Legends to supplemental Figures

Supplemental Figure 1: Annotation of Srr1 sequence. The following colour code was used. Blue: signal peptide, yellow: peptide detected in MS experiments, gray: identified glycopeptide, green: LPXTG motif.

Supplemental Figures 2a to 2d: Automated identification of peptides after neutral loss event using X! Tandem . Detection parameters were set to detect fragmentation ions at low signal to noise ratio.

Supplemental Fig 2a: neutral loss of HexNAc on [234-247] peptide.

Supplemental Fig 2b: neutral Loss of HexNAc on [275-285] peptide.

Supplemental Fig 2c: neutral Loss of HexNAc on [214-233] peptide.

Supplemental Fig 2d: neutral Loss of O-AcHexNAc on [214-233] peptide.

The figures were obtained with the Global Proteome Machine XML data viewer.

(http://bacteria.thegpm.org/tandem/thegpm_upview.html).

Supplemental Figures 3a-3t: CID MS/MS spectra of glycopeptides described in

 Table 1. Glycan symbols: HexNAc (Square), Hex (Circle), O-AcHexNAc (Crossed square).

Supplemental Figure 4: Successive neutral loss events of [192-211] peptide modified with +3(HexNAc) detected by CID MS/MS cycles on LTQ-Orbitrap. Precursor ion m/z 911.4414 z=3. Sample Srr1 MSn4. Scan 2236-2240. Peak noted * corresponds to the most abundant ion selected for next CID event.

Supplemental Figures 5a-5ag: HCD MS/MS spectra of glycopeptides described in Table 2. Glycan symbols: HexNAc (Square), Hex (Circle), *O*-AcHexNAc (Crossed square).

Supplemental Figure 6: Extracted ion chromatograms (XIC) of MS spectra of nonglycosylated and glycosylated forms of peptide [192-211] peptide described in Table 2. The reported data were extracted in the time window 29-39 min. The glycan modification is reported in each panel.

Supplemental figure 7: SDS PAGE of medium after overnight cultures of *S. agalactiae* (A) strain H36B *srtA** and (B) strain H36B *srtA** $\Delta gtfCH$. Gel was stained with Coomassie Blue. Arrowheads points to Srr1 bands which were analyzed by MS. Note the apparent molecular weight difference between the two proteins which likely reflects the glycosylation default in H36B *srtA** $\Delta gtfCH$.

Supplemental Figures 8a to 8j: ETD MS/MS spectra of glycopeptides described in

Table 3. The deduced glycosylation sites are underlined. $Z' = Z + H^{\cdot}$.

MSOKTFGKOLTVVDTKSRVKMHKSGKNWVRTVMSHFNLFKAIKGRATVEADVCIODVEKEDRLSSGNLTYLKGI LAAGALVGGASLTSRVYADETPVVQEQSSSVPTLAEQTEVTVKTTTVQNHQDGTVSKNIIDSNSVSMSESASTS TSESVSMSMSGSTLTSVSESVSTSALTSASESISTSASESVSKSTSISEVSNILETQASLTDKGRESFSANQIV TESSLVTDAGKNASVSSLIEITKPK<mark>SELOTSK</mark>MSNESLITPEK<mark>SOVMIASDK</mark>TGNESLTPTIRLKSVIOPR<mark>SMN</mark> LMTLSSEMDLIPLEEVSDTEMLGKDVSSELOKVNIALKDNTLSEPGTVKLDSSENLVLNFAFSIASVNEGDVFT VKLSDNLDTOGIGTILKVODIMDETGOLLATGSYSPLTHNITYTWTRYASTLNNIKARVNMPVWPDORIISKTT SDKQCFTATLNNQVASIEERVQYNSPSVTEHTNVKTNVRSRIMKLDDERQTETYITQINPEGKEMYFASGLGNL YTIIGSDGTSGSPVNLLNAEVKILKTNSKNLTDSMDQNYDSPEFEDVTSQYSYTNDGSKITIDWKTNSISSTTS YVVLVKIPKOSGVLYSTVSDINOTYGSKYSYGHTNISGDSDANAEIKLLSESASTSASTSASTSASMSASTSAS MSASMSASTSASTSSSSSVTSNSSKEK<mark>VYSALPSTG</mark>DQDYSVTATALGLGLMTGATLLGRKKSKKDKN

