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Supplemental information

Decrease in multiple complement proteins associated with development of islet autoimmunity and type 1 diabetes

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Table S1. SRM Statistics for Pre-IA comparison to control. As described in the STAR Methods, Quantification and Statistical Analysis section, P-value and effect size is based on a linear mixed model comparing the difference of SRM protein abundance between CTRL and the data Pre-IA, adjusting for sex, HLA group, and first-degree relative status with a nested random effect for subject and plate number. The average log2 abundance values of all Pre-IA and control samples for each subject within the age range was used to compute log2 fold-changes.

	P-Value	Effect Size	Log2 Fold-Change (Age Ranges)				
			<3	[3,6)	[6,9)	[9,12)	>12
MBL2	0.241	0.248	0.5224	0.1110	0.3067	0.4596	0.4918
C1q	0.057	-0.162	-0.2354	-0.2341	0.0345	0.0539	0.1055
C1r	0.001	-0.107	-0.1717	-0.1390	-0.1201	-0.0528	-0.1229
C1s	0.003	-0.089	-0.1258	-0.1502	-0.1187	-0.0237	-0.0463
C2	0.084	-0.074	-0.1059	-0.0939	-0.1272	-0.1107	-0.0678
C4a	0.003	-0.268	-0.3088	-0.2097	-0.0891	-0.1406	0.3072
C4b	0.006	-0.247	-0.1986	-0.2122	-0.0629	-0.1806	0.3112
CFB	0.294	-0.062	-0.2028	-0.0617	-0.1147	-0.0202	0.2958
PROP	0.431	-0.139	0.0130	-0.2195	-0.6270	-0.4097	-0.4866
C5	0.187	-0.076	-0.3015	0.0042	-0.1279	-0.1928	0.0520
C6	0.025	-0.112	-0.1623	-0.1123	-0.1073	-0.0216	0.0827
C7	0.083	-0.160	-0.5479	-0.0665	-0.1592	-0.0744	0.0855
C8a	0.080	-0.089	-0.1667	-0.1177	-0.0595	-0.0408	0.0615
C8b	0.212	-0.069	-0.0807	-0.0763	-0.1084	-0.1292	0.2606
C8g	0.159	0.140	0.2765	-0.0276	0.2400	-0.0335	0.1179
C9	0.488	-0.052	-0.3856	-0.0438	-0.0132	-0.0718	0.3192
C3	0.034	-0.095	-0.1251	-0.0996	-0.0779	-0.0113	0.0462
CFI	0.084	-0.060	-0.1264	-0.0867	-0.0814	-0.0495	0.1183
CFH	0.146	-0.051	-0.1504	-0.0093	-0.1930	-0.1706	0.0215

Table S2. SRM Statistics for Post-IA comparison to control. As described in the STAR Methods, Quantification and Statistical Analysis section, P-value and effect size is based on a linear mixed model comparing the difference of SRM protein abundance between CTRL and the data Post-IA, adjusting for sex, HLA group, and first-degree relative status with a nested random effect for subject and plate number. The average log2 abundance values of all Pre-IA and control samples for each subject within the age range was used to compute log2 fold-changes.

	P-Value	Effect Size	Log2 Fold-Change (Age Ranges)				
			<3	[3,6)	[6,9)	[9,12)	>12
MBL2	0.156	0.2399	0.3234	0.2856	0.3140	-0.0148	0.5210
C1q	0.019	-0.1558	-0.0942	-0.1599	-0.1814	-0.1205	-0.1095
C1r	0.004	-0.0921	-0.1144	-0.0914	-0.0977	-0.1182	-0.1151
C1s	0.001	-0.1084	-0.0776	-0.1467	-0.1455	-0.1122	-0.1080
C2	0.014	-0.0812	-0.0373	-0.1394	-0.1375	-0.0442	-0.0479
C4a	0.013	-0.1766	-0.0814	-0.1533	-0.1021	-0.0854	-0.0347
C4b	0.041	-0.1606	-0.0223	-0.1867	-0.1043	-0.0714	0.0035
CFB	0.156	-0.0703	-0.0699	-0.0676	-0.0714	-0.0513	-0.0807
PROP	0.698	0.0516	0.4478	0.1331	-0.0439	-0.0560	-0.2041
C5	0.011	-0.1317	-0.1586	-0.1739	-0.1420	-0.2142	0.0012
C6	0.001	-0.1349	-0.1266	-0.1738	-0.1259	-0.0832	-0.1547
C7	0.137	-0.1089	-0.6289	-0.0158	0.0184	-0.2436	-0.0330
C8a	0.028	-0.0881	-0.0902	-0.1279	-0.0607	-0.0635	-0.0973
C8b	0.045	-0.1037	-0.0694	-0.2258	-0.1597	-0.1056	0.0555
C8g	0.837	-0.0164	-0.0229	-0.0913	-0.0449	-0.0830	0.0661
C9	0.280	-0.0620	-0.0779	-0.1026	-0.1011	-0.0401	0.0117
C3	0.007	-0.1036	-0.0549	-0.1643	-0.1348	-0.0551	-0.1085
CFI	0.107	-0.0520	-0.0085	-0.0688	-0.0688	0.0068	-0.0788
CFH	0.018	-0.0898	-0.1293	-0.0922	-0.1225	-0.0876	-0.0135

