Current Background: Homo sapiens

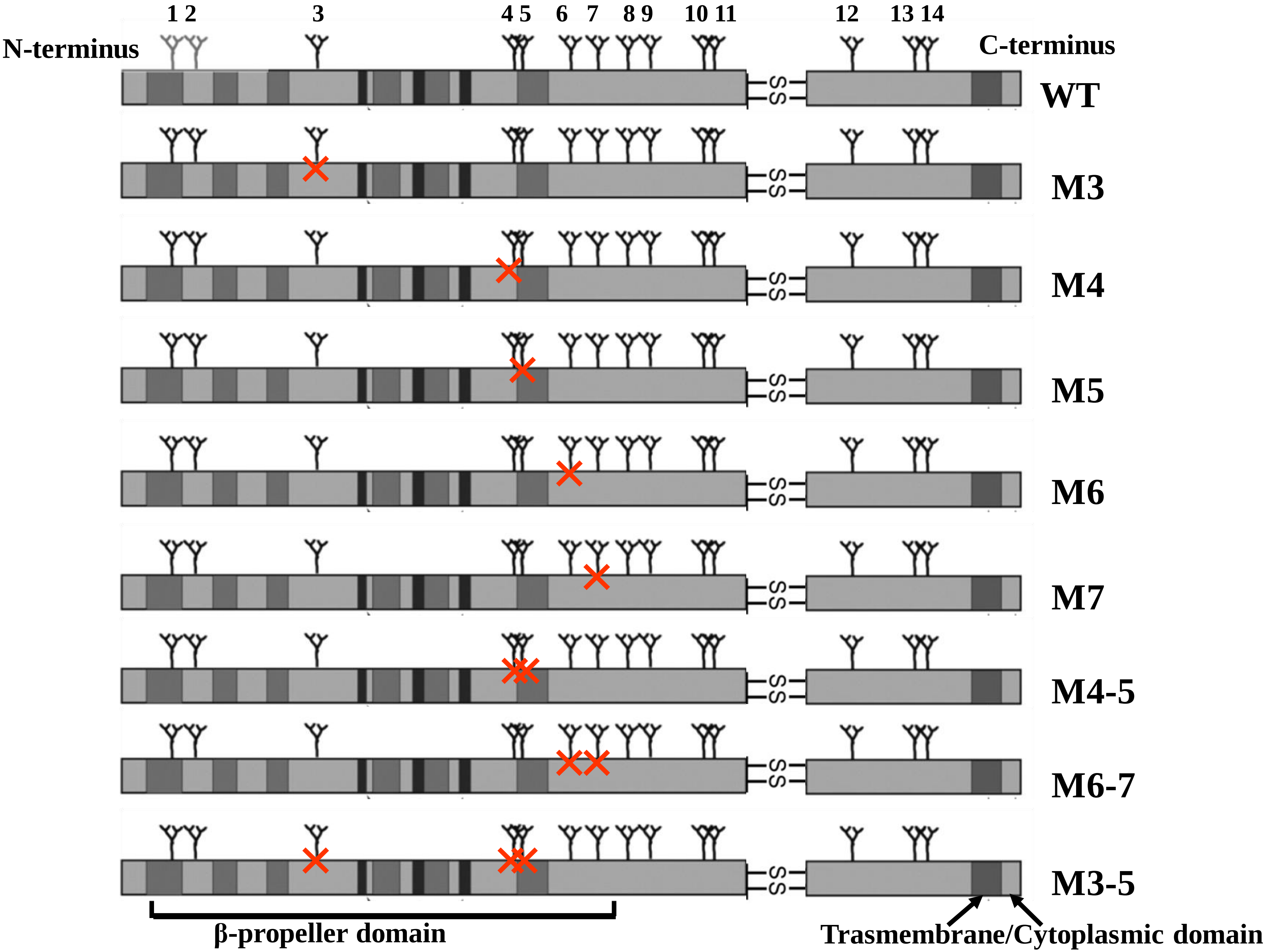
1770 DAVID IDs

