

Supplementary information to

Genome-wide patterns of variation in genetic diversity are shared among populations, species and higher order taxa

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Table S1: Overview of the datasets used for the study with population details for each species.

FC=flycatcher, CR=crow, DF=Darwin's finch.

Clade	Populations/Species	Number of individuals	Publication NCBI accession
CR	<i>C. (c.) cornix</i> (Sweden & Poland)	30	Poelstra et.al. 2014 PRJNA192205
	<i>C. (c.) corone</i> (Germany)	15	
	<i>C. (c.) corone</i> (Spain)	15	
	<i>C. (c.) cornix</i> (Bulgaria & Israel)	10	Vijay et.al. 2016 PRJEB9057
	<i>C. (c.) cornix</i> (Italy)	14	
	<i>C. (c.) cornix</i> (Russia)	6	
	<i>C. (c.) cornix</i> x <i>C. (c.) corone</i> hybrids (Ireland)	6	
	<i>C. (c.) cornix</i> x <i>C. (c.) orientalis</i> hybrids (Russia)	6	
	<i>C. (c.) orientalis</i> (Russia Primorsky)	5	
	<i>C. (c.) orientalis</i> (Russia Yakutsk)	3	
<i>C. (c.) pectoralis</i> (Collared crow - Guangxi)	3		
FC	<i>F. albicollis</i> (Czech Republic)	20	Burri et. al. 2015 PRJEB2984
	<i>F. albicollis</i> (Hungary)	20	
	<i>F. albicollis</i> (Italy)	20	
	<i>F. albicollis</i> (Öland)	20	
	<i>F. hypoleuca</i> (Czech Republic)	20	
	<i>F. hypoleuca</i> (Öland)	19	
	<i>F. hypoleuca</i> (Spain)	20	
	<i>F. hypoleuca</i> (Sweden)	20	
	<i>F. semitorquata</i>	20	
	<i>F. speculigera</i>	20	
DF	<i>C. fusca</i> (Espanola)	10	Lamichhaney et al. 2015 PRJNA301892
	<i>C. fusca</i> (San cristobal)	10	
	<i>C. olivacea</i>	5	
	<i>C. pallidus</i>	5	
	<i>G. conirostris</i> (Espanola)	10	
	<i>G. conirostris</i> (Genevosa)	10	
	<i>G. difficilis</i> (Genevosa)	4	
	<i>G. difficilis</i> (Pinta)	10	
	<i>G. difficilis</i> (Wolf)	8	
	<i>P. inornata</i> (Cocos)	8	

Table S2: GC content correlations between the Zebra finch genome and the focal species used in liftOver. Finally chosen parameter settings are highlighted in bold. *Abbreviations:* CR = crow, FC = flycatcher, DF = Darwin's finch.

Clade	minblocks	minmatch	Direct Correlation (r)	Mapped Correlation (r)	Percent recovery
CR	0.40	0.50	0.83	0.82	90.25
	0.40	0.60	0.85	0.82	87.00
	0.40	0.65	0.86	0.83	84.49
	0.40	0.70	0.87	0.83	80.58
	0.40	0.75	0.89	0.87	73.91
	0.40	0.80	0.91	0.87	61.72
	0.40	0.85	0.93	0.86	40.02
	0.40	0.90	0.97	0.86	12.96
FC	0.40	0.50	0.84	0.82	95.74
	0.40	0.60	0.86	0.83	93.40
	0.40	0.65	0.86	0.83	91.65
	0.40	0.70	0.87	0.83	88.83
	0.40	0.75	0.87	0.83	84.36
	0.40	0.80	0.88	0.82	75.82
	0.40	0.85	0.89	0.85	57.47
	0.40	0.90	0.91	0.84	26.05
DF	0.40	0.50	0.93	0.83	93.70
	0.40	0.60	0.94	0.84	92.01
	0.40	0.65	0.95	0.83	90.89
	0.40	0.70	0.95	0.83	89.24
	0.40	0.75	0.95	0.83	87.22
	0.40	0.80	0.96	0.82	83.97
	0.40	0.85	0.96	0.81	78.66
	0.40	0.90	0.96	0.78	67.09

Table S3: Details of the data processing steps for variant calling in each of the studies. CR = crow, FC = flycatcher, DF = Darwin's finch.

