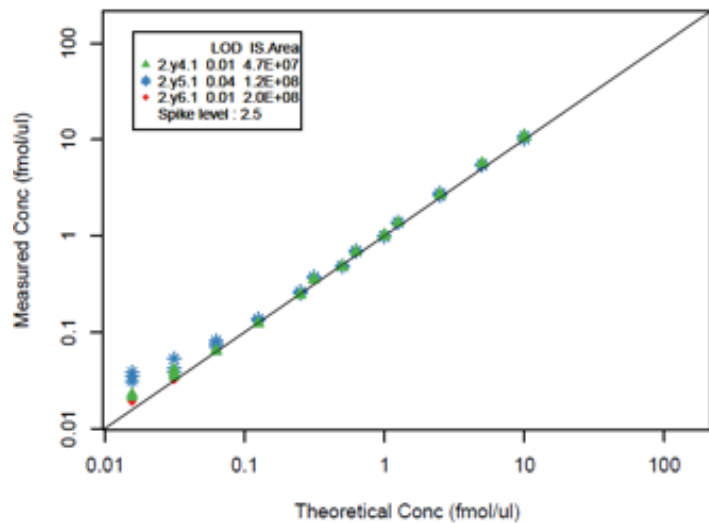
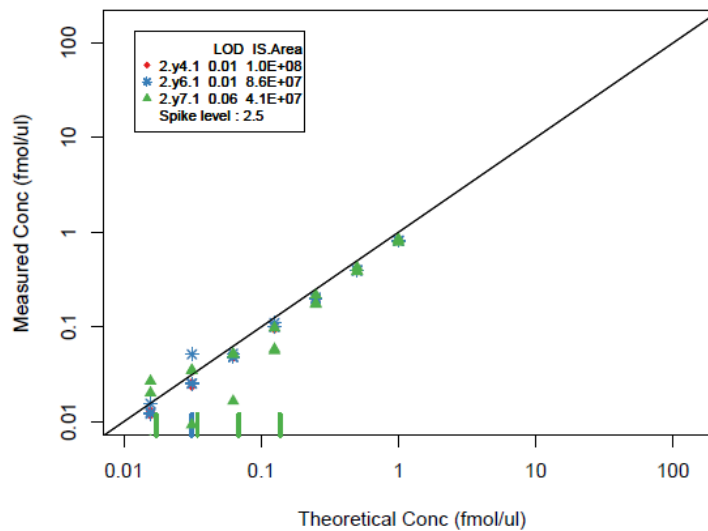


Figure S1. Detection of PD-L1 peptides in long gradient LC-PRM analyses of unfractionated digests from FFPE melanomas.

