

Supplementary Table S1. The plasma N-glycan peaks separated by HILIC and their dominant composition

Glycan peak	Major glycan structure	Description
GP01	FA2	agalactosylated
GP02	M5, FA2B	high mannose (M5), agalactosylated with bisecting GlcNAc (FA2B)
GP03	A2[6]BG1	monogalactosylated with bisecting GlcNAc
GP04	FA2[6]G1	monogalactosylated with core fucose
GP05	FA2[3]G1	monogalactosylated with core fucose
GP06	FA2[6]BG1	monogalactosylated with core fucose and bisecting GlcNAc
GP07	M6	high mannose
GP08	A2G2	digalactosylated
GP09	A2BG2	digalactosylated with bisecting GlcNAc
GP10	FA2G2	digalactosylated with core fucose
GP11	FA2BG2	digalactosylated with core fucose and bisecting GlcNAc
GP12	A2[3]BG1S(3)1	monogalactosylated with bisecting GlcNAc
GP13	FA2[3]G1S(3)1	monogalactosylated and sialylated with core fucose
GP14	A2G2S(6)1	digalactosylated and sialylated
GP15	A2BG2S1	digalactosylated and sialylated with bisecting GlcNAc
GP16	FA2G2S(6)1	digalactosylated and sialylated with core fucose
GP17	FA2BG2S(3)1	digalactosylated and sialylated with bisecting GlcNAc and core fucose
GP18	A2G2S(3,6)2	digalactosylated and disialylated
GP19	M9	high mannose
GP20	A2G2S(3,6)2	digalactosylated and disialylated
GP21	A2BG2S2	digalactosylated and disialylated with bisecting GlcNAc
GP22	FA2G2S(3,6)2	digalactosylated and disialylated with core fucose
GP23	FA2BG2S(3,6)2	digalactosylated and disialylated with bisecting GlcNAc and core fucose
GP24	A3G3S(3,6)2	trigalactosylated and disialylated
GP25	A3BG3S2	trigalactosylated and disialylated with bisecting GlcNAc
GP26	A3G3S(3,3)2	trigalactosylated and disialylated
GP27	A3G3S(3,3,3)3	trigalactosylated and trisialylated
GP28	A3G3S(3,3,6)3	trigalactosylated and trisialylated
GP29	FA3G3S(3,3,3)3	trigalactosylated and trisialylated with core fucose
GP30	A3G3S(3,3,6)3	trigalactosylated and trisialylated
GP31	FA3G3S(3,3,6)3	trigalactosylated and trisialylated with core fucose
GP32	A3F1G3S(3,3,3)3	trigalactosylated and trisialylated with antennary fucose
GP33	A4G4S(3,3,3)3	tetragalactosylated and trisialylated
GP34	A4G4S(3,3,6)3	tetragalactosylated and trisialylated
GP35	A4F1G3S(3,3,3)3	tetragalactosylated and trisialylated with antennary fucose
GP36	A4G4S(3,3,3,3)4	tetragalactosylated and tetrasialylated
GP37	A4G4S(3,3,3,6)4	tetragalactosylated and tetrasialylated
GP38	A4G4S(3,6,6,6)4	tetragalactosylated and tetrasialylated
GP39	A4F1G4S(3,3,3,6)4	tetragalactosylated and tetrasialylated with antennary fucose

Structure abbreviations: all N-glycans have two core N-acetylglucosamines (GlcNAcs); F at the start of the abbreviation indicates core fucose α 1-6 linked to the inner GlcNAc; Mx, number (x) of mannose on the core GlcNAcs; Ax, number of antennae (GlcNAc) on the trimannosyl core; B, bisecting GlcNAc linked β 1-4 to β 1-3 mannose; Gx, number (x) of β 1-4 linked galactose on the antenna; [3]G1 and [6]G1 indicates that the galactose is present on the antenna of the α 1-3 or α 1-6 mannose; F(x), number (x) of fucose linked α 1-3 to the antenna GlcNAc; Sx, number (x) of sialic acids linked to galactose; the numbers 3 or 6 or in parentheses after S indicate whether the sialic acid is in a α 2-3 or α 2-6 linkage. If there is no linkage number, the exact link is unknown.

Supplementary Table S2. The list of the N-glycan peaks with their p-values (p_{BH}) obtained by the univariate analysis (corrected with the Benjamini-Hochberg procedure), the correlation coefficients values ($p(corr)$), and variable importance in the projection (VIP) obtained by the Supervised Orthogonal Partial Least Square – Discriminant Analysis (OPLS-DA).

Glycan peak	p_{BH}	$p(corr)$	VIP
GP01	0.857	-0.084	0.396
GP02	0.962	0.092	0.757
GP03	0.526	0.253	0.773
GP04	0.039	-0.449	1.207
GP05	0.010	-0.527	1.348
GP06	0.459	-0.116	0.869
GP07	0.009	-0.071	0.750
GP08	0.011	0.330	0.799
GP09	0.839	0.133	0.885
GP10	0.016	-0.461	1.215
GP11	0.078	-0.055	0.921
GP12	0.700	-0.040	0.437
GP13	0.117	-0.354	1.040
GP14	0.002	0.375	0.937
GP15	0.649	0.131	0.769
GP16	0.008	-0.424	1.306
GP17	0.249	0.022	0.819
GP18	0.343	-0.262	0.681
GP19	0.002	-0.455	1.102
GP20	0.924	0.063	0.776
GP21	0.903	0.195	0.488
GP22	0.039	-0.349	0.839
GP23	0.577	-0.023	0.678
GP24	0.335	-0.126	0.486
GP25	0.963	0.050	0.524
GP26	0.687	0.015	0.534
GP27	0.001	0.700	1.715
GP28	0.588	-0.311	0.868
GP29	0.140	-0.227	0.726
GP30	0.919	-0.183	0.722
GP31	0.095	-0.386	1.089
GP32	0.050	0.377	1.112
GP33	0.001	0.688	1.699
GP34	0.259	0.092	0.852
GP35	0.015	0.502	1.302
GP36	<0.001	0.605	1.590
GP37	0.348	0.010	0.515
GP38	<0.001	0.437	1.250
GP39	<0.001	0.693	1.706