Processing step	CR	FC	DF
Quality control	FASTQC & PMDTools	NA	FASTQC
Read mapping	BWA 0.7.8 default settings	BWA 0.7.4 with a soft-clipping base-quality threshold of 5 to avoid low-quality bases in alignments Repeat masking before read mapping	BWA 0.6.2
Duplicate read check	PICARD	PICARD	PICARD
Read group information	Library, lane and sample identity	NA	NA
Variant calling	Below steps done across all crow populations <ul style="list-style-type: none"> Local realignment with GATK Base quality score recalibration (BQSR) Variant discovery for all individuals using HaplotypeCaller using GATK version 3.3.0 Variant quality score recalibration (VQSR) 	<ul style="list-style-type: none"> Local realignment with GATK Below steps are population specific <ul style="list-style-type: none"> Base quality score recalibration (BQSR) Variant quality score recalibration (VQSR) Unified genotype caller 	No population specific steps <ul style="list-style-type: none"> Base quality recalibrations Insertion/deletion (INDEL) realignment SNP and INDEL discovery and genotyping GATK best practice recommendations followed
Quality filtering of the raw variant calls	Variants within repeat regions were removed. Sites that had missing data in more than half the individuals in either population were also excluded.	Variants within repeat regions were removed. Sites that had missing data in more than half the individuals in either population were also excluded.	SNP quality > 100, base quality > 30, mapping quality > 50, haplotype score < 10, Fisher strand bias <60, mapping quality rank sum > -4.0, read position rank sum >

			-2.0, quality by depth > 2.0, minimum depth (summing all 120 samples) > 125, and maximum depth (summing all 120 samples) < 1,875
Phasing /missing data inference	Statistical phasing with fastPHASE with population labels across all crows without including American crow (outgroup species)	Statistical phasing with fastPHASE v1.4.0 <ul style="list-style-type: none"> • All individuals of the four flycatcher species together, sub-population structure was provided as species designation • Coded heterozygous positions with <80% posterior phasing support as missing data 	Inferred separately for each population using BEAGLE
Independent validation	Population genetic statistics were independently estimated using ANGSD and were found to be strongly correlated with estimates obtained using GATK followed by Hierfstat	NA	NA

Table S4: Genome-wide mean estimates of F_{ST} and d_{xy} between populations within clades. *Abbreviations:* CR=crow, FC=flycatcher, DF=Darwin's finch. Consult Vijay et al. (2016) for population sampling in crows, Burri et al. (2015) for flycatchers and Lamichhaney et al. (2015) for Darwin's finches.

Comparison	Mean F_{ST}	Mean d_{xy}	Clade
Bulgaria & Israel vs China (Collared crow)	0.15	0.0018	CR
Bulgaria & Israel vs Russia (Kirov, Tyumen, Novosibirsk)	0.03	0.0015	
Bulgaria & Israel vs Russia (Krasnoyarsky, Tuva)	0.06	0.0016	
Bulgaria & Israel vs Russia (Primorsky)	0.13	0.0017	
Bulgaria & Israel vs Russia (Yakutsk)	0.18	0.0016	
China (Collared crow) vs American crow	0.35	0.0016	
Germany vs <i>C. brachyrhynchos</i>	0.28	0.0016	
Germany vs Bulgaria & Israel	0.03	0.0015	
Germany vs China (Collared crow)	0.14	0.0018	
Germany vs Italy	0.03	0.0015	
Germany vs Russia (Kirov, Tyumen, Novosibirsk)	0.03	0.0015	
Germany vs Russia (Krasnoyarsky, Tuva)	0.06	0.0016	
Germany vs Russia (Primorsky)	0.12	0.0017	
Germany vs Russia (Yakutsk)	0.17	0.0017	
Germany vs Spain	0.1	0.0016	
Italy vs Bulgaria & Israel	0.02	0.0015	
Italy vs China (Collared crow)	0.16	0.0018	
Italy vs Russia (Kirov, Tyumen, Novosibirsk)	0.03	0.0015	
Italy vs Russia (Krasnoyarsky, Tuva)	0.07	0.0016	
Italy vs Russia (Primorsky)	0.14	0.0018	
Italy vs Russia (Yakutsk)	0.18	0.0017	
Poland & Sweden vs Bulgaria & Israel	0.02	0.0015	
Poland & Sweden vs China (Collared crow)	0.15	0.0017	
Poland & Sweden vs Germany	0.02	0.0015	
Poland & Sweden vs Italy	0.02	0.0015	
Poland & Sweden vs Russia (Kirov, Tyumen, Novosibirsk)	0.02	0.0015	
Poland & Sweden vs Russia (Krasnoyarsky, Tuva)	0.06	0.0016	
Poland & Sweden vs Russia (Primorsky)	0.13	0.0017	
Poland & Sweden vs Russia (Yakutsk)	0.16	0.0016	

