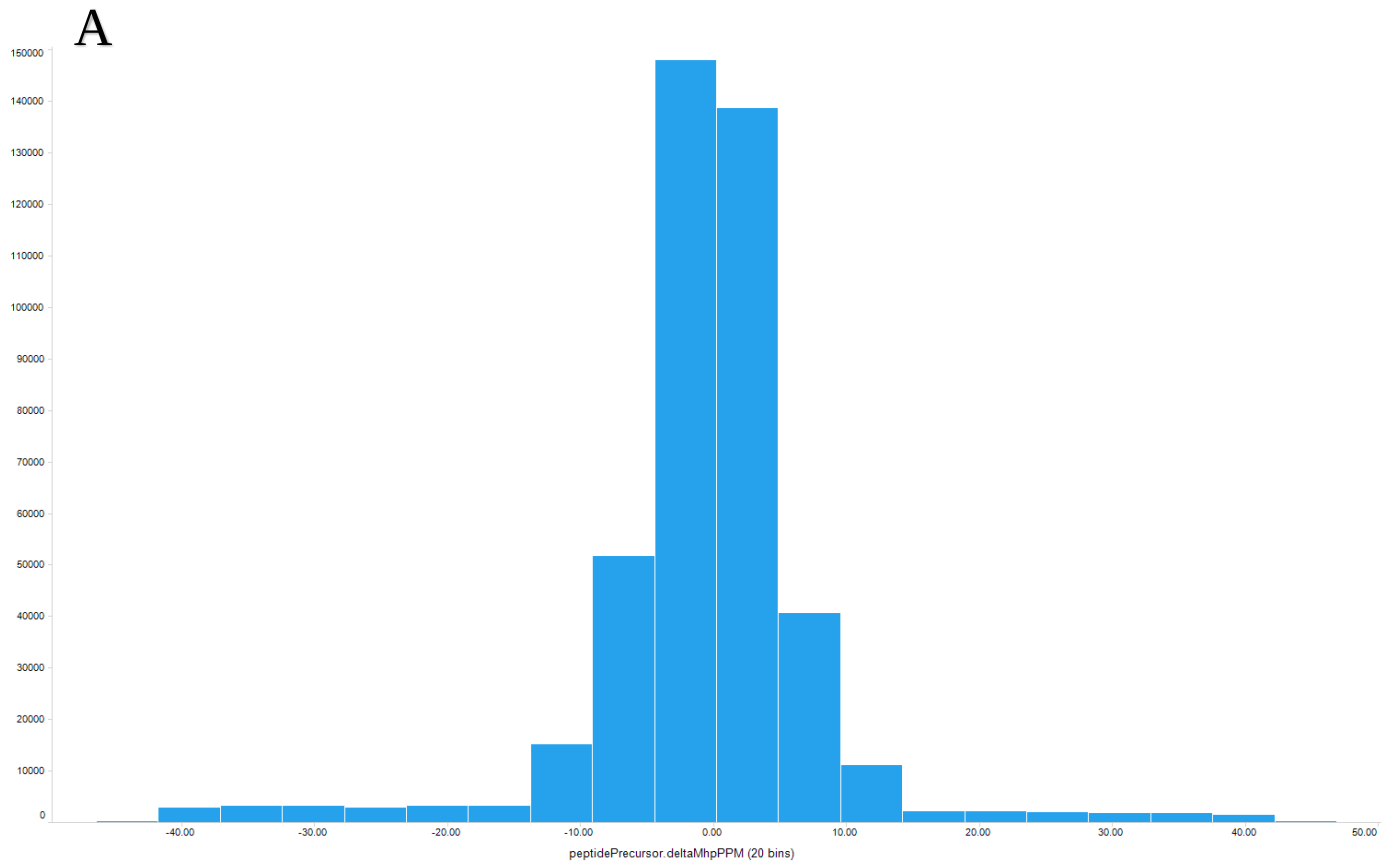
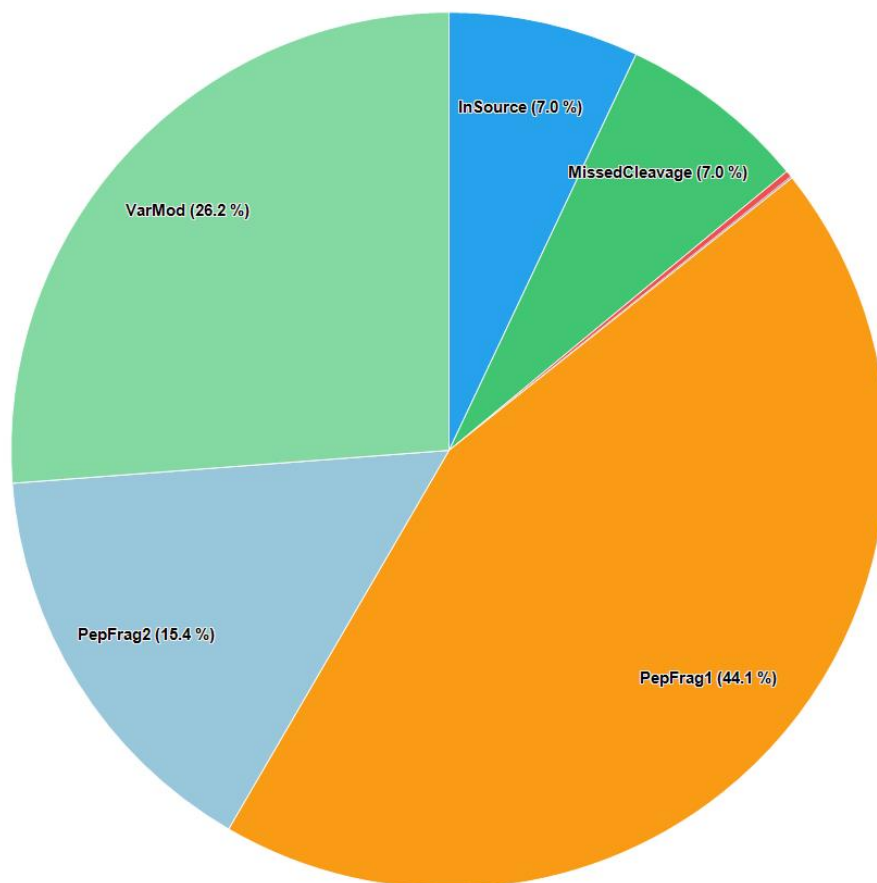


**Additional file 1: Figure S1.** Quality control of the proteins identified by LC-MS. A: normal distribution of 10 ppm error of the total identified peptides. B: peptide detection type. PepFrag1 and PepFrag2 correspond to the peptide matches obtained by comparison to the database by Progenesis QIP, VarMod corresponds to variable modifications, InSource corresponds to fragmentation that occurred at the ionization source, and MissedCleavage corresponds to missed trypsin cleavage. C: drift time for ions of 1+ (blue), 2+ (green), 3+ (red), 4+ (yellow) and 5+ (purple) charge states. D: repeat rate indicating the number of times that an identified protein appears in the replicates: 3 of 3 (blue) and 2 of 3 (red). E: principal component analysis, biological replicates (n = 3) of GBS strains; NEM316 (red), SA16 (blue), SA20 (yellow), SA53 (gray), SA81 (green) and SA95 (black).



B



C

