

Supplementary Material

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Supplementary Tables

Supplementary Table 1: List of 29 genes surveyed, organized by step in the meiotic recombination pathway. Adapted from Table 1 in Dapper and Payseur (2019).

Gene	Complex	Function	Direct Interactions	Citation
(A) Double strand break formation				
<i>HORMAD1</i>		Associates with unsynapsed chromosomes, required for accumulation of MCD recombisomes	<i>IHO1</i>	Fukuda et al. (2010)
<i>MEI4</i>	MCD Recombinosome	Component of a complex that promotes DSB formation by activating SPO11	<i>REC114</i>	Kumar et al. (2010)
<i>REC114</i>	MCD Recombinosome	Component of a complex that promotes DSB formation by activating SPO11	<i>MEI4, IHO1</i>	Kumar et al. (2018)
<i>IHO1</i>	MCD Recombinosome	Component of a complex that promotes DSB formation by activating SPO11	<i>REC114, HORMAD1</i>	Stanzione et al. (2016)
<i>SPO11</i>		Generates double strand breaks		Romanienko and Camerini-Otero (2000)
(B) Double strand break processing				
<i>HORMAD2</i>		Associates with unsynapsed chromosomes, detects chromosome asynapsis		
<i>MRE11</i>	MRN complex	Part of complex that processes newly formed DSB, trims off SPO11	<i>NBS1, RAD50</i>	Stracker and Petrini (2011)
<i>NBS1</i>	MRN complex	Part of complex that processes newly formed DSB, responsible for nuclear localization of the complex	<i>MRE11, RAD50</i>	Oh et al. (2016)
<i>RAD50</i>	MRN complex	Part of complex that processes newly formed DSB, holds broken DNA ends together	<i>NBS1, MRE11</i>	Lamarche et al. (2010)
<i>BRCC3</i>		Involved in DNA repair		Dumont and Payseur (2011)
(C) Homology search and strand invasion				
<i>DMC1</i>		Mediates/catalyzes homologous chromosome pairing	<i>RAD51</i>	Tarsounas et al. (1999)
<i>RAD51</i>		Mediates/catalyzes homologous chromosome pairing	<i>DMC1</i>	Cloud et al. (2012)
<i>SPATA22</i>		Required for the completion of strand invasion	<i>MEIOB</i>	Xu et al. (2017)
<i>MEIOB</i>		Required for the completion of strand invasion	<i>SPATA22</i>	Luo et al. (2013)
<i>MCMD2</i>		Required for the formation or stabilization of DNA strand invasion events		Finsterbusch et al. (2016)
(D) Synapsis				
<i>REC8</i>	Cohesion complex	Maintains sister-chromatid cohesion		Xu et al. (2005)
<i>RAD21L</i>	Cohesion complex	Maintains sister-chromatid cohesion, initiates synapsis		Lee and Hirano (2011)
<i>SYCP1</i>	Synaptonemal complex	Binds homologous chromosomes, transverse filament	<i>SYCP2</i>	de Vries et al. (2005)
<i>SYCP2</i>	Synaptonemal complex	Binds homologous chromosomes, lateral element	<i>SYCP1, TEX11</i>	Winkel et al. (2009)
<i>TEX12</i>	Synaptonemal complex	Binds homologous chromosomes, central element		Hamer et al. (2006)
(E) Crossover/non-crossover decision				
<i>TEX11</i>		Required for the recruitment of proteins that designate crossovers	<i>SYCP2, SHOC1</i>	Yang et al. (2008)
<i>SHOC1</i>		Required for the recruitment of proteins that designate crossovers	<i>TEX11</i>	Guiraldelli et al. (2018)
<i>RNF212</i>		Selectively localizes to a subset of DSB, stabilizing MSH4/MSH5	<i>mutS Complex</i>	Reynolds et al. (2013)
<i>MSH4</i>	mutS complex	Localizes to a subset of DSB, regulating crossover number	<i>MSH5</i>	Santucci-Darmanin et al. (2000)
<i>MSH5</i>	mutS complex	Localizes to a subset of DSB, regulating crossover number	<i>MSH4</i>	de Vries et al. (1999)
(F) Resolution				
<i>HFM1/MER3</i>		Required for correct localization of MLH1 and crossover formation		Guiraldelli et al. (2013)
<i>CNTD1</i>		Required crossover maturation and recruitment of MLH1/MLH3	<i>mutL Complex</i>	Holloway et al. (2014)
<i>MLH1</i>	mutL complex	Mismatch repair gene that localizes to and resolves crossovers	<i>MLH3</i>	Baker et al. (1996)
<i>MLH3</i>	mutL complex	Mismatch repair gene that localizes to and resolves crossovers	<i>MLH1</i>	Lipkin et al. (2002)

Supplementary Table 2: NCBI Reference Bird Genomes

Species	Assembly	RefSeq Accession	WGS Project Reference
<i>Anas platyrhynchos</i>	ZJU1.0	GCF_015476345.1	(Li et al. 2021)
<i>Anser cygnoides domesticus</i>	AnsCyg_PRJNA183603_v1.0	GCF_000971095.1	(Lu et al. 2015)
<i>Apteryx rowi</i>	aptRow1	GCF_003343035.1	(Sackton et al. 2019)
<i>Aquila chrysaetos chrysaetos</i>	bAquChr1.4	GCF_900496995.4	(Institute 2021)
<i>Athene cucularia</i>	athCun1	GCF_003259725.1	(Mueller et al. 2018)
<i>Calidris pugnax</i>	ASM143184v1	GCF_001431845.1	(Andersson et al. 2015)
<i>Camarhynchus parvulus</i>	STF_HiC	GCF_901933205.1	(Enbody and Pettersson 2022)
<i>Catharus ustulatus</i>	bCatUst1.pri.v2	GCF_009819885.2	(Delmore et al. 2020)
<i>Columba livia</i>	Cliv_2.1	GCA_000337935.2	(Shapiro et al. 2013)
<i>Corvus moneduloides</i>	bCorMon1.pri	GCF_009650955.1	(Rutz et al. 2019)
<i>Coturnix japonica</i>	Coturnix japonica 2.1	GCF_001577835.2	(Rutz et al. 2019)
<i>Cyanistes caeruleus</i>	cyaCae2	GCF_002901205.1	(Mueller et al. 2016)
<i>Dromolus novaehollandiae</i>	droNov1	GCF_003342905.1	(Sackton et al. 2019)
<i>Ficedula albicollis</i>	FicAlb1.5	GCF_000247815.1	(Ellegren et al. 2012)
<i>Gallus gallus</i>	bGalGal1.mat.broiler.GRCg7b	GCF_016699485.2	(Warren et al. 2022)
<i>Hirundo rustica</i>	bHirRus1.pri.v3	GCF_015227805.2	(Secomandi et al. 2021)
<i>Lepidothrix coronata</i>	Lepidothrix_coronata-1.0	GCF_001604755.1	(Warren et al. 2016)
<i>Lonchura striata domestica</i>	lonStrDom2	GCF_005870125.1	(Mets et al. 2019)
<i>Meleagris gallopavo</i>	Turkey_5.1	GCF_000146605.3	(Dalloul et al. 2010)
<i>Melospittacus undulatus</i>	bMelUnd1.mat.Z	GCF_012275295.1	(Gedman et al. 2020)
<i>Motacilla alba alba</i>	Motacilla_alba_V1.0_pri	GCF_015832195.1	(Enbody et al. 2020)
<i>Nothoprocta perdicaria</i>	notPer1	GCF_003342845.1	(Sackton et al. 2019)
<i>Numida meleagris</i>	NumMel1.0	GCF_002078875.1	(Vignal and Warren 2017)
<i>Parus major</i>	Parus_major1.1	GCF_001522545.3	(Laine et al. 2016)
<i>Phasianus colchicus</i>	ASM414374v1	GCF_004143745.1	(Wang 2019)
<i>Serinus canaria</i>	cibio_Scana_2019	GCF_007115625.1	(Gazda et al. 2019)
<i>Strigops habroptila</i>	bStrHab1.2.pri	GCF_004027225.2	(Rhie et al. 2021)
<i>Struthio camelus australis</i>	ASM69896v1	GCF_000698965.1	(Zhang et al. 2014)
<i>Taeniopygia guttata</i>	bTaeGut1.4.pri	GCF_003957565.2	(Rhie et al. 2021; Formenti et al. 2021)

Supplementary Table 3: Evolutionary rates and tests for positive selection in mammals. Previously published in Dapper and Payseur (2019).

