

Table S3 Primers used in this study

Primer	Sequence (5'-3')
SS001FRAG1_F	GCAAGACGTTTCCCGTTGAATATGGCTCATAATGCTGCTTCTTCGATGAT
SS001FRAG1_R	ACAGAAATACAAACCCCTCACCTG
SS001FRAG2_F	TGTAACCTGGATAGCAACACACC
SS001FRAG2_R	TAGAACCCTCGAACGCTACGTC
SS001FRAG3_F	AAGTCACCCTACAAGGAGCCTG
SS001FRAG3_R	ACGGAGCATGGTGTGCCTAATAC
SS001FRAG4_F	TCCAAGGAAATCTGAATACGAGGG
SS001FRAG4_R	ACAGCGTCCTTTCTTTGAAGTC
SS001FRAG5_F	ATGAACTTCACCCCTACTGAACTC
SS001FRAG5_R	ATGAGTAAACTGCTGGTTCCGG
SS001FRAG6_F	AGTGGTTCCTCTCAACTTAGCC
SS001FRAG6_R	CGTGATGAAAAGGACCCAGGTGGCACTTTTCGCCCACTTAACCGAAGAG
SS002FRAGYT_F	CGAAAAGTGCCACCTGGGTC
SS002FRAGYT_R	GTGAGTTTAGTATACATGCA
SS002FRAGBK_F	AGTAAATGCATGTATACTAAACTCACCTGCAGCAATGGCAACAACG
SS002FRAGBK_R	TTAATCATGACATCATCGAAGAAGCAGCATTATGAGCCATATTCAAC
SS002FRAG1_F	GGCCGCTTTCCTGGCTTTGCTTCCCAATTAATAATGACAATTAAGTTCC
SS002FRAG1_R	GACTGTAAGAGGAATTGTCAGAGGC
SS002FRAG2_F	GTTATTAAGCCCTATCCCTAAGTCC
SS002FRAG2_R	GCCAACTTGATTAGTTAGGGAAGGC
SS002FRAG3_F	GAAAGCCACCGCCGTTGCCGTTGCC
SS002FRAG3_R	GCCAGATAACTTAATGCTTTCAGTC
SS002FRAG4_F	GATTAGGAAGATTCAGGGAGTACC
SS002FRAG4_R	CTTCAGGAAACTTGTTAACTAATC
SS002FRAG5_F	GAAACCAACTCTCTTATGTCGAAC
SS002FRAG5_R	GAAAAGGACCCAGGTGGCACTTTTCGGGAACGTTTACCATTGATTTCTAAC
SS002FRAGYT_F	GTTAGAAATCAATGGTAAACGTTCCCGAAAAGTGCCACCTGGGTCTTTTC
SS002FRAGYT_R	CAACCGTGGCTCCCTCACTTTCTGGCTGTGAGTTTAGTATACATGCATTTAC
SS002FRAGBK_F	GTAATGCATGTATACTAAACTCACAGCCAGAAAAGTGAGGGAGCCACGG
SS002FRAGBK_R	GGAACCTAATTGCTATTTTAATTGGGAAGCAAAGCCAGGAAAGCGGCC
PHUPL_US2_F	CAGGGCGCGTACTATGGTTAGCTGTGGCTGATCCCCAGC
PHUPL_US2_R	CGAAATATTAACAAAATCTACTTTAATAAGTATCCTGAGC
PHUPL_PSSR2227_F	GCTCAGGATACTTATTAAGTAGATTTTGTAAATATTTTCG
PHUPL_PSSR2227_R	GCAGCATAAAAACATTAGCCATTGATAATTTATTTCTCGTAG
PHUPL_HUPS_F	CTACGAGAAATAAATTATCAATGGCTAATGTTTTATGGCTGC
PHUPL_HUPL_R	GGTTATCATGAGACCGGTCTTAATTAGTACGGAACCTGGC
PHUPL_TRRN_B_F	GCCAGGTTCCGTAATAAAGACCGGTCTCATGATAACC
PHUPL_SPEC_F	CAGTAATACAAGGGGTGTTATGAGGAGGATATATTTGAATAC
PHUPL_SPEC_R1	TACAACCAATTAACCAATTCTGATTATAATTTTTTAACTG
PHUPL_SPEC_R2	CCATGGTACCGCTCTGCCAGTGTTACAACCAATTAACCAATTC
PHUPL_SPEC_R3	GGTCACTGCGGCCTGAAAAGCCATGGTACCGCTCTGCCAG
PHUPL_DS2_F	CTGGCAGAGCGGTACCATGGCTTTTCAGGCCGCACTGACC
PHUPL_DS2_R	CCTGGCCTTTTGTGGCCTTGTTCGCGGAGAATTTTGC