⊞ Options Classification Stringency Medium

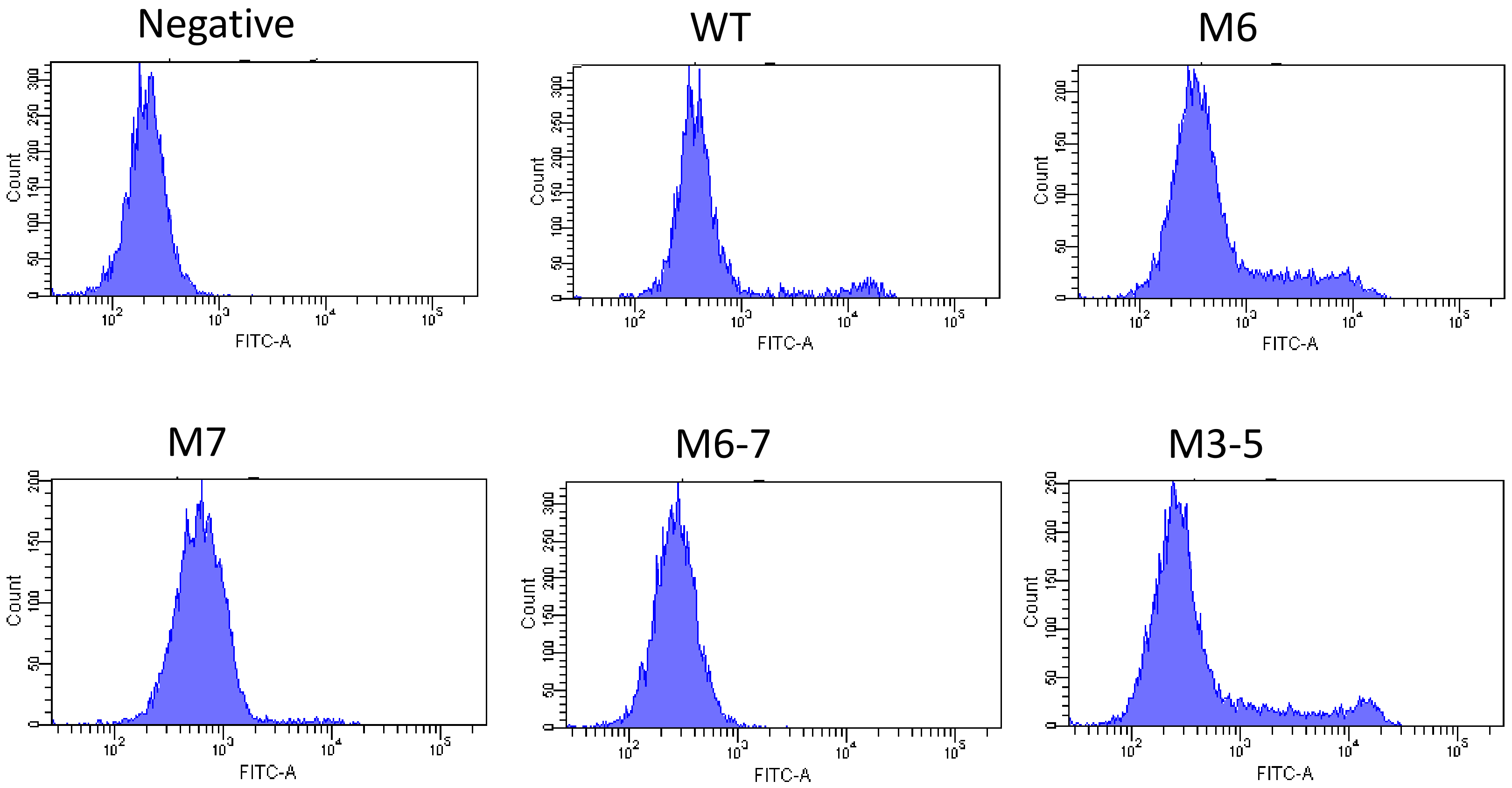
83 Cluster(s)

