

Table S1. Sequence divergence between *G. gallus* gametologs

Gene pair (Z/W)	Gene ID ^a (Z/W)	Position on <i>G. gallus</i> Z (mb)	<i>G. gallus</i> d _s (SE) ^b	<i>G. gallus</i> d _N (SE) ^b	Putative stratum	Divergence (MYA)
<i>CHD1Z/CHD1W</i>	14642/ <i>CHDW</i> ¹	51.10	0.390 (0.0246)	0.0322 (0.0029)	Conserved I	103
<i>HINT1Z/HINT1W</i>	00428/ 22690	44.76	0.404 (0.1087)	0.275 (0.0503)	Conserved I	106
<i>RASA1Z/RASA1W</i>	17706/ 22611	60.83	0.241 (0.0526)	0.028 (0.0094)	Conserved II	63
<i>KCMF1Z/KCMF1W</i>	15391/ 14441	53.60	0.271 (0.0371)	0.036 (0.0068)	Conserved II	71
<i>SPINZ/SPINW</i>	14916/ <i>SPINW</i> ¹	43.03	0.178 (0.0347)	0.007 (0.0035)	Galliform-specific III	47
<i>HNRNPKZ/HNRNPKW</i>	12591/ 14366	39.94	0.268 (0.0351)	0.003 (0.0019)	Galliform-specific III	71
<i>BTF3Z/BTF3W</i>	13512/ 00395	24.60	0.245 (0.0526)	0.024 (0.0087)	Galliform-specific III	64
<i>ZSWIM6Z/ZSWIM6W</i>	14734/ 27170	18.95	0.156 (0.0210)	0.024 (0.0048)	Galliform-specific III	41
<i>MIER3Z/MIER3W</i>	14721/ 00140	17.22	0.210 (0.0426)	0.025 (0.0077)	Galliform-specific III	55
<i>NIPBLZ/NIPBLW</i>	03605/ 13312	11.23	0.198 (0.0111)	0.023 (0.0018)	Galliform-specific IV	52
<i>RPL17LZ/RPL17LW</i>	02696/ 22174	10.80	0.169 (0.0212)	0.000 (0.0000)	Galliform-specific IV	44
<i>ZFRZ/ZFRW</i>	03235/ 14545	9.61	0.158 (0.0157)	0.018 (0.0029)	Galliform-specific IV	42
<i>VCPZ/VCPW</i>	01986/ 00386	8.40	0.162 (0.0214)	0.000 (0.0009)	Galliform-specific IV	43
<i>UBAP2Z/UBAP2W</i>	13809/ 05785	7.22	0.194 (0.0165)	0.049 (0.0049)	Galliform-specific IV	51
<i>UBE2R2Z/UBE2R2W</i>	01668/ 09227	7.16	0.257 (0.0258)	0.000 (0.0000)	Galliform-specific IV	68
<i>ATP5A1Z/ATP5A1W</i>	14644/ 01756	2.15	0.193 (0.0231)	0.019 (0.0042)	Galliform-specific IV	51
<i>CZH18ORF25Z/CZH18ORF25W</i>	01763/ 01585	2.10	0.139 (0.0294)	0.072 (0.0126)	Galliform-specific IV	37
<i>MADH2Z/MADH2W</i>	14697/ 10056	1.52	0.191 (0.0251)	0.005 (0.0023)	Galliform-specific IV	50
<i>ZNF532Z/ZNF532W</i>	02852/ 14003	0.86	0.152 (0.0151)	0.032 (0.0039)	Galliform-specific IV	40
<i>SIAT8CZ/SIAT8CW</i>	03049/ 26991	0.44	0.173 (0.0266)	0.021 (0.0053)	Galliform-specific IV	45

^aEnsembl gene ID Ensgalg000000...^bStandard errors generated in Paml.¹Ayers et al (2013) Genome Biol