Variables with $p_{BH} \leq 0.05$, absolute $p(corr) \geq 0.30$, and $VIP > 1.000$ were considered the significant contributors in discriminating the diagnostic groups and are denoted in bold. Negative $p(corr)$ indicates diminished glycan concentrations in the plasma of PTSD patients versus control participants, whereas positive $p(corr)$ values indicate increased glycan concentrations in PTSD patients.

Supplementary Table S3. The associations of the rs6573604 and rs11621121 polymorphisms (genetic and allelic model) with the plasma N-glycan levels in the control participants and the patients with PTSD.

Glycan peak	Group	rs6573604						rs11621121					
		Genetic model			Allelic model			Genetic model			Allelic model		
		H	p	p _{BH}	U	p	p _{BH}	H	p	p _{BH}	U	p	p _{BH}
GP01	Control	1.566	0.457	0.775	20518.5	0.786	0.876	0.930	0.628	0.742	28566.0	0.342	0.534
	PTSD	0.480	0.786	0.929	23138.5	0.615	0.923	0.836	0.658	0.778	40804.5	0.420	0.546
GP02	Control	1.278	0.528	0.735	20120.5	0.565	0.787	2.315	0.314	0.510	28078.0	0.208	0.406
	PTSD	1.551	0.461	0.782	23344.5	0.712	0.926	1.871	0.392	0.637	39552.5	0.156	0.304
GP03	Control	5.631	0.060	0.334	18534.5	0.074	0.241	2.640	0.267	0.548	27566.0	0.113	0.367
	PTSD	3.388	0.184	0.652	21940.5	0.199	0.776	0.156	0.925	0.925	42282.5	0.933	0.933
GP04	Control	1.997	0.368	0.718	20160.5	0.586	0.737	6.027	0.049	0.478	26852.0	0.041	0.200
	PTSD	1.128	0.569	0.888	22270.5	0.285	0.695	0.751	0.687	0.788	40668.5	0.382	0.514
GP05	Control	1.450	0.484	0.726	20092.5	0.551	0.796	1.109	0.574	0.700	28440.0	0.303	0.514
	PTSD	3.373	0.185	0.601	22926.5	0.521	0.813	0.343	0.842	0.888	41230.5	0.549	0.630
GP06	Control	2.510	0.285	0.654	18780.5	0.110	0.268	1.629	0.443	0.596	28188.0	0.234	0.415
	PTSD	2.718	0.257	0.626	21776.5	0.164	0.711	7.353	0.025	0.139	37042.5	0.008	0.052
GP07	Control	0.286	0.867	0.939	20124.5	0.567	0.763	3.157	0.206	0.502	27666.0	0.128	0.357
	PTSD	3.765	0.152	0.741	23338.5	0.709	0.953	3.153	0.207	0.449	39672.5	0.174	0.308
GP08	Control	0.056	0.973	0.999	20754.5	0.928	0.978	9.067	0.011	0.215	25454.0	0.003	0.059
	PTSD	3.143	0.208	0.624	21110.5	0.068	0.332	5.332	0.070	0.248	38938.5	0.086	0.224
GP09	Control	2.193	0.334	0.686	20334.5	0.681	0.781	2.468	0.291	0.516	27882.0	0.166	0.341
	PTSD	4.004	0.135	1.053	23158.5	0.624	0.901	2.856	0.240	0.468	39076.5	0.099	0.241
GP10	Control	1.907	0.385	0.715	19020.5	0.157	0.360	4.097	0.129	0.503	27860.0	0.162	0.351
	PTSD	0.107	0.948	0.999	23438.5	0.758	0.924	1.449	0.484	0.699	40448.5	0.327	0.455
GP11	Control	1.135	0.567	0.763	19508.5	0.297	0.610	0.923	0.630	0.723	29108.0	0.546	0.761
	PTSD	3.837	0.147	0.819	22398.5	0.325	0.704	5.560	0.062	0.242	37500.5	0.015	0.059
GP12	Control	1.748	0.417	0.739	19690.5	0.366	0.714	0.088	0.957	0.957	29596.0	0.769	0.857
	PTSD	0.448	0.799	0.917	23572.5	0.826	0.920	0.338	0.845	0.867	41502.5	0.642	0.696
GP13	Control	0.492	0.782	0.924	19874.5	0.446	0.696	1.488	0.475	0.598	29310.0	0.634	0.824
	PTSD	0.896	0.639	0.923	22522.5	0.366	0.751	5.167	0.076	0.228	37634.5	0.018	0.059
GP14	Control	0.621	0.733	0.893	19956.5	0.484	0.726	4.610	0.100	0.650	26820.0	0.039	0.254
	PTSD	5.176	0.075	0.731	20324.5	0.019	0.185	7.801	0.020	0.195	36918.5	0.007	0.055
GP15	Control	0.343	0.843	0.939	20200.5	0.607	0.717	4.482	0.106	0.517	26818.0	0.039	0.217
	PTSD	2.347	0.309	0.709	22288.5	0.291	0.668	2.447	0.294	0.521	39134.5	0.104	0.239
GP16	Control	2.709	0.258	0.629	18734.5	0.102	0.265	3.169	0.205	0.533	28132.0	0.220	0.409
	PTSD	0.179	0.915	0.991	23364.5	0.722	0.908	11.512	0.003	0.039	35666.5	0.001	0.020
GP17	Control	0.123	0.941	0.992	20770.5	0.937	0.962	4.371	0.112	0.485	26798.0	0.038	0.296
	PTSD	2.053	0.358	0.698	22696.5	0.429	0.761	6.680	0.035	0.171	37424.5	0.014	0.068
GP18	Control	0.445	0.801	0.919	20142.5	0.577	0.750	2.436	0.296	0.502	29370.0	0.662	0.807
	PTSD	6.913	0.032	0.416	20228.5	0.016	0.208	1.292	0.524	0.705	41508.5	0.644	0.679
GP19	Control	3.829	0.147	0.478	18164.5	0.039	0.169	3.240	0.198	0.552	27456.0	0.098	0.347
	PTSD	0.409	0.815	0.908	23588.5	0.834	0.904	2.777	0.249	0.462	41054.5	0.494	0.602
GP20	Control	4.085	0.130	0.563	18362.5	0.055	0.195	2.224	0.329	0.513	29748.0	0.844	0.890
	PTSD	2.816	0.245	0.683	22042.5	0.224	0.794	7.233	0.027	0.156	36544.5	0.005	0.049
GP21	Control	8.104	0.017	0.166	20168.5	0.590	0.719	3.696	0.158	0.474	27106.0	0.060	0.234
	PTSD	1.808	0.405	0.752	22764.5	0.455	0.772	0.470	0.791	0.857	41118.5	0.514	0.607
GP22	Control	1.563	0.458	0.744	19856.5	0.437	0.710	21.000	<0.001	0.001	23408.0	<0.001	0.001
	PTSD	0.054	0.974	1.000	23552.5	0.816	0.936	19.336	<0.001	0.002	33526.5	<0.001	0.001
GP23	Control	0.037	0.981	0.981	20638.5	0.858	0.930	5.494	0.064	0.499	30006.0	0.974	1.000
	PTSD	0.939	0.625	0.938	23606.5	0.843	0.865	12.784	0.002	0.039	35466.5	0.001	0.013
GP24	Control	2.807	0.246	0.640	18586.5	0.081	0.243	2.726	0.256	0.587	29694.0	0.817	0.885
	PTSD	1.173	0.556	0.904	22202.5	0.266	0.741	3.312	0.191	0.466	39296.5	0.123	0.267
GP25	Control	2.331	0.312	0.676	18728.5	0.101	0.281	2.031	0.362	0.523	29358.0	0.656	0.825

