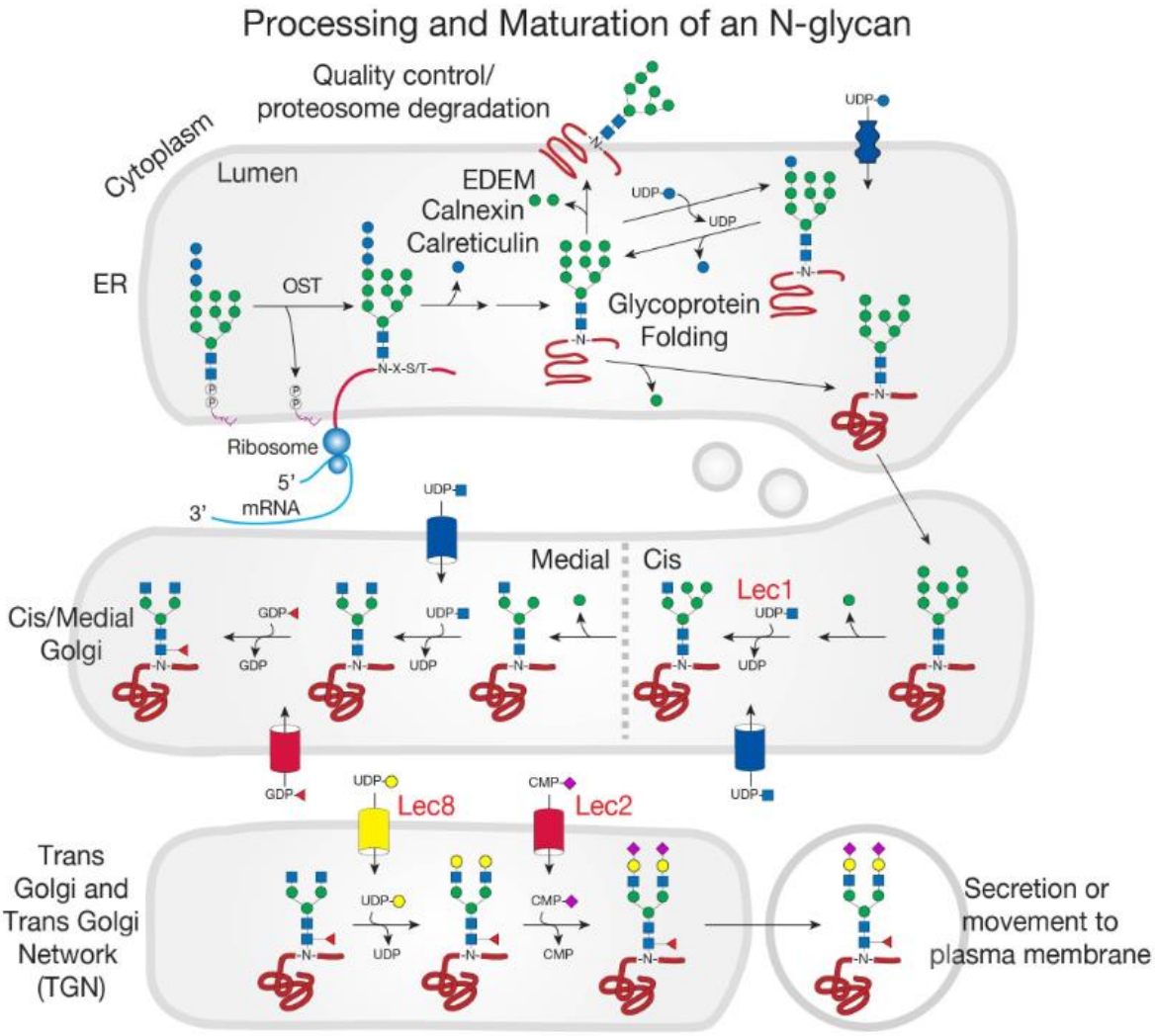
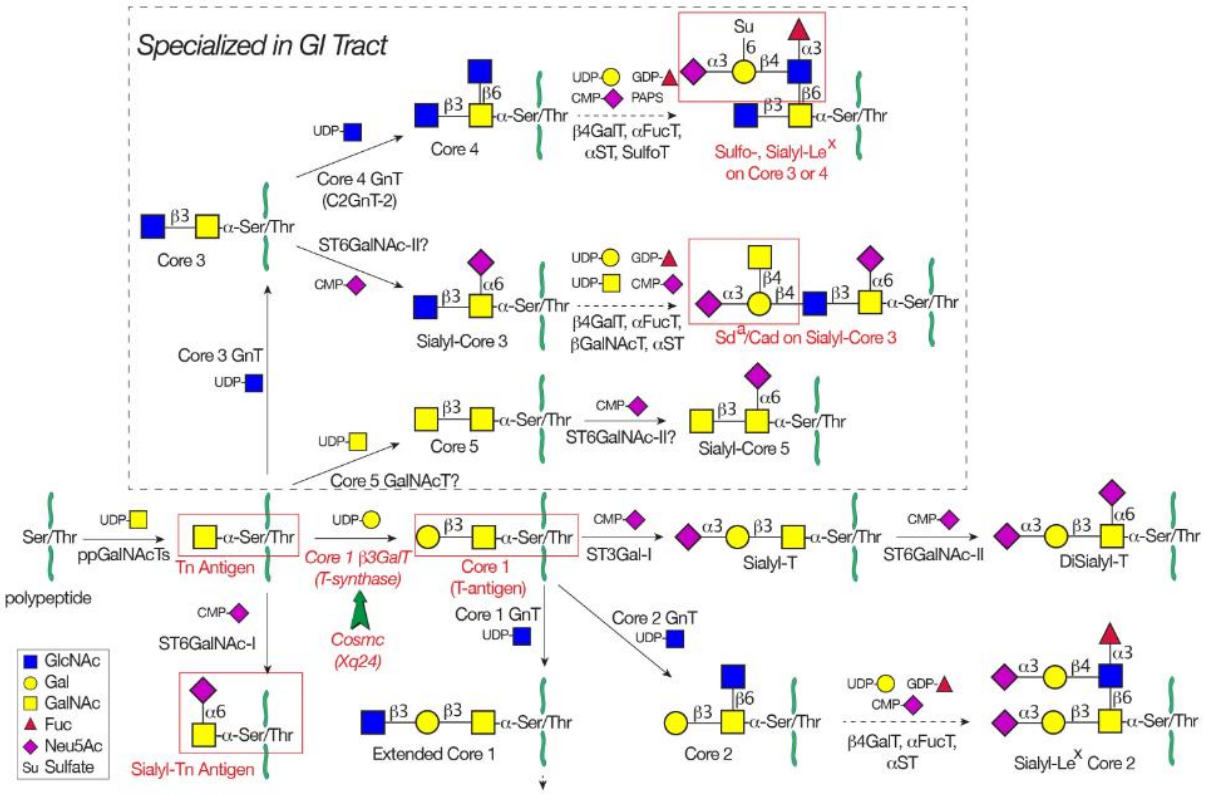
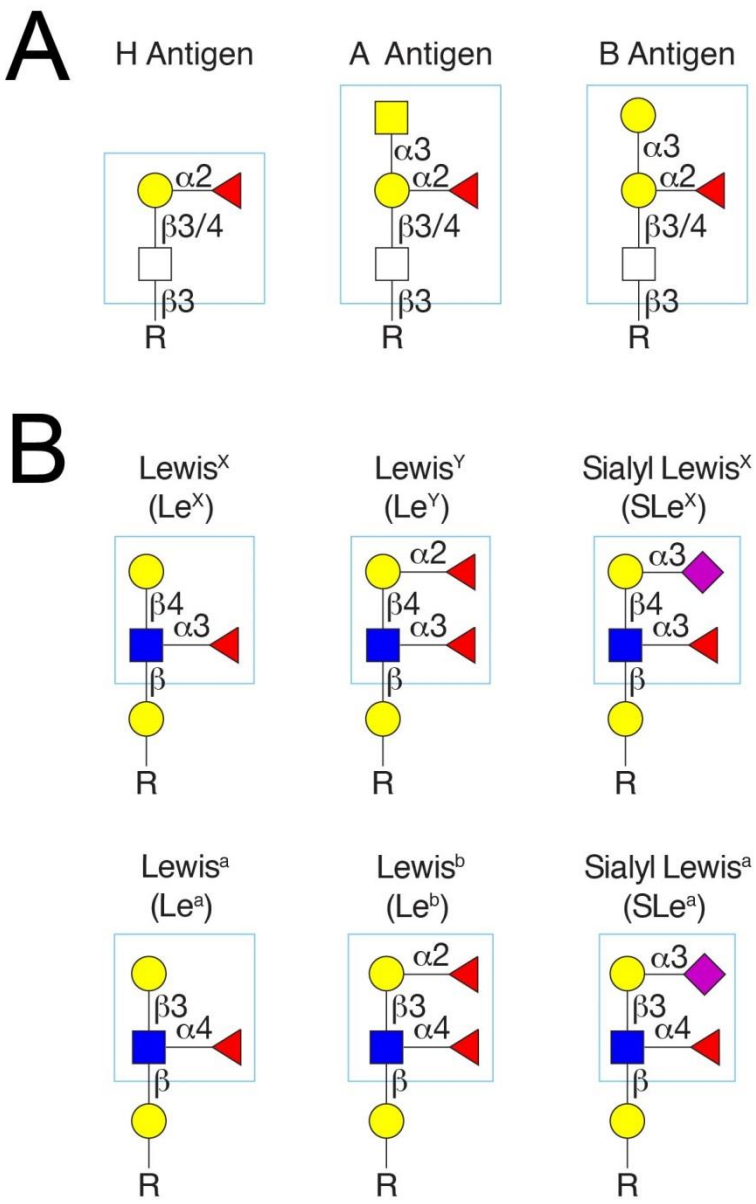


Supplementary Figure 1. N-glycan synthesis and processing. A $Glc_3Man_9GlcNAc_2$ precursor is synthesized on the cytoplasmic face of the endoplasmic reticulum on a dolichol-pyrophosphate precursor before being flipped to the ER lumen (as $Man_5GlcNAc_2$) and transferred to asparagine in the Asn-X-Ser/Thr sequon on nascent polypeptides through the oligosaccharyltransferase (OST) multiprotein complex. Glucosidases remove terminal glucose residues, calnexin and calreticulin assist in

folding, and the glycoprotein is interrogated by the protein folding and quality control machinery. Improperly folded proteins are retrotranslocated by the lectin EDEM, whereas properly folded proteins are marked with removal of the