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Supporting Information

for

A systems-based framework to computationally describe putative transcription factors and signaling pathways regulating glycan biosynthesis

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Comparison of wet-lab studies and entries in DBs as well as Alluvial plots for all cancer types

Level of agreement between wet-lab studies and corresponding entries in the databases.

Proposition: We determined if findings reported in literature (see Introduction section) have corresponding entries in bioinformatics databases that present TF–(glyco)gene relationships. Such comparisons were made with Cistrome DB, GTRD, and Regulatory Circuits DB (see table below). The footnote explains the metrics used for this comparison.

Conclusion: The analysis concludes that experimental data reported in literature only have partial support in currently established databases. The lack of agreement was due to several reasons: i) Sometimes, the TF was not included in the curation of the database; ii) sometimes, the TF in question was filtered out due to the database criteria for establishing TF–gene relationships; and iii) the putative TF–glycogene relationship is present in some cell systems, but not the cell system reported in literature. This suggests that the same TF–glycogene relationship may not hold for all cell types.

Table S1: To what degree are interactions reported in literature observed in various databases?

literature reports[a]			GTRD[b]	Cistrome database[c]	Regulatory Circuits[d]
glycogene	TF	expt. cell system	cell system where TF–glycogene relationship was found in database		
B4GALT1	SP1	A549	A375 (malignant melanoma); GM12878 (female B-cells lymphoblastoid cell line); HCT-116 (colon carcinoma); HEK293 (embryonic kidney); HUES64 (embryonic stem cells); liver	SP1 not present in DB	107 tissue-specific relationships with conf $\geq$0.1, significant
ST6Gal1	HNF1a	HepG2	not found (N.F.)	HNF1A not present in DB	2 with conf$\geq$0.1, (hepatocyte, spinal cord)
MGAT5	ETS2	NIH3T3	N.F.	N.F.	N.F.
ST6Gal2	HNF1a	HepG2	N.F.	HNF1A not in DB	N.F.
B3GNT8	c-JUN	Gastric Carcinoma	A549 (lung carcinoma); Dexamethasone-treated HUVEC-C. Metaclusters are absent in gastric carcinoma	N.F.	N.F.
HS3ST1	ZNF263	HeLa	HEK293 (embryonic kidney) K562 (myelogenous leukemia). Metaclusters are absent in HeLa.	ZNF263 not in DB	ZNF263 not in DB
HS3ST3A1	ZNF263	HeLa	K562 (myelogenous leukemia). Metaclusters are absent in HeLa	ZNF263 not in DB	ZNF263 not in DB

[a] Reported in literature (see Introduction section in the main manuscript). [b] GTRD: The GTRD curates TF binding sites on the genome by employing 4 different ChIP-Seq peak calling algorithms. Any binding region identified by more than one ChIP-Seq peak finding algorithm is designated as a metacluster. Thus, metaclusters represent TF binding regions with support from multiple ChIP-Seq peak calling algorithms. In our analysis, we parsed glycogene transcriptional start sites (TSSs) from Ensembl BioMart. Only transcripts with an Ensembl support level of 1 were used. To identify regulating TFs, the distance between the center of a metacluster and a glycogene TSS was computed. TF metaclusters identified 2 kb upstream from any glycogene TSS constituted a TF–glycogene relationship. This yielded a total 5,190 TF–glycogene interactions across 302 biological systems. [c] Cistrome DB: TF–glycogene relationships were parsed from Cistrome Cancer DB by picking regulatory potential ≥ 0.5 and correlation values ≥ 0.4. This yielded 22,654 TF–glycogene interactions in Cistrome Cancer DB. These thresholds were selected to find long- and short-range TF–glycogene interactions. [d] Regulatory Circuits: TF–glycogene relationships with a confidence score ≥ 0.1 were parsed from each of the 394 tissue-specific networks from Regulatory Circuits. This yielded 66,071 relationships across all 394 tissue systems.

Details: The following is a detailed explanation of our findings for each interaction and cell system:

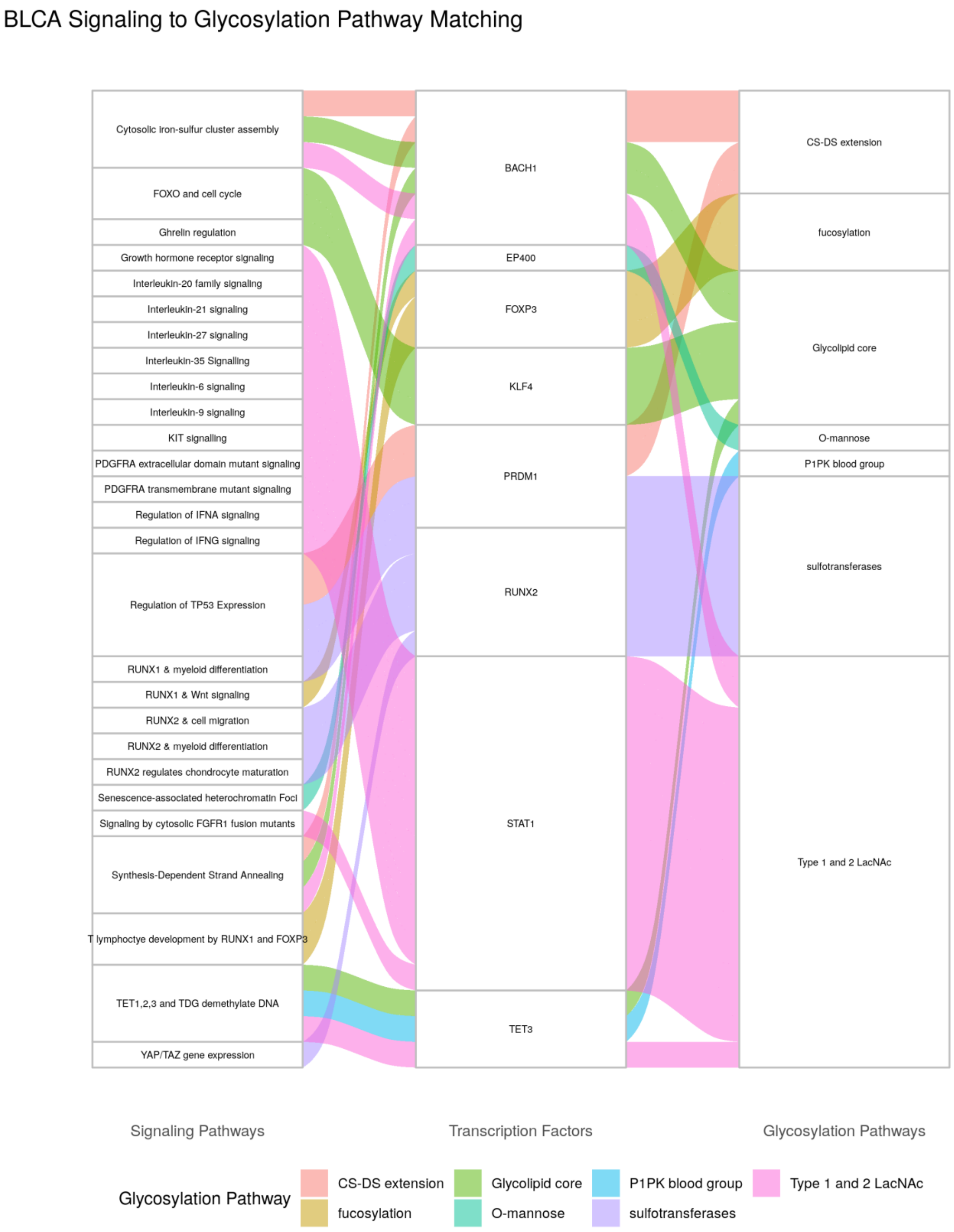
SP1→B4GALT1 in A549 cell line:
i) Cistrome DB: This relationship was not found in Cistrome DB since this TF was not included in the database. It is unclear if SP1 has been filtered from the database due to low tumor expression specificity, or if it was not included in the analysis.
ii) GTRD: SP1 was found in the promoter region of 6 different cell systems: A375, GM12878, HCT-116, HEK293, HUES64, and the “liver” system. In the A549 data (wet-lab data are reported in literature for this system), however, the SP1→B4GALT1 relation was not supported by the multiple ChIP-Seq algorithm used by GTRD. In this regard, while the SP1→B4GALT1 relation was reported in A549 using the MACS algorithm in one study. Three other algorithms used in GTRD (GEM, PICS, SISSRS) do not support a SP1→B4GALT1 relationship in A549. Thus, the SP1→B4GALT1 metacluster for A549 is not reported in the GTRD.
iii) Regulatory Circuits: This relation was observed in large cell lung carcinoma cell line network, which is derived from NCI-H460 and IA-LM cell lines (confidence threshold = 0.105). Since this network does not contain the A549 relationship, we conclude that SP1→B4GALT1 relation does not exist in A549 in Regulatory Circuits.

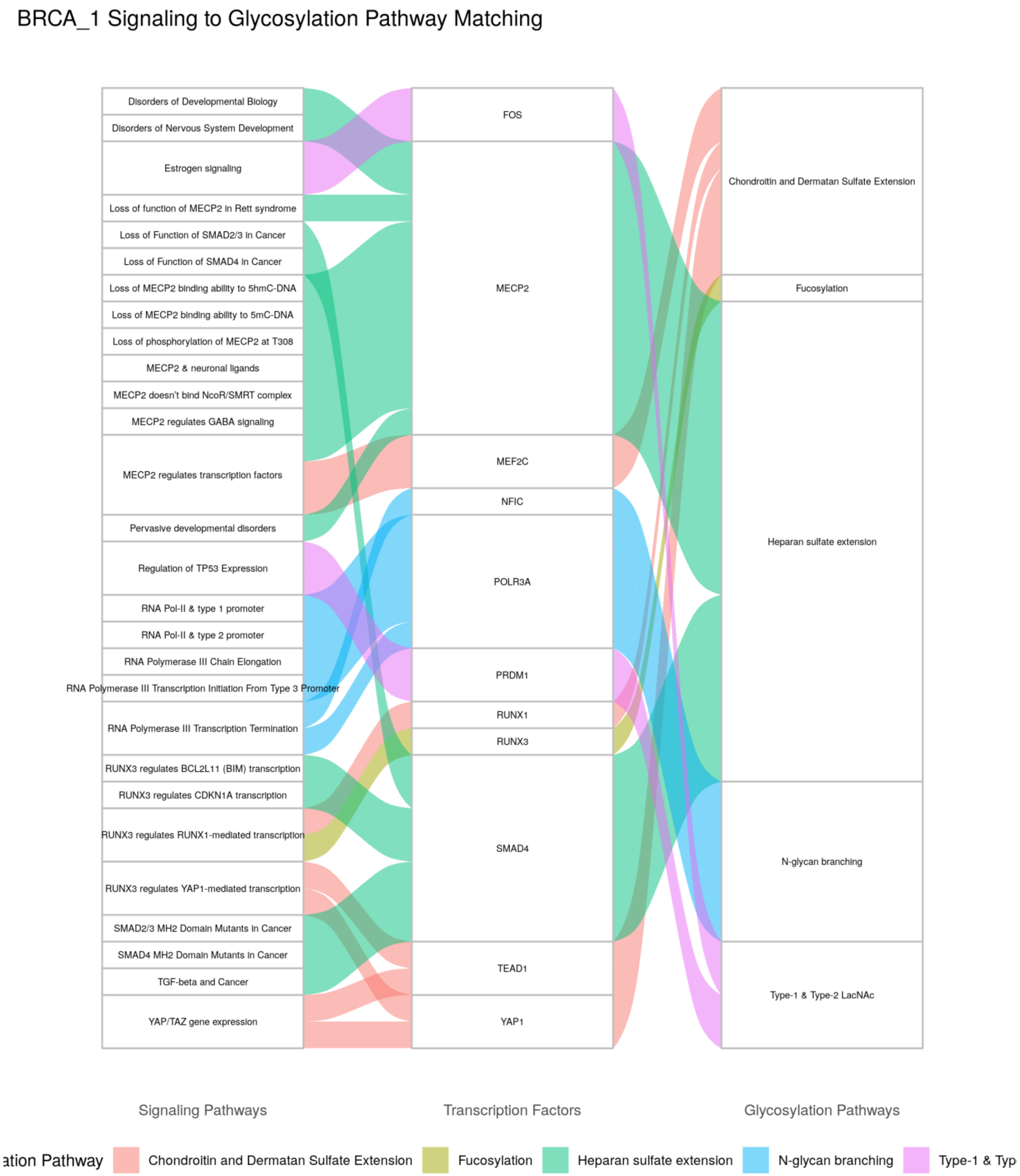
HNF1A→ST6Gal1/2 in HepG2 cell line:
i) Cistrome DB: HNF1A was not found in the downloaded Cistrome DB dataset. It was also not found upon searching the online database portal (http://cistrome.org/CistromeCancer/CancerTarget/). This may be due to low expression of this TF across TCGA cancers.
ii) GTRD: HNF1A data were available for 6 different cell systems across 9 distinct experiments. None of these systems supported a HNF1A→ST6GAL1 or HNF1A→ST6GAL1 metacluster relationship. Peaks called by GEM, MACS2, PICS, and SISSRS were loaded into the UCSC genome browser to see if individual algorithms supported the HNF1→ST6GAL1/2 relationship. No peak calling algorithm found HNF1A binding in the ST6GAL1 promoter.
iii) Regulatory Circuits: The HNF1A→ST6GAL1 relationship exists in the “hepatocyte” (confidence = 0.110) and “spinal cord adult” (confidence = 0.103) networks. However, the HNF1A→ST6GAL1 confidence threshold for three HepG2 CAGE sequencing replicates, called “hepatocellular carcinoma cell line”, was low and below our cutoff criterion (confidence value = 0.013).