PHUPL_BONE_F	GCAAAATCTCCGGCAAACAAGGCCAGCAAAGGCCAGG
PHUPL_BONE_R	GCTGGGGATCAGCCACAGCTAAACCATAGTACGCGCCCTG
PHUPW_US_F	GCGCGTACTATGGTTGTGGTCTATGATAGCTTC
PHUPW_US_R	GGTTTTCTAGACGTCAAACGCAGAAAAGGCCACCCG
PHUPW_PTRC_F	GGCCTTTCTGCGTTTGACGTCTAAGAAACCATTATTATC
PHUPW_PTRC_R	CTAGGTCAGTCTCCATAAATGTGTGAAATTGTTATCCGCTC
PHUPW_HUPW_F	TTTATGGAGGACTGACCTAGATGTTAACAGTTATTGGGTGTG
PHUPW_HUPW_R1	CATTATTTATTTGAGTTATCTTTTAAATAAAAAATC
PHUPW_HUPW_R2	CGCTTGCGCGGGCTTTTTACATTATTTATTTGAGTTATC
PHUPW_HUPW_R3	TCCATAAAAAAACCCGCTTGCGCGGGCTTTTTAC
PHUPW_HUPW_R4	AGAGTTTACCTGGCGGTTTTTCCATAAAAAAACCCGCTTG
PHUPW_DSBK_F	CAATCGAGGGGCTTTTTTTTGCCTTTTCAGGCCGCACTGAC
PHUPW_DSBK_R	TATCATAGACACCACAACCATAGTACGCGCCCTGTAG
KOPLAS MID_BB_F	AAGGCCAGCAAAGGCCAG
KOPLAS MID_BB_R	AACCATAGTACGCGCCCTGTAG
KOPLAS MID_PPSBA2_F	GAAAAACCGCCAGGTAACCTC
KOPLAS MID_PPSBA2_R	CCAGTGATTTTTTCTCCATTTGGTTATAATTCCTTATGTATTTG
KOPLAS MID_CM_F	ACATAAGGAATTATAACCAATGGAGAAAAAAATCACTGG
KOPLAS MID_CM_R1	GAAGCGGGTTTTTACGTTATTACGCCCGCCCTGCCAC
KOPLAS MID_CM_R2	CTCATAAAAAAACCCGCGAAGCGGGTTTTTACGTTATTAC
KOPLAS MID_CM_R3	GCAAAAAAAGCCCTCGATTGAGGGGCTCATAAAAAAACCCGCGC
KOPLAS MID_USHESA_F	CCGCTACAGGGCGCGTACTATGGTTGTTTACGGGATGCTCATCGC
KOPLAS MID_USHESA_R	AGAAGAGTTTACCTGGCGGTTTTTTCGGTGAGGTGTTGAGAGTGTAC
KOPLAS MID_DSHESAB_F	CCTCAATCGAGGGGCTTTTTTTTGCGGCCAAGCTACTTCTTGTAGC

(Table S3 continued)

Primer	Sequence (5'-3')
KOPLASMID_DSHEB_R	CGGTTCTGGCCCTTTGCTGGCCTTCTGTGGTATGGTGCACTCTC
KOPLASMID_USHEB_F	CCGCTACAGGGCGCGTACTATGGTTAACTTCACCCCTACTGAACTC
KOPLASMID_USHEB_R	AGAAGAGTTTACCTGGCGGTTTTCCAGCTTTTTCAGTAAGAGTGAC
KOPLASMID_USTZ_F	CCGCTACAGGGCGCGTACTATGGTTCATGTGGTCAAAGGTAGCTATC
KOPLASMID_USTZ_R	AGAAGAGTTTACCTGGCGGTTTTCTCTTCCCTCCAGTTTTTTCGGGC
KOPLASMID_DST_F	CCTCAATCGAGGGGCTTTTTTGTCTACTTTCATAGCGTAACTC
KOPLASMID_DST_R	CGGTTCTGGCCCTTTTGTGGCCTTAAATGGGTTAGGAGAAAGGGC
KOPLASMID_DSZ_F	CCTCAATCGAGGGGCTTTTTTGCCTTTCCTCCATTTCAAAGC
KOPLASMID_DSZ_R	CGGTTCTGGCCCTTTTGTGGCCTTATCTTGTGGGATCGGTTAC
KOPLASMID_USW_F	CCGCTACAGGGCGCGTACTATGGTTGATAGCTGCTTTCTGAACTGC
KOPLASMID_USW_R	AGAAGAGTTTACCTGGCGGTTTTTCAGGGTTCTTGGGGTATCAGC
KOPLASMID_DSW_F	CCTCAATCGAGGGGCTTTTTTGTCAACCTCCAGTCTTTAGAAAC
KOPLASMID_DSW_R	CGGTTCTGGCCCTTTTGTGGCCTTGTATATGGACGACGTTTGGC
