

Supplementary Materials

Full title: The wild species genome ancestry of domestic chickens

Short title: Chicken genome ancestry

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The content of this supplementary materials is as below:

Fig. S1A and B: Exon phylogeny and TreeMix

Fig. S2 – S4: Plots for the introgression from domestic chicken/Red junglefowl to Grey junglefowl

Fig. S5 – S11: Plots for the introgression from Grey junglefowl to domestic chicken/Red junglefowl

Fig. S12: Genome *fd* plots for the comparison between Ceylon junglefowl and domestic chicken

Fig. S13 – S14: Plots for the introgression from Ceylon junglefowl to domestic chicken.

Fig. S15: Genome *fd* plots for the comparison between Green junglefowl and domestic chicken

Fig. S16: Plots for the introgression from Green junglefowl to domestic chicken

Table S1: Sampling, mapping and variants statistics

Table S2A and B: Candidate introgressed regions

Table S3: Functional annotations for the enriched genes within the introgressed regions

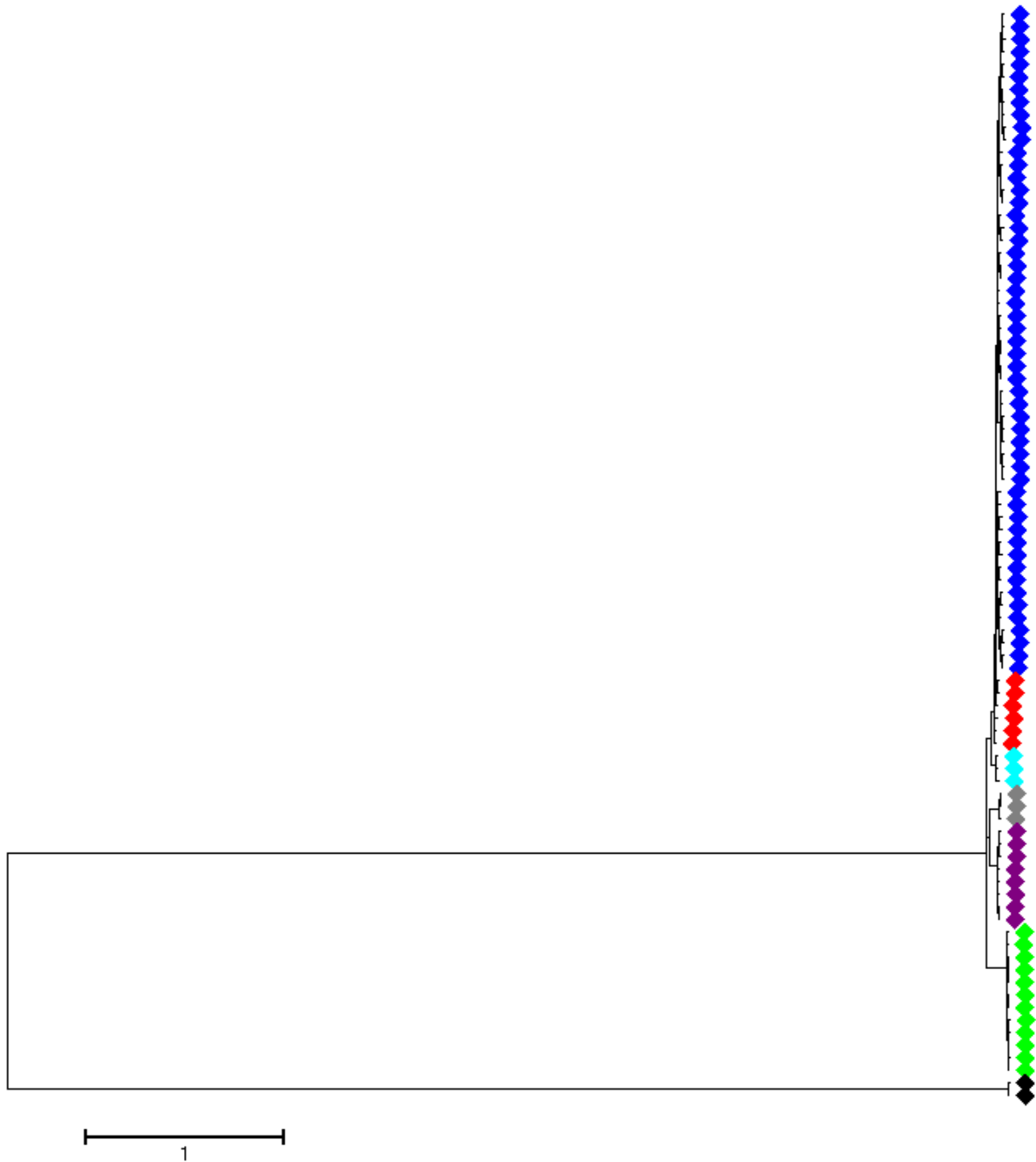


Fig. S1A. Maximum likelihood tree generated from 1,849,580 exon SNPs with GTR model. All branches are supported by 100% bootstrap values. The colour for the taxon markers are ◆: Domestic chicken, ◆: Red junglefowl, ◆: Javan red junglefowl, ◆: Grey junglefowl, ◆: Ceylon junglefowl, ◆: Green junglefowl, ◆: common Pheasant.

