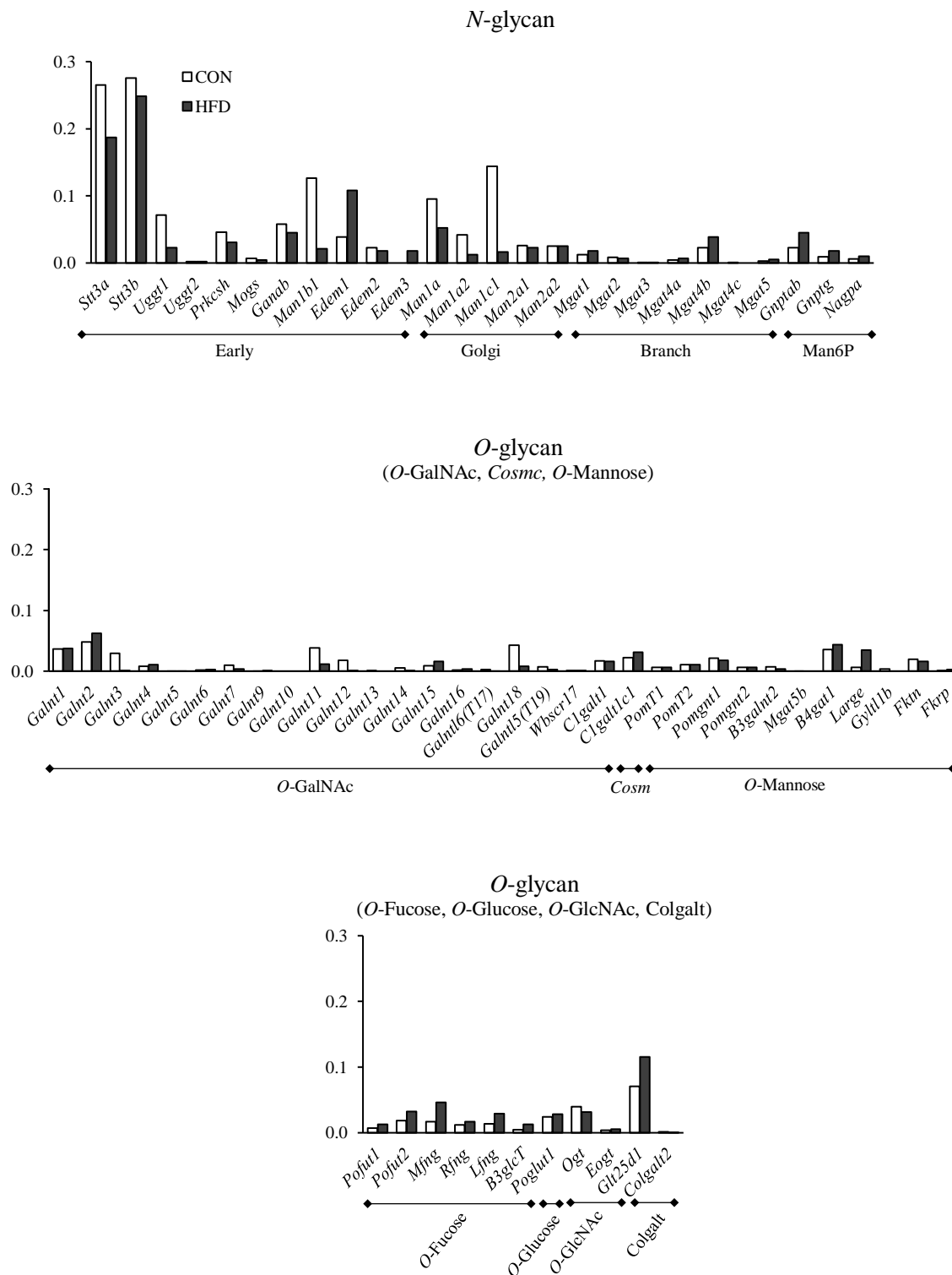
