

>EM29-396-uc483 (FLR)

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GGTGTCTAGAGCCACTGTGGACATCAAATCAGAGTGACCCCGTGGAG

>EMFLREM22UC483

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>EM1T7-1

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>EM2T7-1

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>EM3T7-1

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>EM4T7-1

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>EM5T7-1

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>EM7T7-1

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>EM8T7-1

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AGGGGTTGGACCTGCAGGGACATCAGAGAAGAGTGACCCCGTGGAG

>EM9T7-1

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GCAGGATGCAGCTGAGTTCTCCTTTGCTGTCACAAACCTGGAGGACGCCGGGACATATCAGTGTCCGTACCA
GGTGTCTAGAGCCACTGTGGACATCAAATCAGAGTGACCCCGTGGAG

Fig. S1, page 1 of 1. Sequences of 39 clones of 190 base pairs from two independent amplifications of exon 2 from a line 6₁ chicken, plus the two FLRs

>EM10T7-1
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GTGTCAGAGCCACTGTGGACATCAAATCAGAGTGACCCCGTGGAG

>EM11T7-1
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CAGGAAATGGCAGAGTTCTCCTTCCGTAGCGCAAGTCATGATCAAGCAGGTACATATTTGTGCCAGTACCAGG
TGTCTGAGTCAGAGGACGTATCAGTGATGAGTGACCCTGTGGAG

>EM12T7-1
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GTGTCTGAGTCAGAGGACGTATCAGTGATGAGTGACCCCGTGGAG

>EM13T7-1
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TGTGTCTGAGCCACTGGGGACTTCAGAGAAGAGCGATCCTGTGGAG

>EM14T7-1
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>EM15T7-1
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>EM16T7-1
GCCCCGCATGGCTGCCTGGGTCCAGCTCTGGCACAATGGAACCTCTGAGATTTAACAAGGAAAAAGACAAGGA
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>EM17T7-1
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>EM18T7-1
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>EM19T7-1
GCCCCGCATGGCTGCCTGGGTCCAGCTCTGGCTCAATGGAACCTCTGAGATTTAACGAGGAAAAAGACAAGGA
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GTGTCAGAGCCTCTGAGGACATCCAAAAAGAGTGACCCTGTGGAG

Fig. S1, continued page 2 of 4. Sequences of 39 clones of 190 base pairs from two independent amplifications of exon 2 from a line 6₁ chicken, plus the two FLRs

>EM20T7-1

GCCCCAGCCAGCTGCCTGGGTCTGGCTGTACCAGGAGGGAGGTTGGTCGTACAACAAGGGGAAGGAGAAGG
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>EM22T7-1

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AGGGGTTGGCACCTGCAGGGACATCAGAGAAGAGTGACCCCGTGGAG

>EM23T7-1

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GGGAGTCTTGGTCAGTAGGGGCATCAGAGAAGAGTGACCCCGTGGAG

>EM24T7-1

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GGTTTTGGAGCCACCAGGGATGTCAGGGAAGAGTGACCCCGTGGAG

>EM2T7-2

GCCCCGGTTAACCTTACAAGCTGAGCTCTGCCAGAACGGCCATTTGAGATCCAAGAAAGACATGGACAGACTT
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GGTTTTGGAGCCACCGGGGACATCAGGGAAGAGTGACCCCGTGGAG

>EM4T7-2 curated

GCCCCGCATGGCTGCCTGGGTCCAGCTCTGGCACAATGGAACCTGAGATTTGACAAGGAAAAAGACAAGGA
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GGTGTCAAGCCACTGTGGACATCAAATCAGAGTGACCCCGTGGAG

>EM5T7-2

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AGGGGTTGGCACCTGCAGGGACATCAGAGAAGAGTGACCCCGTGGAG

>EM6T7-2 curated

GCCCCAGCTGGCTGCACAAGTTGAGCTCTACCAGAACGGACATATGAGATCCAAGAAAGACATGGACATGCT
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GGTTTTAGAGCCACCAGGGATGCCAGGGAAGAGTGACCCCGTGGAG

