

Species	Gene	Position	Sequence
Hs	DND1_140030567	1	TACTAACCCAGGGGTTTAAT-ATAAATACAACCAGCATAGAAAGACCCAAAACCTATACAGAAA-CCAAAAC
Ptr	DND1_142431156	1	TACTAACCCAGGGGTTTAAT-ATAAATACAACCAGCATAGAAAGACCCAAAACCTATACAGAAA-CCAAAAC
Hs	chr17_41692196	1	TACTAACCCAGGGGTTTAAC-ATAAATACAACCAGCATAGAAAGACCCAAAACCTATACAGAAA-CCAAAAC
Hs	chr17_h2R	1	TACTAACCCAGGGGTTTAAC-ATAAATACAACCAGCATAGAAAGACCCAAAACCTATACAGAAA-CCAAAAC
Hs	chr17_41019840	1	TACTAACCCAGGGGTTTAAT-ATAAATACAACCAGCATAGAAAGACCCAAAACCTATACAGAAA-CCAAAAC
Ptr	chr17_11917365	1	TACTAACCCAGGGGTTTAAT-ATAAATACAACCAGCATAGAAAGACCCAAAACCTATACAGAAA-CCAAAAC
Hs	chr17_h2F	1	TACTAACCCAGGGGTTTAAT-ATAAATACAACCAGCATAGAAAGACCCAAAACCTATACAGAAA-CCAAAAC
Ppy	chr17_43819715	1	TACTAACCCAGGGGTTTAAT-ATAAATACAACCAGCATAGAAAGACCCAAAACCTATACAGAAA-CCAAAAC
Ppy	DND1_	1	TACTAACCCAGGGGTTTAAT-ATAAATACAACCAGCATAGAAAGACCCAAAACCTATACAGAAA-CCAAAAC
Mmu	DND1_580548182	1	TACTATCCAGGGGTTTAAT-TATAATACAACCAGCATAGAAAGACCCAAAACCTACACAGAAA-CCAAAAC
Mmd	DND1_36923507	1	-----AGGGGTTTAAT-ATAAATATAACCAGCATAGAAAACCTCAAAACTACACACGCA-CCAAAAC
Ef	DND1_36233886	1	----AACCAGGGGTTTAAT-ATAAATACAACCAGCATAGAAAGATTCAAAACTACACATACA-CCAAAAC
Bt	DND1_51121458	1	-----AGGGGTTTAAT-ATAAATATAACCAGCATAGAAAACCTCAAAACTACACACGCA-CCAAAAC
Cf	DND1_38675152	1	-----AGGGGTTTAAT-ATAAATATAACCAGCATAGAAAACCTCAAAACTACACACGCA-CCAAAAC
Hs	DND1_140030567	69	CAGAATGCCATGTGGTGGAGGCAAAGGGCAGAATTTCTGACCCCTTTGGCTCAGCTGCCCTTCCCCACAA
Ptr	DND1_142431156	69	CAGAATGCCATGTGGTGGAGGCAAAGGGCAGAATTTCTGACCCCTTTGGCTCAGCTGCCCTTCCCCACAA
Hs	chr17_41692196	69	CAGAATGCCATGTGGTGGAGGCAAAGGGCAGAATTTCTGACCCCTTTGGCTCAGCTGCCCTTCCCCACAA
Hs	chr17_h2R	69	CAGAATGCCATGTGGTGGAGGCAAAGGGCAGAATTTCTGACCCCTTTGGCTCAGCTGCCCTTCCCCACAA
Hs	chr17_41019840	69	CAGAATGCCATGTGGTGGAGGCAAAGGGCAGAATTTCTGACCCCTTTGGCTCAGCTGCCCTTCCCCACAA
Ptr	chr17_11917365	69	CAGAATGCCATGTGGTGGAGGCAAAGGGCAGAATTTCTGACCCCTTTGGCTCAGCTGCCCTTCCCCACAA
Hs	chr17_h2F	69	CAGAATGCCATGTGGTGGAGGCAAAGGGCAGAATTTCTGACCCCTTTGGCTCAGCTGCCCTTCCCCACAA
Ppy	chr17_43819715	68	CAGAATGCCATGTGGTGGAG-CAAAGGGCAGAATT-CTGACCC-TTTGGCTCAGCTGCC-TTCCCCACAA
Ppy	DND1_	69	CAGAATGCCATGTGTGGTGGAGGCAAAGGGCAGAATTTCTGACCCCTTTGGCTCAGCTGCCCTTCCCCACAA
Mmu	DND1_580548182	71	CAGAATGCCATGTGGTGGAG-CAAAGGGCAGAATTTCTGACCCCTTTGGCTCAGCTGCCCTTCCCCACAA
Mmd	DND1_36923507	1	-----AGGGGTTTAAT-ATAAATATAACCAGCATAGAAAACCTCAAAACTACACACGCA-CCAAAAC
Ef	DND1_36233886	61	CAGAATGCCAAGTGGTAGGGACAAAAGGCAGATTT-CTGATACCTTTGGCTCA-CCAGCCCCCAAATAAAA
Bt	DND1_51121458	65	CATAA--CCAAGTGGTGGGGGCAA--GGCAGATGT-TTGACCCCTTTGGTTCCACAGCCCTCAAATAAAA
