

Figure S1

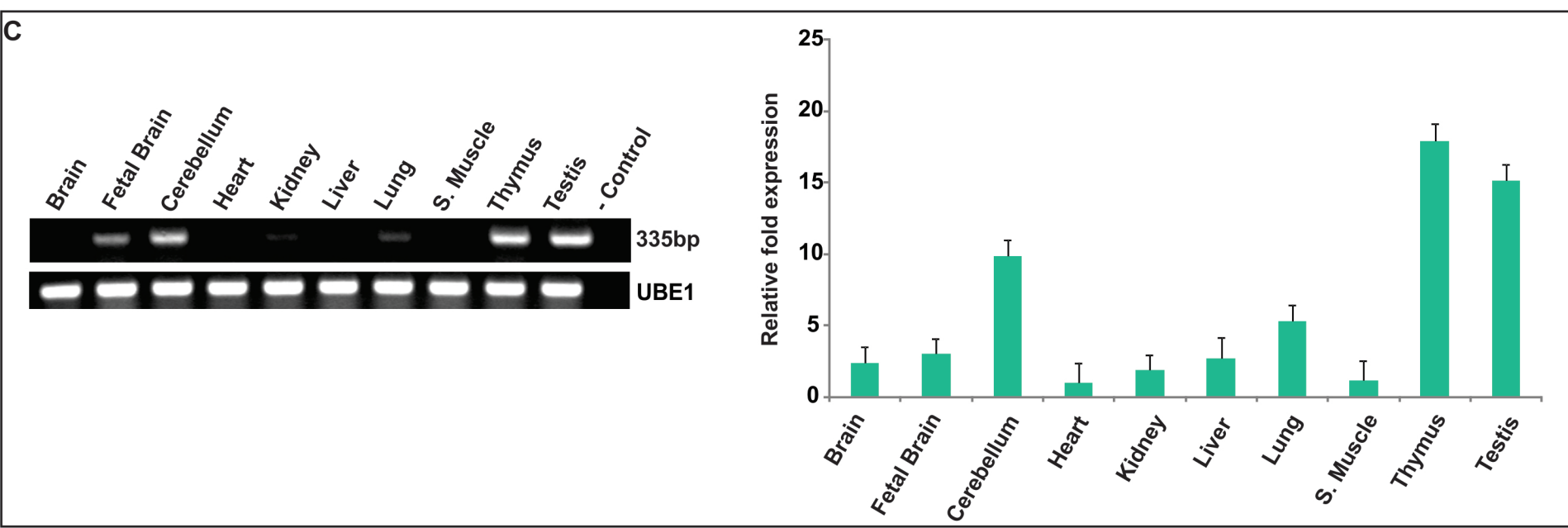
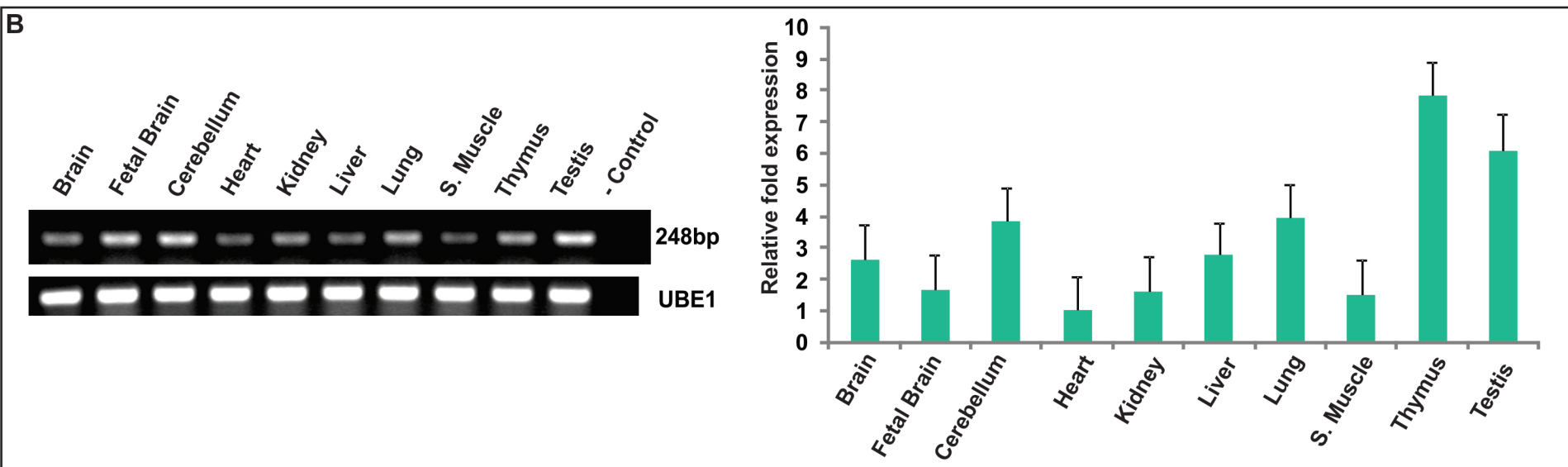
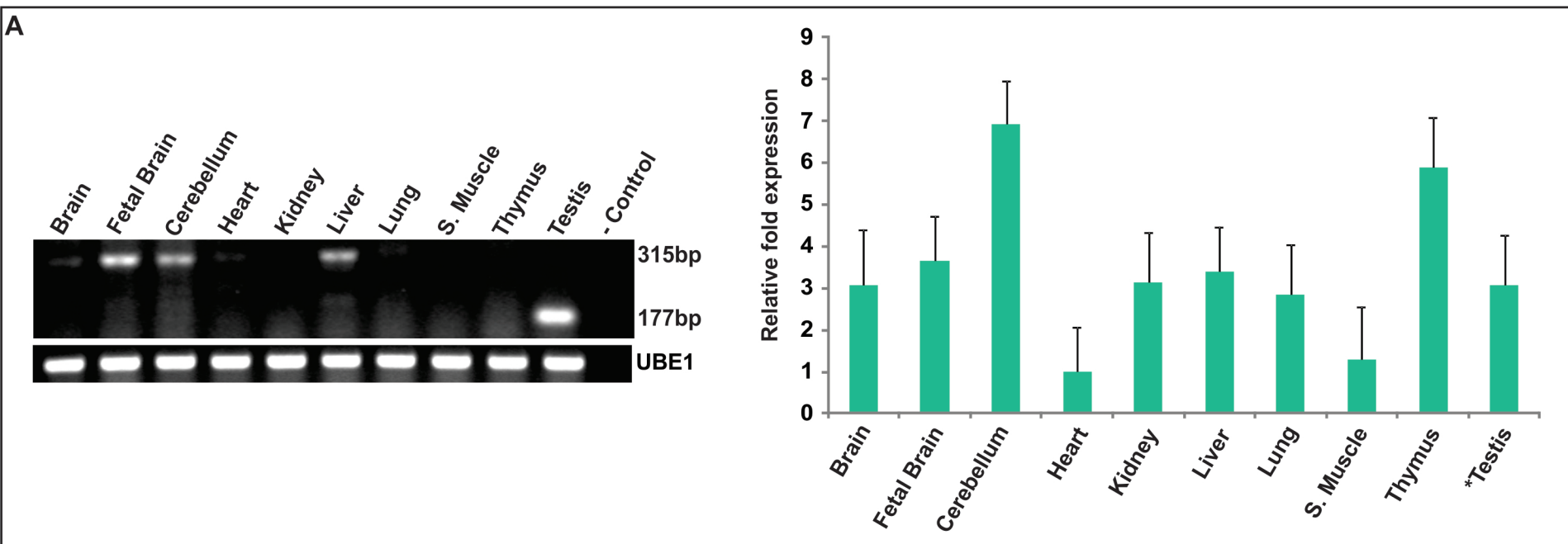