>EM7T7-2

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AGGGGTTGGAGCAACCAGGGACATCGGAGAAGAGTGACCCCGTGGAG

>EM9T7-2 curated

GCCCCACATGGCTGCCTGGGTCTGGTTGTACCACGAAGAAGGTCGGTCGTACAACAAGGGGAAGAAGAAGG
AGCAGGACGCGGCCGCGTTCTTTTTTGTAGCACACTGCAGGAACACGCAGGTCGTTACTGGTGTCACTACCG
GGTGTCTGAGTCAGCCGAGGTGTCAAGAGTGACCCCTGTGGAG

Fig. S1, continued page 3 of 4. Sequences of 39 clones of 190 base pairs from two independent amplifications of exon 2 from a line 6₁ chicken, plus the two FLRs

>EM11T7-2
 GCCCCAGTTGCACTTACAAGTTCAGCTCTGCCAGAACGGACATATGAGATCCAAGAAAGACGCGGAGATGCT
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 GGTTCCTGGAGCCACCGGGGACATCAGGGAAGAGTGACCCCGTGGAG

>EM12T7-2
 GCCCCGCATGGCTGCCTGGGTCTGGCTGTACCAGGAAAGAGGTTGGTCGTACAACAAGGGGAAGGAGAAGG
 AGCAGAACGCGGCCGAGTTCTTCTTTGTTAGCACAAAGCGGGAACACGCAGGTCGTTATCGGTGTCAGTACC
 GGGTGTCTTGGTCAGTAGGGGCATCAGAGAAGAGTGACCCCGTGGAG

>EM13T7-2 curated
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 AGCAGGACGTGGCTGAGTTCTCCTTGACTGGAATTAAGCAGGAAGATGCAGTGAGATATCAGTGCCAGTACC
 AGGGGTTGGAGCCTGCAGGGACATCGCAGAAGAGTGACCCCGTGGAG

>EM14T7-2
 GCCCCGGCCGGCTGCCTGGGTGAGCTGTACAAGGAGGGAAAGTGGAGATCCAGAAAAGAAATGGACCAGG
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 AGGGGTTGGAGCAACCAGGGACATCGGAGAAGAGTGACCCCGTGGAG

>EM15T7-2
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 GGTGTCTGAGTCAGCCGAGTTGTCACTGGAGAGTGACCCCGTGGAG

>EM16T7-2 curated
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 CAGGAAATGGCAGAGTTCTCCTTGACTGGAATTAAGCAGGTAGATGCAGTGAGATATCAGTGCCAGTACCAG
 GGGTTGGAGCAACCAGGCACATCAAATCAGAGTAACCCCGTGGAG

>EM18T7-2 curated
 GCCCTGGTTGCCCTTACAAGTTGAGCTCTGCCAGAACGGACATTTGAGATCCAAGAAAGACGTGGAGATGCTT
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 GTTTTGGAGCCACCAGGGACATCAGGGAAGAGTGACCCCGTGGAG

>EM20T7-2 curated
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 ACAGAACACAGTTGAGTTTTCTTGCTTAGTGTAGAGAAGGAAGATGCAGAGAAGTATCGGTGCCTGTACCG
 GGTTCCTGGAGCCACCAGGGATGTCAGGGAAGAGTGACCCCGTGGAG

>EM21T7-2 curated
 GCCCCGGCCAGCTACCAGGGTCGAGCTGTATCAGGATGGACAGTGGAGATCCAGAAAGGAAATGGACCAGG
 AGCAGGACGTGGCTGAGTTCTCCTTGGCTGGAATAAAGAAGAAAGATTGCGGGGACATATCAGTGCCAGTACC
 AGGGGTTGGCACCTGCAGGGACATCAGAGAAGAGTGACCCCGTGGAG

Fig. S1, continued page 4 of 4. Sequences of 39 clones of 190 base pairs from two independent amplifications of exon 2 from a line 6₁ chicken, plus the two FLRs