KOPLASMID_USX_F	CCGCTACAGGGCGCGTACTATGGTTTCTCATTTGTCTCTGGGGAC
KOPLASMID_USX_R	AGAAGAGTTTACCTGGCGGTTTTTCAAAGTGAGCGTTAACATGGAC
KOPLASMID_DSX_F	CCTCAATCGAGGGGCTTTTTTGTCACTTTAAAAGGAAATCCGCC
KOPLASMID_DSX_R	CGGTTCTGGCCCTTTTGTGGCCTTCTCAGCGAGATCGTGAAGTC
RTPCR_NIFT_F	ATGAAAGTGATCTTAAGCAGAG
RTPCR_NIFT_R	AGGTTAGGAAATTGTAATTC
RTPCR_NIFZ_F	GTATAATCCAGGTGAAATTG
RTPCR_NIFZ_R	AACCTGAGACTCTGTAGAG
RTPCR_NIFV_F	GATACGGTGGGCATTCTTAAC
RTPCR_NIFV_R	GGACTTTCATGGTTAAAC
RTPCR_NIFB_F	ATTTATCCTTGGGTTCCGG
RTPCR_NIFB_R	GCGTTGGCTTTCTTTGGGC
RTPCR_NIFS_F	CAAGTCGCATCCTTACTCGG
RTPCR_NIFS_R	AACGGGTTCTTTACGCAC
RTPCR_NIFU_F	GAACGATTACGGAGAAAGG
RTPCR_NIFU_R	CGCTAAACAAGAGCCACATC
RTPCR_NIFH_F	GAGAATCAACTATGCGTCAG
RTPCR_NIFH_R	GTACATCGCCATCATTCC
RTPCR_NIFD_F	GATGCTTGGTCTAGCCGTATC
RTPCR_NIFD_R	AGCCAGTGGTCCGTTTGTAG
RTPCR_NIFK_F	CTTTCTTAGGAAATGCTCGTC
RTPCR_NIFK_R	CTTTAGGAATCGGTTTGCCAG
RTPCR_NIFE_F	GAATATACCACCGCTTACGAC
RTPCR_NIFE_R	CGACCACTTCCATCCCTAAG
RTPCR_NIFN_F	GTCCTCGTGCGTCATTTTC
RTPCR_NIFN_R	GAGATACCAAACCTTCAATG
RTPCR_HESB_F	TTATACGGGAACTCAAAC
RTPCR_HESB_R	GAAAGACTTACCGCAGCCAC
CCE_0545_RTPCR_F	GCAGCAGGTCACAATTTAG
CCE_0545_RTPCR_R	GACTACGGGGACAAGTTTC
CCE_0546_RTPCR_F	ATTTTCGTCCTCCTCGTTTCGC
CCE_0546_RTPCR_R	AAATCCAATGGTCAATCAAAGC
CCE_0550_RTPCR_F	CAAATCTTTGTAATTGGGTTAC
CCE_0550_RTPCR_R	TTTCAGTGCTGTCATGGAAGC
CCE_0551_RTPCR_F	GGCTAAGAGATAAGGCAGAAAC
CCE_0551_RTPCR_R	TTGGGGTATCCCAAGTGGCGGAC
CCE_0552_RTPCR_F	GTATCCCAACATCGCTCCAG
CCE_0552_RTPCR_R	GGAGTGTTTACCAACGTCTCC
CCE_0555_RTPCR_F	CTTCTTTAGTTTCTTCAACCC
CCE_0555_RTPCR_R	GTTTAGGCTAGGAAAACAACG
CCE_0556_RTPCR_F	GTATTAAGTGTCTCGTTGTGCG
CCE_0556_RTPCR_R	GTTGAAATTTCTGGGAGTAAGC
CCE_0562_RTPCR_F	ATGGTTATGACGAGTCTACTC
CCE_0562_RTPCR_R	GATCGACATTTTACCACAAAC
CCE_0571_RTPCR_F	GCTACTTATCAAGTTCGCCTG
CCE_0571_RTPCR_R	CAGTTAGAACGAGGATAAGC
CCE_0572_RTPCR_F	GACAATAACGTGCTTTCTCTG
CCE_0572_RTPCR_R	TACAATCTCCAGGGGAGAATC
CCE_0573_RTPCR_F	GAGTATCGCCATCTTGTAAAC
CCE_0573_RTPCR_R	AAAGTTCCAACCAAAGACGAGG
CCE_0574_RTPCR_F	TTCTAACAGGTTGTGGCAAAG
CCE_0574_RTPCR_R	CAATCATATTGACAGCAAGGAC
CCE_0575_RTPCR_F	CCATTGAAAGGGTGATAGAATC

(Table S3 continued)

Primer	Sequence (5'-3')
CCE_0575_RTPCR_R	GATTAACAGAGAAATTCTCGGC