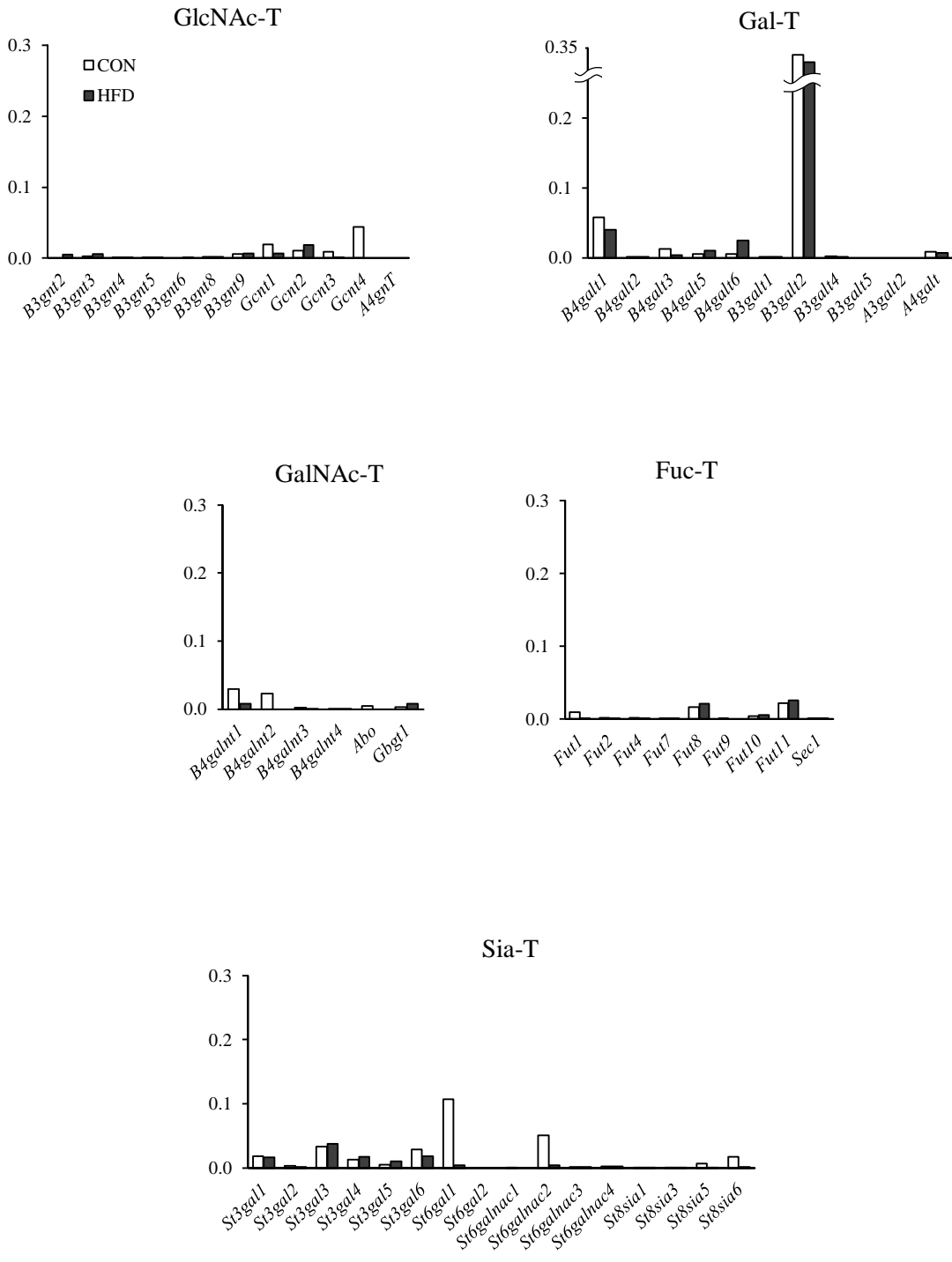