Poland & Sweden vs Spain	0.14	0.0016	
Poland vs Germany	0.03	0.0015	
Russia (Kirov, Tyumen, Novosibirsk) vs China (Collared crow)	0.15	0.0017	
Russia (Kirov, Tyumen, Novosibirsk) vs Russia (Krasnoyarsky, Tuva)	0.05	0.0016	
Russia (Kirov, Tyumen, Novosibirsk) vs Russia (Primorsky)	0.12	0.0017	
Russia (Kirov, Tyumen, Novosibirsk) vs Russia (Yakutsk)	0.18	0.0016	
Russia (Krasnoyarsky, Tuva) vs American crow	0.33	0.0016	
Russia (Krasnoyarsky, Tuva) vs China (Collared crow)	0.11	0.0017	
Russia (Krasnoyarsky, Tuva) vs Russia (Primorsky)	0.08	0.0017	
Russia (Krasnoyarsky, Tuva) vs Russia (Yakutsk)	0.14	0.0016	
Russia (Primorsky) vs American crow	0.31	0.0016	
Russia (Primorsky) vs China (Collared crow)	0.04	0.0016	
Russia (Primorsky) vs Russia (Yakutsk)	0.16	0.0017	
Russia (Yakutsk) vs American crow	0.49	0.0016	
Russia (Yakutsk) vs China (Collared crow)	0.2	0.0017	
Spain (Pied) vs Czech Republic (Pied)	0.07	0.0033	
Spain vs American crow	0.34	0.0016	
Spain vs Bulgaria & Israel	0.16	0.0016	
Spain vs China (Collared crow)	0.21	0.0018	
Spain vs Italy	0.16	0.0017	
Spain vs Russia (Kirov, Tyumen, Novosibirsk)	0.16	0.0016	
Spain vs Russia (Krasnoyarsky, Tuva)	0.17	0.0017	
Spain vs Russia (Primorsky)	0.2	0.0018	
Spain vs Russia (Yakutsk)	0.26	0.0017	
Sweden vs Bulgaria & Israel	0.02	0.0015	
<i>F. albicollis</i> (Czech Republic) vs <i>F. hypoleuca</i> (Czech Republic)	0.29	0.0048	FC
<i>F. albicollis</i> (Czech Republic) vs <i>F. albicollis</i> (Öland)	0.03	0.0040	
<i>F. hypoleuca</i> (Czech Republic) vs <i>F. hypoleuca</i> (Öland)	0.02	0.0031	
<i>F. albicollis</i> (Hungary) vs <i>F. albicollis</i> (Czech Republic)	0.02	0.0040	
<i>F. albicollis</i> (Hungary) vs <i>F. albicollis</i> (Öland)	0.03	0.0040	
<i>F. albicollis</i> (Hungary) vs <i>F. hypoleuca</i> (Sweden)	0.29	0.0048	
<i>F. albicollis</i> (Italy) vs <i>F. albicollis</i> (Czech Republic)	0.03	0.0040	
<i>F. albicollis</i> (Italy) vs <i>F. albicollis</i> (Hungary)	0.02	0.0040	
<i>F. albicollis</i> (Italy) vs <i>F. albicollis</i> (Öland)	0.04	0.0040	
<i>F. albicollis</i> (Italy) vs <i>F. semitorquata</i>	0.33	0.0050	