SKKDKN covered sequence SKKDKN LPXTG site SKKDKN Signal peptide MSNESLITPEK Glycopeptide identified in the present study

Supplemental Figure 1

NASVSSLIEITKPK+ (HexNAc)1, m/z [2+] = 743.92

#	log (e)	log (I)	m+h	delta
1633	-5	4.25	1689.9273	0.0001



.

matched/total:	# ions: 48%	intensi	ty: 91%	σ: 0.16 Da		
bond	⁺¹ y	+1y-17	⁺¹ Y ⁻¹⁸	+1b	+1b-17	+1b-18
N_1	1575.884	1558.858	1557.874	115.05	98.024	97.04
A ₂	1504.847	1487.821	1486.837	186.087	169.061	168.077
S3	1417.815 ²⁺	1400.789	1399.805	273.119	256.093	255.109
V_4	1318.747 +1,2	1301.72	1300.736	372.188	355.161	354.177
S ₅	1231.715	1214.688	1213.704	459.22	442.193	441.209
S6	941.603	924.577	923.593	749.331	732.305	731.321
L ₇	828.519	811.493	810.509	862.415	845.389	844.405
18	715.435	698.409	697.425	975.499	958.473	957.489
E ₉	586.393	569.366	568.382	1104.542	1087.515	1086.531
110	473.309	456.282	455.298	1217.626	1200.6	1199.616
T ₁₁	372.261	355.234	354.25	1318.674 +1,2	1301.647	1300.663
K ₁₂	244.166	227.139	226.155	1446.769	1429.742	1428.758
P ₁₃	147.113	130.087	129.103	1543.821 ⁺²	1526.795	1525.811





Supplemental Figure 2a

TGNESLTPTIR+ (HexNAc)1 m/z [2+] = 594.81

#	log (e)	log (I)	m+h	delta
1219	-2.1	4.69	1391.7017	0.0006



.

.

-0.5

.

.

0.5 error (Da)

matched/total:	# ions: 38%	intensi	ty: 14%	σ: 0.40 Da		
bond	⁺¹ y	⁺¹ Y ⁻¹⁷	⁺¹ Y ⁻¹⁸	+1b	+1b-17	+1b-18
T ₁	1290.654	1273.627	1272.643	102.055	85.029	84.045
G ₂	1233.632 ⁺²	1216.606	1215.621	159.077	142.05	141.066
N ₃	1119.589	1102.563	1101.579	273.119	256.093	255.109
E ₄	990.547	973.52	972.536	402.162	385.136	384.151
S ₅	903.515	886.488	885.504	489.194	472.168	471.184
L ₆	790.43	773.404	772.42	602.278	585.252	584.268
Τ ₇	486.304	469.277	468.293	906.405 +1,2	889.378	888.394
P ₈	389.251	372.224	371.24	1003.458 +2	986.431	985.447
T ₉	288.203	271.177	270.193	1104.505	1087.479	1086.495
I ₁₀	175.119	158.093	157.109	1217.589	1200.563	1199.579

Other observed ions:

lon type	m/z
by[3-4]	244.093
ay[2-4]	273.119
by[7-8]	402.187
by[3-6]	444.209
ay[3-6]	416.214
by[5-8]	602.303
by[8-11]	468.293
ay[4-8]	703.35
by[5-9]	703.35
ay[3-7]	720.341
(parent-H ₂ O) ⁺²	687.349
(parent-2H ₂ O) ⁺²	678.841
(parent-NH ₃)+2	687.8411