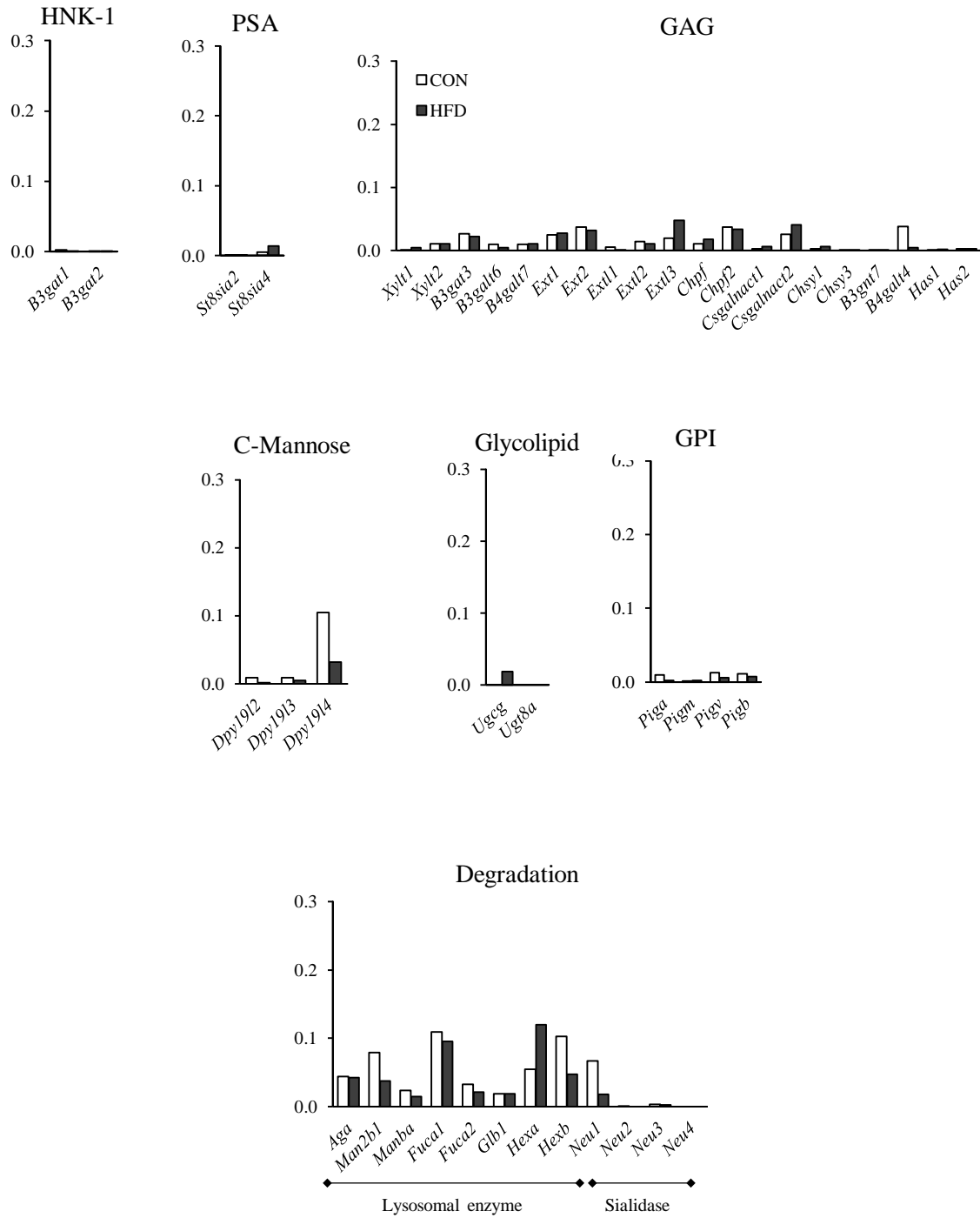
Supplemental Figure 1



Supplemental Figure 1 mRNA abundance relative to house keeping genes (Actb, B2m, Gapdh, and Hsp90ab1).



Supplemental Figure 1 mRNA abundance relative to house keeping genes (Actb, B2m, Gapdh, and Hsp90ab1).



Supplemental Figure 1 mRNA abundance relative to house keeping genes (Actb, B2m, Gapdh, and Hsp90ab1).