Cf	DND1_38675152	1	-----AGGGGTTTAAT-ATAAATATAACCAGCATAGAAAACCTCAAAACTACACACGCA-CCAAAAC
Hs	DND1_140030567	139	ATAAAAACCAACAAAGAGGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Ptr	DND1_142431156	139	ATAAAAACCAACAAAGAGGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Hs	chr17_41692196	139	ATAAAAACCAACAAAGAGGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Hs	chr17_h2R	139	ATAAAAACCAAA-----GAGGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Hs	chr17_41019840	139	ATAAAAACCAACAAAGAGGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Ptr	chr17_11917365	139	ATAAAAACCAACAAAGAGGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Hs	chr17_h2F	139	ATAAAAACCAACAAAGAGGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Ppy	chr17_43819715	134	ATAAAAACCAACAAAGAGGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Ppy	DND1_	139	ATAAAAACCAACAAAGAGGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Mmu	DND1_580548182	141	ATAAAAACCAACA--AAAGACAAATCAGGACAATAAAGAAGATTTCATGCTAAGCTGTGGCAGAGGG-GGG
Mmd	DND1_36923507	1	-----AGGGGTTTAAT-ATAAATATAACCAGCATAGAAAACCTCAAAACTACACACGCA-CCAAAAC
Ef	DND1_36233886	130	AC--CAACAACGAAGACAAATCAAGAAAAATAACAAACAAAGATTTCATGCTAAGCTGTGGCAGAGGG-GAG
Bt	DND1_51121458	131	ACTTCAACAAGAAGACAAACAGGGGAAATAAGAAACAAAGATTTCATACTAACTGTGGGAGGAGGAGAG
Cf	DND1_38675152	1	-----AGGGGTTTAAT-ATAAATATAACCAGCATAGAAAACCTCAAAACTACACACGCA-CCAAAAC
Hs	DND1_140030567	208	AAGGTATGATCGGGTGGGGGTGGGACAAGGAACGGCCATGGAAGATCACTGGGTGAG-----
Ptr	DND1_142431156	208	AAGGTATGATCGGGTGGGGGTGGGACAAGGAACGGCCATGGAAGATCACTGGGTGAG-----
Hs	chr17_41692196	208	AAGGTATGATCGGGTGGGGGTGGGATAAGGAATGGCCATGGAAGATAACTGGGTGAG-----
Hs	chr17_h2R	204	AAGGTATGATCGGGTGGCGGTGGGACAAGGAATGGCCATGGAAGATAACTGGGTGAG-----
Hs	chr17_41019840	208	AAGGTATGATCGGGTGGGGGTGGGACAAGGAATGGCCAAGGAAGATAACTGGGTGAG-----
Ptr	chr17_11917365	208	AAGGTATGATCGGGTGGGGGTGGGACAAGGAATGGCCATGGAAGATAACTGGGTGAG-----
Hs	chr17_h2F	208	AAGGTATGATCGGGTGGGGGTGGGACAAGGAATGGCCATGGAAGATAACTGGGTGAG-----
Ppy	chr17_43819715	203	AAGGTATGATCGGGTGGGGGTGGGACAAGGAATGGCCATGGAAGATAACTGGGTGAG-----
Ppy	DND1_	205	AAGGTATGATCGGGTGGGGGTGGGACAAGGAATGGCCAAGGAAGATAACTGGGTGAG-----
Mmu	DND1_580548182	207	AAGTTATGATCGGGTGGGTGTGGGACAAGGAATGGCCATGGAAGACCAAGGGTACC-----
Mmd	DND1_36923507	1</	

Hs_chr17_h2F	265	-----
Ppy_chr17_43819715	260	-----
Ppy_DND1_	275	AGGGGAGGCAAGCCCTCACACAATAAGCAAAGCTGCTCCAGGGGGTGGGACAAAGTATGGCCCAGG
Mmu_DND1_580548182	264	-----
