Supporting Information

Gongora *et al.* 10.1073/pnas.0801991105

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        11222222222233334
        69111223445611354
        79027257366105057

Ref     TTCATACATTTCCTCTC

140-CH  ...GC..GCCCTTC..T
9-CH    ...GC....CCTTC..T
5-CH    .C.GC...CCCTTC..T
8-CH    ...GC...CCCTTC..T
11-CH   .................
141-CH  ...............C.
17-CH   C.TG..T..C...C...
128-CH  ...GCG..CCCTTCT.T
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Fig. S1. Haplotypes identified among Chilean chickens. Numbers indicate the site position of the variable sites. Dots indicate identity with the reference sequence (GenBank accession no. AB098668) (1), and different base letters denote substitution.

1. Komiyama T, Ikeo K, Gojobori T (2003) Where is the origin of the Japanese gamecocks? *Gene* 317:195–202.

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HapID                                        Nucleotide Position                                         Frequency
        0000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000
        0000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000000
        0000111111112222222222222222222222222222222222222222222222233333333333333333333333333333444444444444444444445555555555555
        2457135567770001111222222222233333333444444445555556667888999999000001111112233444555566677790022222333344455666811111222222333
        2460245682580192469012345679012567890124568901268137123434567924569123468051446816895672579471368912351568926711378903467823 4

     1 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG120
     2 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
     3 CGATTATCTTACTACAATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCACCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  2
     4 CGATCATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTGCAAATCCTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
     5 CGATTATCTTACCACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTGCTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  2
     6 CGATTATTTTACCACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG 24
     7 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTTTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 21
     8 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTACAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  5
     9 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG115
    10 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGTTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG 11
    11 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCTAAGCTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  5
    12 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG121
    13 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  5
    14 CGATTATCTTACTACAATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 11
    15 CGATTATCTTACTACAATACTCATTTCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
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    17 CGATTATCTTACTGCGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  4
    18 CGATTATCTTACTATGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 10
    19 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 34
    20 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  2
    21 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTCATCCTACAAATCCTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  2
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    23 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCATCCTGCAAATCCTTCATCTTCCCATTCTAAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  7
    24 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTTAAACCCATCCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG 30
    25 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG 31
    26 CGATCATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 16
    27 CGATTATTTTACTACGATATTCATTCCCCTCTACAGACGCTTAAACCCATCCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
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    29 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACCGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  9
    30 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTATCCTACAAATCTTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
    31 CGATTATTTTACTGCAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  4
    32 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCTTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 25
    33 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
    34 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
    35 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATCCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG 18
    36 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCCACTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  6
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    50 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
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    65 CGATTATTTTACCACGATACTCATTCCCCTCTACAGACGCTTAAACCCATCCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    66 CGATTATTTTATCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTGAACTTACTTTATTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
    67 CGATTATTTTATCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTAAACTTACTTTATTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    68 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTCACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  7
    69 CGATTATTTTACTACAATACTTATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    70 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCTTATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    71 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCTAAACTTACCTTACTGTGCACTCACAG-TCAT-TCCCTACGCCTTCCCG  1
    72 CGATTATCTTACTACGATACTTATTTCCCTCCATAGACGCTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
    73 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCTAAACTTATCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
    74 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCTAAGCTTATCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    75 CGATTATCCTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
    76 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATCCTACAAATCCTTCATCTTCCTCTTCTGAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
    77 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACCGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
    78 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCGTCCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTGCTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
    79 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATTCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  7
    80 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCACCCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    81 CGATTATTTTACTACGATACTCATTCCTCTCTACAGACGCTCAAACCCATTCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    82 CGATTATTTAACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    83 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTGAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  6
    84 CGATTATCTTACTGCGATACTCATTTCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
    85 CGATTATTTTACCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCACCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  2
    86 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTTAAACCCATCCTACAAATCCTTCACCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    87 CGATTATTTTACTACAATACTCACTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCTTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 16
    88 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATCCTGCAAATCCTTCATCTTCCTCTTCTGAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    89 CGATTATTTTTCTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATTCTGCAAATCCTTCACCTTCCCATTCTGAACTTACTTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 12
    90 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATCCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACCGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    91 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTCCCCATTCTAAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  6
    92 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  4
    93 CGATTATCTTACCACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTGCTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  7
    94 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTGAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
    95 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCTAAACTTACCTTACTATGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
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Fig. S2a. Haplotypes and frequencies used for networks analyses from the 534-bp alignment including indels. Because of the differences in the number of polymorphic sites, it was not possible to keep the same haplogroup numbers for both the complete and truncated alignment analyses.