Figure S2

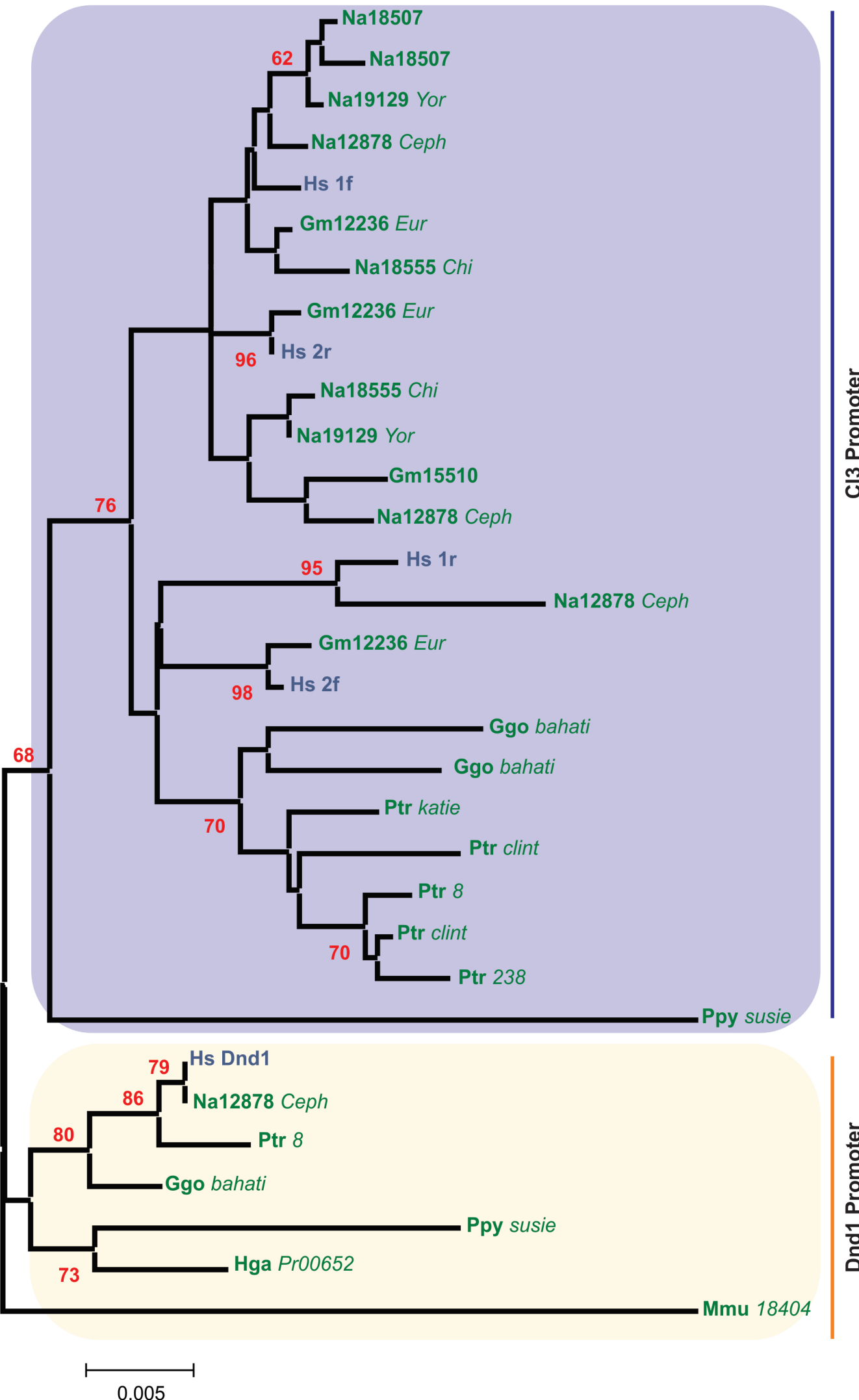
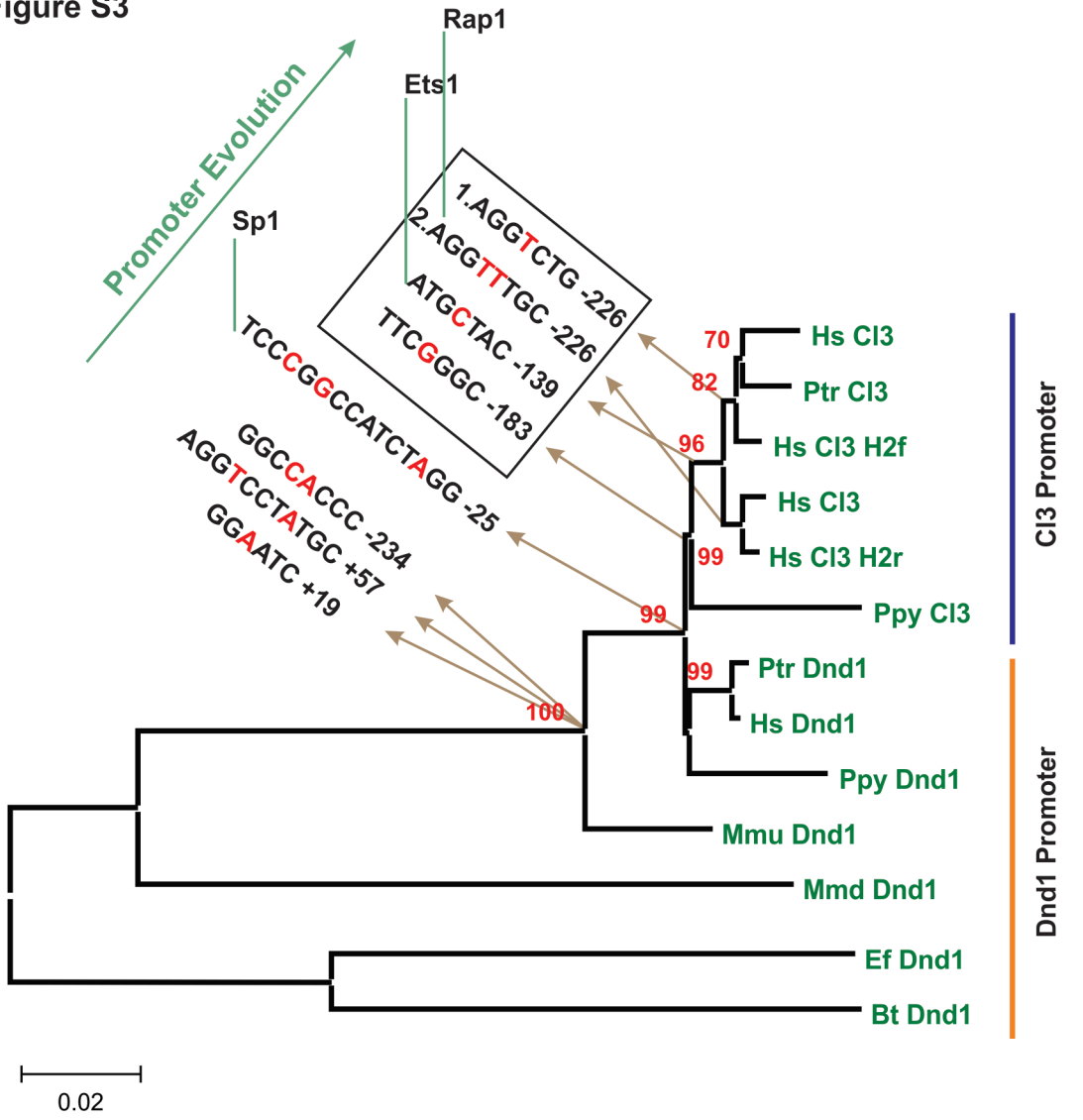