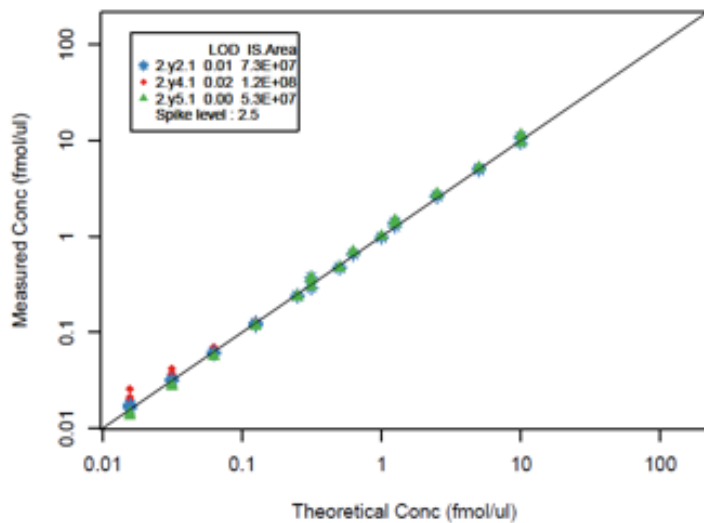
Data points for PD1L1
Peptide: LQDAGVYR



Data points for PD1|NP_005009.2|
Peptide: LAAFPEDR



Data points for PD1L1
Peptide: VNAPYNK



Data points for PDL2
Peptide: TPEGLYQVTSVLR

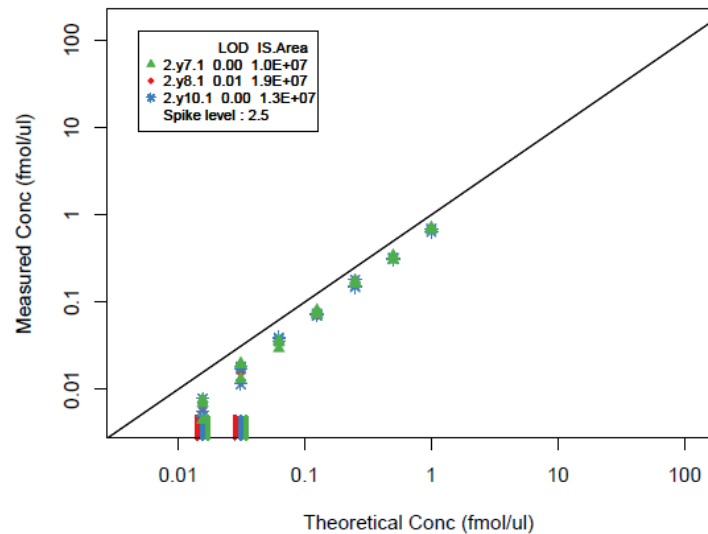


Figure S2. SID calibration curves

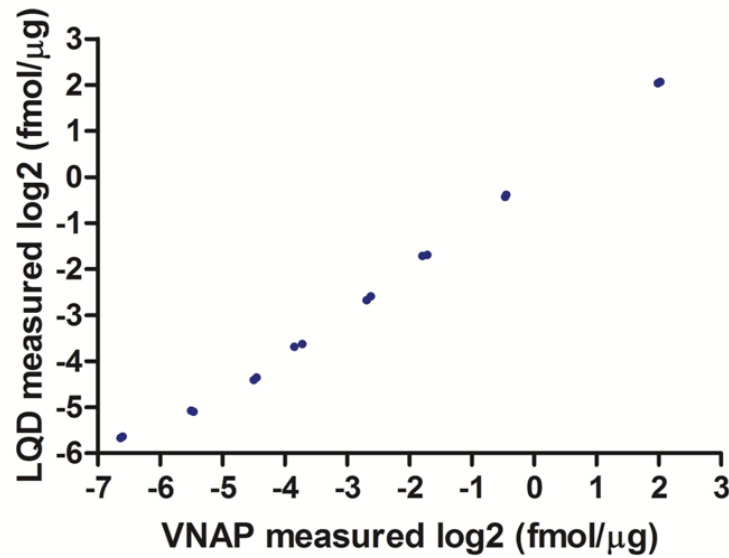
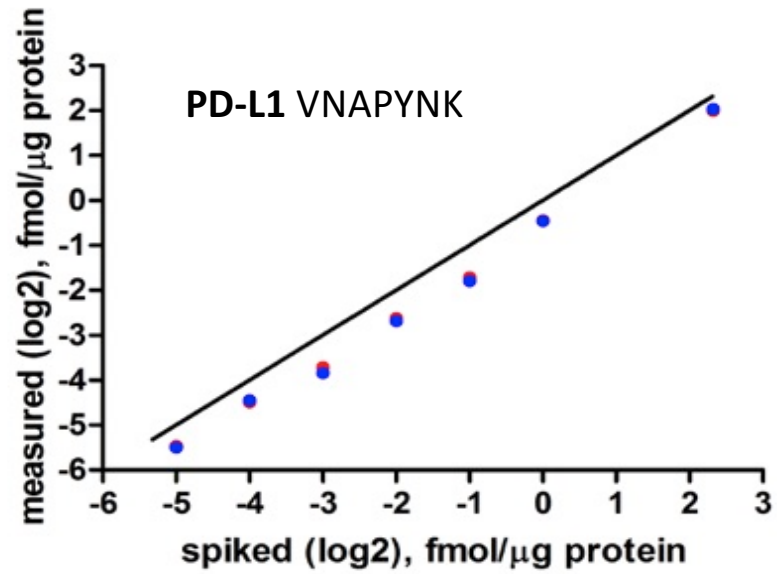
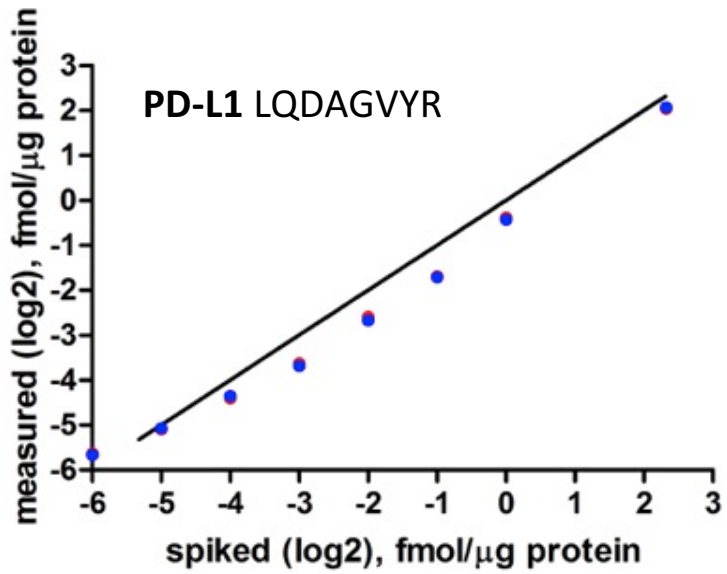
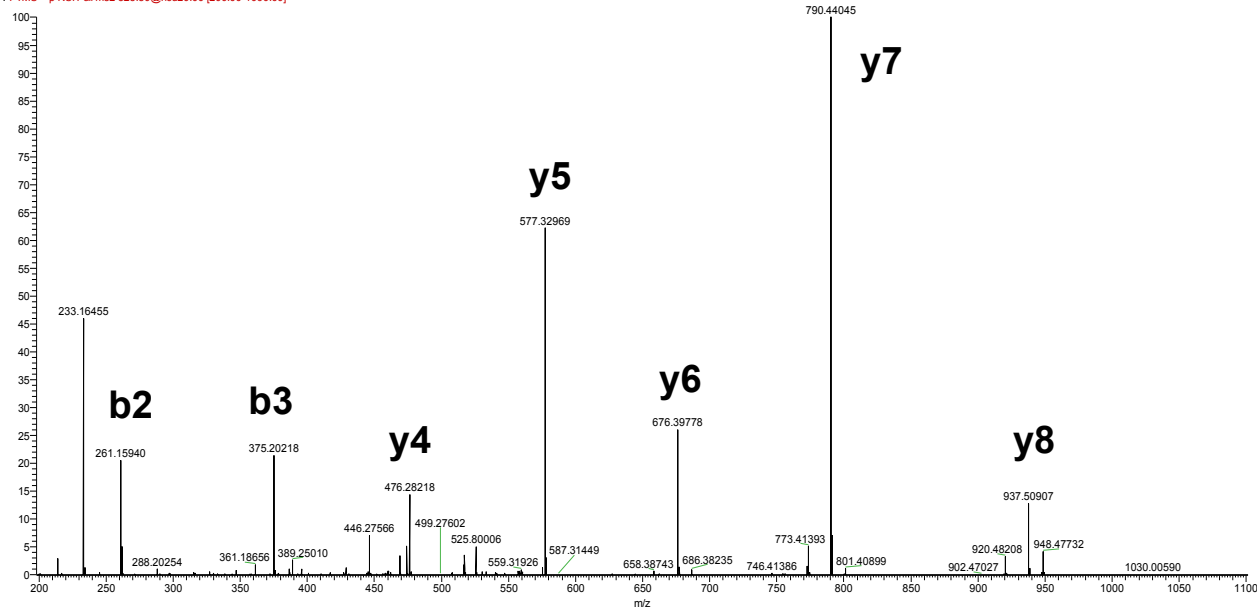


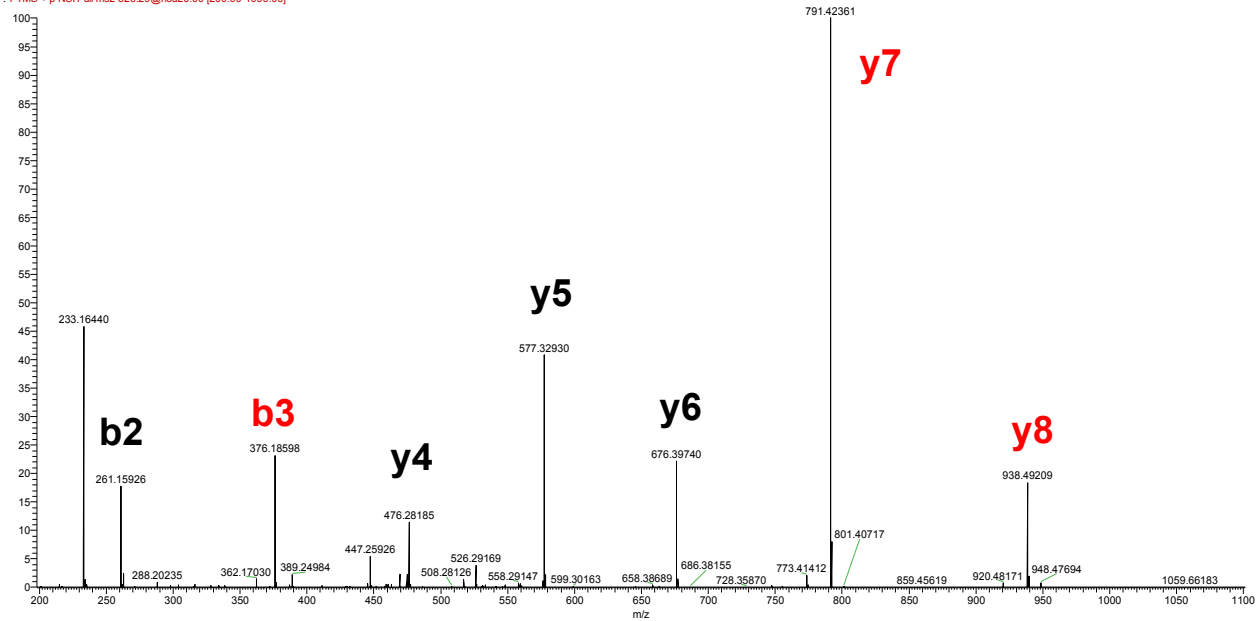
Figure S3. Spike recovery study for recombinant human PD-L1 100 μ g HEK293 cell lysate 0.031, 0.063, 0.125, 0.25, 0.5, 1 or 5 fmol/microgram protein.

