SUPPORTING INFORMATION

The mucinous domain of pancreatic carboxyl-ester lipase (CEL) contains core 1/core 2 O-glycans that can be modified by ABO blood group determinants

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TABLE S1. **List of compounds in the Tn microarray and their observed binding affinities to mAb16D10 and the anti-Tn antibody.** Chart ID refers to the structures' position in the array; STDV is the SD value calculated from four technical replicates. An asterisk within the sequence indicates that the residue before it contains a GalNAc residue, and the number between parentheses indicates how many times the preceding residue is repeated.

			mAb16D10		anti-Tn	
Chart ID	**Detail**	**Sequence**	**Average**	**STDEV**	**Average**	**STDEV**
1	a-100uM	AcPT*TTPLKNH2	1509	688	1	1
2	b-100uM	AcPTT*TPLKNH2	272	215	2	2
3	c-100uM	AcPTTT*PLKNH2	743	288	6	11
4	d-100uM	AcPT*T*TPLKNH2	2996	1951	76	75
5	e-100uM	AcPT*TT*PLKNH2	4240	321	76	150
6	f-100uM	AcPTT*T*PLKNH2	1071	241	1925	594
7	g-100uM	AcPT*T*T*PLKNH2	4383	1581	4774	1952
8	R-100uM	AcPTTTPLKNH2	73	142	1	2
9	I-100uM	AcPPTTTTKKPNH2	166	172	2	1
10	II-100uM	H-GTTPSPVPT*TSTTSAP-OH	72	148	20	14
11	III-100uM	AcPTTDSTT*PAPTTKNH2	25	230	11	6
12	EA2 -1-100uM	Ac-PTTDSTTPAPTTK-HH2	60	113	3	5
13	EA2 -2-100uM	Ac-PPT*T*T*T*KKP-HN2	165	98	2	2
14	EA2 -3-100uM	NH2-TSAPDT*RDAP-NH2	252	204	1	1
15	EA2 -4-100uM	NH2-TSAPDTRPAP-NH2	152	293	5	6
16	G-8-Pep-100uM	H-APGS*T*APP-NH2	6287	2287	7898	1724
17	P-8-mer-100uM	H-APGSTAPP-NH2	321	308	2	3
18	PADRE-Tn3-100uM	C107H178N26O38 - Sequence not given	4757	1818	4158	738
19	Tn3-linker-100uM	C41H72N8O22 - Sequence not given	10640	7146	5284	2121
20	Tn-linker-100uM	C17H32N4O8 - Sequence not given	3521	1316	27	10
21	Peptide-4-100uM	AcHN-KTTT-CONH2	100	149	7	12
22	Peptide-5-100uM	AcHN-KTTTG-CONH2	8	55	6	3
23	Ser1-100uM	H-Ser(a-D-GalNAc)-NH2	-104	365	15	2
24	S2-100uM	H-Ser(a-D-GalNAc)-OH	357	418	6	8
25	Thr1-100uM	H-Thr(a-D-GalNAc)-NH2	-133	358	3	2
26	T1-100uM	H-Thr(a-D-GalNAc)-OH	-90	164	2	3
27	IgA-Pep01-100uM	KPVPST*PPT*PS*C	7466	369	11	7
28	IgA-Pep02-100uM	KPVPSTPPTPSC	630	507	1728	3449
29	S-GalNAc-100uM	S-GalNAc	2521	1181	0	1
30	T-GalNAc-100uM	T-GalNAc	-111	88	153	187

