	GAGCTTGATCCCTCTCCTTTGG	ATTTGTTGTTTAAAATAACGGTGTGGGA
NeosH ITS_1.8107	AGGGACTCGGTCCTGGA	ACATTATAGTTTTTAGTAGGTAATCTGAAAGCG
EEErPmerase_1.1.129103	TACACCAGTGACAAGCCTCCT	CTGTAACCCCTTTTGGTTCCAT
EEErPmerase_1.1.72623	CGTAAACCTAAACCAGGCAAACGA	CTGGTGTACTGGAGGGTATCTGA
EEErPmerase_1.3.114610	CTTTGTGCCTGTTAAGGCCAAG	CCCTTCTCCTGACTCTTGAGC
EEErPmerase_1.3.14226	ACACCGCACCTGATTTTACAC	CCGATAATTGTGGTTAACGGGTATCTG
EEErPmerase_1.3.194592	TGCCGTCTCCAGTAGTGAAATG	ATCTGCAGATCTCCAGCTGAC
EEErPmerase_1.3.51867	ATTATCGGGTTATGCACCTGTGT	GTGGGATAAGCGTCTGCATCC
EEErPmerase_1.3.7079	AAGGGAACCCACATGGATGG	CAGCAAAGTAACGCCAGGAGTA
EEErPmerase_1.4.86402	CTGCAGATGTCTACGTCAATGGTG	GTGAAAGGTGTGTGCACGATAC
EEErPmerase_1.4.92029	CTTCGAACGATGGAAAAGGGACAA	GAATTGGACAGTTTCTGCTTTACTG
C_perf_beta_1.1.30019	GGCAAACCTACTACTATAACTAGAAATAAGACA	AATTGCAGTAGAATTAGTAACATCATGCAA
C_perf_beta_1.1.36446	TCAAGTGTGAAAAGAGCAATGTTTCAT	ATCTTCATTTTTACTTGAAGAGTCAACAGATT
C_perf_beta_1.1.38216	TCGATGATAAATATTCATCTGAAATGACAAC	TTGAACCTCTATTTTGTATCCCATTGT
AMPL1652244	CGCTACAGTGATGTCTCTCAGT	GCCAGCATCTGCATTTGTCTTA
AMPL1652273_1	CCCTAGTGTTCCTTTTCCAAAAACC	TTCTTGCATGACCGGTACGAA
AMPL1652273_2	CCCCTGTGTTCCTTTTCCAAAAACC	TTCTTGCATGACCGGTACGAA
AMPL1652202	ACTTTCGATTTTGGCTATCTCCGTT	TTTCGTTTGTCCCTGGGATTGT

Targeted NGS panel for detection of equine pathogens

AMPL1652203	GCCAAGCCTAAAAAGCTCTTTTGTC	GCGTCGCTTACTAAGTCTCCATC
AMPL1652196	CGGCAGTATCTGGTTCAGTGAT	CATCACTCATCTTCGCTGCTAAAAA
AMPL1652197	AAACGGAAGTTGAATATTTCTGTTCCAA	CCAAATGACAAAGGAACAGAAAGAGTC
TM01_1.3313	TCGGACACCCTCTGAACGA	GGGAAGACGGTATAAGAAGTCTCG
TM01_2.3313	TCGGACACCCTCTGAACGA	GGGAAGACGGTATAAGAAGTCTCG
AMPL1652282_1	GGGTGAACTGTCCAAGCTTCAT	GCAGCATGTTTAGCGCGATTATAATATAAC
AMPL1652282_2	GGGTGAACTGTCCAAGCTTCAT	GCAGCATGTTTAGCGCGATTATAATATATA
AMPL1652282_3	TGGTGAACGTGTCCAAGCTTCAT	GCAGCATGTTTAGCGCGATTATAATATAAC
AMPL1652274_1	CACTACATCAAGTGTCACCTCCATACA	GAGGTGCATCTCGACATAAAGCT
AMPL1652274_2	CACTACATCAAGTGTCACCTACATACA	GAGGTGCATCTCGACATAAAGCT
AMPL1652274_3	CACTACATCAAGTGTCACCTCTCATACA	GAGGTGCATCTCGACATAAAGCT
AMPL1652274_4	CACTACATCAAGTGTCACCTCTATACA	GAGGTGCATCTCGACATAAAGCT
AMPL1652274_5	CACTACATCAAGTGTCACCTCCACACA	GAGGTGCATCTCGACATAAAGCT
AMPL1652275	CCAAGTCTACGCACATGATGCA	ATGGTCTCGGAGATCTTTGTGC
AMPL1652182	GCGCAAAAATTTGAGCCCAAGT	CGTTCTCCATCTTGTCGTGGAA
AMPL1652183	CAAGCTCAGCAACATGAACCAG	TGGTGTGATCTCCTCCTTGAT
AMPL1652278	CTTGGAATGAGCAACAGAGACTTC	CCTTGTCTGCACACAAAAGCTG
AMPL1652200	AGTAAAAGTCGTAACAAGGTTTCCGT	ATCGATGCCGGAACCAAGAGAT
TM12_1.1051	CTTTCCCCGTCAGCGATC	ACTTCAACAGGCCAGTCT
TM12_2.1051	CTTTCCCCGTCAGCGATC	ACTTCAACAGGCCAGTCT
TM13_1.868	GGGAAGGAAATCTCATTGTGGAAGT	AAATCGTACAGGTACGGTTTCCC
TM13_2.868	GGGAAGGAAATCTCATTGTGGAAGT	AAATCGTACAGGTACGGTTTCCC
AMPL1652250_1	AACGTGGAGCCGTTCTTAATGT	GGGCTTATGTAAGTCAATGTCATAGTGA
AMPL1652250_2	AACGTGGAGCCGTTCTTAATGT	GGGCTTATGTAAGTCAACGTCATAGTGA
AMPL1652250_3	AACGTTGAGCCGTTCTTAATGT	GGGCTTATGTAAGTCAATGTCATAGTGA
AMPL1652212_1	GCTGGCCGATGTCTTTTTCAA	GCAAGTTTGTATGTACGGACACTGA
AMPL1652212_2	GCTAGCCGATGTCTTTTTCAA	GCAAGTTTGTATGTACGGACACTGA
AMPL1652213	CACTTTCGGGTTATGCCTGGAA	GAGGTGCATCTCCTTAATGTCCTTTCC
AMPL1652195	CACTGCTAGCTATTATCTTAGGTGGTATG	ACTGTTCATAGAACCAGACCAGTCA
AMPL1652267_1	GACTGCATTTATTCTGCAGACTTTGG	GGTCGACTTTATGTGGTTCTCCAATTAT
AMPL1652267_2	GACTGCATTTATTCTGCAGACTTTGG	GGTCGACCTTATGTGGTTCTCCAATTAT