061116_PDL1_PNG_25ng #9055-9082 RT: 42.35-42.45 AV: 4 NL: 2
F: FTMS + p NSI Full ms2 525.80@hcd20.00 [200.00-1090.00]



LFNVTSTLR

061116_PDL1_PNG_25ng #9354-9400 RT: 43.74-43.91 AV: 7 NL: 1.82
F: FTMS + p NSI Full ms2 526.29@hcd20.00 [200.00-1090.00]

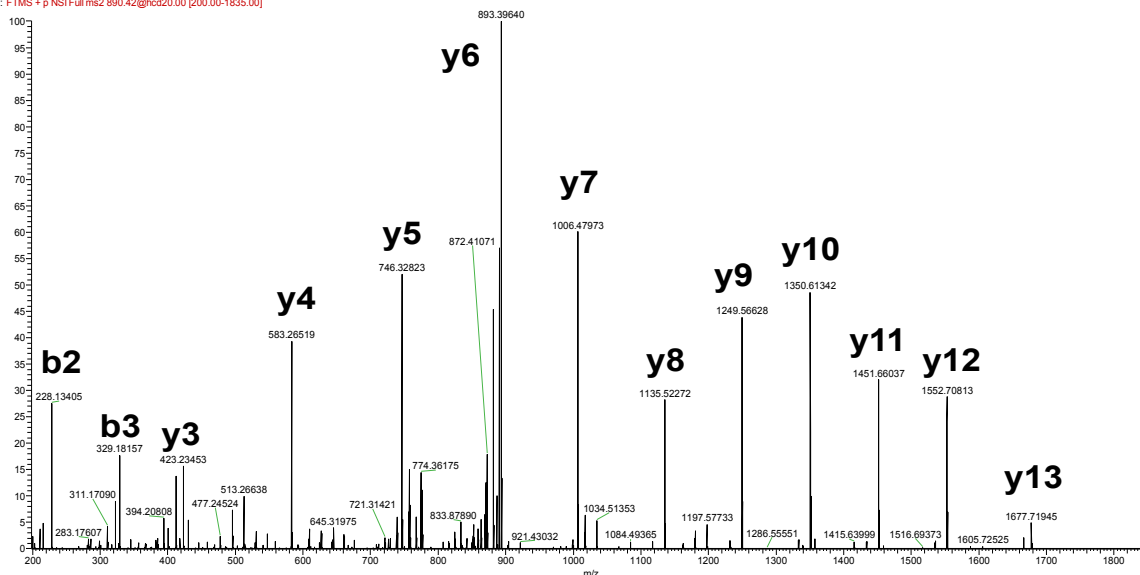


LFDVTSTLR

(fragments with m/z shift
from N → D substitution
labeled in red)

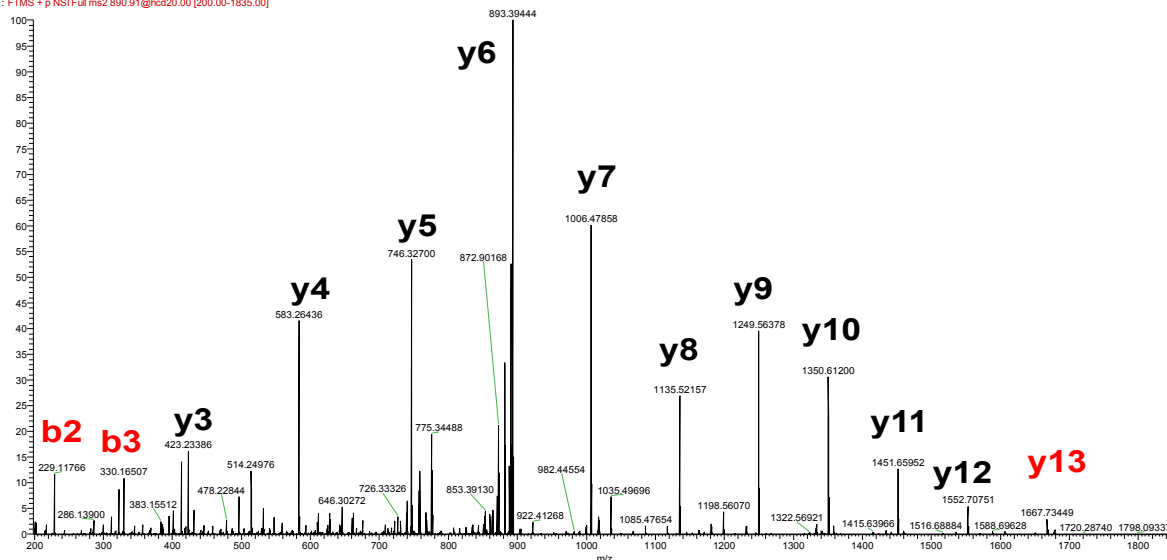
Figure S4. MS/MS spectra of PD-L1 LFNVTSTLR peptide and LFDVTSTLR peptide released by PNGase F treatment of recombinant human PD-L1 tryptic digest.

061116_PDL1_PNG_25ng #10437-10483 RT: 48.82-48.98 AV: 6 NL: 1
F: FTMS + p NSI Full ms2 890.42@hcd20.00 [200.00-1835.00]



INTTTNEIFYCTFR

061116_PDL1_PNG_25ng #10640-10699 RT: 49.75-50.01 AV: 9 NL: 4
F: FTMS + p NSI Full ms2 890.91@hcd20.00 [200.00-1835.00]

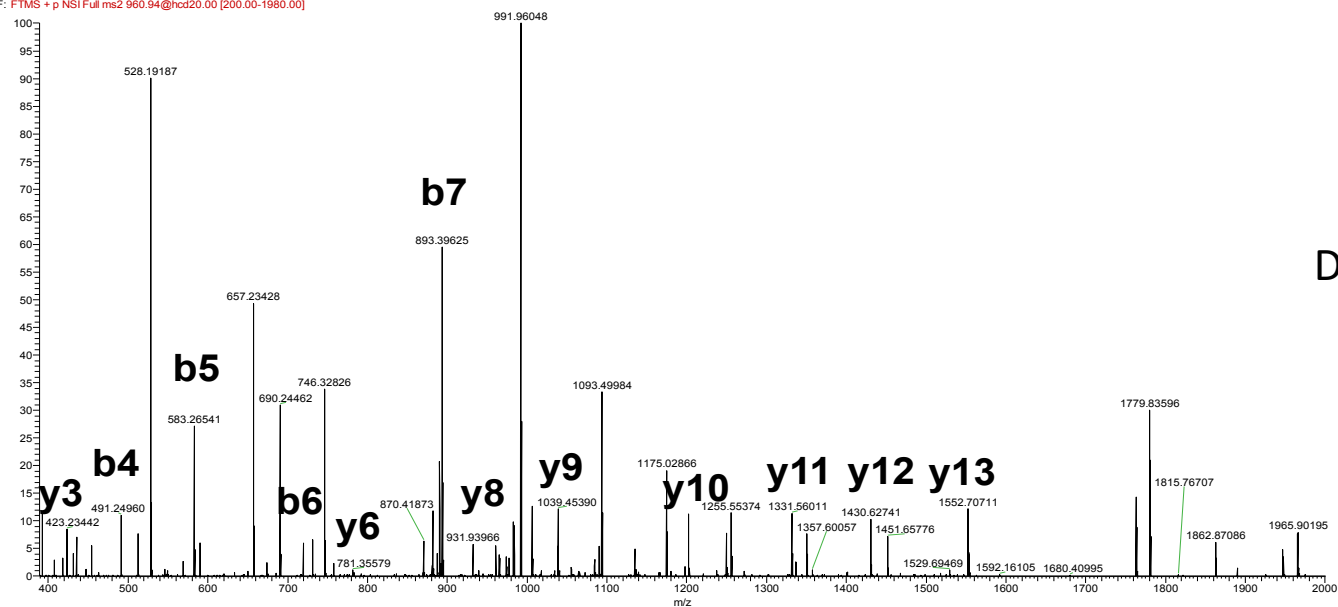


IDTTTNEIFYCTFR

(fragments with m/z shift
from N → D substitution
labeled in red)