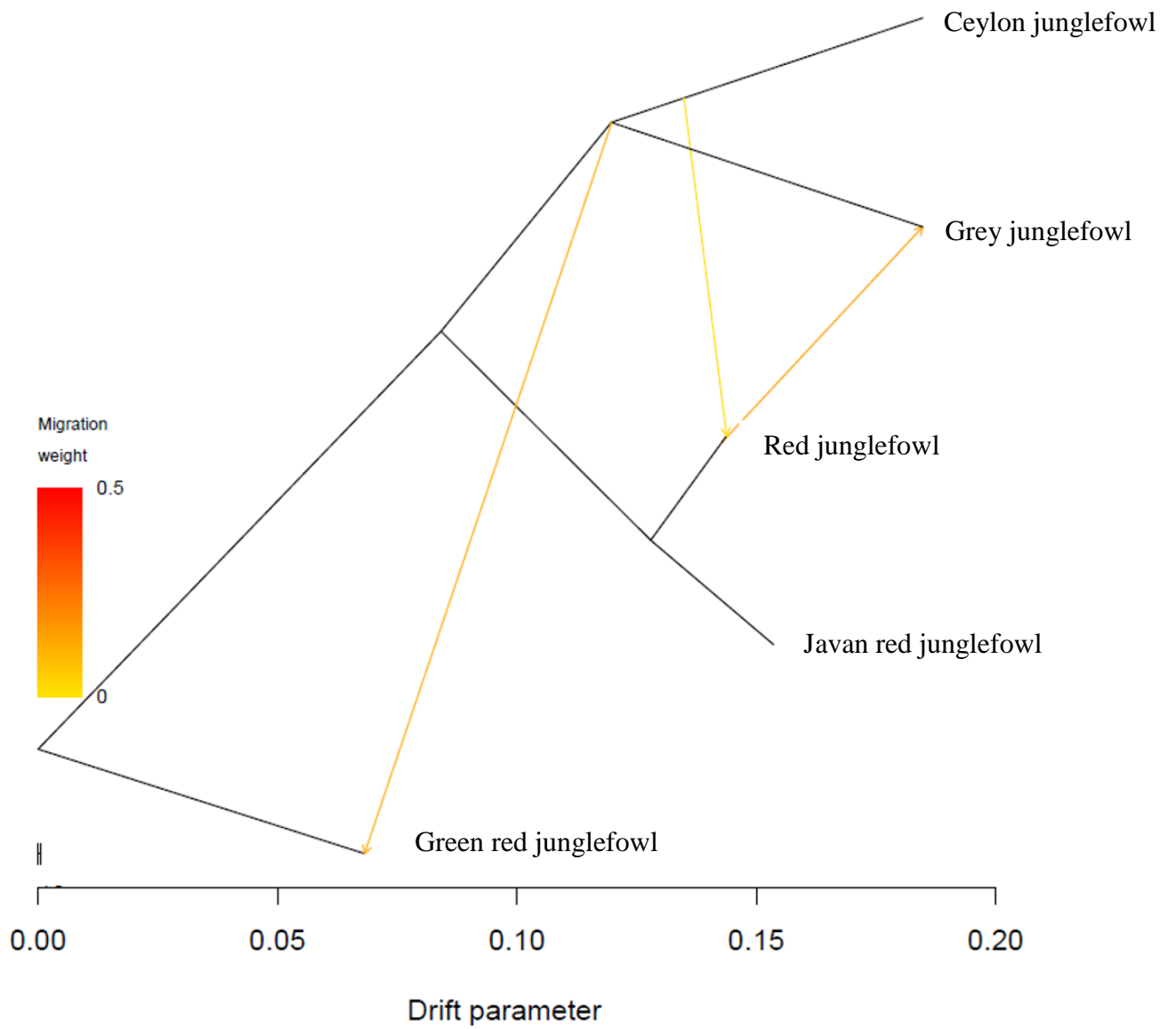


Fig. S1B. TreeMix across the autosomal genome

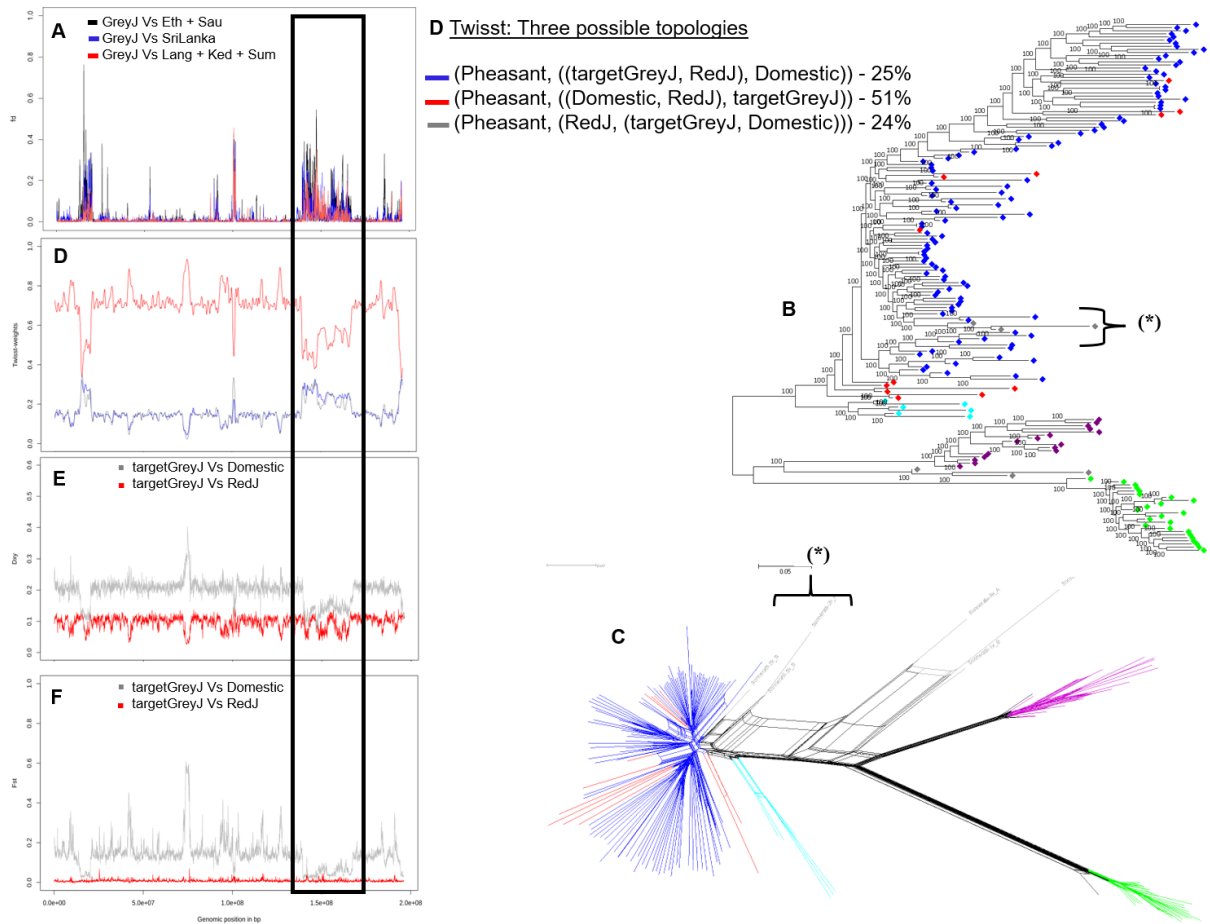


Fig. S2. A 26 Mb (Chr1: 141287737 - 167334186 bp) introgressed region from domestic chicken into Grey junglefowl. **(A)** fd plot for chromosome 1, **(B)** haplotype-based network and **(C)** maximum likelihood tree for the introgressed region, **(D)** *Twisst* plot and the proportion of each topology in the introgressed region, **(E)** D_{XY} and **(F)** F_{ST} . Eth, Sau, SriLanka, Lang, Ked, Sum represent chicken samples from Ethiopia, Saudi, Sri Lanka, Langshan, Kedu Hitam and Sumatra, respectively, GreyJ represent Grey junglefowl, and targetGreyJ are the introgressed (*) Grey junglefowl haplotypes. domestic include all the domestic chicken populations. The colours for **(B)** and **(C)** defining each species are; \blacklozenge : Domestic chicken \blacklozenge : Red junglefowl, \blacklozenge : Javan red junglefowl, \blacklozenge : Grey junglefowl, \blacklozenge : Ceylon junglefowl, \blacklozenge : Green junglefowl, \blacklozenge : common Pheasant.

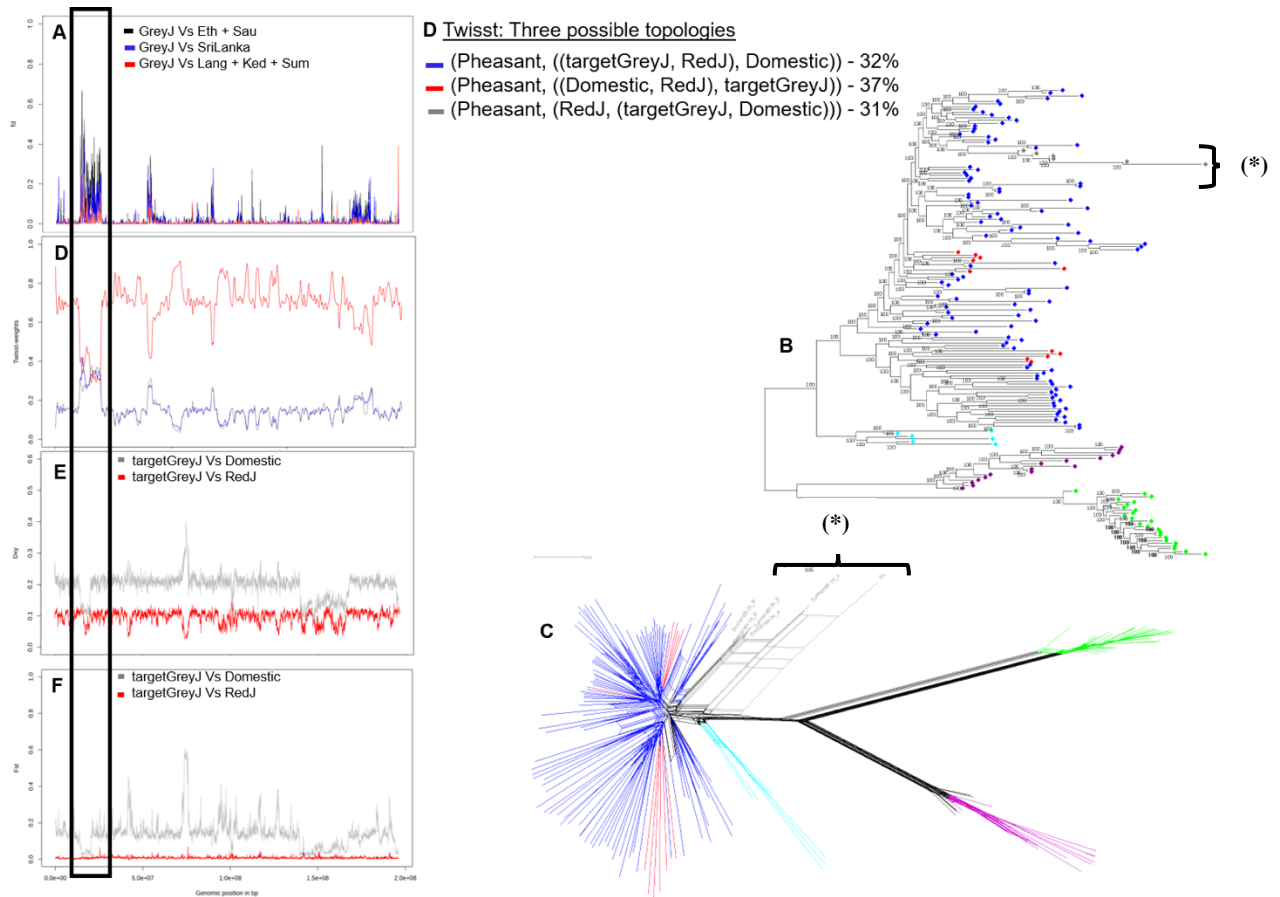


Fig. S3. A 9 Mb (Chr2: 11022874 - 19972089 bp) introgressed region from domestic chicken to Grey junglefowl. **(A)** fd plot for chromosome 1, **(B)** maximum likelihood tree for the introgressed region, **(C)** haplotype-based network, **(D)** *Twisst* plot and the proportion of each topology in the introgressed region, **(E)** D_{XY} and **(F)** F_{ST} . Eth, Sau, SriLanka, Lang, Ked, Sum represent chicken samples from Ethiopia, Saudi, Sri Lanka, Langshan, Kedu Hitam and Sumatra, respectively, GreyJ represent Grey junglefowl, and targetGreyJ are the introgressed (*) Grey junglefowl haplotypes. Domestic include all the domestic chicken populations. The colours for **(B)** and **(C)** defining each species are; \blacklozenge : Domestic chicken \blacklozenge : Red junglefowl, \blacklozenge : Javan red junglefowl, \blacklozenge : Grey junglefowl, \blacklozenge : Ceylon junglefowl, \blacklozenge : Green junglefowl, \blacklozenge : common Pheasant.