Figure S3





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Ppy\_chr17\_43819715 260 -----  
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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--GGACCCCTGGGCTG--GGAGCGGGAG--GGCAAGGCCCTCACCACA  
Ptr\_DND1\_142431156 265 -----GTT--GGACCCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA  
Hs\_chr17\_41692196 265 -----GTT--GGACCCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA  
Hs\_chr17\_h2R 261 -----GTT--GGACCCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA  
Hs\_chr17\_41019840 265 -----GTT--GGACCCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA  
Ptr\_chr17\_11917365 265 -----GTT--GGACCCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA  
Hs\_chr17\_h2F 265 -----GTT--GGACCCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA  
Ppy\_chr17\_43819715 260 -----GTT--G--ACCCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA  
Ppy\_DND1\_ 345 TAAGATCCACTTGGTCA GTTTGGAACCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA  
Mmu\_DND1\_580548182 264 -----TT--GGACCCCTGGGCTG--GGAGGGGGAG--GGCAAGGCCCTCACCACA  
Mmd\_DND1\_36923507 1 -----GACCCCTGGGCTC--ACTGGGGGAG--GGCAAGGTTCCCTCAC--  
Ef\_DND1\_36233886 254 -----TAGGCTGGGAGG--GGGCTGGGAG--GGCAAGGTTCCCTCACCACA  
Bt\_DND1\_51121458 258 -----GGGTCCATGAAACCCAGAAATGGGAGAAAGGAAGTCCCTCACCACA  
Cf\_DND1\_38675152 1 -----GACCCCTGGGCTG--GGAGGGGGAG--GGCAAGGTTCCCTCACCACA

Hs\_DND1\_140030567 310 ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAGGGAGGCTG-----A  
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Ptr\_chr17\_11917365 310 ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAGGGAGGCTG-----A  
Hs\_chr17\_h2F 310 ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTTCCTGTCCAGCAGGGAGGCTG-----A  
Ppy\_chr17\_43819715 304 ACTTAAGCCAAACCTAAGCTGCCCCAGGTGCCATAGGTCCCTGTCCAGCAAGGAGGCTG-----A  
Ppy\_DND1\_ 408 ACTTAAGCCAAACCTAAGCTGCTCCAGGTGCCACAGGTTCCTGTCCAGCAGGGAGGCTG-----A  
Mmu\_DND1\_580548182 308 ACTTAAGCCAAACCTAAGCTGCTCCAGGTGCCCTAGGTCCCTGTCCAGCAGGGAGGCTG-----A  
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Bt\_DND1\_51121458 306 ACTTTGGCCAAACCTGAGCTGCCCCAGGTGCTTCTGGGGCCCTGCCAGCTGGGAGGCTGTGTCAAGTC  
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Mmd\_DND1\_36923507 87 -----CTGTCAACCCAGCCCTG-----GGCTGCCAGGCCTGCTGGGCTGGG  
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Bt\_DND1\_51121458 376 TAGGGCAGGGCCATGCTCCCTCCCTTTCTT--GGAGTCAGATAGTGGCTGCCAGGCCTGCTGGGCTGGG  
Cf\_DND1\_38675152 109 TAGGGCAGGACCTGTGTCTT--CCCTCCTT--GAGATCAGATGGTGGCTGCCAGGCCTGCTGGGCTGGG

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Ptr\_DND1\_142431156 442 GC-CTGACACAGGCTCTGCATG--CCCATTTCAGGCTGCCTGTGGAGAGAAGAATGGAGTCACTGTTTAACCA  
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Hs\_chr17\_h2R 438 GC-CTGACACAGGCTCTGCATG--CCCATTTCGGCTGCCTGTGGAGAGAGAATGGAGTCACTGTTTAACCA  
Hs\_chr17\_41019840 442 GC-CTGACACAGGCTCTGCATG--CCCATTTCGGCTGCCTGTGGAGAGAGAATGGAGTCACTGTTTAACCA  
Ptr\_chr17\_11917365 442 GC-CTGACACAGGCTCTGCATG--CCGATTTCGCTGCCTGTGGAGAGAGAATGGAGTCACTGTTTAACCG  
Hs\_chr17\_h2F 442 GC-CTGACACAGGCTCTGCATG--CCCATTTCGGCTGCCTGTGGAGAGAGAATGGAGTCACTGTTTAACCA  
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Ppy\_DND1\_ 540 GC-CTGCACAGGCTCTGCATG--CCCATTTCAGGCTGCCTGTGGAGAGAGAATGGAGTCACTGTTTAACCA  
Mmu\_DND1\_580548182 438 GC-CTGACACAGGCTCTGCCTG--CCCATTTCAGGCTGCCTGTGGAGAGAGAATGGAGTCACTGTTTAACCA  
Mmd\_DND1\_36923507 128 GGGTTGGCACAGGCTCTGCTTA--CCCATTTCAGGCTGCCTGTAAAAGAA--GGGGTCACTGCTTAACCA  
Ef\_DND1\_36233886 433 GA-CTGACACAGGCTCTGCTTA--CTCATTTCAGGCTGCCGCTGAGAGGA--TGGGGTCACTGCTTAACCA  
Bt\_DND1\_51121458 444 TG-CAGACAAGGCTC-----CCTGTGGAGAGGA--TAAGGTCACTGTTCAACCA  
Cf\_DND1\_38675152 175 GA-CTGACACAGGCTCTGCCA--TGTCTTCAGGCTGCCTGTGAAGAAGA--CAGGGTCACTGCTTAACCA

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Ptr\_DND1\_142431156 510 TGGTACCT---GCCTCAGCCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG  
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Bt\_DND1\_51121458 491 TGGTACCTCCTCGCTCAGCCCCAGTAGACCAAGGAGGCTGGCCCTAGACTCACTCATTTGCTTCCAGCAG  
Cf\_DND1\_38675152 241 CCATACCT---GCCTCAGCCCCAGCAGACCACAGGAGGTTGGCCCCAGACTCACTGAGTGCCTGCAGCAG