<i>F. albicollis</i> (Italy) vs <i>F. hypoleuca</i> (Spain)	0.28	0.0048	
<i>F. albicollis</i> (Öland) vs <i>F. hypoleuca</i> (Öland)	0.31	0.0048	
<i>F. hypoleuca</i> (Spain) vs <i>F. hypoleuca</i> (Öland)	0.06	0.0033	
<i>F. hypoleuca</i> (Spain) vs <i>F. semitorquata</i>	0.4	0.0050	
<i>F. hypoleuca</i> (Sweden) vs <i>F. hypoleuca</i> (Czech Republic)	0.02	0.0031	
<i>F. hypoleuca</i> (Sweden) vs <i>F. hypoleuca</i> (Öland)	0.01	0.0031	
<i>C. fusca</i> (Espanola) vs <i>C. olivacea</i>	0.87	0.0041	DF
<i>C. fusca</i> (Espanola) vs <i>C. pallidus</i>	0.89	0.0044	
<i>C. fusca</i> (Espanola) vs <i>P. inornata</i> (Cocos)	0.9	0.0044	
<i>C. fusca</i> (Espanola) vs <i>G. conirostris</i> (Espanola)	0.8	0.0044	
<i>C. fusca</i> (Espanola) vs <i>G. conirostris</i> (Genevosa)	0.75	0.0044	
<i>C. fusca</i> (Espanola) vs <i>G. difficilis</i> (Genevosa)	0.84	0.0044	
<i>C. fusca</i> (Espanola) vs <i>G. difficilis</i> (Pinta)	0.86	0.0045	
<i>C. fusca</i> (Espanola) vs <i>G. difficilis</i> (Wolf)	0.86	0.0044	
<i>C. fusca</i> (San cristobal) vs <i>C. olivacea</i>	0.71	0.0040	
<i>C. fusca</i> (San cristobal) vs <i>C. pallidus</i>	0.74	0.0043	
<i>C. fusca</i> (San cristobal) vs <i>P. inornata</i> (Cocos)	0.77	0.0043	
<i>C. fusca</i> (San cristobal) vs <i>G. conirostris</i> (Espanola)	0.69	0.0043	
<i>C. fusca</i> (San cristobal) vs <i>G. conirostris</i> (Genevosa)	0.64	0.0043	
<i>C. fusca</i> (San cristobal) vs <i>G. difficilis</i> (Genevosa)	0.67	0.0043	
<i>C. fusca</i> (San cristobal) vs <i>G. difficilis</i> (Pinta)	0.75	0.0044	
<i>C. fusca</i> (San cristobal) vs <i>G. difficilis</i> (Wolf)	0.74	0.0043	
<i>C. olivacea</i> vs <i>C. pallidus</i>	0.79	0.0046	
<i>C. olivacea</i> vs <i>P. inornata</i> (Cocos)	0.83	0.0046	
<i>C. olivacea</i> vs <i>G. conirostris</i> (Espanola)	0.72	0.0046	
<i>C. olivacea</i> vs <i>G. conirostris</i> (Genevosa)	0.66	0.0046	
<i>C. olivacea</i> vs <i>G. difficilis</i> (Genevosa)	0.71	0.0046	
<i>C. olivacea</i> vs <i>G. difficilis</i> (Pinta)	0.79	0.0047	
<i>C. olivacea</i> vs <i>G. difficilis</i> (Wolf)	0.78	0.0046	
<i>C. pallidus</i> vs <i>P. inornata</i> (Cocos)	0.73	0.0028	
<i>C. pallidus</i> vs <i>G. difficilis</i> (Genevosa)	0.49	0.0025	
<i>C. pallidus</i> vs <i>G. difficilis</i> (Pinta)	0.67	0.0029	
<i>C. pallidus</i> vs <i>G. difficilis</i> (Wolf)	0.62	0.0026	
<i>P. inornata</i> (Cocos) vs <i>G. difficilis</i> (Genevosa)	0.61	0.0028	
<i>P. inornata</i> (Cocos) vs <i>G. difficilis</i> (Pinta)	0.72	0.0030	
<i>P. inornata</i> (Cocos) vs <i>G. difficilis</i> (Wolf)	0.7	0.0028	

<i>G. conirostris</i> (Espanola) vs <i>C. pallidus</i>	0.51	0.0026
<i>G. conirostris</i> (Espanola) vs <i>P. inornata</i> (Cocos)	0.6	0.0028
<i>G. conirostris</i> (Espanola) vs <i>G. conirostris</i> (Genevosa)	0.23	0.0022
<i>G. conirostris</i> (Espanola) vs <i>G. difficilis</i> (Genevosa)	0.3	0.0022
<i>G. conirostris</i> (Espanola) vs <i>G. difficilis</i> (Pinta)	0.56	0.0028
<i>G. conirostris</i> (Espanola) vs <i>G. difficilis</i> (Wolf)	0.47	0.0024
<i>G. conirostris</i> (Genevosa) vs <i>C. pallidus</i>	0.38	0.0024
<i>G. conirostris</i> (Genevosa) vs <i>P. inornata</i> (Cocos)	0.52	0.0028
<i>G. conirostris</i> (Genevosa) vs <i>G. difficilis</i> (Genevosa)	0.19	0.0023
<i>G. conirostris</i> (Genevosa) vs <i>G. difficilis</i> (Pinta)	0.49	0.0028
<i>G. conirostris</i> (Genevosa) vs <i>G. difficilis</i> (Wolf)	0.37	0.0024
<i>G. difficilis</i> (Genevosa) vs <i>G. difficilis</i> (Pinta)	0.54	0.0028
<i>G. difficilis</i> (Genevosa) vs <i>G. difficilis</i> (Wolf)	0.44	0.0023
<i>G. difficilis</i> (Pinta) vs <i>G. difficilis</i> (Wolf)	0.62	0.0027

Table S5: Overlap of peaks with peri-centromeric / telomeric regions and list of populations used.