					Count	P_Value	Benjamini
Annotation Cluster 1		**Enrichment Score: 21.41**	G		**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		101	1.7E-34	1.3E-31
☐	SP_PIR_KEYWORDS	glycoprotein	RT		101	5.2E-33	1.4E-30
☐	SP_PIR_KEYWORDS	signal	RT		85	4.2E-29	5.9E-27
☐	UP_SEQ_FEATURE	signal peptide	RT		85	6.7E-29	2.6E-26
☐	SP_PIR_KEYWORDS	disulfide bond	RT		58	1.3E-12	9.3E-11
☐	SP_PIR_KEYWORDS	transmembrane	RT		70	1.4E-8	4.2E-7
☐	UP_SEQ_FEATURE	transmembrane region	RT		69	2.7E-8	3.5E-6
Annotation Cluster 2		**Enrichment Score: 13.84**	G		**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	cell adhesion	RT		27	1.0E-16	1.0E-14
☐	GOTERM_BP_FAT	cell adhesion	RT		34	1.5E-15	2.0E-12
☐	GOTERM_BP_FAT	biological adhesion	RT		34	1.6E-15	1.0E-12
☐	KEGG_PATHWAY	ECM-receptor interaction	RT		14	1.7E-10	1.5E-8
Annotation Cluster 3		**Enrichment Score: 7.04**	G		**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		61	1.7E-11	4.4E-9
☐	SP_PIR_KEYWORDS	membrane	RT		84	7.1E-10	4.0E-8
☐	UP_SEQ_FEATURE	topological domain:Extracellular	RT		50	2.1E-9	3.2E-7
☐	SP_PIR_KEYWORDS	transmembrane	RT		70	1.4E-8	4.2E-7
☐	UP_SEQ_FEATURE	transmembrane region	RT		69	2.7E-8	3.5E-6
☐	GOTERM_CC_FAT	intrinsic to membrane	RT		79	1.5E-3	1.6E-2
☐	GOTERM_CC_FAT	integral to membrane	RT		75	4.0E-3	3.6E-2
Annotation Cluster 4		**Enrichment Score: 6.24**	G		**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	lysosome	RT		13	1.4E-9	6.5E-8
☐	KEGG_PATHWAY	Lysosome	RT		12	9.7E-7	2.1E-5
☐	GOTERM_CC_FAT	lysosome	RT		13	3.4E-6	1.5E-4
☐	GOTERM_CC_FAT	lytic vacuole	RT		13	3.4E-6	1.5E-4
☐	GOTERM_CC_FAT	vacuole	RT		14	3.9E-6	1.3E-4