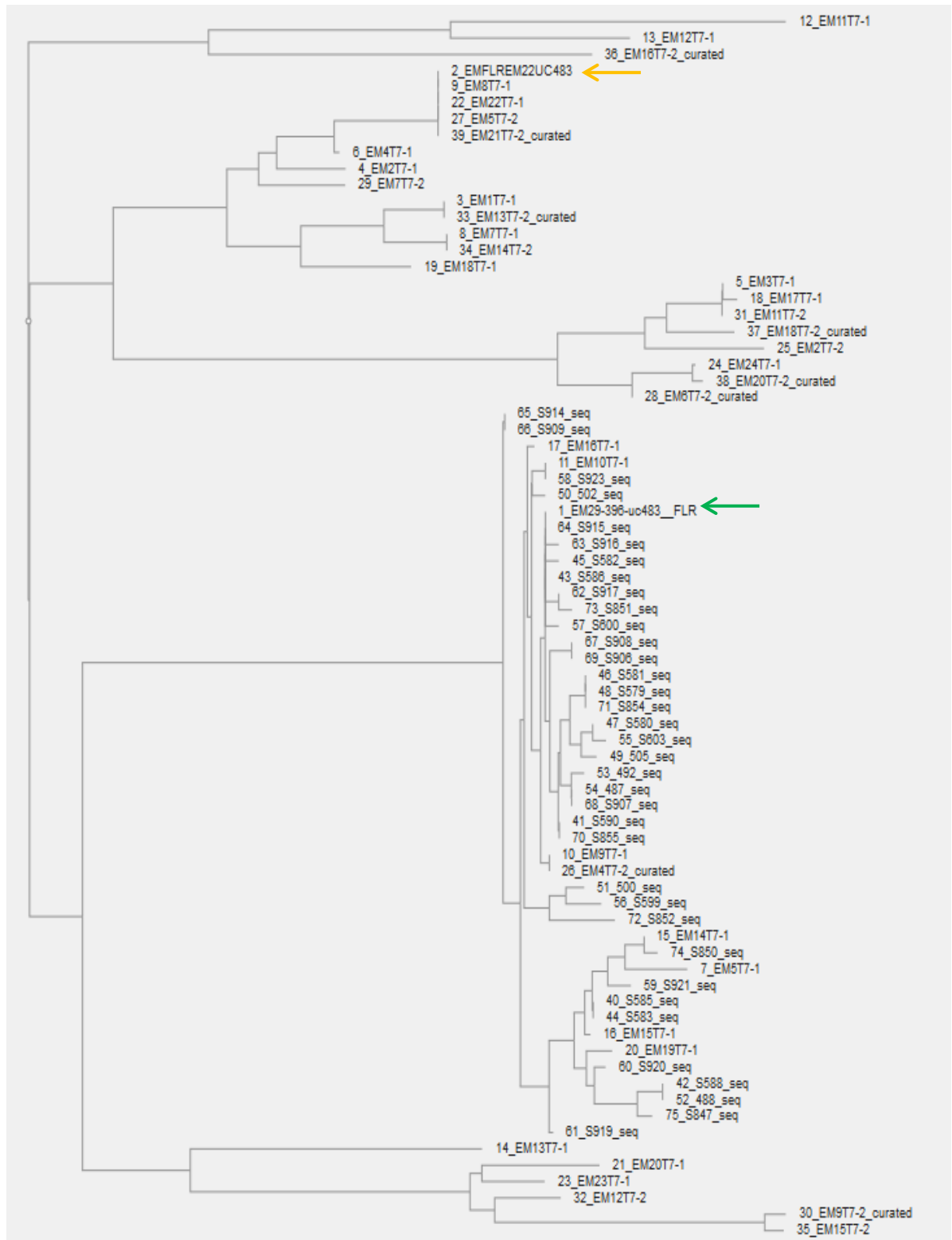


Fig. S2. Neighbour joining tree of 36 cloned sequences from Munich lines M11 and R11 (all indicated by names starting with S), and 39 sequences from a line 6₁ chicken (all indicated by names starting with EM), plus the two FLRs (indicated by arrows, orange for FLR22 and green for FLR29). The tree was constructed using MAFFT (<https://mafft.cbrc.jp/alignment/server/>) displayed using Archaeopteryx.js available on the same website.