Gene	bp	N	ω	M	M1-M2	p-value	M7-M8	p-value	M8a-M8	p-value	BEB
(A) DSB formation											
<i>HORMAD1</i>	1212	16	0.3036	7	0	1.000	1.795	0.4076	—	—	0
<i>MEI4</i>	1170	16	0.4332	7	0	1.000	0.005	0.9976	—	—	0
<i>REC114</i>	870	15	0.4003	7	0	1.000	5.384	0.0677	—	—	0
<i>IHO1</i>	1824	16	0.7095	8	13.061	0.0015	17.571	0.0002	14.527	0.0001	1
<i>SPO11</i>	1188	15	0.1654	7	0	1.000	4.648	0.0980	—	—	0
(B) DSB processing											
<i>HORMAD2</i>	981	15	0.3153	7	0	1.000	3.650	0.1612	—	—	0
<i>MRE11</i>	2136	16	0.1688	8	0.363	0.8342	11.931	0.0026	4.706	0.0301	0
<i>NBS1</i>	2289	15	0.4183	8	0	1.000	12.763	0.0017	4.087	0.0432	0
<i>RAD50</i>	3936	16	0.1006	7	0	1.000	0.301	0.8605	—	—	0
<i>BRCC3</i>	954	15	0.0602	7	0	1.000	0.250	0.8826	—	—	0
(C) Homology search and strand invasion											
<i>DMC1</i>	1020	15	0.0351	1	0.488	0.7835	5.000	0.0821	—	—	1
<i>RAD51</i>	1017	16	0.0268	7	0	1.000	0	1.000	—	—	0
<i>SPATA22</i>	1101	16	0.4893	7	0	1.000	0.429	0.8070	—	—	0
<i>MEIOB</i>	1425	16	0.2341	7	0	1.000	0.665	0.7172	—	—	0
<i>MCMDC2</i>	2052	16	0.2239	7	0	1.000	0.628	0.7307	—	—	0
(D) Synapsis											
<i>REC8</i>	1833	16	0.3698	8	0	1.000	14.690	0.0006	5.927	0.0149	0
<i>RAD21L</i>	1686	15	0.503	8	12.124	0.0023	32.050	>0.0001	12.049	0.0005	4
<i>SYCP1</i>	3015	16	0.4337	8	8.711	0.0128	26.860	>0.0001	9.243	0.0024	3
<i>SYCP2</i>	4650	16	0.5572	8	11.584	0.0031	37.200	>0.0001	15.838	0.0001	0
<i>TEX12</i>	369	14	0.2297	7	0.0565	0.9721	1.549	0.4610	—	—	0
(E) CO/NCO decision											
<i>TEX11</i>	2844	15	0.8483	8	60.872	>0.0001	82.665	>0.0001	61.141	>0.0001	14
<i>SHOC1</i>	4644	16	0.6113	8	12.447	0.0020	30.561	>0.0001	15.645	0.0001	0
<i>RNF212</i>	948	16	0.5014	8	0	1.000	16.366	0.0003	5.202	0.0226	1
<i>RNF212B</i>	906	14	0.4066	7	0	1.000	0.500	0.7788	—	—	0
<i>MSH4</i>	2814	16	0.2132	8	16.608	0.0002	39.447	>0.0001	23.238	>0.0001	6
<i>MSH5</i>	2565	15	0.1642	7	0	1.000	4.214	0.1216	—	—	0
(F) Resolution											
<i>MER3</i>	4458	16	0.3633	8a	0	1.000	12.838	0.0016	3.109	0.0779	0
<i>CNTD1</i>	1026	15	0.2496	7	0	1.000	0.936	0.6263	—	—	0
<i>HEI10</i>	831	15	0.1226	7	0	1.000	0.250	0.8826	—	—	0
<i>MLH1</i>	2313	15	0.1652	8a	0	1.000	12.221	0.0022	0.280	0.5970	0
<i>MLH3</i>	4419	16	0.4444	7	0	1.000	3.757	0.1528	—	—	0
<i>MUS81</i>	1665	16	0.2124	7	0	1.000	0.628	0.7304	—	—	0

Supplementary Table 4: NCBI Reference Fish Genomes

Species	Assembly	RefSeq Accession	WGS Project Reference
<i>Amphiprion ocellaris</i>	AmpOce1.0	GCF_002776465.1	(Tan et al. 2017)
<i>Astyanax mexicanus</i>	Astyanax_mexicanus-2.0	GCF_000372685.2	(Rohner and Warren 2019)
<i>Boleophthalmus pectinirostris</i>	BP.fa	GCF_000788275.1	(You et al. 2014)
<i>Chanos chanos</i>	fChaCha1.1	GCF_902362185.1	(Wellcome Sanger Institute 2019a)
<i>Clupea harengus</i>	Ch_v2.0.2	GCF_900700415.2	(Pettersson 2019)
<i>Cynoglossus semilaevis</i>	Cse_v1.0	GCF_000523025.1	(Chen et al. 2014)
<i>Cyprinodon variegatus</i>	C_variegatus-1.0	GCF_000732505.1	(Warren and Nacci 2014)
<i>Danio rerio</i>	GRCz11	GCF_00002035.6	(Howe et al. 2013)
<i>Electrophorus electricus</i>	fEleEle1.pri	GCF_013358815.1	(Myers et al. 2020b)
<i>Esox lucius</i>	fEsoLuc1.pri	GCF_011004845.1	(Myers et al. 2020a)
<i>Gadus morhua</i>	gadMor3.0	GCF_902167405.1	(Wellcome Sanger Institute 2019b)
<i>Gouania wilidenowi</i>	fGouWii2.1	GCF_900634775.1	(Institute" 2019)
<i>Haplochromis burtoni</i>	NCSU_Asbu1	GCF_018398535.1	(Peterson et al. 2021)
<i>Hippocampus comes</i>	H_comes_QL1_v1.1	GCF_001891065.2	(Lin 2022)
<i>Ictalurus punctatus</i>	IpCoco_1.2	GCF_001660625.2	(Liu et al. 2016)
<i>Mastacembelus armatus</i>	fMasArm1.2	GCF_900324485.2	(Wellcome Sanger Institute 2019c)
<i>Myripristis murdjan</i>	fMyrMur1.1	GCF_902150065.1	(Wellcome Sanger Institute 2019d)
<i>Oncorhynchus mykiss</i>	USDA_Omyka_1.1	GCF_013265735.2	(Gao et al. 2021)
<i>Oreochromis niloticus</i>	O_niloticus_UMD_NMBU	GCF_001858045.2	(Conte et al. 2017)
<i>Oryzias melastigma</i>	ASM292280v2	GCF_002922805.2	(Kim et al. 2018)
<i>Pygocentrus nattereri</i>	fPygNat1.pri	GCF_015220715.1	(Myers et al. 2020c)
<i>Salmo salar</i>	Ssal_v3.1	GCF_905237065.1	(Nome and Gillard 2022)
<i>Sceloporus formosus</i>	fSciFor1.1	GCF_900964775.1	(Wellcome Sanger Institute 2019e)
<i>Takifugu rubripes</i>	fTakRub1.2	GCF_901000725.2	(Wellcome Sanger Institute 2019f)

Supplementary Table 5: Evolutionary rates and tests for positive selection in teleost fish.