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 96 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTGAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
 97 CGATTATCTTACTACGATACTCATTTCCCTCCATAGGCGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
 98 CGATTATTTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
 99 CGATTATCTTACTACGATACTCATTCCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
100 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCACCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  4
101 CGATTATTTTCCTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
102 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCACCCTACAAATCCTTCATCTTCCCATTTTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
103 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTAAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
104 CGATTATTTTACCACAATACTCATTCCCCTCCGTAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
105 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCACCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTGT-TCCCTACGCCTTCCCG  1
106 CGATTATTTTACTACGATACCCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTTACCTTCCCATTCTAAACTTACCTTAATGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
107 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTTTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  3
108 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTGAACTTACCTTACTGTGCACTCACAG-CTAG-TCCCTACGCCTTCCCG  1
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111 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
112 CGATTATCTTACCACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCGTGCTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
113 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
114 CGATTATCTTACTGCGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTATCGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
115 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTATACTTACCCTACAAATCCTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
116 CGATTATTTTCTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATTCTGCAAATCCTTCACCTTCCCATTCTGAACTTACTTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
117 CGATTATTTTACTACGATACCCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  6
118 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTTCCG  1
126 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  5
127 CGATTATTTTACTACGATACTCATCCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTGAACTTACCTTACTGTGCACTCACAG-CTGT-TCCCTACGCCTTCCCG  1
128 CGATTATTTTACTACAATACTCATTCCCTTCCATAGATGCTCAAACTCAACCTACAAATCCTTCACCTTCCCATTCTAAATCCACCTTATTGTGTACTCACAG-TCAT-TCCCTACGCCTTCCCG  1
129 CGATTATTTTACTACAATACTCATTCCCTTCCATAGACGCCCAAACTCAACCTACAAATCCTTCACCTTCCCATTCTAAATCTACTTTATTGTGTACTCACAG-TCAT-TCCCTACGCCTTCCCG  1
130 CGATTATTCTTCCACATTTCT-AGTCTATTCCATAAGCGCTTAA-CTCAACCTACAACTCTTTCACCCTCCCATTCTAAACTTACCTCATTGTGTACTCACAGCTCAT-TCCCTACGCCTTCCCG  1
131 CGATTATTCTTCCACATTTCT-AGTCTATTCCATAAGCGCTTAA-CTCAACCTACAACTCCTTCATCTTCCCATTCTAAACTTATCTTATTGTGTACTCACAG-TCAT-TCCCTACGCCTTCCCG  1
132 CGATTATTCTTCCACATTTCT-AGTCTATTCCATAAGCGCTTAA-CTCAACCCACAACTCTTTCATCTTCCCATTCTGAACTTATCTTATTGTGTACTCACAG-TCAT-TCCCTACGCCTTCCCG  1
133 CGATTATTTTACTACAATACTCATTCCTCTCCATGGACGCTTAAACTCACCCTGCAAATTCTTCATCTTCCCATTCTAAACTCACTTTATTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
134 CGATTATTTTACTACAATACTCATTCCCCTTCATAGACGCTCAAACTCATCCTGCAAATCCCTCATCTTCCCATTCTAAACTCACTTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
135 CGATTATTTTACCACGATACTCATTCCCCTCCATAGACGCTCAAATTCATCCTACAAATCCTTCATCTTCCTCTTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
136 CGATTGTTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATCCTAAACTTACCTTATTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
137 CGATTATTCTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTGAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
138 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATTCTACAAATCCTTCATCTTCCTCTTCTGAATTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
139 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAGTCTTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
140 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCTTTCATCTCCCTATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
141 CGATTATTTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATCCTACAAATCCTTCATCTTCCTCTTCTAAGCTTACCTTACCGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
142 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTTAAGCTCATCCTACAAATCCTTCATCTTCCCATTCTAGACTCACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  2
143 CGATTATTTTTCTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATTCTGCAAATCCTTCACCTTCCCATTCTAAACTTACTTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
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145 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCACCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  5
146 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAACCCTTCACCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
147 CGATTATTTTACTACGACACTCATCCCCCTCCATAGACGCTTAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
148 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTGAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
149 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTAATGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
150 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTGCTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
153 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTAAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 12