Abbreviations: CR=crow, FC=flycatcher, DF=Darwin's finch.

Clade	Population comparison	Overlap distance	Percent overlap
CR	Spain vs Russia (Primorsky) $F_{ST} = 0.196$	0	21.95
		10000	21.95
		50000	21.95
		100000	21.95
		200000	21.95
		300000	24.39
		400000	26.83
		500000	26.83
	China vs <i>C. brachyrhynchos</i> $F_{ST} = 0.353$	0	31.71
		10000	34.15
		50000	34.15
		100000	34.15
		200000	34.15
		300000	36.59
400000		36.59	
500000		39.02	
FC	<i>F. hypoleuca</i> (Spain) vs <i>F. hyperythra</i> $F_{ST} = 0.960$	0	58.54
		10000	60.98
		50000	60.98
		100000	60.98
		200000	60.98
		300000	60.98
		400000	63.41
		500000	63.4
	<i>F. speculigera</i> vs <i>F. parva</i> $F_{ST} = 0.940$	0	60.98
		10000	65.85
		50000	65.85
		100000	65.85
		200000	65.85
		300000	65.85
400000		65.85	

		500000	65.85
DF	<i>C. fusca</i> (Espanola) vs <i>P. inornata</i> $F_{ST} = 0.897$	0	14.63
		10000	17.07
		50000	17.07
		100000	19.51
		200000	26.83
		300000	34.15
		400000	34.15
		500000	34.15
	<i>C. olivacea</i> vs <i>C. pallidus</i> $F_{ST} = 0.790$	0	29.27
		10000	29.27
		50000	29.27
		100000	29.27
		200000	29.27
		300000	36.59
		400000	36.59
500000		36.59	

Table S6: Correlations within clades for ρ , λ , F_{ST} , PBS and d_{xy} in 50 kb windows. *Abbreviations:* CR=crow, FC=flycatcher, DF=Darwin's finch.

Clade	Statistics	Within/between clade	Minimum	Lower 5%	Mean	Max
CR	ρ	within	-0.023	0.027	0.187	0.572
FC			0.328	0.348	0.432	0.603
DF			0.152	0.161	0.268	0.398
CR	λ	within	0.336	0.479	0.702	0.964
FC			0.908	0.910	0.947	0.997
DF			0.150	0.196	0.493	0.736
CR	F_{ST}	within	0.047	0.077	0.364	0.979
FC			0.012	0.100	0.428	0.994
DF			0.071	0.185	0.462	0.920
CR	PBS	within	0.128	0.171	0.468	0.988
FC			0.110	0.122	0.421	0.984
DF			0.462	0.482	0.643	0.982
CR	d_{xy}	within	0.413	0.539	0.853	0.999
FC			0.498	0.555	0.721	0.990
DF			0.849	0.858	0.937	0.999

Table S7: Correlations between clades for ρ , π , F_{ST} , PBS and d_{xy} in 50 kb windows. *Abbreviations:* CR=crow, FC=flycatcher, DF=Darwin's finch.

Clade	Statistics	Minimum	Lower 5%	Mean	Max
CR vs DF	ρ	0.010	0.025	0.102	0.239
FC vs DF		0.073	0.089	0.172	0.256
CR vs FC		0.008	0.028	0.099	0.192
CR vs DF	π	0.056	0.132	0.204	0.301
FC vs DF		-0.015	-0.011	0.082	0.149
CR vs FC		0.057	0.060	0.271	0.364
CR vs DF	F_{ST}	0.020	0.041	0.163	0.341
FC vs DF		0.078	0.014	0.138	0.287
CR vs FC		0.044	0.038	0.115	0.293
CR vs DF	PBS	0.075	0.108	0.185	0.283
FC vs DF		0.091	0.122	0.231	0.353
CR vs FC		0.136	0.150	0.223	0.361
CR vs DF	d_{xy}	0.087	0.197	0.268	0.387
FC vs DF		0.100	0.160	0.224	0.306
CR vs FC		0.089	0.131	0.342	0.454