Inhibitory role of α 2,6-Sialylation in Adipogenesis

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Supplemental Figure 2

Gene symbol	Category	Subcategory	CON	HFD	Log Fold change (v.s. CON)
<i>Stt3a</i>	N-glycan	Early	0.2651	0.1867	-0.51
<i>Stt3b</i>	N-glycan	Early	0.2756	0.2481	-0.15
<i>Uggt1</i>	N-glycan	Early	0.0718	0.0227	-1.66
<i>Uggt2</i>	N-glycan	Early	0.0024	0.0018	-0.45
<i>Prkcsb</i>	N-glycan	Early	0.0460	0.0307	-0.58
<i>Mogs</i>	N-glycan	Early	0.0065	0.0043	-0.59
<i>Ganab</i>	N-glycan	Early	0.0578	0.0453	-0.35
<i>Man1b1</i>	N-glycan	Early	0.1264	0.0208	-2.60
<i>Edem1</i>	N-glycan	Early	0.0386	0.1078	1.48
<i>Edem2</i>	N-glycan	Early	0.0226	0.0184	-0.30
<i>Edem3</i>	N-glycan	Early	N.D.	0.0181	-
<i>Man1a</i>	N-glycan	Golgi mannosidase	0.0956	0.0525	-0.86
<i>Man1a2</i>	N-glycan	Golgi mannosidase	0.0423	0.0126	-1.74
<i>Man1c1</i>	N-glycan	Golgi mannosidase	0.1440	0.0161	-3.16
<i>Man2a1</i>	N-glycan	Golgi mannosidase	0.0263	0.0230	-0.19
<i>Man2a2</i>	N-glycan	Golgi mannosidase	0.0254	0.0253	-0.01
<i>Mgat1</i>	N-glycan	Branch	0.0123	0.0178	0.54
<i>Mgat2</i>	N-glycan	Branch	0.0081	0.0071	-0.20
<i>Mgat3</i>	N-glycan	Branch	0.0004	0.0001	-1.71
<i>Mgat4a</i>	N-glycan	Branch	0.0041	0.0071	0.78
<i>Mgat4b</i>	N-glycan	Branch	0.0228	0.0386	0.76
<i>Mgat4c</i>	N-glycan	Branch	0.0001	N.D.	-
<i>Mgat5</i>	N-glycan	Branch	0.0027	0.0054	1.02
<i>Gnptab</i>	N-glycan	Man6P	0.0231	0.0455	0.98
<i>Gnptg</i>	N-glycan	Man6P	0.0089	0.0183	1.04
<i>Nagpa</i>	N-glycan	Man6P	0.0060	0.0102	0.77
<i>Galnt1</i>	O-Glycan	O-GalNAc	0.0366	0.0375	0.04
<i>Galnt2</i>	O-Glycan	O-GalNAc	0.0488	0.0627	0.36
<i>Galnt3</i>	O-Glycan	O-GalNAc	0.0296	0.0016	-4.19
<i>Galnt4</i>	O-Glycan	O-GalNAc	0.0085	0.0108	0.35
<i>Galnt5</i>	O-Glycan	O-GalNAc	0.0001	0.0001	0.20
<i>Galnt6</i>	O-Glycan	O-GalNAc	0.0022	0.0033	0.58
<i>Galnt7</i>	O-Glycan	O-GalNAc	0.0104	0.0036	-1.53
<i>Galnt9</i>	O-Glycan	O-GalNAc	0.0008	0.0017	1.07
<i>Galnt10</i>	O-Glycan	O-GalNAc	N.D.	N.D.	-
<i>Galnt11</i>	O-Glycan	O-GalNAc	0.0390	0.0121	-1.68
<i>Galnt12</i>	O-Glycan	O-GalNAc	0.0182	0.0014	-3.66
<i>Galnt13</i>	O-Glycan	O-GalNAc	0.0015	N.D.	-
<i>Galnt14</i>	O-Glycan	O-GalNAc	0.0057	0.0012	-2.20
<i>Galnt15</i>	O-Glycan	O-GalNAc	0.0095	0.0161	0.76
<i>Galnt16</i>	O-Glycan	O-GalNAc	0.0023	0.0038	0.72
<i>Galnt16(T17)</i>	O-Glycan	O-GalNAc	0.0033	0.0006	-2.53
<i>Galnt18</i>	O-Glycan	O-GalNAc	0.0427	0.0080	-2.41
<i>Galnt15(T19)</i>	O-Glycan	O-GalNAc	0.0071	0.0027	-1.41
<i>Wbscr17</i>	O-Glycan	O-GalNAc	0.0011	0.0013	0.21
<i>Clgalt1</i>	O-Glycan	O-GalNAc	0.0177	0.0163	-0.12
<i>Clgalt1c1</i>	O-Glycan	<i>Cosmc</i>	0.0228	0.0315	0.46
<i>PomT1</i>	O-Glycan	O-Mannose	0.0064	0.0064	0.01
<i>PomT2</i>	O-Glycan	O-Mannose	0.0115	0.0110	-0.07
<i>Pomgnt1</i>	O-Glycan	O-Mannose	0.0215	0.0181	-0.25
<i>Pomgnt2</i>	O-Glycan	O-Mannose	0.0068	0.0069	0.04
<i>B3galnt2</i>	O-Glycan	O-Mannose	0.0078	0.0038	-1.02
<i>Mgat5b</i>	O-Glycan	O-Mannose	0.0001	N.D.	-