154 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTAAACTTACTCTACTGTTCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
155 CGTTTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
156 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTAAACTTACTCTACTGTGCCCTCACAG-CTAT-TCCCTACGCCTTCCCG  1
157 CGATTATTTTACTACGATACTCATTCCCCCCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG 13
158 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTCACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  8
159 CAATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCATCTCCAG-CTAT-TCCCTACCAGGCCTTC  1
160 CGAGTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
162 CGATTATCTTACTACGATACCCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  2
163 CGATTATTTTATCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCACCTTCCCATTCTAAGCTTACTTTATTGTGCACTCACTAGTTAT-TCCTACCGCCTTCCCG  1
164 CGATTATTTTATCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCACCTTCCCATTCTAAGCTTACTTTATTGTGCACTCACAG-TTAT-CCCCTACGCCTTCCCG  1
165 CGATTATTTTATCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCACCTTCCCATTCTAAGCTTACTTTATTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  9
166 CGATTATTTTACTACGATACTCATTCCCCCCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
167 CGATTATTTTATCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCACCTTCCCATTCTAAGCTTACTTTATTGTGCACTCACAG-TTAT-TTCCTACGCCTTCCCG  1
168 CGATTATTTTACTACGATACTCATTCCCCCCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTATGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
169 CGATTATTTTACTACGATACTCATTCCCCCCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCGGAACTTACTCTACTATGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
170 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTATTTCCCTACGCCTTCCCG  1
171 CGATTATTTTACTACGATACTCATTCCCCCCCATAGACACTCAAACTCACCCTGCAAATTCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
172 CGATTATTTTACTACGATACTCATTCCCCCCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAAGCTAT-TCCCTACGCCTTCCCG  1
173 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCAGAG-CTATATCCCTACGCCTTCCCG  1
174 CGATTATTTTACTACGATACTCATTCCCCCCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-GCCCTACGCCTTCCCG  1
175 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTATGCCTTCCCG  1
176 CGATTATTTTACTACGATACTCATTCCCCCCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-CCCCTACGCCTTCCCG  1
177 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTCACCTTACTGTGCACTCACAG-CTAT-TCGCTACGCCTTCCCG  1
178 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAAGCTAT-TCCCTACGCCTTCCCG  1
179 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
180 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
181 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTTAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  3
182 TGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTTAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
183 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCCCTCACAG-CTAT-TCCCTACGCCTTCCCG  1
184 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTCACCTTACTGTGCACTCACAG-CTAT-TCCCAACGCCTTCCCG  1
185 CGATTATTTTACCACGACACTCATTCCCCTCCATAGACGCTCAAACTTATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  3
186 CGATTATTCTACTACGATACTCATTCCCCTCCATAGACGCTCTAACTCATCCTGCAAATCCTTCACCTCCCCATTCTGAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  2
188 CGATTATTTTACTACGACACTCGTTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTTTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  7
189 CGATTATTTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTATTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  1
190 CGATTATCTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCTTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
191 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTGAACTTATTTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  2
193 CGATTATTTTACTACAATACTCATTCCCTTCCATAGATGCTCAAACTCAACCTACAAATCCTTCACCTTCCCATTCTAAATCTACCTTATTGTGTACTCACAG-TCAT-TCCCTACGCCTTCCCG  1
194 CGATTATTTTACTACAATACTCATTCCTCTCCATGGACGCTTAAACTCACCCTGCAAATCCTTCATCTTCCCATTCTAAACTCACTTTATTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
196 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCTGAACTTATTTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCN  1
202 CGATTAATTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATTCTACAAATCCTTCATCTTCCTCTTCTGAATTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCN  1
204 CGATTATCTTACTACGATACTCATTTCCCTCCATAGGCGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
205 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCTTTCACCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
206 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCTTTCACCTTCCCATTCTAAACTTACCTTATTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
207 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCCTCCCATTCTGAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
208 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCCTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
209 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATTTTCCCATTCTAAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
210 CGATTATTTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTTCCATTCTGAACTTACTCTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
211 CGATTATTTTACTACAATACTCATTCCTCTCCATGGACGCTTAAGCTCACCCTGCAAATCCTTCATCTTCCCATTCTAAACTCACTTTATTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1
212 CGATTATTTTACTACGACACTCATTCCCCTCCATGGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCTAAACTTACCTTACTGTGCACTCACAG-TTAT-TCCCTACGCCTTCCCG  4
213 CGATTATTTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCTAAACTCACCTTACTGTGCACTCACAG-CTAT-TCCCTACGCCTTCCCG  1

