Electronic Supplemental Material

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Parviainen A, Härkönen T, Ilonen J, But A, Knip M, and the Finnish Pediatric Diabetes Register. Heterogeneity of Type 1 Diabetes at Diagnosis Supports Existence of Age-related Endotypes. *Diabetes Care*

-Investigators of the Finnish Pediatric Diabetes Register

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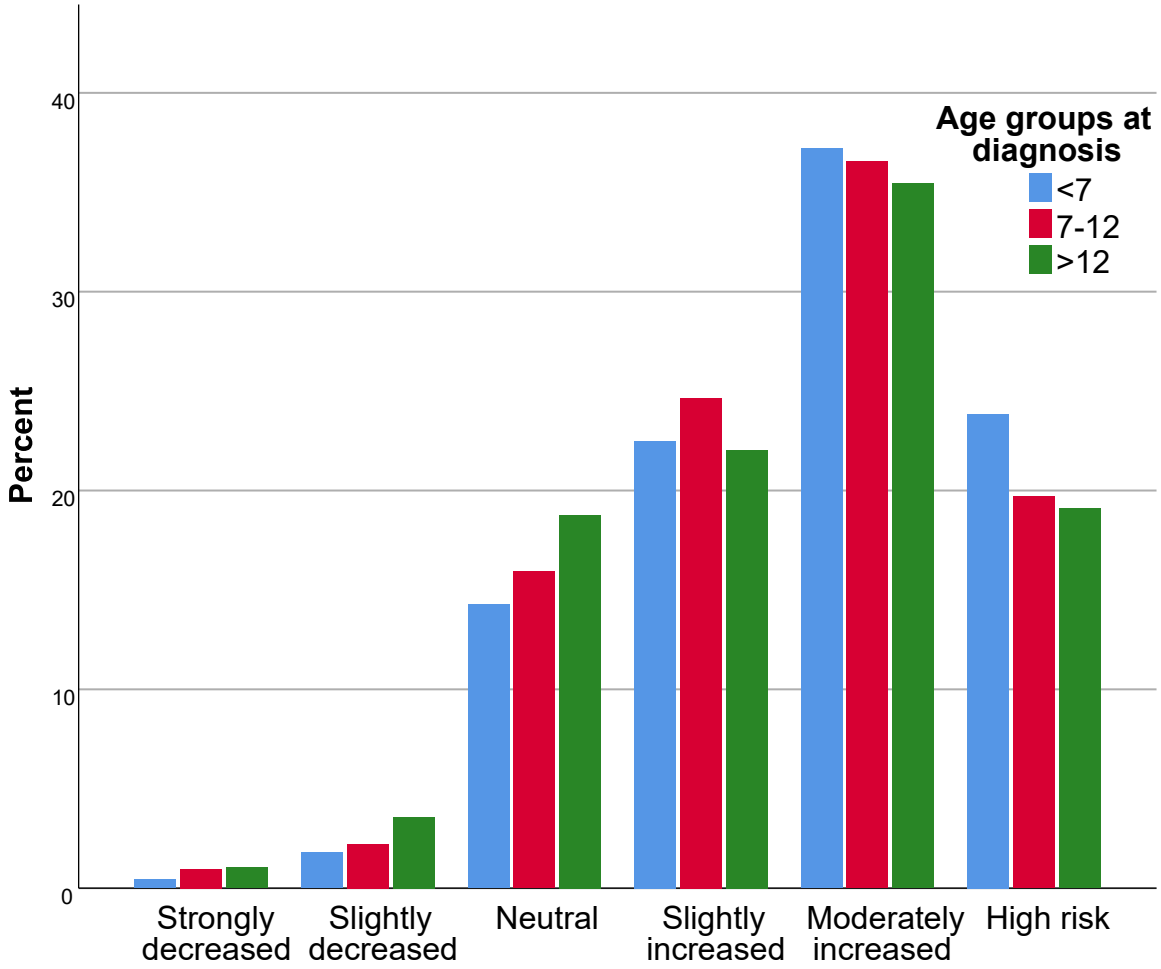