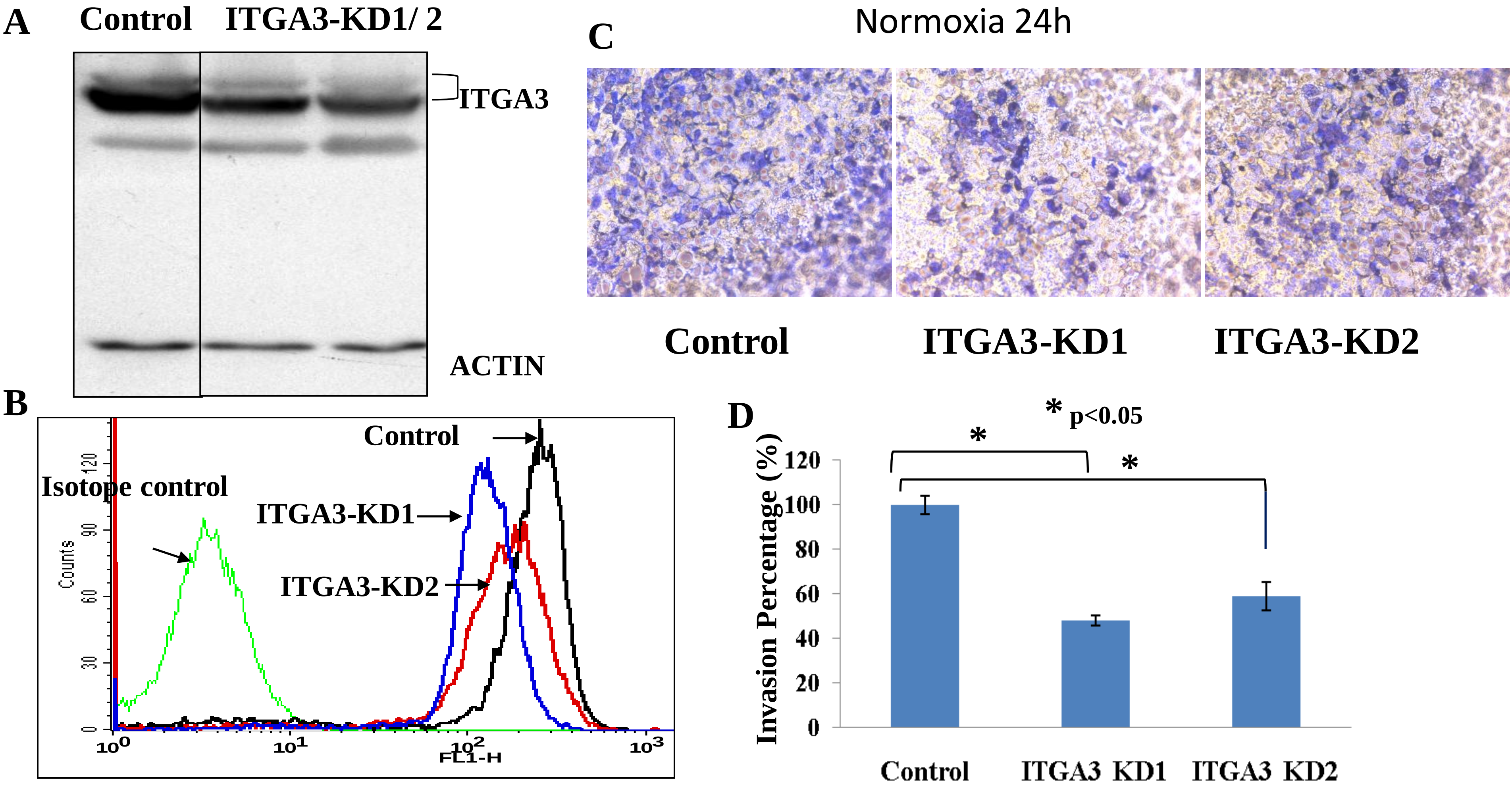
Supplemental Figure S1: Clustering results of identified putative glycoproteins by David Functional Annotation Clustering tool.



Supplemental Figure S2. **Schematic illustration of the locations of mutated N-glycosylation sites in the ITGA3 subunit.** A total of 14 putative N-glycosylation sites exist in the ITGA3 subunit. Crosses represent the unglycosylation of each N-glycan site by site-directed mutagenesis from N to Q.



Supplemental Figure S3: Flow cytometry analysis of membrane ITGA3 expression in the pool of stable cell lines selected by hygromycin B. Only M6-7 had no membrane ITGA3 detected.



Supplemental Figure S4: Knockdown of ITGA3 suppressed A431 invasion.

The lower whole and membrane ITGA3 in knockdown cell lines was confirmed by WB and FACS(A and B). The less invasion of knockdown cell lines was observed in transwell invasion assay (C and D). 1μg/ml laminin 5 was coated on the membrane and 5% FBS in the media was added in the lower chambers of transwells. Control: cells transfected with shRNA fragments of Luciferase; ITGA3-KD1/2: the two clones picked up from the cells transfected with ITGA3 shRNA fragments.