1010101010101000021002101010100010101010101010101000101010101010101010101010100210001010021010021000101010001010101010100210101010101010001010021002101010001010101002100202101010001010101010
1010101010101010100000101010001010101010101010101010101010
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Fig. S2b. Continued.

HapID	Nucleotide Position	Frequency
	00000000000000000000000000000000000000000000000000000000000000000000000000000000000	
	00000000000000000000000000000000000000000000000000000000000000000000000000000000000	
	00000000000000000000000000000000000000000000111111111111111111111111111111111111122	
	00013344445555555566666667777777788888899900111222233333444444555667778889999900	
	148134257923456789023458901234578912345914604567678902578924567913847179149128905	
1	CTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	157
2	CTTACTACAATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCACCTCCCCATTCGTAAACTTACCT	2
3	CTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTGCAAATCCTTCATCTCCCTATTCGTAAACTTACCT	1
4	CTTACCACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	9
5	TTTACCACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCGTAAACTTACCT	29
6	TTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTTGTAAACTTACCT	21
7	TTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTACAAATCCTTCATCTTCCCATTCGTGAACTTACTC	5
8	TTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCGTAAACTTACCT	124
9	TTTACTACGACACTCATTCCCCTCCATAGACGTTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCGTAAACTTACCT	12
10	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCGTAAGCTTACCT	5
11	TTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCGTAAACTTACCT	130
12	CTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTTCCCATTCGTAAACTTACCT	5
13	CTTACTACAATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	11
14	CTTACTACAATACTCATTTCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTTCCCATTCGTAAACTTACCT	1
15	TTTACTACGATACTCATTCCCCTCCATAGACATTCAACCTCACCCTGCAAATCCTTCATCTTCCCATTCGTGAACTTACTT	1
16	CTTACTGCGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	5
17	CTTACTATGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	11
18	TTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCGTGAACTTACTC	38
19	CTTACTACGATACTCATTTCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	2
20	TTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTCATCCTACAAATCCTTCATCTCCCTATTCGTAAACTTACCT	2
21	TTTGCTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCGTAAACTTACCT	1
22	TTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCATCCTGCAAATCCTTCATCTTCCCATTCGTAAACTTACTC	7
23	TTTACTACGATACTCATTCCCCTCTACAGACGCTTAAACCCATCCTACAAATCCTTCATCTTCCTCTTCGTAAACTTACCT	31
24	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCGTAAACTTACCT	33
25	TTTACTACGATATTCATTCCCCTCTACAGACGCTTAAACCCATCCTACAAATCCTTCATCTTCCTCTTCGTAAACTTACCT	2
26	TTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTATCCTACAAATCTTTCATCTCCCTATTCGTAAACTTACCT	1
27	TTTACTGCAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCGTAAACTTACCT	4
28	TTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCTTTCATCTCCCTATTCGTAAACTTACCT	28
29	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTCTTCGTAAACTTACCT	4
30	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTATTCGTAAACTTACCT	2
31	TTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATCCTACAAATCCTTCATCTTCCTCTTCGTAAACTTACCT	19
32	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCCACTCGTAAACTTACCT	6
33	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACGAATCATTTATCTTCCTACTCGTAAACTCACCT	1
34	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTCCCTACTCGTAAACTTACCT	2
35	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCATTTATCTTCCTCTTCGTAAACTTACCT	1
36	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCATTTATCTTCCTACTCGTAAACTTACCT	3
37	TTTACTACGACACTCGTTCCCCTCCATAGACGCTCAAGCTCATCCTGCAAATCCTTCATCTTCCCATTCGTAAACTCACCT	2
38	TTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACATATCCTTCATCTCCCTATTCGTAAACTTACCT	1
39	TTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAGTCTTTCATCTCCCTATTCGTAAACTTACCT	2
40	CTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCACCTCCCCATTCGTAAACTTACCT	1
41	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCTTACAAATCATTTATCTTCTTACTCGTAAACTTACCT	1
42	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCGTAAACTCACCT	1
43	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATCTATCTTCCTACTCGTAAACTTACCT	1
44	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTTATCCTACAAATCATTTGTCTTCCTATTCGTAAACTTACCT	3
45	TTTACTACAATATTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCGTAAACTTACCT	1
46	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTCATCTTCCTAATCGTAAACTTACCT	2
47	CTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTATCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	2
48	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAACCATTTATCTTCCTACTCGTAAACTTATCT	1
49	TTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCGTAAACTTATCT	2
50	TTTACTACAATACTCATTCCCCTCCATAGACGTTTAAACTCACCCTACAAATCCTTCATCTCCCTATTCGTAAACTTACCT	2
51	CTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTTCCT	2
52	TTTACCACGATACTCATTCCCCTCTACAGACGCTTAAACCCATCCTACAAATCCTTCATCTTCCTCTTCGTAAACTTACCT	1
53	TTTATCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCGTGAACTTACTT	2
54	TTTATCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCGTAAACTTACTT	1
55	CTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTCACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	7
56	TTTACTACAATACTTATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCGTAAACTTACCT	1
57	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCTTATTCGTAAACTTACCT	1
58	CTTACTACGATACTTATTTCCCTCCATAGACGCTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	1
59	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCGTAAACTTATCT	2
60	TTTACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCGTAAGCTTATCT	1
61	CCTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	1
62	TTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATCCTACAAATCCTTCATCTTCCTCTTCGTGAACTTACCT	2
63	TTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCTCTTCGTAAACTTACCT	2
64	TTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCGTCCTACAAATCCTTCATCTTCCTCTTCGTAAACTTACCT	2
65	TTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCATTCTACAAATCCTTCATCTTCCTCTTCGTAAACTTACCT	7
66	TTTACTACGATACTCATTCCCCTCTACAGACGCTCAAACCCACCCTACAAATCCTTCATCTTCCTCTTCGTAAACTTACCT	1
67	TTTACTACGATACTCATTCCTCTCTACAGACGCTCAAACCCATTCTACAAATCCTTCATCTTCCTCTTCGTAAACTTACCT	1
68	TTAACTACAATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCATTTATCTTCCTACTCGTAAACTTACCT	1
69	TTTACTACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCGTGAACTTACCT	7
70	CTTACTGCGATACTCATTTCCCTCCATAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCT	1
71	TTTACCACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCACCTTCCCATTCGTAAACTTACCT	2
72	TTTACTACGATACTCATTCCCCTCTACAGACGCTTAAACCCATCCTACAAATCCTTCACCTTCCTCTTCGTAAACTTACCT	1
73	TTTACTACAATACTCACTCCCCTCCATAGACGTTTAAACTTACCCTACAAATCTTTCATCTCCCTATTCGTAAACTTACCT	16
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84	TTTACTACGATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCGTAAACTTACTC	1
85	TTTACCACAATACTCATTCCCCTCCGTAGACGTTTAAACTTACCCTACAAATCCTTCATCTCCCTATTCGTAAACTTACCT	1
86	TTTACTACGATACCCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTTACCTTCCCATTCGTAAACTTACCT	1
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88	CTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTGAACTTACCT	1
89	TTTACTACAATACTCATTCCCCTCCATAGACACTCAAACTCACCCTGCAAATCCTTCATCTTCCCATTCGTAAACTTACTC	15
90	CTTACCACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTTACCG	1
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92	TTTACTACAATACTCATTCCCCTCCATAGACGTTTATACTTACCCTACAAATCCTTCATCTCCCTATTCGTAAACTTACCT	1
93	TTTACTACGATACCCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCGTAAACTTACCT	6
94	TTTACTACGGTACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCGTGAACTTACCT	1
95	TTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCGTGAACTTACCT	6
96	TTTACTACGATACTTATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCCTCCCATTCGTAAACTTACCT	1