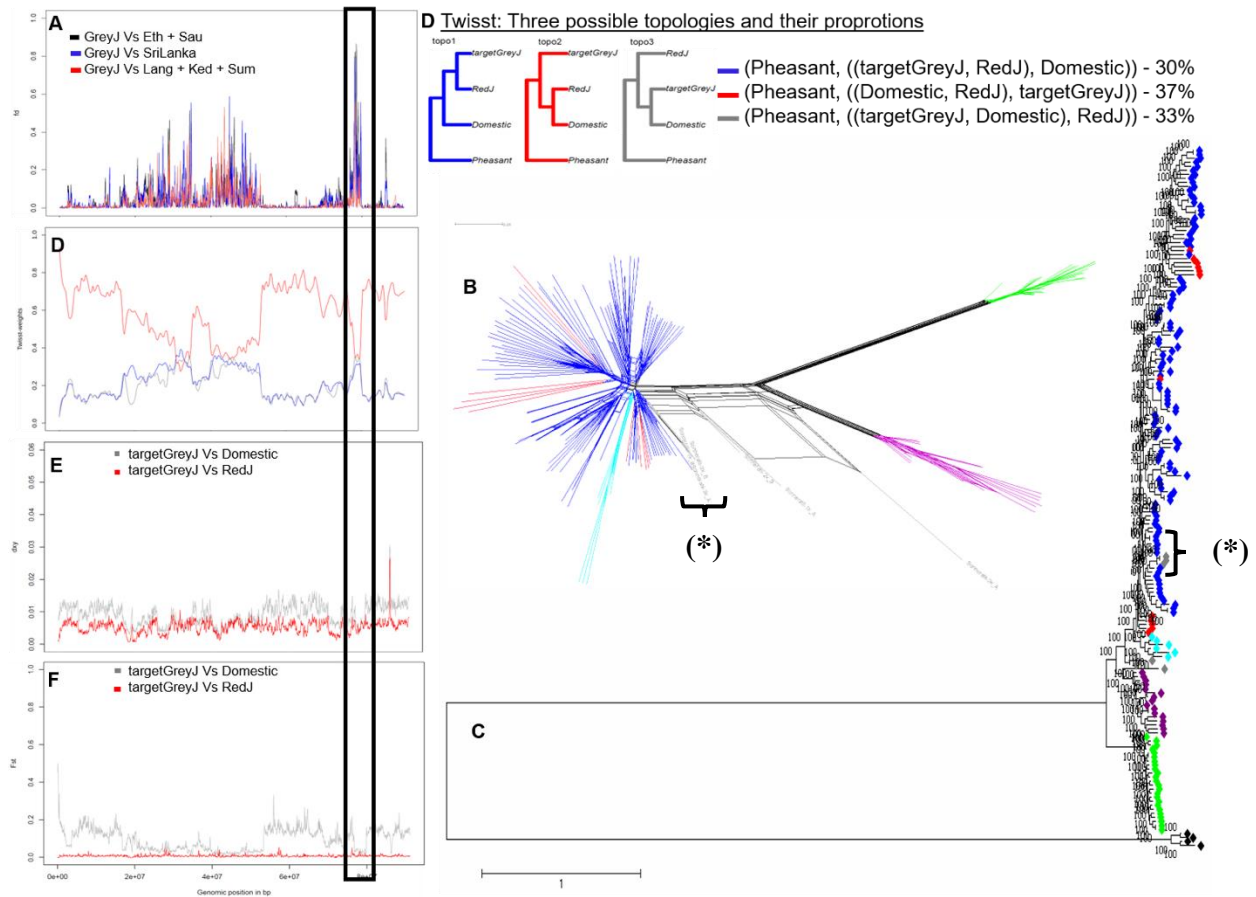


Fig. S4. A 2.8 Mb (Chr4: 76429662 - 79206239bp) introgressed region from domestic chicken/Red junglefowl into Grey junglefowl. (A) f_d plot for chromosome 4, (B) haplotype-based network, (C) maximum likelihood tree, (D) *Twisst* plot, its topologies and their proportions, (E) D_{XY} and (F) F_{ST} . Eth, Sau, SriLanka, Lang, Ked and Sum are domestic chicken from Ethiopia, Saudi, Sri Lanka and Langshan, KeduHitam and Sumatra breeds, respectively. GreyJ is Grey junglefowl, and targetGreyJ are the introgressed Grey junglefowl haplotypes (*). Domestic includes all the chicken domestic populations. ◆: Domestic chicken; ◆: Red junglefowl, ◆: Javan red junglefowl, ◆: Grey junglefowl, ◆: Ceylon junglefowl, ◆: Green junglefowl, ◆: common Pheasant.

Description for **Fig. S5 - S11**

The plots are zoomed close to the region. **(A)** fd plot, **(B)** haplotype-based network and **(C)** maximum likelihood tree for the introgressed region **(D)** *Twisst* plot and the proportion of each topology in the introgressed region **(E)** D_{XY} and **(F)** F_{ST} . Eth, Sau, SriLanka, Lang, Ked, Sum represent chicken samples from Ethiopia, Saudi, Sri Lanka, Langshan, Kedu Hitam and Sumatra, respectively, GreyJ represent Grey junglefowl, and targetDom are the introgressed (*) domestic haplotypes. The colours for **(B)** and **(C)** defining each species are \blacklozenge : Domestic chicken \blacklozenge : Red junglefowl, \blacklozenge : Javan red junglefowl, \blacklozenge : Grey junglefowl, \blacklozenge : Ceylon junglefowl, \blacklozenge : Green junglefowl, \blacklozenge : common Pheasant.

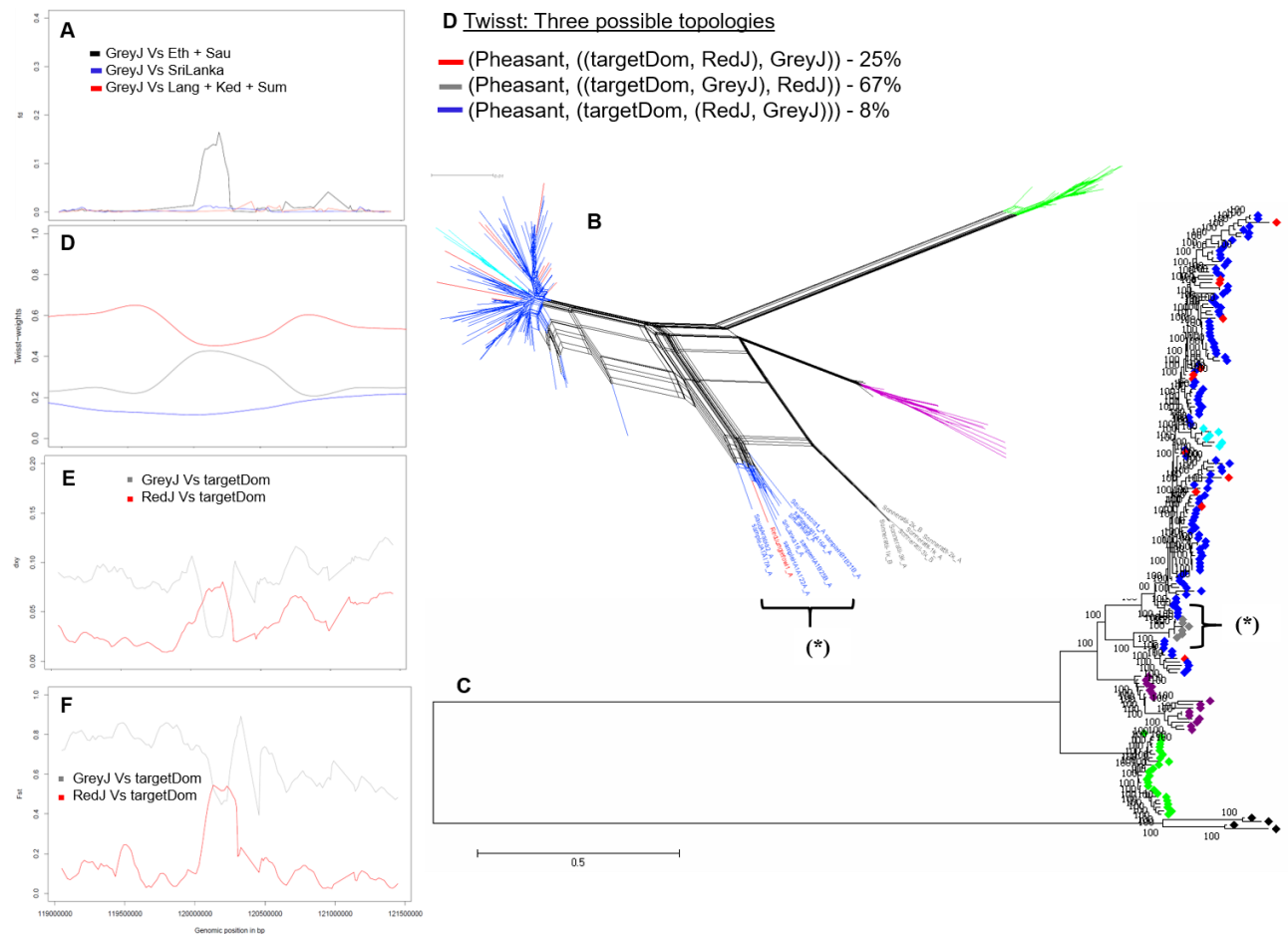


Fig. S5. A 220 kb (Chr 2: 119676880 - 119901132bp) candidate introgressed region from Grey junglefowl to domestic chicken/Red junglefowl. targetDom here include the introgressed domestic chicken and a single Red junglefowl haplotypes (*).

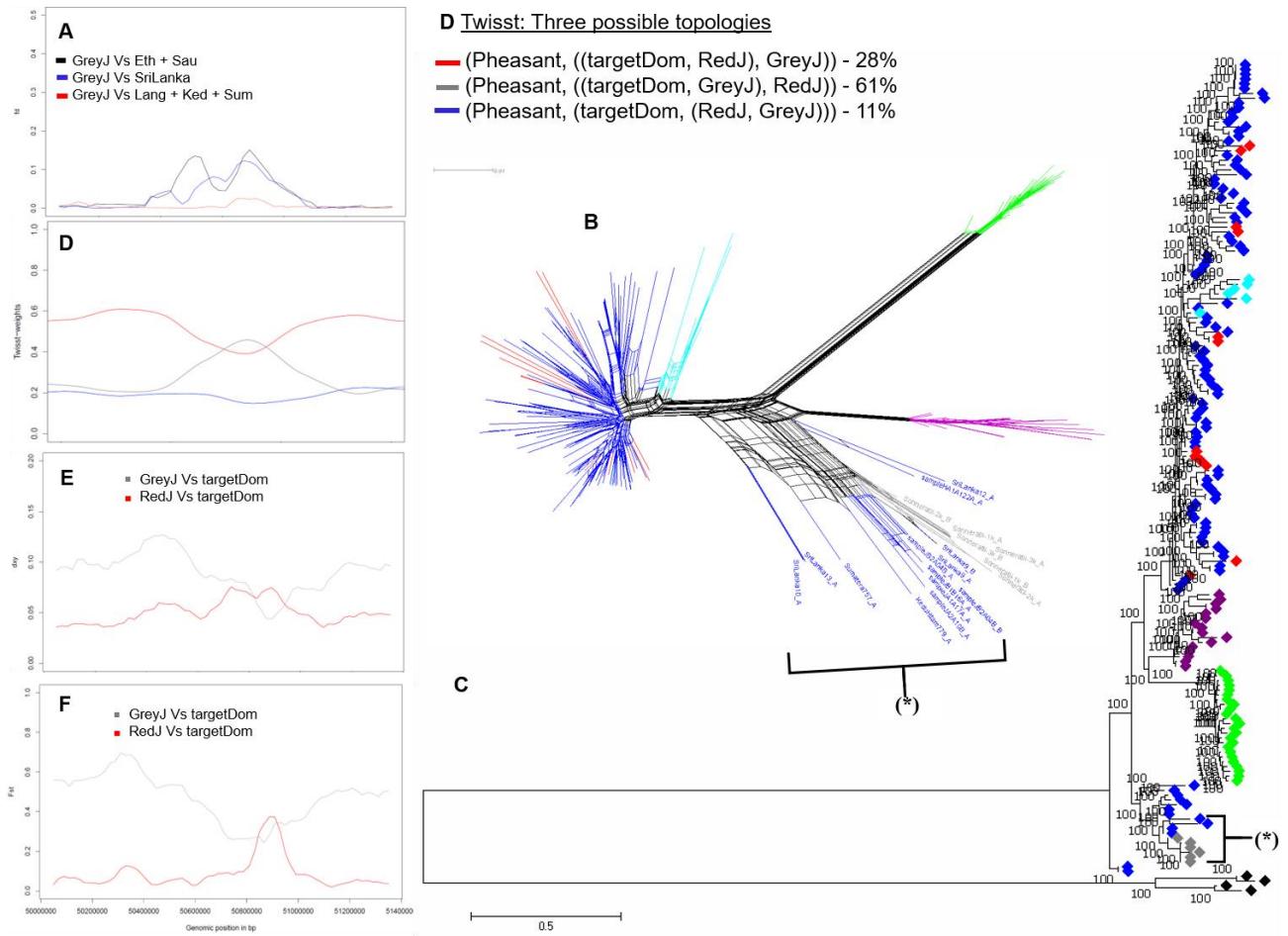


Fig. S6. A 100 kb (Chr 3: 50759656 - 50859645 bp) introgressed region from Grey junglefowl into domestic chicken.