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Hs\_chr17\_41019840 577 CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCAGATG  
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Hs\_chr17\_h2F 577 CCGTACAGACACAGCATCCTTGGCCACCTCATGCCCATCCCGGCCATCTAGGGTCAGCACAAACCAGATG  
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Mmd\_DND1\_36923507 259 CTGTGCGGACACAGCATCCTTGGCCACCTCATGCCCATCCTGCCAATCAGAGGCCAACACAACCCAAATG  
Ef\_DND1\_36233886 566 CCGTGTAGACACAGCATCCTTGGCCACCTCATGCCCATCCTGCCATCTGGGCCAGCACAAACCAGATG  
Bt\_DND1\_51121458 561 CCGTGCAGATACATGCATCCTTAGCCACCTCATGCCCATCCTGCCATCTGGGTCAGCACAAACCAGATG  
Cf\_DND1\_38675152 308 CCTTGCAGACACAGCATCCTTAGCCACTTCATGCCCCTTCCTGCCCTTCTGAGCCAGCACAAACCAGATG

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Hs\_chr17\_41692196 647 AGGCCGCTGAAGGGCACC GGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC  
Hs\_chr17\_h2R 643 AGGCCGCTGAAGGGCACC GGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC  
Hs\_chr17\_41019840 647 AGGCCGCTGAAGGGCACC GGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC  
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Ppy\_chr17\_43819715 641 AGGCCGCTGAAGGGCACC GGATGCCAGGAATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGTC  
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Mmu\_DND1\_580548182 643 AGGCCACTGAAAGGCACC GGATGCCAGGAATCACCACCTGATACCAGAAGCGGTGCCAGCCAGCAGGTC  
Mmd\_DND1\_36923507 329 AGGCCACTGAAAGGCACC TGGATGCCAGGATCACCACCTGGTACCAGAAAGCCTGCCAGCCAGCAGGCC  
Ef\_DND1\_36233886 636 AGGCCGCTGAAGGGCAC TGGATGCCAGGATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGGC  
Bt\_DND1\_51121458 631 AGGCCACTGAAAGGGCACC GGATGCCCGGGATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGGC  
Cf\_DND1\_38675152 378 AGGCCGCTGAAGGGCACC GGTGTCGGGATCACCACCTGGTACCAGAAGCGGTGCCAGCCAGCAGGGC

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  
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Figure S5

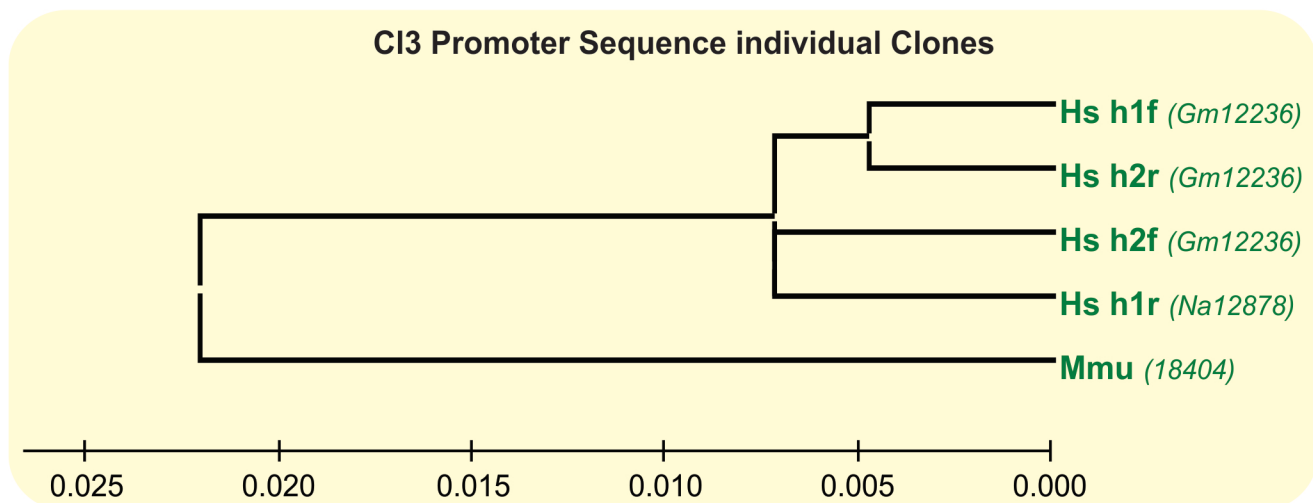
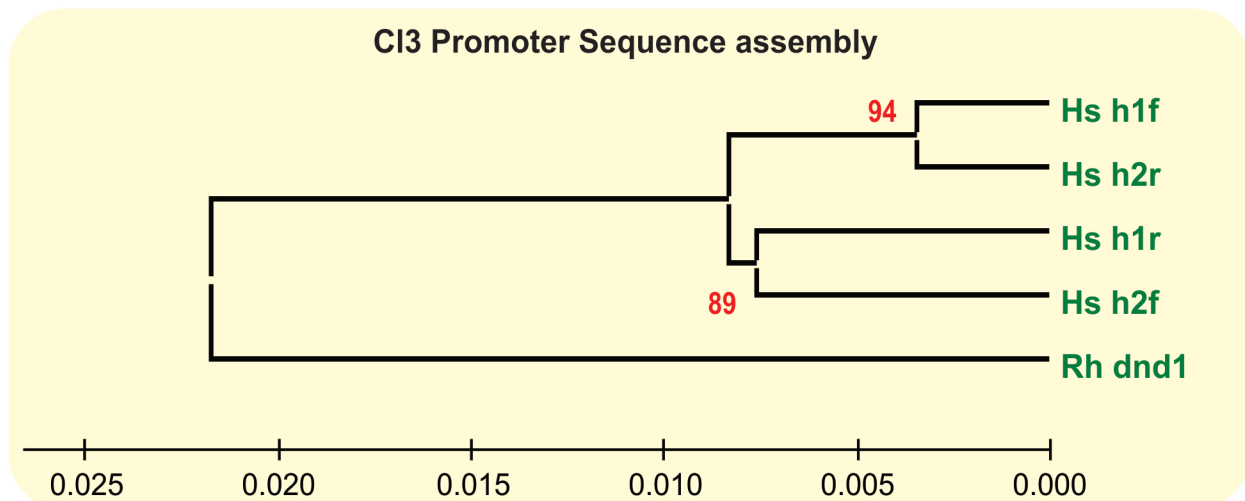
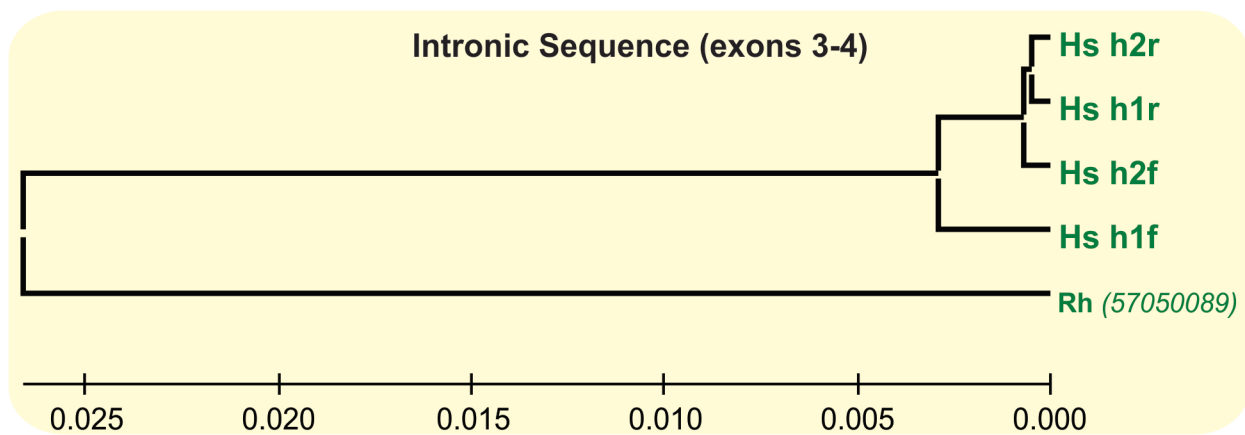
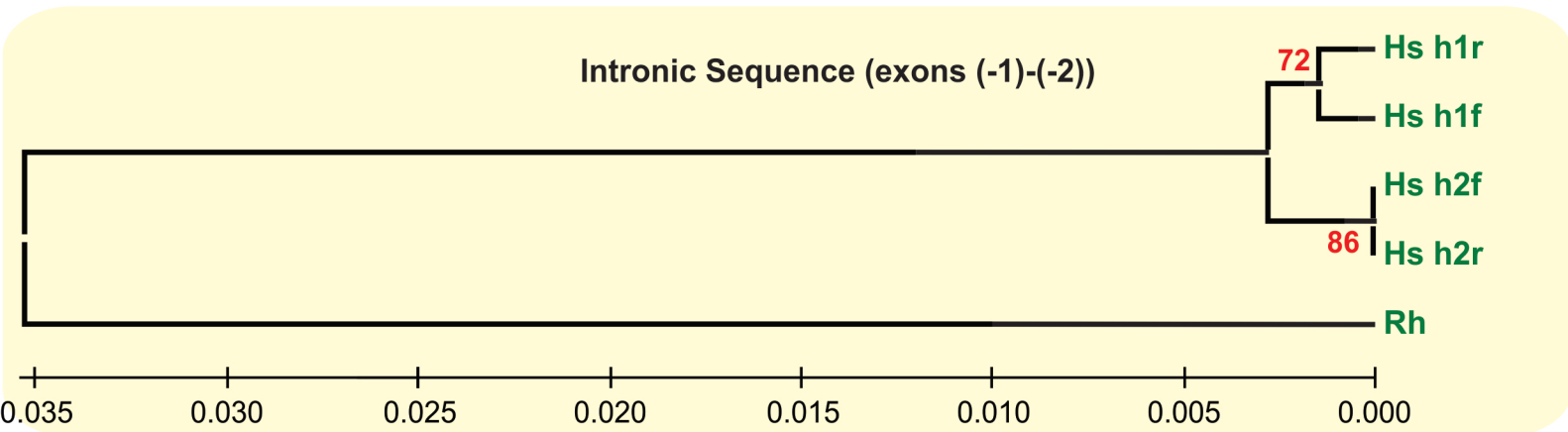