Fig. S3a. Haplotypes and frequencies used for networks analyses from the 205-bp alignment including the archaeological DNA sequences. Because of the differences in the number of polymorphic sites, it was not possible to keep the same haplogroup numbers for both the complete and truncated alignment analyses.

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 97 TTTACTACGATACTCATCCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCCTTCACCTTCCCATTCGTGAACTTACCT  1
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119 CTTACTACGATACTCATTTCCCTCCATAGACGTTCAAACTTACCCTACAAATCCTTCATCTCCCCATTCGTAAACTCACCT 10
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146 NTTACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCTTTCACCTTCCCATTCRTGAACTTACCT  2
147 NNNACYACGACACTCATTCCCCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCRTAAACTTACCT  1
148 NNNACTACGATACTCATTCCCCTCCATAGACGCTCAAACTCATCCTGCAAATCTTTCACCTTCCCATTCCTGAACTTACCT  1
149 NNNNCTACGACACTCATTCCTCTCCATAGACGCTCAAACTCATCCTACAAATCCTTCATCTTCCCATTCGTAAACTTACCT  1

101010101010101001101010101010101010101010101010101010101010101010011010101010101001101010011010101010101010101010101010011010101010101010100110101010101010101010
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Fig. S3b. Continued.

Origin	Region	Color
China	Indo China	🟥
Tibet		
Laos		
Malaysia		
Thailand		
Myanmar		
Vietnam		
Japan	Japan	🟩
Europe	Europe	🟦
United kingdom		⬜
Indonesia	Indonesia	▨
Chile	Chile	🟨
India	India	🟧
Philippines	Philippines	🟩
Iran	Western Asia	🟪
Turkmenistan		
Azerbaijan		
Madagascar	Madagascar	🟫
Easter Island	Easter Island	🟪
Tonga		🟩
Niue		
Hawaii		
American Samoa		
Unknown location	Unknown location	🟦

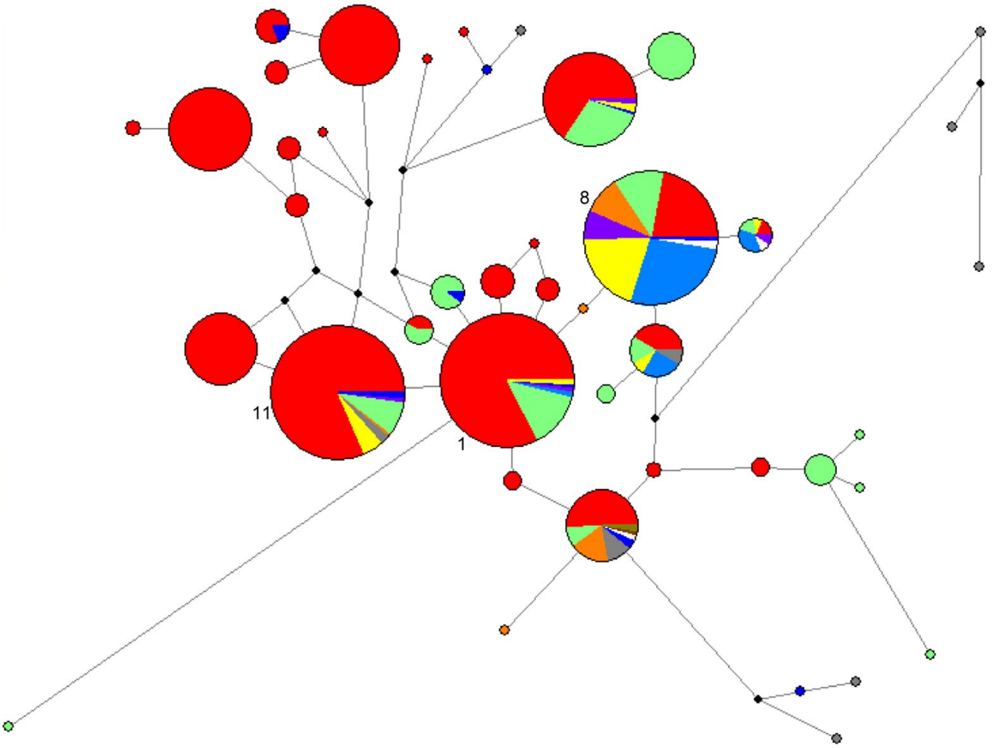
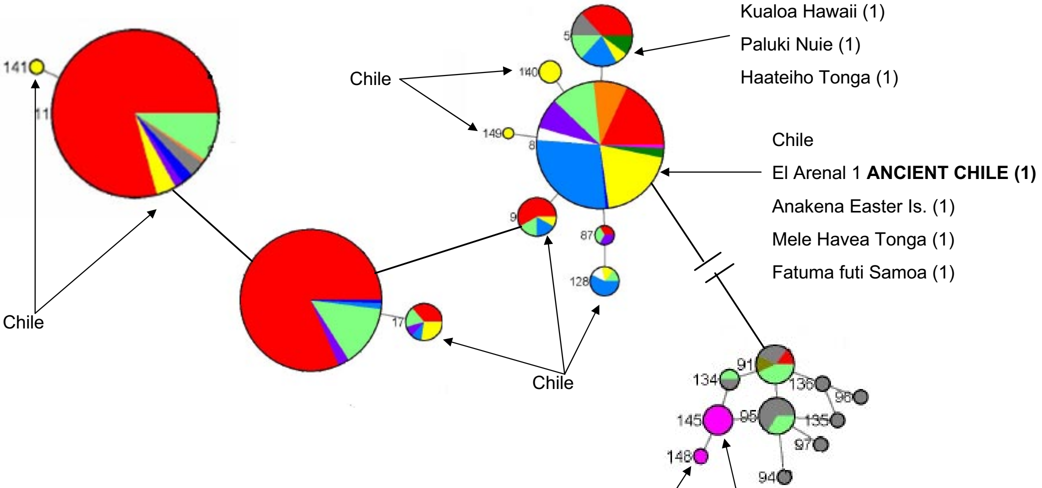