Mmd_DND1_36923507	1	-----
Ef_DND1_36233886	254	-----
Bt_DND1_51121458	258	-----
Cf_DND1_38675152	1	-----

Hs_DND1_140030567	265	-----GTT--GGACCCTGGGCTG--GGAGCGGGAG--GGCAAGGCCCTCACCACA
Ptr_DND1_142431156	265	-----GTT--GGACCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA
Hs_chr17_41692196	265	-----GTT--GGACCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA
Hs_chr17_h2R	261	-----GTT--GGACCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA
Hs_chr17_41019840	265	-----GTT--GGACCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA
Ptr_chr17_11917365	265	-----GTT--GGACCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA
Hs_chr17_h2F	265	-----GTT--GGACCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA
Ppy_chr17_43819715	260	-----GTT--G--ACCCTGGGCTG--GGATGGGGAG--GGCAAGGCCCTCACCACA
Ppy_DND1_	345	TAAGATCCACTTGGTCACTTGGGACCTTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA
Mmu_DND1_580548182	264	-----TTT--GGACCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA
Mmd_DND1_36923507	1	-----GACCCTGGGCTC--AGTGGGGAG--GGCAAGGTTCCCTCAC---
Ef_DND1_36233886	254	-----TAGGCTGGGGAG--GGGCTGGGAG--GGCAAGGTTCCCTCACCACA
Bt_DND1_51121458	258	-----GGGTCCAATGAAACCCAGAAATGGGAGAAAGGAAGTTCCCTCACCACA
Cf_DND1_38675152	1	-----GACCCTGGGCTG--GGAGGGGGAG--AGCAAAGTCCCTCCACCACA

Hs_DND1_140030567	310	ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAGGGAGGCTG-----A
Ptr_DND1_142431156	310	ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAGGGAGGCTG-----A
Hs_chr17_41692196	310	ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAGGGAGGCTG-----A
Hs_chr17_h2R	306	ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAGGGAGGCTG-----A
Hs_chr17_41019840	310	ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAGGGAGGCTG-----A
Ptr_chr17_11917365	310	ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAGGGAGGCTG-----A
Hs_chr17_h2F	310	ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTTCCTGTCCAGCAGGGAGGCTG-----A
Ppy_chr17_43819715	304	ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAGGGAGGCTG-----A
Ppy_DND1_	408	ACTTAAGCCAAACCTAAGCTGCTCCAGGTGCCACAGGTTCCTGTCCAGCAGGGAGGCTG-----A
Mmu_DND1_580548182	308	ACTTAAGCCAAACCTAAGCTGCTCCAGGTGCCCTAGGTCCCTGTCCAGCAGGGAGGCTG-----A
Mmd_DND1_36923507	38	-----AACTAAAGTAGCACTTAGGTGGAACAGGGCCCTGTCCAGCAGGGAAAG-----
Ef_DND1_36233886	296	ACTG--GGCCAAACCTGAGCTGCTCACAGGTGTGCTGGGGCCCTGCCAGCTGGGACGCTGTGTCAGGTC
Bt_DND1_51121458	306	ACTTTGGCCAAACCTGAGCTGCCCCAGGTGTTCTGGGGCCCTGCCAGCTGGGAGGCTGTGTCAGGTC