31	Blood group A Tetra-AEAB-100uM		22673	10527	37	60
32	Blood group A penta-AEAB-100uM		13755	6708	60	116
33	LNnT-100uM		573	144	274	429
34	Man5-100uM		117	230	6	9
35	Crypto peptide 01-50uM	H-ETS*EAAAT*VDLFAFT*LDGGK-NH2	10697	5063	102	192
36	Crypto peptide 02-50uM	H-ETSEAAAT*VDLFAFT*LDGGK-NH2	3014	576	12	19
37	Crypto peptide 03-50uM	H-ETS*EAAATVDLFAFT*LDGGK-NH2	9042	1926	13	6
38	Crypto peptide 04-50uM	H-ETSEAAATVDLFAFT*LDGGK-NH2	2056	1519	110	218
39	Crypto peptide 05-50uM	H-ETS*EAAAT*VDLFAFTLDGGK-NH2	16332	3763	89	58
40	Crypto peptide 06-50uM	H-ETSEAAAT*VDLFAFTLDGGK-NH2	13248	6132	45	47
41	Crypto peptide 07-50uM	H-ETS*EAAATVDLFAFTLDGGK-NH2	8165	1893	13	23
42	Crypto peptide 08-50uM	H-ETSEAAATVDLFAFTLDGGK-NH2	316	115	17	14
43	Crypto peptide 09-50uM	H-ETT*EAAAS*VDLFAFS*LDGGK-NH2	18958	2203	30	3
44	Crypto peptide 10-50uM	H-ETTEAAASVDLFAFSLDGGK-NH2	1608	2215	2	2
45	Crypto peptide 11-50uM	H-DVPVEGSS*(7)TSTVAPANK-NH2	4695	1544	2311	638
46	Crypto peptide 12-50uM	H-DVPVEGSS(7)TSTVAPANK-NH2	1143	841	27	36
47	Crypto peptide 13-50uM	H-DVPVEGSS*(16)TSTVAPANK-NH2	7407	3419	4676	1496
48	Crypto peptide 14-50uM	H-DVPVEGSS(16)TSTVAPANK-NH2	249	131	1	2
49	Crypto peptide 15-50uM	H-DVPVEGSS*(23)TSTVAPANK-NH2	25484	4147	5651	2361
50	Crypto peptide 16-50uM	H-DVPVEGSS(23)TSTVAPANK-NH2	-68	286	2	3
51	Cp17 protein-200ug/ml		5324	1297	15	11
52	Cp23 protein-200ug/ml		308	473	62	8
53	PBS		182	317	25	29
54	PBS		191	332	3	2
55	PBS		400	185	6	7
56	Biotin		267	166	3	3