Fig. S4. Median-joining network start showing the position of 41 Chilean modern chickens (yellow) among native and wild junglefowl from Asia, Africa, and Europe. Only major and relevant networks are presented here by using 534 bp of the mtDNA CR. Circle size is proportional to the frequency of the corresponding haplotypes, and the geographical origin of the haplotypes are distinguished by use of color codes described in the table next to the figure. Most of the Chilean chickens cluster with Indian subcontinental/European/Chinese chickens, whereas other Chilean chickens cluster with haplogroups predominant of South and eastern Chinese/Japanese/Indonesian chickens.

Origin	Region	Color
China	Indo China	🟥
Tibet		
Laos		
Malaysia		
Thailand		
Myanmar		
Vietnam		
Japan	Japan	🟩
Europe	Europe	🟦
United kingdom		⬜
Indonesia	Indonesia	⬛
Chile	Chile	🟨
India	India	🟧
Philippines	Philippines	🟩
Iran	Western Asia	🟪
Turkmenistan		
Azerbaijan		
Madagascar	Madagascar	🟫
Easter Island	Easter Island	🟪
Tonga		🟩
Niue		
Hawaii		
American Samoa		
Unknown location	Unknown location	🟦



Chile

Kualoa Hawaii (1)

Paluki Nuie (1)

Haateiho Tonga (1)

Chile

Chile

El Arenal 1 **ANCIENT CHILE (1)**

Anakena Easter Is. (1)

Mele Havea Tonga (1)

Fatuma futi Samoa (1)

Chile

Chile

Anakena Easter Is. (4)

Hangahahave Easter Is. (1)

Fig. S5. Simplified median-joining networks showing the relationships and clustering of 205 bp of the mtDNA control region from worldwide, Chilean Araucana, pre-Columbian, and ancient Pacific/Polynesian chickens. The numbers next to the circles correspond to the haplotype clade number. The area of each circle is proportional to the frequency of the corresponding haplotypes, and the geographical origins of the haplotypes are distinguished by use of color codes described in the table next to the figure. Most of the Chilean chickens cluster with Indian subcontinental/European/Chinese chickens, more specifically with haplotype numbers 5, 8, 9, 128, and 140. The other Chilean chickens cluster with haplotypes predominant in South and eastern Chinese/Japanese/Indonesian chickens (haplotypes numbers 11, 17, and 141). Pre-Columbian sequence clusters with haplotype number 8. A more complete description of this MJN is presented in Fig. 1. Certain closely related haplotypes described in this and other figures have collapsed into others because of ambiguities and different length sequences.

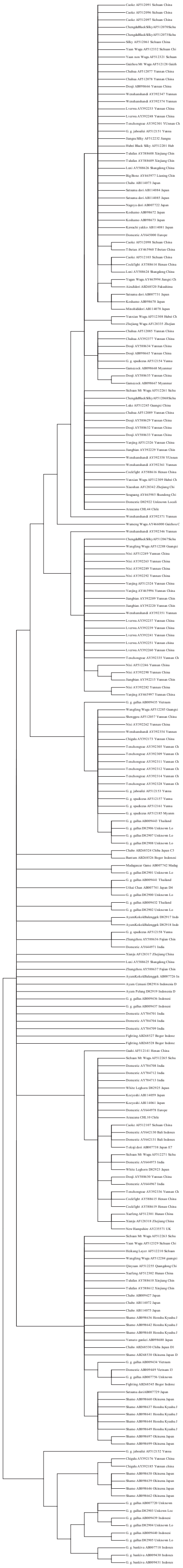


Fig. S6. Strict consensus MP tree. It was constructed from 30,276 trees left as described in *Materials and Methods*.