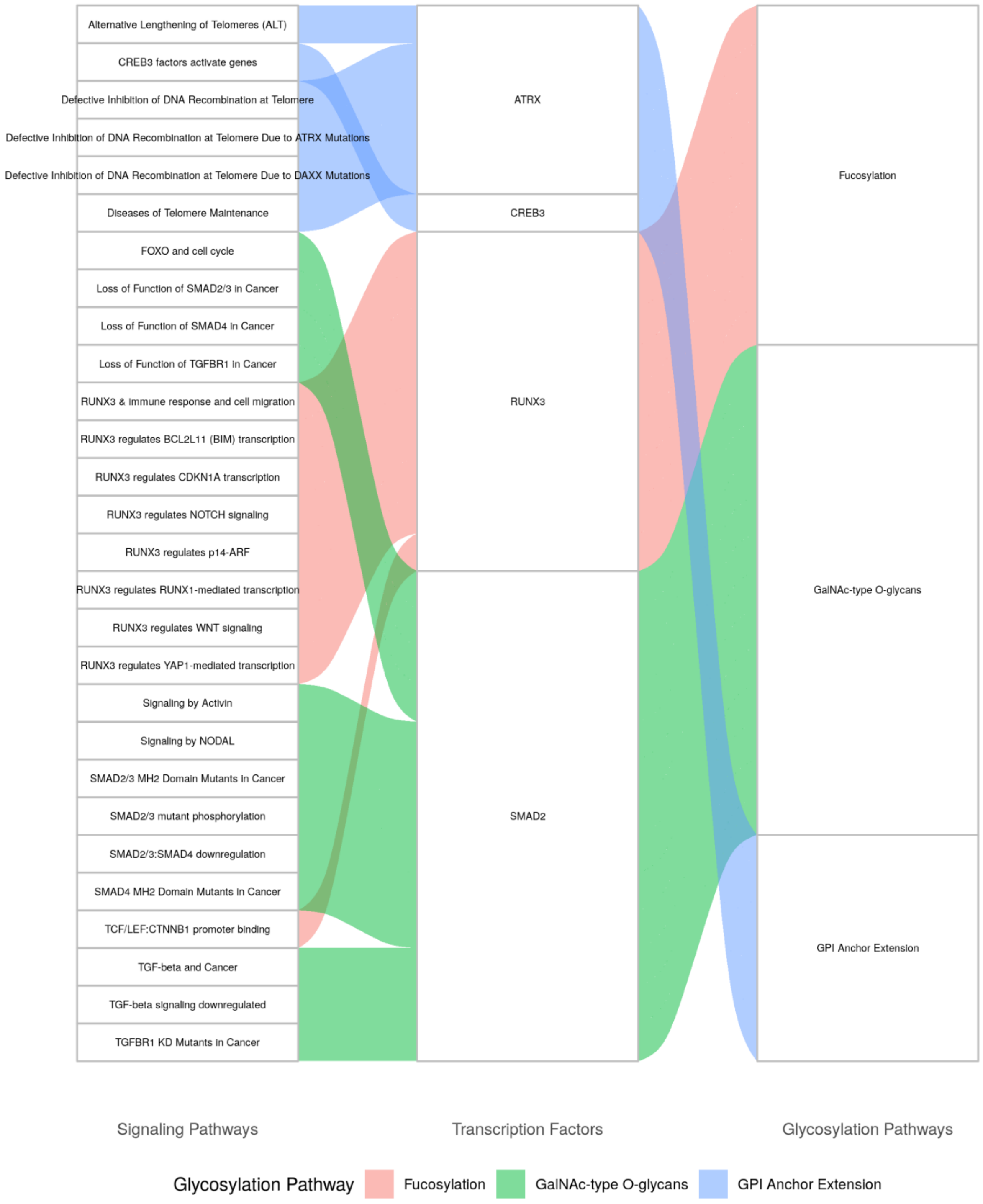
ETS2→MGAT5 in NIH3T3 cell line:
i) Cistrome DB: ETS2 was not found in the downloaded Cistrome DB, nor was it searchable from the database portal (http://cistrome.org/CistromeCancer/CancerTarget/). This could be due to the lack of expression in the TCGA dataset.
ii) GTRD: No metaclusters were identified supporting the ETS2→MGAT5 relationship.

iii) Regulatory Circuits: No ETS2→MGAT5 relationships were found in any of the tissue-specific networks in Regulatory Circuits
c-JUN—B3GNT8 in gastric carcinoma:
i) Cistrome DB: None of the correlation data or regulatory potential data present in Cistrome DB lists B3GNT8 being regulated by c-JUN. It is unclear for what reason this relationship was omitted.
ii) GTRD: dexamethasone-treated HUVEC-C cells and A549 cells support the c-JUN→B3GNT8 relationship. But this relationship is missing in gastric carcinoma systems, tissues and cell lines, and thus there is no evidence supporting this relationship.
iii) Regulatory Circuits: The B3GNT8 gene is absent in the regulatory networks of this database (see the other supplementary data files). Thus, we cannot assess validity of this relationship in Regulatory Circuits.

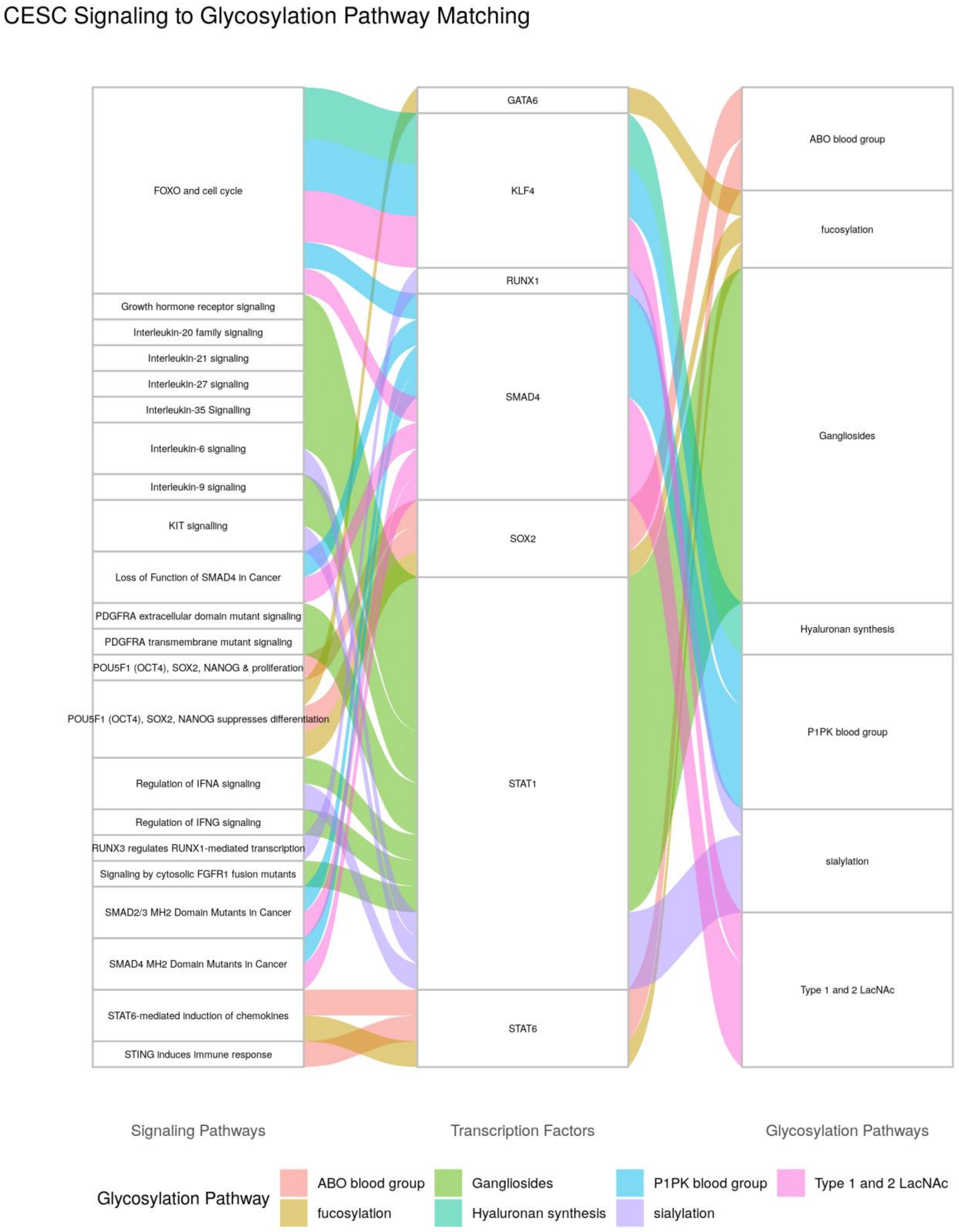
HS3ST1/HS3ST3A1→ZNF263 in HeLa cells:
i) Cistrome DB: ZNF263 was not found in the downloaded Cistrome DB, nor was it searchable from their database portal (http://cistrome.org/CistromeCancer/CancerTarget/). Low expression of this TF across TCGA cancers could potentially explain its absence.
ii) GTRD: ZNF263 has metaclusters in the promoter region of HS3ST1 in both HEK293, as well as K562 cells. ZFN263 also has metaclusters in the promoter region of HS3ST3A1 in K562. However, this relationship was absent in HeLa cells.
iii) Regulatory Circuits: ZNF263 was not considered in the construction of tissue-specific networks. There is no position weight matrix (PWM) information present for ZNF263 (see Regulatory Circuits supplemental material).


BLCA Signaling to Glycosylation Pathway Matching
Cytosolic iron-sulfur cluster assembly
FOXO and cell cycle
Ghrelin regulation
Growth hormone receptor signaling
Interleukin-20 family signaling
Interleukin-21 signaling
Interleukin-27 signaling
Interleukin-35 Signalling
Interleukin-6 signaling
Interleukin-9 signaling
KIT signalling
PDGFRA extracellular domain mutant signaling
PDGFRA transmembrane mutant signaling
Regulation of IFNA signaling
Regulation of IFNG signaling
Regulation of TP53 Expression
RUNX1 & myeloid differentiation
RUNX1 & Wnt signaling
RUNX2 & cell migration
RUNX2 & myeloid differentiation
RUNX2 regulates chondrocyte maturation
Senescence-associated heterochromatin Foci
Signaling by cytosolic FGFR1 fusion mutants
Synthesis-Dependent Strand Annealing
T lymphoctye development by RUNX1 and FOXP3
TET1,2,3 and TDG demethylate DNA
YAP/TAZ gene expression
BACH1
EP400
FOXP3
KLF4
PRDM1
RUNX2
STAT1
TET3
CS-DS extension
fucosylation
Glycolipid core
O-mannose
P1PK blood group
sulfotransferases
Type 1 and 2 LacNAc
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
CS-DS extension
fucosylation
Glycolipid core
O-mannose
P1PK blood group
sulfotransferases
Type 1 and 2 LacNAc

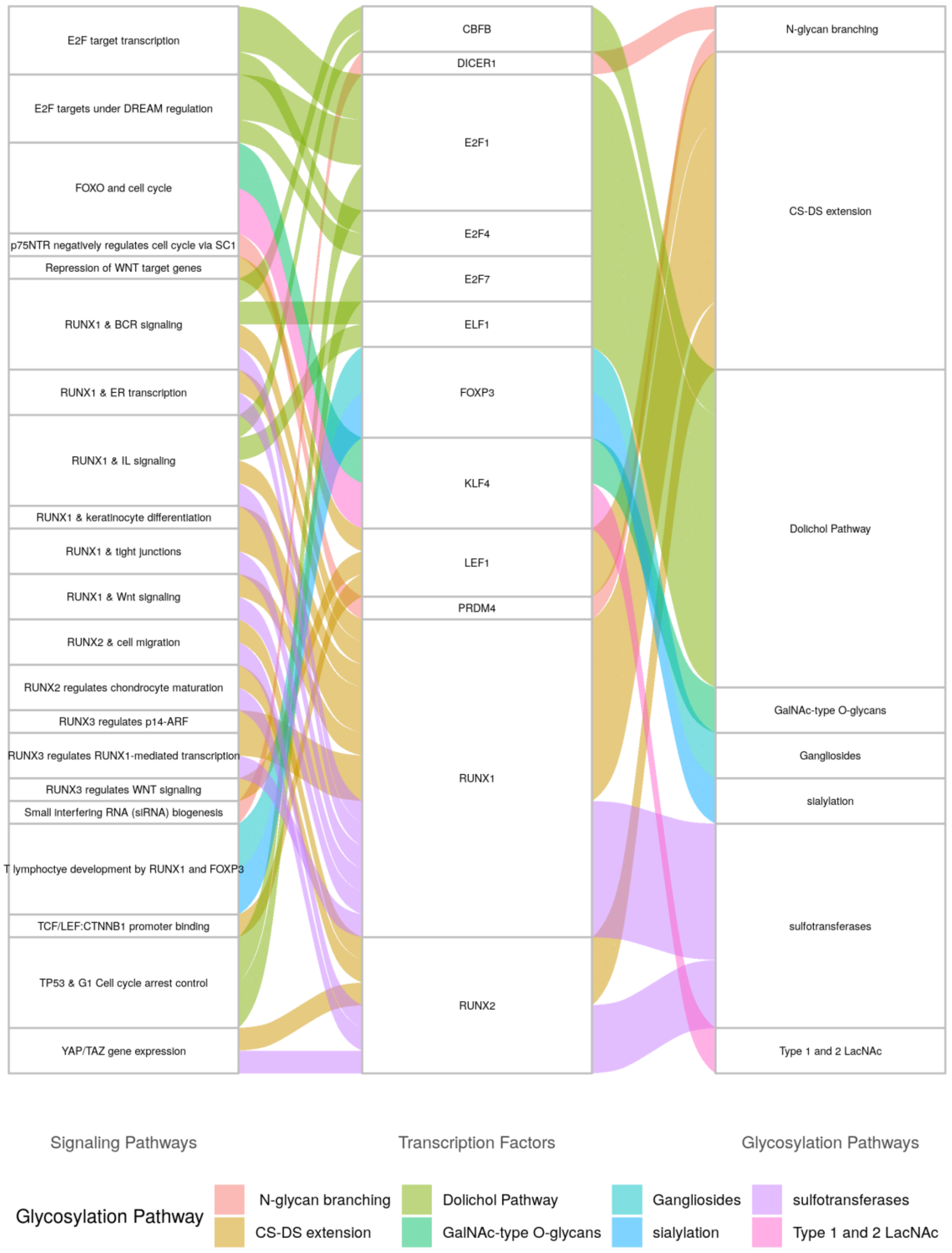

BRCA_1 Signaling to Glycosylation Pathway Matching
Disorders of Developmental Biology
Disorders of Nervous System Development
Estrogen signaling
Loss of function of MECP2 in Rett syndrome
Loss of Function of SMAD2/3 in Cancer
Loss of Function of SMAD4 in Cancer
Loss of MECP2 binding ability to 5hmC-DNA
Loss of MECP2 binding ability to 5mC-DNA
Loss of phosphorylation of MECP2 at T308
MECP2 & neuronal ligands
MECP2 doesn't bind NcoR/SMRT complex
MECP2 regulates GABA signaling
MECP2 regulates transcription factors
Pervasive developmental disorders
Regulation of TP53 Expression
RNA Pol-II & type 1 promoter
RNA Pol-II & type 2 promoter
RNA Polymerase III Chain Elongation
RNA Polymerase III Transcription Initiation From Type 3 Promoter
RNA Polymerase III Transcription Termination
RUNX3 regulates BCL2L11 (BIM) transcription
RUNX3 regulates CDKN1A transcription
RUNX3 regulates RUNX1-mediated transcription
RUNX3 regulates YAP1-mediated transcription
SMAD2/3 MH2 Domain Mutants in Cancer
SMAD4 MH2 Domain Mutants in Cancer
TGF-beta and Cancer
YAP/TAZ gene expression
FOS
MECP2
MEF2C
NFIC
POLR3A
PRDM1
RUNX1
RUNX3
SMAD4
TEAD1
YAP1
Chondroitin and Dermatan Sulfate Extension
Fucosylation
Heparan sulfate extension
N-glycan branching
Type-1 & Type-2 LacNAc
Signaling Pathways
Transcription Factors
Glycosylation Pathways
ation Pathway
Chondroitin and Dermatan Sulfate Extension
Fucosylation
Heparan sulfate extension
N-glycan branching
Type-1 & Typ