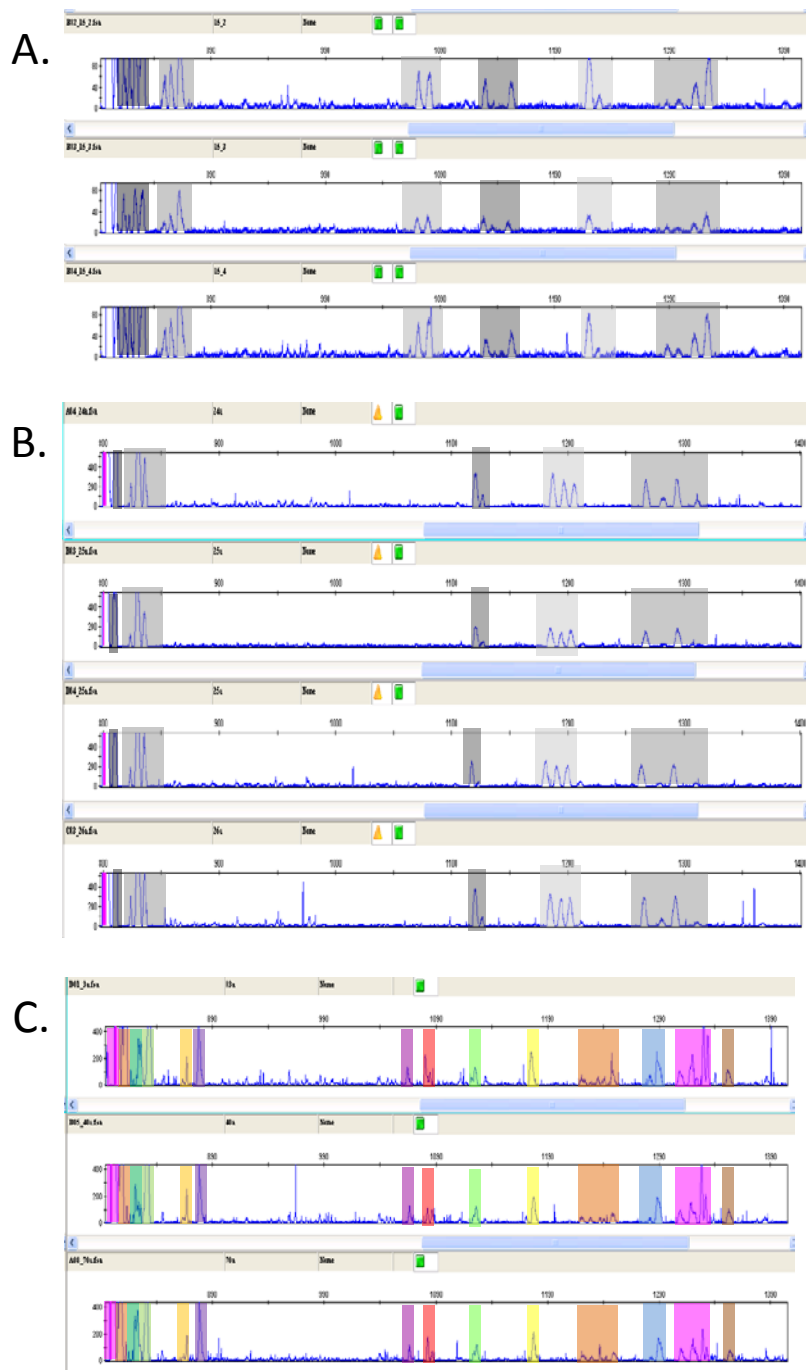


Fig. S3. RSCA of ChIR-AB1 amplicons using FLR29 show that patterns can be very reproducible between different individuals within a class of patterns on the same run.