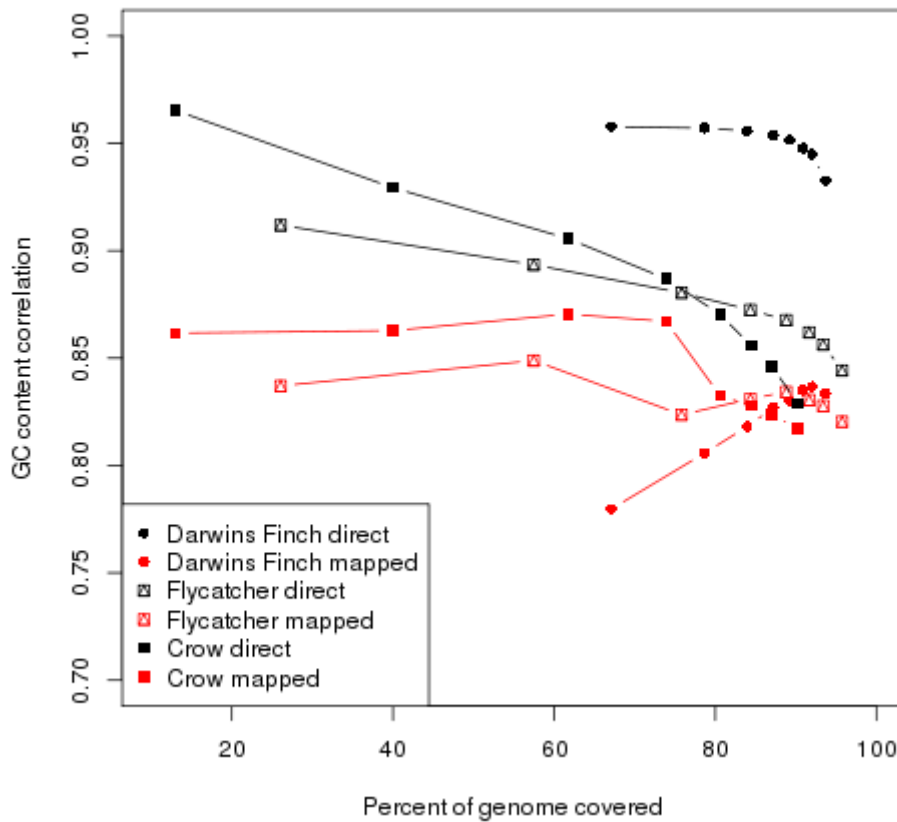


Fig. S1: Pearson's correlation coefficients of GC content between focal species and zebra finch plotted in relationship to the fraction of the genome recovered after liftover. 'Direct' refers to the correlation between the original 50kb windows of the focal species with the new, orthologous positions successfully lifted over to the Zebra Finch genome. 'Mapped' refers to comparisons of GC content from the focal genome with fixed windows of the same size in orthologous coordinates of the zebra finch genome. This value is expected to be lower since it represents the mean of original, potentially overlapping regions in the new windows. Each single point reflects the combination of parameter settings controlling stringency ('minmatch') and cohesion ('minblocks').

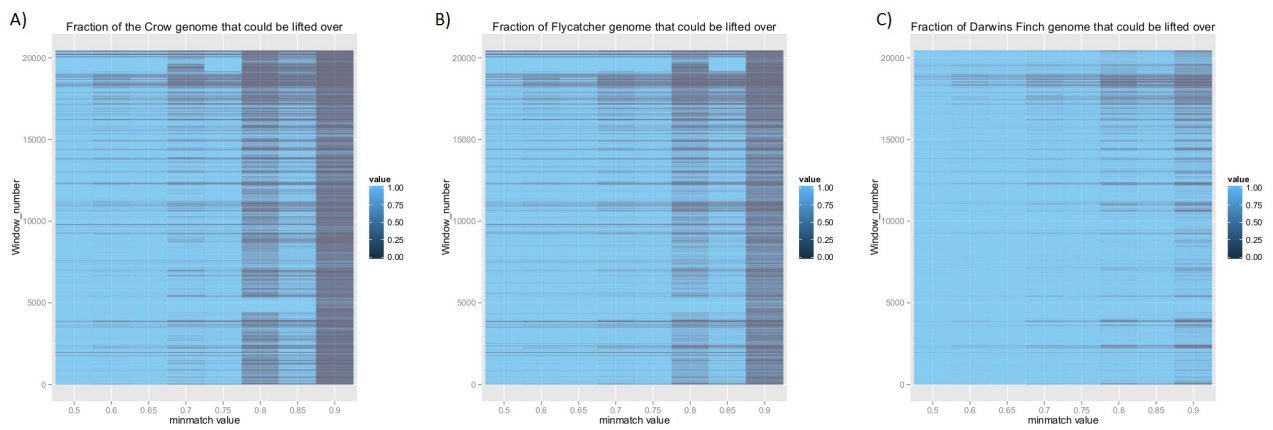


Fig. S2: Fraction of the windows along each genome that were successfully lifted over from each focal species to the Zebra Finch genome as a function of stringency ('minmatch') liftOver parameter. A) Crow B) Flycatcher C) Darwin's Finch.