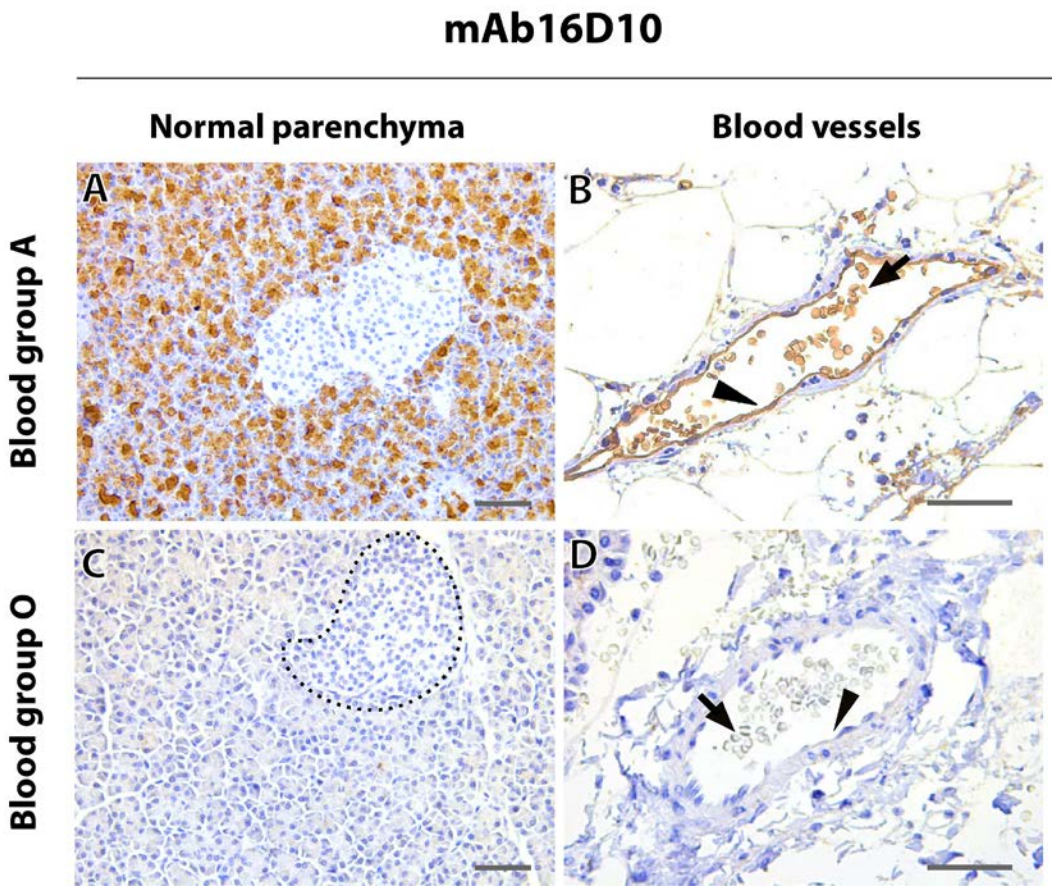

FIGURE S1. **mAb16D10 cross-reacts with blood group A antigens in normal pancreas tissue.** *A* and *C*, normal pancreatic parenchyma of subjects with blood group A and O, respectively, immunostained with mAb16D10. Only specimens from blood group A subjects reacted with the antibody. *B* and *D*, blood vessels of the same specimens. The black arrows point at red blood cells, whereas the arrowheads point at the endothelial lining of the vessels. Pancreatic islets (unstained region in *A*; circumscribed by dotted line in *C*) were negative for both blood groups. Scale bars represent 100 µm.

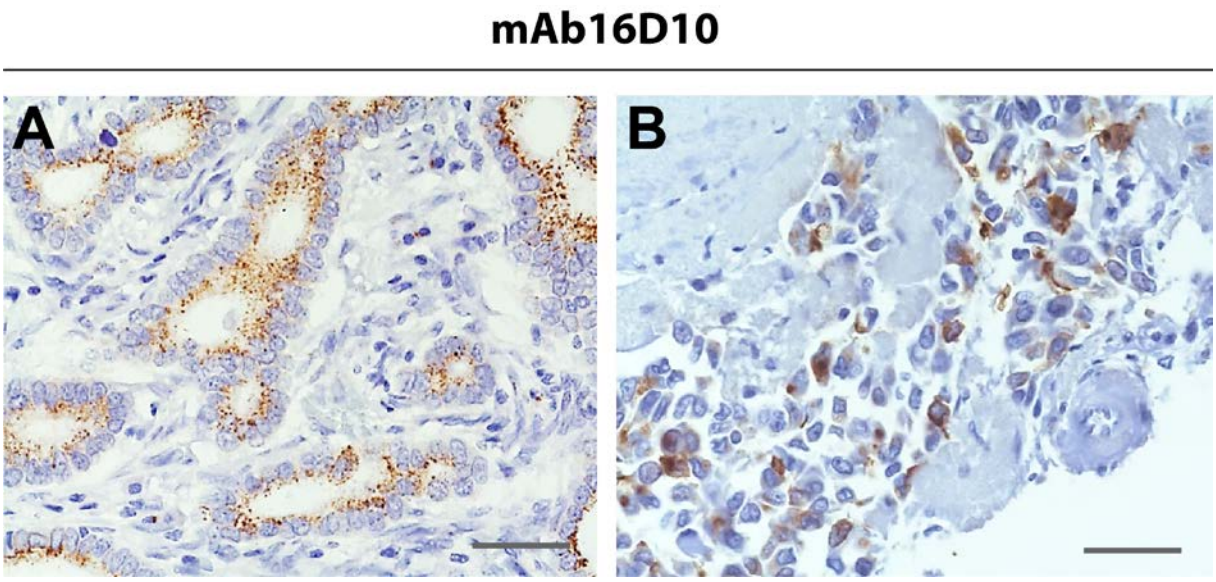

FIGURE S2. **mAb16D10 stains gastric and breast cancer tissue.** *A, B,* sections from gastric and breast cancer, respectively, both from non-A individuals. Scale bars represent 100 µm.