Glycan peak	Group	rs6573604						rs11621121					
		Genetic model			Allelic model			Genetic model			Allelic model		
		H	p	p _{BH}	U	p	p _{BH}	H	p	p _{BH}	U	p	p _{BH}
	PTSD	6.996	0.030	0.585	19704.5	0.006	0.234	3.326	0.190	0.494	39522.5	0.152	0.312
GP26	Control	1.097	0.578	0.751	19744.5	0.389	0.690	2.511	0.285	0.529	28838.0	0.438	0.633
	PTSD	2.785	0.248	0.645	22232.5	0.274	0.712	4.870	0.088	0.245	37846.5	0.024	0.072
GP27	Control	1.000	0.606	0.762	20838.5	0.979	0.979	0.199	0.905	0.954	29402.0	0.676	0.799
	PTSD	0.535	0.765	0.962	23526.5	0.802	0.948	2.215	0.330	0.560	39884.5	0.209	0.354
GP28	Control	3.167	0.205	0.571	18332.5	0.052	0.203	2.034	0.362	0.504	28456.0	0.308	0.501
	PTSD	3.438	0.179	0.698	20964.5	0.055	0.358	0.546	0.761	0.848	41616.5	0.682	0.700
GP29	Control	3.986	0.136	0.530	18026.5	0.030	0.167	4.068	0.131	0.464	27664.0	0.128	0.333
	PTSD	7.226	0.027	1.000	19704.5	0.006	0.117	0.954	0.621	0.781	41356.5	0.591	0.659
GP30	Control	5.343	0.069	0.336	17752.5	0.017	0.111	1.536	0.464	0.603	30018.0	0.980	0.980
	PTSD	0.782	0.676	0.942	22652.5	0.412	0.803	3.093	0.213	0.437	38896.5	0.082	0.228
GP31	Control	3.945	0.139	0.493	18042.5	0.031	0.151	8.694	0.013	0.169	25588.0	0.004	0.052
	PTSD	2.337	0.311	0.674	22074.5	0.232	0.754	6.571	0.037	0.160	37016.5	0.008	0.045
GP32	Control	3.642	0.162	0.486	19726.5	0.381	0.708	3.927	0.140	0.455	27034.0	0.054	0.234
	PTSD	3.645	0.162	0.702	20904.5	0.050	0.390	5.311	0.070	0.228	37562.5	0.017	0.060
GP33	Control	1.459	0.482	0.752	19818.5	0.420	0.712	0.348	0.840	0.910	29212.0	0.590	0.793
	PTSD	0.654	0.721	0.937	23588.5	0.834	0.879	1.660	0.436	0.654	40166.5	0.263	0.395
GP34	Control	6.657	0.036	0.281	17340.5	0.007	0.068	2.569	0.277	0.540	27578.0	0.115	0.345
	PTSD	2.070	0.355	0.729	22688.5	0.426	0.791	1.320	0.517	0.720	40026.5	0.235	0.382
GP35	Control	1.444	0.486	0.702	19230.5	0.210	0.455	2.669	0.263	0.570	27672.0	0.129	0.314
	PTSD	0.495	0.781	0.952	22836.5	0.484	0.787	1.244	0.537	0.698	40096.5	0.249	0.388
GP36	Control	15.133	0.001	0.020	16010.5	<0.001	0.003	4.583	0.101	0.563	26752.0	0.035	0.341
	PTSD	0.686	0.710	0.955	23168.5	0.629	0.876	7.540	0.023	0.150	37424.5	0.014	0.061
GP37	Control	15.139	0.001	0.013	15514.5	<0.001	0.001	0.096	0.953	0.978	29586.0	0.764	0.876
	PTSD	3.877	0.144	0.936	21044.5	0.062	0.345	1.705	0.426	0.665	40344.5	0.302	0.436
GP38	Control	17.400	<0.001	0.007	15342.5	<0.001	0.001	0.853	0.653	0.728	28706.0	0.390	0.585
	PTSD	1.702	0.427	0.757	22152.5	0.252	0.756	3.287	0.193	0.443	39568.5	0.158	0.293
GP39	Control	5.976	0.050	0.325	17626.5	0.013	0.101	2.196	0.334	0.501	27760.0	0.144	0.330
	PTSD	0.004	0.998	0.998	23874.5	0.981	0.981	0.931	0.628	0.765	41018.5	0.483	0.608