Targeted NGS panel for detection of equine pathogens

AMPL1652267_3	GACTGCATTTATTCCGCAGACTTTGG	GGTCGACTTTATGTGGTTCTCCAATTAT
AMPL1652218_1	TTAATATTGCATGATAAGGCAACTTCAGT	AGATGGAGATGAGAAAAAGTGATCTATATTACC
AMPL1652218_2	TTAATATTGCATGATAAGGCAACTTCAGT	ATATGGAGATGAGAAAAAGTGATCTATATTACC
AMPL1652219	GGGATCAGGACACACAGTGA	CTCTTGAAGGAGCATTAGGTAACATCATTAA
AMPL1652265_1	GAGGAGCACATCGTCTACACTG	GAACAAGACCTCCTGGTAGAACTC
AMPL1652265_2	GAGGAGCACATCGTCTACACTG	GAACAAGACCTCCTGGTAGAAGTC
AMPL1652266_1	AGAAGGACGGTGATAAGTGGGT	CCATCAATCAACTCAGTCTTGCCAT
AMPL1652266_2	AGAAGGACGGTGATAAGTGGGT	CCATCAATCAACTCAGTCTCGCCAT
AngioCntnITS_1.113368	TGTGTGCACGTTTTGCGT	ATACATCCTGTGTATCTCGTTCCA
AngioCntnITS_1.116442	TTGAATTGCTGGATATGGTTGATAGTG	TATCTCGTTCCACATTTTCACGTGT
AngioCntnITS_1.95464	TCGCTAAAGTTGGTGGTATCGT	TGCACACACATGCATACACG
AMPL1652299	GTGTCCATCGCCAAGGAGAT	TCCTTGGTCTCGACCTCCTT
AMPL1652300	CGTCACCAACCGTCTGCT	CCTTCCTTGCCGACCTTG
AMPL1652179	CAAGCAGGCTTTTCGCGAATATG	GCTAGCTTATACCCAAGCATTATCCAG
AMPL1652204	GGGTCGATAACATGGGATCTTAAGTTT	GACCGCTTATAAGCTACTGGTTTCA
AMPL1652205	GTGAAAAGAACCCTTGTTAAGGGAGT	TCCTCCACAAGGTCTTACCCAT
AMPL1652225_1	CCCAAGGCTTTGCACCATTTTC	CCACCGATTCAAATTTAGCTTGATATACAT
AMPL1652225_2	CCCAAGGCTTTGCACCATTTTC	CCACCGATTCAAATCTAGCTTGATATACAT
AMPL1652225_3	CCCAAGGCTTTGCACCATTTTC	CCACCGATTCAAACCTAGCTTGATATACAT
AMPL1652226_1	GTATAGGACTCTGATGAGTGTCAAAATAGG	CCATCAGTCATTACCCAATAACAGTCTC
AMPL1652226_2	GTATAGGACTCTGATGAGTGTCAAAATAGG	CCATCAGTCATTACCCAATAACAGTTTC
AMPL1652226_3	GTATAGGACTTTGATGAGTGTCAAAATAGG	CCATCAGTCATTACCCAATAACAGTCTC
EHV_4_1	CTCTGGAGCCAATTAGGAAATGTAAAC	GTTTCAGTTGGTAGAAGCGTTTG
TM02_1.243	GGTTTTGAAGTCGTTGTTCTAACTCC	CTTGAGTACGAGGCGGTGGA
TM02_2.243	GGTTTTGAAGTCGTTGTTCTAACTCC	CTTGAGTACGAGGCGGTGGA
NetF_1.49778	GATATGACCAAAATTCGTATCATGCTCT	TGGTTCTTTTGCAACACGATTTTCT
NetF_1.59223	GTTATAGTATTGGTGGAAATGTTCCGT	TCTTGTTAAACACTATGTTCCAAGAAGC
NetF_1.64905	TAGGGAATATTACACAAGTAAAAGCTAATTCC	TGCACTGTAATAAGTTCTGTTTTAATTAATC
NetF_1.85319	TTGCTCTTAAGGCACCAAAAGG	ATAAATTCTACAGTATGATTCTCCAATCAAG
AMPL1652296	CGCACATTTCCGAACCTTCACTT	TGGGACTTGTTTCAGGTTGTTCTG
AMPL1652298	CCAACGACGGCATCTCGAT	CGATGCGGTTGATTTCTTCCAG