Gene	bp	N	ω	M	M1-M2	p-value	M7-M8	p-value	M8a-M8	p-value	BEB
(A) DSB formation											
<i>HORMAD1</i>	1657	22	0.2188	7	0	1	1.715	4.243e-1	—	—	—
<i>MEI4</i>	1345	22	0.3425	7	0	1	0.573	7.507e-1	—	—	—
<i>REC114</i>	786	24	0.2984	7	0	1	0	1	—	—	—
<i>IHO1</i>	542	21	0.3602	7	0	1	1.514	4.690e-1	—	—	—
<i>SPO11</i>	1588	24	0.1962	7	0	1	3.453	1.779e-1	—	—	—
(B) DSB processing											
<i>HORMAD2</i>	305	24	0.1763	7	0	1	0	1	—	—	—
<i>MRE11</i>	700	24	0.1244	7	0	1	5.245	7.264e-2	—	—	—
<i>NBS1</i>	2457	23	0.2417	7	0	1	0.719	6.979e-1	—	—	—
<i>RAD50</i>	4123	24	0.1101	8	0	1	17.423	1.647e-4	23.606	>0.0001	0
<i>BRCC3</i>	2951	23	0.0451	7	0	1	2.656	0.265	—	—	—
(C) Homology search and strand invasion											
<i>DMC1</i>	1324	22	0.0572	8	0	1	57.485	>0.0001	4.556	3.281e-2	0
<i>RAD51</i>	1380	18	0.0272	8a	0	1	10.626	4.928e-3	3.636	5.653e-2	—
<i>SPATA22</i>	3072	24	0.2907	8a	0	1	6.203	4.498e-2	1.593	2.069e-1	—
<i>MEIOB</i>	2417	23	0.2088	7	0	1	0	1	—	—	—
<i>MCMDC2</i>	2608	24	0.2043	8a	0	1	19.179	6.845e-5	1.230	2.674e-1	—
(D) Synapsis											
<i>REC8</i>	564	23	0.3072	7	0	1	1.122	5.707e-1	—	—	—
<i>RAD21L</i>	2209	23	0.2409	7	0	1	1.920	3.829e-1	—	—	—
<i>SYCP1</i>	3579	23	0.2907	7	0	1	4.397	1.110e-1	—	—	—
<i>SYCP2</i>	1616	16	0.2997	7	0	1	2.593	2.735e-1	—	—	—
(E) CO/NCO decision											
<i>TEX11</i>	3181	21	0.2217	8a	0	1	11.604	3.021e-3	1.514	2.185e-1	—
<i>SHOC1</i>	305	14	0.3952	8a	0	1	36.591	1.133e-8	0	1	—
<i>RNF212</i>	1372	21	0.2336	7	0	1	0	1	—	—	—
<i>MSH4</i>	2654	22	0.1130	7	0	1	0.335	8.457e-1	—	—	—
<i>MSH5</i>	2779	21	0.1716	8a	0	1	20.329	3.9e-5	2.984	8.409e-2	—
(F) Resolution											
<i>MER3</i>	3705	23	0.1788	7	0	1	0	1	—	—	—
<i>CNTD1</i>	966	23	0.2901	7	0	1	1.507	4.706e-1	—	—	—
<i>MLH1</i>	2407	24	0.0856	7	0	1	2.681	2.618e-1	—	—	—
<i>MLH3</i>	3656	24	0.1865	7	0	1	0	1	—	—	—

Supplementary Table 6: Combined evolutionary rates and model of best fit for mammals, birds, and teleost fish.

Gene	Mammal Omega	Mammal Model	Bird Omega	Bird Model	Fish Omega	Fish Model
(A) DSB formation						
<i>HORMAD1</i>	0.3036	7	0.1896	7	0.2188	7
<i>MEI4</i>	0.4432	7	0.4446	8	0.3425	7
<i>REC114</i>	0.4003	7	0.3402	8	0.2984	7
<i>IHO1</i>	0.7095	8	0.4641	8	0.3602	7
<i>SPO11</i>	0.1654	7	0.2981	8	0.1962	7
(B) DSB processing						
<i>HORMAD2</i>	0.3153	7	0.2904	7	0.1763	7
<i>MRE11</i>	0.1688	8	0.2445	8	0.1244	7
<i>NBS1</i>	0.4183	8	0.4453	8	0.2417	7
<i>RAD50</i>	0.1006	7	0.1724	8a	0.1101	8
<i>BRCC3</i>	0.0602	7	0.0137	7	0.0451	7
(C) Homology search and strand invasion						
<i>DMC1</i>	0.0351	1	0.034	7	0.0572	8
<i>RAD51</i>	0.0268	7	0.0191	7	0.0272	8a
<i>SPATA22</i>	0.4893	7	0.5132	8	0.2907	8a
<i>MEIOB</i>	0.2341	7	0.2094	8a	0.2088	7
<i>MCMD2</i>	0.2239	7	0.2066	7	0.2043	8a
(D) Synapsis						
<i>REC8</i>	0.3698	8	0.1391	8	0.3072	7
<i>RAD21L</i>	0.503	8	0.4658	8	0.2409	7
<i>SYCP1</i>	0.4337	8	0.4472	8	0.2907	7
<i>SYCP2</i>	0.5572	8	0.5487	8	0.2997	7
<i>TEX12</i>	0.2297	7	0.4182	7	-	-
(E) CO/NCO decision						
<i>TEX11</i>	0.8483	8	0.3152	8	0.2217	8a
<i>SHOC1</i>	0.6113	8	0.5778	8	0.3952	8a
<i>RNF212</i>	0.5014	8	0.5242	8	0.2336	7
<i>MSH4</i>	0.2132	7	0.2041	8	0.113	7
<i>MSH5</i>	0.1642	8	0.2441	8	0.1716	8a
<i>HFM1/MER3</i>	0.3633	7	0.3727	8	0.1788	7
(F) Resolution						
<i>CNTD1</i>	0.2496	7	0.3021	8	0.2901	7
<i>MLH1</i>	0.1652	8a	0.1754	8a	0.0856	7
<i>MLH3</i>	0.4444	7	0.4378	8	0.1865	7

Supplementary Table 7: Evolutionary rates and tests for positive selection across birds at recombination genes after removal of potential MNM sites.

Gene	bp	N	omega	M	M1-M2	P	M7-M8	P	M8a-M8	P	BEB
<i>MEI4</i>	1724	29	0.4451	8	10.791	0.0045	14.786536	0.0006	6.999	0.0082	1
<i>REC114</i>	1776	29	0.3020	8	0	1.0000	14.17213	0.0008	4.936	0.0263	1
<i>IHO1</i>	3133	24	0.4641	8	9.767	0.0076	17.288	0.0002	10.088	0.0015	1
<i>SPO11</i>	3525	29	0.2981	8	14.256	0.0008	30.404	<0.0001	16.258	0.0001	4
<i>MRE11</i>	2103	28	0.2385	8	0	1.0000	22.494354	<0.0001	7.750	0.0054	1
<i>NBS1</i>	2533	29	0.4441	8a	0	1.0000	15.193354	0.0005	3.192	0.0740	0
<i>SPATA22</i>	2398	29	0.5030	8	12.062	0.0024	21.499556	<0.0001	15.150	0.0001	3
<i>REC8</i>	2571	29	0.1391	8	17.211	0.0002	37.628	<0.0001	22.989	<0.0001	6
<i>RAD21L</i>	2906	29	0.4337	8	0	1.0000	10.594238	0.0050	4.778	0.0288	0
<i>SYCP1</i>	3577	26	0.4472	8	21.222	<0.0001	47.481	<0.0001	17.056	<0.0001	6
<i>SYCP2</i>	5508	26	0.5309	8	22.423	<0.0001	65.897896	<0.0001	31.662	<0.0001	4
<i>TEX11</i>	4555	29	0.3152	8	17.872	0.0001	41.211	<0.0001	12.249	0.0005	3
<i>SHOC1</i>	7924	29	0.5508	8	33.225	<0.0001	67.399394	<0.0001	44.382	<0.0001	12
<i>RNF212</i>	3074	29	0.5242	8	12.592	0.0018	17.743	0.0001	17.004	<0.0001	4
<i>MSH4</i>	3167	28	0.2041	8	21.487	<0.0001	57.911	<0.0001	22.879	<0.0001	4
<i>MSH5</i>	5681	29	0.1864	8a	2.180	0.3362	12.329216	0.0021	3.600	0.0578	0
<i>HFM1/MER3</i>	8134	29	0.3656	8	22.639	<0.0001	47.277202	<0.0001	32.456	<0.0001	1
<i>CNTD1</i>	3168	29	0.2386	7	0	1.0000	1.779072	0.4108	-	-	0
<i>MLH3</i>	5051	29	0.4640	8	31.062	<0.0001	68.60557	<0.0001	38.745	<0.0001	11

Supplementary Table 8: Evolutionary rates and tests for positive selection across mammals at recombination genes after removal of potential MNM sites.