Figure S6

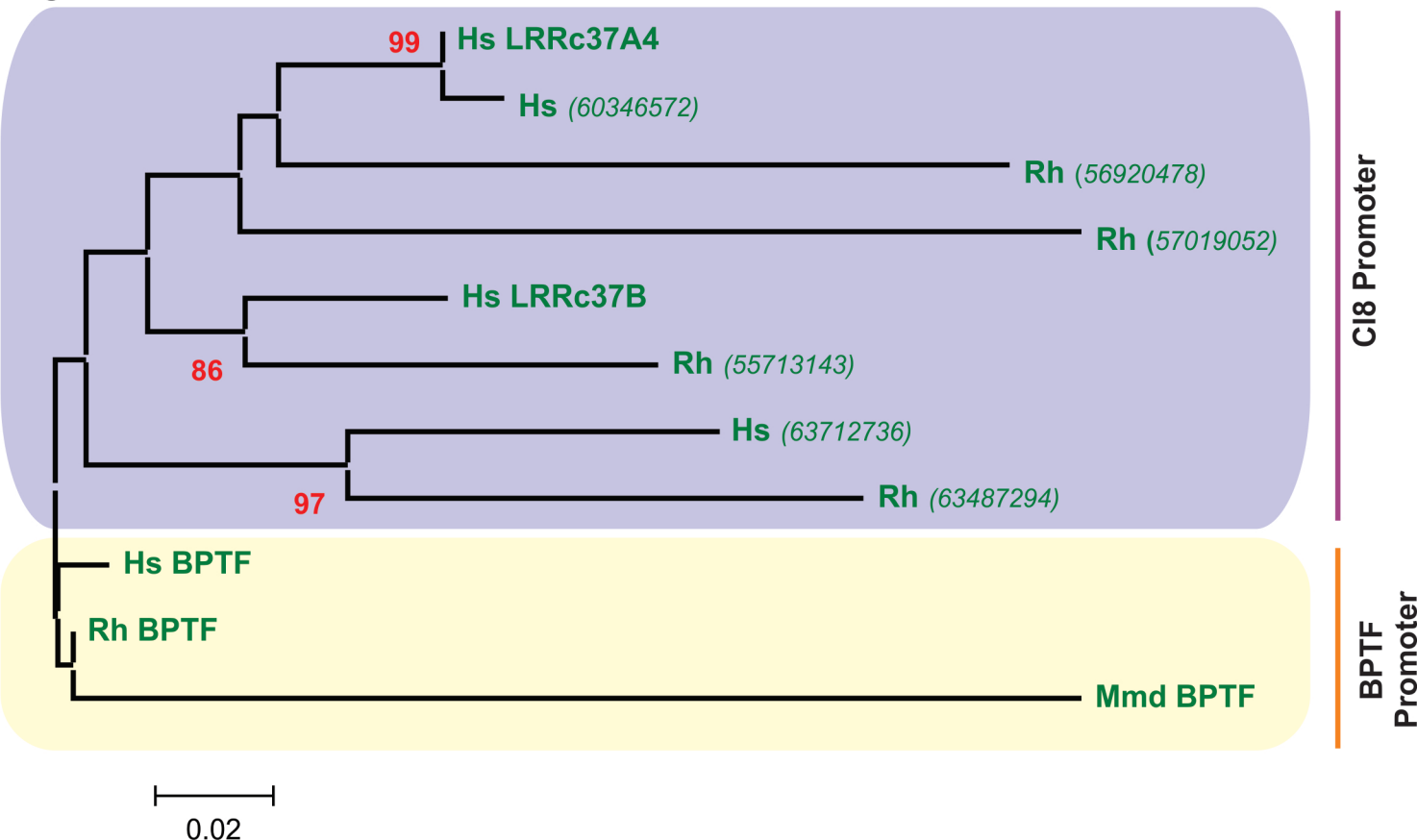
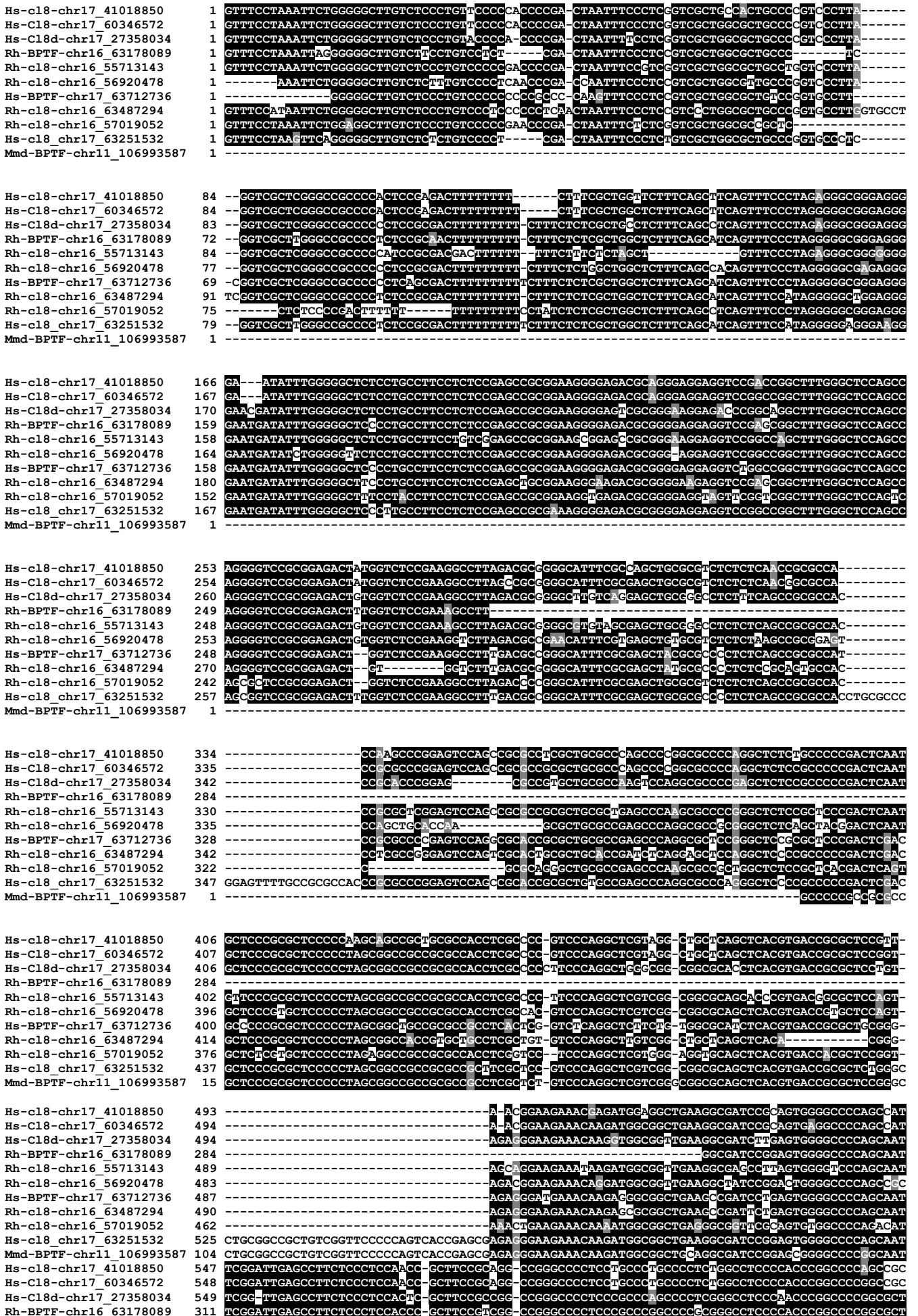