Targeted NGS panel for detection of equine pathogens

AMPL1652258	TGCAATTTGGTTATACAAGTCGCAGTA	CCTTCATATCTACACACATCAGGTTGTTT
AMPL1652259_1	TTTATTAGAACTGGTAGTTGGTGGAGTTTC	CGACACCTTAGCAACAGTAACATAAAC
AMPL1652259_2	TTTATTAGAACTGGTAGTTGGTGGAGTTTC	CGACACCTTAGCTACAGTAACATAAAC
AMPL1652259_3	TTTATTAGAACTGGCAGTTGGTGGAGTTTC	CGACACCTTAGCAACAGTAACATAAAC
Klebsiella_1	CGACCTGATTGCATTTCGCCAC	AGCACGTAGATGAACTCTTCCTCAT
TM06_1.42	AAGAATAGCAGCGTTCGGAGGA	TCTTCGATCTCGAGAGGAACTC
TM06_2.42	AAGAATAGCAGCGTTCGGAGGA	TCTTCGATCTCGAGAGGAACTC
AMPL1652242_1	CTACTGCTGAACAAAAGTCTATGCAAC	CATATGAATTCACTGTTGCTCACTGTTG
AMPL1652242_2	CTACTGCTGAACAAAAGTCTATGCAAC	CATATGAACTCACTGTTGCTCACTGTTG
AMPL1652242_3	CTACTGCTGAATAAAAAGTCTATGCAAC	CATATGAATTCACTGTTGCTCACTGTTG
AMPL1652243_1	CGAGGGCTCATTCTACTCCATT	CCCATCAGTCATTACCACTACACAAG
AMPL1652243_2	CGAGGGCTCATTCTACTCCATT	CCCATCAGTCATCACCCTACACAAG
AMPL1652271_1	GCGACAGCCTACAAGCTACAAT	CCAAGTACGGTATACGTGAGT
AMPL1652271_2	GCGACAGCCTACAAGCTACAAT	CCAAGTACGGTGTACGTGAGT
AMPL1652246_1	GAATTATTAGCAGATGTAGACAGCATTCCCT	CAGTTGATGTGATTTCAAGCTTACCA
AMPL1652246_2	GAATTATTAGCAGATGTAGACAGCATTCCCT	CAGTTGATGTGATTTCAAGCTGACCA
AMPL1652246_3	GAATTATTAGCAGATGTAAACAGCATTCCCT	CAGTTGATGTGATTTCAAGCTTACCA
AMPL1652246_5	GAATTATTAGCAGATGTAAAGCAGCATTCCCT	CAGTTGATGTGATTTCAAGCTTACCA
AMPL1652198	GTAGTTTCAAGTCTAAGTAGCTCAGCAA	CACTTGCTTCAGGACCATATTTCTCT
AMPL1652199	TGATACACCTGAAACAAAGCATCCT	GCTTCACTTTTTCTTAAAAGTTGTTTCATGT
AMPL1652301_1	GGGTTGACCTTAGGTGGTGATT	GTATGCGCCAACCTATAAATATATCGGTAT
AMPL1652301_2	GGGTTGACCTTAGGTGGTGACT	GTATGCGCCAACCTATAAATATATCGGTAT
AMPL1652302_1	TGTAGTATGTATTTGTGTGCTGTGTGTAG	TTTTGGCATTTTTGGTCGATTTTGAAC
AMPL1652302_2	TGTAGTATGTATTTGTGTGCTGTGTGTAG	TTTTGGCATTTTTGGCCGATTTTGAAC
AMPL1652302_3	TGTAGTATGTATTTGTGTGCTGTGTGTAG	TTTTGGCATTTCGGCCGATTTTGAAC
AMPL1652302_4	TGTAGTATGTATTTGTGTGCTGCGTGTAG	TTTTGGCATTTTTGGTCGATTTTGAAC
PHF_1	CACAAGTTGGTTCAATTTCTGC	ATTTTCTCCGGGTTTGTATAAAGT
PHF_2	CACAAGTTGGTTCAATTTCTGC	ATTTTCTCCGGATTTGTATAAAGT
AMPL1652255_1	GCTCGCAATAAGACTGGTCGTT	TGTCGCTTCGTAAGGTTCACTC
AMPL1652255_2	GCTCGCAATAAGACTGGTCGTT	TGTCGCTTTGTGAGATTCACTC
AMPL1652255_3	GTTTCGCAATAAGACTGGTCGTT	TGTCGCTTCGTAAGGTTCACTC