ESFSANQIVTESSLVTDAGK + (HexNAc)1 m/z [2+] = 1042.01

#	log (e)	log (I)	m+h	delta
2102	-7.2	4.69	2286.0988	-0.003



matched/total:	# ions: 72%	intensit	ty: 95%	σ: 0.07 Da		
bond	⁺¹ y	+1y-17	⁺¹ Y ⁻¹⁸	*1b	+1b-17	+1b-18
E1	2157.056	2140.03	2139.045	130.05	113.023	112.039
S ₂	2070.024	2052.997	2052.013	217.082	200.055	199.071
F ₃	1922.956	1905.929	1904.945	364.15	347.124	346.14
S ₄	1835.924	1818.897	1817.913	451.182	434.156	433.172
A ₅	1764.886	1747.86	1746.876	522.22	505.193	504.209
N ₆	1650.844	1633.817	1632.833	636.262	619.236	618.252
Q ₇	1522.785	1505.758	1504.774	764.321	747.295	746.311
I ₈	1409.701	1392.674	1391.69	877.405	860.379	859.395
V ₉	1310.632	1293.606	1292.622	976.474	959.447	958.463
T ₁₀	1209.585	1192.558	1191.574	1077.521	1060.495	1059.511
E ₁₁	1080.542	1063.516	1062.532	1206.564	1189.537	1188.553
S ₁₂	993.51	976.484	975.5	1293.596	1276.569	1275.585
S ₁₃	703.399	686.372	685.388	1583.707	1566.681	1565.697
L ₁₄	590.315	573.288	572.304	1696.791	1679.765	1678.781
V ₁₅	491.246	474.22	473.236	1795.86	1778.833	1777.849
T ₁₆	390.199	373.172	372.188	1896.907	1879.881	1878.897
D ₁₇	275.172	258.145	257.161	2011.934 +2	1994.908	1993.924
A18	204.135	187.108	186.124	2082.971 +2	2065.945	2064.961
G ₁₉	147.113	130.087	129.103	2139.993	2122.966	2121.982

Other observed ions:

lon type	m/z
by[12-14]	491.235
by[13-18]	790.383
by[12-19]	934.436
ay[7-14]	1033.541
by[3-12]	1077.521
by[10-18]	1107.505
by[8-18]	1319.658
by[5-17]	1561.759
by[3-17]	1795.86
by[12-15]	590.303
by[12-18]	877.415
by[11-18]	1006.458
by[2-11]	1077.521
ay[9-17]	1107.542
by[9-18]	1206.574
by[7-18]	1447.716
by[6-18]	1561.759

Supplemental Figure 2c

ESFSANQIVTESSLVTDAGK + (O-AcHexNAc)1 m/z [2+] = 1042.01

#	log (e)	log (I)	m+h	delta
2194	-8.8	3.71	2328.1107	-0.0047



matched/total:	# ions: 52%	intensity: 28%		σ: 0.10 Da		
bond	⁺¹ y	+1y-17	⁺¹ Y ⁻¹⁸	+1b	+1b-17	+1b-18
E1	2199.067	2182.04	2181.056	130.05	113.023	112.039
S ₂	2112.035	2095.008	2094.024	217.082	200.055	199.071
F ₃	1964.966	1947.94	1946.956	364.15	347.124	346.14
S_4	1877.934	1860.908	1859.924	451.182	434.156	433.172
A ₅	1806.897	1789.87	1788.886	522.22	505.193	504.209
N ₆	1692.854	1675.828	1674.844	636.262	619.236	618.252
Q ₇	1564.796	1547.769	1546.785	764.321	747.295	746.311
I ₈	1451.711	1434.685	1433.701	877.405	860.379	859.395
V ₉	1352.643	1335.617	1334.632	976.474	959.447	958.463
T ₁₀	1251.595	1234.569	1233.585	1077.521	1060.495	1059.511
E ₁₁	1122.553	1105.526	1104.542	1206.564	1189.537	1188.553
S ₁₂	1035.521	1018.494	1017.51	1293.596	1276.569	1275.585
S ₁₃	703.399	686.372	685.388	1625.718	1608.691	1607.707
L ₁₄	590.315	573.288	572.304	1738.802	1721.775	1720.791
V ₁₅	491.246	474.22	473.236	1837.87	1820.844	1819.86
T ₁₆	390.199	373.172	372.188	1938.918	1921.891	1920.907
D ₁₇	275.172	258.145	257.161	2053.945	2036.918	2035.934
A18	204.135	187.108	186.124	2124.982	2107.955	2106.971
G ₁₉	147.113	130.087	129.103	2182.003	2164.977	2163.993