<i>B4gat1</i>	O-Glycan	O-Mannose	0.0358	0.0440	0.30
<i>Large</i>	O-Glycan	O-Mannose	0.0069	0.0347	2.33
<i>Gylt11b</i>	O-Glycan	O-Mannose	0.0041	N.D.	-
<i>Fktn</i>	O-Glycan	O-Mannose	0.0200	0.0166	-0.27
<i>Fkrp</i>	O-Glycan	O-Mannose	0.0018	0.0027	0.62
<i>Pofut1</i>	O-Glycan	O-Fucose	0.0071	0.0130	0.87
<i>Pofut2</i>	O-Glycan	O-Fucose	0.0187	0.0327	0.81
<i>Mfng</i>	O-Glycan	O-Fucose	0.0170	0.0461	1.43
<i>Rfng</i>	O-Glycan	O-Fucose	0.0117	0.0166	0.51
<i>Lfng</i>	O-Glycan	O-Fucose	0.0138	0.0295	1.10
<i>B3glcT</i>	O-Glycan	O-Fucose	0.0050	0.0125	1.32
<i>Poglut1</i>	O-Glycan	O-Glucose	0.0239	0.0283	0.24
<i>Ogt</i>	O-Glycan	O-GlcNAc	0.0396	0.0317	-0.32
<i>Eogt</i>	O-Glycan	O-GlcNAc	0.0039	0.0055	0.49
<i>Gl25d1</i>	O-Glycan	Colgalt	0.0711	0.1158	0.70
<i>Colgalt2</i>	O-Glycan	Colgalt	0.0011	0.0010	-0.20
<i>B3gnt2</i>	GlcNAc-T		N.D.	0.0053	-
<i>B3gnt3</i>	GlcNAc-T		0.0025	0.0056	1.14
<i>B3gnt4</i>	GlcNAc-T		0.0008	0.0008	0.07
<i>B3gnt5</i>	GlcNAc-T		0.0002	0.0003	0.29
<i>B3gnt6</i>	GlcNAc-T		N.D.	0.0002	-
<i>B3gnt8</i>	GlcNAc-T		0.0017	0.0022	0.34
<i>B3gnt9</i>	GlcNAc-T		0.0057	0.0068	0.26
<i>Gcnt1</i>	GlcNAc-T		0.0195	0.0069	-1.51
<i>Gcnt2</i>	GlcNAc-T		0.0105	0.0189	0.84
<i>Gcnt3</i>	GlcNAc-T		0.0094	0.0001	-6.82
<i>Gcnt4</i>	GlcNAc-T		0.0443	N.D.	-
<i>A4gnT</i>	GlcNAc-T		N.D.	N.D.	-
<i>B4galt1</i>	Gal-T		0.0582	0.0404	-0.53
<i>B4galt2</i>	Gal-T		0.0013	0.0014	0.15
<i>B4galt3</i>	Gal-T		0.0127	0.0041	-1.61
<i>B4galt5</i>	Gal-T		0.0053	0.0105	0.98
<i>B4galt6</i>	Gal-T		0.0055	0.0247	2.16
<i>B3galt1</i>	Gal-T		0.0018	0.0013	-0.38
<i>B3galt2</i>	Gal-T		0.3410	0.3017	-0.18
<i>B3galt4</i>	Gal-T		0.0022	0.0015	-0.56
<i>B3galt5</i>	Gal-T		N.D.	N.D.	-
<i>A3galt2</i>	Gal-T		N.D.	N.D.	-
<i>A4galt</i>	Gal-T		0.0085	0.0075	-0.18
<i>B4galnt1</i>	GalNAc-T		0.0294	0.0083	-1.83
<i>B4galnt2</i>	GalNAc-T		0.0227	N.D.	-
<i>B4galnt3</i>	GalNAc-T		0.0024	0.0002	-3.83
<i>B4galnt4</i>	GalNAc-T		0.0008	0.0001	-2.47
<i>Abo</i>	GalNAc-T		0.0045	N.D.	-
<i>Gbgt1</i>	GalNAc-T		0.0031	0.0081	1.38
<i>Fut1</i>	Fuc-T		0.0094	0.0000	-8.04
<i>Fut2</i>	Fuc-T		0.0014	0.0004	-1.75
<i>Fut4</i>	Fuc-T		0.0018	0.0001	-3.71
<i>Fut7</i>	Fuc-T		0.0002	0.0006	1.69
<i>Fut8</i>	Fuc-T		0.0162	0.0208	0.35
<i>Fut9</i>	Fuc-T		0.0007	N.D.	-
<i>Fut10</i>	Fuc-T		0.0039	0.0056	0.52
<i>Fut11</i>	Fuc-T		0.0218	0.0256	0.23
<i>Sec1</i>	Fuc-T		0.0008	0.0002	-1.68
<i>St3gal1</i>	Sia-T		0.0183	0.0170	-0.11
<i>St3gal2</i>	Sia-T		0.0030	0.0021	-0.57
<i>St3gal3</i>	Sia-T		0.0331	0.0379	0.19
<i>St3gal4</i>	Sia-T		0.0133	0.0174	0.40
<i>St3gal5</i>	Sia-T		0.0053	0.0107	1.03
<i>St3gal6</i>	Sia-T		0.0285	0.0184	-0.63
<i>St6gal1</i>	Sia-T		0.1070	0.0044	-4.61

Supplemental Figure 2 mRNA abundance relative to house keeping genes (Actb, B2m, Gapdh, and Hsp90ab1).