Targeted NGS panel for detection of equine pathogens

AMPL1652255_5	GCTCGCAATAAGACTGGTCGTC	TGTCGCTTCGTAAGGTTCACTC
AMPL1652256_1	TGGTCGTTGCTTGGCTTTTCTA	CGCTATTAACGCTGGGCTTTTG
AMPL1652256_2	TGGTCGTCACCTGGCTGTTCTA	CGCTATTAACGCTGGGCTTTTG
AMPL1652256_3	TGGTCGTTACTTGGCTGTTCTA	CGCTATTAACGCTGGGCTTTTG
AMPL1652256_4	TGGTCGTCACCTGGCTTTTCTA	CGCTATTAACGCTGGGCTTTTG
AMPL1652190	TGAAACAACATGACGGGAGGTAA	GGGAATCAAAATAAAGATTCCCTCTATGCT
AMPL1652231_1	TTTATTAGCATCGCCATTATATGCAAATGG	GTTCCCTCTCGCGTGATCATAAAGATTAATA
AMPL1652231_2	TTTATTAGCATCGCCATTATATGCTAATGG	GTTCCCTCTCGCGTGATCATAAAGATTAATA
AMPL1652232	GGGCATAATGAGTACTTCGATAGAGGA	GAGGGCTGTATACGCCTAATACATC
AMPL1652233	ATATGTTATAGCGACAGCACCAAATATGT	TGTAATACCGGTCTCTATATTCCCTGTTAC
AMPL1652214	GGATGGATTGATTGGCTATGATTTGG	GTTTGTAACACTCCACTTTGGTTGAA
AMPL1652215	CTTCAATTGGAGAGACAATAATTGATGACA	AGCTTTACCTGTTTCTGGGCTAAAAT
AMPL1652216	GGAGCTGTAGAATGGAAAGAATTAGATGG	GCCATCTATTTTCAGTGTAACCTACTTTCAT
AMPL1652279	TGACGCGACGTACTCGAAAAAT	CATATGCAGGCCATCGACTTCT
AMPL1652280	CAGAAACAGGAATGCTCGGGTAT	GTCACCGGACATTCCTGAATTG
AMPL1652277_1	TTGCTCGGGAAAAGAAGCCAAG	TACCAGATAGCCCTGCTTCCTT
AMPL1652277_2	TTGCTCGGGAAAAGAAGCCAAG	TACCAGATAGCTCTGCTTCCTT
AMPL1652277_3	TTGCCCGGGAAAAGAAGCCAAG	TACCAGATAGCCCTGCTTCCTT
AMPL1652269_1	CGTACGGCGACTCCAAGATTAT	CCCATCAGGTTTATCATTAAACATCGATGA
AMPL1652269_2	CGTACGGCGACTCCAATAATTAT	CCCATCAGGTTTATCATTAAACATCGATGA
TM05_1.687	GTTTACGATGTGATCTACTTCGACACA	CCCCGAACACTTCTTTGAAAACC
TM05_2.687	GTTTACGATGTGATCTACTTCGACACA	CCCCGAACACTTCTTTGAAAACC
AMPL1652010_1	AATGCGACATTGACTACAAAATCAGC	TGTATTTCTATTCCAAGTCATCAGCA
AMPL1652010_2	AATGCGACATTGACTACAAAATCAGC	TGTATTTCTATTCCAAGTCATCAGCA
AMPL1652010_3	AATGCGACATCGACTACAAAATCAGC	TGTATTTCTATTCCAAGTCATCAGCA
AMPL1652237	CTCAGGGCGTGGGTATTAATGAG	CTGTTCCGGCTTTTCCAGATTA
AMPL1652238	GAGTAAAATAGGAGGAACCGCTGAA	AAAAATGAGCCAAGCTGGTTAAGC
AMPL1652201	CGGAGGGATCATTACCGAGTTT	GTGCGTTCAAAGATTCGATGATTCA
AMPL1652257	CATTGTCGGTTCTGGGAGCTAT	GCTGAAGGTCATTTGTGAAGAGAGT
Lyme_1	AGCAAATTTAGGTGCTTTCCAA	GCAATCATTGCCATTGCAGA
AMPL1652234	TCGTCAAGATGGAGTTTCTATGC	GGGTCATTGATAAAATCGTCTGGAGTATAG