Other observed ions:

lon type	m/z
by[4-11]	843.421
by[12-19]	976.447
(parent-2H ₂ O) ⁺²	1146.548
by[10-19]	1206.537
ay[7-16]	1275.668
by[5-12]	843.421
ay[8-15]	1046.562
(parent-H ₂ O) ⁺²	1155.553
ay[4-13]	1234.58



Supplemental Figure 2d

Supplemental Figure 3a

STSISEVSNILETQASLTDK nude m/z =1062.54 (z=2) scan 2385 RT 28.81



STSISEVSNILETQASLTDK +(HexNAc) m/z =1163.57 (z=2), scan 2383 RT 27.22



Supplemental Figure 3c

STSISEVSNILETQASLTDK +(HexNAc)₂ m/z=1265.61 z=2, scan 2299 RT 26.53



Supplemental Figure 3d

STSISEVSNILETQASLTDK +(HexNAc)₃ m/z= 912.11, z=3, scan 2245 RT 26.13



Supplemental Figure 3e

STSISEVSNILETQASLTDK +(HexNAc)₄ m/z= 979.46 z=3, scan 1946 RT 23.83



STSISEVSNILETQASLTDK + $(\text{HexNAc})_4$ (Hex)₂ m/z= 1088.17 z=3, scan 1883 RT 23.36



Supplemental Figure 3g

STSISEVSNILETQASLTDK + $(\text{HexNAc})_4$ (Hex)₃ m/z= 1141.85 z=3, scan 1877 RT 23.30



STSISEVSNILETQASLTDK +(AcHexNAc) m/z= 790.39 z=3, scan 2345 RT 26.89



Supplemental Figure 3i

STSISEVSNILETQASLTDK +(AcHexNAc) +(HexNAc) m/z= 857.75 z=3, scan 2338 RT 26.84



STSISEVSNILETQASLTDK +(AcHexNAc) +(HexNAc)₂ m/z= 926.44 z=3, scan 2330 RT 26.77



Supplemental Figure 3k

STSISEVSNILETQASLTDK +(AcHexNAc) +(HexNAc)₃ m/z= 993.80 z=3, scan 2048 RT 24.62



ESFSANQIVTESSLVTDAGK nude m/z= 1042.51 z=2, scan 2178 RT 25.60



ESFSANQIVTESSLVTDAGK +(HexNAc) m/z= 1143.55 z=2, scan 2113 RT 25.12



ESFSANQIVTESSLVTDAGK +(AcHexNAc) m/z=1165.05 z=2, scan 2197 RT 25.75



Supplemental Figure 30

NASVSSLIEITKPK nude m/z= 743.93 z=2, scan 1601 RT 21.04



NASVSSLIEITKPK +(HexNAc) m/z= 845.46 z=2, scan 1498 RT 20.21



Supplemental Figure 3q

NASVSSLIEITKPK +(HexNAc)₂ m/z 631.67 z=3, scan 1340 RT 18.91



TGNESLTPTIR +(HexNAc) z=2 m/z= 696.85 z=2, scan 1045 RT 16.51



Supplemental Figure 3s

SQVMIASDKTGNESLTPTIR nude m/z= 722.04 z=3, scan 1348 RT 19.75



SQVMIASDKTGNESLTPTIR +(HexNAc) m/z= 789.73 z=3, scan 1316 RT 19.47





Supplemental Figure 4



Supplemental Figure 5a S192TSISEVSNILETQASLTDK211 SpectrumFinder Reference m/z= 1062.04 (+2) ech 96, scan 9577 SpectrumFinder score: 0.00E+00 Precision: 0.37 ppm

Supplemental Figure 5b S192TSISEVSNILETQASLTDK211 + 2 HexNAc m/z= 843.7487 (+3) ech 96, scan 8871 SpectrumFinder score: 3.25E-09 Precision: 0.04 ppm