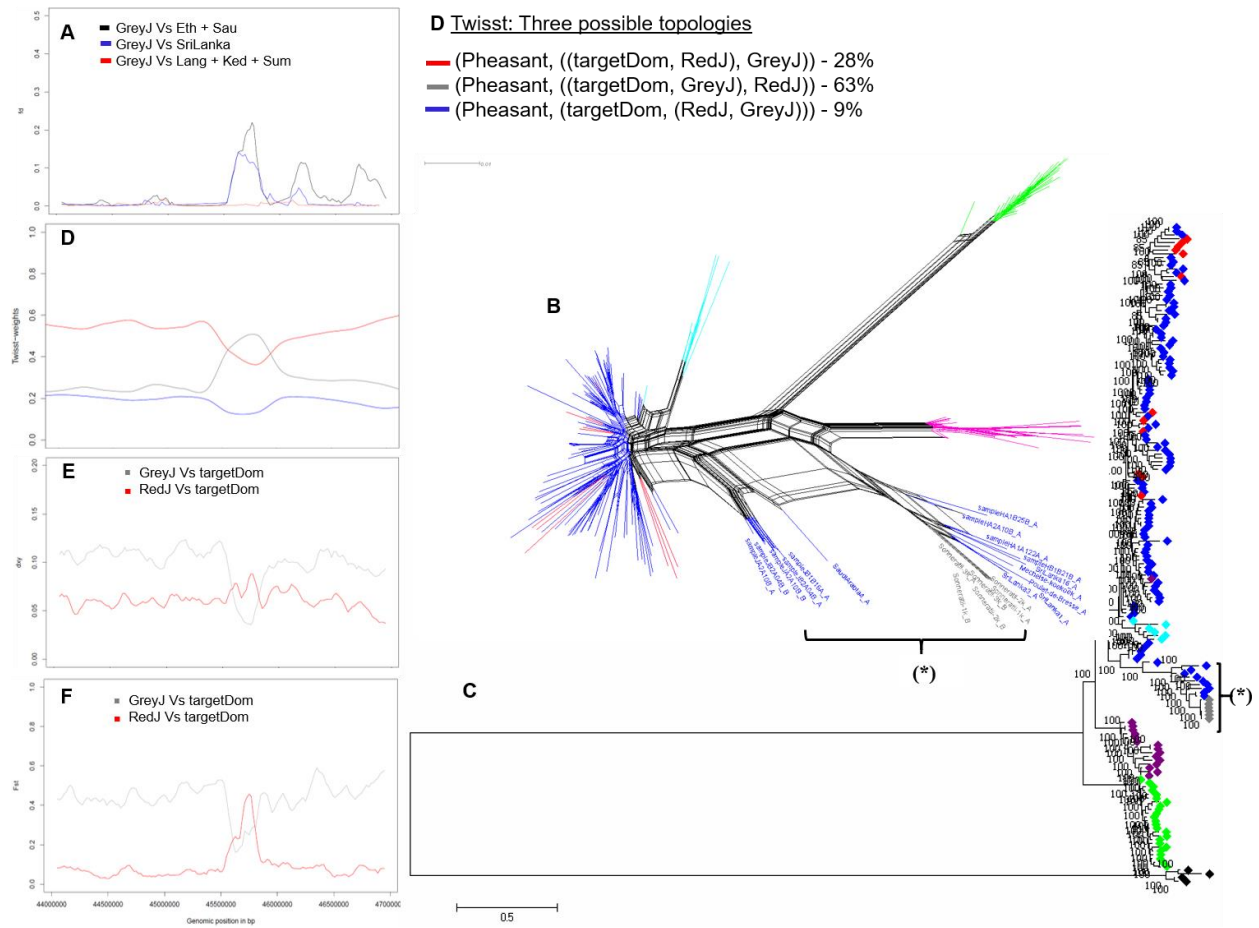


Fig. S8. A 280 kb (Chr 5: 45674368 - 45954418 bp) introgressed region from Grey junglefowl into domestic chicken.

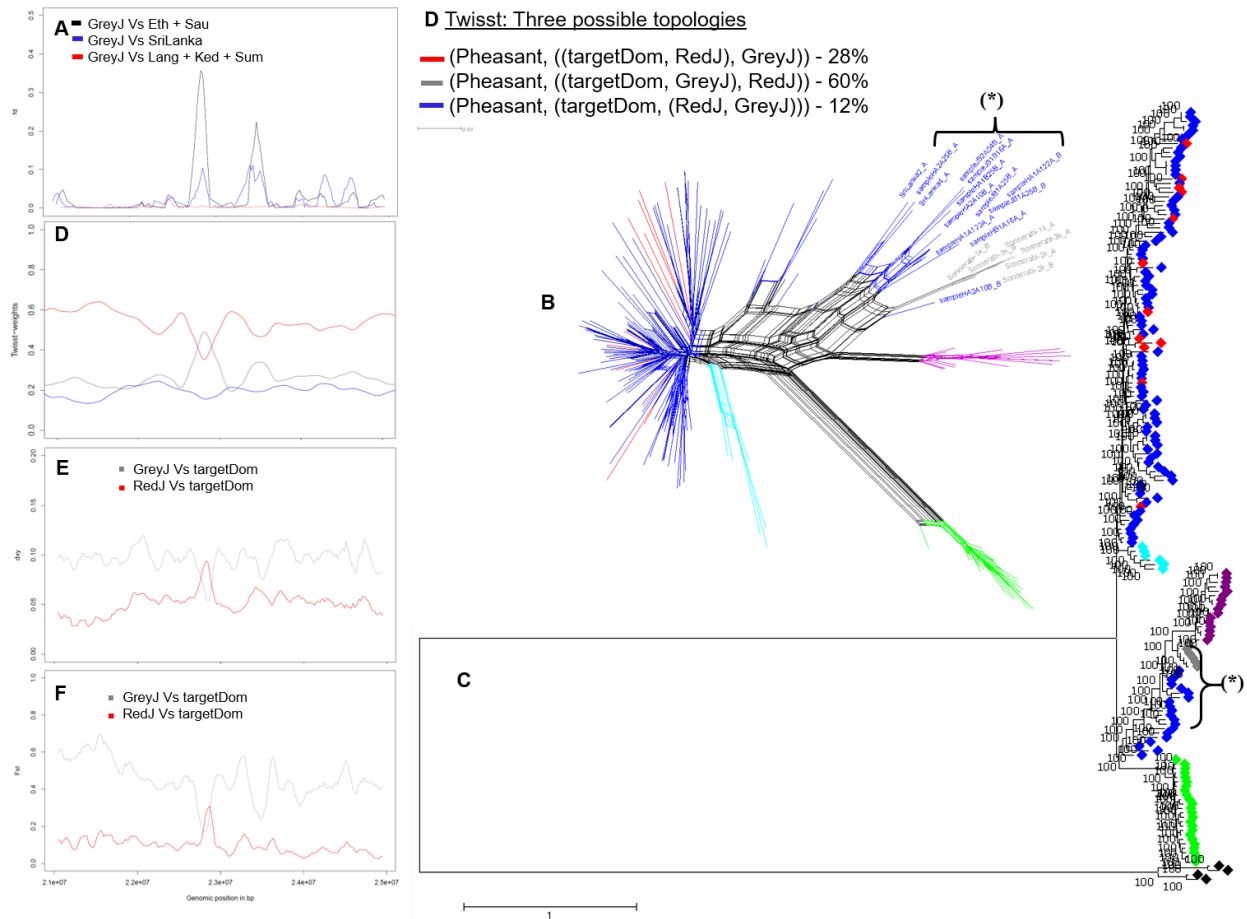


Fig. S9. A 140 kb (Chr 7: 22652767 - 22792759 bp) introgressed region from Grey junglefowl into domestic chicken.