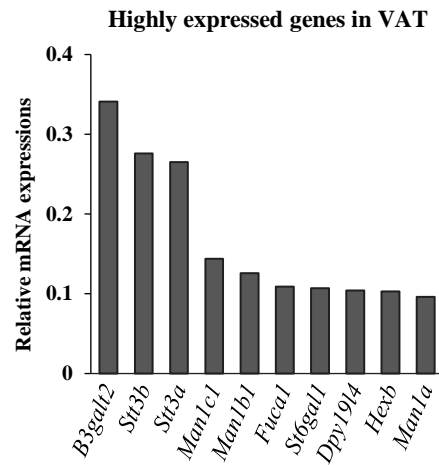
<i>St6gal2</i>	Sia-T		N.D.	N.D.	-
<i>St6galnac1</i>	Sia-T		0.0001	N.D.	-
<i>St6galnac2</i>	Sia-T		0.0514	0.0046	-3.49
<i>St6galnac3</i>	Sia-T		0.0016	0.0013	-0.29
<i>St6galnac4</i>	Sia-T		0.0023	0.0023	0.02
<i>St8sia1</i>	Sia-T		0.0004	0.0004	-0.02
<i>St8sia3</i>	Sia-T		0.0007	0.0002	-1.94
<i>St8sia5</i>	Sia-T		0.0071	0.0002	-5.44
<i>St8sia6</i>	Sia-T		0.0176	0.0014	-3.64
<i>B3gat1</i>	HNK-1		0.0020	0.0001	-4.19
<i>B3gat2</i>	HNK-1		0.0005	0.0003	-0.97
<i>St8sia2</i>	PSA		0.0004	0.0003	-0.38
<i>St8sia4</i>	PSA		0.0049	0.0140	1.51
<i>Xylt1</i>	GAG	Core	0.0011	0.0045	2.04
<i>Xylt2</i>	GAG	Core	0.0110	0.0102	-0.11
<i>B3gat3</i>	GAG	Core	0.0261	0.0222	-0.23
<i>B3galt6</i>	GAG	Core	0.0096	0.0045	-1.10
<i>B4galt7</i>	GAG	Core	0.0100	0.0103	0.05
<i>Ext1</i>	GAG	Heparan sulfate	0.0246	0.0275	0.16
<i>Ext2</i>	GAG	Heparan sulfate	0.0368	0.0316	-0.22
<i>Extl1</i>	GAG	Heparan sulfate	0.0053	0.0006	-3.27
<i>Extl2</i>	GAG	Heparan sulfate	0.0140	0.0109	-0.37
<i>Extl3</i>	GAG	Heparan sulfate	0.0192	0.0480	1.32
<i>Chpf</i>	GAG	Chondroitin sulfate	0.0107	0.0179	0.75
<i>Chpf2</i>	GAG	Chondroitin sulfate	0.0372	0.0339	-0.13
<i>Csgalnact1</i>	GAG	Chondroitin sulfate	0.0023	0.0062	1.43
<i>Csgalnact2</i>	GAG	Chondroitin sulfate	0.0258	0.0402	0.64
<i>Chsy1</i>	GAG	Chondroitin sulfate	0.0024	0.0059	1.29
<i>Chsy3</i>	GAG	Chondroitin sulfate	0.0007	0.0003	-1.07
<i>B3gnt7</i>	GAG	Keratan sulfate	0.0008	0.0010	0.23
<i>B4galt4</i>	GAG	Keratan sulfate	0.0379	0.0043	-3.14
<i>Has1</i>	GAG	Hyaluronic acid	0.0008	0.0021	1.43
<i>Has2</i>	GAG	Hyaluronic acid	0.0023	0.0028	0.28
<i>Dpy1911</i>	C-Mannose		0.0098	0.0196	1.00
<i>Dpy1912</i>	C-Mannose		0.0085	0.0014	-2.65
<i>Dpy1913</i>	C-Mannose		0.0085	0.0051	-0.75
<i>Dpy1914</i>	C-Mannose		0.1043	0.0316	-1.72
<i>Ugcg</i>	Glycolipid		0.0188	0.0205	0.13
<i>Ugt8a</i>	Glycolipid		N.D.	N.D.	-
<i>Piga</i>	GPI		0.0096	0.0020	-2.25
<i>Pigm</i>	GPI		0.0015	0.0017	0.24
<i>Pigv</i>	GPI		0.0122	0.0060	-1.01
<i>Pigb</i>	GPI		0.0113	0.0071	-0.68
<i>Aga</i>	Degradation	Lysosomal enzyme	0.0437	0.0426	-0.04
<i>Man2b1</i>	Degradation	Lysosomal enzyme	0.0790	0.0375	-1.08
<i>Manba</i>	Degradation	Lysosomal enzyme	0.0237	0.0151	-0.65
<i>Fuca1</i>	Degradation	Lysosomal enzyme	0.1091	0.0957	-0.19
<i>Fuca2</i>	Degradation	Lysosomal enzyme	0.0330	0.0217	-0.60
<i>Glb1</i>	Degradation	Lysosomal enzyme	0.0190	0.0191	0.01
<i>Hexa</i>	Degradation	Lysosomal enzyme	0.0548	0.1199	1.13
<i>Hexb</i>	Degradation	Lysosomal enzyme	0.1032	0.0471	-1.13
<i>Neu1</i>	Degradation	Sialidase	0.0668	0.0178	-1.91
<i>Neu2</i>	Degradation	Sialidase	0.0004	N.D.	-
<i>Neu3</i>	Degradation	Sialidase	0.0036	0.0023	-0.61
<i>Neu4</i>	Degradation	Sialidase	N.D.	N.D.	-

Supplemental Figure 2 mRNA abundance relative to house keeping genes (Actb, B2m, Gapdh, and Hsp90ab1). Fig. 1B shows down-regulated glycosyltransferases in HFD mice compared with CON mice, with mRNA abundance being greater than 0.1 in VATs of CON mice.

