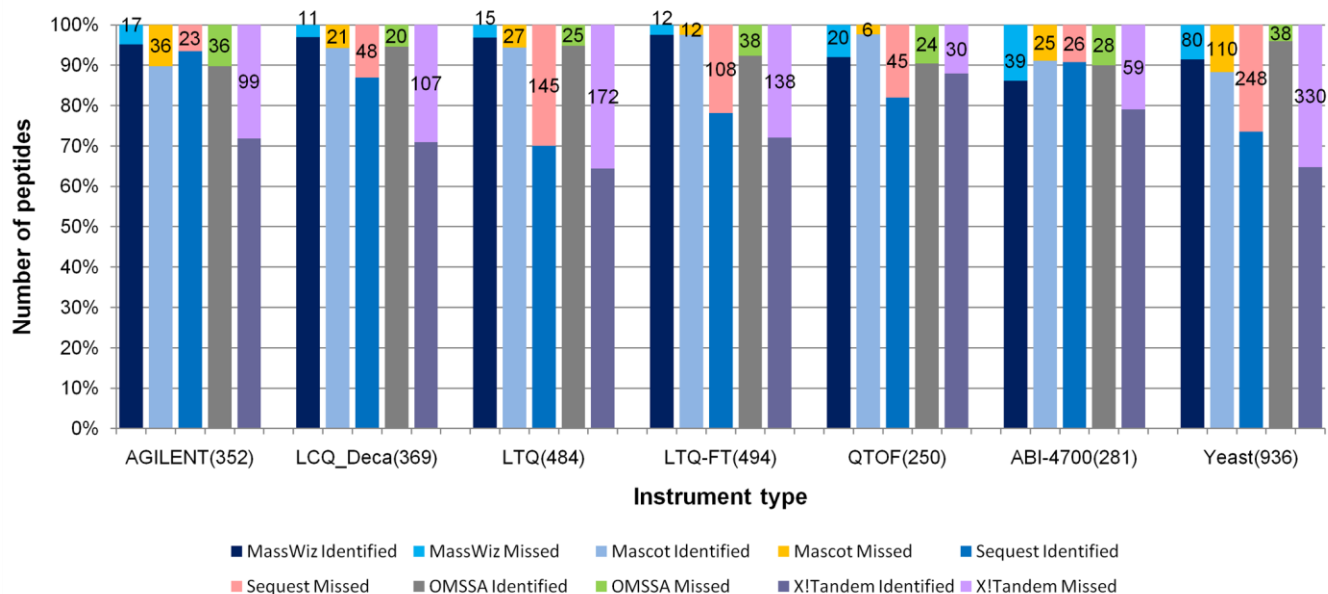Supplementary Table 1A: Comparison of high-confidence peptides for different instrument types in 18 mix datasets
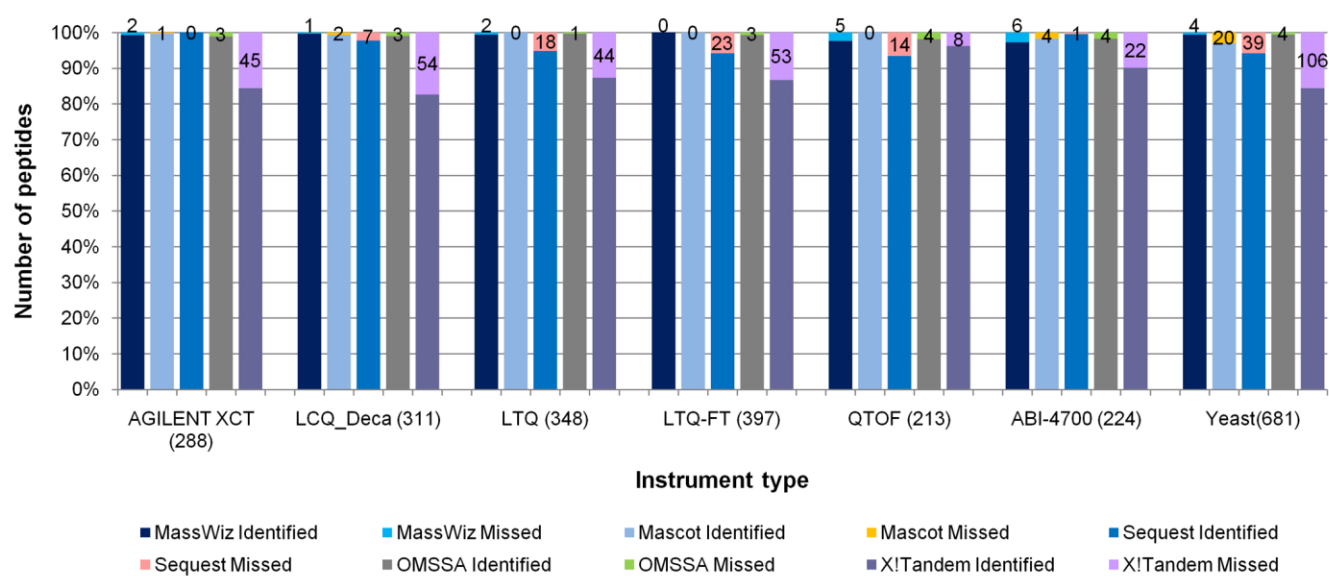
Dataset	High Confidence peptides	MassWiz		Mascot		Sequest		OMSSA		X!Tandem	
		Identified	Missed	Identified	Missed	Identified	Missed	Identified	Missed	Identified	Missed
AGILENT XCT	320	316	4	307	13	312	8	304	16	246	74
LCQ_Deca	345	342	3	335	10	316	29	337	8	260	85
LTQ	437	430	7	431	6	337	100	433	4	311	126
LTQ-FT	459	458	1	454	5	382	77	446	13	352	107
QTOF	230	223	7	227	3	204	26	221	9	210	20
ABI-4700	255	234	21	243	12	244	11	243	12	212	43
TOTAL	2046	2003	43	1997	49	1795	251	1984	62	1591	455

Supplementary Table 1B: Comparison of high-confidence peptides in Yeast dataset

Dataset	High Confidence peptides	MassWiz		Mascot		Sequest		OMSSA		X!Tandem	
		Identified	Missed	Identified	Missed	Identified	Missed	Identified	Missed	Identified	Missed
YEAST	813	795	18	763	50	672	141	806	7	592	221

Supplementary Figure 1: Comparison of peptides identified by two or more algorithms. MassWiz, Mascot, Sequest, OMSSA and X!Tandem are compared for standard mixture on different instruments (first six data series) and mid-log phase Yeast data (last series) at 1% FDR.

Supplementary Figure 2: Comparison of peptides identified by four or more algorithms. MassWiz, Mascot, Sequest, OMSSA and X!Tandem are compared for standard mixture on different instruments (first six data series) and mid-log phase Yeast data (last series) at 1% FDR.