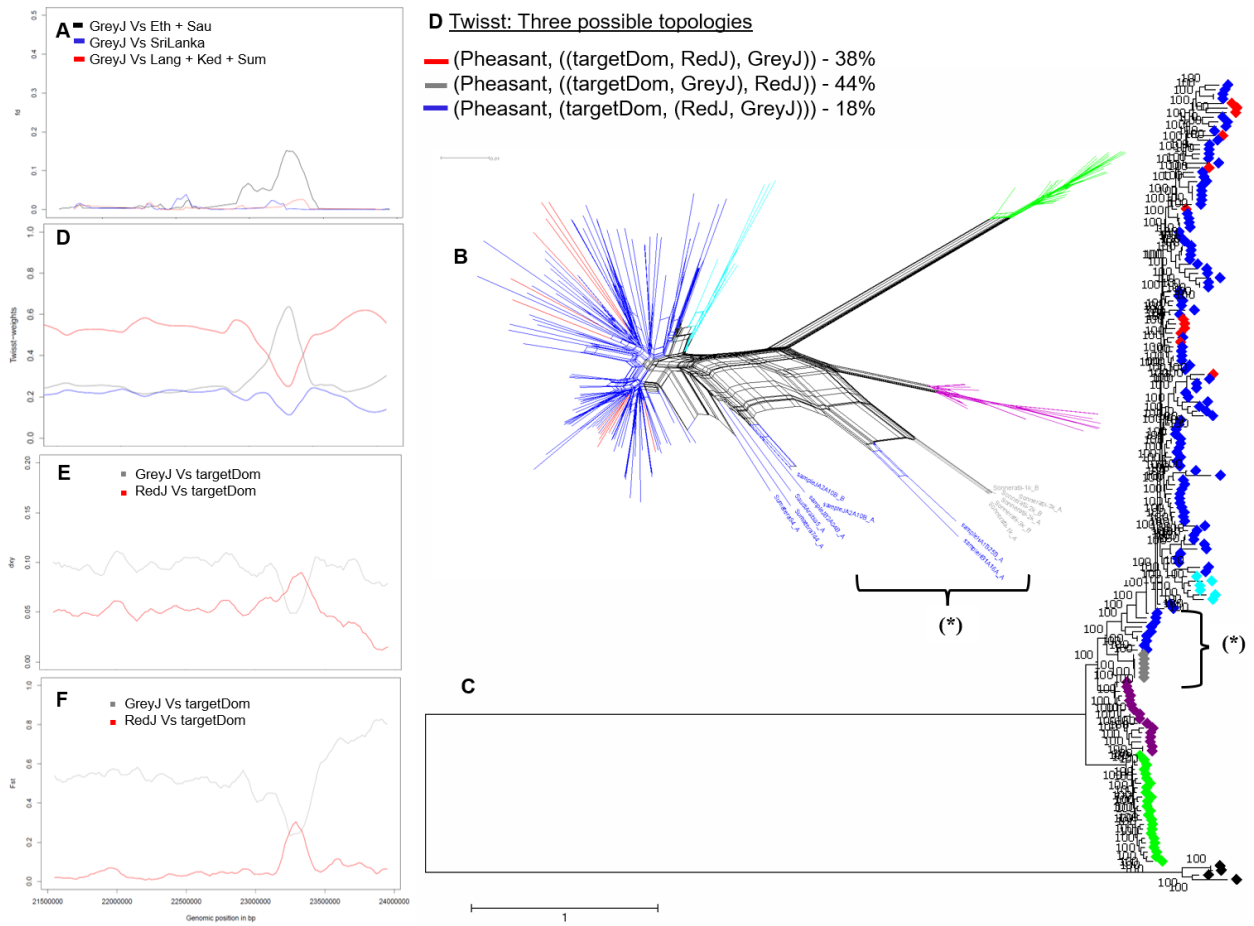


Fig. S10. A 500 kb (Chr 9: 23052049 - 23552045 bp) introgressed region from Grey junglefowl into domestic chicken.

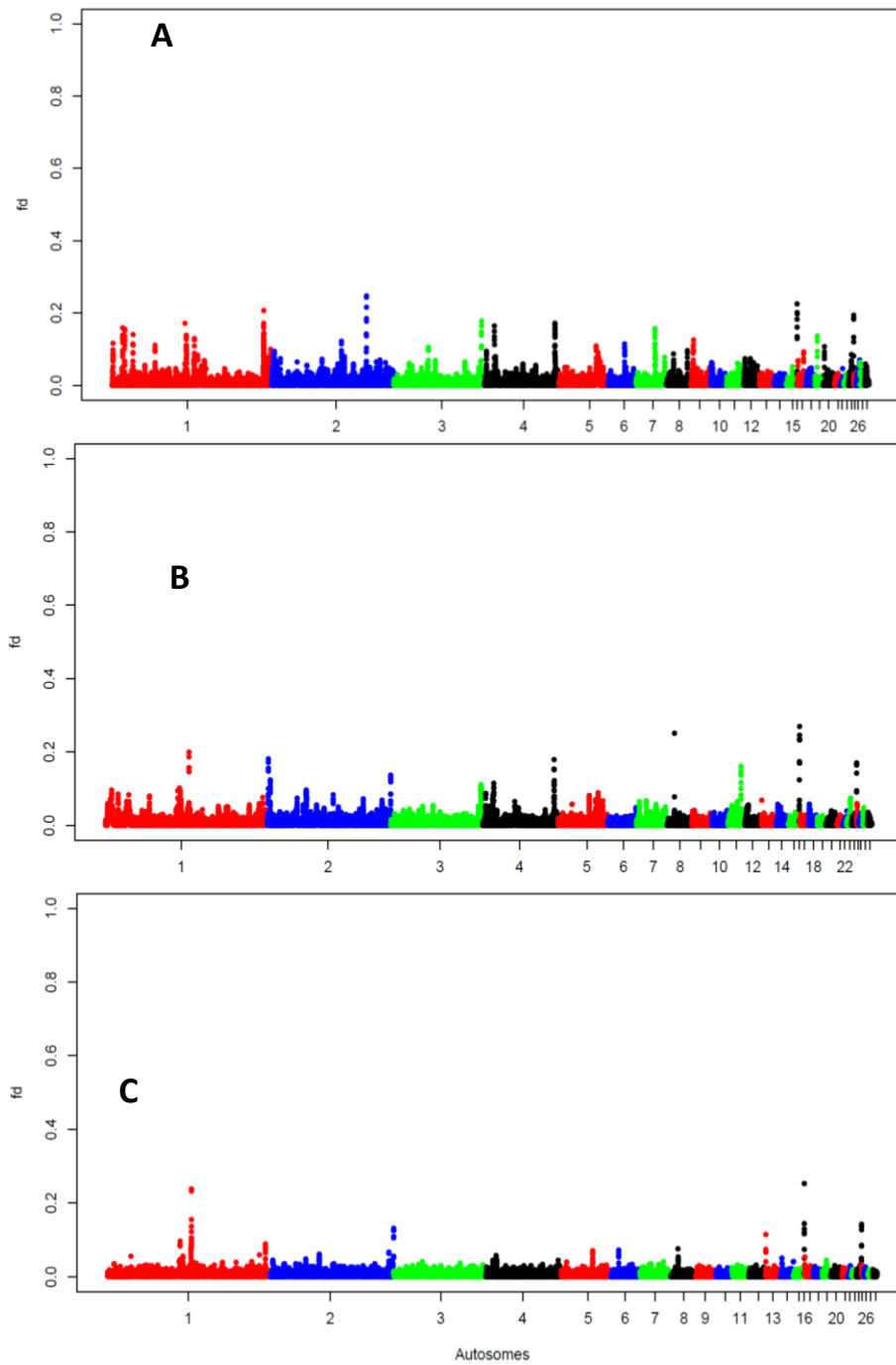


Fig. S12. The *fd* plots test for the comparison between Ceylon junglefowl and domestic chicken population from (A) Ethiopia and Saudi, (B) Sri Lanka and (C) Southeast and East Asia. The Y-axis *fd* value and X-axis 1 – 28 autosomes.

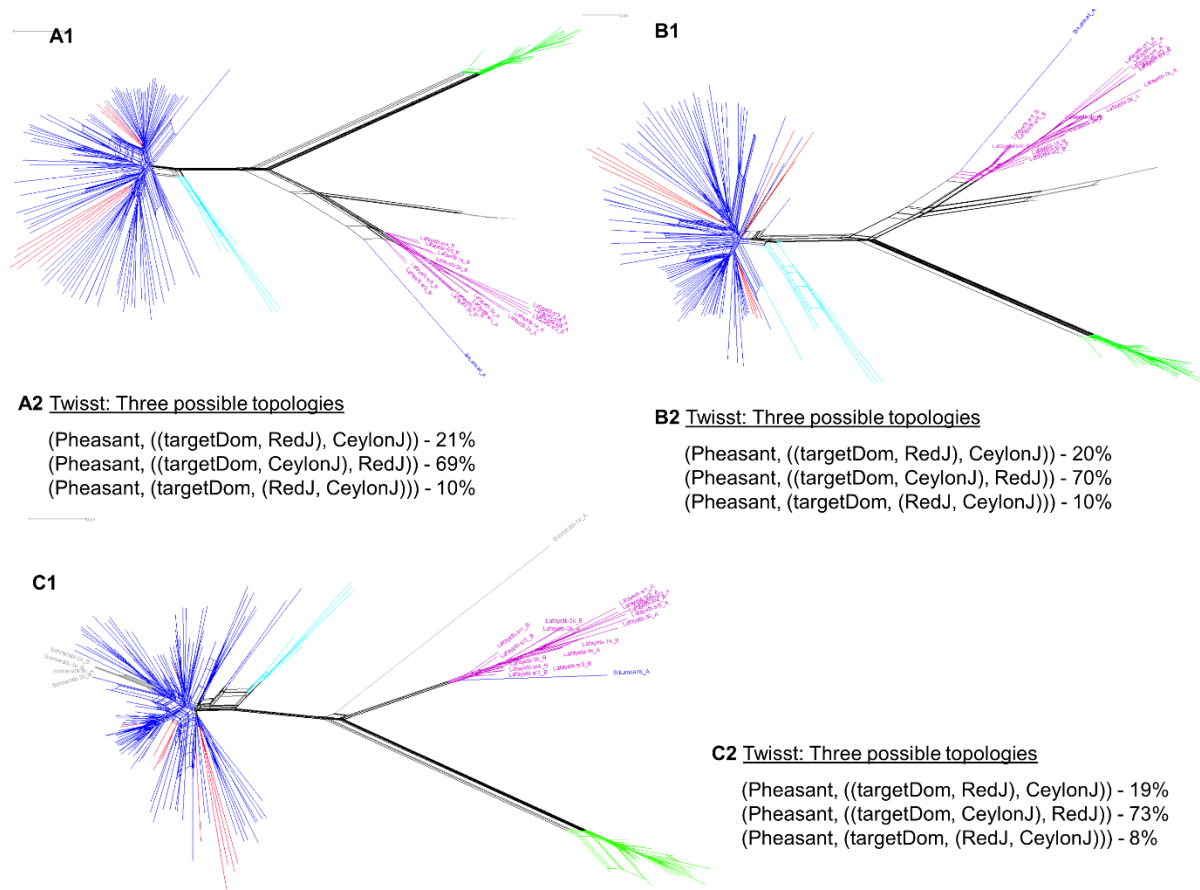


Fig. S13. Network and *Twisst* proportion of topologies for three Ceylon candidate introgressed regions into domestic chicken (**A - C**). (**A1**) and (**A2**) 6.52 Mb region Chr 1: 2895616 - 9418660 bp, (**B1**) and (**B2**) 3.95 Mb Chr 1: 25261354 - 29205161 bp, (**C1**) and (**C2**) 1.38 Mb region Chr 1: 147936229 - 149316591 bp. (**C1**) also shows support for introgression from domestic chicken to some Grey junglefowl haplotypes at the same region.