Targeted NGS panel for detection of equine pathogens

AMPL1652235_1	ATCAAACAGTGAAGCTCAACGAGA	CCTTACTAATCAAGAGTGGAATTGCAAAAG
AMPL1652235_2	ATCAAACAGTGAGGCTCAACGAGA	CCTTACTAATCAAGAGTGGAATTGCAAAAG
AMPL1652236	GGTTTGGCGACAAATGCAGTATT	CGACAATTTGATTATCTTCATCACTAAGCT
AMPL1652239	TGCAAGTGCGGGAATCTATAAAACA	TCTACGATTCAATGCGCTAATAGAGAAATT
Listeria_23S_1.2.207564	TGTCAAGAAAAGCCTCTAGGAAGAGTAG	CGGTTTTGCAGAGACCTGTGT
Listeria_23S_1.2.29471	AGACAACCAGGATGTTGGCTTA	CCTTAGATATTCGGTGGAAAGGGATTCT
Listeria_23S_1.2.49805	ATCTAAGGTTTCCTGAGGAAGGC	TCTTGACAGCGTGAAATCAGGA
Listeria_23S_1.2.83661	CGACACAGGTAGATGAGGAGAGA	GCCGAAGCTAAGCACTCCT
Listeria_23S_1.3.105784	GCTTCGGCGAAGGTACGA	ACACGTCTCTTCGGCTCCT
Listeria_23S_1.3.18366	AGACAGTTCGGTCCCTATCCG	TTTGTCCGCTCCATGTATCGC
Listeria_23S_1.3.92992	GATGGACACACCGCTGGT	TTGGTTAAGTCCTCGATCGATTAGTATTT
AMPL1652261	GTGGGTGACGTCATCGGTAAATA	CGACGAAATCCACCGTCTCTTTTT
AMPL1652262_1	CGAAGATCGCCCATGAACTGAT	GCTGATGTCTTCGTTTTCAACGTAG
AMPL1652262_2	CGAAGATCGCCCATGAACTGAT	GCTGATGTCTTCATTTTCAACGTAG
AMPL1652262_3	CGAAGATCGCCCATGAGCTGAT	GCTGATGTCTTCGTTTTCAACGTAG
AMPL1652191_1	CTATACCACGCTACAGCGTGTT	CCAGTTCAATGTAAGATCAACATCTTCAG
AMPL1652191_2	CTATACCACGTTACAGCGTGTT	CCAGTTCAATGTAAGATCAACATCTTCAG
AMPL1652192	GATGATCTCAGTGGGCGTTCTTA	GTAATCCCACGGACTCTTCCATC
AMPL1652294	AAGTGGCTGGGTAGTTATACGC	CCCGTACTCTCTTGAGAAAAGTAGC
AMPL1652295_1	CCGCCTACTACTAACTATGTACTGTACT	GGCATAAAGTTAAACATTGACCCGTAA
AMPL1652295_2	CCGCCTACTACTAACTATGTACTtagt	GGCATAAAGTTAAACATTGACCCGTAA
TM03_1.958	GGTGTGAAGGAGTCTCTCGTT	ACCGATGGGAACCCTCAC
TM03_2.958	GGTGTGAAGGAGTCTCTCGTT	ACCGATGGGAACCCTCAC
S_equi_type_1	atgctgagagttgatcaaaacactt	ccattttattcccccttttgtttta
AMPL1652224	GTTTATGTGCTTCGGCACGTTT	AAGTCCAACAGGTAATAAAACCCGA
AMPL1652289	GGTAGTTCACTGGACTTCTTATTACCG	CGGAAATAGCCGTTAACGCTACT
AMPL1652220_1	GTCACCTCTGACTAAAGGGATTTTAGG	TGCCACTTCGGTTGTAATAGTTCC
AMPL1652220_2	GTCACCTCTGACTAAAGGGATTTTAGG	TGCCACTTCGGTTGTAACAGTTCC
AMPL1652221	GCCAGTTGCATGGGACTCATAT	ATCTGCCTAGCCCTACTAGCAA
AMPL1652303	AAAGTTCTGTATAGATCCCATTTCTCTTAAGT	GGAAAAGGAAAAGTTAAACTAGTTGGTCCTA
AMPL1652304	TTTTTCGAAAAGCAATTCATATGGTTG	AGATCTTGTTGGGAAAAGTGTGGT