final glucose by glucosidase II. The glycoprotein is then transported to the cis-Golgi network and processed further by mannosidase II before addition of a terminal GlcNAc by GnT1 (which is defective in LEC1-mutant cells), initiating the first N-glycan branch. After additional processing, GnT2 adds GlcNAc to form the second branch of a biantennary $GlcNAc_2Man_3GlcNAc_2$ glycan, which is further modified by addition of a 'core' α1,6 fucose by *FUT8*. This structure is transferred to the trans-Golgi network (TGN) for addition of a terminal galactose (which is absent in UDP-Gal transporter-mutant Lec8 cells) as well as a terminal sialic acid (which is absent in CMP-sialic acid transporter-mutant Lec2 cells). The fully matured glycoprotein is secreted extracellularly or transported to the cell surface. A parallel pathway targeting N-glycoproteins to the lysosome with mannose-6-phosphate is not shown.



Supplementary Figure 2. O-glycan synthesis. Synthesis of the major core (1–4) O-glycans is shown, with structures implicated in inflammatory bowel disease highlighted in red. Mucin-type O-glycosylation is initiated by a family of 20 polypeptide GalNAc transferases (ppGalNacTs) to form the Tn antigen, which is typically modified either by addition of galactose to form core 1 (also known as T antigen) and subsequently core 2 or extended core 1, or by addition of GlcNAc to form core 3 and subsequently core 4 structures. All cores can be further modified by Gal, GlcNAc, Fuc, Sia and sulfate to form terminal epitopes. Core 1-based and core 2-based structures are found in all tissues, whereas core 3-based and core 4-based structures are restricted to the intestinal epithelia.



