

Supplementary Table 1 | Flicker plumage traits and phenotypic scoring of hybrids. Details on the six plumage patch coloration differences between red-shafted and yellow-shafted flickers. Individuals are scored from 0 (pure yellow-shafted) to 4 (pure red-shafted) for each trait. An overall phenotype score is calculated by summing across the six traits and transforming to range from 0-1 (to allow comparisons between the sexes). Phenotypic scoring is adapted from Short (1965).

Phenotype score	Description
<i>Wings and tail ("shaft") color, Carotenoid</i>	
0	Bright yellow, as in yellow-shafted
1	Yellow-orange traces, faint in all feathers or heavy in one or several
2	Orange to red rachises with yellow-orange vanes
3	Orange-red
4	Deep salmon red, as in red-shafted
<i>Nuchal patch presence, Carotenoid</i>	
0	Present and broad, as in yellow-shafted
1	Present and restricted in width (less than one-half of normal width)
2	Present and broken in one or more places
3	Traces present, usually at sides of nape
4	Absent, as in red-shafted
<i>Crown color, Melanin</i>	
0	Gray, as in yellow-shafted
1	Gray with brown traces in forehead and crown
2	Mixed gray and brown (crown half brown with more gray on hind neck)
3	Crown brown with hind neck gray toward back
4	Brown confluent with back color, as in red-shafted
<i>Ear covert color, Melanin</i>	
0	Tan, as in yellow-shafted
1	Tan with gray traces
2	Mixed gray and tan
3	Gray with tan traces (especially below eye)
4	Gray, as in red-shafted
<i>Throat color, Melanin</i>	
0	Tan, as in yellow-shafted
1	Tan with gray traces (usually on lower throat)
2	Mixed gray and tan
3	Gray with tan traces (usually near chin)
4	Gray, as in red-shafted
<i>Malar stripe color (males only), Melanin and Carotenoid</i>	
0	Black, as in yellow-shafted
1	Black with <20% red
2	Mixed black and red
3	Red with <20% black
4	Red, as in red-shafted

Supplementary Table 2 | Sample information

Individual ID	Taxa	Sex	Year	County, State	Phenotype score
LSU B48981	Yellow-shafted	Male	2002	Brevard, FL	-
LSU B48980	Yellow-shafted	Male	2002	Escambia, FL	-
LSU B50722	Yellow-shafted	Male	2003	Escambia, FL	-
LSU B59061	Yellow-shafted	Male	2004	Escambia, FL	-
LSU B59422	Yellow-shafted	Male	2005	Escambia, FL	-
CUMV 51231	Yellow-shafted	Male	2004	Tompkins, NY	-
CUMV 52455	Yellow-shafted	Male	2006	Tompkins, NY	-
CUMV 52999	Yellow-shafted	Male	2009	Tompkins, NY	-
CUMV 54562	Yellow-shafted	Male	2011	Tompkins, NY	-
CUMV 58977	Yellow-shafted	Male	2017	Tompkins, NY	-
1803-25407	Hybrid	Male	2016	Lincoln, NE	0.000
CUMV 56730	Hybrid	Female	2016	Butler, NE	0.050
CUMV 57686	Hybrid	Male	2017	Deuel, NE	0.083
1803-25405	Hybrid	Male	2016	Keith, NE	0.083
1803-25403	Hybrid	Male	2016	Keith, NE	0.083
1803-25410	Hybrid	Female	2016	Sedgwick, CO	0.100
CUMV 56731	Hybrid	Male	2016	Buffalo, NE	0.125
CUMV 58091	Hybrid	Male	2018	Keith, NE	0.125
CUMV 56715	Hybrid	Female	2016	Lancaster, NE	0.150
CUMV 56717	Hybrid	Male	2016	Buffalo, NE	0.167
CUMV 58065	Hybrid	Male	2018	Garden, NE	0.167
CUMV 56728	Hybrid	Male	2016	Keith, NE	0.167
1803-25404	Hybrid	Male	2016	Keith, NE	0.167
CUMV 57607	Hybrid	Female	2017	Logan, CO	0.200
CUMV 56716	Hybrid	Female	2016	Polk, NE	0.200
CUMV 58072	Hybrid	Male	2018	Logan, CO	0.208
CUMV 56725	Hybrid	Male	2016	Morrill, NE	0.208
CUMV 58060	Hybrid	Female	2018	Morgan, CO	0.250
1803-25406	Hybrid	Male	2016	Lincoln, NE	0.292
CUMV 56724	Hybrid	Male	2016	Morrill, NE	0.292
CUMV 58090	Hybrid	Male	2018	Morgan, CO	0.333
CUMV 58084	Hybrid	Male	2018	Logan, CO	0.375
CUMV 58067	Hybrid	Male	2018	Weld, CO	0.375
CUMV 57608	Hybrid	Female	2017	Logan, CO	0.400
CUMV 56734	Hybrid	Female	2016	Morrill, NE	0.400
1833-36504	Hybrid	Female	2016	Sedgwick, CO	0.400
CUMV 58076	Hybrid	Female	2018	Weld, CO	0.450
CUMV 57988	Hybrid	Male	2017	Morgan, CO	0.458
CUMV 58148	Hybrid	Male	2018	Garden, NE	0.500
CUMV 56726	Hybrid	Male	2016	Scotts Bluff, NE	0.500
CUMV 57610	Hybrid	Female	2017	Logan, CO	0.550
CUMV 58085	Hybrid	Female	2018	Logan, CO	0.550
1833-36502	Hybrid	Male	2016	Morgan, CO	0.583
CUMV 58079	Hybrid	Male	2018	Morgan, CO	0.583
1803-25408	Hybrid	Female	2016	Morgan, CO	0.600
1803-25409	Hybrid	Male	2016	Sedgwick, CO	0.625
CUMV 58068	Hybrid	Male	2018	Scotts Bluff, NE	0.667
CUMV 57967	Hybrid	Male	2017	Weld, CO	0.667
CUMV 58080	Hybrid	Male	2018	Morgan, CO	0.708
CUMV 58069	Hybrid	Male	2018	Weld, CO	0.708
CUMV 58070	Hybrid	Male	2018	Weld, CO	0.750
CUMV 56723	Hybrid	Female	2016	Kimball, NE	0.800