CCE_0576_RTPCR_F	GTTTACGCAAACCTTTACCATC
CCE_0576_RTPCR_R	TGTTCTTCAACTTTCCACCAC
CCE_0577_RTPCR_F	CTATTCCTATCGCCATTTTAGG
CCE_0577_RTPCR_R	GTCGGAATAATTAATTCTCCGC
CCE_0578_RTPCR_F	GTATGCTGCGGTAATTGCGGC
CCE_0578_RTPCR_R	CTCGATGGGGTTGGGTAGAAC
CCE_0579_RTPCR_F	GGAGGACACTTATTATGGC
CCE_0579_RTPCR_R	CACAGGTAAAGGGGCGTGAG
RTPCR_RNPB_F	GTTAGGGAGGGAGTTGCG
RTPCR_RNPB_R	CTGTTCCAGGATGCGAGGC
RT_Q_PCR-HUPS-F	GGCCTGTTCTGGGAATACAATTTT
RTPCR-HUPS-R	CTGGGTAAAGCTACGGAAGAAG
RTPCR-HUPL-F	AAGTGCCTCGTAATGCTATCC
RTPCR-HUPL-R	CAGGACCACCACCATACTTATC
RTPCR-HUPW-F	ACAGTTATTGGGTGTGGTAATC
RTPCR-HUPW-R	TCCCATCGAAAGTCATGTAAC
QPCR_NIFH_F	GCGAGAATCAACTATGCG
QPCR_NIFH_R	TAGGGTCACAACCAACAATC
QPCR_NIFD_F	ACGGTGGTGTCTGTTC
QPCR_NIFD_R	GTTAGCGATGTGGTGTCC
QPCR_NIFK_F	GTATGGCTGAGGTTATTG
QPCR_NIFK_R	AGGTGTATGAGCGAAAGG
QPCR_RNPB_F	AAAGGTGCGGTAAGAGC
QPCR_RNPB_R	TGGGGAGTTATCTATCTGG
QPCR_CPCB_F	GCTGAAGGCAACAAACGG
QPCR_CPCB_R	ATGTCACGCAAACAAGCAGC
OripCA_Spec_F	ATGGTAAACGTTTCTAACCCAGGCATCAAATAAAACGAAAG
OripCA_Spec_R1	TTTAATATTTAAGCTCCATGGTACCGCTCTGCCAG
OripCA_Spec_R2	AGAAATATTAATAATTTAATATTTAAGCTCCATGG
OripCA_pca2.4_F	AGCTTAAATATTAATTTAATATTTT
OripCA_DS_F2	GCTATTTTCTTAATTGAGTAAGTCTATTACAATTAATG
OripCA_pca2.4_R	TAATAGACTTACTCAATTAAGAAAATAGC
OripCA_DS_F1	TTGAGTAAGTCTATTACAATTAATGACAATTAAGTCC
OripCA_DS_R1	CTTTTGCTGGCCTTGAATTCATGAGGTAGGTTGGAAACGC
OripCA_DS_R2	TTTACGGTTCCTGGCCTTTTCTGGCCTTGAATTC
OripCA_US_F2	ATGCGCCGCTACAGGGCGCGTACTATGGTTGGATCCCCTGAC
OripCA_US_F1	TACTATGGTTGGATCCCCTGACATCGAAGTCGAAGC
OripCA_spec_R3	AATACCAGAACTCCCCTGGTACCGCTCTGCCAG
OripCA_pcB2.4_F	AGAGCGGTACCATGGGGAGTTTCTGGTATTTTCTAGC
OripCA_pcB2.4_R	CAATTTGACTAATAGTTTTGATATTTTATTAC
OripCA_DS_F4	TAAAATATCAAACTATTAGTCAAATTTGCAATTAATG
OripCA_DS_F3	TATTAGTCAAATTTGCAATTAATGACAATTAAGTTC
Orichange_pCCSpec_R4	GCTTTAATAATCTCGCCATGGTACCGCTCTGCCAG
Orichange_pCC5.2_F	AGAGCGGTACCATGGCGAGATTATTAAGCCAAGACGG
Orichange_pCC5.2middle_R	CGGGAGTACCCTAGGGTAGTC
Orichange_pCC5.2middle_F	CAGGGCATTATTGACCGCTAC
Orichange_pCC5.2_R	TTGTCATTTAATTGCCTTATCAGTCTTGGTAGCGATC
Orichange_pCCDS_F5	CCAAGACTGATAAGGCAATTAATGACAATTAAGTTCCTGTC
Orichange_pCCDS_R3	CTTTTGCTGGCCTTGTGACATGAGGTAGGTTGGAAACGC
Orichange_pCCDS_R4	TTTTACGGTTCCTGGCCTTTTCTGGCCTTGTGCGAC