Cf_DND1_38675152	42	CTTA--GCCAAACCTGAGCT--TTCCAGGTGCCCTGGGGCCCTGTGCCAGCTGGGAGGCTGTGTCAGAGG

Hs_DND1_140030567	372	TGGGCCCTGGGCCCAGTCCCCCTCCCCACCTTTGGGGGTGAGAAAGTGGCCACCAGGCCTGCTGGGATGGG
Ptr_DND1_142431156	372	TGGGCCCTGGGCCCAGTCCCCCTCCCCACCTTTGGGGGTGAGAAAGTGGCCACCAGGCCTGCTGGGATGGG
Hs_chr17_41692196	372	TGGGCCCTGGGCCCAGTCCCCCTCCCCACCTTTGGGGGTGAGATAGTGGCCACCAGGTTTGCTGGGTTGGG
Hs_chr17_h2R	368	TGGGCCCTGGGCCCAGTCCCCCTCCCCACCTTTGGGGGTGAGATAGTGGCCACCAGGTTTGCTGGGTTGGG
Hs_chr17_41019840	372	TGGGCCCTGGGCCCAGTCCCCCTCCCCACCTTTGGGGGTGAGATAGTGGCCACCAGGTTTGCTGGGTTGGG
Ptr_chr17_11917365	372	TGGGCCCTGGGCCCAGTCCCCCTCCCCACCTTTGGGGGTGAGATAGTGGCCACCAGGTTTGCTGGGTTGGG
Hs_chr17_h2F	372	TGGGCCCTGGGCCCAGTCCCCCTCCCCACCTTTGGGGGTGAGATAGTGGCCACCAGGTTTGCTGGGTTGGG
Ppy_chr17_43819715	366	TGGGCCCTGGGCCCAGTCCCCCTCCCCACCTTTGGGGGTGAGATAGTGGCCACCAGGCTGCTGGGTTGGG
Ppy_DND1_	470	AGGGCCCTGGGCCCAGTCCCCCTCCCCACCTTTGGGGGTGAGATAGTGGCCACCAGGCTGCTGGGTTGGG
Mmu_DND1_580548182	369	TGG--CCTGCAACCATGCTCTCCCCACCTTTGGGAGTCAGATAGTGGCCACCAGGCTGCTGGGCTGGG
Mmd_DND1_36923507	87	-----CTGTCACCAAGCCCTG-----GGCTGCCAGGCCTGCTGGGCTGGG
Ef_DND1_36233886	365	CAGGGCAGGGCCCAGTCTCTCCCTTTGTTT--GGGATCAGGTGGTGGCTGCCAGGCCTGCTGGGCTGGT
Bt_DND1_51121458	376	TAGGGCAGGGCCTATGCTCTCTCCCTTTCTT--GGAGTCAGATAGTGGCTGCCAGGCCTGCTGGGCTGGG
Cf_DND1_38675152	109	TAGGGCAGGACCTGTGTCT--CCCTCTTT--GAGATCAGATGGTGGCTGCCAGGCCTGCTGGGCTGGG

Hs_DND1_140030567	442	GC-CTGACACAGGCTCTGCATG--CCCATTTCAGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCA
Ptr_DND1_142431156	442	GC-CTGACACAGGCTCTGCATG--CCCATTTCAGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCA
Hs_chr17_41692196	442	GC-CTGATACAGGCTCTGCATG--CCCATTTCGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCA
Hs_chr17_h2R	438	GC-CTGACACAGGCTCTGCATG--CCCATTTCGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCA
Hs_chr17_41019840	442	GC-CTGACACAGGCTCTGCATG--CCCATTTCGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCA
Ptr_chr17_11917365	442	GC-CTGACACAGGCTCTGCATG--CGCATTTCGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCG
Hs_chr17_h2F	442	GC-CTGACACAGGCTCTGCATG--CCCATTTCGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCA
Ppy_chr17_43819715	436	GC-CTGACACAGGCTCTGCATG--CCCATTTCGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCA
Ppy_DND1_	540	GC-CTGCACAGGCTCTGCATG--CCCATTTCAGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCA
Mmu_DND1_580548182	438	GC-CTGACACAGGCTCTGCCTG--CCCATTTCAGGCTGCCTGTGGAGAGAGAATGGAGTCACCTGTTTAACCA