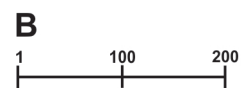
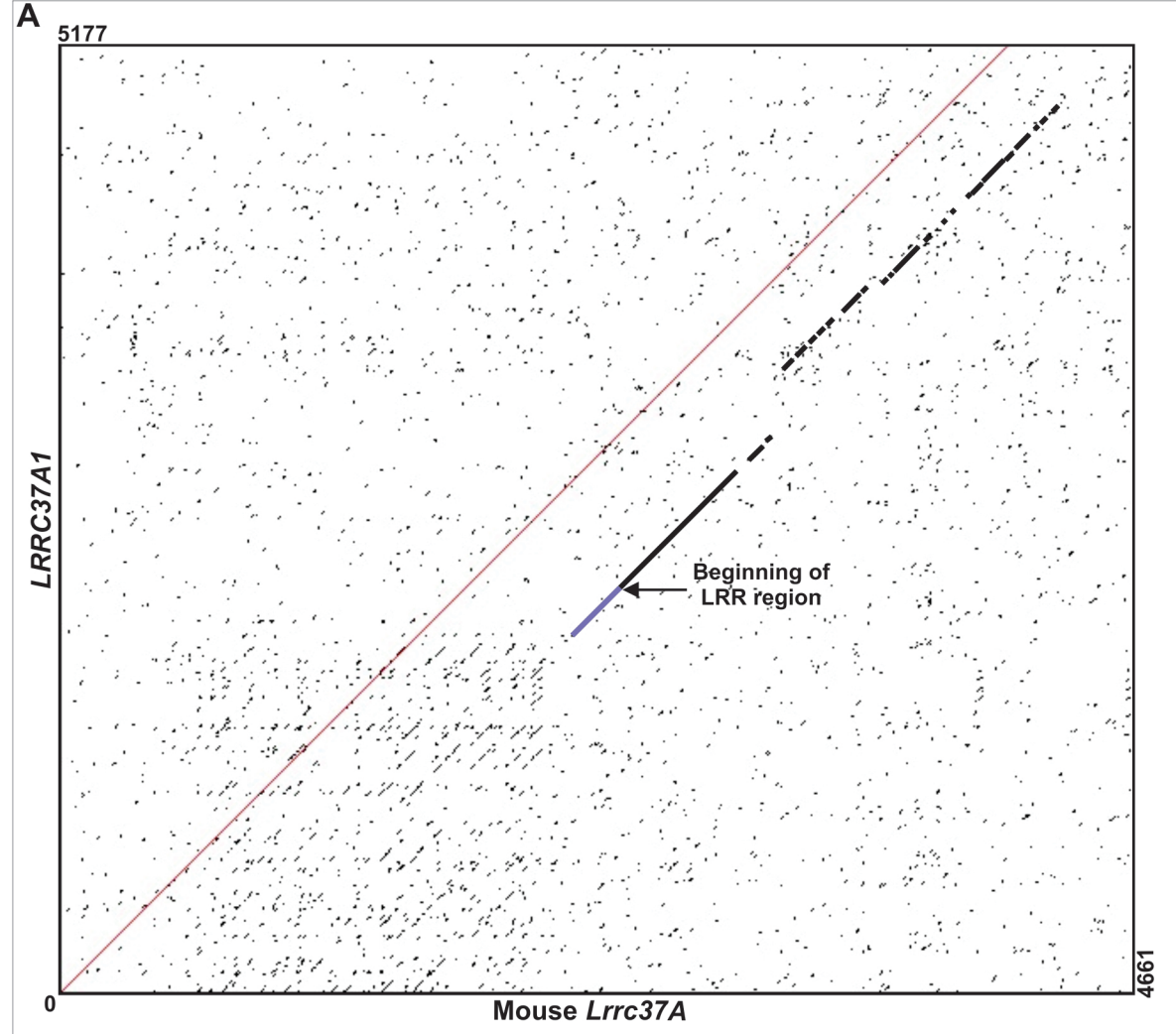