CUMV 56736	Hybrid	Male	2016	Scotts Bluff, NE	0.833
CUMV 58078	Hybrid	Male	2018	Larimer, CO	0.875
CUMV 56727	Hybrid	Male	2016	Scotts Bluff, NE	0.917
CUMV 58063	Hybrid	Male	2018	Larimer, CO	0.958
CUMV 58077	Hybrid	Male	2018	Larimer, CO	0.958
1833-36503	Hybrid	Male	2016	Larimer, CO	1.000
BURKE 109367	Red-shafted	Male	2002	Josephine, OR	-
BURKE 113386	Red-shafted	Male	2002	Josephine, OR	-
BURKE 112778	Red-shafted	Male	2002	Josephine, OR	-
BURKE 101882	Red-shafted	Male	2002	Josephine, OR	-
BURKE 101883	Red-shafted	Male	2002	Josephine, OR	-
BURKE 100969	Red-shafted	Male	2003	Inyo, CA	-
LSU B34359	Red-shafted	Male	1999	San Bernardino, CA	-
LSU B24273	Red-shafted	Male	2000	San Bernardino, CA	-
LSU B60069	Red-shafted	Male	2007	San Bernardino, CA	-
BURKE 66173	Red-shafted	Male	1996	Tulare, CA	-

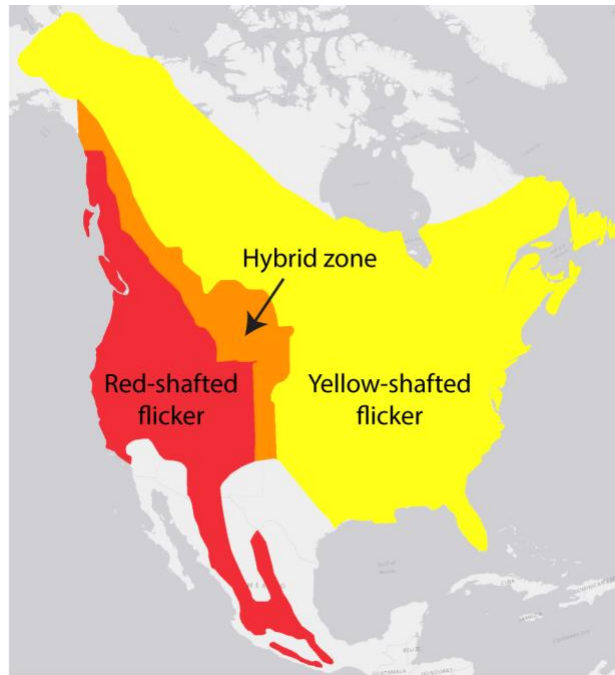
Supplementary Table 3 | Genomic regions identified in the GWAs. List of regions identified as significant in the six genome-wide association (GWA) analyses of hybrid flickers. Each region includes information on the trait (or traits) it was significantly associated with, the number of significant SNPs in the region, and the number of identified genes. Chromosomal and base pair positional information is based on alignment to the zebra finch genome.