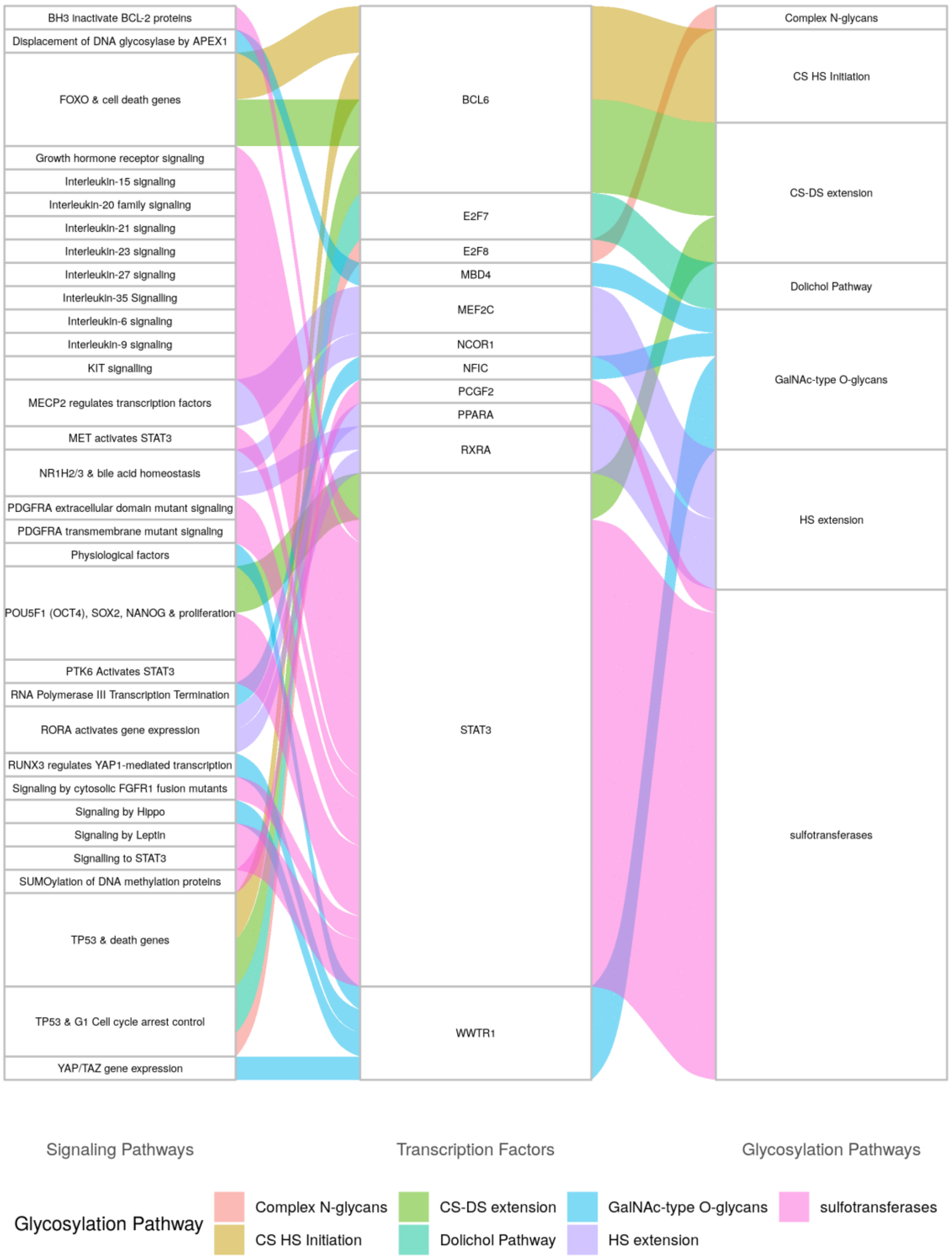
BRCA_2 Signaling to Glycosylation Pathway Matching

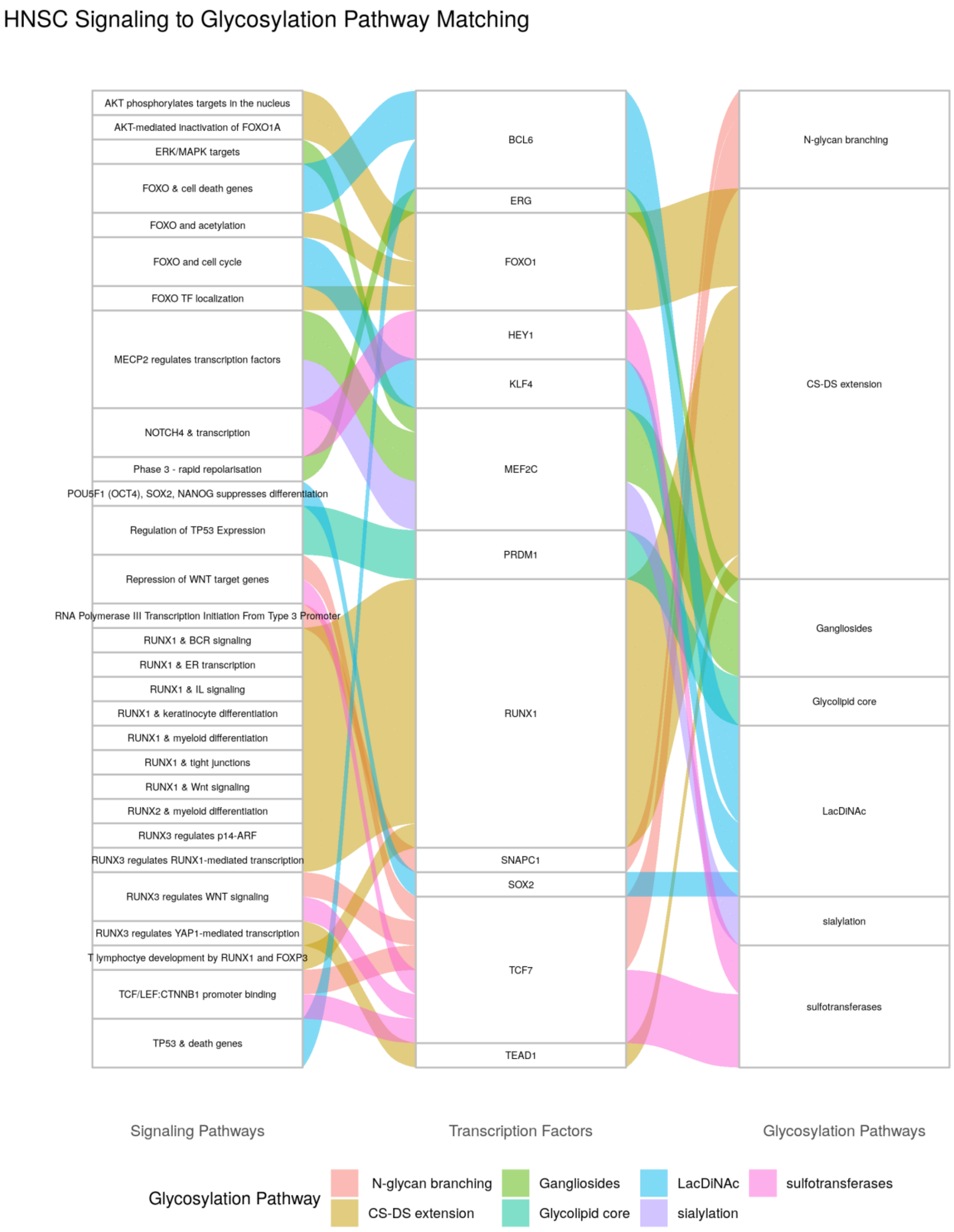

CESC Signaling to Glycosylation Pathway Matching
FOXO and cell cycle
Growth hormone receptor signaling
Interleukin-20 family signaling
Interleukin-21 signaling
Interleukin-27 signaling
Interleukin-35 Signalling
Interleukin-6 signaling
Interleukin-9 signaling
KIT signalling
Loss of Function of SMAD4 in Cancer
PDGFRA extracellular domain mutant signaling
PDGFRA transmembrane mutant signaling
POU5F1 (OCT4), SOX2, NANOG & proliferation
POU5F1 (OCT4), SOX2, NANOG suppresses differentiation
Regulation of IFNA signaling
Regulation of IFNG signaling
RUNX3 regulates RUNX1-mediated transcription
Signaling by cytosolic FGFR1 fusion mutants
SMAD2/3 MH2 Domain Mutants in Cancer
SMAD4 MH2 Domain Mutants in Cancer
STAT6-mediated induction of chemokines
STING induces immune response
GATA6
KLF4
RUNX1
SMAD4
SOX2
STAT1
STAT6
ABO blood group
fucosylation
Gangliosides
Hyaluronan synthesis
P1PK blood group
sialylation
Type 1 and 2 LacNAc
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
ABO blood group
fucosylation
Gangliosides
Hyaluronan synthesis
P1PK blood group
sialylation
Type 1 and 2 LacNAc