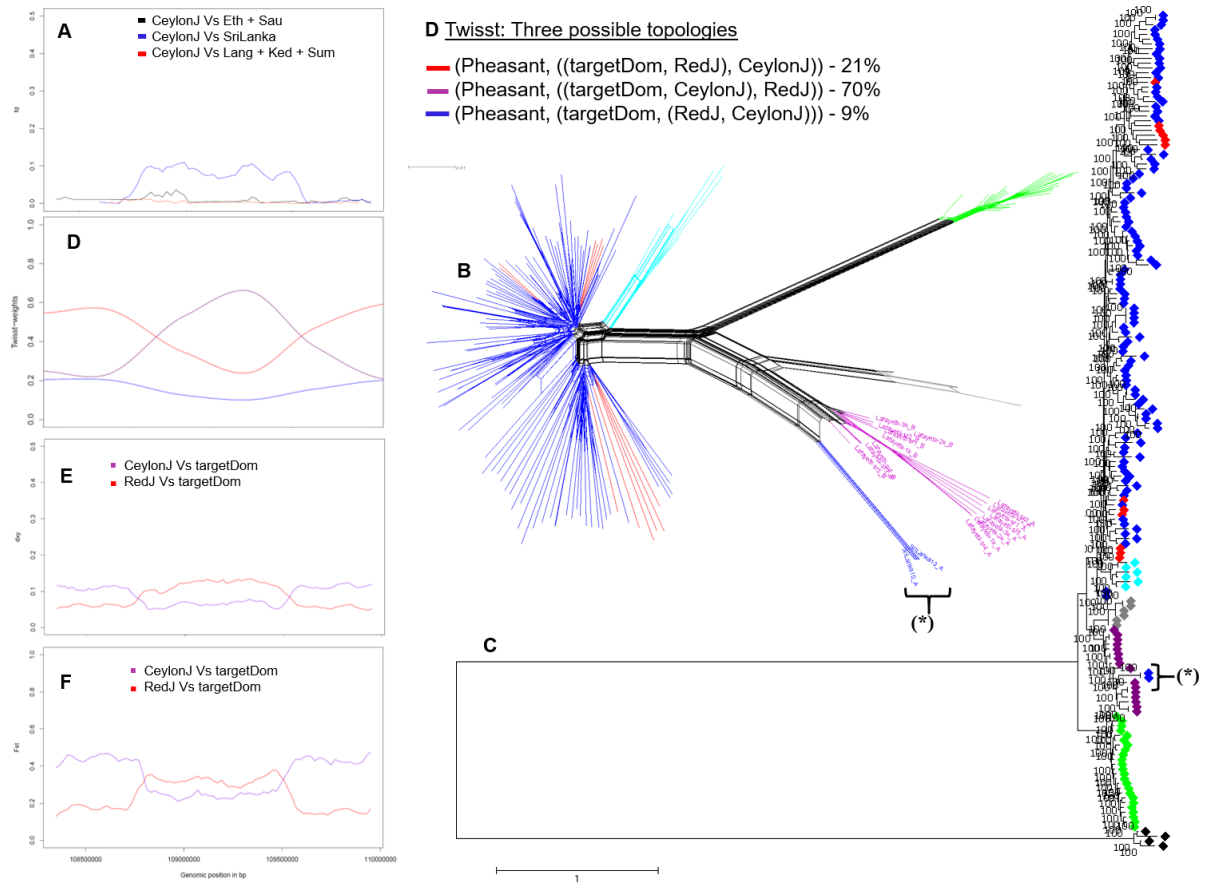


Fig. S14. A 600 kb (Chr 3: 108325801 - 108925723 bp) introgressed region from Ceylon junglefowl to domestic chicken. (A) *fd* plot (B) haplotype-based network, (C) maximum likelihood tree, (D) *Twisst* plot and the proportion of each topology, (E) D_{XY} and (F) F_{ST} . Eth, Sau, SriLanka, Lang, Ked, Sum are domestic chicken from Ethiopia, Saudi, Sri Lanka and Langshan, Kedu Hitam and Sumatra breeds, respectively, CeylonJ is Ceylon junglefowl and targetDom are the introgressed domestic chicken haplotypes (*). ◆: Domestic chicken; ◆: Red junglefowl, ◆: Javan red junglefowl, ◆: Grey junglefowl, ◆: Ceylon junglefowl, ◆: Green junglefowl, ◆: common Pheasant.

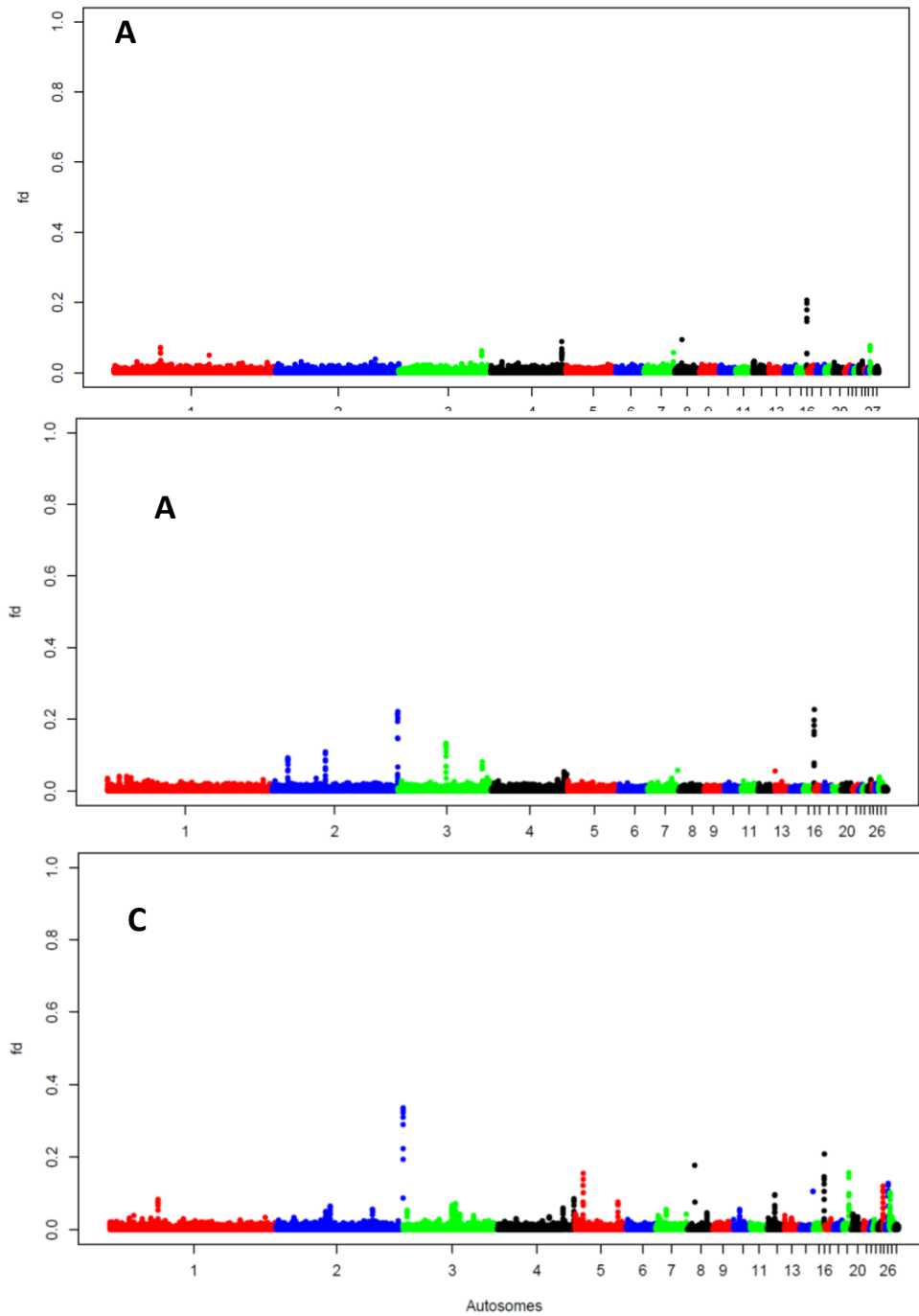


Fig. S15. The *fd* plots test for the comparison between Green junglefowl and domestic chicken population from (A) Ethiopia and Saudi, (B) Sri Lanka and (C) Southeast and East Asia. The Y-axis *fd* value and X-axis 1 – 28 autosomes.

Table S1. Sampling, mapping and variants statistics. HomAA and HetRA are the proportion of homozygous and heterozygous SNPs to the reference (*Galgal5.0*), respectively.