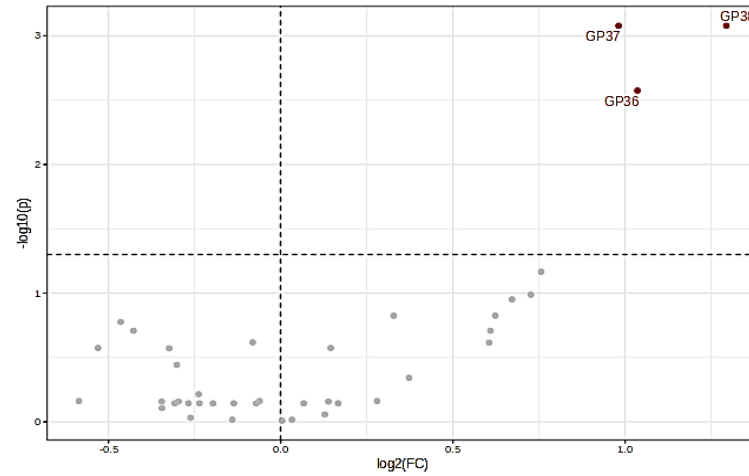
The data are represented as the Kruskal-Wallis H value or the Mann-Whitney U value, the original p-value, and the p-value corrected with the Benjamini-Hochberg procedure (p_{BH}). Significant p_{BH} are denoted in bold.

Supplementary Table S4. The associations of the rs10483776 and rs4073416 polymorphisms (genetic and allelic model) with the plasma N-glycan levels in the control participants and the patients with PTSD.