Targeted NGS panel for detection of equine pathogens

EHV_3_gB_1	gtttgctccgattacgtgtattat	ctgaatctcgctgtagtcataag
Neospora_1	GCCAGTGCCTCAATCCTGTAAC	CTCGCCAGTCAACCTACGTCTTCT
Neospora_2	GCCAGTGCCTCAATCCTGTAAC	CTCGCCAGTCCACCTACGTCTTCT
Neospora_2_1	GGAGGTATAGCAGAGAGAATTCGTG	AGGCTGATTTCAACGTGACGAA
Neospora_2_2	GGAGGTATAGCAGAGAGAATTCGTG	AGGCTCATTTC AACGTGACGAA
Neospora_3	CCCAGTGCCTCAATCCTGTAAC	CTCGCCAGTCAACCTACGTCTTCT
TM08_1.410	CGGGAAAAACGGTGGGTAC	GTGAGGCCCTGTACTCAAGC
TM08_2.410	CGGGAAAAACGGTGGGTAC	GTGAGGCCCTGTACTCAAGC
LstriaMHly_1.1.23870	ACACGCGGATGAAATCGATAAGTAT	TTACAGGGAGAACATCTGGTTGATTTT
LstriaMHly_1.1.4447	AAACGTGATTCATTAACACTCAGCATTG	ATTGCGCCGAAGTTTACATTCAA
LstriaMHly_1.1.48307	ATCTTTAGAAGCGAATTCGCCAATATT	TGTTTCTTTTCGATTGGCGTCTT
LstriaMHly_1.2.114389	GCAAGCGCTTGGAGTGAA	GGTTGCCGTCGATGATTTGAA
LstriaMHly_1.2.117774	GCCTGGTAACGCGAGAAATATTAATGT	AATTTACGAAGAGTGCAAAACAAGCTT
LstriaMHly_1.2.119256	GCGCAATCAGTGAAGGGAAAATG	CGCTTACGGCAGCATCAAAAAG
LstriaMHly_1.2.160507	TCCATTGCTTATACAACAAACTTCCTA	TACCAGGCAAATAGATGGACGATGT
LstriaMHly_1.2.87399	CGGCAACCTCGGAGACTT	GAGCAACGTATCCTCCAGAGT
TM10_1.360	CGTTTCTCGAGGCTGTGAG	TCTGTAGACAGGAACGAGTGG
TM10_2.360	CGTTTCTCGAGGCTGTGAG	TCTGTAGACAGGAACGAGTGG
Histo_hcp_1	GTTTACATCGACTACGGCAACTC	AATGTCCGTTACCAAGGTATC
C_perf_iap_1.4.4902	acaatttgtctatctttatgctatagcttgt	tgcgtttaataaagaaataagaacagaaaatca
C_perf_iap_1.5.11298	ttaagaaaatcttctggtctttcaataaaagc	attgaatcttaataaactgaattaggagggga
C_perf_iap_1.6.22287	ttcaagcatctgtagaatatggattttgaat	aacacatctttaccaactcaattaatgaac
C_perf_iap_1.6.664	aaaggagatggttggatattaagtaaacct	acatactcatttgaacagtagttgtag
AMPL1652263_1	AAATGCTGAAATTCGGCAAATTTGC	CCTTTCAGGTCTTTTCGCGTGTA
AMPL1652263_2	AAATGCTGAAATTCGGCAAATTTGC	CCTTTCAGGTCTTTGGCGTGTA
AMPL1652264	CCACCTTCTACTTCGAGTACGACA	CTCTTTACCATAGGAAACCAGTTCCA
Myco_gen_1	ACCTCCTTTCTACGGAGTACACTT	CTTCATCGACTTCCAGACCCAA
AMPL1652247	CATTAGGCGTGAATTATTCATTATCGGAA	ACCTTCATTTTCCAAATATTGAACGCT
Histo_M_1	ACAAGAGACGACGGTAGCTTCACG	GCGTTGGGGATCAAGCGATGAGCC
AMPL1652305	TATAACAATAATGAGCACATTGTAGGTTATCCG	CAATTAATATATCCCTATTTGGATCGTTGCCT
AMPL1652306_1	TGCATCTTTAGGATTAGTAGGTACCCAT	AGGTACAAAGTACCAATCACATGTTAAAGT

