Supplemental Table I

A list of the features used in Percolator v2.04 to train Percolator support vector machines.

#	Feature	Description
1	Original Score	MS Amanda score for MS Amanda; Xcorr for SEQUEST; Ion score for Mascot.
2	Delta Score	Score of the best hit minus the score of the next best non-isobaric peptide match
3	Binomial Score	Peptide score as described in reference 17
4	Isolation Interference	Fraction of ion current in the isolation window not attributed to the identfied precursor (%)
5	Mass	Calculated monoisotopic peptide mass
6	Delta mass	Difference beween calculated and observed mass (in Dalton and ppm)
7	Absolute delta mass	Absolute value of the delta mass (in Dalton and ppm)
8	Peptide length	Number of amino acids in one peptide
9	Charge	Precursor charge state
10	Missed cleavages	Number of missed cleavages
11	Log peptide matched	Number of candidates in the precursor mass window (log)
12	Log total intensity	Total ion current of the fragment spectrum (log)
13	Fraction matched intensity	Matched ion current divided by total ion current (%)
14a	Fragment coverage series A, B, C	Coverage of the N-terminal fragement ion series (%). The coverage is separately calculated for each series used and the maximum coverage is used.
14b	Fragment coverage series X, Y, Z	Coverage of the N-terminal fragement ion series (%). The coverage is separately calculated for each series used and the maximum coverage is used.
15	Log matched fragment series intensities	Ion current of matched fragment ions (log)
16	Longest sequence series	longest consecutive run of matched fragment ions in any ion series
17	IQR fragment delta mass	Interquartile range of fragment mass error (in Dalton and ppm)
18	Mean fragment delta mass	Arithmetic mean fragment mass error (in Dalton and ppm)
19	Mean absolute fragment delta mass	Arithmetic mean absolute fragment mass error (in Dalton and ppm)