Table S3. Exsera Statistics for Pre-IA comparison to control. As described in the STAR Methods, Quantification and Statistical Analysis section, P-value and effect size is based on a linear mixed model comparing the difference of Exsera protein abundance between CTRL and the data Pre-IA, adjusting for sex, HLA group, and first-degree relative. The average log2 abundance values of all Pre-IA and control samples for each subject within the age range was used to compute log2 fold-changes.

	P-Value	Effect Size	Log2 Fold-Change (Age Ranges)				
			<3	[3,6)	[6,9)	[9,12)	>12
MBL2	0.025	0.812	0.5624	0.7268	0.9747	0.4303	-0.5290
C1q	0.839	-0.016	-0.0750	0.0548	0.0611	-0.0274	0.2499
C2	0.375	-0.223	-0.3005	-0.2105	-0.5097	-0.6208	0.5873
C4	0.147	-0.121	-0.1380	-0.0393	0.0849	0.0469	0.4764
C4b	0.961	-0.008	-0.0796	0.1354	0.3403	0.4579	1.2143
CFB	0.457	0.042	-0.0295	0.0387	0.0255	-0.0147	0.5161
CFD	0.548	0.041	0.1109	-0.0274	-0.0607	0.0768	0.0068
PROP	0.322	-0.045	-0.0600	-0.0373	-0.0704	-0.0637	0.1225
C5	0.049	-0.166	-0.1460	-0.2055	-0.2717	-0.1004	0.0615
C5a	0.015	-0.870	-0.6220	-0.9313	-1.5790	-1.5748	-1.3607
C5b	0.001	-0.306	-0.3022	-0.1490	-0.5107	-0.3833	0.1621
C3	0.000	-0.693	-0.3802	-0.6167	-1.1095	-0.7525	0.0311
C3a	0.003	-0.370	-0.4002	-0.5084	-0.4000	-0.2470	0.6287
C3b	0.000	-0.980	-0.7252	-0.9002	-1.2046	-0.4898	0.7396
CFI	0.803	0.012	-0.1788	0.0551	0.0636	0.0168	0.2295
CFH	0.960	0.002	-0.0458	0.0148	-0.0206	-0.0224	0.2705

Table S4. Exsera Statistics for Post-IA comparison to control. As described in the STAR Methods, Quantification and Statistical Analysis section, P-value and effect size is based on a linear mixed model comparing the difference of Exsera protein abundance between CTRL and the data Post-IA, adjusting for sex, HLA group, and first-degree relative. The average log2 abundance values of all Pre-IA and control samples for each subject within the age range was used to compute log2 fold-changes.

	P-Value	Effect Size	Log2 Fold-Change (Age Ranges)				
			<3	[3,6)	[6,9)	[9,12)	>12
MBL2	0.009	0.785	0.6353	0.2483	0.6286	0.7061	0.5308
C1q	0.495	-0.035	0.0250	0.0339	-0.0403	0.0025	0.0549
C2	0.419	-0.186	-0.6146	-0.1645	-0.3836	-0.1518	0.4128
C4	0.731	-0.024	0.0288	0.0488	0.0237	0.0544	0.1346
C4b	0.599	-0.064	-0.1940	-0.0481	-0.1478	0.0064	0.1773
CFB	0.968	0.002	0.0253	0.0354	0.0163	0.0425	0.0193
CFD	0.809	-0.015	-0.0179	-0.0452	-0.0262	0.0220	0.1259
PROP	0.496	-0.030	0.0393	0.0215	-0.0602	0.0192	0.0047
C5	0.168	-0.101	0.0722	-0.0429	-0.0297	-0.0759	-0.0303
C5a	0.042	-0.586	-0.0506	-0.2828	0.0232	-0.2557	-0.5014
C5b	0.018	-0.189	-0.2138	-0.1417	-0.3615	-0.1179	-0.0922
C3	0.014	-0.375	-0.3590	-0.6522	-0.8530	-0.1941	-0.1310
C3a	0.042	-0.203	-0.3821	-0.4990	-0.1902	-0.0977	0.1583
C3b	0.075	-0.412	-0.6937	-0.7346	-1.0911	0.0004	0.4066
CFI	0.069	-0.077	-0.1025	-0.0935	-0.0966	-0.0318	-0.0088
CFH	0.758	-0.013	-0.0251	-0.0164	-0.0220	0.0242	0.0307