- A. three individuals from line 15I (pattern 2),
- B. four individuals from line C-B4 (pattern 4c),
- C. three individuals from the first commercial broiler line

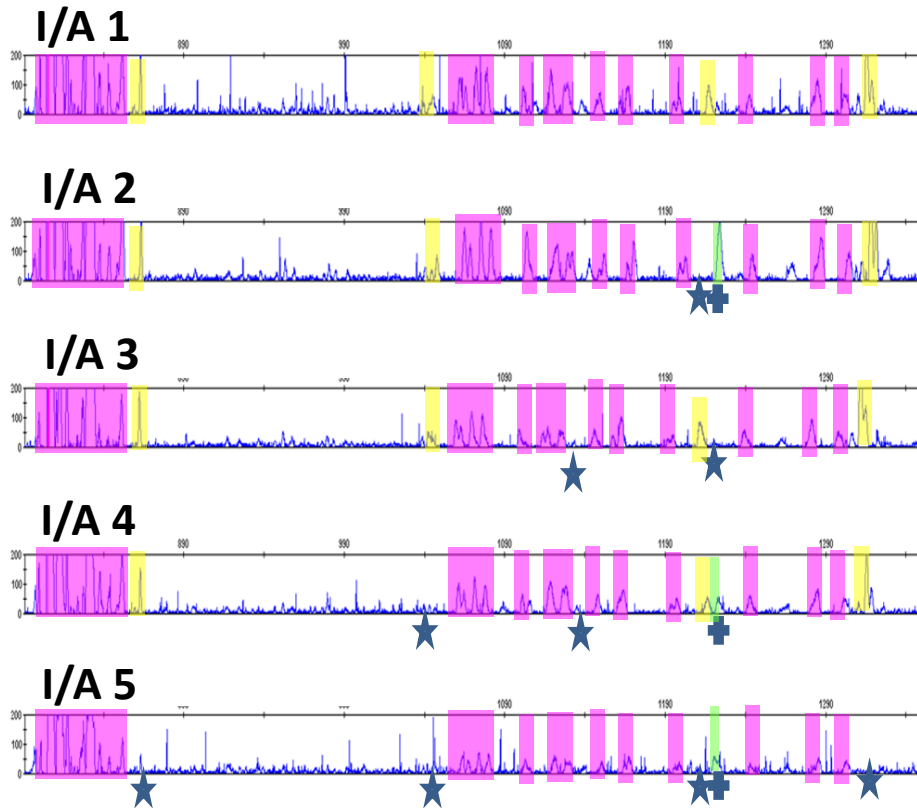


Fig. S4. RSCA of ChIR-AB1 amplicons from one group of commercial broiler chickens using FLR29 shows peaks that appear or disappear. Purple highlight indicates peaks common to all patterns shown, yellow highlight and star indicate peaks shared with pattern I/A-1, green highlight and plus sign indicate peaks not shared with pattern I/A-1.