Gene	bp	N	omega	M	M1-M2	P	M7-M8	P	M8a-M8	P	BEB
<i>IHO1</i>	1824	16	0.7100	8	13.065	0.0015	17.49	0.0002	14.513526	0.0001	1
<i>MRE11</i>	2136	16	0.1687	8	0	1.0000	11.931	0.0026	4.673254	0.0306	0
<i>MSH4</i>	2814	16	0.2131	8	16.611	0.0002	39.451	<0.0001	23.24	<0.0001	6
<i>NBS1</i>	2289	15	0.4186	8	0	1.0000	13.025	0.0015	4.036	0.0445	0
<i>RAD21L</i>	1686	15	0.5023	8	12.407	0.0020	32.908	<0.0001	12.544	0.0004	4
<i>REC8</i>	1833	16	0.3690	8	0	1.0000	14.727	0.0006	5.917	0.0150	0
<i>RNF212</i>	948	16	0.4058	7	0	1.0000	0.357	0.8370	-	-	0
<i>SHOC1</i>	4644	16	0.6128	8	12.652	0.0018	30.691	<0.0001	15.837	<0.0001	0
<i>SYCP1</i>	3015	16	0.4322	8	8.871	0.0119	26.905	<0.0001	9.399	0.0022	3
<i>SYCP2</i>	4650	16	0.5553	8	11.147	0.0038	36.585	<0.0001	15.471	<0.0001	0
<i>TEX11</i>	2844	15	0.8481	8	60.798	<0.0001	82.532	<0.0001	61.061	<0.0001	14

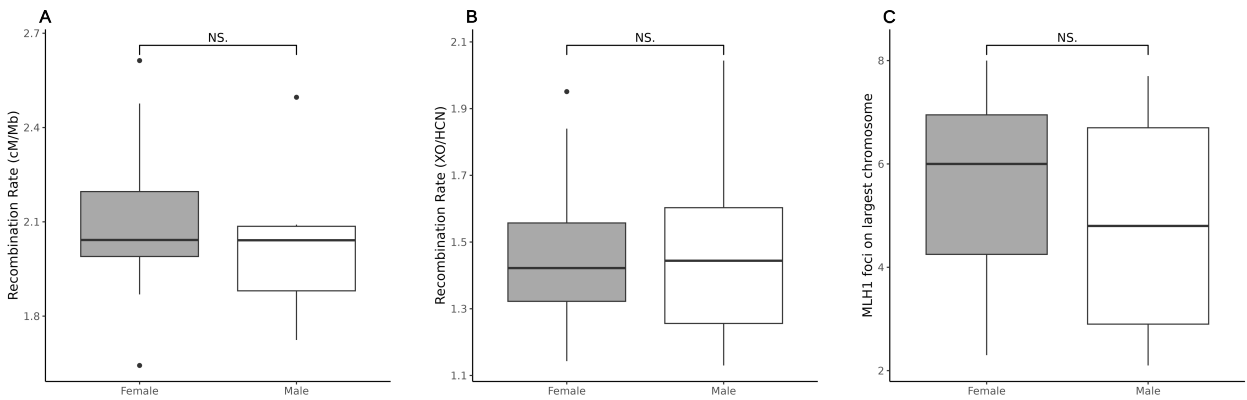
Supplementary Table 9: Correlations between substitution rate and recombination rate, measured as XO/HCN across 7 species of birds for 29 recombination genes. Posterior probabilities are given in parenthesis.

Gene	Correlation coefficient			Partial correlation coefficient		
	dS - ω	dS - XO/HCN	ω - XO/HCN	dS - ω	dS - XO/HCN	ω - XO/HCN
(A) DSB formation						
<i>HORMAD1</i>	0.274 (0.66)	-0.538 (0.18)	-0.492 (0.20)	0.115 (0.58)	-0.343 (0.28)	-0.298 (0.30)
<i>MEI4</i>	0.134 (0.58)	0.466 (0.81)	0.17 (0.61)	0.137 (0.59)	0.287 (0.70)	0.107 (0.57)
<i>REC114</i>	-0.109 (0.42)	-0.00443 (0.51)	0.125 (0.58)	-0.0549 (0.47)	0.00215 (0.50)	0.113 (0.57)
<i>IHO1</i>	0.476 (0.80)	-0.072 (0.43)	0.133 (0.58)	0.572 (0.84)	-0.116 (0.41)	0.193 (0.62)
<i>SPO11</i>	-0.312 (0.31)	0.362 (0.81)	-0.0936 (0.42)	-0.328 (0.30)	0.191 (0.65)	0.0152 (0.51)
(B) DSB processing						
<i>HORMAD2</i>	0.0162 (0.50)	-0.208 (0.30)	0.0413 (0.51)	0.0863 (0.55)	-0.121 (0.40)	0.0616 (0.53)
<i>MRE11</i>	-0.0489 (0.47)	0.181 (0.61)	0.016 (0.51)	-0.0132 (0.49)	0.113 (0.58)	0.0101 (0.50)
<i>NBS1</i>	0.518 (0.82)	0.472 (0.87)	0.361 (0.77)	0.527 (0.83)	0.209 (0.65)	0.114 (0.57)
<i>RAD50</i>	-0.574 (0.14)	0.663 (0.97)	-0.415 (0.21)	-0.458 (0.21)	0.407 (0.80)	-0.0876 (0.44)
<i>BRCC3</i>	0.0205 (0.51)	0.39 (0.73)	0.101 (0.55)	0.00663 (0.50)	0.239 (0.66)	0.0616 (0.54)
(C) Homology search and strand invasion						
<i>DMC1</i>	-0.0263 (0.48)	-0.0554 (0.46)	-0.000482 (0.50)	-0.0157 (0.48)	-0.033 (0.47)	-0.000285 (0.50)
<i>RAD51</i>	-0.189 (0.40)	-0.735 (0.088)	0.148 (0.58)	-0.134 (0.42)	-0.441 (0.20)	0.0181 (0.52)
<i>SPATA22</i>	0.085 (0.54)	0.862 (0.99)	0.138 (0.57)	-0.0231 (0.49)	0.531 (0.85)	0.125 (0.59)
<i>MEIOB</i>	-0.223 (0.38)	-0.103 (0.44)	0.419 (0.73)	-0.128 (0.41)	0.0113 (0.51)	0.281 (0.68)
<i>MCMD2</i>	0.172 (0.61)	0.512 (0.92)	0.152 (0.59)	0.146 (0.59)	0.255 (0.72)	0.102 (0.56)
(D) Synapsis						
<i>REC8</i>	0.937 (1)	0.225 (0.74)	0.235 (0.75)	0.841 (1)	-0.0224 (0.48)	0.0562 (0.55)
<i>RAD21L</i>	0.638 (0.87)	-0.502 (0.08)	-0.388 (0.18)	0.659 (0.89)	-0.201 (0.35)	-0.00548 (0.50)
<i>SYCP1</i>	-0.335 (0.29)	-0.238 (0.28)	0.0765 (0.57)	-0.342 (0.30)	-0.115 (0.40)	0.0109 (0.51)
<i>SYCP2</i>	-0.913 (0.0029)	-0.0758 (0.42)	0.0344 (0.53)	-0.93 (0.0037)	-0.0897 (0.43)	-0.0829 (0.44)
<i>TEX12</i>	-0.0786 (0.46)	0.248 (0.72)	0.0708 (0.54)	-0.0981 (0.44)	0.128 (0.61)	0.1 (0.56)
(E) CO/NCO decision						
<i>TEX11</i>	0.0929 (0.55)	-0.0198 (0.48)	0.127 (0.59)	0.124 (0.57)	-0.0212 (0.48)	0.132 (0.59)
<i>SHOC1</i>	-0.051 (0.46)	-0.0826 (0.40)	0.0572 (0.53)	-0.0318 (0.47)	-0.0378 (0.46)	0.0678 (0.54)
<i>RNF212</i>	-0.0479 (0.47)	-0.00572 (0.49)	-0.0592 (0.47)	-0.00861 (0.49)	-0.00895 (0.49)	-0.0454 (0.47)
<i>MSH4</i>	-0.0619 (0.45)	0.0298 (0.54)	0.132 (0.58)	-0.0425 (0.47)	0.0377 (0.55)	0.13 (0.57)
<i>MSH5</i>	-0.0762 (0.46)	0.0211 (0.52)	0.0826 (0.55)	-0.0517 (0.47)	0.0172 (0.52)	0.0699 (0.54)
(F) Resolution						
<i>HFM1/MER3</i>	0.2 (0.64)	-0.174 (0.31)	-0.161 (0.39)	0.207 (0.63)	-0.0617 (0.44)	-0.149 (0.41)
<i>CNTD1</i>	0.366 (0.74)	0.554 (0.87)	0.223 (0.72)	0.407 (0.75)	0.481 (0.79)	-0.0719 (0.46)
<i>MLH1</i>	-0.00945 (0.49)	0.0265 (0.51)	0.0994 (0.56)	0.0286 (0.51)	0.0232 (0.51)	0.0744 (0.55)
<i>MLH3</i>	0.335 (0.71)	0.23 (0.73)	0.0704 (0.57)	0.369 (0.73)	0.124 (0.61)	-0.00817 (0.51)

