

Table S5. Relative allele frequency for all the MHC alleles found along the latitudinal gradient. N= number of individual per population, A_s = Alleles within sampling areas.

A _s	Germany			Skane			Uppsala		Umeå		Luleå	
N	14	10	10	20	20	19	18	19	19	19	20	19
Raar_DAB*01	0.071	0	0	0	0	0	0	0	0	0	0	0
Raar_DAB*02	0.321	0.1	0.1	0	0	0	0	0	0	0	0	0
Raar_DAB*03	0.107	0	0	0	0	0	0	0	0	0	0	0
Raar_DAB*04	0.143	0.1	0.15	0	0	0	0	0	0	0	0	0
Raar_DAB*05	0.071	0.2	0.15	0	0	0	0	0	0	0	0	0
Raar_DAB*06	0.036	0	0	0	0.05	0	0	0	0	0	0	0
Raar_DAB*07	0.143	0	0	0	0	0	0	0	0	0	0	0
Raar_DAB*08	0.107	0	0.05	0	0	0	0	0	0	0	0	0
Raar_DAB*09	0	0	0	0	0	0	0.167	0	0.026	0.026	0	0
Raar_DAB*10	0	0	0	0	0	0	0.028	0	0	0	0	0
Raar_DAB*11	0	0	0	0	0	0	0.028	0	0	0	0	0
Raar_DAB*12	0	0	0	0	0	0	0.139	0.026	0	0	0	0
Raar_DAB*13	0	0	0	0	0	0	0.056	0.026	0	0	0	0
Raar_DAB*14	0	0.05	0	0	0	0	0.25	0	0	0	0	0
Raar_DAB*15	0	0.2	0.2	0.05	0.125	0.053	0.167	0	0.105	0.289	0	0
Raar_DAB*16	0	0	0	0	0	0	0.028	0	0	0	0	0
Raar_DAB*17	0	0	0	0	0	0	0.028	0.421	0	0	0	0
Raar_DAB*18	0	0	0	0	0	0	0.028	0	0	0.053	0	0
Raar_DAB*19	0	0	0	0	0	0	0.083	0	0	0	0	0
Raar_DAB*20	0	0	0	0	0	0	0	0	0.447	0.395	0.825	0.711
Raar_DAB*21	0	0	0	0	0	0	0	0	0.395	0.053	0.125	0.237
Raar_DAB*22	0	0	0	0	0	0.053	0	0	0.026	0	0	0
Raar_DAB*23	0	0	0	0	0	0	0	0	0	0.026	0	0
Raar_DAB*24	0	0	0	0	0	0	0	0	0	0.105	0	0
Raar_DAB*25	0	0	0	0	0	0	0	0	0	0.026	0	0
Raar_DAB*26	0	0	0	0	0.025	0	0	0	0	0.026	0	0
Raar_DAB*27	0	0	0	0.45	0.075	0.184	0	0	0	0	0	0
Raar_DAB*28	0	0	0.1	0.35	0.325	0.658	0	0	0	0	0	0
Raar_DAB*29	0	0	0	0.075	0	0	0	0	0	0	0	0
Raar_DAB*30	0	0	0	0.05	0	0	0	0	0	0	0	0
Raar_DAB*31	0	0	0	0.025	0.05	0	0	0	0	0	0	0
Raar_DAB*32	0	0	0	0	0	0	0	0	0	0	0.025	0
Raar_DAB*33	0	0	0	0	0	0	0	0	0	0	0.025	0
Raar_DAB*34	0	0	0	0	0.1	0	0	0	0	0	0	0
Raar_DAB*35	0	0	0	0	0.025	0	0	0	0	0	0	0
Raar_DAB*36	0	0	0	0	0.025	0	0	0	0	0	0	0
Raar_DAB*37	0	0	0	0	0.05	0.026	0	0	0	0	0	0
Raar_DAB*38	0	0	0	0	0.025	0	0	0	0	0	0	0
Raar_DAB*39	0	0	0	0	0.025	0	0	0	0	0	0	0
Raar_DAB*40	0	0	0	0	0.05	0	0	0	0	0	0	0