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AMPL1652306_2	TGCATCTTTAGGATTAGTAGGTACCCAT	AGGTACAAAGTACCAATCACATcctaaaat
AMPL1652306_3	TGCATCTTTAGGACTAGTAGGTACCCAT	AGGTACAAAGTACCAATCACATGTAAAGT
TM07_1.780	CTGTGATCGATCCGTGGAAGG	TCGTCTCCAGCGAGAGTACC
TM07_2.780	CTGTGATCGATCCGTGGAAGG	TCGTCTCCAGCGAGAGTACC
AMPL1652272	GCATTCGAAGGTGTCGAGATCA	GGTTCAGTCTTAAAGAATTTAAGGGTTG
AMPL1652186_1	CAATTTAAATCCAATGGTGTTCGAAAATGC	TGATTGGCTAAAGGTACCTGTTTCATTA
AMPL1652186_2	CAATTTAAATCCAATGGTGTTCGAAAATGC	TGATTGGCTAAAGGTGCCTGTTTCATTA
AMPL1652284	TGCGATAAGCTTGATGAGTTGATAAGA	TCGAATACGGGACTATCACCCCTT
TM09_1.923	TATCGTTGTAGCGTAACCTGGTC	CGCGATGATCGATGGTGCA
TM09_2.923	TATCGTTGTAGCGTAACCTGGTC	CGCGATGATCGATGGTGCA
AMPL1652270_1	GCATTTGCAGTCAGGTCCCTAA	CTAAGTCGTGGAAGTAACTGTGGT
AMPL1652270_2	GCGTTTGCAGTCAGGTCCCTAA	CTAAGTCGTGGAAGTAACTGTGGT
APhgcytAnk_1.2.196638	GTCGCTACCAGCACTTGACAT	GTATACCCGCAGAAATAGCTGGT
APhgcytAnk_1.3.109934	CTGCTAAGTTGCTCTTGGATAAAGGG	AAGCAAGTCTTTGAAAGATGAGTCTGA
APhgcytAnk_1.3.137325	GCCTGAAAGTCCAACCTCCTTTTAA	CCTTAGATGACGCCGCATCTG
APhgcytAnk_1.3.146371	GCTGAAGCACTAACGAATGGTCA	TACTTGCCTCATTGCGCGCTT
APhgcytAnk_1.3.164485	GGTATACAAGGAGGGTGCTTTCAG	CAGTCTTATGGTTGCCAGCAG
APhgcytAnk_1.4.93641	GCAGAACGAACATCTTCTTCTGG	AGCTCAGCTGCAAAAGAGCTA
CEM_1	GCAGCATAAGGAGAGCTTGCT	GTAAAAGGTCATCTCTGATCC
AMPL1652308	ATGAACAACGTTCTGAAATTCTCTGC	GGCTGGCTTTTTCCAGCATG
AMPL1652187_1	ATGTTTTTCATGTTTTCTTATTGTTGGAGCA	TCAAAAGATTTTCAGTTGTTGGTTAGGATCA
AMPL1652187_2	ATGTTTTTCATGTTTTCTTATTGTTGGAGCA	TCAAAAGATTTTAGTTGTTGGCTAGGATCA
AMPL1652187_3	ATGTTTTTCATATTTCTTATTGTTGGAGCA	TCAAAAGATTTTCAGTTGTTGGTTAGGATCA
AMPL1652187_5	ATGTTTTTCATGTTTTCTTATTGTTGGGAGCA	TCAAAAGATTTTCAGTTGTTGGTTAGGATCA
AMPL1652281_1	CAGGGAAACGTCCCTTCTACAA	CGCTTCCAGTGACTCATCATCG
AMPL1652281_2	CAGGGAAACGTCCCTTCTACAA	TGCTTCCAGTGACTCATCATCG
AMPL1652281_3	CAGGGAAACGTCCCTTCTACAA	CGCTTCTAGTGACTCATCATCG
AMPL1652281_4	CAGGGAAACGTCCCTTCTATAA	CGCTTCCAGTGACTCATCATCG
AMPL1652193	GGAACGTTCCGGAATGCAAATC	CGGAAGCACATTGCTGATTCTC
AMPL1652194	GAAGAAGTGGACCTCACACTGA	GAAAAGCAGCTGCGGTATTACTTT
AMPL1652176	TGCACTCGGCTGATCGTTTT	CGGATAGTTCAGGGTTGTTTGGT

