

**Cell Reports Medicine, Volume 4**

**Supplemental information**

**Plasma protein biomarkers predict the development  
of persistent autoantibodies and type 1 diabetes  
6 months prior to the onset of autoimmunity**

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## Appendix 1

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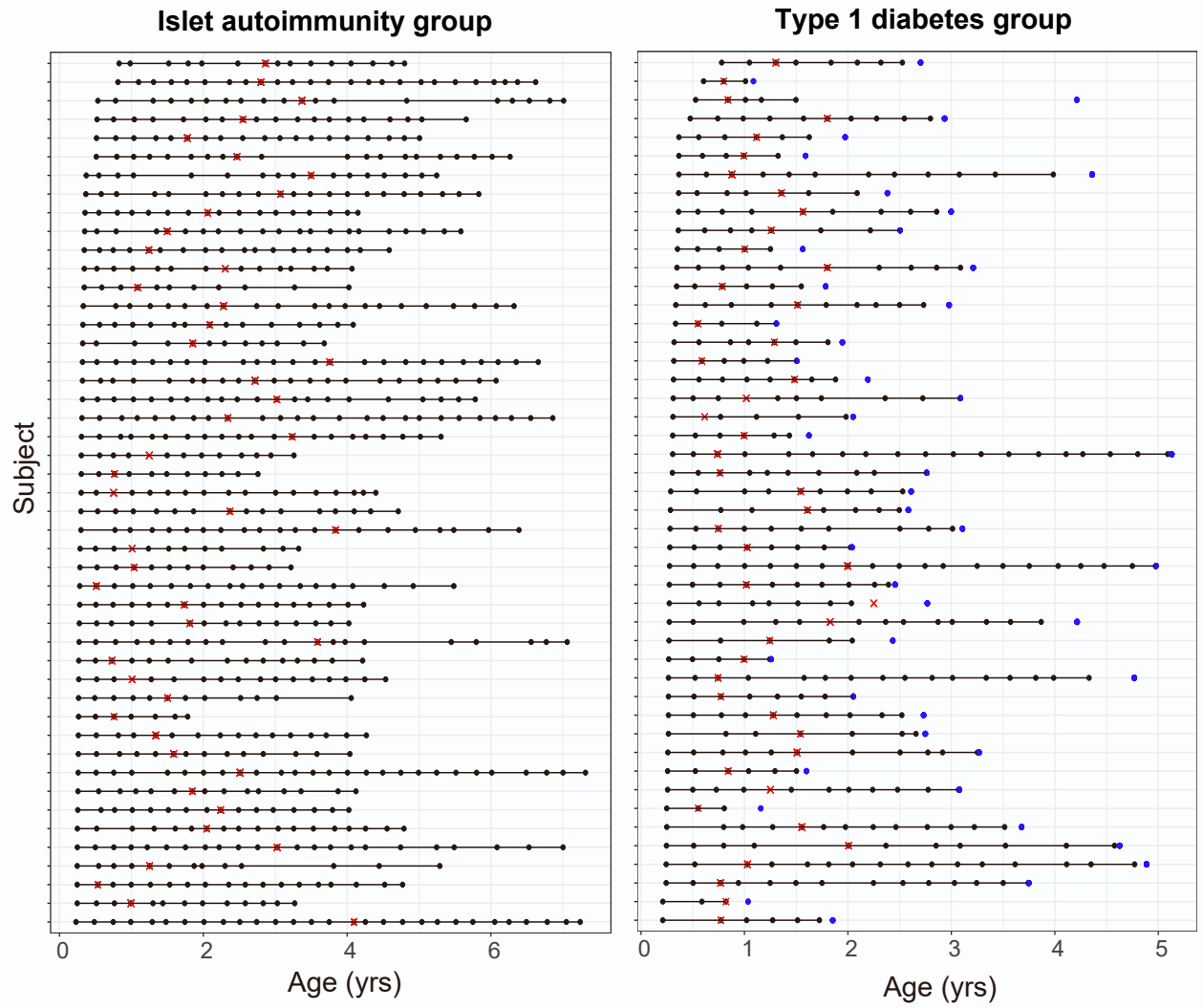
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**Repository:** Chris Deigan. NIDDK Biosample Repository at Fisher BioServices, Rockville, MD, USA. (Previously Ricky Schrock, Polina Malone, Sandra Ke, Niveen Mulholland, Ph.D.)