Inhibitory role of α 2,6-Sialylation in Adipogenesis

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Supplemental Figure 3



Supplemental Figure 3 Highly expressed glycosyltransferase and related enzyme genes in VATs of CON mice (> 0.1 relative to housekeeping genes; average of *Actb*, *B2m*, *Gapdh*, and *Hsp90ab1*).

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Mascot Search Results

User : superuser
Email : superuser
Search title : 151015_L_294_Kaburagi_sample.mgf
MS data file : C:\Xcalibur\data\2015\15-294_Kaburagi\151015_L_294_Kaburagi_sample.mgf
Database : SwissProt 2015_09 (549215 sequences; 195767212 residues)
Taxonomy : Mus musculus (house mouse) (16726 sequences)
Timestamp : 15 Oct 2015 at 10:00:05 GMT
Enzyme : Trypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 1.5 Da
Fragment Mass Tolerance : ± 0.8 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 4969

Protein hits : [SPA3K_MOUSE](#) Serine protease inhibitor A3K OS=Mus musculus GN=Serpina3k PE=1 SV=2
[ITIH4_MOUSE](#) Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=2
[K1C10_MOUSE](#) Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=3
[K2C75_MOUSE](#) Keratin, type II cytoskeletal 75 OS=Mus musculus GN=Krt75 PE=1 SV=1
[ITB1_MOUSE](#) Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1
[MUC18_MOUSE](#) Cell surface glycoprotein MUC18 OS=Mus musculus GN=Mcam PE=1 SV=1
[K2C1B_MOUSE](#) Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt77 PE=1 SV=1
[A2M_MOUSE](#) Alpha-2-macroglobulin OS=Mus musculus GN=A2m PE=1 SV=3
[K2C8_MOUSE](#) Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4
[CAD13_MOUSE](#) Cadherin-13 OS=Mus musculus GN=Cdh13 PE=1 SV=2

	SwissProt	Decoy	False discovery rate
Peptide matches above identity threshold	51	5	9.80 %
Peptide matches above homology or identity threshold	73	13	17.81 %

Select Summary Report

Format As	Select Summary (protein hits) <input type="text"/>	Help
Significance threshold p<	<input type="text" value="0.05"/>	Max. number of hits <input type="text" value="AUTO"/>
Standard scoring <input checked="" type="radio"/>	MudPIT scoring <input type="radio"/>	Ions score or expect cut-off <input type="text" value="0.05"/>
Show pop-ups <input checked="" type="radio"/>	Suppress pop-ups <input type="radio"/>	Show sub-sets <input type="text" value="0"/>
Preferred taxonomy	<input type="text" value="All entries"/>	Require bold red <input checked="" type="checkbox"/>

All queries
 Unassigned
 Below homology threshold
 Below identity threshold

1. [SPA3K_MOUSE](#) Mass: 47021 Score: 639 Matches: 26(26) Sequences: 9(9) emPAI: 1.05
 Serine protease inhibitor A3K OS=Mus musculus GN=Serpina3k PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1419	498.6588	995.3029	995.5764	-0.2734	0	38	0.018	1	U	K.LSVSQVVK.A
1620	582.1216	1162.2286	1161.5951	0.6335	0	61	9.6e-005	1	U	K.TMEEILEGLK.F 1618
1650	590.0821	1178.1496	1177.5900	0.5596	0	(61)	0.00011	1	U	K.TMEEILEGLK.F
1929	672.1654	1342.3163	1341.6928	0.6234	0	61	8.4e-005	1	U	K.DLQILAEFHEK.T 1928
1963	687.0972	1372.1798	1371.6955	0.4842	0	55	0.00042	1	U	R.LEEDVLPENGIK.E 1961 1962 1964
2433	815.9222	1629.8299	1628.8192	1.0107	0	102	6.3e-009	1	U	R.MQOVEASLQPETLR.K 2427 2431 2434
2705	587.0090	1758.0051	1756.9141	1.0909	1	46	0.0022	1	U	R.MQOVEASLQPETLRK.W
3307	1071.5416	2141.0687	2141.1328	-0.0641	0	101	6.1e-009	1	U	K.AVLDVAETGTEAAAATGVIGGIR.K 3305 3308
3309	714.9377	2141.7914	2141.1328	0.6586	0	(96)	2e-008	1	U	K.AVLDVAETGTEAAAATGVIGGIR.K 3311 3312
3348	1079.5435	2157.0724	2158.0219	-0.9495	0	86	1.9e-007	1	U	R.ALYQTEAFTADFQOPTAK.N 3350
3440	1105.5427	2209.0709	2208.9739	0.0970	0	88	1.1e-007	1	U	K.ISFDPQDTFESEFYLDEK.R 3442 3443