Fig. S7. MJN showing eight haplotypes of 41 modern Chilean chickens based by using 530 bp of the mtDNA CR sequences. The area of each circle is proportional to the frequency of the corresponding haplotypes described in supporting information (SI) Table S1. Clustering of these sequences among native chickens and wild junglefowl from Asia, Africa, and Europe is shown in yellow in Fig. 1 and Figs. S4 and S5.

Table S1. Voucher information of modern Chilean chicken samples collected from latitudes 33° to 40° S

Sample ID	Breed or type	Flock	Sex (♀/♂)	Chilean haplotype name	Haplotype no. as indicated in network analyses
CHL1	Ketro	A Pirque 1, Santiago (Lat 33° 40′ S, Long 70° 28′ W)	♂	11-CH	11
CHL2	Kollonca	♂	8-CH	8	
CHL3	Kollonca	♀			
CHL4	Kollonca	♀			
CHL5	Creole/naked neck	♂	17-CH	17	
CHL6	Kollonca	♀	11-CH	11	
CHL7	Creole	B Pirque 2, Santiago (Lat 33° 39′ S, Long 70° 27′ W)	♂	8-CH	8
CHL8	Kollonca	C Antiquina, Arauco (Lat 38° 11′ S, Long 73° 25′ W)	♂	8-CH	8
CHL9	Kollonca	♂	8-CH	8	
CHL10	Ketro	♀	140-CH	140	
CHL11	Kollonca de Aretes	♀	8-CH	8	
CHL12	Kollonca	♀	8-CH	8	
CHL13	Kollonca	♂	8-CH	8	
CHL14	Creole	D Malihue, Valdivia (Lat 39° 44′ S, Long 72° 38′ W)	♀	8-CH	8
CHL15	Creole	♀	8-CH	8	
CHL16	Kollonca	G Cañete, Arauco (Lat 37° 47′ S, Long 73° 23′ W)	♂		
CHL17	Ketro	♂	11-CH	11	
CHL18	Kollonca	♂	8-CH	8	
CHL19	Creole	E Ninhue, Chillán (Lat 36° 21′ S, Long 72° 23′ W)	♀	8-CH	8
CHL20	Creole	F Yumbel, Chillán (Lat 37° 02′ S, Long 72° 32′ W)	♀	140-CH	140
CHL21	Kollonca	G Cañete, Arauco (Lat 37° 47′ S, Long 73° 23′ W)	♂	8-CH	8
CHL22	Ketro	♀	140-CH	140	
CHL23	Ketro	♀	5-CH	5	
CHL24	Kollonca	♀	9-CH	9	
CHL25	Ketro	♀	8-CH	8	
CHL26	Kollonca	♀	5-CH	5	
CHL27	Kollonca	♀	8-CH	8	
CHL28	Ketro	♂	8-CH	8	
CHL29	Ketro	♀	140-CH	140	
CHL30	Kollonca	♀	8-CH	8	
CHL31	Kollonca	B Pirque 2, Santiago (Lat 33° 39′ S, Long 70° 27′ W)	♂	17-CH	17
CHL32	Kollonca	♀	128-CH	128	
CHL33	Ketro	♀	8-CH	8	
CHL34	Japanese Long Tail ancestry	♂	8-CH	8	
CCHL35	Kollonca	♂	8-CH	8	
CHL36	Kollonca	♀	11-CH	11	
CHL37	Ketro	♂	11-CH	11	
CHL38	Creole	♀	8-CH	8	
CHL39	Passion fowl	♀	8-CH	8	
CHL41	Passion fowl	H Viña del Mar, Valparaíso (Lat 32° 59′ S, Long 71° 33′ W)	♂	8-CH	8
CHL40	Passion fowl	♂	8-CH	8	
CHL42	Passion fowl	♀	8-CH	8	
CHL43	Ketro	J Melipilla, Santiago (Lat 33° 42′ S, Long 71° 13′ W)	♂	8-CH	8
CHL44	Passion fowl/Sebright ancestro	I El Monte, Santiago (Lat 33° 42′ S, Long 70° 58′ W)	♀	141-CH	141

Creole translates from ‘‘criollo’’ and stands for an unselected smallholder chicken typical of the countryside. DNA extraction precedures failed for samples 3, 4, and 16.