COAD_READ. Signaling to Glycosylation Pathway Matching

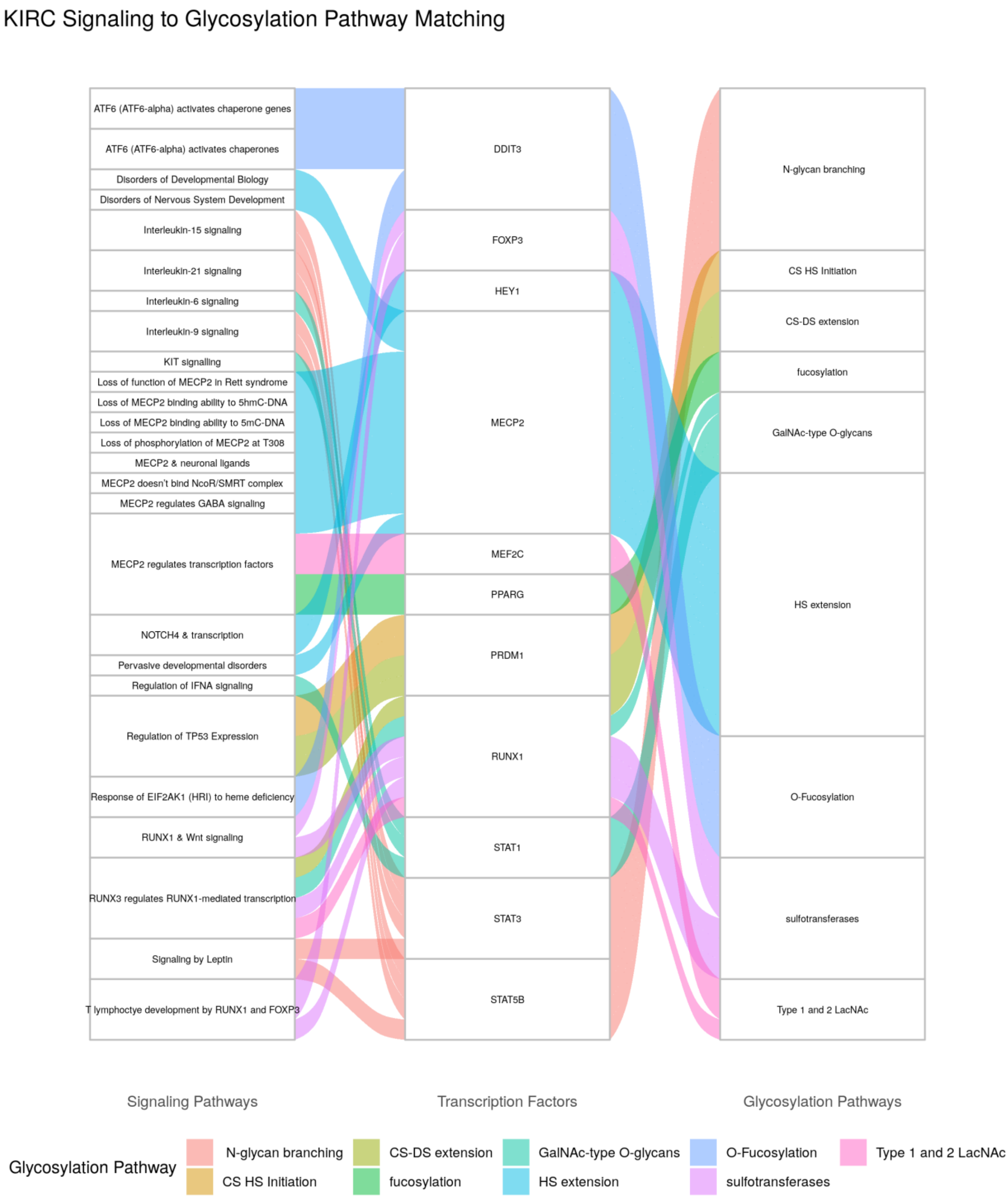


GBM. Signaling to Glycosylation Pathway Matching

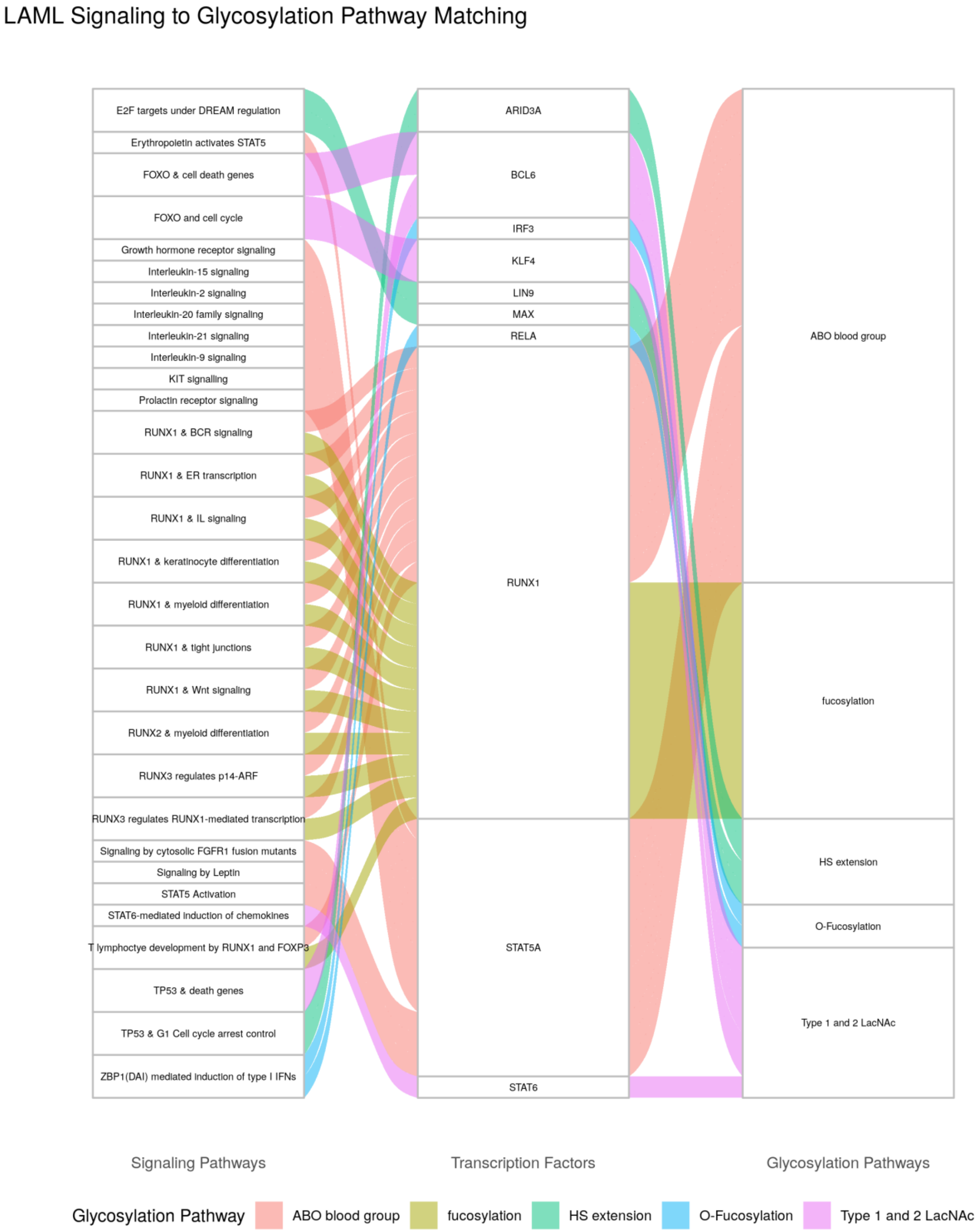


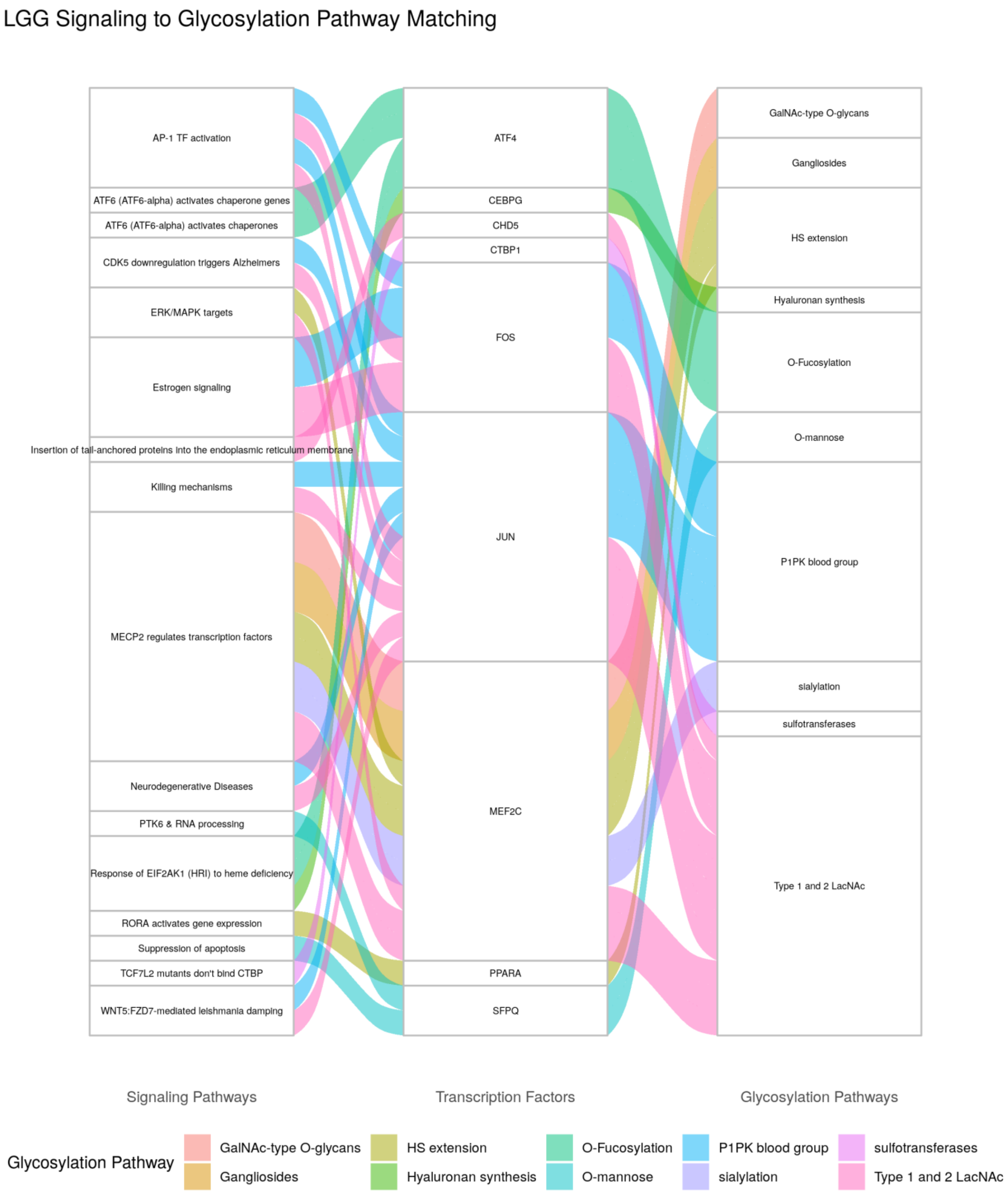

HNSC Signaling to Glycosylation Pathway Matching
AKT phosphorylates targets in the nucleus
AKT-mediated inactivation of FOXO1A
ERK/MAPK targets
FOXO & cell death genes
FOXO and acetylation
FOXO and cell cycle
FOXO TF localization
MECP2 regulates transcription factors
NOTCH4 & transcription
Phase 3 - rapid repolarisation
POU5F1 (OCT4), SOX2, NANOG suppresses differentiation
Regulation of TP53 Expression
Repression of WNT target genes
RNA Polymerase III Transcription Initiation From Type 3 Promoter
RUNX1 & BCR signaling
RUNX1 & ER transcription
RUNX1 & IL signaling
RUNX1 & keratinocyte differentiation
RUNX1 & myeloid differentiation
RUNX1 & tight junctions
RUNX1 & Wnt signaling
RUNX2 & myeloid differentiation
RUNX3 regulates p14-ARF
RUNX3 regulates RUNX1-mediated transcription
RUNX3 regulates WNT signaling
RUNX3 regulates YAP1-mediated transcription
T lymphoctye development by RUNX1 and FOXP3
TCF/LEF:CTNNB1 promoter binding
TP53 & death genes
BCL6
ERG
FOXO1
HEY1
KLF4
MEF2C
PRDM1
RUNX1
SNAPC1
SOX2
TCF7
TEAD1
N-glycan branching
CS-DS extension
Gangliosides
Glycolipid core
LacDiNAc
sialylation
sulfotransferases
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
N-glycan branching
CS-DS extension
Gangliosides
Glycolipid core
LacDiNAc
sialylation
sulfotransferases

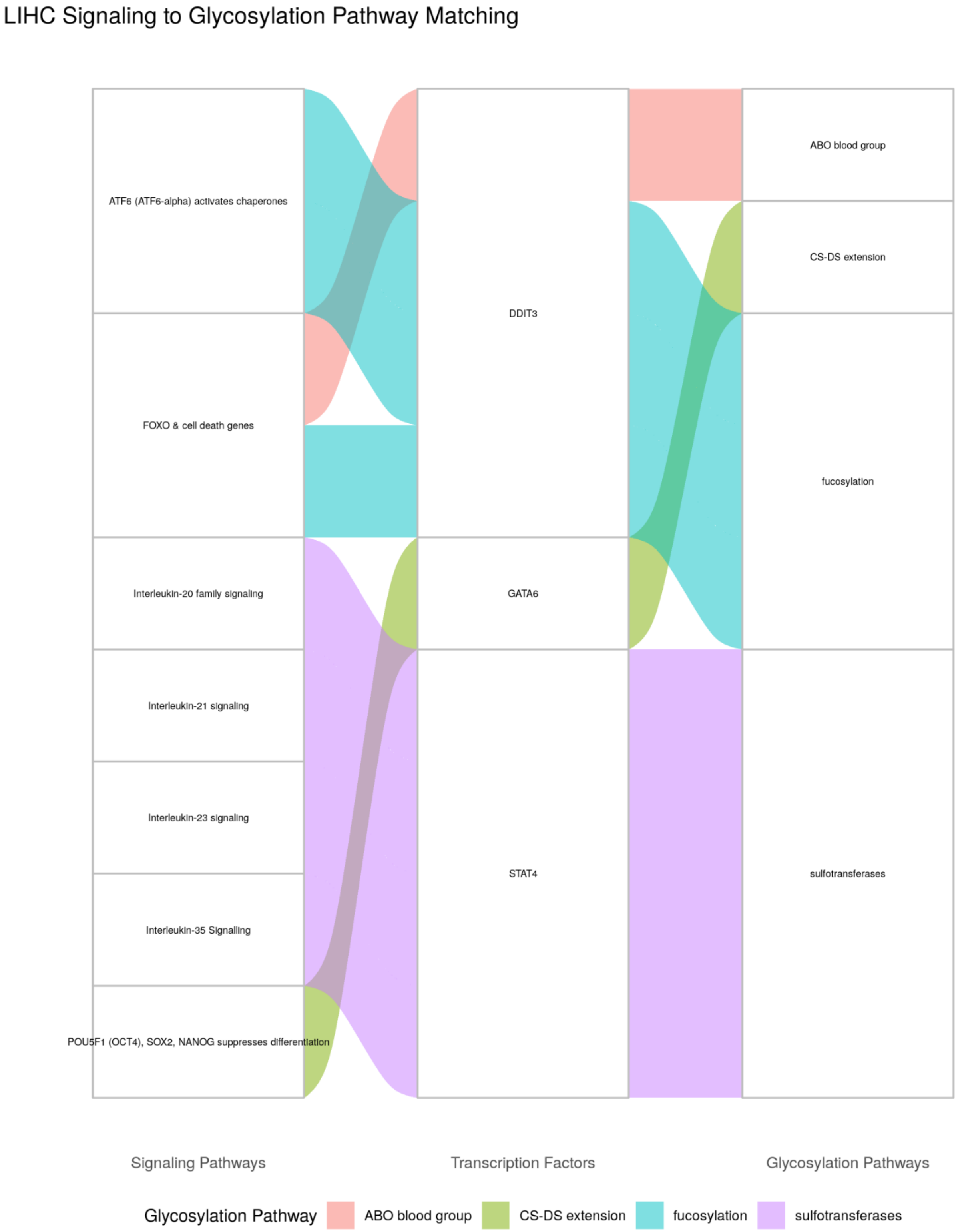

KICH Signaling to Glycosylation Pathway Matching

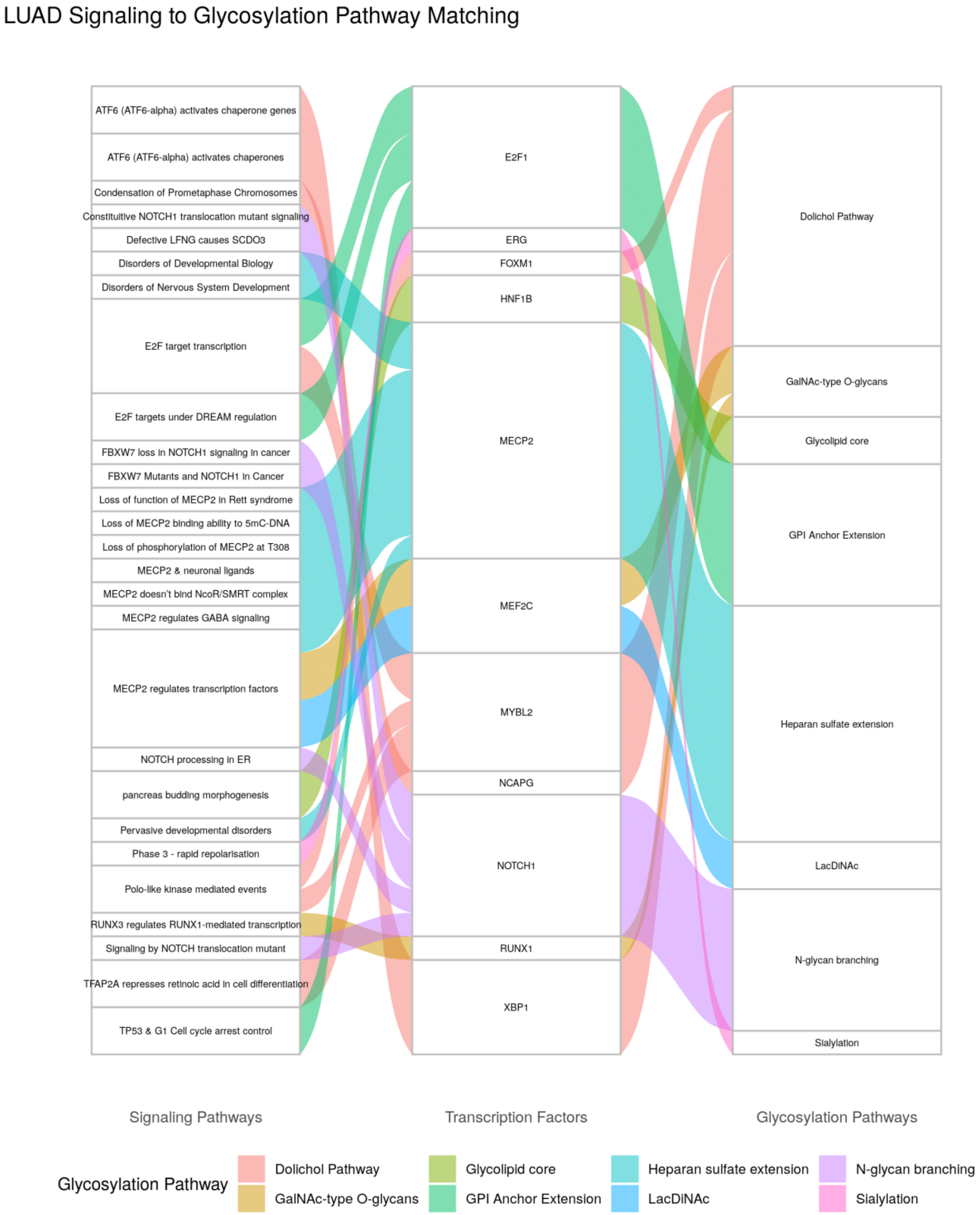

KIRC Signaling to Glycosylation Pathway Matching
ATF6 (ATF6-alpha) activates chaperone genes
ATF6 (ATF6-alpha) activates chaperones
Disorders of Developmental Biology
Disorders of Nervous System Development
Interleukin-15 signaling
Interleukin-21 signaling
Interleukin-6 signaling
Interleukin-9 signaling
KIT signalling
Loss of function of MECP2 in Rett syndrome
Loss of MECP2 binding ability to 5hmC-DNA
Loss of MECP2 binding ability to 5mC-DNA
Loss of phosphorylation of MECP2 at T308
MECP2 & neuronal ligands
MECP2 doesn't bind NcoR/SMRT complex
MECP2 regulates GABA signaling
MECP2 regulates transcription factors
NOTCH4 & transcription
Pervasive developmental disorders
Regulation of IFNA signaling
Regulation of TP53 Expression
Response of EIF2AK1 (HRI) to heme deficiency
RUNX1 & Wnt signaling
RUNX3 regulates RUNX1-mediated transcription
Signaling by Leptin
T lymphoctye development by RUNX1 and FOXP3
DDIT3
FOXP3
HEY1
MECP2
MEF2C
PPARG
PRDM1
RUNX1
STAT1
STAT3
STAT5B
N-glycan branching
CS HS Initiation
CS-DS extension
fucosylation
GalNAc-type O-glycans
HS extension
O-Fucosylation
sulfotransferases
Type 1 and 2 LacNAc
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
N-glycan branching
CS HS Initiation
CS-DS extension
fucosylation
GalNAc-type O-glycans
HS extension
O-Fucosylation
sulfotransferases
Type 1 and 2 LacNAc