2. [ITIH4_MOUSE](#) Mass: 104765 Score: 498 Matches: 13(13) Sequences: 8(8) emPAI: 0.30
 Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1233	426.3312	850.6479	850.4297	0.2182	0	54	0.00053	1	U	K.QYSAAVGR.G
1298	439.4031	876.7917	876.4375	0.3542	0	69	2e-005	1	U	K.GSEMVVAGK.L
1520	543.8196	1085.6246	1085.5717	0.0530	0	50	0.0014	1	U	R.SNQAELLPSK.S 1519
1569	561.4141	1120.8137	1120.5877	0.2260	0	51	0.0011	1	U	K.VQGVLYLATR.E 1570
1833	648.8306	1295.6466	1295.7085	-0.0619	0	74	4.2e-006	1	U	K.LQDQGPVLLAK.V 1834
2126	738.0449	1474.0753	1472.7471	1.3282	0	65	3.6e-005	1	U	K.QSLVQATEENLNK.A
2153	745.4677	1488.9207	1488.7824	0.1383	0	80	9.6e-007	1	U	K.LFVDPSQGLEVTGK.Y 2155
2799	904.6213	1807.2281	1806.8748	0.3533	0	54	0.00031	1	U	K.SQSEQDTVLNGDFIVR.Y 2800

3.	K1C10_MOUSE	Mass: 57906	Score: 125	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.12					
Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=3											
	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	1525	545.9040	1089.7935	1089.5237	0.2699	0	45	0.0051	1	U	R.VTMQNLNDR.L
	1978	691.4297	1380.8448	1380.6408	0.2040	0	83	6e-007	1	U	R.ALEESNYELEGK.I
4.	K2C75_MOUSE	Mass: 59932	Score: 119	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.12					
Keratin, type II cytoskeletal 75 OS=Mus musculus GN=Krt75 PE=1 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	1845	652.2750	1302.5354	1301.7078	0.8275	0	71	9.1e-006	1	U	R.SLDLDSIIAEVK.A
	2130	738.6626	1475.3106	1475.7984	-0.4877	1	50	0.0011	2	U	R.FLEQQNKVLETK.W
5.	ITB1_MOUSE	Mass: 91424	Score: 115	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.08					
Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	1444	508.4224	1014.8302	1014.5710	0.2592	0	63	8.2e-005	1	U	K.SAVTTVVNPK.Y
	1584	570.8734	1139.7323	1139.5095	0.2228	0	52	0.00078	1	U	R.DNTNEIYSGK.F
6.	MUC18_MOUSE	Mass: 72470	Score: 96	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.10					
Cell surface glycoprotein MUC18 OS=Mus musculus GN=Mcam PE=1 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	1543	555.8283	1109.6419	1108.6353	1.0067	0	50	0.0012	1	U	K.GPVLQLNVR.R
	3029	649.2312	1944.6718	1944.0065	0.6653	0	46	0.0019	1	U	K.APEEPTIQANVVGIVHVD.R
7.	K2C1B_MOUSE	Mass: 61379	Score: 72	Matches: 2(2)	Sequences: 1(1)	emPAI: 0.06					
Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt77 PE=1 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	2130	738.6626	1475.3106	1474.7780	0.5327	0	72	7.9e-006	1	U	R.FLEQQNQVLQTK.W 2129
Proteins matching the same set of peptides:											
	K2C1_MOUSE	Mass: 66079	Score: 72	Matches: 2(2)	Sequences: 1(1)						
Keratin, type II cytoskeletal 1 OS=Mus musculus GN=Krt1 PE=1 SV=4											
	K2C71_MOUSE	Mass: 57860	Score: 72	Matches: 2(2)	Sequences: 1(1)						
Keratin, type II cytoskeletal 71 OS=Mus musculus GN=Krt71 PE=1 SV=1											
	K2C73_MOUSE	Mass: 59502	Score: 72	Matches: 2(2)	Sequences: 1(1)						
Keratin, type II cytoskeletal 73 OS=Mus musculus GN=Krt73 PE=1 SV=1											
	K2C74_MOUSE	Mass: 55340	Score: 72	Matches: 2(2)	Sequences: 1(1)						
Keratin, type II cytoskeletal 74 OS=Mus musculus GN=Krt74 PE=3 SV=1											
8.	A2M_MOUSE	Mass: 167116	Score: 40	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.02					
Alpha-2-macroglobulin OS=Mus musculus GN=A2m PE=1 SV=3											
	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	2038	706.5985	1411.1825	1411.7500	-0.5675	0	40	0.01	1	U	K.TVQGAFFGVPVYK.D
9.	K2C8_MOUSE	Mass: 54531	Score: 35	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06					
Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4											
	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	1987	692.6489	1383.2833	1382.7194	0.5639	1	35	0.041	1	U	K.SLNNKFASFIDK.V
10.	CAD13_MOUSE	Mass: 78536	Score: 34	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04					
Cadherin-13 OS=Mus musculus GN=Cdh13 PE=1 SV=2											
	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	1591	573.1916	1144.3687	1143.6248	0.7440	0	34	0.049	1	U	K.VNSDGTLVALR.N