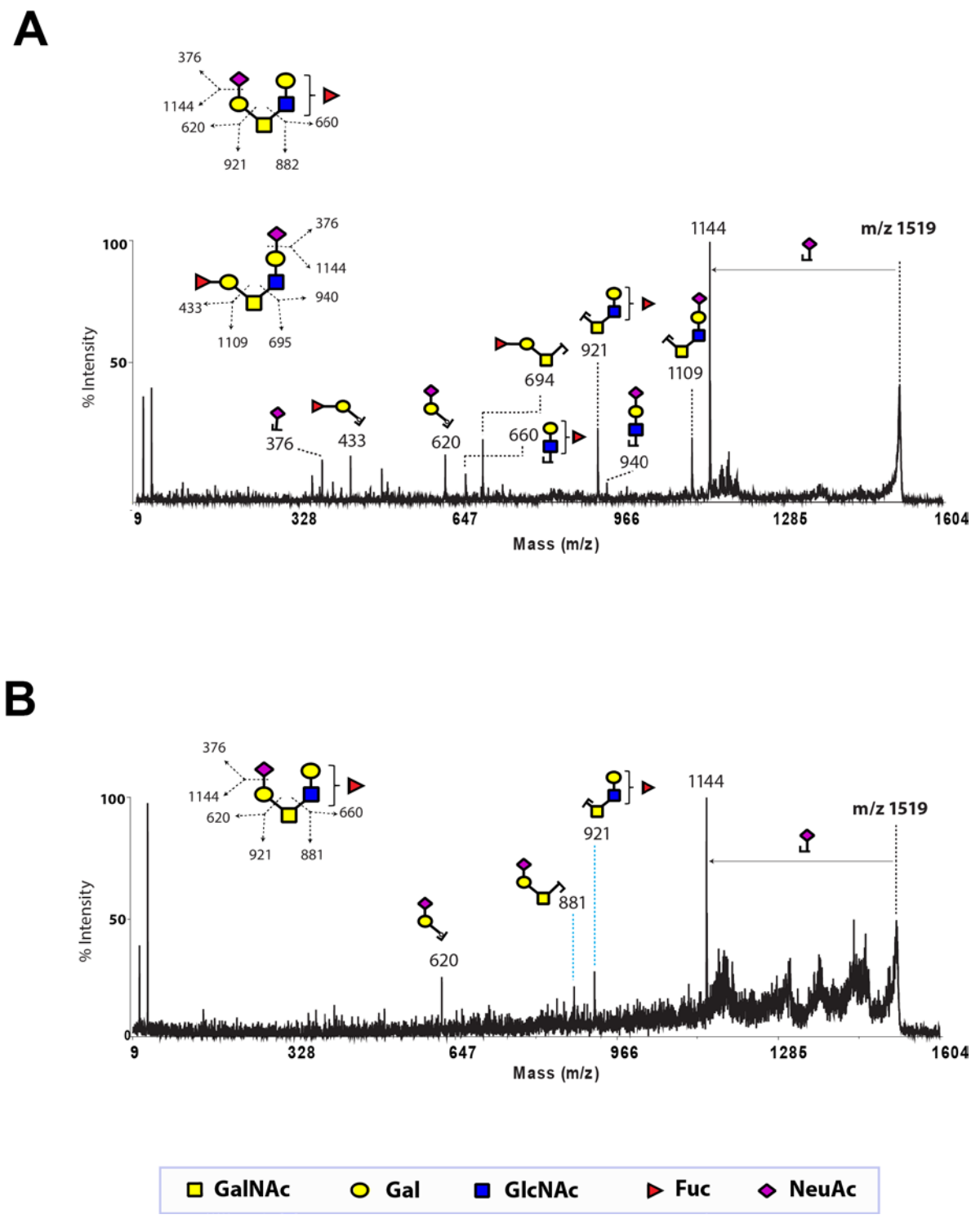

FIGURE S3. **MALDI-TOF/TOF-MS/MS fragmentation spectra of the selected molecular ion m/z 1519 from two samples with different secretor status.** *A*, fragmentation spectra of the molecular ion 1519 from the blood group O/*FUT2*-positive (secretor) case; *B*, same from the blood group O/*FUT2*-negative (non-secretor) case. All fragment ions are [M+Na]+. When structures have not been unequivocally defined from MS/MS information, the monosaccharide is shown after a bracket.