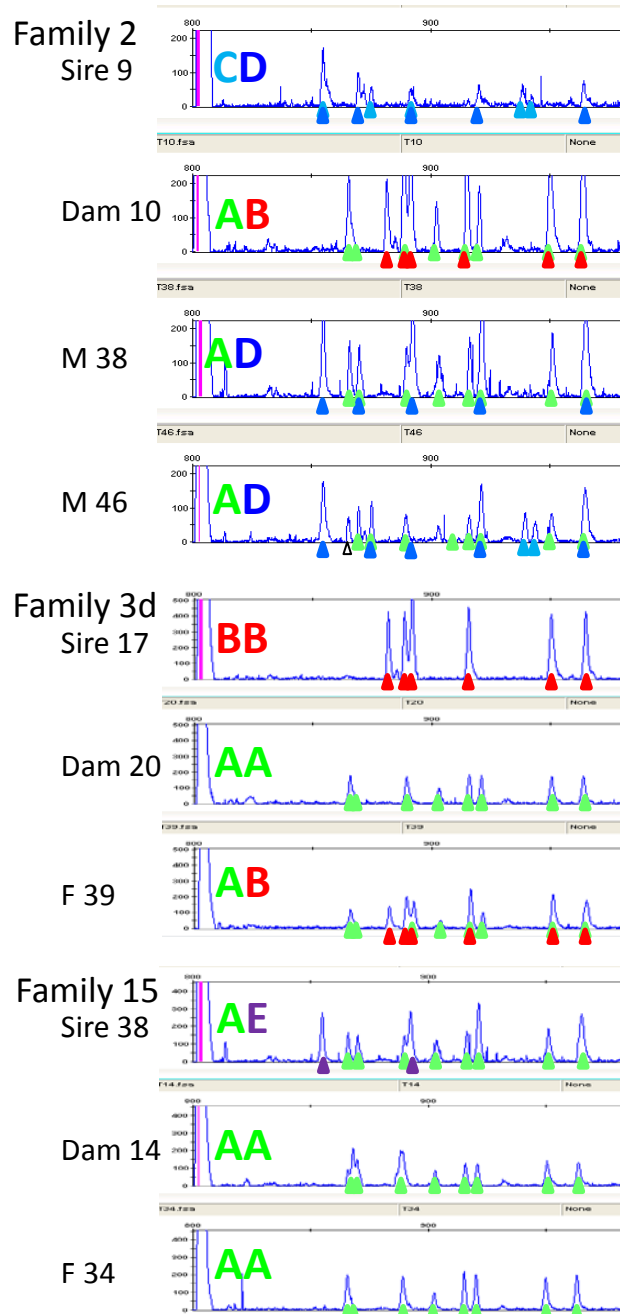


Fig. S5. Families (trios) in a line of commercial birds allow haplotypes to be discerned by analysis of RSCA patterns using FLR22. Letters indicate haplotypes with colours of triangles indicating peaks assigned to that haplotype. Page 1 of 2.