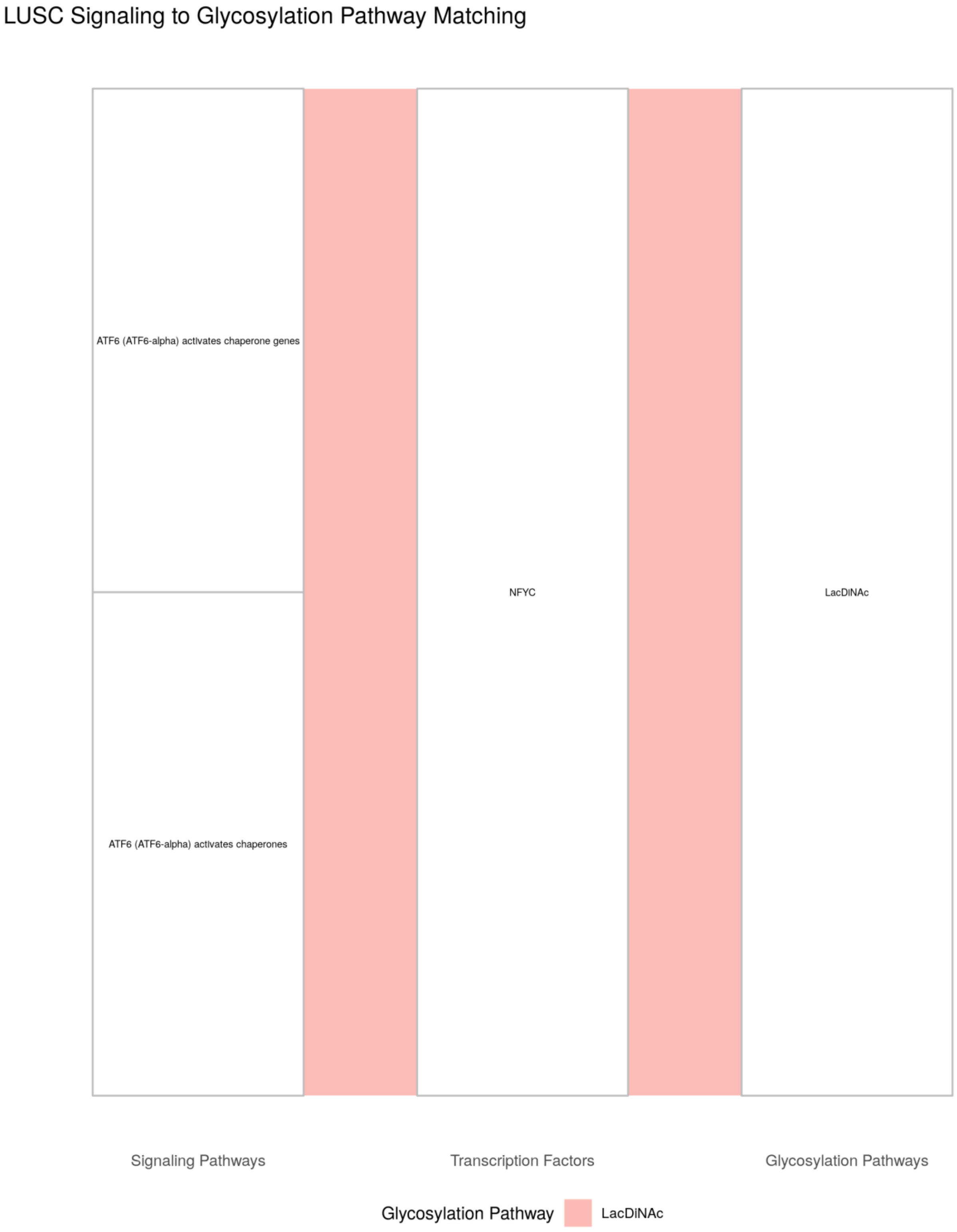

KIRP Signaling to Glycosylation Pathway Matching
AP-2 regulates cell cycle
ATF6 (ATF6-alpha) activates chaperone genes
ATF6 (ATF6-alpha) activates chaperones
BH3 inactivate BCL-2 proteins
E2F targets under DREAM regulation
FOXO & cell death genes
FOXO and cell cycle
IGFR mRNA binding proteins
Interleukin-15 signaling
Interleukin-21 signaling
Interleukin-23 signaling
Interleukin-27 signaling
Interleukin-35 Signalling
Interleukin-6 signaling
Interleukin-9 signaling
MET activates STAT3
NOCTH2 & transcription
NOTCH4 & transcription
p75NTR negatively regulates cell cycle via SC1
pancreas budding morphogenesis
PDGFRA extracellular domain mutant signaling
PDGFRA transmembrane mutant signaling
POU5F1 (OCT4), SOX2, NANOG & proliferation
PTK6 Activates STAT3
Repression of WNT target genes
RUNX3 regulates NOTCH signaling
RUNX3 regulates WNT signaling
Signaling by Leptin
Signalling to STAT3
TCF/LEF:CTNNB1 promoter binding
HES1
KLF4
MYC
NFYC
PRDM4
STAT3
N-glycan branching
Gangliosides
sialylation
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
N-glycan branching
Gangliosides
sialylation

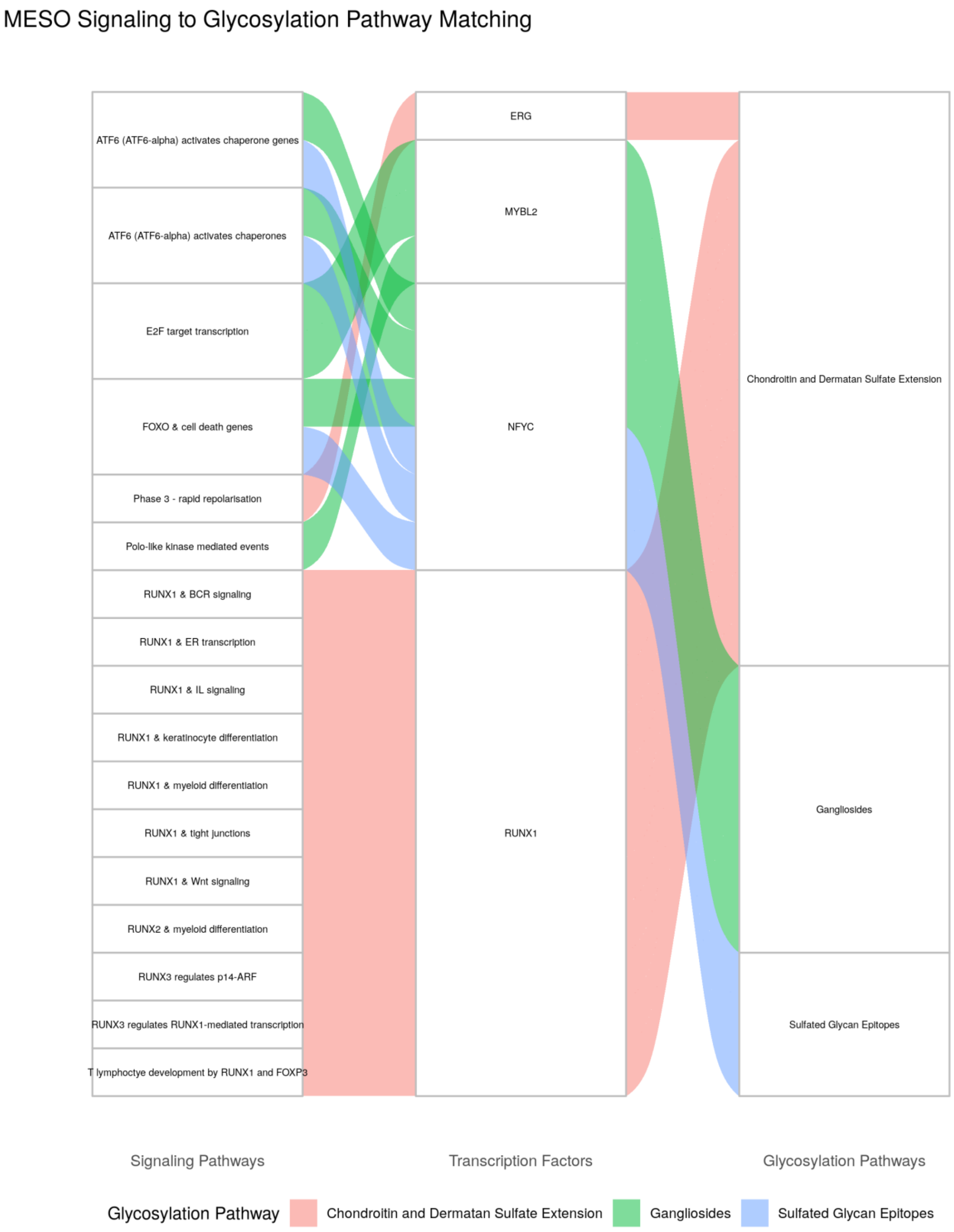

LAML Signaling to Glycosylation Pathway Matching
E2F targets under DREAM regulation
Erythropoietin activates STAT5
FOXO & cell death genes
FOXO and cell cycle
Growth hormone receptor signaling
Interleukin-15 signaling
Interleukin-2 signaling
Interleukin-20 family signaling
Interleukin-21 signaling
Interleukin-9 signaling
KIT signalling
Prolactin receptor signaling
RUNX1 & BCR signaling
RUNX1 & ER transcription
RUNX1 & IL signaling
RUNX1 & keratinocyte differentiation
RUNX1 & myeloid differentiation
RUNX1 & tight junctions
RUNX1 & Wnt signaling
RUNX2 & myeloid differentiation
RUNX3 regulates p14-ARF
RUNX3 regulates RUNX1-mediated transcription
Signaling by cytosolic FGFR1 fusion mutants
Signaling by Leptin
STAT5 Activation
STAT6-mediated induction of chemokines
T lymphoctye development by RUNX1 and FOXP3
TP53 & death genes
TP53 & G1 Cell cycle arrest control
ZBP1(DAI) mediated induction of type I IFNs
ARID3A
BCL6
IRF3
KLF4
LIN9
MAX
RELA
RUNX1
STAT5A
STAT6
ABO blood group
fucosylation
HS extension
O-Fucosylation
Type 1 and 2 LacNAc
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
ABO blood group
fucosylation
HS extension
O-Fucosylation
Type 1 and 2 LacNAc


LGG Signaling to Glycosylation Pathway Matching
AP-1 TF activation
ATF6 (ATF6-alpha) activates chaperone genes
ATF6 (ATF6-alpha) activates chaperones
CDK5 downregulation triggers Alzheimers
ERK/MAPK targets
Estrogen signaling
Insertion of tail-anchored proteins into the endoplasmic reticulum membrane
Killing mechanisms
MECP2 regulates transcription factors
Neurodegenerative Diseases
PTK6 & RNA processing
Response of EIF2AK1 (HRI) to heme deficiency
RORA activates gene expression
Suppression of apoptosis
TCF7L2 mutants don't bind CTBP
WNT5:FZD7-mediated leishmania damping
ATF4
CEBPG
CHD5
CTBP1
FOS
JUN
MEF2C
PPARA
SFPQ
GalNAc-type O-glycans
Gangliosides
HS extension
Hyaluronan synthesis
O-Fucosylation
O-mannose
P1PK blood group
sialylation
sulfotransferases
Type 1 and 2 LacNAc
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
GalNAc-type O-glycans
Gangliosides
HS extension
Hyaluronan synthesis
O-Fucosylation
O-mannose
P1PK blood group
sialylation
sulfotransferases
Type 1 and 2 LacNAc

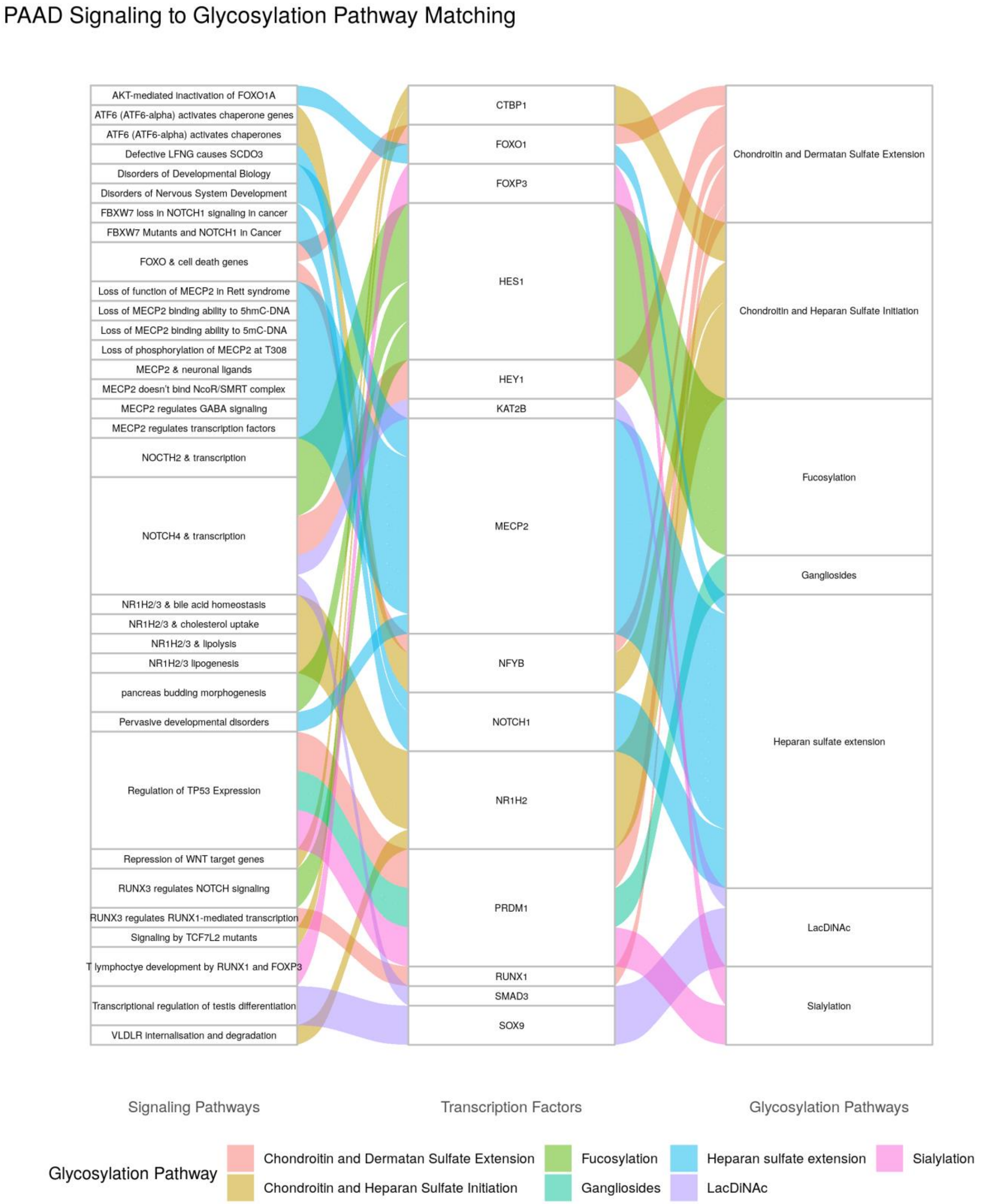

LIHC Signaling to Glycosylation Pathway Matching
ATF6 (ATF6-alpha) activates chaperones
FOXO & cell death genes
Interleukin-20 family signaling
Interleukin-21 signaling
Interleukin-23 signaling
Interleukin-35 Signalling
POU5F1 (OCT4), SOX2, NANOG suppresses differentiation
DDIT3
GATA6
STAT4
ABO blood group
CS-DS extension
fucosylation
sulfotransferases
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
ABO blood group
CS-DS extension
fucosylation
sulfotransferases