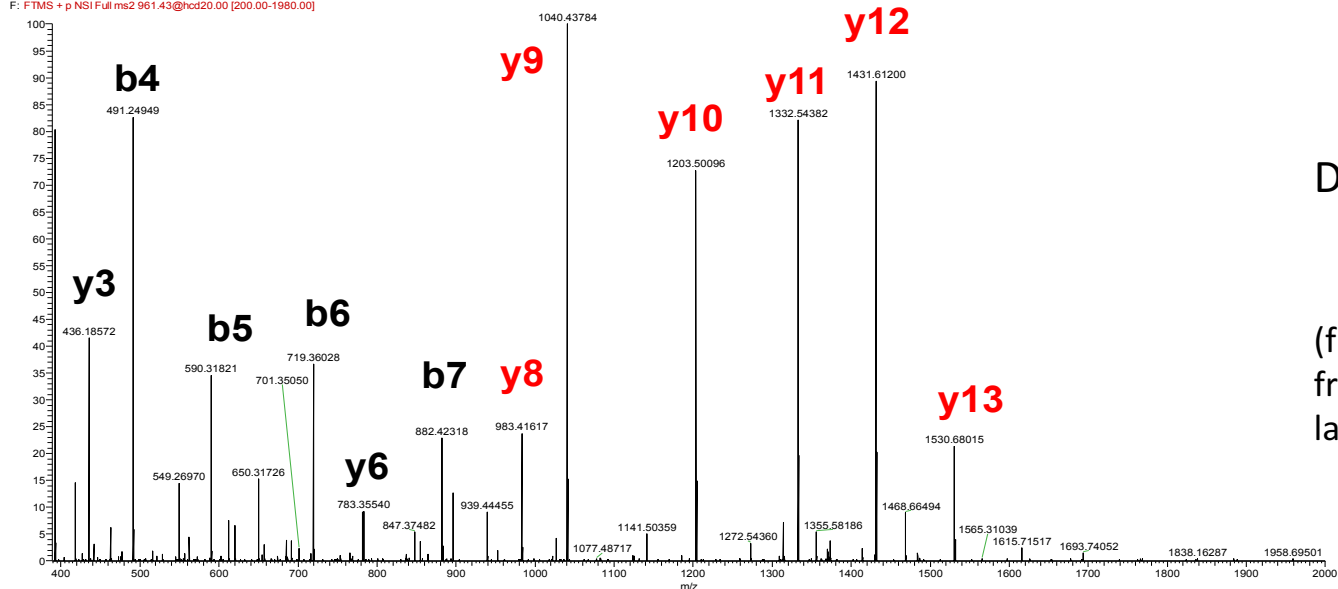
Figure S5. MS/MS spectra of PD-L1 INTTTNEIFYCTFR peptide and L1 IDTTTNEIFYCTFR peptide released by PNGase F treatment of recombinant human PD-L1 tryptic digest.

061116_PDL1_PNG_25ng #10064-10138 RT: 47.04-47.37 AV: 11 NL: 1
F: FTMS + p NSI Full ms2 960.94@hcd20.00 [200.00-1980.00]



DLYVVEYGSNMEIECK

061116_PDL1_PNG_25ng #10315-10362 RT: 48.21-48.41 AV: 7 NL: 2
F: FTMS + p NSI Full ms2 961.43@hcd20.00 [200.00-1980.00]