Mmd_DND1_36923507	128	GGGTGGCACAGGCTCTGCTTA--CCCATTTCAGGCTACCTGTAAAGAGAA--GGGGTCACCTGCTTAACCA
Ef_DND1_36233886	433	GA-CTGACACAGGCTCTGCTTA--CTCATTTCAGGCTGCCGCTGAAGAGGA--TGGGGTCACCTGCTTAACCA
Bt_DND1_51121458	444	TG-CAGACAAAGGCTC-----CCTGTGGAGAGGA--TAAGGTCACCTGTTCAACCA
Cf_DND1_38675152	175	GA-CTGACACAGGCTCTGCCA--TGTCTTCAGGCTGCCTGTGAAGAAGA--CAGGGTCACCTGCTTAACCA

Hs_DND1_140030567	510	TGGTACCT---	GCCTCAGCCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG
Ptr_DND1_142431156	510	TGGTACCT---	GCCTCAGCCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG
Hs_chr17_41692196	510	TGCTACCT---	GCCTCAGCCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG
Hs_chr17_h2R	506	TGCTACCT---	GCCTCAGCCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG
Hs_chr17_41019840	510	TGCTACCT---	GCCTCAGCCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG
Ptr_chr17_11917365	510	TGCTACCT---	GCCTCAGCCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG
Hs_chr17_h2F	510	TGCTACCT---	GCCTCAGTCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG
Ppy_chr17_43819715	504	TGGTACCT---	GCCTCAGCCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG
Ppy_DND1_	608	TGGTACCT---	GCCTCAGCCCCAGCAGAACACAGGAGGTTGGCCCCAGACTCACTAAGTGCCTGCAGCAG
Mmu_DND1_580548182	506	TGGTACCT---	GCCTCAGCCCCAGCAGACCACAGGAGGCTGGCCCCAGACTCACTGAGTGCCTGCAGCAG
Mmd_DND1_36923507	195	TAGTACCT---	GCTTCAGCCCCAGGAGACCACAAG---CTGGTCCTAGGTTCACTCAGTGCCTGCAGCAG
Ef_DND1_36233886	499	CAGTACCT---	GCCTCAGCCCCAGCAGACCACAGGAGGCTAGCCCCAGACTCACTCAGTGCCTGCAGCAG
Bt_DND1_51121458	491	TGGTACCTCCT	GCCTCAGCCCCAGTAGACCACAGGAGGCTGGCCCTAGACTCACTCATTGCTTGCAGCAG
Cf_DND1_38675152	241	CCATACCT---	GCCTCAGCCCCAGCAGACCAGAGAGGCCGGCTCCAGACTCCTCAGTGCCTTGCAGCAG

Hs_DND1_140030567	577	CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCCAGATG
Ptr_DND1_142431156	577	CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCCAGATG
Hs_chr17_41692196	577	CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCCAGATG
Hs_chr17_h2R	573	CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCCAGATG
Hs_chr17_41019840	577	CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCCAGATG
Ptr_chr17_11917365	577	CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCCAGATG
Hs_chr17_h2F	577	CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCCAGATG
Ppy_chr17_43819715	571	CCGTACAGACACAGCATCCTTGGCTACCTCATGTCCATCCCGGCCATCTAGGGTCAGCACAAACCCAGATG