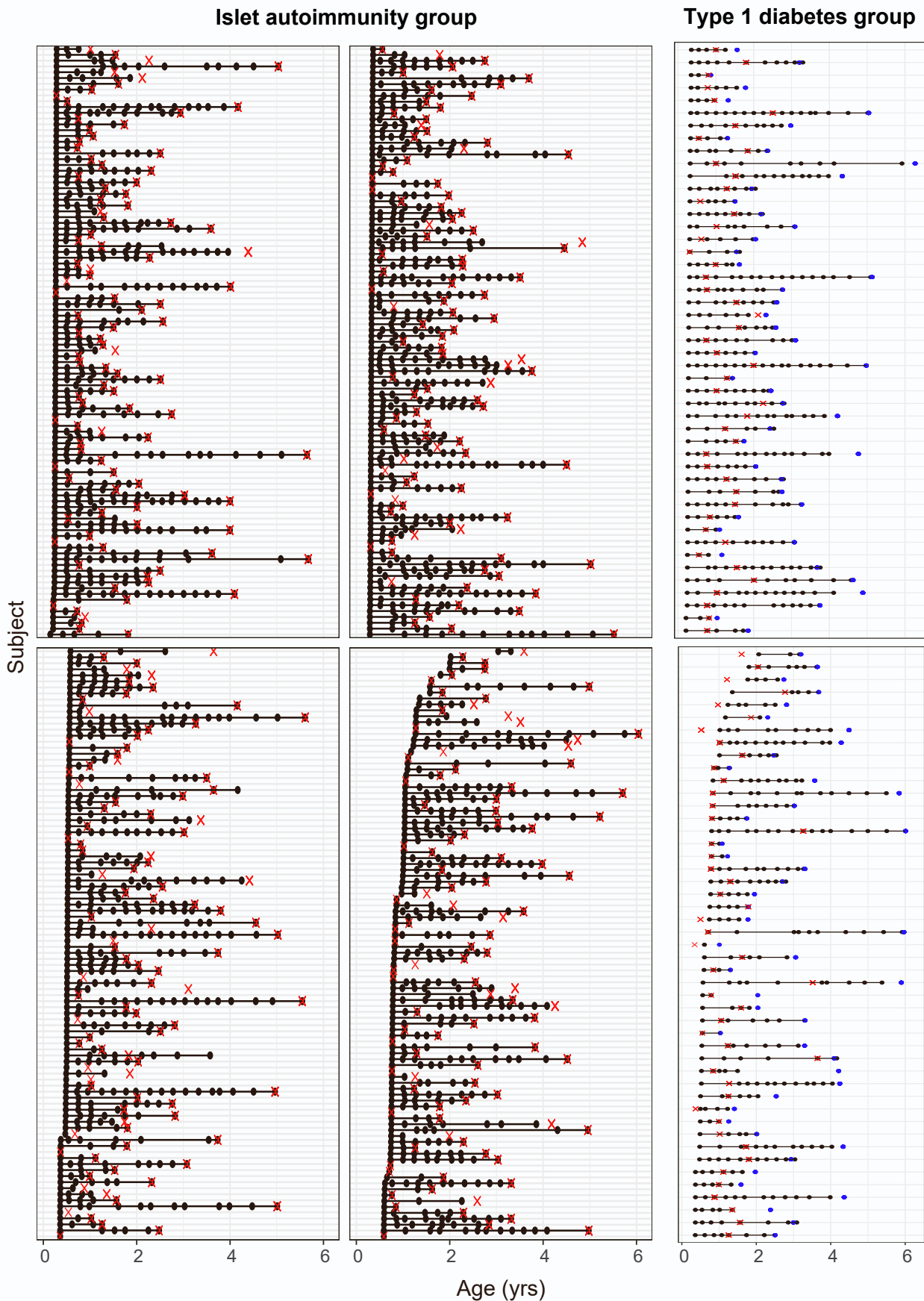
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***Committees:***

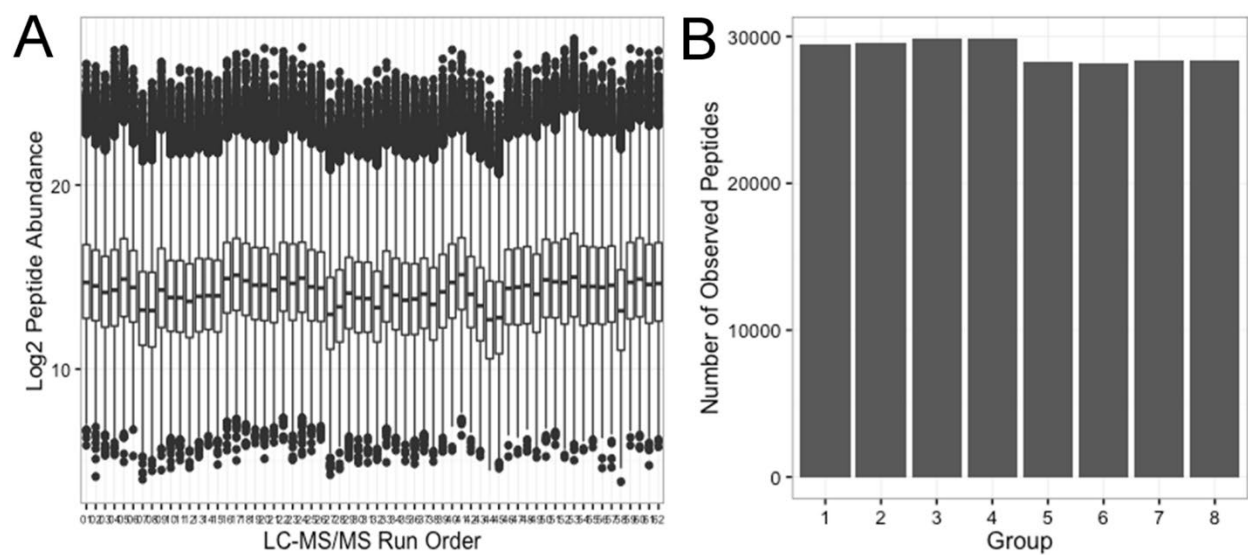
<sup>1</sup>Ancillary Studies, <sup>2</sup>Diet, <sup>3</sup>Genetics, <sup>4</sup>Human Subjects/Publicity/Publications, <sup>5</sup>Immune Markers, <sup>6</sup>Infectious Agents, <sup>7</sup>Laboratory Implementation, <sup>8</sup>Psychosocial, <sup>9</sup>Quality Assurance, <sup>10</sup>Steering, <sup>11</sup>Study Coordinators, <sup>12</sup>Celiac Disease, <sup>13</sup>Clinical Implementation.