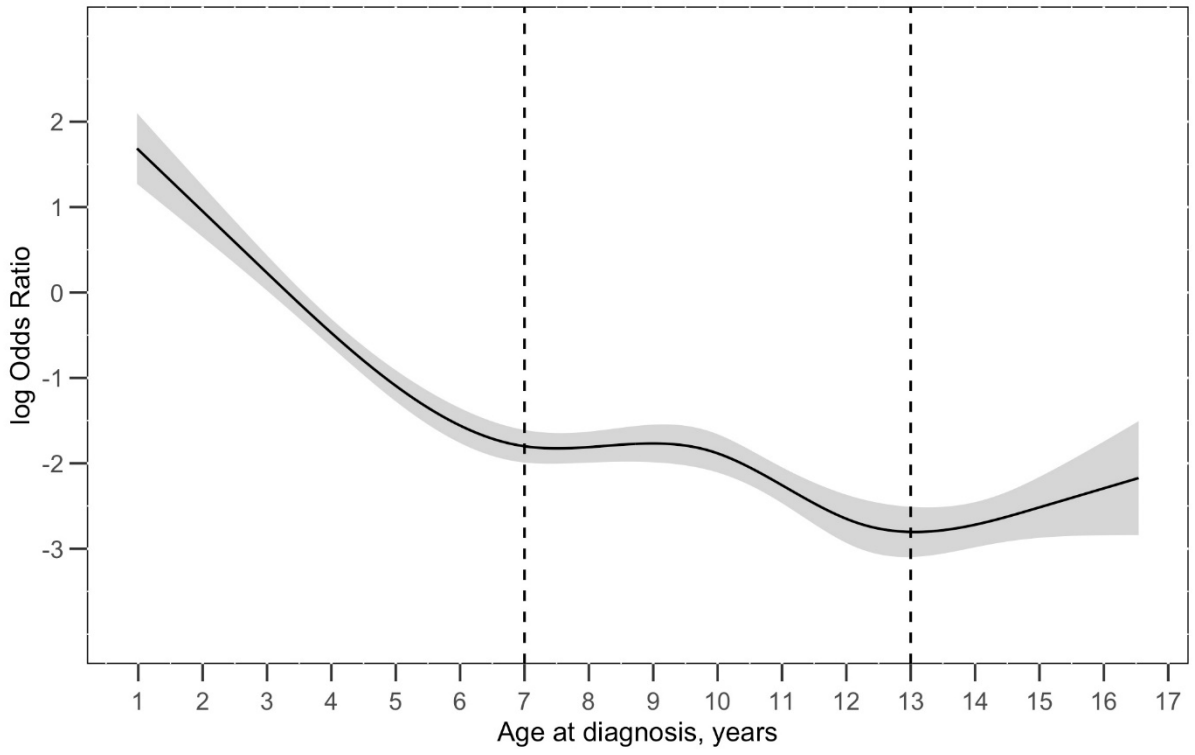
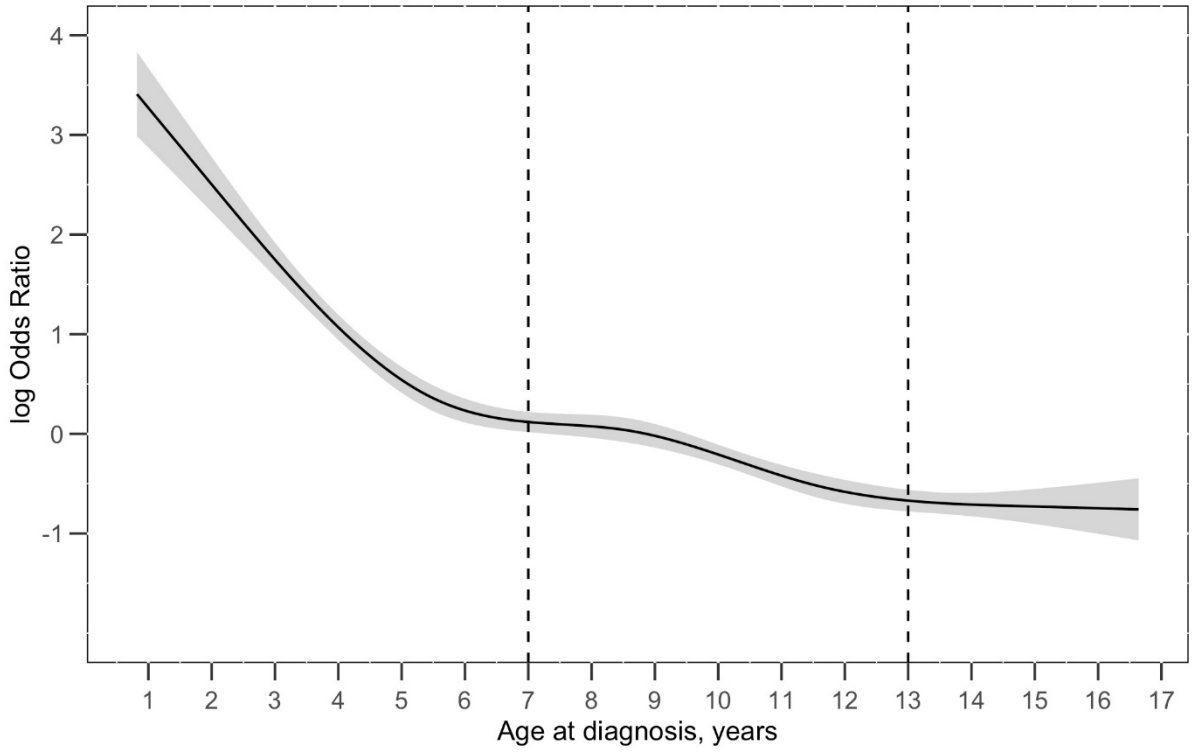
Supplementary Figure S1 – The distribution of HLA-DR/DQ genotype-based risk groups by age at diagnosis. Overall significance $P < 0.001$ (Kruskal-Wallis test). Pairwise comparisons (Mann-Whitney U-test): $P < 0.001$ for both the youngest age group *vs.* the oldest one, and the youngest age group vs. the middle age group.