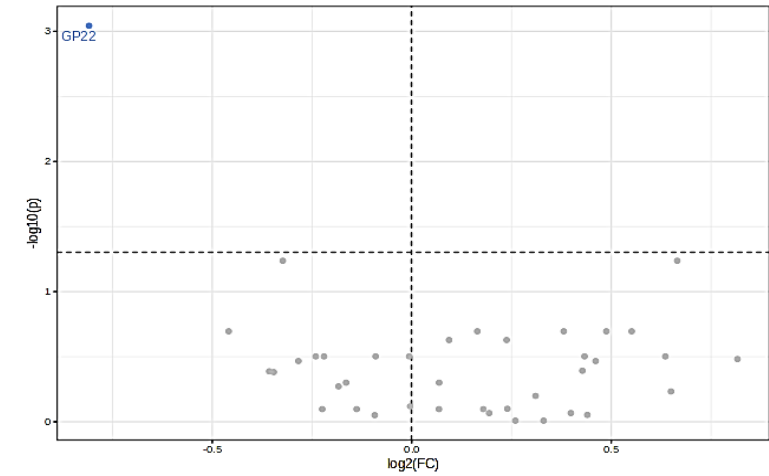
Glycan peak	Group	rs10483776						rs4073416					
		Genetic model			Allelic model			Genetic model			Allelic model		
		H	p	pBH	U	p	pBH	H	p	pBH	U	p	pBH
GP01	Control	2.266	0.322	0.571	17806.5	0.282	0.611	1.984	0.371	0.629	27528.0	0.215	0.399
	PTSD	0.476	0.788	0.878	27984.5	0.524	0.705	0.419	0.811	0.904	41838.5	0.874	0.921
GP02	Control	0.170	0.918	0.968	18746.5	0.743	0.828	3.781	0.151	0.535	27896.0	0.315	0.473
	PTSD	2.669	0.263	0.466	26576.5	0.142	0.346	2.443	0.295	0.677	39138.5	0.138	0.449
GP03	Control	0.081	0.960	0.985	18794.5	0.772	0.814	5.141	0.076	0.329	27312.0	0.168	0.385
	PTSD	1.991	0.370	0.601	27324.5	0.304	0.515	2.189	0.335	0.622	39536.5	0.198	0.429
GP04	Control	2.321	0.313	0.610	17266.5	0.132	0.322	5.919	0.052	0.338	25580.0	0.013	0.101
	PTSD	1.064	0.588	0.791	28396.5	0.694	0.820	1.655	0.437	0.710	41536.5	0.759	0.987
GP05	Control	1.789	0.409	0.638	17826.5	0.289	0.593	2.498	0.287	0.533	27430.0	0.192	0.394
	PTSD	0.310	0.856	0.927	28698.5	0.830	0.925	0.107	0.948	0.948	41694.5	0.819	0.913
GP06	Control	2.488	0.288	0.591	18024.5	0.366	0.595	1.500	0.472	0.736	27584.0	0.228	0.387
	PTSD	5.048	0.080	0.240	25536.5	0.037	0.289	6.773	0.034	0.265	37214.5	0.015	0.293
GP07	Control	2.757	0.252	0.578	17122.5	0.105	0.315	5.384	0.068	0.332	25762.0	0.018	0.117
	PTSD	4.801	0.091	0.237	26324.5	0.106	0.295	0.794	0.672	0.904	41200.5	0.638	0.889
GP08	Control	2.954	0.228	0.593	17330.5	0.145	0.333	10.262	0.006	0.117	24352.0	0.001	0.020
	PTSD	0.501	0.779	0.894	27942.5	0.508	0.708	3.541	0.170	0.663	42126.5	0.987	0.987
GP09	Control	0.652	0.722	0.828	18380.5	0.536	0.697	3.391	0.183	0.446	27246.0	0.155	0.378
	PTSD	5.688	0.058	0.189	25820.5	0.055	0.306	3.098	0.212	0.591	38972.5	0.118	0.418
GP10	Control	3.104	0.212	0.591	17948.5	0.335	0.653	3.314	0.191	0.438	26902.0	0.100	0.325
	PTSD	1.822	0.402	0.627	27732.5	0.432	0.648	1.472	0.479	0.719	39958.5	0.280	0.475
GP11	Control	0.948	0.623	0.784	18276.5	0.483	0.650	0.445	0.801	0.893	28572.0	0.569	0.672
	PTSD	9.244	0.010	0.078	25878.5	0.060	0.234	3.376	0.185	0.555	38664.5	0.086	0.335
GP12	Control	0.271	0.873	0.946	18492.5	0.596	0.726	5.452	0.065	0.362	26056.0	0.029	0.141
	PTSD	0.922	0.631	0.794	28232.5	0.624	0.785	0.357	0.836	0.906	41310.5	0.677	0.910
GP13	Control	2.316	0.314	0.583	17230.5	0.125	0.325	7.641	0.022	0.215	27376.0	0.181	0.392
	PTSD	2.709	0.258	0.479	27046.5	0.233	0.478	2.401	0.301	0.652	39160.5	0.141	0.423
GP14	Control	5.245	0.073	0.475	16446.5	0.031	0.202	9.849	0.007	0.091	24472.0	0.001	0.013
	PTSD	4.174	0.124	0.269	25758.5	0.051	0.332	3.677	0.159	0.689	39444.5	0.183	0.446
GP15	Control	0.966	0.617	0.802	18434.5	0.564	0.710	1.728	0.421	0.684	27560.0	0.222	0.394
	PTSD	6.675	0.036	0.156	27052.5	0.235	0.458	4.197	0.123	0.685	38234.5	0.054	0.301
GP16	Control	1.831	0.400	0.650	18098.5	0.399	0.599	3.689	0.158	0.474	27496.0	0.207	0.404
	PTSD	15.503	<0.001	0.017	24838.5	0.013	0.169	6.853	0.033	0.322	37340.5	0.018	0.176
GP17	Control	2.928	0.231	0.563	16988.5	0.084	0.298	3.308	0.191	0.414	26590.0	0.065	0.282
	PTSD	9.725	0.008	0.078	26748.5	0.171	0.392	3.425	0.180	0.585	38640.5	0.084	0.364
GP18	Control	1.349	0.51	0.710	17966.5	0.342	0.635	3.692	0.158	0.440	28566.0	0.566	0.690
	PTSD	1.279	0.527	0.734	28146.5	0.588	0.764	0.139	0.933	0.983	41676.5	0.812	0.931
GP19	Control	2.001	0.368	0.624	18748.5	0.744	0.806	3.720	0.156	0.507	27010.0	0.116	0.323
	PTSD	0.168	0.92	0.970	28564.5	0.768	0.881	0.695	0.706	0.860	41592.5	0.780	0.951
GP20	Control	3.673	0.159	0.517	16706.5	0.051	0.249	3.679	0.159	0.413	26926.0	0.104	0.312
	PTSD	6.194	0.045	0.160	26016.5	0.072	0.255	3.916	0.141	0.687	38474.5	0.070	0.341
GP21	Control	2.755	0.252	0.546	18164.5	0.429	0.620	0.452	0.798	0.915	28716.0	0.633	0.726
	PTSD	1.517	0.468	0.702	27356.5	0.313	0.509	0.492	0.782	0.897	42036.5	0.951	0.976
GP22	Control	22.050	<0.001	<0.001	13506.5	<0.001	<0.001	14.606	0.001	0.039	23952.0	<0.001	0.016
	PTSD	12.924	0.002	0.026	23454.5	0.001	0.039	11.303	0.004	0.156	36856.5	0.009	0.351
GP23	Control	0.522	0.770	0.858	18936.5	0.860	0.883	1.022	0.600	0.807	28022.0	0.356	0.514
	PTSD	9.194	0.010	0.065	26536.5	0.135	0.351	7.693	0.021	0.273	37268.5	0.016	0.208
GP24	Control	1.147	0.563	0.757	18058.5	0.381	0.594	1.105	0.576	0.802	27886.0	0.312	0.487
	PTSD	0.031	0.985	0.985	28978.5	0.96	0.960	1.483	0.476	0.743	39806.5	0.248	0.484
GP25	Control	0.708	0.702	0.830	18654.5	0.688	0.789	0.934	0.627	0.815	28162.0	0.405	0.564