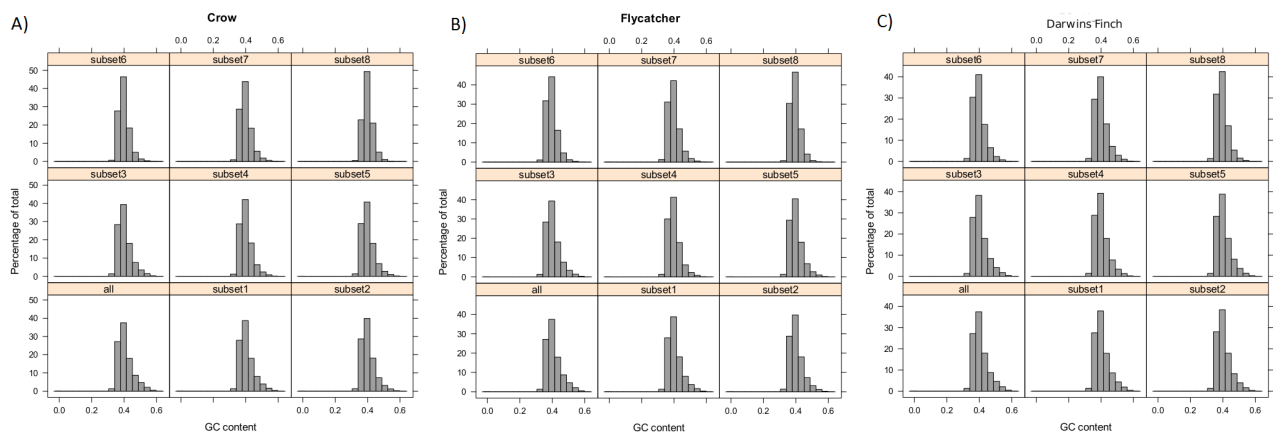


Fig. S3: Distribution of GC content of Zebra Finch genome in 50Kb windows for different subsets of the genome that could be successfully lifted over. A) Crow B) Flycatcher C) Darwin's Finch.

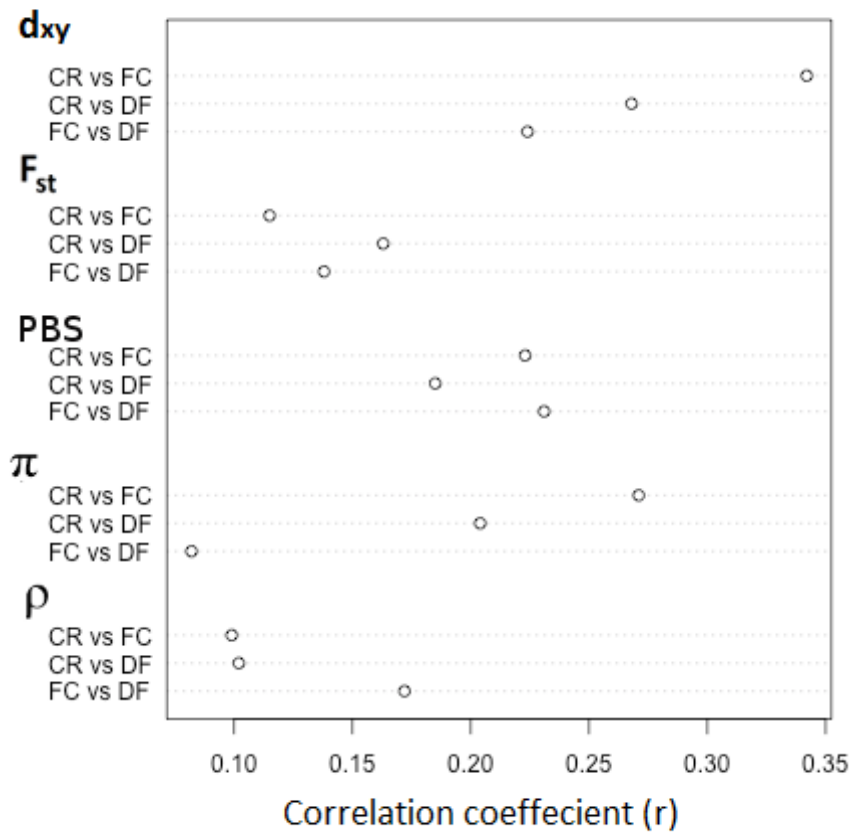


Fig. S4. Mean Pearson's correlation coefficients for population comparisons among clades shown for d_{xy} , F_{ST} , PBS, π and ρ . *Abbreviations:* CR=crow, FC=flycatcher, DF=Darwin's finch. Estimated age of divergence CR vs FC/DF 25-50 mya, FC vs. DF 19-45 mya depending on source (see Methods).