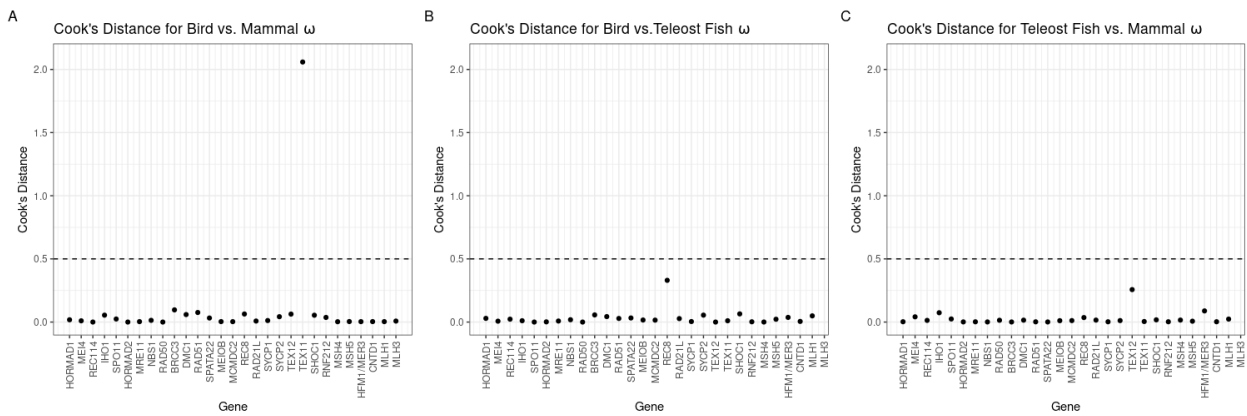
Supplementary Table 10: Evolutionary rates and tests for positive selection across mammals at 18 brain development genes, including likelihood ratio tests for each model, average omega across the gene, and number of codon sites potentially experiencing positive selection (BEB, P >95%).

Gene	bp	N	omega	M	M1-M2	P	M7-M8	P	M8a-M8	P	BEB
<i>BMI1</i>	3540	16	0.0532	7	0	1	4.1900	1.233e-1	-	-	-
<i>CCNA2</i>	2748	16	0.1711	7	0	1	0.2600	8.796e-1	-	-	-
<i>CCNB1</i>	2029	16	0.1644	8a	0	1	6.5500	3.789e-2	2.55	1.104e-1	-
<i>CCND1</i>	4238	16	0.0614	7	0	1	0.2800	8.708e-1	-	-	-
<i>CCND2</i>	6493	16	0.0634	7	0	1	0.0100	9.971e-1	-	-	-
<i>DHH</i>	4683	16	0.0267	7	0	1	0.4700	7.891e-1	-	-	-
<i>EN1</i>	2427	16	0.0838	7	0	1	0.0002	9.999e-1	-	-	-
<i>FOXM1</i>	3507	16	0.2566	7	0	1	3.6200	1.638e-1	-	-	-
<i>GLI1</i>	3972	16	0.1717	7	0	1	3.0500	2.182e-1	-	-	-
<i>GLI2</i>	7136	16	0.1696	7	0	1	0.0000	1	-	-	-
<i>GLI3</i>	8405	16	0.1870	7	0	1	2.1100	3.475e-1	-	-	-
<i>IGF2</i>	5580	16	0.3142	7	0	1	0.5200	7.731e-1	-	-	-
<i>IHH</i>	2473	16	0.0510	7	0	1	0.0002	1	-	-	-
<i>MYCN</i>	2613	16	0.1116	7	0	1	0.3300	8.484e-1	-	-	-
<i>PTCH1</i>	8662	16	0.0605	7	0	1	2.0600	3.563e-1	-	-	-
<i>SHH</i>	4650	16	0.1750	7	0	1	1.7400	4.191e-1	-	-	-
<i>SMO</i>	3977	16	0.0539	8a	0	1	8.1200	1.723e-2	5.66e-4	9.810e-1	-
<i>SUFU</i>	5016	16	0.0702	7	0	1	0.0001	1	-	-	-

Supplementary Figures



Supplementary Figure 1: Comparison of recombination rate, measured as (A) cM/Mb, (B) XO/HCN and (C) MLH1 Foci on largest chromosome in female and male birds.



Supplementary Figure 2: Cook's Distance plots for identifying influential points in recombination gene evolutionary rate comparisons between birds and mammals (A), birds and teleost fish (B), and mammals and teleost fish (C). The significance threshold is set at 0.5 for all three comparisons.