Glycan peak	Group	rs10483776						rs4073416					
		Genetic model			Allelic model			Genetic model			Allelic model		
		H	p	pBH	U	p	pBH	H	p	pBH	U	p	pBH
	PTSD	2.275	0.321	0.544	26940.5	0.21	0.455	0.741	0.690	0.868	40494.5	0.414	0.621
GP26	Control	0.006	0.997	0.997	19126.5	0.98	0.980	2.918	0.233	0.454	26736.0	0.080	0.312
	PTSD	1.408	0.495	0.715	27608.5	0.39	0.608	2.381	0.304	0.624	39878.5	0.263	0.488
GP27	Control	5.551	0.062	0.484	17038.5	0.091	0.296	0.822	0.663	0.834	28166.0	0.406	0.546
	PTSD	6.987	0.03	0.146	25466.5	0.034	0.332	3.531	0.171	0.606	39252.5	0.154	0.429
GP28	Control	4.464	0.107	0.464	16458.5	0.031	0.173	0.257	0.879	0.927	29426.0	0.984	0.984
	PTSD	0.663	0.718	0.875	27750.5	0.438	0.633	1.235	0.539	0.751	41572.5	0.773	0.972
GP29	Control	12.852	0.002	0.020	14608.5	<0.001	0.003	6.997	0.030	0.234	25248.0	0.007	0.068
	PTSD	1.056	0.59	0.767	28820.5	0.886	0.909	0.597	0.742	0.877	41592.5	0.780	0.922
GP30	Control	0.830	0.660	0.804	18018.5	0.364	0.617	2.410	0.300	0.532	27146.0	0.137	0.356
	PTSD	0.051	0.975	1.001	28774.5	0.865	0.937	1.468	0.480	0.693	40226.5	0.343	0.535
GP31	Control	24.363	<0.001	<0.001	13052.5	<0.001	<0.001	1.293	0.524	0.757	27646.0	0.244	0.397
	PTSD	13.755	0.001	0.020	23276.5	0.001	0.020	7.989	0.018	0.351	37588.5	0.025	0.195
GP32	Control	4.618	0.099	0.483	16420.5	0.029	0.226	4.824	0.090	0.351	25960.0	0.025	0.139
	PTSD	3.972	0.137	0.281	26062.5	0.076	0.247	2.194	0.334	0.651	39292.5	0.159	0.413
GP33	Control	4.868	0.088	0.490	17152.5	0.110	0.306	0.723	0.697	0.849	28394.0	0.494	0.621
	PTSD	6.466	0.039	0.152	25860.5	0.058	0.251	2.898	0.235	0.611	39444.5	0.183	0.420
GP34	Control	13.535	0.001	0.013	14452.5	<0.001	0.002	1.376	0.503	0.755	28230.0	0.430	0.559
	PTSD	4.603	0.100	0.229	26212.5	0.092	0.276	2.775	0.250	0.609	39938.5	0.276	0.489
GP35	Control	3.882	0.144	0.511	16942.5	0.077	0.300	3.114	0.211	0.433	26730.0	0.080	0.284
	PTSD	3.324	0.19	0.371	28774.5	0.865	0.912	0.119	0.942	0.967	41776.5	0.851	0.922
GP36	Control	1.444	0.486	0.702	18606.5	0.661	0.781	0.414	0.813	0.881	28718.0	0.634	0.706
	PTSD	8.367	0.015	0.084	25824.5	0.056	0.273	4.843	0.089	0.579	37934.5	0.038	0.247
GP37	Control	3.496	0.174	0.522	16828.5	0.063	0.273	0.185	0.912	0.912	28868.0	0.705	0.743
	PTSD	0.568	0.753	0.890	28290.5	0.648	0.790	0.752	0.687	0.893	41074.5	0.594	0.858
GP38	Control	1.622	0.444	0.666	17988.5	0.351	0.622	0.231	0.891	0.914	29370.0	0.955	0.980
	PTSD	4.700	0.095	0.232	27190.5	0.269	0.500	1.897	0.387	0.656	39558.5	0.202	0.415
GP39	Control	4.202	0.122	0.476	18268.5	0.479	0.667	0.511	0.775	0.916	28724.0	0.637	0.690
	PTSD	5.061	0.08	0.223	27216.5	0.275	0.488	2.064	0.356	0.631	40196.5	0.335	0.544