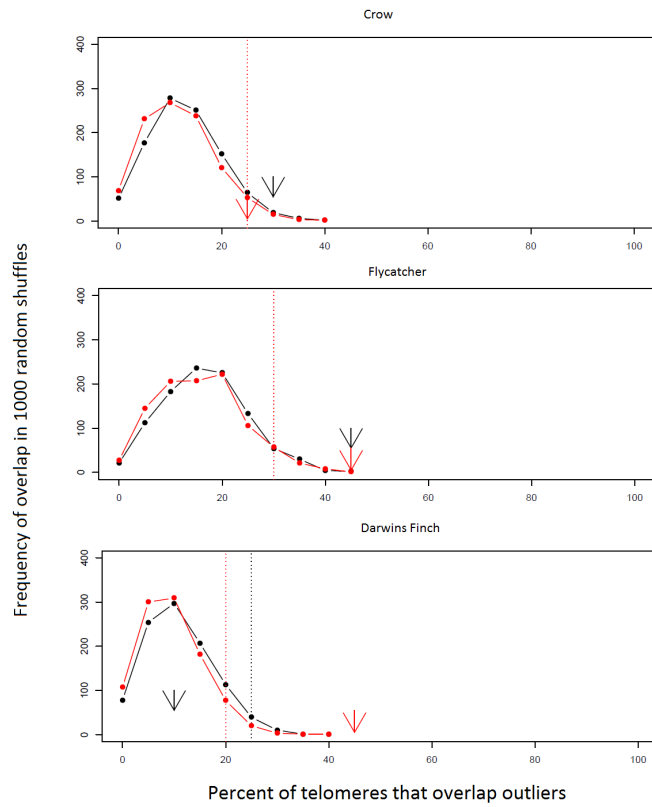


Fig. S5: The degree of overlap between regions of elevated differentiation with combined set of regions adjacent to sub-telomeric regions is quantified for two selected population pairs (red and black arrows) from each taxon. The distributions of random expectation as assessed by permutation for these population pairs are shown in the same colours. The dotted line to the right side are the 95% quantile of the distribution.

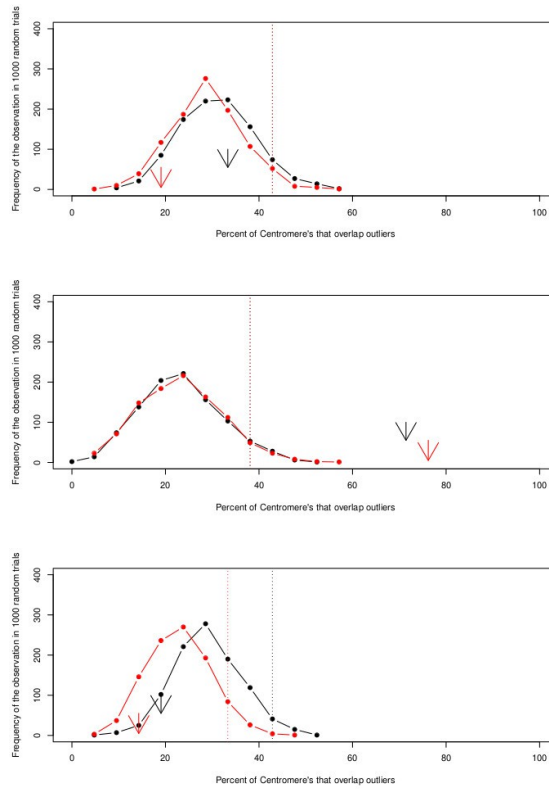


Fig. S6: The degree of overlap between regions of elevated differentiation with combined set of regions adjacent to peri-centromeric regions is quantified for two selected population pairs (red and black arrows) from each taxon. The distributions of random expectation as assessed by permutation for these population pairs are shown in the same colours. The dotted line to the right side are the 95% quantile of the distribution.