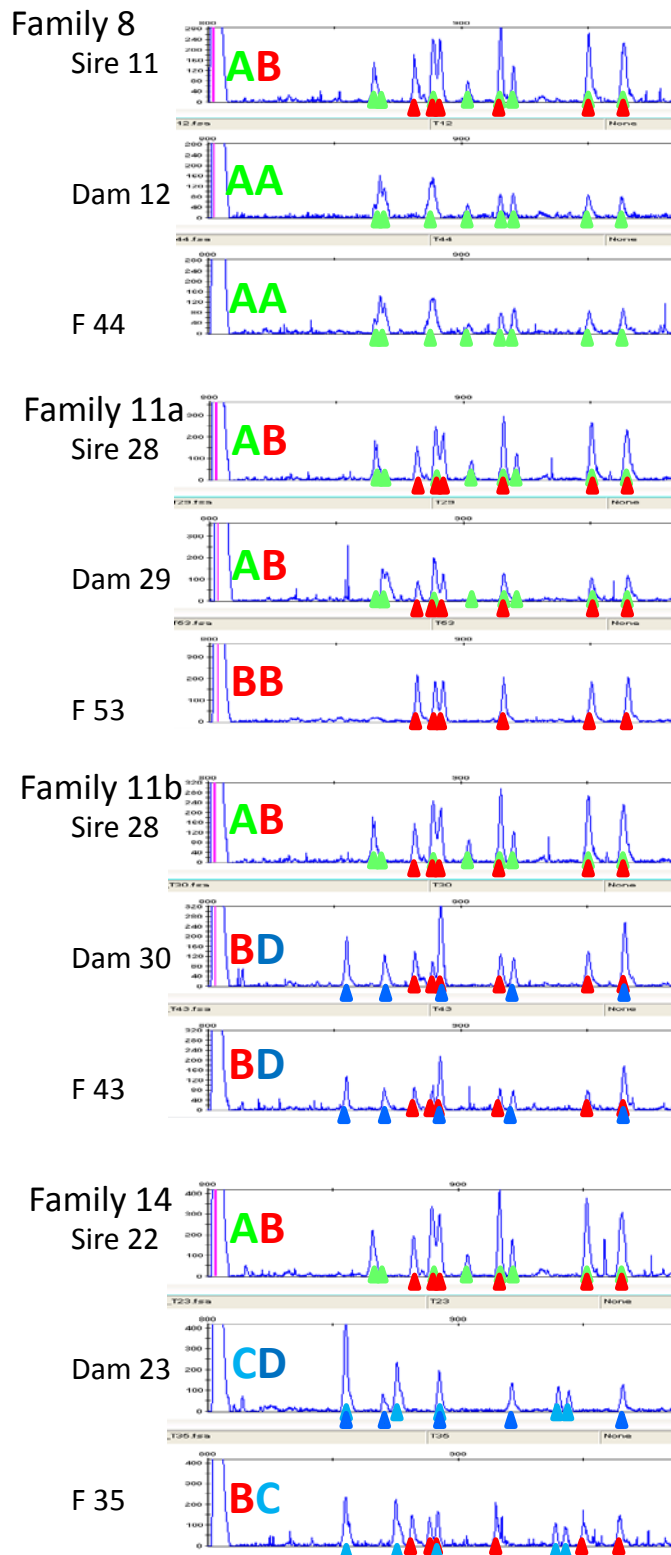


Fig. S5, continued. Families (trios) in a line of commercial birds allow haplotypes to be discerned by analysis of RSCA patterns using FLR22. Letters indicate haplotypes with colours of triangles indicating peaks assigned to that haplotype. Page 2 of 2.

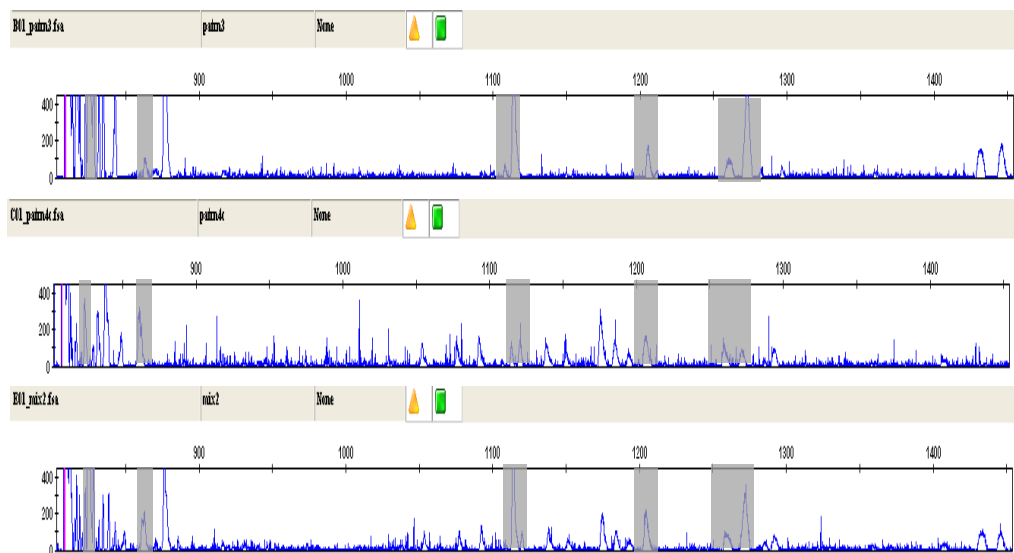


Fig. S6. RSCA with mixed samples identifies peaks with the same mobility, confirming identical peaks. Two samples with different peak patterns (3 and 4c) were analysed either separately (top two panels) or mixed together (half and half to give the same loading volume, bottom panel). The shaded peaks that appear to have the same mobility when analysed separately are confirmed to collapse to a single peak, while other peaks remain unchanged.