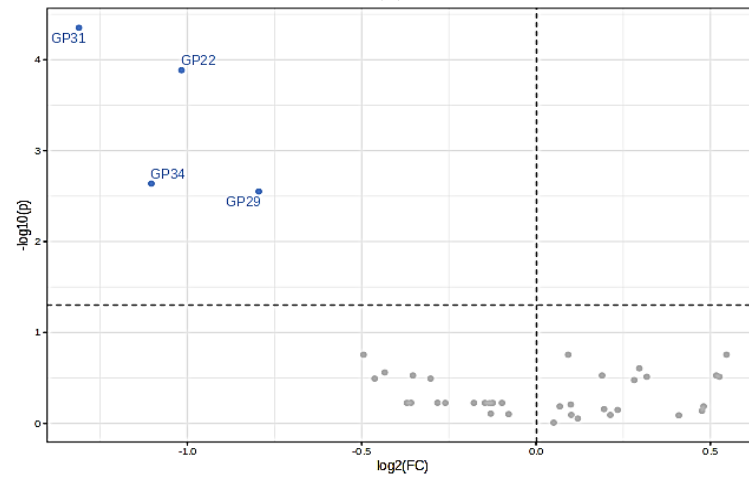
The data are represented as the Kruskal-Wallis H value or the Mann-Whitney U value, the original p-value, and the p-value corrected with the Benjamini-Hochberg procedure (p_{BH}). Significant p_{BH} are denoted in bold.



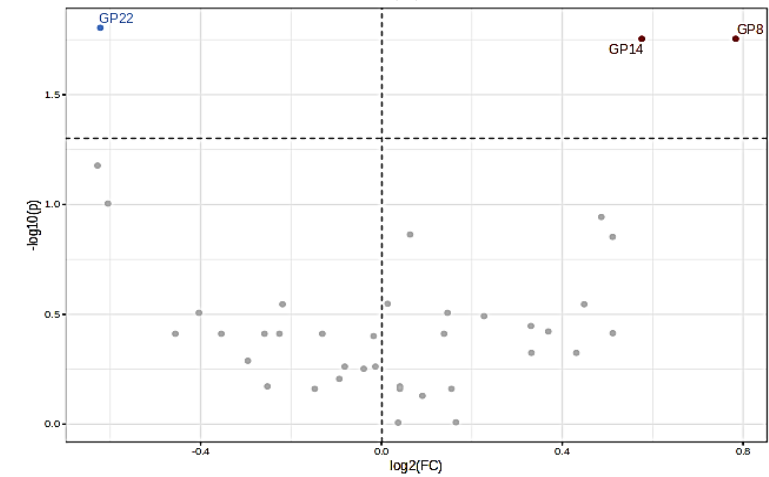
(a)



(b)