Sample Name	Species Name	Geographic Distribution/Collection Point	Mapped Rate	Properly paired rate	HomAA%	HetRA%	Total SNPs (HomAA + HetRA)
HA1A12A	Gallus gallus domesticus	Ethiopia	99.75	96.88	49.78	50.22	5496987
HA1B25B	Gallus gallus domesticus	Ethiopia	99.76	96.43	43.95	56.05	5715229
HA2A10B	Gallus gallus domesticus	Ethiopia	99.74	95.07	44.74	55.26	5702301
HA2A25B	Gallus gallus domesticus	Ethiopia	99.71	95.28	42.42	57.58	5772262
HB1A16A	Gallus gallus domesticus	Ethiopia	99.74	95.98	42.13	57.87	5818311
HB1B21B	Gallus gallus domesticus	Ethiopia	99.74	96.28	42.75	57.25	5779878
JA1A17A	Gallus gallus domesticus	Ethiopia	99.75	96.23	46.25	53.75	5611611
JA2A10B	Gallus gallus domesticus	Ethiopia	99.75	95.99	47.24	52.76	5577330
JB1A25B	Gallus gallus domesticus	Ethiopia	99.76	96.21	52.97	47.03	5345839
JB1B16A	Gallus gallus domesticus	Ethiopia	99.75	96.18	42.44	57.56	5764815
JB2A04B	Gallus gallus domesticus	Ethiopia	99.4	95.97	55.19	44.81	5303913
SaudiArabia1	Gallus gallus domesticus	Saudi Arabia	99.53	93.43	51.31	48.69	5254695
SaudiArabia2	Gallus gallus domesticus	Saudi Arabia	99.45	93.74	41.01	58.99	5685951
SaudiArabia3	Gallus gallus domesticus	Saudi Arabia	99.07	94.8	44.38	55.62	5391149
SaudiArabia4	Gallus gallus domesticus	Saudi Arabia	99.45	95.83	24.23	75.77	6540870
SaudiArabia5	Gallus gallus domesticus	Saudi Arabia	99.16	93.96	41.35	58.65	5562922
SriLanka1	Gallus gallus domesticus	Sri Lanka	99.14	94.21	36.75	63.25	6083602
SriLanka10	Gallus gallus domesticus	Sri Lanka	99.1	94.6	37.4	62.6	6061984
SriLanka12	Gallus gallus domesticus	Sri Lanka	99.21	93.83	35.27	64.73	6175086
SriLanka13	Gallus gallus domesticus	Sri Lanka	99.15	93.42	37.41	62.59	6056414
SriLanka15	Gallus gallus domesticus	Sri Lanka	99.16	93.1	36.98	63.02	6105444
SriLanka16	Gallus gallus domesticus	Sri Lanka	99.12	94.37	36.27	63.73	6159000
SriLanka2	Gallus gallus domesticus	Sri Lanka	99.04	94.38	35.84	64.16	6106133
SriLanka3	Gallus gallus domesticus	Sri Lanka	99.21	94.58	36.76	63.24	6084710
SriLanka4	Gallus gallus domesticus	Sri Lanka	98.98	94.51	35.08	64.92	6196012
SriLanka5	Gallus gallus domesticus	Sri Lanka	99.23	94.38	35.81	64.19	6155422
SriLanka9	Gallus gallus domesticus	Sri Lanka	99.2	94.27	34.83	65.17	6163149

Langshan1	Gallus gallus domesticus	Langshan, China - Collected in UK	99.79	98.99	64.19	35.81	4183574
Langshan2	Gallus gallus domesticus	Langshan, China - Collected in UK	99.89	99.07	62.76	37.24	4219311
Langshan3	Gallus gallus domesticus	Langshan, China - Collected in UK	99.84	98.73	67.7	32.3	4052704
Langshan4	Gallus gallus domesticus	Langshan, China - Collected in UK	99.87	98.3	59.37	40.63	4770695
Langshan5	Gallus gallus domesticus	Langshan, China - Collected in UK	99.89	99.06	61.98	38.02	4090606
Langshan6	Gallus gallus domesticus	Langshan, China - Collected in UK	99.86	99.03	61.29	38.71	4226957
Langshan7	Gallus gallus domesticus	Langshan, China - Collected in UK	99.85	97.49	63.9	36.1	4499626
Langshan8	Gallus gallus domesticus	Langshan, China - Collected in UK	99.87	98.29	62.04	37.96	4280925
Sumatera738	Gallus gallus domesticus	Indonesia	99.14	98.04	50.58	49.42	4556806
Sumatera741	Gallus gallus domesticus	Indonesia	99.12	97.52	57.44	42.56	4508322
Sumatera744	Gallus gallus domesticus	Indonesia	99.1	97.99	58.61	41.39	4450663
Sumatera757	Gallus gallus domesticus	Indonesia	99.1	97.26	51.82	48.18	4659515
Sumatera94	Gallus gallus domesticus	Indonesia	99.05	97.13	55.83	44.17	4193805
KeduHitam761	Gallus gallus domesticus	Indonesia	99.62	98.56	43.22	56.78	5458556
KeduHitam763	Gallus gallus domesticus	Indonesia	99.59	98.48	42.22	57.78	5551599
KeduHitam766	Gallus gallus domesticus	Indonesia	99.63	98.61	53.71	46.29	5205120
KeduHitam767	Gallus gallus domesticus	Indonesia	99.56	98.29	40.28	59.72	5745786
KeduHitam778	Gallus gallus domesticus	Indonesia	98.94	97.66	54.11	45.89	4996704
KeduHitam779	Gallus gallus domesticus	Indonesia	99.3	97.61	44.14	55.86	5324021
KeduHitam780	Gallus gallus domesticus	Indonesia	99.5	97.92	45.98	54.02	5424436
KeduHitam781	Gallus gallus domesticus	Indonesia	99.06	98	56.45	43.55	5035441
KeduHitam783	Gallus gallus domesticus	Indonesia	99.05	97.81	46.95	53.05	5126861
KeduHitam784	Gallus gallus domesticus	Indonesia	99.52	98.35	44.98	55.02	5238868
Mechelse-koekoek	Gallus gallus domesticus	Europe	96.9	91.9	55.47	44.53	5206378
Mechelse-styrian	Gallus gallus domesticus	Europe	97	92.89	34.66	65.34	6163592
Poulet-de-Bresse	Gallus gallus domesticus	Europe	97.63	93.32	47.83	52.17	5554109
RedJunglefowl1	Gallus gallus (Red junglefowl)	Southeast Asia	98.69	93.85	38.55	61.45	6090522
RedJunglefowl2	Gallus gallus (Red junglefowl)	Southeast Asia	99.53	96.65	38.48	61.52	6322049
RedJunglefowl3	Gallus gallus (Red junglefowl)	Southeast Asia	99.52	95.25	37.1	62.9	6721117
RedJunglefowl4	Gallus gallus (Red junglefowl)	Southeast Asia	99.51	96.66	43.85	56.15	6432497
RedJunglefowl5	Gallus gallus (Red junglefowl)	Southeast Asia	99.32	96	34.17	65.83	7055675

RedJungleFowlKoen	Gallus gallus (Red junglefowl)	South/Southeast Asia - Private collection	95.66	92.14	33.62	66.38	6790156
Bankiva650	Gallus gallus bankiva (Javan red junglefowl)	Indonesia	98.85	97.46	60.09	39.91	6880685
Bankiva759	Gallus gallus bankiva (Javan red junglefowl)	Indonesia	98.98	97.57	59.49	40.51	6890215
Bankiva760	Gallus gallus bankiva (Javan red junglefowl)	Indonesia	98.87	97.16	60.1	39.9	6811363
Sonneratii1k	Gallus sonneratii (Grey junglefowl)	Indian subcontinent - Private collection	99.69	95.4	77.76	22.24	10050824
Sonneratii2k	Gallus sonneratii (Grey junglefowl)	Indian subcontinent - Private collection	99.61	88.02	75.64	24.36	10115589
Sonneratii3k	Gallus sonneratii (Grey junglefowl)	Indian subcontinent - Private collection	99.69	95.4	84.74	15.26	9432160
Lafayetii1k	Gallus lafayetti (Ceylon junglefowl)	Sri Lanka - Private collection	99.61	90.84	79.78	20.22	10637322
Lafayetii2k	Gallus lafayetti (Ceylon junglefowl)	Sri Lanka - Private collection	99.66	93.6	79.84	20.16	10619033
Lafayetii3k	Gallus lafayetti (Ceylon junglefowl)	Sri Lanka - Private collection	99.67	95.1	85.73	14.27	10267990
Lafayetiisr1	Gallus lafayetti (Ceylon junglefowl)	Sri Lanka - Private collection	98.93	92.66	74.06	25.94	11126055
Lafayetiisr2	Gallus lafayetti (Ceylon junglefowl)	Sri Lanka	99.05	91.09	74.69	25.31	11091506
Lafayetiisr3	Gallus lafayetti (Ceylon junglefowl)	Sri Lanka	98.88	91.5	72.73	27.27	11216350
Lafayetiisr4	Gallus lafayetti (Ceylon junglefowl)	Sri Lanka	98.98	92.83	72.7	27.3	11215158
Lafayetiisr5	Gallus lafayetti (Ceylon junglefowl)	Sri Lanka	98.75	89.28	72.53	27.47	11218503
Varius1k	Gallus varius (Green junglefowl)	Indonesia - Private collection	99.52	85.65	87.94	12.06	12019627
Varius2k	Gallus varius (Green junglefowl)	Indonesia - Private collection	99.54	90.03	88.04	11.96	12004164
Varius3k	Gallus varius (Green junglefowl)	Indonesia - Private collection	99.61	94.6	86.74	13.26	11958988
VariusJava18	Gallus varius (Green junglefowl)	Indonesia	98.54	96.26	90.56	9.44	10591696
VariusJava19	Gallus varius (Green junglefowl)	Indonesia	98.47	96.51	82.54	17.46	11112951
VariusMandura702	Gallus varius (Green junglefowl)	Indonesia	98.56	95.01	92.29	7.71	11077799
VariusMandura703	Gallus varius (Green junglefowl)	Indonesia	98.83	94.31	88	12	11590408
VariusMandura704	Gallus varius (Green junglefowl)	Indonesia	98.77	94.76	91.51	8.49	10841620
VariusMandura706	Gallus varius (Green junglefowl)	Indonesia	98.71	93.73	89.48	10.52	11414585
VariusMandura710	Gallus varius (Green junglefowl)	Indonesia	98.76	95.26	90.96	9.04	10429506

VariusMandura714	Gallus varius (Green junglefowl)	Indonesia	98.8	94.82	92.26	7.74	10620997
VariusMandura715	Gallus varius (Green junglefowl)	Indonesia	98.69	95.02	90.07	9.93	11322992
PheasantsFemale	Phasianus colchicus	Collected in UK	91.95	81.69	96.01	3.99	53278629
PheasantsMale	Phasianus colchicus	Collected in UK	93	83.47	94.19	5.81	56157598

Table S2A. Candidate introgressed regions from domestic chicken and/or Red junglefowl into Grey/Ceylon junglefowls