2500



Supplemental Figure 5c S192TSISEVSNILETQASLTDK211 + 3 HexNAc m/z= 911.4419 (+3) ech 96, scan 8853 SpectrumFinder score: 1.61E-04 Precision: 0.26 ppm



100



Supplemental Figure 5d S192TSISEVSNILETQASLTDK211 + 1 HexNAc m/z= 776.0549 (+3) ech 96, scan 9429 SpectrumFinder score: 1.08E-09 Precision: -0.56 ppm

Supplemental Figure 5e S192TSISEVSNILETQASLTDK211 + 4 HexNAc m/z= 1468.2003 (+2) ech 96, scan 8385 SpectrumFinder score: 1.31E-03 Precision: -0.41 ppm



100

95

90

85

80



Supplemental Figure 5f S192TSISEVSNILETQASLTDK211

+ 1 O-AcHexNAc + 2 HexNAc m/z= 925.4456 (+3) ech 96, scan 9111 SpectrumFinder score: 5.51E-06 Precision: -0.33 ppm



Supplemental Figure 5g S192TSISEVSNILETQASLTDK211 + 4 HexNAc + 2 Hex m/z= 1087.1693 (+3) ech 96, scan 7581 SpectrumFinder score: 4.61E-03 Precision: -0.64 ppm


Supplemental Figure 5h S192TSISEVSNILETQASLTDK211 + 1 O-AcHexNAc + 1 HexNAc m/z= 857.7518 (+3) ech 96, scan 9293 SpectrumFinder score: 6.73E-08 Precision: -0.21 ppm



Supplemental Figure 5i S192TSISEVSNILETQASLTDK211 + 1 O-AcHexNAc + 3 HexNAc m/z= 1489.2051 (+2) ech 96, scan 8145 SpectrumFinder score: 4.62E-02 Precision: 1.03 ppm



Supplemental Figure 5j S192TSISEVSNILETQASLTDK211 + 1 O-AcHexNAc + 3 HexNAc + 2 Hex m/z= 1101.1737 (+3) ech 96, scan 7777



Supplemental Figure 5k S192TSISEVSNILETQASLTDK211 + 1 O-AcHexNAc m/z= 790.0579 (+3) ech 96, scan 9175 SpectrumFinder score: 7.42E-10 Precision: -0.88 ppm



Supplemental Figure 51 S192TSISEVSNILETQASLTDK211 + 4 HexNAc + 3 Hex m/z= 1141.1898 (+3) ech 96, scan 7547 SpectrumFinder score: 1.13E-03 Precision: 1.91 ppm

3500



Supplemental Figure 5m S192TSISEVSNILETQASLTDK211 + 5 HexNAc + 2 Hex m/z= 1154.8633 (+3) ech 96, scan 7241 SpectrumFinder score: Manual detection Precision: NA



Supplemental Figure 5n S192TSISEVSNILETQASLTDK211 + 2 O-AcHexNAc + 1 HexNAc m/z= 939.4503 (+3) ech 96, scan 9195 SpectrumFinder score: 1.31E-03 Precision: 1.79 ppm





Supplemental Figure 5p S192TSISEVSNILETQASLTDK211 + 2 O-AcHexNAc m/z= 871.7542 (+3) ech 96, scan 9390 SpectrumFinder score: 1.13E-05 Precision: -0.85 ppm



Supplemental Figure 5q S₁₉₂TSISEVSNILETQASLTDK₂₁₁ + 1 *O*-AcHexNAc + 4 HexNAc m/z= 1060.8307 (+3) ech 96, scan 7801 SpectrumFinder score: Manual detection Precision: NA



Supplemental Figure 5r E₂₁₄SFSANQIVTESSLVTDAGK₂₃₃ SpectrumFinder reference m/z= 1042.0123 (+2) ech 96_01, scan 8526 SpectrumFinder score: 1.11E-16 Precision: -0.47 ppm