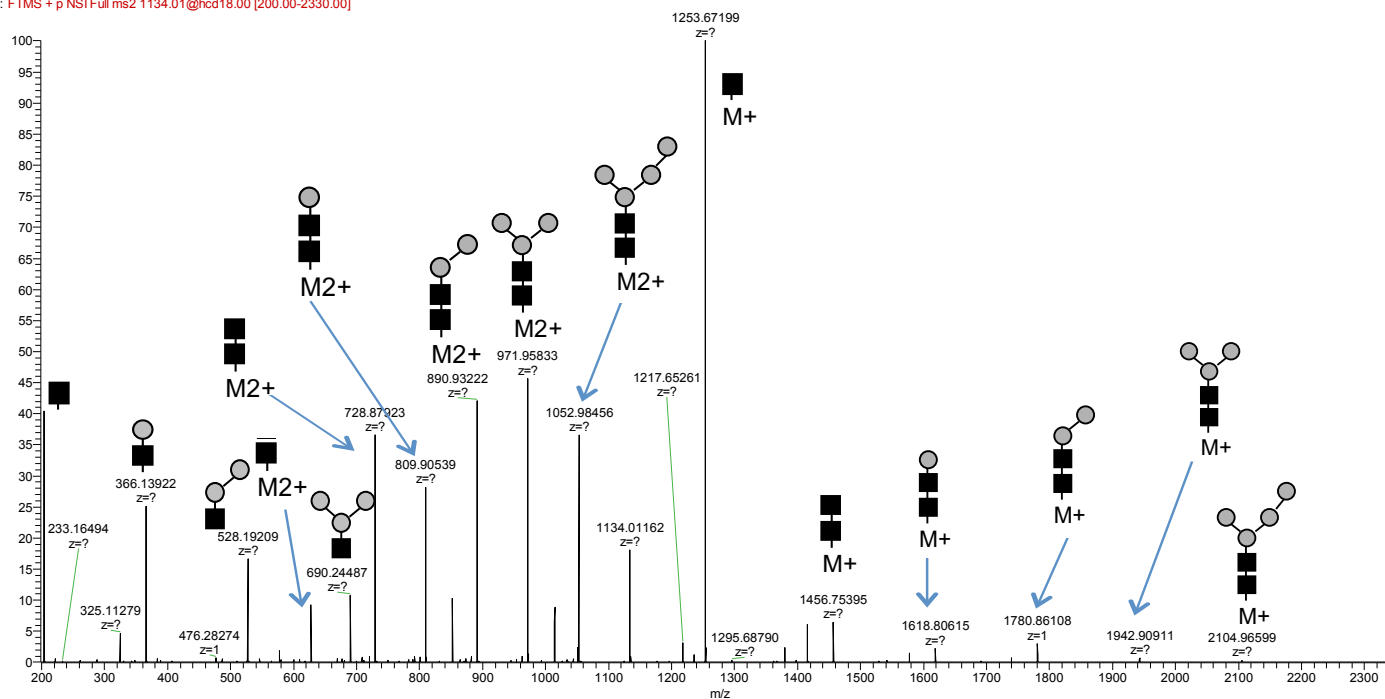


DLYVVEYGS DMEIECK

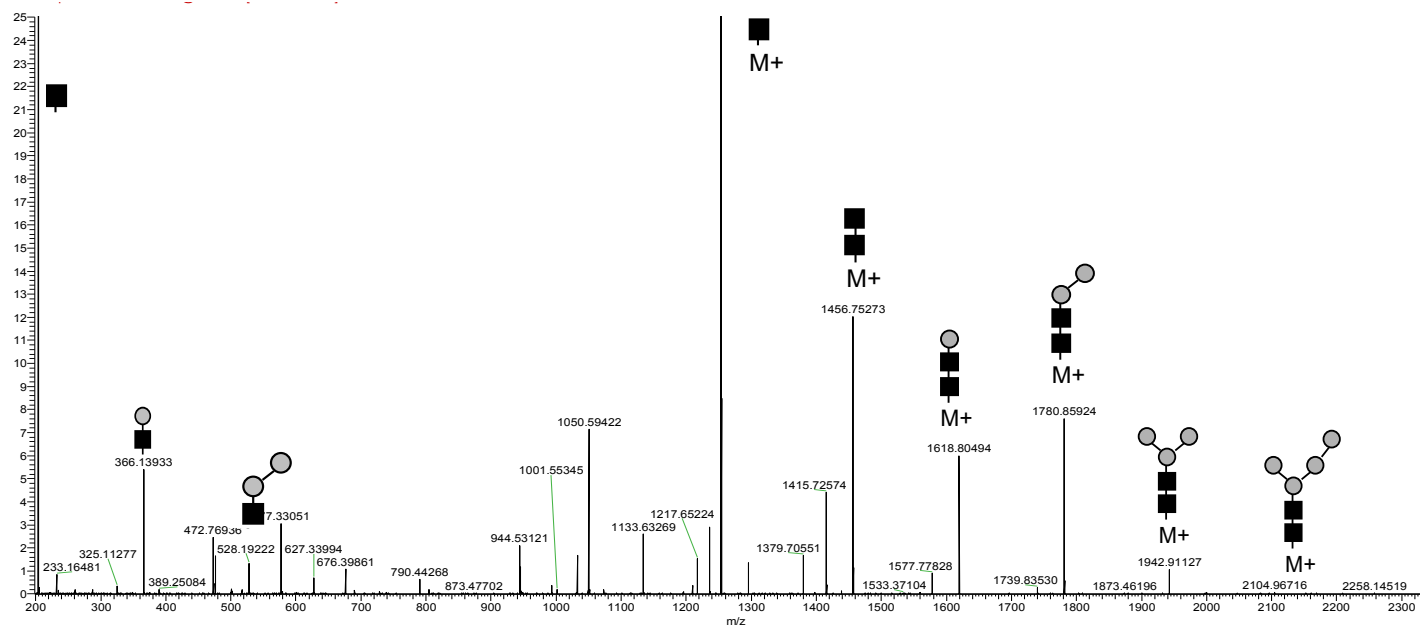
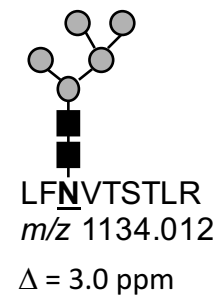
(fragments with m/z shift from N → D substitution labeled in red)

Figure S6. MS/MS spectra of PD-L1 DLYVVEYGSNMEIECK peptide and L1 DLYVVEYGS DMEIECK peptide released by PNGase F treatment of recombinant human PD-L1 tryptic digest.

161019_LFN_All_glyco_#2686-2706 RT: 7.15-7.18 AV: 2 NL: 4.48E7
F: FTMS + p NSI Full ms2 1134.01@hcd18.00 [200.00-2330.00]