Table S2. Sequence divergence between *M. gallopavo* gametologs

Gene pair (Z/W)	Gene ID ^a (Z/W)	Position on <i>G. gallus</i> / <i>M. gallopavo</i> Z (mb)	<i>M. gallopavo</i> d _S (SE) ^b	<i>M. gallopavo</i> d _N (SE) ^b	Putative stratum	Divergence (MYA)
<i>HINT1Z</i> / <i>HINT1W</i>	06655/ 16898	44.76/47.46	0.285 (0.0961)	0.182 (0.0434)	Conserved I	75
<i>RASA1Z</i> / <i>RASA1W</i>	08292/ AH015047.1 ¹	60.83/64.54	0.266 (0.0600)	0.0312 (0.0106)	Conserved II	70
<i>SPINZ</i> / <i>SPINW</i>	02500/ AH015050.1 ¹	43.03/45.85	0.198 (0.0423)	0.0129 (0.0054)	Galliform-specific III	52
<i>NIPBLZ</i> / <i>NIPBLW</i>	01989/ 13606	11.23/12.01	0.182 (0.0453)	0.0087 (0.0051)	Galliform-specific IV	48
<i>UBAP2Z</i> / <i>UBAP2W</i>	01837/ AY188758.1 ¹	7.22/75.78	0.137 (0.0487)	0.0273 (0.0139)	Galliform-specific IV	36
<i>ATP5A1Z</i> / <i>ATP5A1W</i>	09963/ 01414	2.15/2.23	0.141 (0.0326)	0.0076 (0.0044)	Galliform-specific IV	37
<i>MADH2Z</i> / <i>MADH2W</i>	01351/ AH015049.1 ¹	1.52/1.51	0.146 (0.0485)	0.0159 (0.0093)	Galliform-specific IV	38

^aEnsembl gene ID Ensmgag000000...^bStandard errors generated in Paml¹Berlin and Ellegren (2006) J Mol Ev

Table S3. Sequence divergence between *A. platyrhynchos* gametologs

Gene pair (Z/W)	Gene ID ^a (Z/W)	Position on <i>G. gallus</i> Z (mb)	<i>A. platyrhynchos</i> d _s (SE) ^b	<i>A. platyrhynchos</i> d _N (SE) ^b	Putative stratum	Divergence (MYA)
<i>CHD1Z</i> / <i>CHD1W</i>	09965/ 05191	51.10	0.296 (0.0399)	0.0317 (0.0057)	Conserved I	78
<i>RASA1Z</i> / <i>RASA1W</i>	05627/ 05611	60.83	0.171 (0.0346)	0.008 (0.0039)	Conserved II	45
<i>KCMF1Z</i> / <i>KCMF1W</i>	13426/ 03026	53.60	0.198 (0.0343)	0.0371 (0.0081)	Conserved II	52
<i>SPINZ</i> / <i>SPINW</i>	13922/ 02923	43.03	0.014* (0.0000)	0.000 (0.0000)	Anseriform- specific III	4
<i>HNRNPKZ</i> / <i>HNRNPKW</i>	10856/ 10986	39.94	0.148 (0.0249)	0.005 (0.0023)	Anseriform-specific III	39
<i>ZSWIM6Z</i> / <i>ZSWIM6W</i>	06992/ 13555	19.00	0.065* (0.0153)	0.0131 (0.0045)	Anseriform-specific III	17
<i>MIER3Z</i> / <i>MIER3W</i>	06634/ 010850	17.22	0.104 (0.0182)	0.0278 (0.0055)	Anseriform-specific III	27
<i>NIPBLZ</i> / <i>NIPBLW</i>	08473/ 10290	11.23	0.077* (0.0204)	0.0017 (0.0017)	Anseriform-specific III	20
<i>ZFRZ</i> / <i>ZFRW</i>	15627/ 15519	9.61	0.133 (0.0264)	0.0256 (0.0062)	Anseriform-specific III	35
<i>VCPZ</i> / <i>VCPW</i>	04533/ 05806	8.40	0.005* (0.0000)	0.000 (0.0000)	Anseriform-specific III	1
<i>UBE2R2Z</i> / <i>UBE2R2W</i>	03800/ 16000	1.76	0.000* (0.0000)	0.004 (0.0042)	Anseriform-specific III	0