Supplementary Table 4 | Candidate genes. List of candidate genes within the genomic regions of interest shown in Supplementary Table 3. Gene functions of potential relevance to melanin or carotenoid pigmentation are included (e.g., vesicles, WNT signaling pathway). The strongest candidate genes, those with known or suspected roles in pigmentation, are shaded in gray. Chromosomal and base pair positional information is based on alignment to the zebra finch genome.

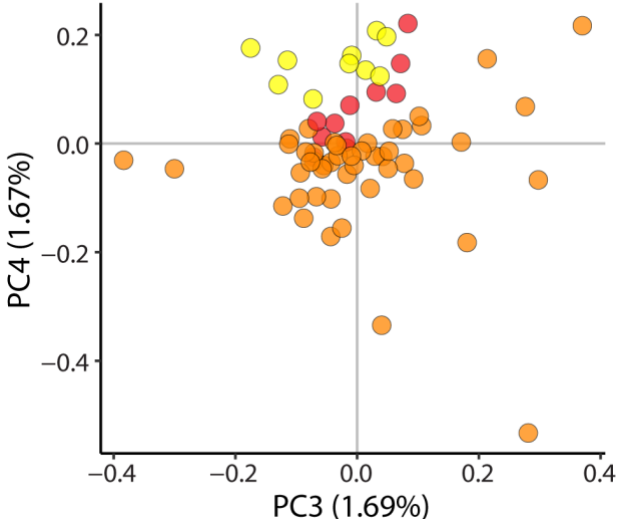
Supplementary Table 5 | Summary statistics averaged across the whole genome

Taxa	Observed Heterozygosity	Nucleotide Diversity	Tajima's D
Red-shafted	0.3630	0.0016	0.0843
Yellow-shafted	0.3979	0.0014	0.1153
Hybrid	0.3115	0.0015	0.6423

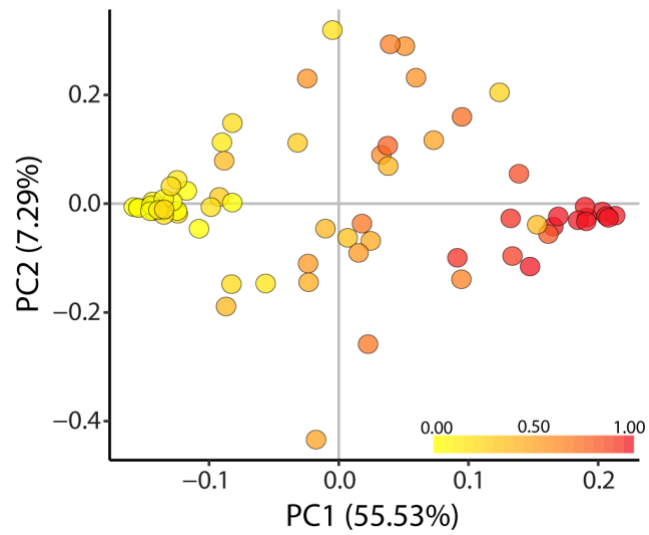
Supplementary Fig. 1 | Distribution of red-shafted and yellow-shafted flickers.
Geographical distribution of the red-shafted and yellow-shafted flickers in North America with the approximate location of the hybrid zone shown in orange.



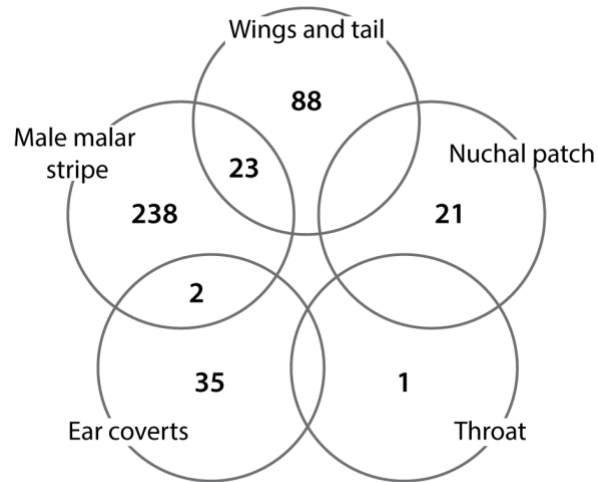
Supplementary Fig. 2 | Additional PC axes. PC3 and PC4 of the principal component analysis (PCA) showing the hybrid flickers (orange points) separating from red-shafted (red points) and yellow-shafted (yellow points) flickers on these axes.