Supplementary Figure S2 − The likelihood of having IAA positivity and familial type 1 diabetes rather than having IAA negativity and non-familial type 1 diabetes in relation to age at diagnosis estimated using binary logistic regression analysis with the restricted cubic spline function of age as the explanatory variable ($P < 0.001$ for non-linearity, $P < 0.001$ for the overall association). The grey area corresponds to the 95% confidence band, and the two vertical dashed lines are set to 7 and 13 years, to demonstrate the division into the three age groups used in the main analyses.



Supplementary Figure S3 – The likelihood of having IAA positivity and non-familial type 1 diabetes rather than having IAA negativity and non-familial type 1 diabetes in relation to age at diagnosis estimated using binary logistic regression analysis with the restricted cubic spline function of age as the explanatory variable ($P < 0.001$ for non-linearity, $P < 0.001$ for the overall association). The grey area corresponds to the 95% confidence band, and the two vertical dashed lines are set to 7 and 13 years, to demonstrate the division into the three age groups used in the main analyses.



Supplementary Figure S4 – The likelihood of having IAA negativity and familial type 1 diabetes rather than having IAA negativity and non-familial type 1 diabetes in relation to age at diagnosis. The likelihood was estimated using binary logistic regression analysis with the restricted cubic spline function of age as the explanatory variable [*P* = 0.529 for non-linearity, *P* = 0.002 for the linear association with a negative slope (OR=0.93, 95% CI 0.92-0.98)]. The grey area corresponds to the 95% confidence band, and the two vertical dashed lines are set to 7 and 13 years, to demonstrate the division into the three age groups used in the main analyses.