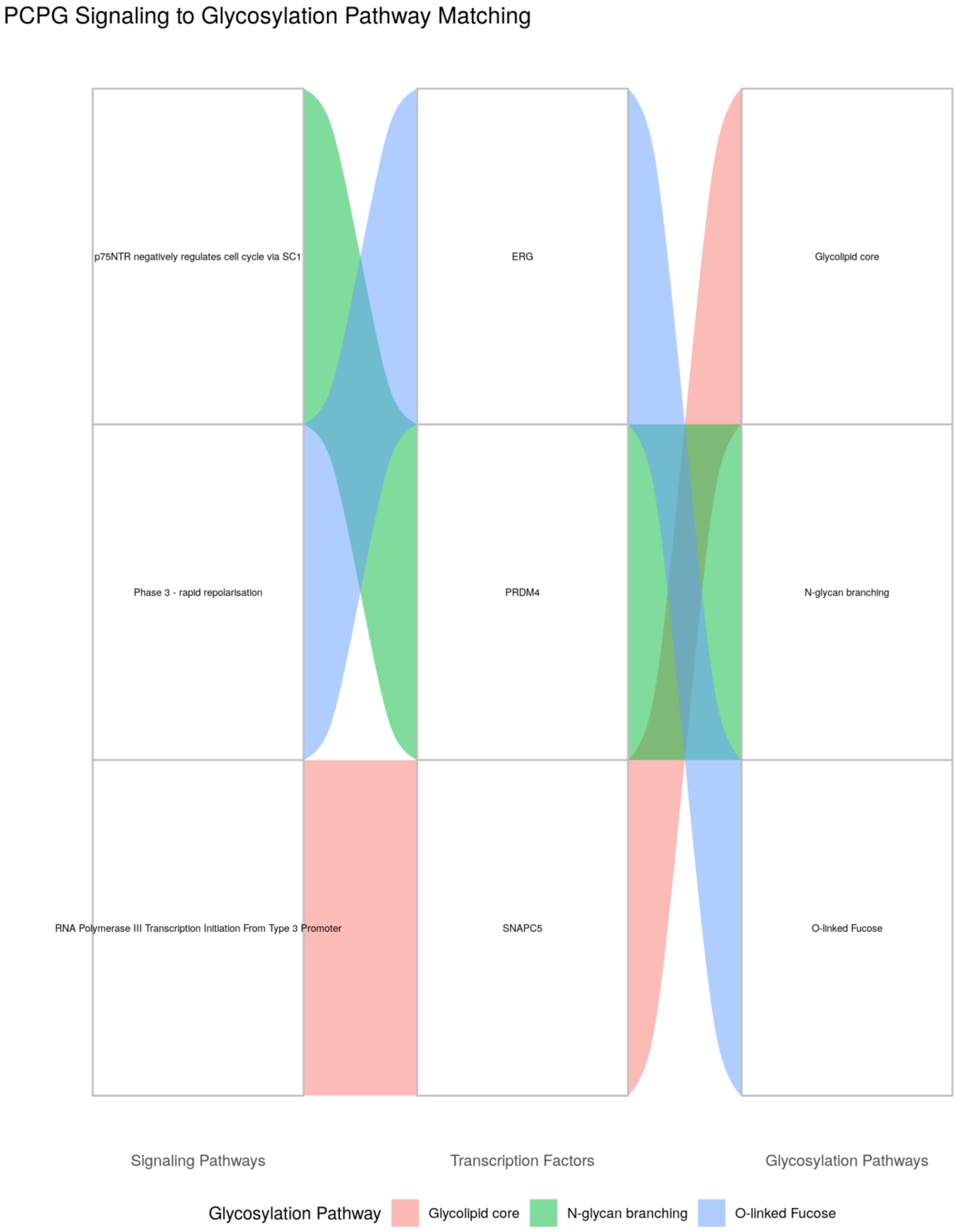

LUAD Signaling to Glycosylation Pathway Matching
ATF6 (ATF6-alpha) activates chaperone genes
ATF6 (ATF6-alpha) activates chaperones
Condensation of Prometaphase Chromosomes
Constitutive NOTCH1 translocation mutant signaling
Defective LFNG causes SCDO3
Disorders of Developmental Biology
Disorders of Nervous System Development
E2F target transcription
E2F targets under DREAM regulation
FBXW7 loss in NOTCH1 signaling in cancer
FBXW7 Mutants and NOTCH1 in Cancer
Loss of function of MECP2 in Rett syndrome
Loss of MECP2 binding ability to 5mC-DNA
Loss of phosphorylation of MECP2 at T308
MECP2 & neuronal ligands
MECP2 doesn't bind NcoR/SMRT complex
MECP2 regulates GABA signaling
MECP2 regulates transcription factors
NOTCH processing in ER
pancreas budding morphogenesis
Pervasive developmental disorders
Phase 3 - rapid repolarisation
Polo-like kinase mediated events
RUNX3 regulates RUNX1-mediated transcription
Signaling by NOTCH translocation mutant
TFAP2A represses retinoic acid in cell differentiation
TP53 & G1 Cell cycle arrest control
E2F1
ERG
FOXM1
HNF1B
MECP2
MEF2C
MYBL2
NCAPG
NOTCH1
RUNX1
XBP1
Dolichol Pathway
GalNAc-type O-glycans
Glycolipid core
GPI Anchor Extension
Heparan sulfate extension
LacDiNAc
N-glycan branching
Sialylation
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
Dolichol Pathway
GalNAc-type O-glycans
Glycolipid core
GPI Anchor Extension
Heparan sulfate extension
LacDiNAc
N-glycan branching
Sialylation

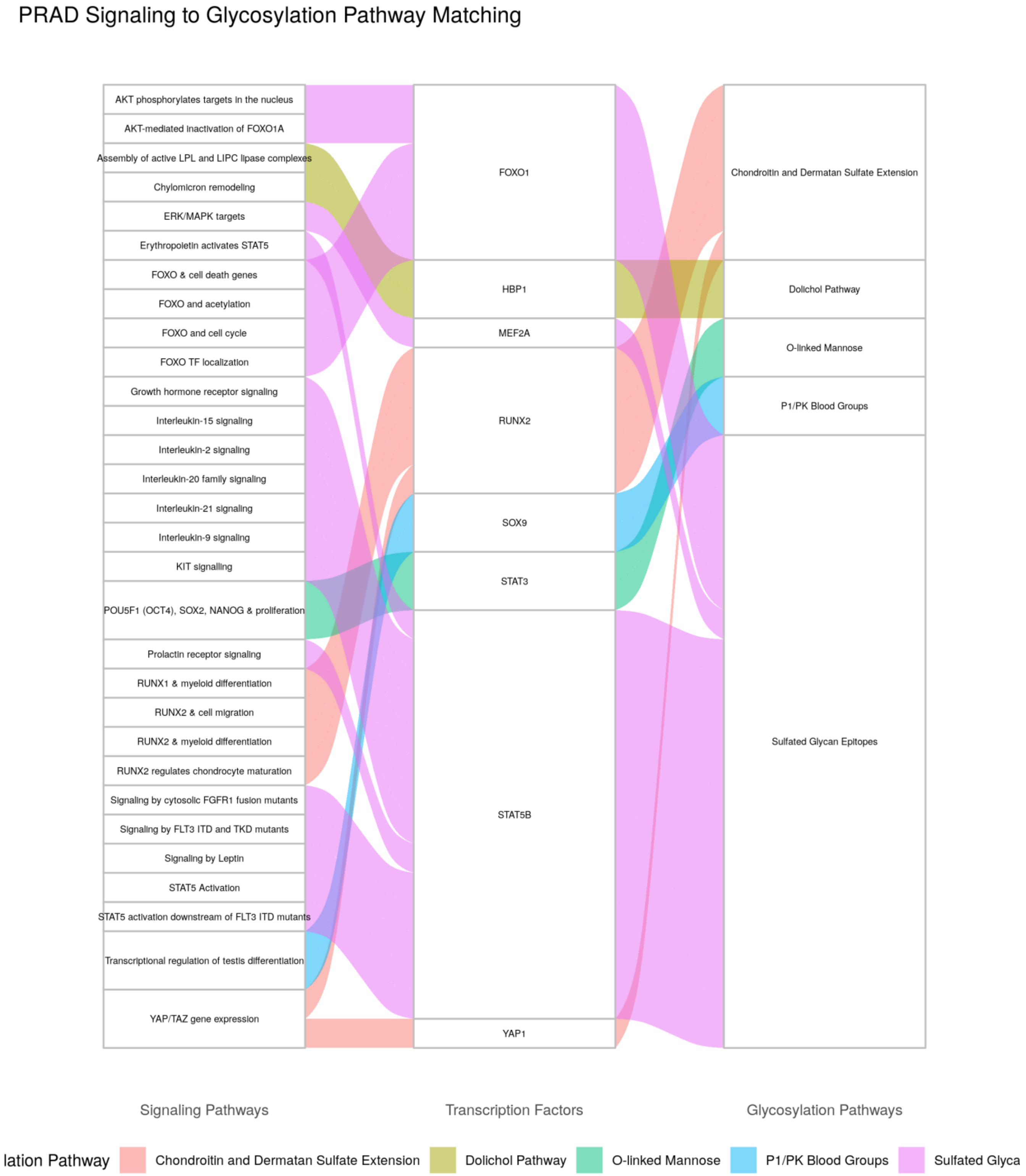

LUSC Signaling to Glycosylation Pathway Matching
ATF6 (ATF6-alpha) activates chaperone genes
ATF6 (ATF6-alpha) activates chaperones
NFYC
LacDiNAc
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
LacDiNAc

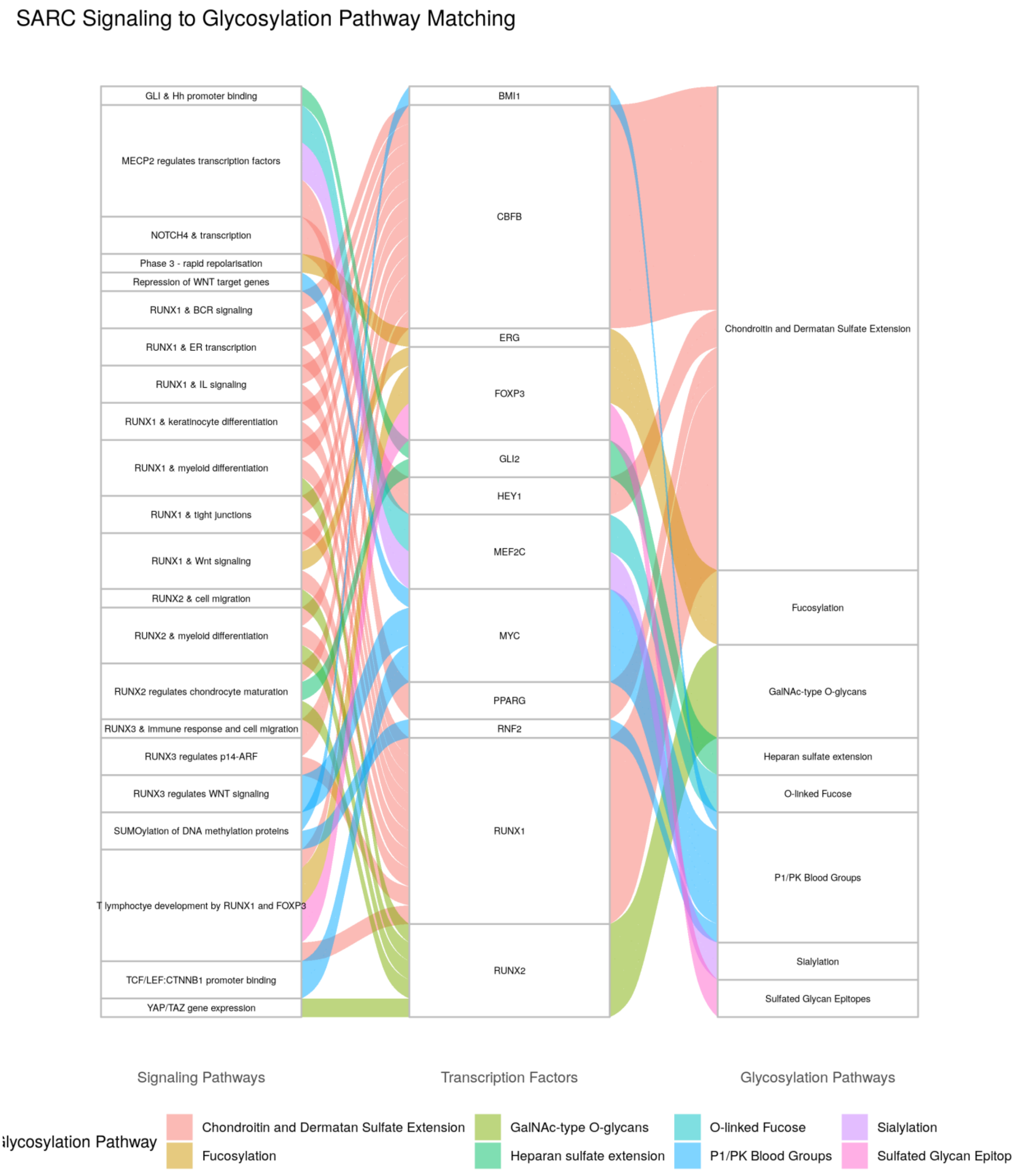

MESO Signaling to Glycosylation Pathway Matching
ATF6 (ATF6-alpha) activates chaperone genes
ATF6 (ATF6-alpha) activates chaperones
E2F target transcription
FOXO & cell death genes
Phase 3 - rapid repolarisation
Polo-like kinase mediated events
RUNX1 & BCR signaling
RUNX1 & ER transcription
RUNX1 & IL signaling
RUNX1 & keratinocyte differentiation
RUNX1 & myeloid differentiation
RUNX1 & tight junctions
RUNX1 & Wnt signaling
RUNX2 & myeloid differentiation
RUNX3 regulates p14-ARF
RUNX3 regulates RUNX1-mediated transcription
T lymphoctye development by RUNX1 and FOXP3
ERG
MYBL2
NFYC
RUNX1
Chondroitin and Dermatan Sulfate Extension
Gangliosides
Sulfated Glycan Epitopes
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
Chondroitin and Dermatan Sulfate Extension
Gangliosides
Sulfated Glycan Epitopes


OV Signaling to Glycosylation Pathway Matching
AP-2 regulates cell cycle
AP-2 TF downregulation
AP-2 TF upregulation
AP-2 TFs regulate other TFs
TFAP2C
ABO blood Group Synthesis
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
ABO blood Group Synthesis