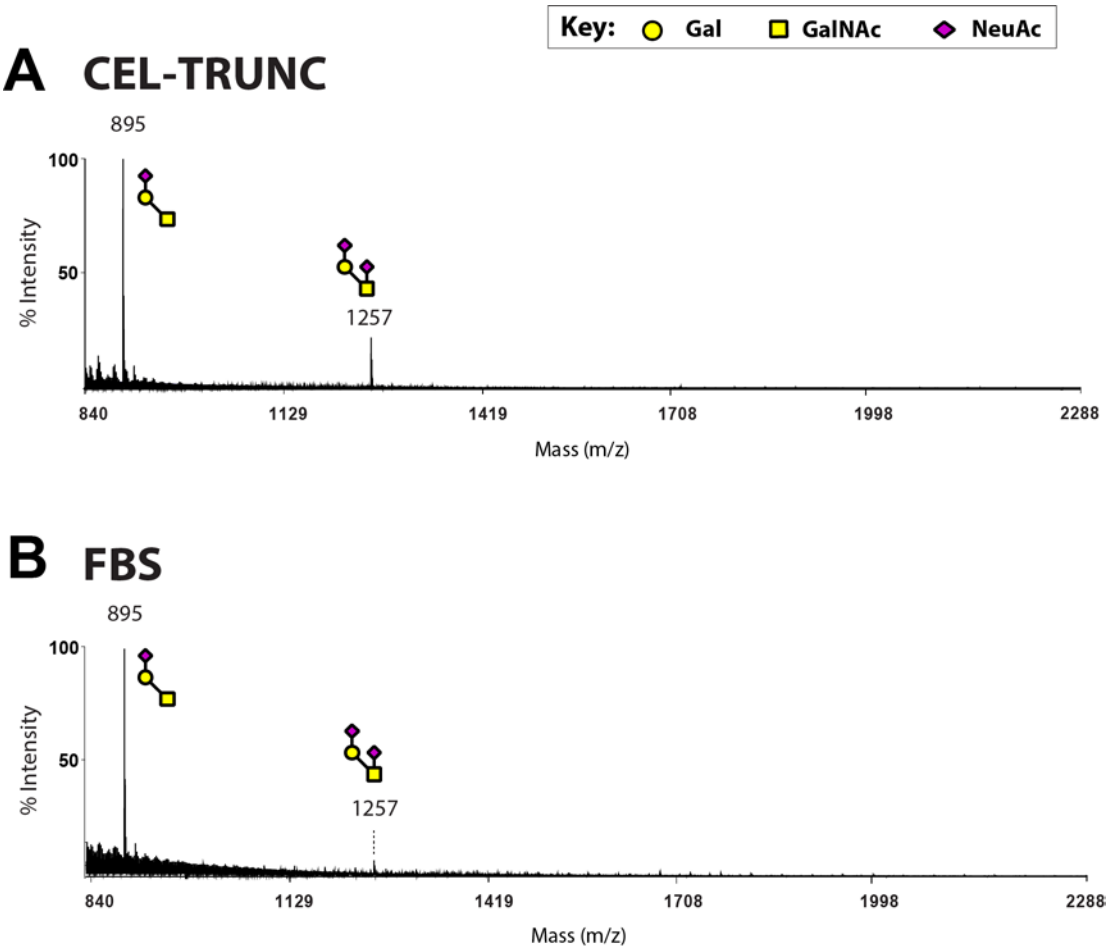

FIGURE S4. **Deletion of CEL´s mucinous domain results in O-glycans only corresponding to the fetal bovine serum background.** *A*, Spectrum from HEK293 cells stably transfected with CEL-TRUNC, a CEL construct containing a stop codon mutation immediately before the VNTR region. *B*, Spectrum from fresh DMEM medium containing 10% FBS. The medium was purified exactly as the other samples (see Experimental Procedures) and the resulting glycans were treated and analyzed in the same way. The nearly identical O-glycan pattern of *A* and *B* shows that the glycans seen when analyzing CEL-TRUNC most likely stem from the serum background.