Table S2. Calibration of one direct date on chicken bone with increasing proportion of marine-derived carbon

ΔR	Marine C, %	Calibration dataset	Radiocarbon on chicken bones from the El Arenal-1, Chile ($n = 622 \pm 35$)
0 ± 0	0	SHCal04	**AD1304–1424**
154 ± 131	10	Mixed marine SoHem	**AD1387–1449**
154 ± 131	20	Mixed marine SoHem	**AD1395–1492**
154 ± 131	30	Mixed marine SoHem	AD1412–1620
154 ± 131	40	Mixed marine SoHem	AD1440–1644
154 ± 131	50	Mixed marine SoHem	AD1439–1796

ΔR of 137 ± 114 based on Ingram and Southon's (1) single bivalve determination from Valparaiso, Chile combined with Taylor and Berger's (2) gastropod date from approximately the same location. Given the problems inherent with the use of gastropods for characterizing marine reservoir effects, the derived ΔR value is used simply for illustrative purposes. All calibrated dates are reported at 2σ. Bold type denotes pre-Columbian values.

1. Ingram BL, Southon JR (1996) Reservoir ages in Eastern Pacific coastal and estuarine waters. *Radiocarbon* 38:573–582.
2. Taylor RE, Berger R (1967) Radiocarbon content of marine shells from the Pacific coasts of Central and South America. *Science* 158:1180–1182.

Table S3. Frequency of modern Chilean chicken haplotypes

Haplotype	Frequency
17-CH	2
11-CH	5
141-CH	1
140-CH	4
5-CH	2
9-CH	1
8-CH	25
128-CH	1
Total	41

Table S4. ΔR values for the west coast of South America (after Reimer and Reimer 2008)

Longitude	Latitude	ΔR	Location	Ref	Collection year	Reservoir age	^{14}C age	Lab no.	Taxa	Diet
−80.00	−3.00	−216 ± 37	Guayaquil, Ecuador*	10	1927	85 ± 38	235 ± 37	UCIA-1249A	Cerithidea valida	Deposit feeder
−80.00	−3.00	84 ± 45	Guayaquil, Ecuador*	10	1927	386 ± 46	536 ± 45	UCLA-1249B	Thais biserialis	Carnivore
−80.00	−10.00	243 ± 49	Northern Peru*	10	1935[†]	544 ± 50	700 ± 49	UCLA-1282	Strombus peruvianus	Herbivore/omnivore
−78.00	−14.00	670 ± 44	Peru*	10	1935[†]	971 ± 45	1127 ± 44	UCLA-1279	Oliva peruviana	Unknown
−70.00	−24.00	175 ± 34	Antofagasta, Chile*	10	1925	477 ± 35	626 ± 34	UCLA-1277	Concholepas concholepas	Carnivore
−72.00	−33.00	313 ± 76	Valparaiso, Chile*	10	1935[†]	614 ± 77	770 ± 76	UCLA-1278	Tequla aler	Unknown
−71.80	−33.10	61 ± 50	Valparaiso, Chile	6	1939[‡]	370 ± 51	520 ± 50	CAMS-17919/1	Mytilus californianus	Suspension feeder
−72.65	−51.70	221 ± 40	Puerto Natales, Chile	6	1939[‡]	530 ± 41	680 ± 40	CAMS-17918	Mytilus californianus	Suspension feeder

Marine reservoir effects for Chile are poorly resolved. There are eight ΔR values published for the west coast of South America between the equator and Cape Horn. All but one of these values can be shown to be problematic. Six of these values were published by Taylor and Berger (10) on the basis of dating of gastropods. Over the last 20 years, several studies have indicated that detrital feeders are potentially problematic because ingested organic carbon from diverse sources can become incorporated into shell structures through metabolic action (5, 9). These effects have been found to be particularly problematic in limestone-dominated areas (1, 4). It is for this reason that the use of suspension feeders, herbivores, and omnivores is recommend in ΔR research. Taylor and Berger's sample contains two carnivores, a deposit feeder, and two other gastropods for which dietary information is lacking. Only the determination on *Strombus peruvianus* from northern Peru is unproblematic as a herbivore/omnivore, resulting in $\Delta R = 243 \pm 49$. In Ingram and Southon's (6) more recent study focused on California included two samples of the suspension-feeding bivalve *Mytilus californianus* from Chile. The sample from Puerto Natales is an estuarine reservoir value, potentially influenced by terrestrial runoff and incomplete exchange with the open ocean and therefore may not reflect open water reservoir conditions (11). This leaves the determination from Valparaiso in central Chile, resulting in $\Delta R = 61 \pm 50$. This single ΔR value provides the single reliable estimate for marine reservoir effect in near-shore open waters in southern South America. However, this value is likely to underestimate ΔR in the region because of heavily depleted Antartic source waters brought to the Chilean coastline by the Antartic circumpolar current. Seven values are reported in the Marine Reservoir Database for northern Antartica (7) giving a combined $\Delta R = 871 \pm 176$ (see refs. 2, 3, 8). We believe, therefore, that the $\Delta R = 61 \pm 50$ from Valparaiso should be treated as a conservative estimate of open water marine reservoir effect in Chile.

*Approximate location.

[†] Mid-point. Collected between 1930–1940 (10).

[‡] Ingram and Southon (1996:574) state that ''*n most cases, it is uncertain whether these specimens were collected live or not.*''

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Other Supporting Information Files

Table S5 (XLS)
Table S6 (XLS)