Supplementary Figure 3. Select terminal glycan structures. (A) ABO(H) blood group antigens. These can be further classified as type-1 or -2, based on β3 or β4 linkage, respectively, of the terminal (H Ag) or subterminal (A/B Ag) galactose to the proximal GlcNAc (i.e. LacNAc) or type-3 or -4 based on β3 linkage to an O-GalNAc-linked glycan or a glycolipid, respectively. **(B)** Lewis antigens. These can be further modified by addition of sulfate to the 6-position of GlcNAc (6-Sulfo-), Gal (6'-Sulfo-), or 3-position of Gal (3'-Sulfo-).

Supplementary Table 1. Inflammatory bowel disease risk genes. Genes are divided by those found in UC, CD, or both (IBD). Those genes implicated in regulating glycosylation are highlighted in red.

CD	UC	IBD				
ADAM30	ADA	ADCY3	CXCR5	IL21	PLA2R1	TRIB1
AKAP1	AHR	ALDH2	DAP	IL23R	PRKAB1	TRIM 35
ATG16L1	CALM3	ARHGEF6	DNMT3B	IL27	PRKCB	TRIM8
CD27	CARD11	ATG4B	DOK3	IL2RA	PTGER4	TSPAN14
CHADL	DLD	ATXN 2	DUSP1	IPMK	PTGS2	TST
CPEB4	FAM55A	BACH2	DUSP22	IRF4	PTK2B	TUBD1
CREB5	FAM55D	BRE	EDG1	IRF8	PTPRC	TYK2
FASLG	GNA12	BTBD8	EPHX2	IRGM	REL	VDR
FUT2	HNF4A	C10orf58	EPO	JAK2	RELA	ZFP36L1
GPX4	IRF5	C1GALT1C1	ERAP1	KIF21B	RORC	ZNF831
HMHA1	ITGAL	C1orf53	ERAP2	LIF	RPS6KA2	ZPBP
IFNAR1	ITIH4	C5orf4	FCGR2A/B	LIFR	RPS6KB1	
IFNGR2	JRKL	CARD9	FCGR3A	LITAF	SELE	
IL31RA	MAML2	CCDC88B	FLJ78302	LOH12CR1	SELL	
IL6ST	MANBA	CCL13	FOS	LPXN	SELP	
JAZF1	MAN2A1	CCL2	FOSL2	LSP1	SH2B3	
L3MBTL2	NFKB1	CCL20	FYB	LTF	SLC30A	
LACC1	NFKBIZ	CCR1	GALC	LY75	SMAD3	
LGALS9	PLCL1	CCR2	GPR18	MAP3K7IP2	SMAD7	
LTBR	PRKCD	CCR3	GPR183	MAP3K8	SMURF1	
NHP2L1	RFTN2	CCR5	GPR35	MARCH7	SOCS1	
NOD2	SLC9A3	CCR6	GPR65	MLH3	SPRED2	
NOS2	TNFRSF14	CD226	HCK	MST1	SPRY4	
PMM1	ZFP90	CD28	HGFAC	MUC19	STAT1	
PTPN22		CD40	IBD5 locus	NDFIP1	STAT3	
RASGRP1		CD48	ICOS	NFATC1	STAT4	
RIPK2		CD6	ICOSLG	NFIL3	TMEM180	
SP140		CEBPB	IFIH1	NFKB2	TMEM258	
SPRED1		CEBPG	IFNG	NKX2-3	TNFAIP3	
TAGAP		CISD1	IKZF1	ORMDL3	TNFRSF18	
TEF		CNTF	IL10	OSM	TNFRSF4	
TFSF11		CNTNAP2	IL12B	OSMR	TNFRSF6B	
TNFRSF 1A		CREM	IL15RA	PDCD1	TNFRSF9	
TNFSF18		CRTC3	IL18RAP	PFKB4	TNFSF15	
UCN		CTLA4	IL1R1	PHACTR2	TNNI2	
USP1		CTSZ	IL2	PLA2G4A	TRAF3IP2	