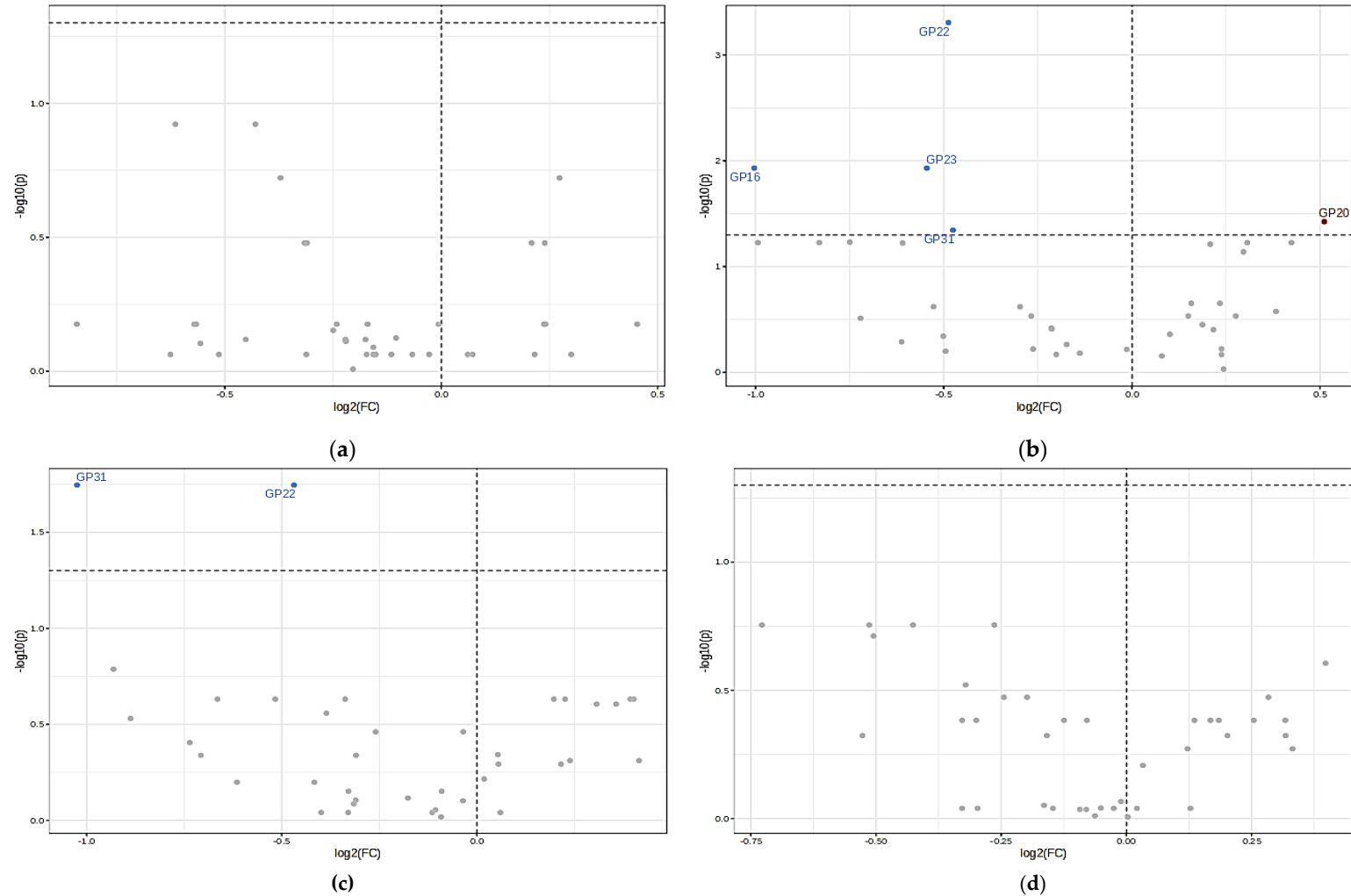


(c)



(d)

Supplementary Figure S1. Direction and size of glycan concentration change in the minor allele carriers compared to carriers of the major allele of (a) rs6573604, (b) rs11621121, (c) rs10483776, and (d) rs4073416 polymorphism in control participants. Significantly increased or decreased glycan peaks are labeled with red or blue circles, respectively, while non-significant glycan peaks are represented with grey circles. $\log_2(\text{FC})$ = logarithm of fold change; $-\log_{10}(p)$ = negative logarithm of FDR corrected p-value (Benjamini-Hochberg method).



Supplementary Figure S2. Direction and size of glycan concentration change in the minor allele carriers compared to carriers of the major allele of (a) rs6573604, (b) rs11621121, (c) rs10483776, and (d) rs4073416 polymorphism in PTSD patients. Significantly increased or decreased glycan peaks are labeled with red or blue circles, respectively, while non-significant glycan peaks are represented with grey circles. $\log_2(\text{FC})$ = logarithm of fold change; $-\log_{10}(p)$ = negative logarithm of FDR corrected p-value (Benjamini-Hochberg method).

Supplementary Table S5. The associations of the rs11621121-rs10483776 haplotypes with the plasma N-glycan levels in the control participants and the patients with PTSD.

Glycan peak	Control participants			Patients with PTSD		
	H	p	p _{BH}	H	p	p _{BH}
GP01	1.300	0.522	0.617	1.670	0.434	0.605
GP02	1.534	0.465	0.585	3.069	0.216	0.401
GP03	4.912	0.086	0.280	1.565	0.457	0.594
GP04	4.479	0.107	0.261	2.249	0.325	0.507
GP05	1.471	0.479	0.584	0.866	0.649	0.723
GP06	1.534	0.464	0.603	7.470	0.024	0.134
GP07	3.306	0.191	0.372	2.752	0.253	0.429
GP08	8.654	0.013	0.101	4.056	0.132	0.343
GP09	2.180	0.336	0.570	3.806	0.149	0.363
GP10	2.049	0.359	0.560	1.070	0.586	0.672
GP11	0.516	0.773	0.815	6.447	0.040	0.173
GP12	0.243	0.886	0.909	0.396	0.820	0.842
GP13	2.054	0.358	0.582	6.453	0.040	0.156
GP14	5.840	0.054	0.351	8.159	0.017	0.111
GP15	5.010	0.082	0.291	3.017	0.221	0.392
GP16	1.569	0.456	0.635	11.877	0.003	0.029
GP17	4.907	0.086	0.258	6.927	0.031	0.151
GP18	0.843	0.656	0.731	1.626	0.444	0.597
GP19	5.335	0.069	0.384	0.402	0.818	0.862
GP20	4.752	0.093	0.242	8.528	0.014	0.109
GP21	3.546	0.170	0.368	0.806	0.668	0.724
GP22	25.182	<0.001	<0.001	20.069	<0.001	0.002
GP23	0.049	0.976	0.976	12.508	0.002	0.026
GP24	1.700	0.427	0.617	3.640	0.162	0.372
GP25	0.652	0.722	0.782	2.328	0.312	0.507
GP26	1.250	0.535	0.614	5.245	0.073	0.219
GP27	3.379	0.185	0.380	4.342	0.114	0.318
GP28	5.022	0.081	0.351	1.774	0.412	0.595
GP29	12.000	0.002	0.020	0.307	0.858	0.858
GP30	1.549	0.461	0.620	3.584	0.167	0.343
GP31	24.234	<0.001	<0.001	13.471	0.001	0.020
GP32	5.325	0.070	0.341	5.924	0.052	0.169
GP33	2.807	0.246	0.436	3.605	0.165	0.358
GP34	14.390	0.001	0.013	3.149	0.207	0.404
GP35	3.618	0.164	0.376	1.355	0.508	0.639
GP36	4.764	0.092	0.256	6.432	0.040	0.142
GP37	5.020	0.081	0.316	1.124	0.570	0.674
GP38	2.883	0.237	0.440	2.120	0.346	0.519
GP39	2.050	0.359	0.539	1.276	0.528	0.644

The data are represented as the Kruskal-Wallis H value, the original p-value, and the p-value corrected with the Benjamini-Hochberg procedure (p_{BH}). Significant p_{BH} values are denoted in bold.