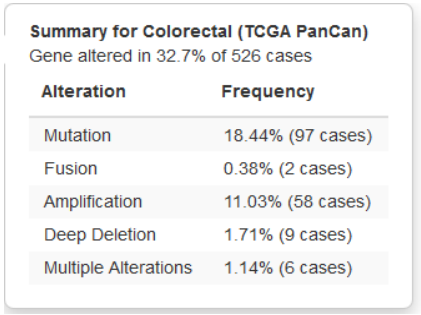
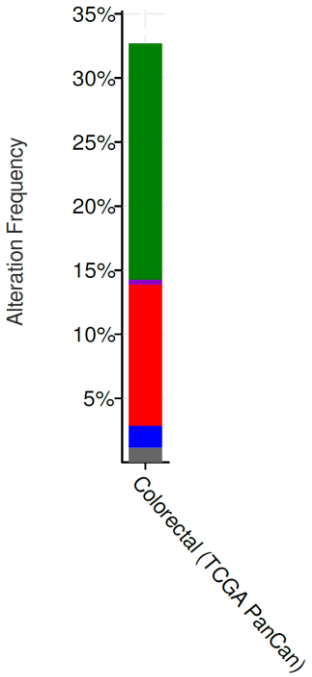
Gene Name	Missense Mutation	Truncating Mutation	Fusion	Amplification	Deep Deletion
DAG1	1.52%	0.38%			0.38%
POMT1	2.47%	0.19%		0.19%	
POMT2	2.47%	0.19%			
POMGNT1	1.71%	0.38%			
POMGNT2	2.47%	0.19%		0.19%	
MGAT5B	2.66%	0.95%		0.76%	
B3GALNT2	0.38%			0.57%	
POMK	0.76%	0.38%	0.19%	3.61%	0.19%
FKTN	1.14%	0.76%			0.19%
FKRP	0.57%				
RXYLT1	0.38%	0.57%			
B4GAT1	1.33%				0.19%
LARGE1	3.04%	0.38%		0.19%	0.76%
LARGE2	1.71%	0.76%		0.19%	
CHST10	3.04%	0.57%			
DPM1	0.57%	0.19%		5.70%	
DPM2	0.19%				
DPM3				0.57%	
DOLK	1.33%	0.19%			
CRPPA	1.52%	0.57%		0.38%	
HK1	2.47%	0.19%	0.19%	0.38%	0.19%
MPI	0.76%	0.38%			
PMM2	0.38%	0.19%			0.19%
GMPPB	0.38%			0.38%	
FURIN	2.47%	0.76%		0.38%	0.19%

TCGA PanCaner Atlas **n=526**





Additional file 12: Mutational status of genes involved in α-DG glycosylation in CRC

We analyzed the genetic status of the indicated genes within the TCGA cohort of 526 colorectal cancer cases (PanCancer Atlas) accessible via the cBioPortal (www.cbioportal.org). Percentages give the frequency of a given genetic alteration found in 526 CRC cases. Note that *LARGE1* and *LARGE2* plus 23 factors known to be involved in α-DG glycosylation were each affected in only a small (3 percent and less) fraction of tumors. Overall, approximately 18.5% of CRC cases harbour mutations in one or several of these genes, and 1.7% of patients were affected by deep deletions on one of the analyzed gene loci.