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HPhalbs28S_1.50258	GAAAACGATTAAGTGGAAGCAAACAGG	ACGAATGAACCTTTACTTTTCATTATGCC
HPhalbs28S_1.58507	GCAGCGAACTGTAGCGTATAGG	CGTTTTACAGTTCTTTTAACCTCTCTCTT
HPhalbs28S_1.7896	AAGCTCAGCGCTGAATCTCT	CCTCACGGTACTTGTTTACTATTGGT
CperfEpsln_1.1.12066	AGTTATTTAGCTTTTCCTAGGGATGGTT	AATCTTATTTTATTCTGGTGCCTTAATAGAA
CperfEpsln_1.1.42002	TGTCCTTCACAAGATATACTAGTACCA	ACTATTAACTCATCTCCATAACTGCACTA
CperfEpsln_1.1.42185	TGTGGGAACTTCGATACAAGCA	AAATAACTAGGTATCTCTCCCCATTAC
AMPL1652290_1	GAGCCGAAGTGCGTTTTCTTTT	TTCCACCCTCCAGGAAAAGCAG
AMPL1652290_2	GAGCCGAAGTGCGTTTTTTTTT	TTCCACCCTCCAGGAAAAGCAG
AMPL1652291	GAGTCGGAGAGGGAGAAGATGT	AGTGCATCTGGATTCTCTCTCTA
AMPL1652217_1	GGTAAATGTGAAATATGGAGAATGGAAGGT	CGGTCTAACAGTTTTGTACCATCATTTTCT
AMPL1652217_2	GGTAAATGTGAAATATGGAGAATGGAAGGT	CGGTCTAACAGTTTTGTGCCATCATTTTCT
AMPL1652217_3	GGTAAATGTGAAATCTGGAGAATGGAAGGT	CGGTCTAACAGTTTTGTACCATCATTTTCT
AMPL1652217_5	GGTAAATGTGAAATCTGGCGAATGGAAGGT	CGGTCTAACAGTTTTGTACCATCATTTTCT
APhgcytGroEL_1.1.101234	GACAAGAACATAGGAAGTAAGATTGCAC	ACCAGCTCTCGCAACGT
APhgcytGroEL_1.1.107649	GATGCAGTTGGTTGACTGCTG	ATGCTAACAATATCAGATCCAGCAGCT
APhgcytGroEL_1.1.18193	AATGGTATTCTCAAGGCTAAGGAAGC	TCAGCATTTGTAACAAAGTAAGGCGAA
APhgcytGroEL_1.1.54030	ATGCTGGTGGAATTTGAAAATCCATAC	ACTACATACTTAGCGCCTACTATTACGG
APhgcytGroEL_1.2.44429	GAGCTGGTAGACCATTGCTTATCAT	AGTTGCGTCTTTTGTGATGCG
TM11_1.601	CAGCTTTGATTGGCATAAGAGACT	AGAAGAGGCTTCATCCTCTCC
TM11_2.601	CAGCTTTGATTGGCATAAGAGACT	AGAAGAGGCTTCATCCTCTCC
AMPL1652310_1	ATCCGAAGGCAACGGAATGCAA	TCATGAACGAAATAACCATTGCTACTATCA
AMPL1652310_2	ATCCGAAGGCAACGGAATGCAA	TCATGAACGAAATCATCATTGCTAATATCA
AMPL1652310_3	ATCCGAAGGCAACAGAATGCAA	TCATGAACGAAATAACCATTGCTACTATCA
AMPL1652240_1	AGTAGACACCCTTACTGAAAAGGGA	CGGATTTTCTGAGTATTTGTCTCAATGTTT
AMPL1652240_2	AGTAGACACCCTTACTGAAAAGGGA	CGGATTTTCTGAGTATTTTCTCAATGTTT
AMPL1652240_3	AGTAGACACCCTTACTGAAAAAGGA	CGGATTTTCTGAGTATTTGTCTCAATGTTT
AMPL1652241_1	GTGATGACATTTGTTATCCAGGCAAATT	GTAGGATTTTGTGATTTGTGGGAATACC
AMPL1652241_2	GTGATGACATTTGTTATCCAGGCAAATT	GTAGGACTTTGTGATTTGTGGAAATACC
AMPL1652241_3	GTAATGACATTTGTTATCCAGGCAAATT	GTAGGATTTTGTGATTTGTGGGAATACC
AMPL1652241_5	GTGATGATATTTGTTATCCAGGCAAATT	GTAGGATTTTGTGATTTGTGGGAATACC
AMPL1652241_7	GTGATGACATTTGCTATCCAGGCAAATT	GTAGGATTTTGTGATTTGTGGGAATACC

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TM04_1.1251	CTCACAGACAGCCCTTCTGTT	GGAGCAACGAGGACTCTGT
TM04_2.1251	CTCACAGACAGCCCTTCTGTT	GGAGCAACGAGGACTCTGT
AMPL1652229_1	GGCGATGGTTAGTCAAGCTTCT	ATGCCACATTCAACGGTCAAAC
AMPL1652229_2	GGCGATGGTTAGTCAAACCTTCT	ATGCCACATTCAACGGTCAAAC
AMPL1652230	CTGACAACAACGGCACCATTGAC	GCCATTGTCGACTCCAGATCAC
AMPL1652286	CAGTGCTCGTTTACGACCTGAA	AAGATAAGACGGCTGGTACTGATTG
AMPL1652184	ACTATAGTCATGCTAGCATGAGTCATAGT	AGTTTTTCCATCCTTTGTTTTGATTCCAAA
AMPL1652185_1	GTGAGAAAGATGCTGGAACAGATG	GGCTTATAAGCATCTGAGAATGCTGTATAT
AMPL1652185_2	GTGAAAAAGATGCTGGAACAGATG	GGCTTATAAGCATCTGAGAATGCTGTATAT
AMPL1652222	AAAACCCAATCAGTGGCAATAACAC	AGCGCTGCTTCTTTCTATAAAGAGG
AMPL1652223	CCACTGTGACGCCTTTCAGTAT	TAAGAGCTTCCAGATTTTGTTAGCCAA
AMPL1652058_1	GCCAGGCTGGTGGATTACAATT	GTTGACTGTGATAGCGCCTGAT
AMPL1652058_2	GCCAGGCTGGTGGATTACAATT	GCTGACTGTGATAGCGCCTGAT
AMPL1652058_3	TCCAGGCTGGTGGATTACAATT	GTTGACTGTGATAGCGCCTGAT
AMPL1652251	ATACAGACCAAGCACGAGAAAAGCTA	TGAGCATGGGCCTTTAGCAAAT
AMPL1652252	CCCTGGAAGAAAAGTGTCCCAA	GTTTTCTGTACCTGTATCCCCTT
AMPL1652253	GCAAGAAGTGGCTGAAACAACC	TGTAGATGGTGGTCGAGGTCAT
AMPL1652254_1	CCGGGAACCAGATGTACAAGTA	GCTGTCCCTGCCATGATCTATG
AMPL1652254_2	CTGGGAACCAGATGTACAAGTA	GCTGTCCCTGCCATGATCTATG