References

- Andersson, A. Barrio, and Fan. 2015. *Calidris pugnax* isolate Ruff, whole genome shotgun sequencing project .
- Chen, S., G. Zhang, C. Shao, Q. Huang, G. Liu, P. Zhang, W. Song, N. An, D. Chalopin, J.-N. Volff, Y. Hong, Q. Li, Z. Sha, H. Zhou, M. Xie, Q. Yu, Y. Liu, H. Xiang, N. Wang, K. Wu, C. Yang, Q. Zhou, X. Liao, L. Yang, Q. Hu, J. Zhang, L. Meng, L. Jin, Y. Tian, J. Lian, J. Yang, G. Miao, S. Liu, Z. Liang, F. Yan, Y. Li, B. Sun, H. Zhang, J. Zhang, Y. Zhu, M. Du, Y. Zhao, M. Scharl, Q. Tang, and J. Wang. 2014. Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. *Nature Genetics* 46(3):253–260. doi:10.1038/ng.2890.
- Conte, M. A., W. J. Gammerdinger, K. L. Bartie, D. J. Penman, and T. D. Kocher. 2017. A high quality assembly of the Nile Tilapia (*Oreochromis niloticus*) genome reveals the structure of two sex determination regions. *BMC Genomics* 18(1):341. doi:10.1186/s12864-017-3723-5.
- Dalloul, R. A., J. A. Long, A. V. Zimin, L. Aslam, K. Beal, L. A. Blomberg, P. Bouffard, D. W. Burt, O. Crasta, R. P. M. A. Crooijmans, K. Cooper, R. A. Coulombe, S. De, M. E. Delany, J. B. Dodgson, J. J. Dong, C. Evans, K. M. Frederickson, P. Flicek, L. Florea, O. Folkerts, M. A. M. Groenen, T. T. Harkins, J. Herrero, S. Hoffmann, H.-J. Megens, A. Jiang, P. de Jong, P. Kaiser, H. Kim, K.-W. Kim, S. Kim, D. Langenberger, M.-K. Lee, T. Lee, S. Mane, G. Marcais, M. Marz, A. P. McElroy, T. Modise, M. Nefedov, C. Notredame, I. R. Paton, W. S. Payne, G. Pertea, D. Prickett, D. Puiu, D. Qioa, E. Raineri, M. Ruffier, S. L. Salzberg, M. C. Schatz, C. Scheuring, C. J. Schmidt, S. Schroeder, S. M. J. Searle, E. J. Smith, J. Smith, T. S. Sonstegard, P. F. Stadler, H. Tafer, Z. J. Tu, C. P. V. Tassell, A. J. Vilella, K. P. Williams, J. A. Yorke, L. Zhang, H.-B. Zhang, X. Zhang, Y. Zhang, and K. M. Reed. 2010. Multi-Platform Next-Generation Sequencing of the Domestic Turkey (*Meleagris gallopavo*): Genome Assembly and Analysis. *PLOS Biology* 8(9):e1000475. doi:10.1371/journal.pbio.1000475.
- Dapper, A. L. and B. A. Payseur. 2019. Molecular evolution of the meiotic recombination pathway in mammals. *Evolution* 73(12):2368–2389. doi:10.1111/evo.13850.
- Delmore, M. Vafadar, G. Formenti, W. Chow, S. Pelan, K. Howe, A. Rhie, J. Mountcastle, B. Haase, O. Fedrigo, and E. D. Jarvis. 2020. *Catharus ustulatus* isolate bCatUst1, whole genome shotgun sequencing project .
- Ellegren, H., L. Smeds, R. Burri, P. I. Olason, N. Backström, T. Kawakami, A. Künstner, H. Mäkinen, K. Nadachowska-Brzyska, A. Qvarnström, S. Uebbing, and J. B. W. Wolf. 2012. The genomic landscape of species divergence in *Ficedula* flycatchers. *Nature* 491(7426):756–760. doi:10.1038/nature11584.
- Enbody, D. E. and Pettersson. 2022. *Camarhynchus parvulus*, whole genome shotgun sequencing project .
- Enbody, E. D., P. Alström, and L. Andersson. 2020. *Motacilla alba alba* isolate MOTALB_02, whole genome shotgun sequencing project .
- Formenti, G., A. Rhie, J. Balacco, B. Haase, J. Mountcastle, O. Fedrigo, S. Brown, M. R. Capodiferro, F. O. Al-Ajli, R. Ambrosini, P. Houde, S. Koren, K. Oliver, M. Smith, J. Skelton, E. Betteridge, J. Dolucan, C. Corton, I. Bista, J. Torrance, A. Tracey, J. Wood, M. Uliano-Silva, K. Howe, S. McCarthy, S. Winkler,

- W. Kwak, J. Korlach, A. Fungtammasan, D. Fordham, V. Costa, S. Mayes, M. Chiara, D. S. Horner, E. Myers, R. Durbin, A. Achilli, E. L. Braun, A. M. Phillippy, E. D. Jarvis, A. N. G. Kirschel, A. Digby, A. Veale, A. Bronikowski, B. Murphy, B. Robertson, C. Baker, C. Mazzoni, C. Balakrishnan, C. Lee, D. Mead, E. Teeling, E. L. Aiden, E. Todd, E. Eichler, G. J. P. Naylor, G. Zhang, J. Smith, J. Wolf, J. Touchon, K. Delmore, K. Jakobsen, L. Komoroske, M. Wilkinson, M. Genner, M. Pšenička, M. Fux-jager, M. Stratton, M. Liedvogel, N. Gemmell, P. Minias, P. O. Dunn, P. Sudmant, P. Morin, Q. Ayub, R. Kraus, S. Vernes, S. Smith, T. Lama, T. Edwards, T. Smith, T. Gilbert, T. Marques-Bonet, T. Einfeldt, B. Venkatesh, W. Johnson, W. Warren, Y. Bukhman, and The Vertebrate Genomes Project Consortium. 2021. Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. *Genome Biology* 22(1):120. doi:10.1186/s13059-021-02336-9.
- Gao, G., S. Magadan, G. C. Waldbieser, R. C. Youngblood, P. A. Wheeler, B. E. Scheffler, G. H. Thorgaard, and Y. Palti. 2021. A long reads-based de-novo assembly of the genome of the Arlee homozygous line reveals chromosomal rearrangements in rainbow trout. *G3: Genes|Genomes|Genetics* 11(4):jkab052. doi:10.1093/g3journal/jkab052.
- Gazda, M. A., S. J. Sabatino, T. Larson, and M. Carneiro. 2019. *Serinus canaria* isolate sc_yellow_7_cibi, whole genome shotgun sequencing project .
- Gedman, G., J. Mountcastle, B. Haase, G. Formenti, T. Wright, J. Apodaca, S. Pelan, W. Chow, A. Rhie, K. Howe, O. Fedrigo, and E. D. Jarvis. 2020. *Melopsittacus undulatus* isolate bMelUnd1, whole genome shotgun sequencing project .
- Howe, K., M. D. Clark, C. F. Torroja, J. Torrance, C. Berthelot, M. Muffato, J. E. Collins, S. Humphray, K. McLaren, L. Matthews, S. McLaren, I. Sealy, M. Caccamo, C. Churcher, C. Scott, J. C. Barrett, R. Koch, G.-J. Rauch, S. White, W. Chow, B. Kilian, L. T. Quintais, J. A. Guerra-Assunção, Y. Zhou, Y. Gu, J. Yen, J.-H. Vogel, T. Eyre, S. Redmond, R. Banerjee, J. Chi, B. Fu, E. Langley, S. F. Maguire, G. K. Laird, D. Lloyd, E. Kenyon, S. Donaldson, H. Sehra, J. Almeida-King, J. Loveland, S. Trevanion, M. Jones, M. Quail, D. Willey, A. Hunt, J. Burton, S. Sims, K. McLay, B. Plumb, J. Davis, C. Clee, K. Oliver, R. Clark, C. Riddle, D. Elliott, G. Threadgold, G. Harden, D. Ware, S. Begum, B. Mortimore, G. Kerry, P. Heath, B. Phillimore, A. Tracey, N. Corby, M. Dunn, C. Johnson, J. Wood, S. Clark, S. Pelan, G. Griffiths, M. Smith, R. Glithero, P. Howden, N. Barker, C. Lloyd, C. Stevens, J. Harley, K. Holt, G. Panagiotidis, J. Lovell, H. Beasley, C. Henderson, D. Gordon, K. Auger, D. Wright, J. Collins, C. Raisen, L. Dyer, K. Leung, L. Robertson, K. Ambridge, D. Leongamornlert, S. McGuire, R. Gilderthorp, C. Griffiths, D. Manthravadi, S. Nichol, G. Barker, S. Whitehead, M. Kay, J. Brown, C. Murnane, E. Gray, M. Humphries, N. Sycamore, D. Barker, D. Saunders, J. Wallis, A. Babbage, S. Hammond, M. Mashreghi-Mohammadi, L. Barr, S. Martin, P. Wray, A. Ellington, N. Matthews, M. Ellwood, R. Woodmansey, G. Clark, J. D. Cooper, A. Tromans, D. Grafham, C. Skuce, R. Pandian, R. Andrews, E. Harrison, A. Kimberley, J. Garnett, N. Fosker, R. Hall, P. Garner, D. Kelly, C. Bird, S. Palmer, I. Gehring, A. Berger, C. M. Dooley, Z. Ersan-Ürün, C. Eser, H. Geiger, M. Geisler, L. Karotki, A. Kirn, J. Konantz, M. Konantz, M. Oberländer, S. Rudolph-Geiger, M. Teucke, C. Lanz, G. Raddatz, K. Osoegawa, B. Zhu, A. Rapp, S. Widaa, C. Langford, F. Yang, S. C. Schuster, N. P. Carter, J. Harrow, Z. Ning, J. Herrero, S. M. J. Searle, A. Enright, R. Geisler, R. H. A. Plasterk, C. Lee, M. Westerfield, P. J. de Jong, L. I. Zon, J. H. Postlethwait, C. Nüsslein-Volhard, T. J. P. Hubbard, H. R. Crollius, J. Rogers, and D. L. Stemple. 2013. The zebrafish reference genome sequence and its relationship to the human genome. *Nature* 496(7446):498–503. doi:10.1038/nature12111.