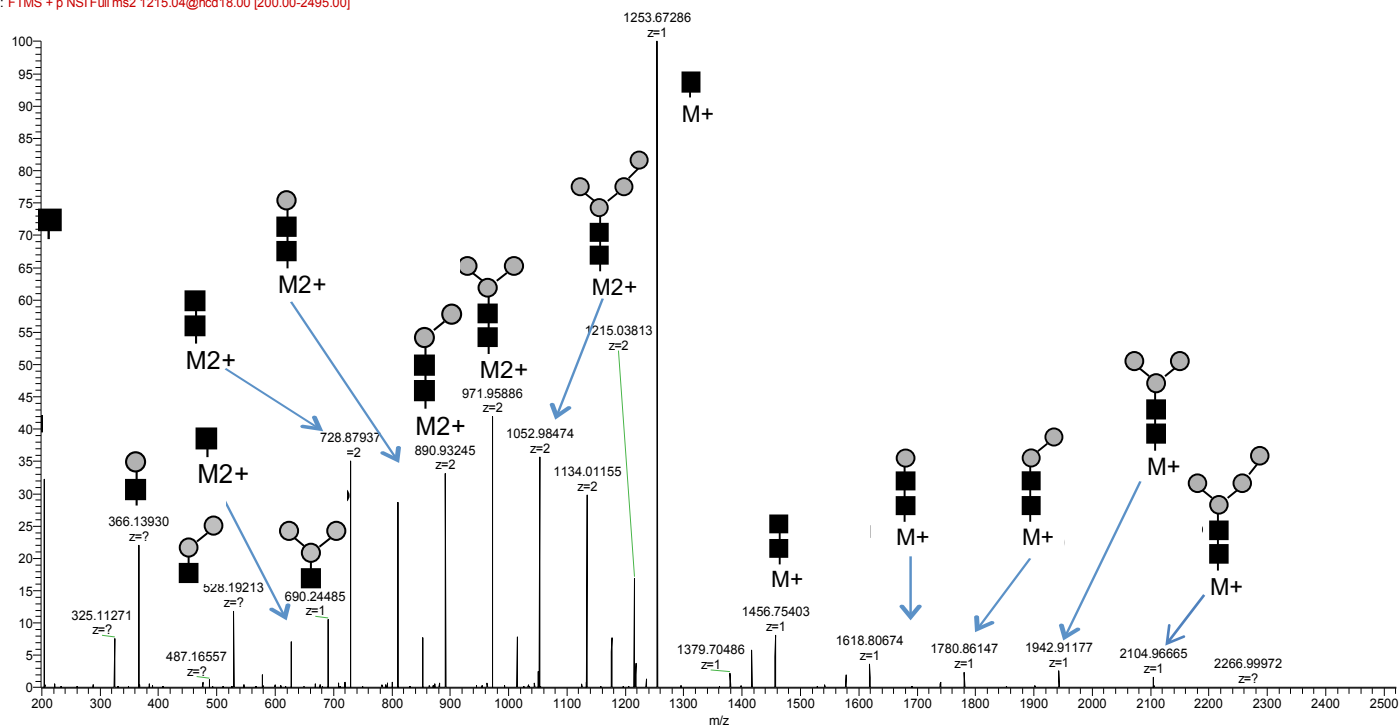


Recomb PD-L1

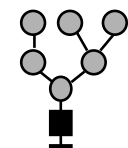


Melanoma B14

Figure S7



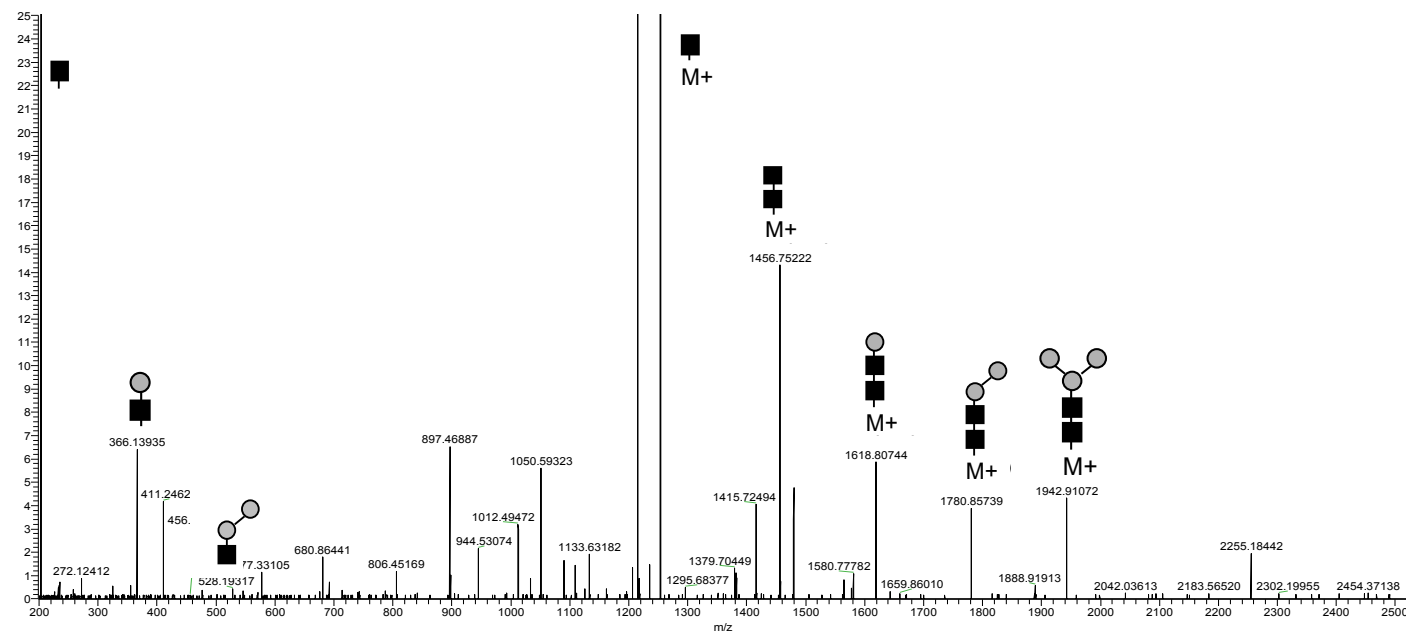
Recomb PD-L1



LFNVTSTLR

m/z 1215.0386 (+2)

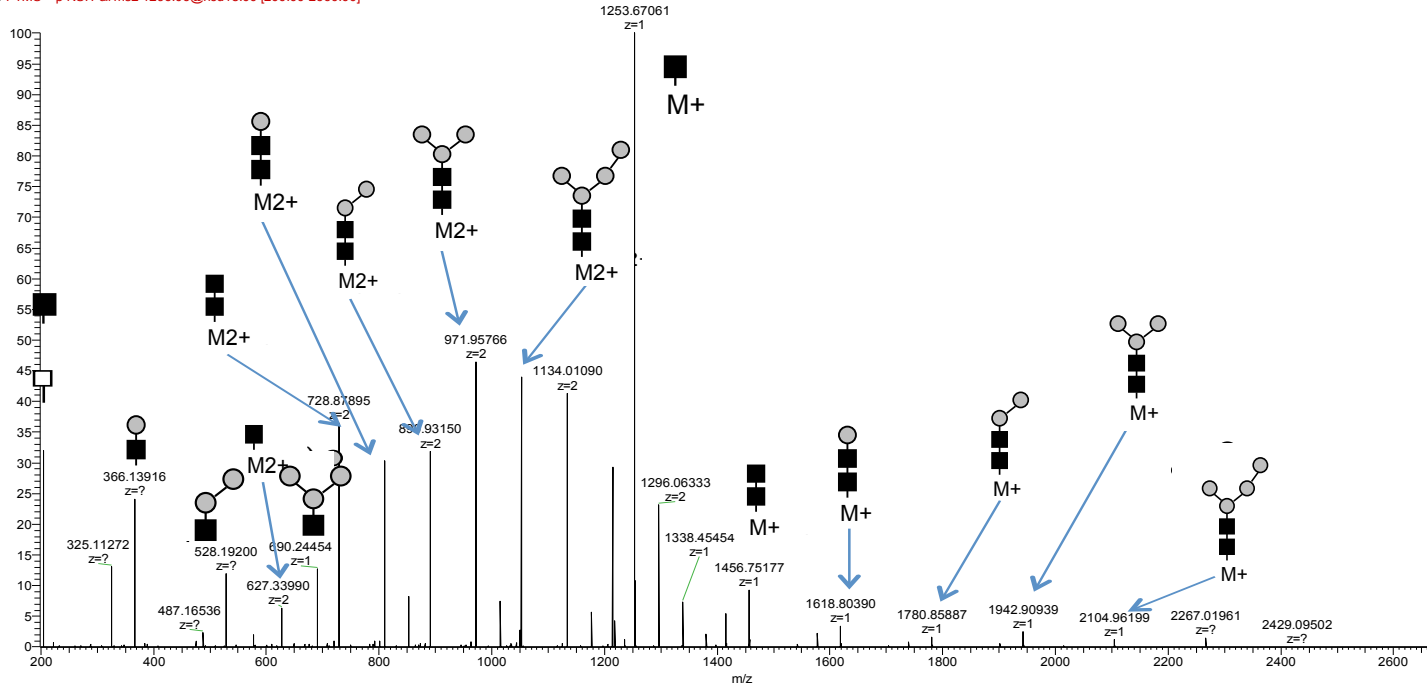
$\Delta = 2.9$ ppm



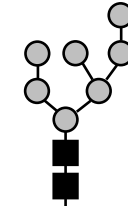
Melanoma B14

Figure S8

161019_LFN_All_glyco #2661-2689 RT: 7.10-7.16 AV: 3 NL: 1.35E7
 F: FTMS + p NSI Full ms2 1296.06@hcd18.00 [200.00-2660.00]

