Multiglycan issues

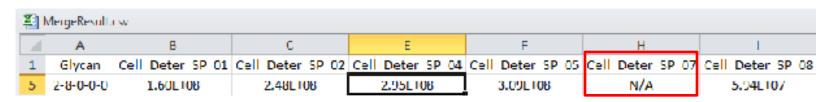
Batch Mode Issue

- The batch mode is not able to handle more than 15 raw files simultaneously. As you can see in the "MergeResult.csv", we tried to process 18 raw files together, the last file shows "N/A" for all glycans. (Some times last two or three samples are all "N/A". In other cases, Multiglycan crushed with >15 files loading.)
- The "pic" folders do not contain all the peak construction information, when batch mode is used. (Most of time, only several of the "pic" folders are empty. The ones we uploaded is the worst case, only "Cell_Deter_SP_01" has 3 pictures.)

Quantitation Issue

- There are two issues with the newest version of Multiglycan.
- 1. Some peaks are not picked.
- 2. Some quantitation results agreed with Xcalibur while some quantitation results did not.
- Examples are shown in the following slides.

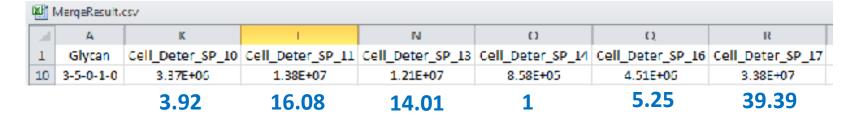
Issue Type 1



EICs of [28000+2H]2+

Clear Peak

Issue Type 2: quantitation of same glycan in different files (Multiglycan and Xcarlibur gives different ratio)



2.56

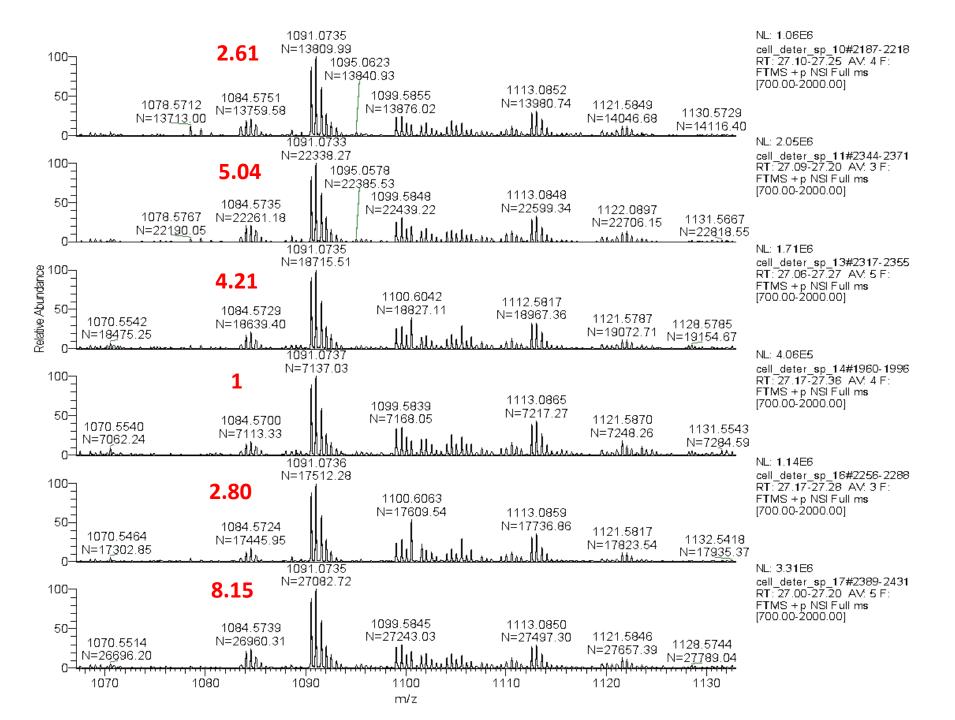
4.78

5.08

1

2.73

9.68



Issue Type 2: quantitation of same glycan in different files (Multiglycan and Xcarlibur gives similar ratio)

al	A	K	T.	N	O	Q	R
1	Glycan	Cell_Deter_SP_10	Cell_Deter_SP_11	Cell_Deter_SP_13	Cell_Deter_SP_1/I	Cell_Deter_SP_16	Cell_Deter_SP_17
2	2-5-0-0-0	1.35E+09	2.11E+09	1.63E+09	4.56E+08	9.50E+08	2.94E+09
		2.96	4.62	3.57	1	2.08	6.44

2.48

3.82

3.06

1

1.68

4.66