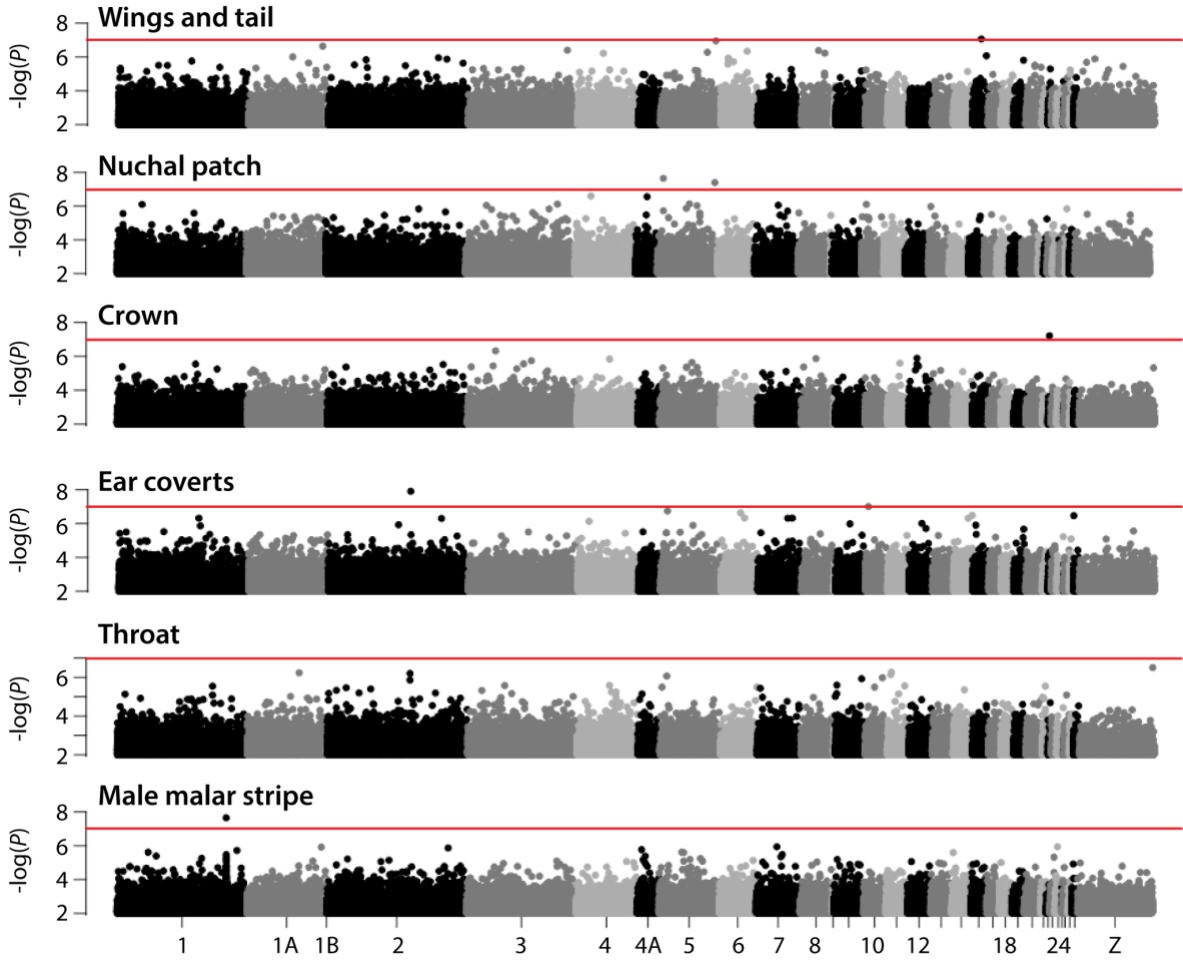
Supplementary Fig. 3 | PCA of fixed SNPs. PCA using 790 fixed SNPs ($F_{ST} = 1$) between allopatric red-shafted and allopatric yellow-shafted flickers with points colored by phenotype score with allopatric samples colored at the ends of the gradient.



Supplementary Fig. 4 | Venn diagram of SNPs identified in the GWAs. Venn diagram showing how individual SNPs identified as significantly associated with coloration traits in the independent GWAs are shared across analyses.



Supplementary Fig. 5 | Associations between genomic SNPs and randomized phenotypes. Results from the GWAs comparing individual SNPs with the six plumage patches after the phenotypes were randomized across individuals. For visualization purposes we show only points with $-\log_{10}(P) > 2$.



Supplementary Fig. 6 | F_{ST} of SNPs identified in the GWAs. Distribution of per-SNP F_{ST} values of SNPs identified as significantly associated with coloration traits in the GWAs.