Figure S7. Alignment of BPTF and C18 promoter region



Rh-c18-chr16_55713143	544	TCGGTTGAGCCTCTCCCTCCACC	GCTTCGCGCGG	CCGGGCGCTCTCGCCCGGCCCA	GGGCCTCCCACCCGGCCCCGGCGCT
Rh-c18-chr16_56920478	538	TCGGATTGAGCCTCTCCCTCCAACC	AC-----CGG	TCCGGACCCTAGTCCCGGCCCTTGGGCTC	CCCAATCCGGCCCCGGCGCT
Hs-BPTF-chr17_63712736	542	TCGGATTGAGCCTTTCCCTCCACC	GCTTCTGCGCA	CCGGGGCCTCCCGCGCGCCCTCC	AGGCCTCCCACCCG-----
Rh-c18-chr16_63487294	545	TCGGATTGAGCCTTTCCCTCCACC	GCTTCTGCGCGG	CCGGGGCGCTCCTCGCGGCCCGCG	GGGCCTCCCACCCGGCCCCGGCGCT
Rh-c18-chr16_57019052	517	TCGGATTGAGCCTTCCCTCTAAC	GCTTCTGCGAG	CCGGGGCGCTCCCGCCCTCCCGCT	CCCGCGCTCCCA-----
Hs-c18-chr17_63251532	615	TCGGATTGAGCCTTTCCCTCCACC	GCTTCTGCGG	CCGGGGCCTCCCGCCCGGCCCA	GGGCCTCCCACCCGGCCCCGGCGCT
Mmd-BPTF-chr11_106993587	194	TCGGATTGAGCCTTTCCCTCCACC	CGCGTTCGCGGG	CCCGGCCCTCCCGCCCGCA	CCCGCGCTCCCTCCCGCTCGCGCGG
Hs-c18-chr17_41018850	635	CCCCA-----CTGGCCCA	TGGGCCCGCCCTTCCCTTCT	CCCTCGGCCTCGG	CTCCACATGAGGGGCGGGCGG
Hs-C18-chr17_60346572	636	CCCCA-----CTGGCCCA	TGGGCCCGCCCTTCCCTTCT	CCCTCGGCCTCGG	CTCCACATGAGGGGCGGGCGG
Hs-C18d-chr17_27358034	636	CCCCA-----CGCGCCCA	CTGGGCCCGCCCTTCCCTTCT	CCCGCCCGCTCGG	CTCCACATGAGGGGCGGGCGG
Rh-BPTF-chr16_63178089	399	CCCCA-----CGCGCCCA	CTGGGCCCGCCCTTCCCTTCT	CCCGCCCGCTCGG	CTCCACATGAGGGGCGGGCGG
Rh-c18-chr16_55713143	631	CCCCA-----CGCGCCCA	CTGGGCCCGCCCTTCCCTTCT	CCCGCCCGCTCGG	CTCCACATGAGGGGCGGGCGG
Rh-c18-chr16_56920478	620	CCCCA-----CGCGCCCA	CTGGGCCCGCCCTTCCCTTCT	CCCGCCCGCTCGG	CTCCACATGAGGGGCGGGCGG
Hs-BPTF-chr17_63712736	619	-----CGCGCCCA	CTGGGCCCGCCCTTCCCTTCT	CCCGCCCGCTCGG	CTCCACATGAGGGGCGGGCGG
Rh-c18-chr16_63487294	633	CCCCA	CCGGCCCGCCCTTCCCTTCT	CCCGCCCGCTCGG	CTCCACATGAGGGGCGGGCGG
Rh-c18-chr16_57019052	595	-----CTTCCCGCA	CTGGGCCCGCCCTTCCCTTCT	CCCGCCCGCTCGG	CTCCACATGAGGGGCGGGCGG
Hs-c18-chr17_63251532	703	CCCCA-----CGCGCCCA	CTGGGCCCGCCCTTCCCTTCT	CCCGCCCGCTCGG	CTCCACATGAGGGGCGGGCGG
Mmd-BPTF-chr11_106993587	284	GGGCG-----CCCGCGCG	CTTCCCGCA	CCCGCCCGCTCGG	CTCCACATGAGGGGCGGGCGG
Hs-c18-chr17_41018850	718	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGT	-----
Hs-C18-chr17_60346572	719	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGC	-----
Hs-C18d-chr17_27358034	719	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGC	-----
Rh-BPTF-chr16_63178089	481	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGC	-----
Rh-c18-chr16_55713143	715	GGCAGGCCGACCAAGCAT	CCCGCGGGTCCCT-----	GCTCGCGCCCGGCC	-----GCCGCGCGC
Rh-c18-chr16_56920478	703	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGC	-----
Hs-BPTF-chr17_63712736	685	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGC	-----
Rh-c18-chr16_63487294	716	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGC	-----
Rh-c18-chr16_57019052	672	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGC	-----
Hs-c18-chr17_63251532	785	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGC	-----
Mmd-BPTF-chr11_106993587	367	GGCAGGCCGACCAAGCAGCCCGGGCT	CCCTCTCGCGGAGCGCTGCGCCCGGCC	-----GCCGCGCGC	-----
Hs-c18-chr17_41018850	783	-----GCCGCGCG	CCAGCTCCGGACCCATCGGGG	TTCCGCTCGCGGCA	CCCGGTAGC
Hs-C18-chr17_60346572	784	-----GCCGCGCG	CCAGCTCCGGACCCATCGGGG	TTCCGCTCGCGGCA	CCCGGTAGC
Hs-C18d-chr17_27358034	784	-----GCCGCGCG	CCAGCTCCGGACCCATCGGGG	TTCCGCTCGCGGCA	CCCGGTAGC
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Hs-BPTF-chr17_63712736	763	-----CCGCCG	CCAGCTCCGGACCCATCGGGG	TTCCGCTCGCGGCA	CCCGGTAGC
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Rh-c18-chr16_57019052	850	-----GCCGCGCG	CCAGCTCCGGACCCATCGGGG	TTCCGCTCGCGGCA	CCCGGTAGC
Hs-c18-chr17_63251532	457	CCACCGCCGCG	CCAGCTCCGGACCCATCGGGG	TTCCGCTCGCGGCA	CCCGGTAGC
Hs-c18-chr17_41018850	854	CGCCGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Hs-C18-chr17_60346572	855	CGCCGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Hs-C18d-chr17_27358034	852	AGCCGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Rh-BPTF-chr16_63178089	622	CGCCGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Rh-c18-chr16_55713143	837	AGCCGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Rh-c18-chr16_56920478	836	CGCCGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Hs-BPTF-chr17_63712736	847	CGCCGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Rh-c18-chr16_63487294	809	TCGGGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Rh-c18-chr17_63251532	925	CGCCGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Mmd-BPTF-chr11_106993587	543	CGCCGCC	AGGCTGAGGTGGCGCCCAAGACCGC	CTGAGCTCGCCAGG	ATGGGCAGCAGTAGCCGGACA
Hs-c18-chr17_41018850	938	-GCCCCAC	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----
Hs-C18-chr17_60346572	942	AGCCCCAC	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----
Hs-C18d-chr17_27358034	939	CGCCCCAC	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----
Rh-BPTF-chr16_63178089	708	CGCCCCAC	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----
Rh-c18-chr16_55713143	924	C-----CCG	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----
Rh-c18-chr16_56920478	921	-----CCG	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----
Hs-BPTF-chr17_63712736	934	-----CCG	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----
Rh-c18-chr16_63487294	891	-----CAG	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----
Rh-c18-chr16_57019052	1014	CGCCCCAC	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----
Hs-c18-chr17_63251532	632	CCTCG	CCAGCACCCAGCCCGCCCGG	CGGGGGAGGGGGGGG	-----

