CORRECTION

Correction to: Evolution at two time frames: ancient structural variants involved in post-glacial divergence of the European plaice (*Pleuronectes platessa*)

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Published online: 29 April 2021

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Correction to: *Heredity*

<https://doi.org/10.1038/s41437-020-00389-3>

The original version of this article unfortunately contained mistakes. The presentation of Table 2 and Fig. 4 was incorrect. The corrected Table 2 and Fig. 4 are given below.

Table 2 Summary table of the divergence history between the populations from Iceland and Norway inferred with (SV incl.) and without (SV excl.) the chromosomes carrying putative SVs.

Data	Model	AIC	Δ_{AIC}	W_{AIC}	T_S	$T_{SC \text{ or } AM}$	P
SVs incl.	SC_af_2m	1678.00	0.00	0.67	57.91	28.19	1.47
	SC_af_rf_2m	1680.00	2.00	0.25	67.46	28.26	1.60
	IM_af_2m	1684.00	6.00	0.03	96.40	–	49.89
	IM_af_rf_2m	1684.00	6.00	0.03	96.60	–	0.55
	AM_af_2m	1687.00	9.00	0.01	96.35	0.27	49.62
	AM_af_rf_2m	1688.00	10.00	0.01	97.48	0.16	49.42
SVs excl.	SC_af_2m	1620.00	0.00	0.59	54.56	26.74	1.05
	SC_af_rf_2m	1622.00	2.00	0.22	60.71	31.36	0.87
	IM_af_rf_2m	1623.00	3.00	0.13	89.37	–	0.44
	IM_af_2m	1625.00	5.00	0.05	93.68	–	49.90
	AM_af_2m	1628.00	8.00	0.01	92.85	0.16	47.38
	AM_af_rf_2m	1630.00	10.00	0.00	96.32	0.19	48.65

In order of appearance, the table shows the dataset used for the inferences, the six best models sorted by AIC, their AIC, the difference of AIC with the best model (Δ_{AIC}), the weighted AIC (W_{AIC}), the time of split between populations (T_S), the time of secondary contact or ancestral migration ($T_{AM \text{ or } SC}$), and the percentage of the genome affected by reduced migration rate (P). The best model for each pairwise comparison is highlighted in bold.

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Fig. 4 Detailed analyses of structural variants. Sample-specific data for the European plume structural variants SV19 (a, c, e, g, i) and SV21 (b, d, f, h, j): a, b sample-specific allele frequencies (yellow=allele found twice in haplogroup 1 and once in haplogroup 2, and blue=allele found twice in haplogroup 3 and once in haplogroup 2); c, d differentiation between different pairs of populations and

between haplogroups 1 and 3 along the two chromosomes carrying the SVs, each dot is the F_{ST} value of an individual locus and the lines represent the smoothed upper 1% quantile (one color is one comparison, $\alpha=0.3$); e, f smoothed average π for the three haplogroups identified in the DAPC (span = 0.3); g, h variation of LD along the chromosomes and i, j LD heatmaps for pairwise SNP comparisons.