PAAD Signaling to Glycosylation Pathway Matching

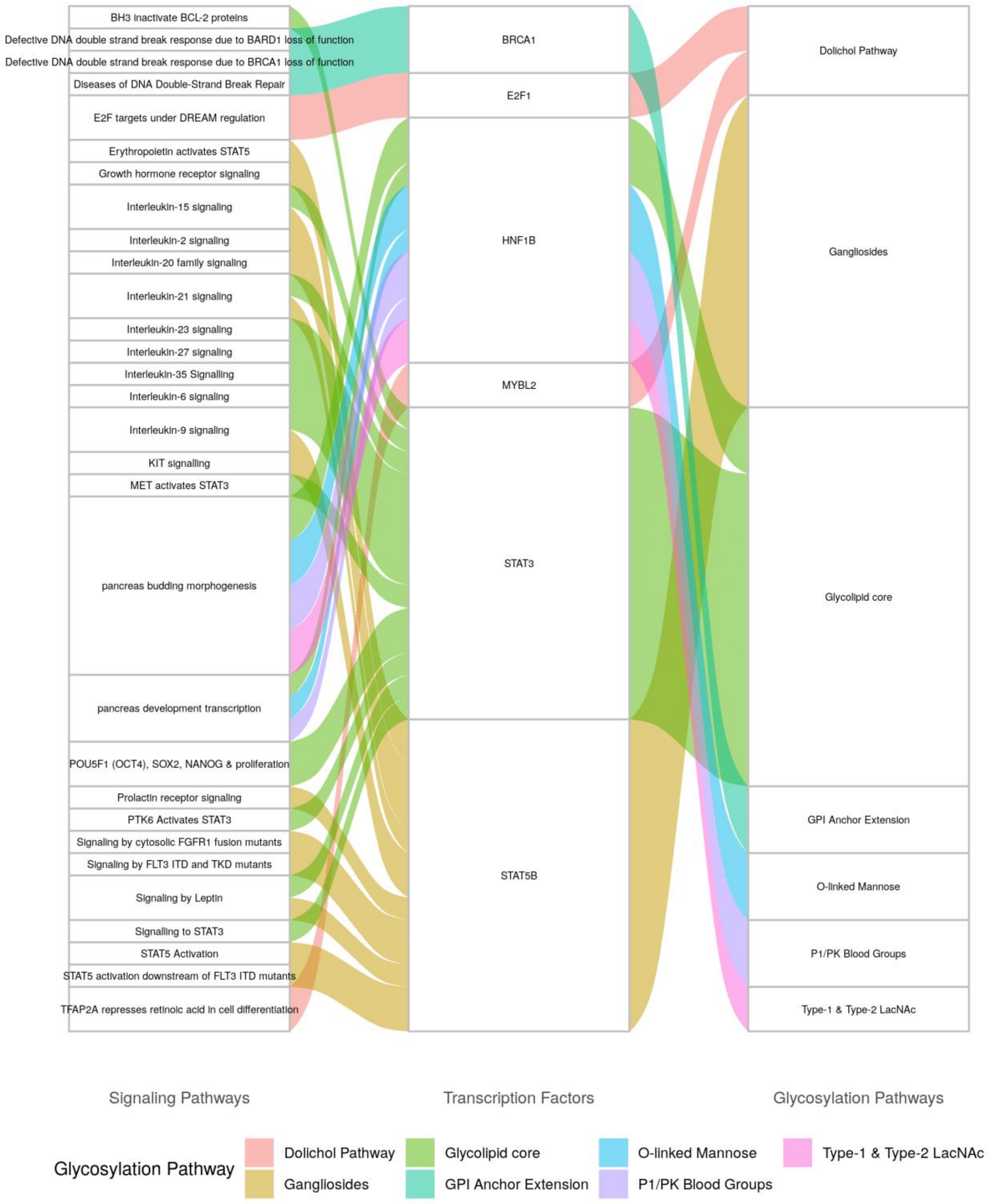

PCPG Signaling to Glycosylation Pathway Matching

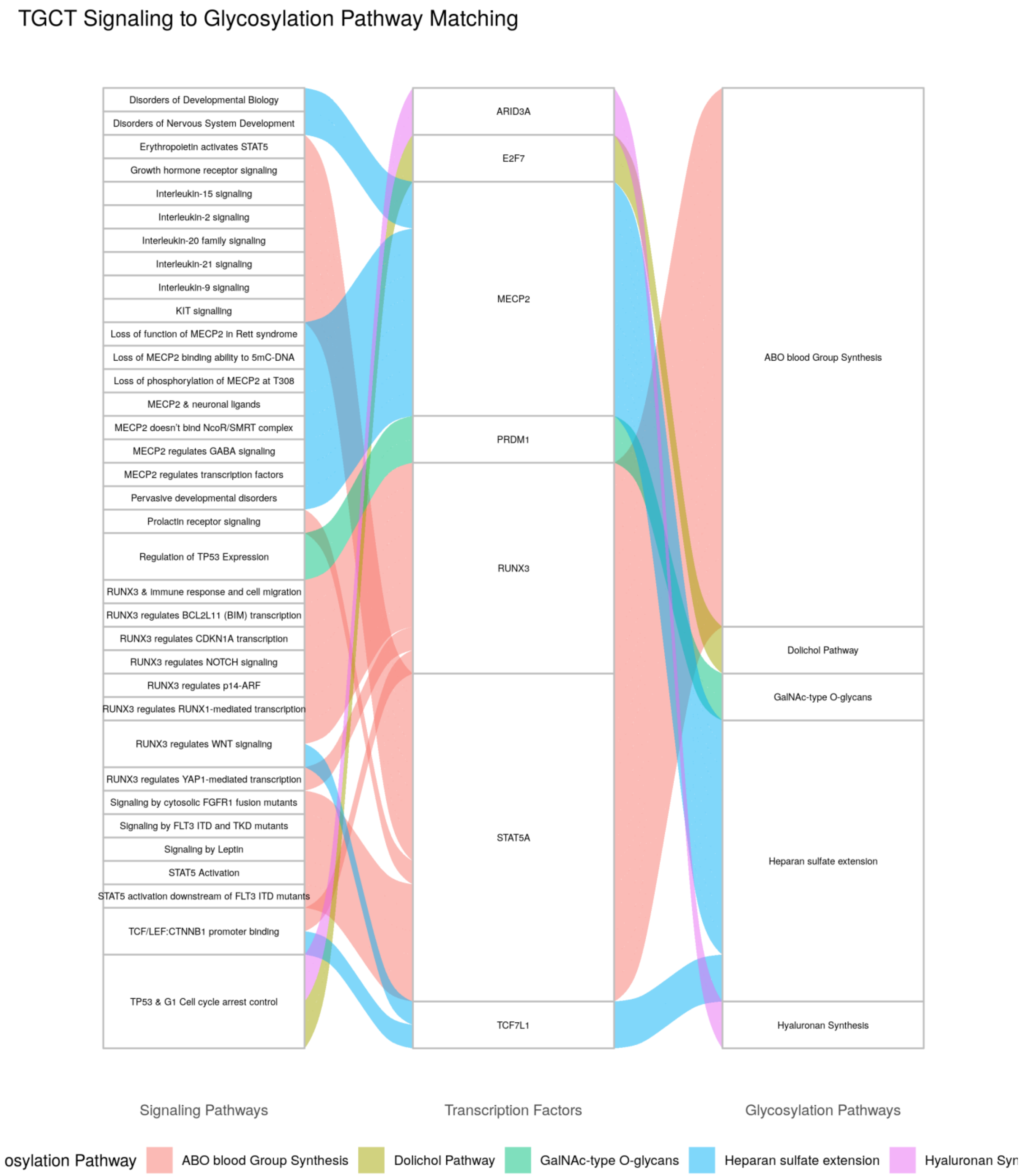

PRAD Signaling to Glycosylation Pathway Matching
AKT phosphorylates targets in the nucleus
AKT-mediated inactivation of FOXO1A
Assembly of active LPL and LIPC lipase complexes
Chylomicron remodeling
ERK/MAPK targets
Erythropoietin activates STAT5
FOXO & cell death genes
FOXO and acetylation
FOXO and cell cycle
FOXO TF localization
Growth hormone receptor signaling
Interleukin-15 signaling
Interleukin-2 signaling
Interleukin-20 family signaling
Interleukin-21 signaling
Interleukin-9 signaling
KIT signalling
POU5F1 (OCT4), SOX2, NANOG & proliferation
Prolactin receptor signaling
RUNX1 & myeloid differentiation
RUNX2 & cell migration
RUNX2 & myeloid differentiation
RUNX2 regulates chondrocyte maturation
Signaling by cytosolic FGFR1 fusion mutants
Signaling by FLT3 ITD and TKD mutants
Signaling by Leptin
STAT5 Activation
STAT5 activation downstream of FLT3 ITD mutants
Transcriptional regulation of testis differentiation
YAP/TAZ gene expression
FOXO1
HBP1
MEF2A
RUNX2
SOX9
STAT3
STAT5B
YAP1
Chondroitin and Dermatan Sulfate Extension
Dolichol Pathway
O-linked Mannose
P1/PK Blood Groups
Sulfated Glycan Epitopes
Signaling Pathways
Transcription Factors
Glycosylation Pathways
lation Pathway
Chondroitin and Dermatan Sulfate Extension
Dolichol Pathway
O-linked Mannose
P1/PK Blood Groups
Sulfated Glyca

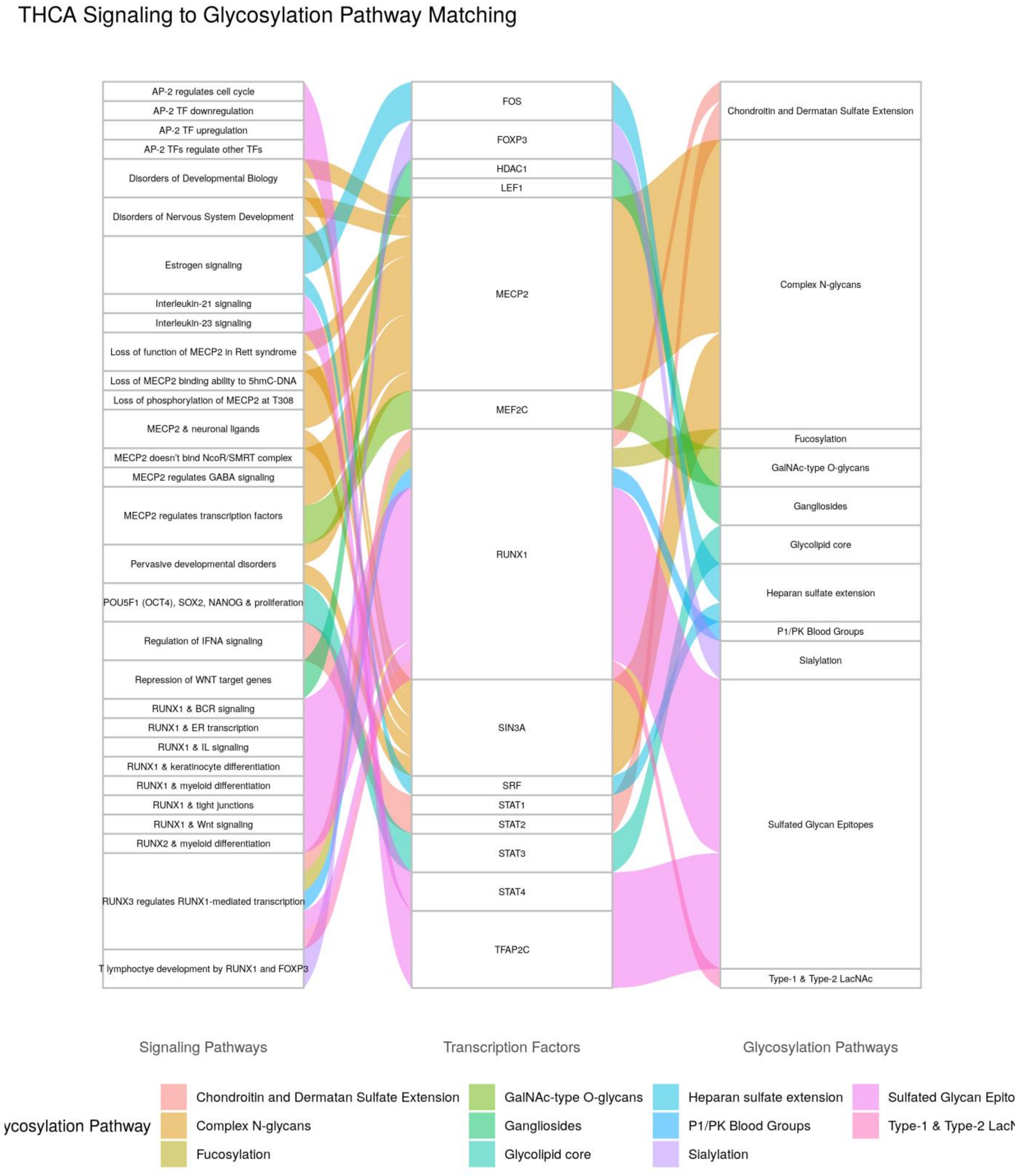

SARC Signaling to Glycosylation Pathway Matching
GLI & Hh promoter binding
MECP2 regulates transcription factors
NOTCH4 & transcription
Phase 3 - rapid repolarisation
Repression of WNT target genes
RUNX1 & BCR signaling
RUNX1 & ER transcription
RUNX1 & IL signaling
RUNX1 & keratinocyte differentiation
RUNX1 & myeloid differentiation
RUNX1 & tight junctions
RUNX1 & Wnt signaling
RUNX2 & cell migration
RUNX2 & myeloid differentiation
RUNX2 regulates chondrocyte maturation
RUNX3 & immune response and cell migration
RUNX3 regulates p14-ARF
RUNX3 regulates WNT signaling
SUMOylation of DNA methylation proteins
T lymphoctye development by RUNX1 and FOXP3
TCF/LEF:CTNNB1 promoter binding
YAP/TAZ gene expression
BMI1
CBFB
ERG
FOXP3
GLI2
HEY1
MEF2C
MYC
PPARG
RNF2
RUNX1
RUNX2
Chondroitin and Dermatan Sulfate Extension
Fucosylation
GalNAc-type O-glycans
Heparan sulfate extension
O-linked Fucose
P1/PK Blood Groups
Sialylation
Sulfated Glycan Epitopes
Signaling Pathways
Transcription Factors
Glycosylation Pathways
ilycosylation Pathway
Chondroitin and Dermatan Sulfate Extension
Fucosylation
GalNAc-type O-glycans
Heparan sulfate extension
O-linked Fucose
P1/PK Blood Groups
Sialylation
Sulfated Glycan Epitop

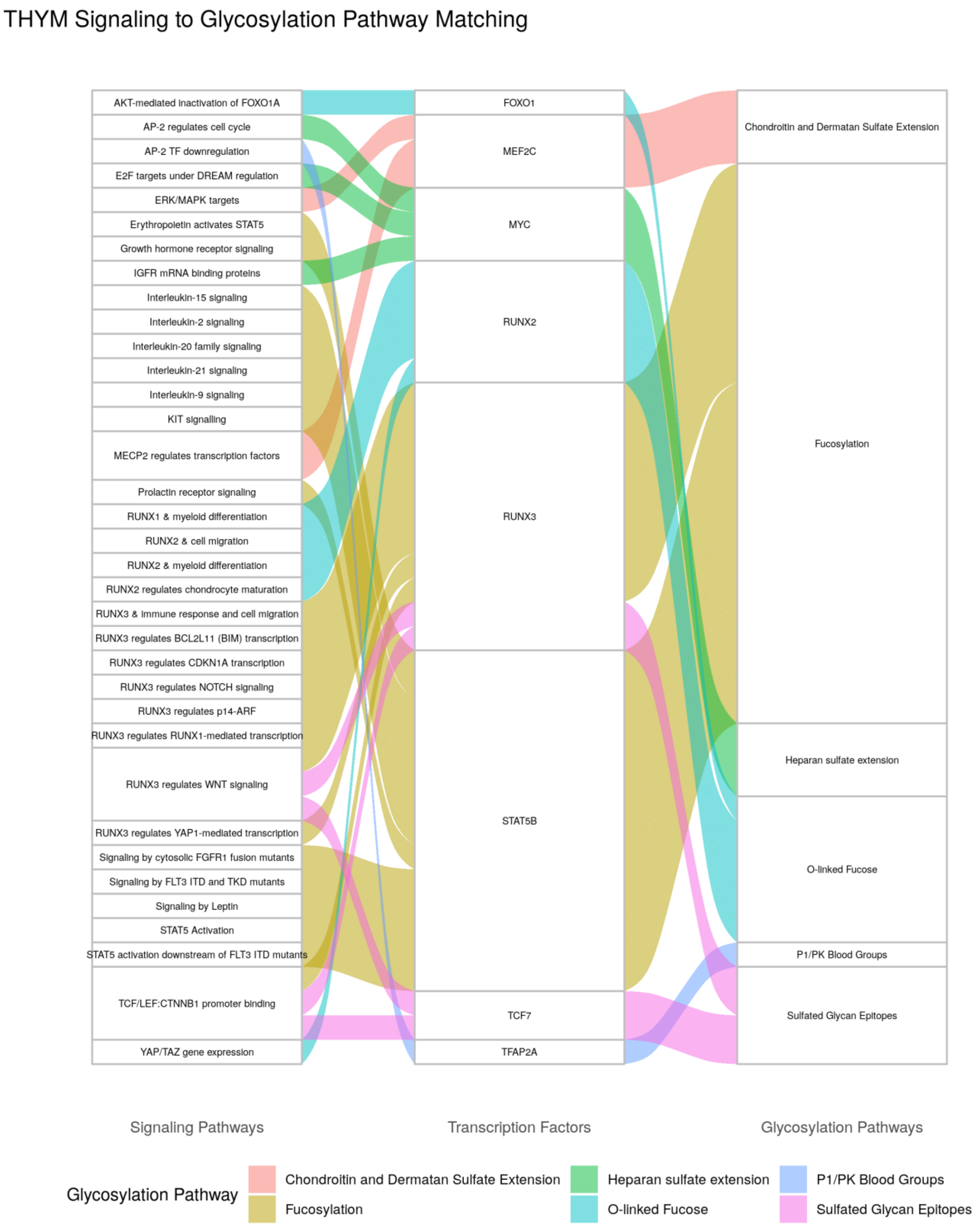

SKCM Signaling to Glycosylation Pathway Matching
ATF6 (ATF6-alpha) activates chaperone genes
ATF6 (ATF6-alpha) activates chaperones
FOXO & cell death genes
FOXO and acetylation
Notch-HLH transcription pathway
NOTCH4 & transcription
pancreas budding morphogenesis
Physiological factors
Regulation of TP53 Expression
RUNX3 regulates NOTCH signaling
YAP/TAZ gene expression
KAT2B
NFYA
PRDM1
Gangliosides
GPI Anchor Extension
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
Gangliosides
GPI Anchor Extension