Figure S8



Human LRRC37A Protein Structure

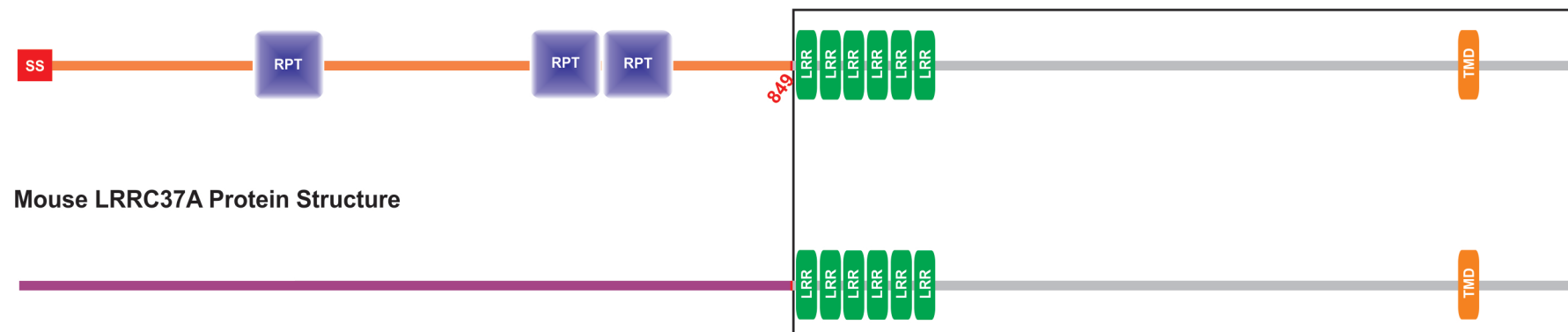


Figure S9

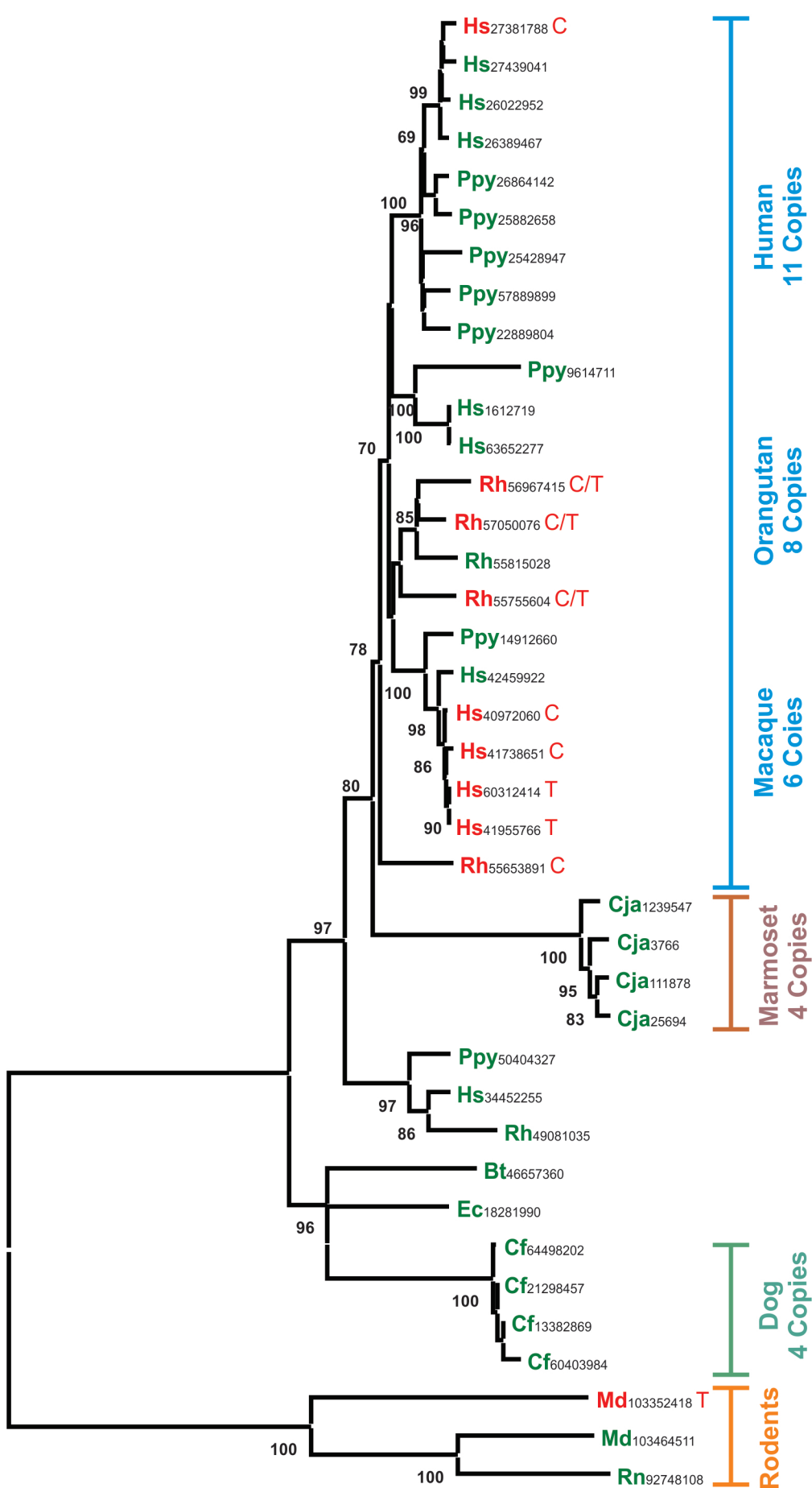


Figure S10