Supplemental Figure 5s E₂₁₄SFSANQIVTESSLVTDAGK₂₃₃ + 1 HexNAc m/z= 1143.5543 (+2) ech 96_01, scan 8238 SpectrumFinder score: 0.00E+00 Precision: 0.95 ppm



Supplemental Figure 5t

E₂₁₄SFSANQIVTESSLVTDAGK₂₃₃ + 1 *O*-AcHexNAc m/z= 776.707 (+3) ech 96_01, scan 8433 SpectrumFinder score: 0.00E+00 Precision: -0.75 ppm



Supplemental Figure 5u E₂₁₄SFSANQIVTESSLVTDAGK₂₃₃ + 2 HexNAc m/z= 1245.0939 (+2) ech 96_01, scan 7636 SpectrumFinder score: 9.07E-05 Precision: 1.03 ppm

2500



Supplemental Figure 5v

2500

E₂₁₄SFSANQIVTESSLVTDAGK₂₃₃ + 1 *O*-AcHexNAc + 1 HexNAc m/z= 844.3998 (+3) ech 96_01, scan 7926 SpectrumFinder score: 1.21E-07 Precision: -0.68 ppm



Supplemental Figure 5w

N₂₃₄ASVSSLIEITKPK₂₄₇ SpectrumFinder reference m/z= 743.9276 (+2) ech 96_01, scan 7059 SpectrumFinder score: 6.66E-16 Precision: -1.17 ppm



Supplemental Figure 5x

Peptide 1486.8503 N₂₃₄ASVSSLIEITKPK₂₄₇ + 1 HexNAc m/z= 845.4673 (+2)) ech 96_01, scan 6994 SpectrumFinder score: 1.11E-16 Precision: 0.12 ppm





Supplemental Figure 5z

M₂₅₅SNESLITPEK ₂₆₅ SpectrumFinder reference m/z= 624.8124 (+2) SpectrumFinder score: 0.00E+00 Precision: 1.89 ppm



Supplemental Figure 5aa

M₂₅₅SNESLITPEK ₂₆₅ + 1 HexNAc + Oxid. Methionine m/z= 734.3477 (+2) ech 96, scan 4524 SpectrumFinder score: 5.71E-09 Precision: -0.90 ppm



Supplemental Figure 5ab

1400

S₂₆₆QVMIASDKTGNESLTPTIR₂₈₅ SpectrumFinder reference m/z= 716.704 (+3) ech 96, scan 5122 SpectrumFinder score: 3.33E-16 Precision: -0.35 ppm



Supplemental Figure 5ac T₂₇₅GNESLTPTIR₂₈₅ + 1 HexNAc m/z= 696.3559 (+2) ech 96, scan 4797 SpectrumFinder score: 2.01E-07 Precision: 1.53 ppm



T₂₇₅GNESLTPTIR₂₈₅ + 1 *O*-AcHexNAc m/z= 717.359 (+2) ech 96, scan 5481 SpectrumFinder score: 0.00E+00 Precision: 0.00 ppm

Supplemental Figure 5ad



Supplemental Figure 5ae

T₄₄₇ATLNNQVASIEER₄₆₄ SpectrumFinder reference m/z= 773.3971 (+2) ech 96_01, scan 5875 SpectrumFinder score: 4.20E-05 Precision: -0.60 ppm





Supplemental Figure 5ag

2000

T₄₄₇ATLNNQVASIEER₄₆₄ + 2 *O*-AcHexNAc m/z= 679.6598 (+3) ech 96_01, scan 8518 SpectrumFinder score: 2.77E-03 Precision: -5.53 ppm

Supplemental Figure 6







Supplemental Figure 7







Z16 Z15 Z14 Z13 Z12 Z11 Z10 Z9 Z8 Z7 Z6 **Y**4 Z5 A D K S S T S S Q Т E Ν Ε <u>S</u> L C11 C15 C16 C7 C9 C12 Сз C5 C8 C10 C14







m/z












Z12 Z11 Z10 Z9 Z6 Z13 Z8 Z7 Z5 Ζ4 Z3 Z2 S E Ν 0 Е V Ν R T C5 Ce C1 Сз C4 C12 C13