- Institute”, W. S. 2019. *Gouania willdenowi*, whole genome shotgun sequencing project .
- Institute, W. S. 2021. *Aquila chrysaetos chrysaetos*, whole genome shotgun sequencing project .
- Kim, H.-S., B.-Y. Lee, J. Han, C.-B. Jeong, D.-S. Hwang, M.-C. Lee, H.-M. Kang, D.-H. Kim, D. Lee, J. Kim, I.-Y. Choi, and J.-S. Lee. 2018. The genome of the marine medaka *Oryzias melastigma*. *Molecular Ecology Resources* 18(3):656–665. doi:10.1111/1755-0998.12769.
- Laine, V. N., T. I. Gossmann, K. M. Schachtschneider, C. J. Garroway, O. Madsen, K. J. F. Verhoeven, V. de Jager, H.-J. Megens, W. C. Warren, P. Minx, R. P. M. A. Crooijmans, P. Corcoran, B. C. Sheldon, J. Slate, K. Zeng, K. van Oers, M. E. Visser, and M. A. M. Groenen. 2016. Evolutionary signals of selection on cognition from the great tit genome and methylome. *Nature Communications* 7(1):10474. doi:10.1038/ncomms10474.
- Li, J., J. Zhang, J. Liu, Y. Zhou, C. Cai, L. Xu, X. Dai, S. Feng, C. Guo, J. Rao, K. Wei, E. D. Jarvis, Y. Jiang, Z. Zhou, G. Zhang, and Q. Zhou. 2021. A new duck genome reveals conserved and convergently evolved chromosome architectures of birds and mammals. *GigaScience* 10(1):giaa142. doi:10.1093/gigascience/giaa142.
- Lin, Q. 2022. *Hippocampus comes* isolate QL1, whole genome shotgun sequencing project .
- Liu, Z., S. Liu, J. Yao, L. Bao, J. Zhang, Y. Li, C. Jiang, L. Sun, R. Wang, Y. Zhang, T. Zhou, Q. Zeng, Q. Fu, S. Gao, N. Li, S. Koren, Y. Jiang, A. Zimin, P. Xu, A. M. Phillippy, X. Geng, L. Song, F. Sun, C. Li, X. Wang, A. Chen, Y. Jin, Z. Yuan, Y. Yang, S. Tan, E. Peatman, J. Lu, Z. Qin, R. Dunham, Z. Li, T. Sonstegard, J. Feng, R. G. Danzmann, S. Schroeder, B. Scheffler, M. V. Duke, L. Ballard, H. Kucuktas, L. Kaltenboeck, H. Liu, J. Armbruster, Y. Xie, M. L. Kirby, Y. Tian, M. E. Flanagan, W. Mu, and G. C. Waldbieser. 2016. The channel catfish genome sequence provides insights into the evolution of scale formation in teleosts. *Nature Communications* 7(1):11757. doi:10.1038/ncomms11757.
- Lu, L., Y. Chen, Z. Wang, X. Li, W. Chen, Z. Tao, J. Shen, Y. Tian, D. Wang, G. Li, L. Chen, F. Chen, D. Fang, L. Yu, Y. Sun, Y. Ma, J. Li, and J. Wang. 2015. The goose genome sequence leads to insights into the evolution of waterfowl and susceptibility to fatty liver. *Genome Biology* 16(1):89. doi:10.1186/s13059-015-0652-y.
- Mets, D. G., B. M. Colquitt, and M. S. Brainard. 2019. *Lonchura striata domestica* isolate Mets1, whole genome shotgun sequencing project .
- Mueller, J. C., H. Kuhl, S. Boerno, J. L. Tella, M. Carrete, and B. Kempenaers. 2018. Evolution of genomic variation in the burrowing owl in response to recent colonization of urban areas. *Proceedings of the Royal Society B: Biological Sciences* 285(1878):20180206. doi:10.1098/rspb.2018.0206.
- Mueller, J. C., H. Kuhl, B. Timmermann, and B. Kempenaers. 2016. Characterization of the genome and transcriptome of the blue tit *Cyanistes caeruleus*: Polymorphisms, sex-biased expression and selection signals. *Molecular Ecology Resources* 16(2):549–561. doi:10.1111/1755-0998.12450.
- Myers, G., N. Karagic, A. Meyer, M. Pippel, M. Reichard, S. Winkler, A. Tracey, Y. Sims, K. Howe, A. Rhie, G. Formenti, R. Durbin, O. Fedrigo, and E. D. Jarvis. 2020a. *Esox lucius* isolate fEsoLuc1, whole genome shotgun sequencing project .

- Myers, G., A. Meyer, O. Fedrigo, G. Formenti, A. Rhie, A. Tracey, Y. Sims, and E. D. Jarvis. 2020b. *Electrophorus electricus* isolate fEleEle1, whole genome shotgun sequencing project .
- Myers, G., A. Meyer, N. Karagic, M. Pippel, S. Winkler, A. Tracey, J. Wood, G. Formenti, K. Howe, O. Fedrigo, and E. D. Jarvis. 2020c. *Pygocentrus nattereri* isolate fPygNat1, whole genome shotgun sequencing project .
- Nome, T. and G. Gillard. 2022. *Salmo salar*, whole genome shotgun sequencing project .
- Peterson, E. N., A. Elias, N. B. Roberts, and R. B. Roberts. 2021. *Haplochromis burtoni* strain Fernald_Lab_line, whole genome shotgun sequencing project .
- Pettersson, E. M. 2019. *Clupea harengus*, whole genome shotgun sequencing project .
- Rhie, A., S. A. McCarthy, O. Fedrigo, J. Damas, G. Formenti, S. Koren, M. Uliano-Silva, W. Chow, A. Functammasan, J. Kim, C. Lee, B. J. Ko, M. Chaisson, G. L. Gedman, L. J. Cantin, F. Thibaud-Nissen, L. Haggerty, I. Bista, M. Smith, B. Haase, J. Mountcastle, S. Winkler, S. Paez, J. Howard, S. C. Vernes, T. M. Lama, F. Grutzner, W. C. Warren, C. N. Balakrishnan, D. Burt, J. M. George, M. T. Biegler, D. Iorns, A. Digby, D. Eason, B. Robertson, T. Edwards, M. Wilkinson, G. Turner, A. Meyer, A. F. Kautt, P. Franchini, H. W. Detrich, H. Svoldal, M. Wagner, G. J. P. Naylor, M. Pippel, M. Malinsky, M. Mooney, M. Simbirsky, B. T. Hannigan, T. Pesout, M. Houck, A. Misuraca, S. B. Kingan, R. Hall, Z. Kronenberg, I. Sović, C. Dunn, Z. Ning, A. Hastie, J. Lee, S. Selvaraj, R. E. Green, N. H. Putnam, I. Gut, J. Ghurye, E. Garrison, Y. Sims, J. Collins, S. Pelan, J. Torrance, A. Tracey, J. Wood, R. E. Dagnew, D. Guan, S. E. London, D. F. Clayton, C. V. Mello, S. R. Friedrich, P. V. Lovell, E. Osipova, F. O. Al-Ajli, S. Secomandi, H. Kim, C. Theofanopoulou, M. Hiller, Y. Zhou, R. S. Harris, K. D. Makova, P. Medvedev, J. Hoffman, P. Masterson, K. Clark, F. Martin, K. Howe, P. Flicek, B. P. Walenz, W. Kwak, H. Clawson, M. Diekhans, L. Nassar, B. Paten, R. H. S. Kraus, A. J. Crawford, M. T. P. Gilbert, G. Zhang, B. Venkatesh, R. W. Murphy, K.-P. Koepfli, B. Shapiro, W. E. Johnson, F. Di Palma, T. Marques-Bonet, E. C. Teeling, T. Warnow, J. M. Graves, O. A. Ryder, D. Haussler, S. J. O'Brien, J. Korlach, H. A. Lewin, K. Howe, E. W. Myers, R. Durbin, A. M. Phillippy, and E. D. Jarvis. 2021. Towards complete and error-free genome assemblies of all vertebrate species. *Nature* 592(7856):737–746. doi:10.1038/s41586-021-03451-0.
- Rohner, N. and W. C. Warren. 2019. *Astyanax mexicanus* isolate Rio Sabinas/Rio Valles surface cross, whole genome shotgun sequencing project .
- Rutz, C., C. Functammasan, J. Mountcastle, G. Formenti, W. Chow, K. Howe, M. P. Steele, J. Fernandes, M. T. P. Gilbert, O. Fedrigo, E. D. Jarvis, and N. Gemmell. 2019. *Corvus moneduloides* isolate bCorMon1, whole genome shotgun sequencing project .
- Sackton, T. B., P. Grayson, A. Cloutier, Z. Hu, J. S. Liu, N. E. Wheeler, P. P. Gardner, J. A. Clarke, A. J. Baker, M. Clamp, and S. V. Edwards. 2019. Convergent regulatory evolution and loss of flight in paleognathous birds. *Science* 364(6435):74–78. doi:10.1126/science.aat7244.
- Secomandi, S., G. Formenti, A. Rhie, O. Fedrigo, J. Mountcastle, B. Haase, J. Balacco, J. Collins, W. Chow, K. Howe, G. R. Gallo, L. Gianfranceschi, A. Bonisoli-Alquati, N. Saino, and E. D. Jarvis. 2021. *Hirundo rustica* isolate bHirRus1, whole genome shotgun sequencing project .