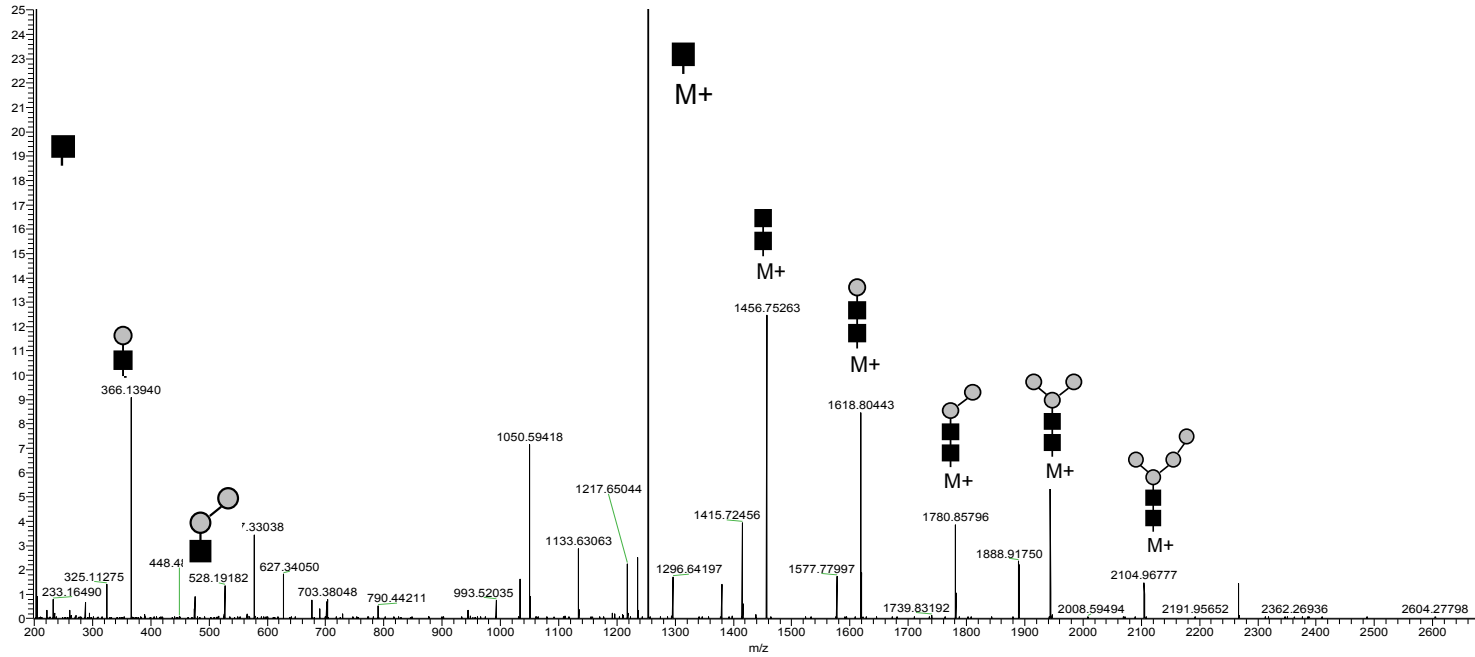


Recomb PD-L1



LFNVTSTLR
 m/z 1296.065 (+2)

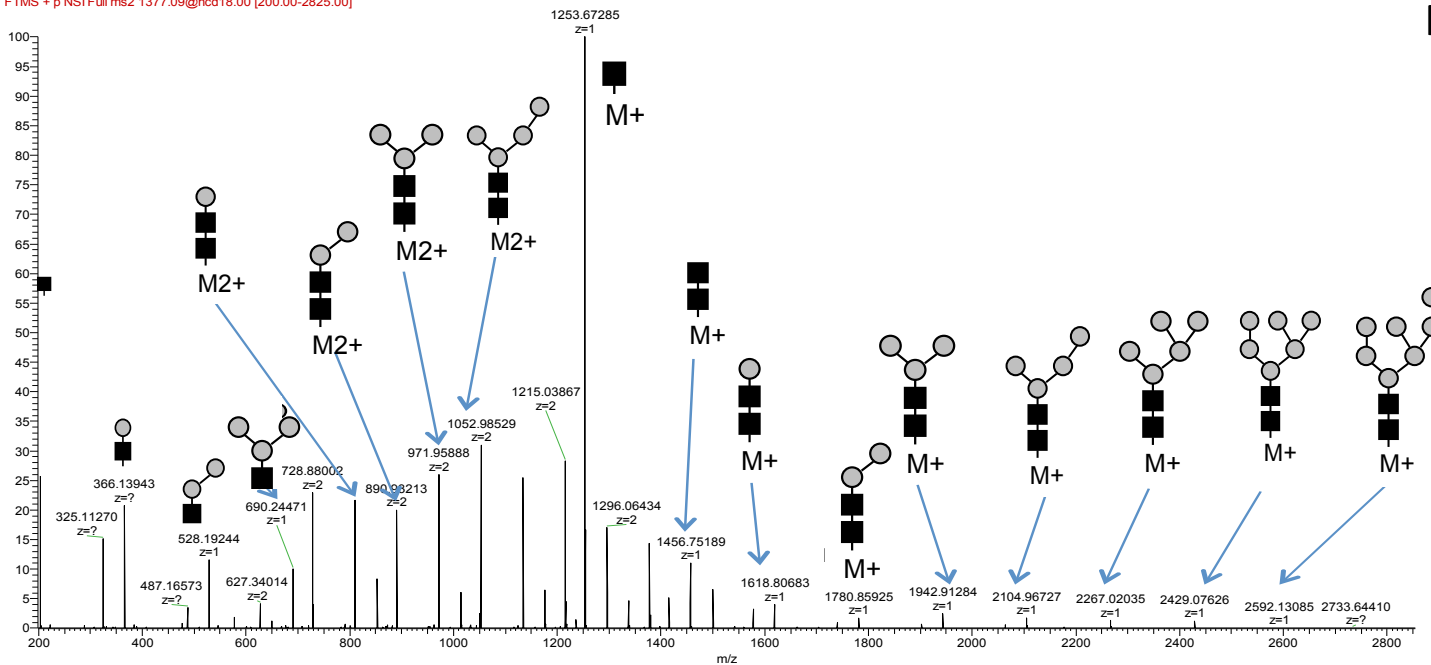
$\Delta = 3.0$ ppm



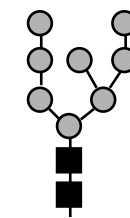
Melanoma B14

Figure S9

161019_LFN_All_glyco #2656-2683 RT: 7.07-7.13 AV: 3 NL: 2.53E6
F: FTMS + p NSI Full ms2 1377.09@hcd18.00 [200.00-2825.00]