Ppy_DND1_	675	CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCCAGATG
Mmu_DND1_580548182	573	CCGAACAGACACAGCATCCTTGGCCACCTCATGCCCATCCTGGCCATCTAGGGTCAGCACAAACCCAGATG
Mmd_DND1_36923507	259	CTGTGCGGACACAGCATCCTTGGCCACCTCATGCCCATCCTGCCATCCTGCCAATCAGAGGCCAACACAACCCAAATG
Ef_DND1_36233886	566	CCGTGTAGACACAGCATCCTTGGCCACCTCATGCCCATCCTGCCATCTGGGGCCAGCACAAACCCAGATG
Bt_DND1_51121458	561	CCGTGCAGATACATGCATCCTTAGCCACCTCATGCCCATCCTGCCATCTGGGGTCAGCACAAACCCAGATG
Cf_DND1_38675152	308	CCTTGCAGACACAGCATCCTTAGCCACCTCATGCCCCTCCTGCCCTTCTGGAGCCAGCACAAACCCAGATG

Hs_DND1_140030567	647	AGGCCGCTGAAGGGCACCAGGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC
Ptr_DND1_142431156	647	AGGCCGCTGAAGGGCACCAGGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC
Hs_chr17_41692196	647	AGGCCGCTGAAGGGCACCAGGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC
Hs_chr17_h2R	643	AGGCCGCTGAAGGGCACCAGGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC
Hs_chr17_41019840	647	AGGCCGCTGAAGGGCACCAGGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC
Ptr_chr17_11917365	647	AGGCCGCTGAAGGGCACCAGGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC
Hs_chr17_h2F	647	AGGCCGCTGAAGGGCACCAGGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC
Ppy_chr17_43819715	641	AGGCCGCTGAAGGGCACCAGGATGCCAGGAATCACCACCTGTACCAGAAGCGGTGCCAGCCAGCAGGTC
Ppy_DND1_	745	AGGCCGCTGAAGGGCACATGGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC
Mmu_DND1_580548182	643	AGGCCACTGAAAGGCACCAGGATGCCAGGAATCACCACCTGATACCAGAAGCGGTGCCAGCCAGCAGGTC
Mmd_DND1_36923507	329	AGGCCACTGAAAGGCACATGGATGCCAGGATCACCACCTGGTACCAAAAGCCATGCCAGCCAGCAGGCC
Ef_DND1_36233886	636	AGGCCGCTAAGGGCACATGGATGCCAGGATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGGC
Bt_DND1_51121458	631	AGGCCACTGAAGGGCACCAGGATGCCCGGGGATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGGC
Cf_DND1_38675152	378	AGGCCGCTGAAGGGCACCAGGTGTCCCGGATCACCACCTGGTACCAGAAGCGGTGCCAGCCTGCAGGGC

Hs_DND1_140030567	717	CTATGCCCAAACACTTGG
Ptr_DND1_142431156	717	CTATGCCCAAACACTTGG
Hs_chr17_41692196	717	CTATGCCCAAACACTTGG
Hs_chr17_h2R	713	CTATGCCCAAACACTTGG
Hs_chr17_41019840	717	CTATGCCCAAACACTTGG
Ptr_chr17_11917365	717	CTATGCCCAAACACTTGG
Hs_chr17_h2F	717	CTATGCCCAAACACTTGG
Ppy_chr17_43819715	711	CTGTGCCCAAACACTTGG
Ppy_DND1_	815	CTATGCCCAAACACTTGG
Mmu_DND1_580548182	713	CTATGCCCAAACACTTAG
Mmd_DND1_36923507	399	CTGTTCCTAAACACTTGG
Ef_DND1_36233886	706	CTGTGCCCAAACACTTGG
Bt_DND1_51121458	701	TTGTGCCCAAACACTTGG
Cf_DND1_38675152	448	CTGTGCCCAAACACTTGG