Candidate introgressed regions*	Length	Genes within the candidate introgressed regions***
<i>Domestic chicken/Red junglefowl into Grey Junglefowl</i>		
Chr1: 141.0 – 167.0	26 Mb	<i>TNFSF13B, ABHD13, LIG4, FAM155A, ARGLU1, EFN2, SLC10A2, ERCC5, BIVM, KDELC1, TEX30, METTL21C, TPP2, FHF-4, ITGBL1, NALCN, TMTC4, GGACT, PCCA, ZIC2, ZIC5, CLYBL, TM9SF2, gga-mir-2984, UBAC2, GPR183, GPR18, DOCK9, SLC15A1, STK24, FARP1, gga-mir-1555, IPO5, RAP2A, MBNL2, UGGT2, DNAJC3, DZIP1, CLDN10, ABCC4, SOX21, GPR180, TGDS, DCT, RF00066, GPC5, gga-mir-92-1, gga-mir-19b, gga-mir-20a, gga-mir-19a, gga-mir-18a, gga-mir-17, SLITRK6, SLITRK1, SPRY2, NDFIP2, RBM26, RNF219, POU4F1, EDNRB, SLAIN1, MYCBP2, FBXL3, CLN5, GATD3A, ACOD1, KCTD12, LMO7, UCHL3, TBC1D4, KLF12, KLF5, PIBF1, DIS3, BORA, MZT1, DACH1, gga-mir-1743, KLHL1, PCDH9, RF00154, gga-mir-7445-2, TDRD3, DIAPH3, PCDH17, RF02271, RF00493, RF00494, OLFM4, PCDH8, CNMD, SUGT1, ELF1, WBP4, MTRF1, RGCC, VWA8</i>
Chr2: 11.0 – 20.0	9 Mb	<i>PFKP, PITRM1, KLF6, gga-mir-6628, GJD4, CCNY, CREM, CUL2, PARD3, RF02271, NR1, ITGB1, EPC1, gga-mir-1768, KIF5B, ARHGAP12, ZEB1, ZNF438, SVIL, JCAD, MTPAP, MAP3K8, BAMBI, WAC, MPP7, ARMC4, MKX, RAB18, YME1L1, MASTL, ACBD5, ABI1, PDSS1, APBB1IP, GAD2, MYO3A, GPR158, THNSL1, ENKUR, PRTFDC1, ARHGAP21, KIAA1217, PTF1A, ARMC3, PIP4K2A, SPAG6, gga-mir-12240, BMI1, COMMD3, DNAJC1, MLLT10, RF00001, NEBL, PLXDC2, MALRD1, ARL5B, NSUN6, CACNB2, SLC39A12, MMR1L2, MMR1L1, MMR1L3, MMR1L4, MRC1, STAM, HACD1, VIM, ST8SIA6, gga-mir-1661, TRDMT1, CUBN</i>
Chr4: 76.4 – 79.2	2.8 Mb	<i>TAPT1, Prom1, FGFBP2, CD38, BST1, FBXL5, CC2D2A, C1QTNF7, CPEB2, NKX3-2, RAB28, HS3ST1, ZNF518B, WDR1, SLC2A9, DRD5, OTOP1, TMEM128, LYAR, ZBTB49, NSG1, STX18, MSX1, CYTL1, STK32B, EVC2, EVC, CRMP1B</i>
<i>Domestic chicken into Ceylon junglefowl</i>		
Chr5: 49.33 – 49.43	100 kb	<i>No gene</i>

*Positions along the chromosome in megabase (Mb),

Table S2B. Candidate introgressed regions from non-red junglefowls into domestic chicken/Red junglefowl

Candidate introgressed regions*	Length	Proportion of haplotypes introgressed in each population (%)**							Genes within the candidate introgressed regions***
		Ethiopia (n = 22)	Saudi Arabia (n = 10)	Sri Lanka (n = 22)	SEA Langshan (n = 16)	SEA Kedu Hitam (n = 20)	SEA Sumatra (n = 10)	Red Junglefowl (n = 12)	
<i>Introgressed regions from Grey junglefowl to domestic chicken/Red junglefowl</i>									
Chr2:119.68 – 119.90	220 kb	23	20	9	0	0	0	8	-
Chr3:50.75 – 50.85	100 kb	27	0	23	0	5	10	0	<i>NOX3</i>
Chr4:62.10 – 62.30	200 kb	14	0	0	0	0	0	0	<i>RF00003</i>
Chr5:45.67 – 45.95	280 kb	41	10	9	0	0	0	0	<i>PPP4R4, SERPINA10, SPIA4, SPIA1, GSC</i>
Chr6:20.72 – 20.84	120 kb	45	0	0	0	0	0	0	<i>IDE, Mar-05, CPEB3</i>
Chr7:22.65 – 22.79	140 kb	50	0	9	0	0	0	0	-
Chr9:23.05 – 23.55	500 kb	23	10		0	0	20	0	<i>KCNAB3, GMPS, gga-mir-1658, C3orf33, PLCH1, MME, GPR149, DHX36, RAP2B, ARHGEF26, P2RY1, MBNL1</i>
Chr12: 12.54 – 12.64	100 kb	27	0	0	0	0	0	0	<i>FHIT</i>
<i>Introgressed regions from Ceylon junglefowl to domestic chicken</i>									
Chr1:2.90 – 9.42	6.52 Mb	0	0	5	0	0	0	0	<i>PLXNA4, gga-mir-6621, PODXL, MKLN1, gga-mir-29b-1, gga-mir-29a, K123, IL2RA, RBM17, PFKFB3, SFMBT2, ITIH5, ITIH2, KIN, ATP5F1C, TAF3, GATA3, CELF2, gga-mir-1626, gga-mir-1596, USP6NL, ECHDC3, UPF2, DHTKD1, SEC61A2, NUDT5, CDC123, CAMK1D, CCDC3, OPTN, MCM10, PHYH, SEPHS2L, BEND7, FRMD4A, gga-mir-1460, FAM107B, HSPA14, SUV39H2, DCLRE1C, MEIG1, TMEM243, DMTF1, RF02271, KIAA1324L, GRM3, SEMA3D, SEMA3A</i>
Chr1:25.25 – 29.21	3.95 Mb	0	0	5	0	0	0	0	<i>TES, TFEC, MDFIC, FOXP2, PPP1R3A, GPR85, gga-mir-1695, BMT2, TMEM168, LSMEM1, IFRD1, ZNF277, DOCK4, IMMP2L, LRRN3,</i>

Chr1:147.94 – 149.32	1.38 Mb	0	0	5	0	0	0	0	<i>DNAJB9, THAP5, AVPR2, PNPLA8, NRCAM, gga-mir-12208, CNTN1, PDZRN4 GPC6, RF00066, GPC5</i>
Chr3:108.33 – 108.93	600 kb	0	0	9	0	0	0	0	<i>CRISP3, CRISP2, RHAG, CYP2AC1, CYP2AC2, CENPQ, MMUT, OPN5L2, FOXP2</i>
<i>Introgressed region from Green junglefowl to domestic chicken</i>									
Chr5: 9.54 – 9.64	100 kb	0	0	0	63	0	0	0	<i>SWAP70, WEE1, ZNF143, IPO7, RF00319</i>

*Positions along the chromosome in megabase (Mb), **SEA (South-East and East Asia), ***Ensembl release version 96

1 **Table S3.** Functional annotations for the enriched genes within the introgressed regions

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Gene ontology for introgressed genes from domestic chicken to Grey junglefowl			
Term	Biological function	P-Value	Genes
GO:0002042	cell migration involved in sprouting angiogenesis	0.003885481	<i>NRP1, EFNB2, ITGB1</i>
GO:0030890	positive regulation of B cell proliferation	0.004098509	<i>BMII, GPR183, CD38, BST1</i>
			<i>GPR183, RAP2A, SLC2A9, GPR158, OLFM4, NRP1, BST1, VIM, EFNB2, PCDH9, CLDN10, PCDH8, LIG4, PCDH17, APBB1IP, WBP4, ITGB1, CD38, GPC5, SVIL,</i>
GO:0005886	plasma membrane	0.004886068	<i>NALCN, BAMBI, PIP4K2A, DNAJC1</i>
GO:0007224	smoothened signaling pathway	0.015997843	<i>EVC2, EVC, DZIP1, CC2D2A</i>
			<i>DCT, ZBTB49, KLF6, NRP1, ZNF518B, KLF12, DZIP1, MBNL2, LIG4, ZEB1,</i>
GO:0046872	metal ion binding	0.01615502	<i>ITGB1, ZNF438, PCCA, RBM26</i>
GO:0045595	regulation of cell differentiation	0.017578595	<i>SPRY2, SOX21, STK24</i>
GO:0003953	NAD ⁺ nucleosidase activity	0.022841738	<i>CD38, BST1</i>
	transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific		
GO:0001227	binding	0.033003736	<i>MSX1, KLF12, ZEB1</i>
GO:0045814	negative regulation of gene expression, epigenetic	0.047610409	<i>BMII, EPC1</i>
Gene ontology for introgressed genes from Grey junglefowl to domestic chicken			
GO:0050435	Beta-amyloid metabolic process	0.009746297	<i>IDE, MME</i>
GO:0003725	Double-stranded RNA binding	0.044235391	<i>DHX36, MBNL1</i>
Gene ontology for introgressed genes from Ceylon junglefowl to domestic chicken			
GO:0030212	hyaluronan metabolic process	0.021181	<i>ITIH5, ITIH2</i>
GO:0009791	Post-embryonic development	0.025842519	<i>MUT, GATA3, FOXP2</i>
GO:0000380	alternative mRNA splicing, via spliceosome	0.036777	<i>CELF2, RBM17</i>
GO:0045786	negative regulation of cell cycle	0.04704	<i>GATA3, THAP5</i>
			<i>TAF3, CENPQ, THAP5, CDC5L, OPTN, KIN, SUV39H2, FOXP2, DMTF1, MDFIC, TFEC, GATA3, CELF2, IFRD1, CAMK1D, TES</i>
GO:0005634	nucleus	0.039752	
	transcription factor activity, RNA polymerase II		
GO:0001135	transcription factor recruiting	0.019549	<i>DMTF1, CDC5L</i>
GO:0038191	neuropilin binding	0.048175	<i>SEMA3D, SEMA3A</i>
GO:0044212	transcription regulatory region DNA binding	0.049902	<i>DMTF1, GATA3, CDC5L</i>