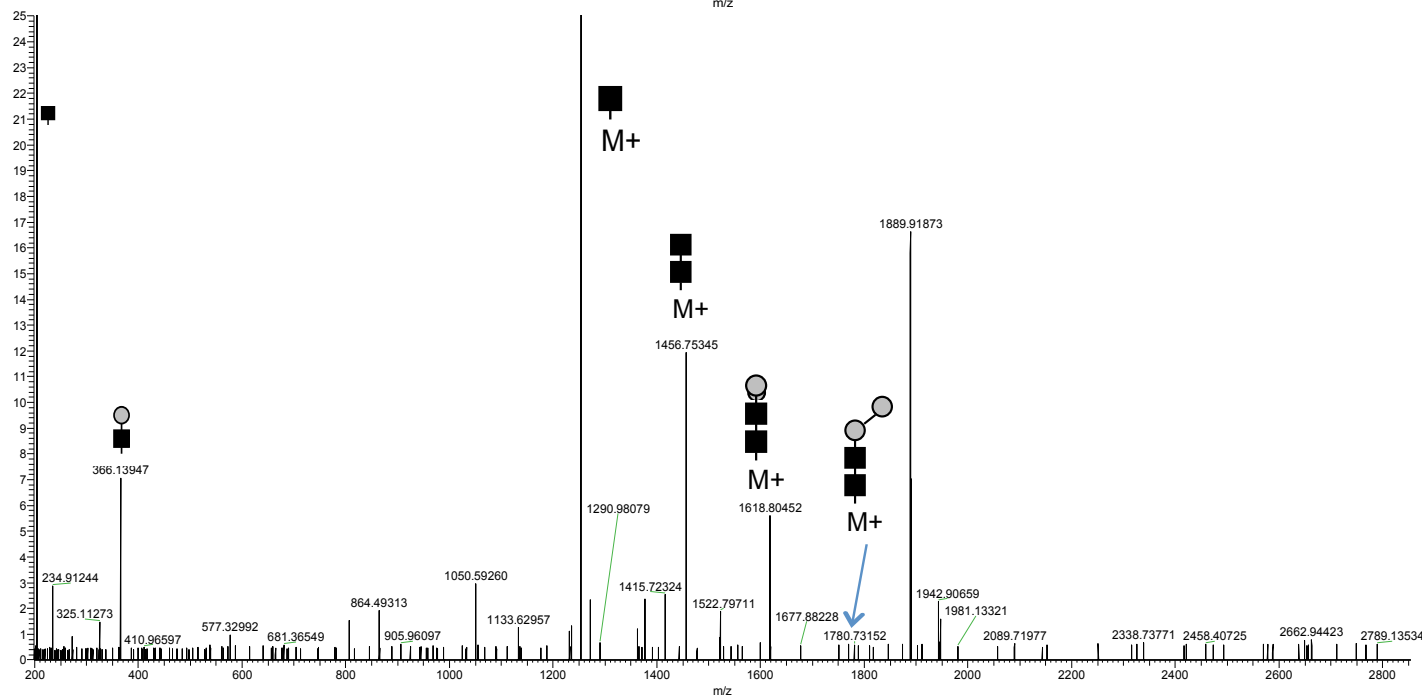
Recomb PD-L1



LFNVTSTLR

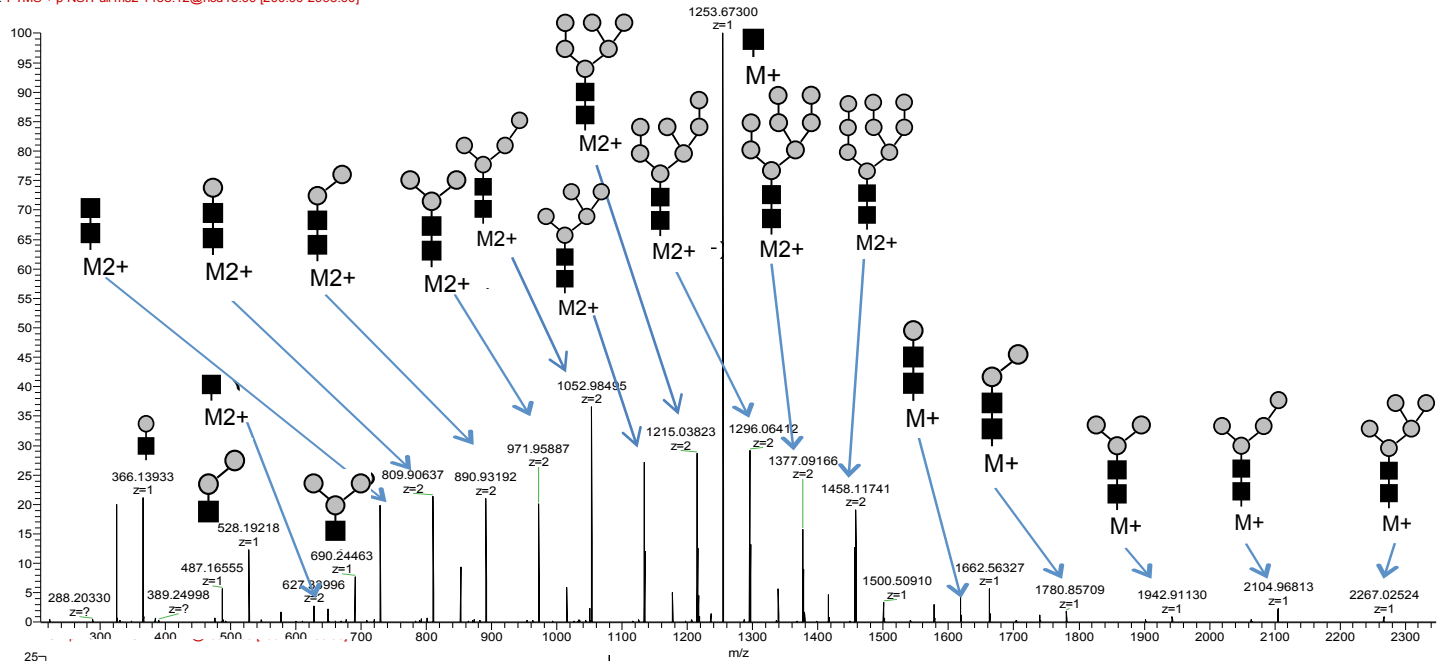
m/z 1377.0914 (+2)

$\Delta = 2.5$ ppm

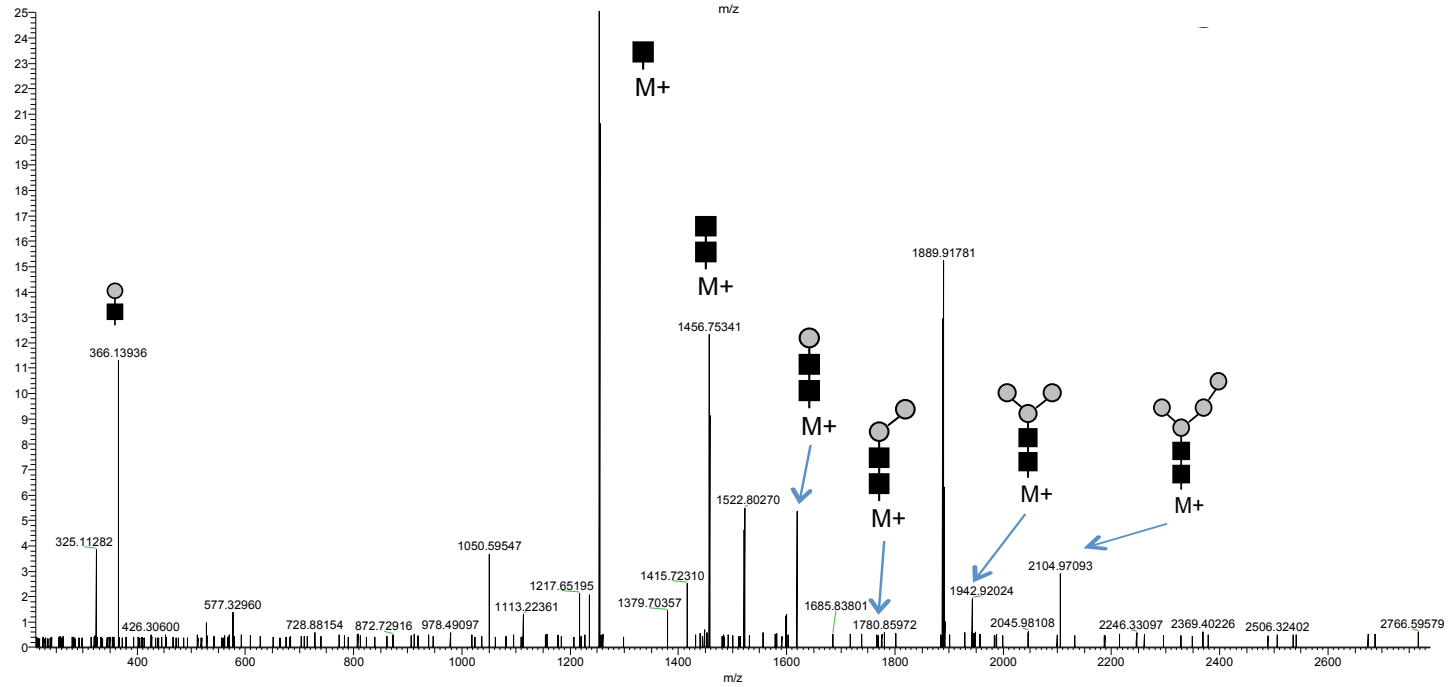
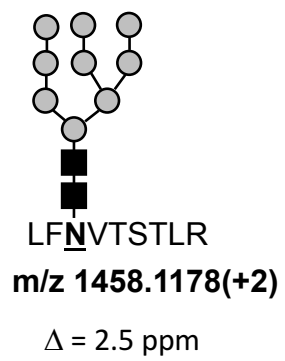


Melanoma B14

Figure S10



Recomb PD-L1



Melanoma B14

Figure S11