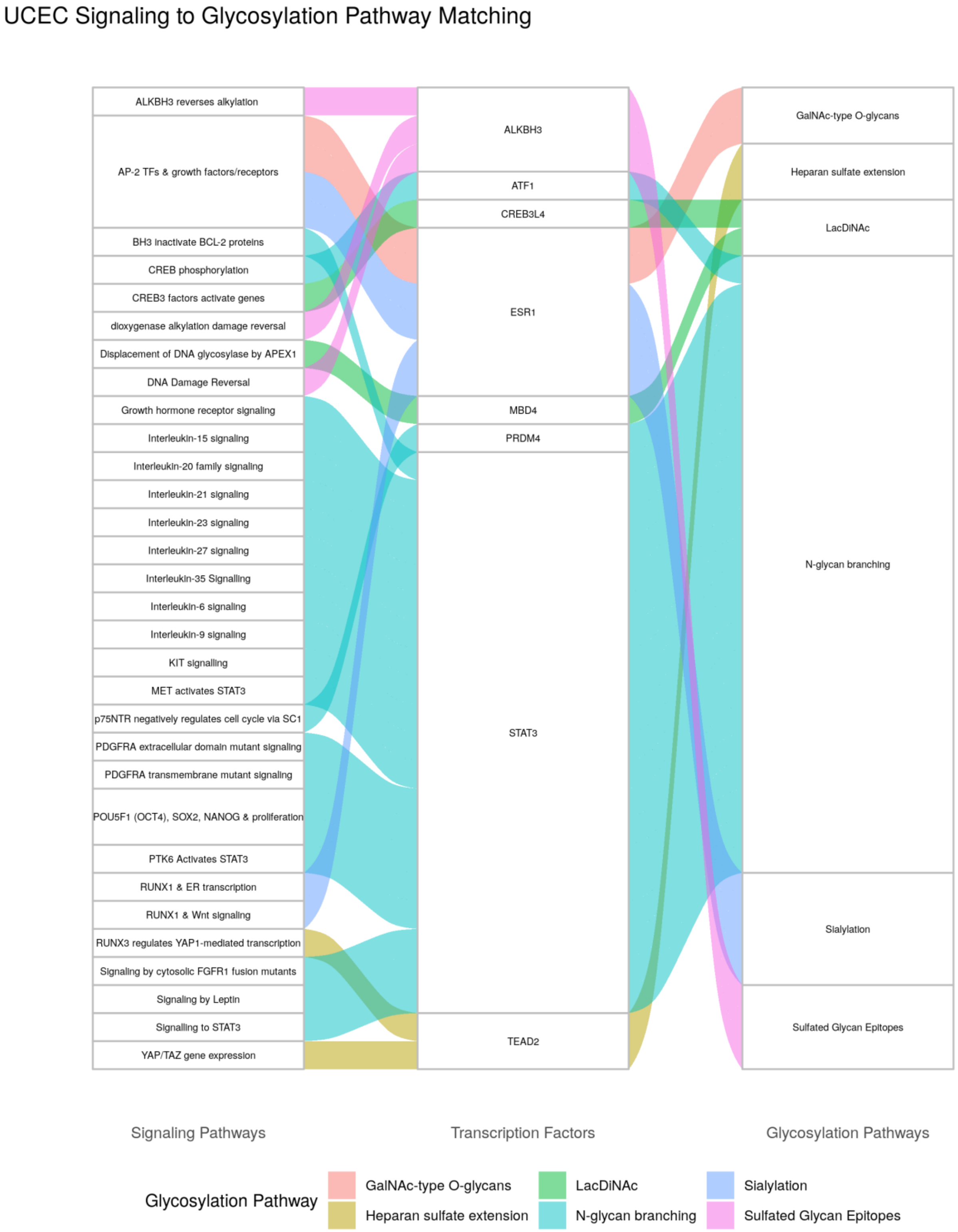
STES. Signaling to Glycosylation Pathway Matching

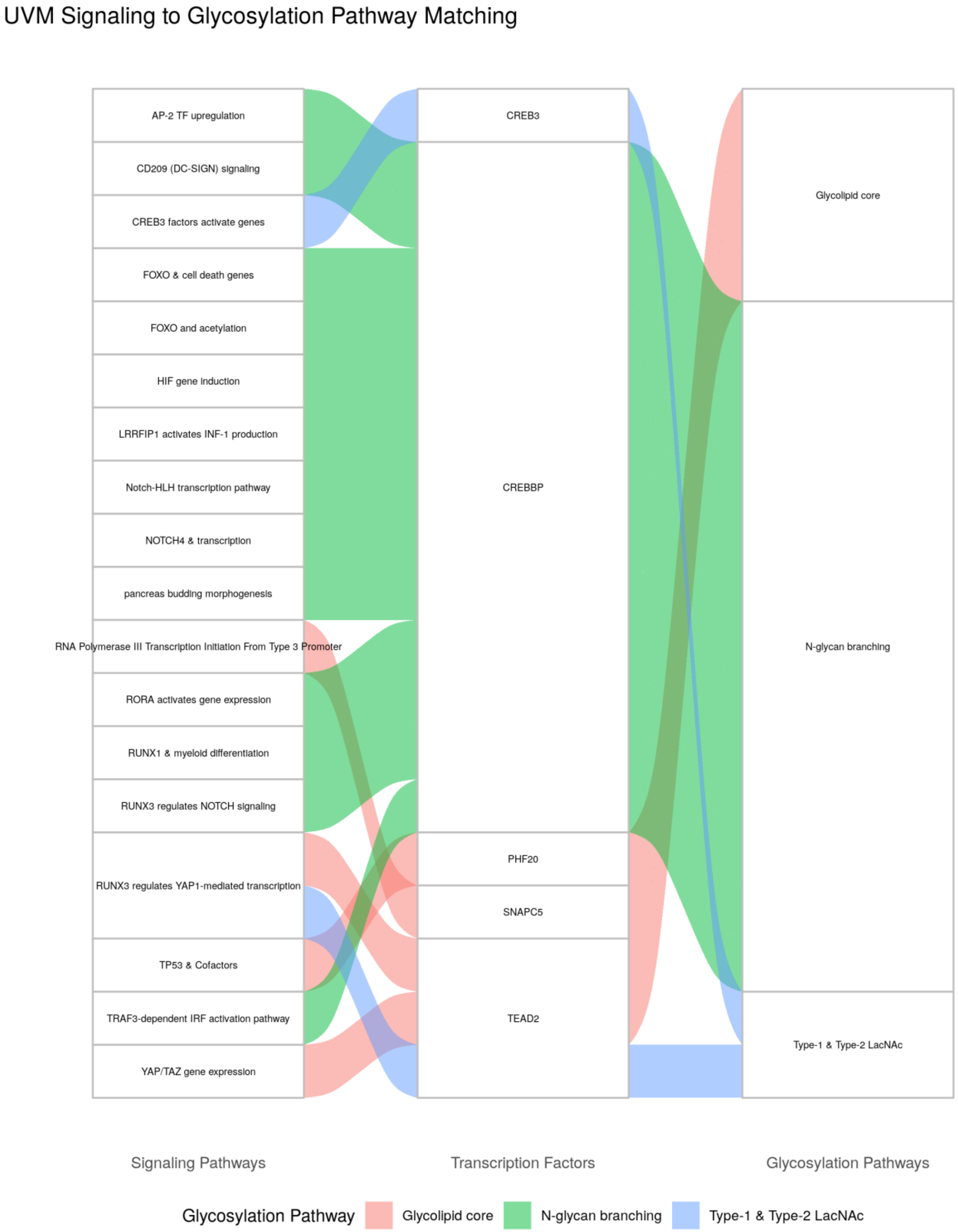



TGCT Signaling to Glycosylation Pathway Matching
Disorders of Developmental Biology
Disorders of Nervous System Development
Erythropoietin activates STAT5
Growth hormone receptor signaling
Interleukin-15 signaling
Interleukin-2 signaling
Interleukin-20 family signaling
Interleukin-21 signaling
Interleukin-9 signaling
KIT signalling
Loss of function of MECP2 in Rett syndrome
Loss of MECP2 binding ability to 5mC-DNA
Loss of phosphorylation of MECP2 at T308
MECP2 & neuronal ligands
MECP2 doesn't bind NcoR/SMRT complex
MECP2 regulates GABA signaling
MECP2 regulates transcription factors
Pervasive developmental disorders
Prolactin receptor signaling
Regulation of TP53 Expression
RUNX3 & immune response and cell migration
RUNX3 regulates BCL2L11 (BIM) transcription
RUNX3 regulates CDKN1A transcription
RUNX3 regulates NOTCH signaling
RUNX3 regulates p14-ARF
RUNX3 regulates RUNX1-mediated transcription
RUNX3 regulates WNT signaling
RUNX3 regulates YAP1-mediated transcription
Signaling by cytosolic FGFR1 fusion mutants
Signaling by FLT3 ITD and TKD mutants
Signaling by Leptin
STAT5 Activation
STAT5 activation downstream of FLT3 ITD mutants
TCF/LEF:CTNNB1 promoter binding
TP53 & G1 Cell cycle arrest control
ARID3A
E2F7
MECP2
PRDM1
RUNX3
STAT5A
TCF7L1
ABO blood Group Synthesis
Dolichol Pathway
GalNAc-type O-glycans
Heparan sulfate extension
Hyaluronan Synthesis
Signaling Pathways
Transcription Factors
Glycosylation Pathways
osylation Pathway
ABO blood Group Synthesis
Dolichol Pathway
GalNAc-type O-glycans
Heparan sulfate extension
Hyaluronan Syn


THCA Signaling to Glycosylation Pathway Matching
AP-2 regulates cell cycle
AP-2 TF downregulation
AP-2 TF upregulation
AP-2 TFs regulate other TFs
Disorders of Developmental Biology
Disorders of Nervous System Development
Estrogen signaling
Interleukin-21 signaling
Interleukin-23 signaling
Loss of function of MECP2 in Rett syndrome
Loss of MECP2 binding ability to 5hmC-DNA
Loss of phosphorylation of MECP2 at T308
MECP2 & neuronal ligands
MECP2 doesn't bind NcoR/SMRT complex
MECP2 regulates GABA signaling
MECP2 regulates transcription factors
Pervasive developmental disorders
POU5F1 (OCT4), SOX2, NANOG & proliferation
Regulation of IFNA signaling
Repression of WNT target genes
RUNX1 & BCR signaling
RUNX1 & ER transcription
RUNX1 & IL signaling
RUNX1 & keratinocyte differentiation
RUNX1 & myeloid differentiation
RUNX1 & tight junctions
RUNX1 & Wnt signaling
RUNX2 & myeloid differentiation
RUNX3 regulates RUNX1-mediated transcription
T lymphoctye development by RUNX1 and FOXP3
FOS
FOXP3
HDAC1
LEF1
MECP2
MEF2C
RUNX1
SIN3A
SRF
STAT1
STAT2
STAT3
STAT4
TFAP2C
Chondroitin and Dermatan Sulfate Extension
Complex N-glycans
Fucosylation
GalNAc-type O-glycans
Gangliosides
Glycolipid core
Heparan sulfate extension
P1/PK Blood Groups
Sialylation
Sulfated Glycan Epitopes
Type-1 & Type-2 LacNAc
Signaling Pathways
Transcription Factors
Glycosylation Pathways
ycosylation Pathway
Chondroitin and Dermatan Sulfate Extension
Complex N-glycans
Fucosylation
GalNAc-type O-glycans
Gangliosides
Glycolipid core
Heparan sulfate extension
P1/PK Blood Groups
Sialylation
Sulfated Glycan Epito
Type-1 & Type-2 LacN


THYM Signaling to Glycosylation Pathway Matching
AKT-mediated inactivation of FOXO1A
AP-2 regulates cell cycle
AP-2 TF downregulation
E2F targets under DREAM regulation
ERK/MAPK targets
Erythropoietin activates STAT5
Growth hormone receptor signaling
IGFR mRNA binding proteins
Interleukin-15 signaling
Interleukin-2 signaling
Interleukin-20 family signaling
Interleukin-21 signaling
Interleukin-9 signaling
KIT signalling
MECP2 regulates transcription factors
Prolactin receptor signaling
RUNX1 & myeloid differentiation
RUNX2 & cell migration
RUNX2 & myeloid differentiation
RUNX2 regulates chondrocyte maturation
RUNX3 & immune response and cell migration
RUNX3 regulates BCL2L11 (BIM) transcription
RUNX3 regulates CDKN1A transcription
RUNX3 regulates NOTCH signaling
RUNX3 regulates p14-ARF
RUNX3 regulates RUNX1-mediated transcription
RUNX3 regulates WNT signaling
RUNX3 regulates YAP1-mediated transcription
Signaling by cytosolic FGFR1 fusion mutants
Signaling by FLT3 ITD and TKD mutants
Signaling by Leptin
STAT5 Activation
STAT5 activation downstream of FLT3 ITD mutants
TCF/LEF:CTNNB1 promoter binding
YAP/TAZ gene expression
FOXO1
MEF2C
MYC
RUNX2
RUNX3
STAT5B
TCF7
TFAP2A
Chondroitin and Dermatan Sulfate Extension
Fucosylation
Heparan sulfate extension
O-linked Fucose
P1/PK Blood Groups
Sulfated Glycan Epitopes
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
Chondroitin and Dermatan Sulfate Extension
Fucosylation
Heparan sulfate extension
O-linked Fucose
P1/PK Blood Groups
Sulfated Glycan Epitopes


UCEC Signaling to Glycosylation Pathway Matching
ALKBH3 reverses alkylation
AP-2 TFs & growth factors/receptors
BH3 inactivate BCL-2 proteins
CREB phosphorylation
CREB3 factors activate genes
dioxygenase alkylation damage reversal
Displacement of DNA glycosylase by APEX1
DNA Damage Reversal
Growth hormone receptor signaling
Interleukin-15 signaling
Interleukin-20 family signaling
Interleukin-21 signaling
Interleukin-23 signaling
Interleukin-27 signaling
Interleukin-35 Signalling
Interleukin-6 signaling
Interleukin-9 signaling
KIT signalling
MET activates STAT3
p75NTR negatively regulates cell cycle via SC1
PDGFRA extracellular domain mutant signaling
PDGFRA transmembrane mutant signaling
POU5F1 (OCT4), SOX2, NANOG & proliferation
PTK6 Activates STAT3
RUNX1 & ER transcription
RUNX1 & Wnt signaling
RUNX3 regulates YAP1-mediated transcription
Signaling by cytosolic FGFR1 fusion mutants
Signaling by Leptin
Signalling to STAT3
YAP/TAZ gene expression
ALKBH3
ATF1
CREB3L4
ESR1
MBD4
PRDM4
STAT3
TEAD2
GalNAc-type O-glycans
Heparan sulfate extension
LacDiNAc
N-glycan branching
Sialylation
Sulfated Glycan Epitopes
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
GalNAc-type O-glycans
Heparan sulfate extension
LacDiNAc
N-glycan branching
Sialylation
Sulfated Glycan Epitopes


UVM Signaling to Glycosylation Pathway Matching
AP-2 TF upregulation
CD209 (DC-SIGN) signaling
CREB3 factors activate genes
FOXO & cell death genes
FOXO and acetylation
HIF gene induction
LRRFIP1 activates INF-1 production
Notch-HLH transcription pathway
NOTCH4 & transcription
pancreas budding morphogenesis
RNA Polymerase III Transcription Initiation From Type 3 Promoter
RORA activates gene expression
RUNX1 & myeloid differentiation
RUNX3 regulates NOTCH signaling
RUNX3 regulates YAP1-mediated transcription
TP53 & Cofactors
TRAF3-dependent IRF activation pathway
YAP/TAZ gene expression
CREB3
CREBBP
PHF20
SNAPC5
TEAD2
Glycolipid core
N-glycan branching
Type-1 & Type-2 LacNAc
Signaling Pathways
Transcription Factors
Glycosylation Pathways
Glycosylation Pathway
Glycolipid core
N-glycan branching
Type-1 & Type-2 LacNAc