- Shapiro, M. D., Z. Kronenberg, C. Li, E. T. Domyan, H. Pan, M. Campbell, H. Tan, C. D. Huff, H. Hu, A. I. Vickrey, S. C. Nielsen, S. A. Stringham, H. Hu, E. Willerslev, M. T. P. Gilbert, M. Yandell, G. Zhang, and J. Wang. 2013. Genomic diversity and evolution of the head crest in the rock pigeon. *Science (New York, N.Y.)* 339(6123):1063–1067. doi:10.1126/science.1230422.
- Tan, M. H., H. M. Gan, Y. P. Lee, M. P. Hammer, and C. M. Austin. 2017. *Amphiprion ocellaris* isolate DU_AmpOce, whole genome shotgun sequencing project .
- Vignal, A. and W. Warren. 2017. *Numida meleagris* breed g44 Domestic line isolate 19003, whole genome shotgun sequencing project .
- Wang, B. 2019. *Phasianus colchicus* isolate SZU-A5-319, whole genome shotgun sequencing project .
- Warren, W., G. Formenti, O. Fedrigo, B. Haase, J. Mountcastle, J. Balacco, A. Tracey, V. Schneider, R. Okimoto, H. Cheng, R. Hawken, K. Howe, and E. D. Jarvis. 2022. *Gallus gallus* breed Cross of Broiler mother + white leghorn layer father isolate bGalGal1, whole genome shotgun sequencing project .
- Warren, W., B. Loiselle, M. Braun, and B. Ryder. 2016. *Lepidothrix coronata* voucher LSUMZ:110521 isolate B3197, whole genome shotgun sequencing project .
- Warren, W. and D. Nacci. 2014. *Cyprinodon variegatus* isolate N-32, whole genome shotgun sequencing project .
- Wellcome Sanger Institute. 2019a. *Chanos chanos*, whole genome shotgun sequencing project.
- Wellcome Sanger Institute. 2019b. *Gadus morhua*, whole genome shotgun sequencing project .
- Wellcome Sanger Institute. 2019c. *Mastacembelus armatus*, whole genome shotgun sequencing project .
- Wellcome Sanger Institute. 2019d. *Myripristis murdjan*, whole genome shotgun sequencing project .
- Wellcome Sanger Institute. 2019e. *Scleropages formosus*, whole genome shotgun sequencing project .
- Wellcome Sanger Institute. 2019f. *Takifugu rubripes*, whole genome shotgun sequencing project .
- You, X., C. Bian, Q. Zan, X. Xu, X. Liu, J. Chen, J. Wang, Y. Qiu, W. Li, X. Zhang, Y. Sun, S. Chen, W. Hong, Y. Li, S. Cheng, G. Fan, C. Shi, J. Liang, Y. Tom Tang, C. Yang, Z. Ruan, J. Bai, C. Peng, Q. Mu, J. Lu, M. Fan, S. Yang, Z. Huang, X. Jiang, X. Fang, G. Zhang, Y. Zhang, G. Polgar, H. Yu, J. Li, Z. Liu, G. Zhang, V. Ravi, S. L. Coon, J. Wang, H. Yang, B. Venkatesh, J. Wang, and Q. Shi. 2014. Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. *Nature Communications* 5(1):5594. doi:10.1038/ncomms6594.
- Zhang, G., C. Li, Q. Li, B. Li, D. M. Larkin, C. Lee, J. F. Storz, A. Antunes, M. J. Greenwold, R. W. Meredith, A. Ödeen, J. Cui, Q. Zhou, L. Xu, H. Pan, Z. Wang, L. Jin, P. Zhang, H. Hu, W. Yang, J. Hu, J. Xiao, Z. Yang, Y. Liu, Q. Xie, H. Yu, J. Lian, P. Wen, F. Zhang, H. Li, Y. Zeng, Z. Xiong, S. Liu, L. Zhou, Z. Huang, N. An, J. Wang, Q. Zheng, Y. Xiong, G. Wang, B. Wang, J. Wang, Y. Fan, R. R. da Fonseca, A. Alfaro-Núñez, M. Schubert, L. Orlando, T. Mourier, J. T. Howard, G. Ganapathy, A. Pfenning, O. Whitney, M. V. Rivas, E. Hara, J. Smith, M. Farré, J. Narayan, G. Slavov, M. N. Romanov, R. Borges, J. P. Machado, I. Khan, M. S. Springer, J. Gatesy, F. G. Hoffmann, J. C. Opazo, O. Håstad, R. H. Sawyer, H. Kim, K.-W.

Kim, H. J. Kim, S. Cho, N. Li, Y. Huang, M. W. Bruford, X. Zhan, A. Dixon, M. F. Bertelsen, E. Derryberry, W. Warren, R. K. Wilson, S. Li, D. A. Ray, R. E. Green, S. J. O'Brien, D. Griffin, W. E. Johnson, D. Haussler, O. A. Ryder, E. Willerslev, G. R. Graves, P. Alström, J. Fjeldså, D. P. Mindell, S. V. Edwards, E. L. Braun, C. Rahbek, D. W. Burt, P. Houde, Y. Zhang, H. Yang, J. Wang, Avian Genome Consortium, E. D. Jarvis, M. T. P. Gilbert, J. Wang, C. Ye, S. Liang, Z. Yan, M. L. Zepeda, P. F. Campos, A. M. V. Velazquez, J. A. Samaniego, M. Avila-Arcos, M. D. Martin, R. Barnett, A. M. Ribeiro, C. V. Mello, P. V. Lovell, D. Almeida, E. Maldonado, J. Pereira, K. Sunagar, S. Philip, M. G. Dominguez-Bello, M. Bunce, D. Lambert, R. T. Brumfield, F. H. Sheldon, E. C. Holmes, P. P. Gardner, T. E. Steeves, P. F. Stadler, S. W. Burge, E. Lyons, J. Smith, F. McCarthy, F. Pitel, D. Rhoads, and D. P. Froman. 2014. Comparative genomics reveals insights into avian genome evolution and adaptation. *Science* 346(6215):1311–1320. doi:10.1126/science.1251385.