^aEnsembl gene ID Ensaplg000000...^bStandard errors generated in Paml*Significantly different from *G. gallus* d_s estimates (non-overlapping 95% confidence intervals)

Table S4. Branch models and branch-site test across W-linked branches

Gene name	<i>G. gallus</i> Ensembl ID (Z/W) ^a	<i>A. platyrhynchos</i> Ensembl ID (Z/W) ^b	<i>M. gallopavo</i> Ensembl ID (Z/W) ^c	<i>T. guttata</i> Ensembl ID (Z) ^d	Branch model (ω estimated)		Branch model test ($\omega = 1$)		Branch model test ($\omega = 0$)		Branch-site test ($\omega = 1$)	
					-lnL	ω	-lnL	LR	-lnL	LR	-lnL (ω estimated)	-lnL ($\omega = 1$)
<i>HINT1</i>	00428/22690	-	06655/16898	00395	-365.13	1.10	-365.15	0.05	-2213.65	3697.05**	-362.45	-362.47
<i>CHD1</i>	14642/ <i>CHDW</i> ¹	09965/05191	-	01185	-3027.39	0.14	-3074.62	94.45**	-6533.47	7012.15**	-3009.74	-3009.74
<i>RASA1</i>	17706/22611	05611/05627	08292/AH015047.1 ²	01169	-697.16	0.09	-712.82	31.33**	-1390.63	1386.95**	-697.08	-697.08
<i>KCMF1</i>	15391/14441	13426/03026	-	00265	-1746.53	0.22	-1764.27	35.49**	-4583.88	5674.71**	-1736.81	-1736.92
<i>MIER3</i>	14721/00140	06634/10850	-	02601	-1292.61	0.24	-1301.60	17.97**	-1376.24	167.25**	-1293.55	-1293.55
<i>SPIN</i>	14916/ <i>SPINW</i> ¹	13922/02923	02500/AH015050.1 ²	00468	-1153.90	0.09	-1168.12	28.45**	-2027.39	1749.98**	-1154.67	-1154.67
<i>HNRNPK</i>	12591/14366	10856/10986	-	03138	-2340.51	0.03	-2394.89	108.75**	-2382.62	84.21**	-2332.91	-2332.92
<i>VCP</i>	01986/00386	04533/05806	-	01760	-1081.34	0.03	-1094.13	25.58**	-1090.90	19.13**	-1081.23	-1081.31
<i>ZFR</i>	03235/14545	15627/15519	-	01909	-1973.85	0.18	-1987.42	27.16**	-2060.59	173.50**	-1963.95	-1963.95
<i>NIPBL</i>	03605/13312	08473/10290	-	02047	-1487.07	0.05	-1509.10	44.08**	-1519.02	63.91**	-1487.31	-1487.31
<i>NIPBL</i>	03605/13312	-	13606/01989	02047	-838.30	0.03	-857.50	38.40**	-1010.05	343.5**	-838.37	-838.37
<i>UBAP2</i>	13809/05785	-	01837/AY188758.1 ²	01689	-406.73	0.15	-409.83	6.19*	-584.14	354.82**	-406.74	-406.74
<i>ATP5A1</i>	14644/01756	-	09963/01414	01582	-1101.40	0.09	-1109.67	16.54**	-1426.82	650.83**	-1096.96	-1098.75
<i>MADH2</i>	14697/14184	-	01351/AH015049.1 ²	00016	-1151.96	0.06	-1163.14	22.37**	-1318.71	33.50**	-1149.58	-1149.58
<i>UBE2R2</i>	01668/09227	03800/16000	-	01683	-514.68	0.04	-522.19	15.03**	-523.37	17.39**	-514.68	-514.68
<i>ZSWIM6</i>	06992/13555	14734/27170	-	02716	-1014.36	0.25	-1019.98	11.25**	-1078.80	128.88**	-1014.15	-1014.15

^aEnsgalg000000...

^bEnsaplg000000...

^cEnsmgag000000...

^dEnstgug000000...