**Figure S1 – Time points of samples analyzed in the discovery phase.** Related to Figure1. The black dots represent the time points of sample collection, whereas the red “x” the time of seroconversion and the blue dots, the time of diabetes diagnosis. All the samples were paired with controls of individuals with same characteristics but without islet autoimmunity or type 1 diabetes.



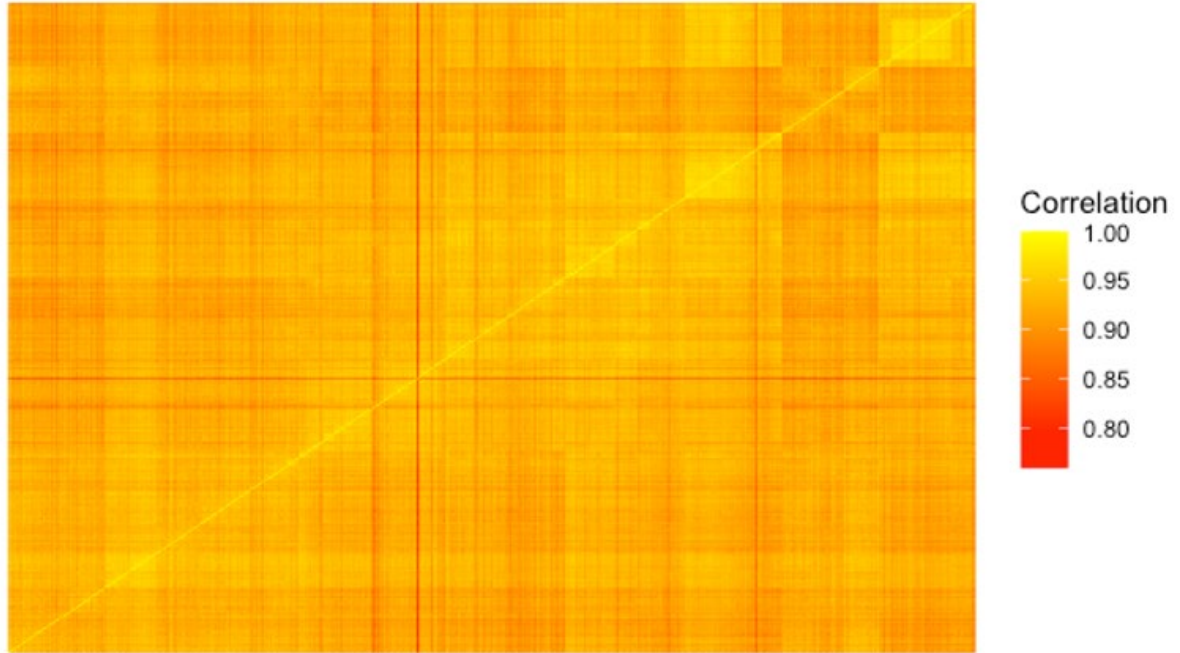
**Figure S2 – Time points of samples analyzed in the discovery phase.** Related to Figure1. The black dots represent the time points of sample collection, whereas the red “x” the time of seroconversion and the blue dots, the time of diabetes diagnosis. All the samples were paired with controls of individuals with same characteristics but without islet autoimmunity or type 1 diabetes.



**Figure S3 - Data quality across the entire discovery phase analysis.** Related to Figure 2.

(A) Overall peptide abundances of the reference sample channel in each of the sixty-two 8-plex iTRAQ sets.

(B) Number of identified peptides in different sample groups.



**Figure S4 - Data quality across the whole plasma proteomics analysis of the validation phase.** Related to Figure 4. The heatmap shows the correlations of the overall peptide abundances across the 6,426 targeted mass spectrometry analyses.