** p-value <0.01

* p-value <0.05

¹Ayers et al (2013) Genome Biol

²Berlin and Ellegren (2006) J Mol Ev

Table S5. Branch models and branch-site test across Z-linked branches

Gene name	<i>G. gallus</i> Ensembl ID (Z/W) ^a	<i>A. platyrhynchos</i> Ensembl ID (Z/W) ^b	<i>M. gallopavo</i> Ensembl ID (Z/W) ^c	<i>T. guttata</i> Ensembl ID (Z) ^d	Branch model (ω estimated)		Branch model test ($\omega = 1$)		Branch model test ($\omega = 0$)		Branch-site test ($\omega = 1$)	
					-lnL	ω	-lnL	LR	-lnL	LR	-lnL (ω estimated)	-lnL ($\omega = 1$)
<i>HINT1</i>	00428/22690	-	06655/16898	00395	-367.32	0.00	-370.99	7.34**	-367.32	0.00	-370.17	-370.17
<i>CHD1</i>	14642/ <i>CHDW</i> ¹	09965/05191	-	01185	-3035.79	0.03	-3122.01	172.44**	-4005.27	1938.96**	-3026.57	-3026.57
<i>RASA1</i>	17706/22611	05611/05627	08292/AH015047.1 ²	01169	-696.13	0.03	-709.51	26.77**	-868.30	344.34**	-697.08	-697.08
<i>KCMF1</i>	15391/14441	13426/03026	-	00265	-1749.50	0.12	-1764.45	29.89**	-3019.36	259.71**	-1740.93	-1740.93
<i>MIER3</i>	14721/00140	06634/10850	-	02601	-1293.87	0.11	-1306.99	26.23**	-1324.28	60.82**	-1294.25	-1294.25
<i>SPIN</i>	14916/ <i>SPINW</i> ¹	13922/02923	02500/AH015050.1 ²	00468	-1156.96	0.02	-1172.79	31.65**	-1326.73	339.55**	-1157.20	-1157.20
<i>HNRNPK</i>	12591/14366	10856/10986	-	03138	-2339.38	0.01	-2393.62	108.49**	-2343.99	9.22**	-2333.75	-2333.75
<i>VCP</i>	01986/00386	04533/05806	-	01760	-1081.20	0.00	-1095.52	28.65**	-1081.20	0.00	-1081.67	-1081.67
<i>ZFR</i>	03235/14545	15627/15519	-	01909	-1975.63	0.12	-2003.04	54.84**	-2055.82	160.38**	-1968.12	-1968.16
<i>NIPBL</i>	03605/13312	08473/10290	-	02047	-1487.64	0.02	-1529.38	83.48**	-1503.87	32.46**	-1488.06	-1488.06
<i>NIPBL</i>	03605/13312	-	13606/01989	02047	-838.46	0.04	-845.81	14.70**	-1008.86	340.80**	-838.47	-838.47
<i>UBAP2</i>	13809/05785	-	01837/AY188758.1 ²	01689	-406.59	0.25	-407.82	2.47	-751.58	689.98**	-406.61	-406.61
<i>ATP5A1</i>	14644/01756	-	09963/01414	01582	-1105.90	0.00	-1132.66	53.53**	-1105.89	-0.01	-1103.10	-1103.10
<i>MADH2</i>	14697/14184	-	01351/AH015049.1 ²	00016	-1152.46	0.02	-1182.98	61.03**	-1485.78	666.65**	-1150.21	-1150.21
<i>UBE2R2</i>	01668/09227	03800/16000	-	01683	-515.67	0.00	-520.67	10.01**	-515.66	0.00	-515.82	-515.82
<i>ZSWIM6</i>	06992/13555	14734/27170	-	02716	-1014.55	0.05	-1021.05	12.99**	-1020.57	12.05**	-1015.06	-1015.06

^aEnsgalg000000...

^bEnsaplg000000...

^cEnsmgag000000...

^dEnstgug000000...

** p-value <0.01

* p-value <0.05

¹Ayers et al (2013) Genome Biol

²Berlin and Ellegren (2006) J Mol Evol