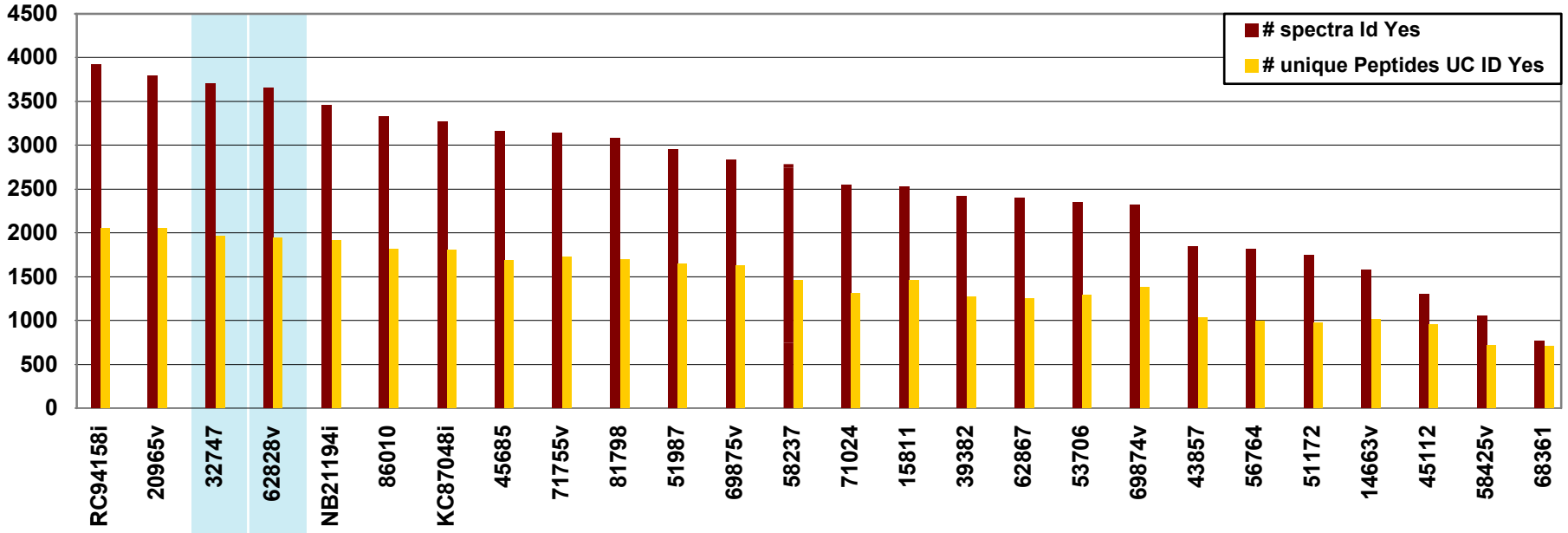
Single Database Search Engine Methods and Results



Spectrum Pre-processing			PK	PK	Re	pF	SM	PK	IH(P)	Xc pF	Xc pF		IH(P)		Ems	Dg	IH(np)	Dg		Dg		MaD Ems		IH(P)	Oth	PK
Peptide Identification	PP	IH(P)	PK	PK	IH(P)	PF	SM	PK	IH(P)	PF	PF	Ma	IH(P)	PP	PF	Ma	Ma	OM	Ma	Ma	Ma	Ma	X!	IH(P)	Oth	PK
Result Filtering	PP	IH(P)	Ex PK Oth	Ex PK	IH(P)	PF	SM	PK	Per IH(P)	IH(P)		Per	Per Ex	PP IH(P)	Ex IH(P)	Per		IH(P)		IH(P)	Ma	Ex	Ex IH(P)	IH(P)	Ex	R
Years Experience	>10	5-10	5-10	5-10	5-10	5-10	>10	5-10	1-2	5-10	1-2	>10	1-2	5-10	3-4	>10	5-10	3-4	>10	>10	3-4	5-10	5-10	1-2	3-4	<1

DTA Generator = Dg
Excel = Ex
Extract_msn = Ems
In-house software (freely available) = IH(P)

In-house software (not public) = IH(np)
Mascot = Ma
Ma Distiller = MaD
OMSSA = OM

Oth = Other
PEAKS = PK
Percolator = Per
pFind = pF

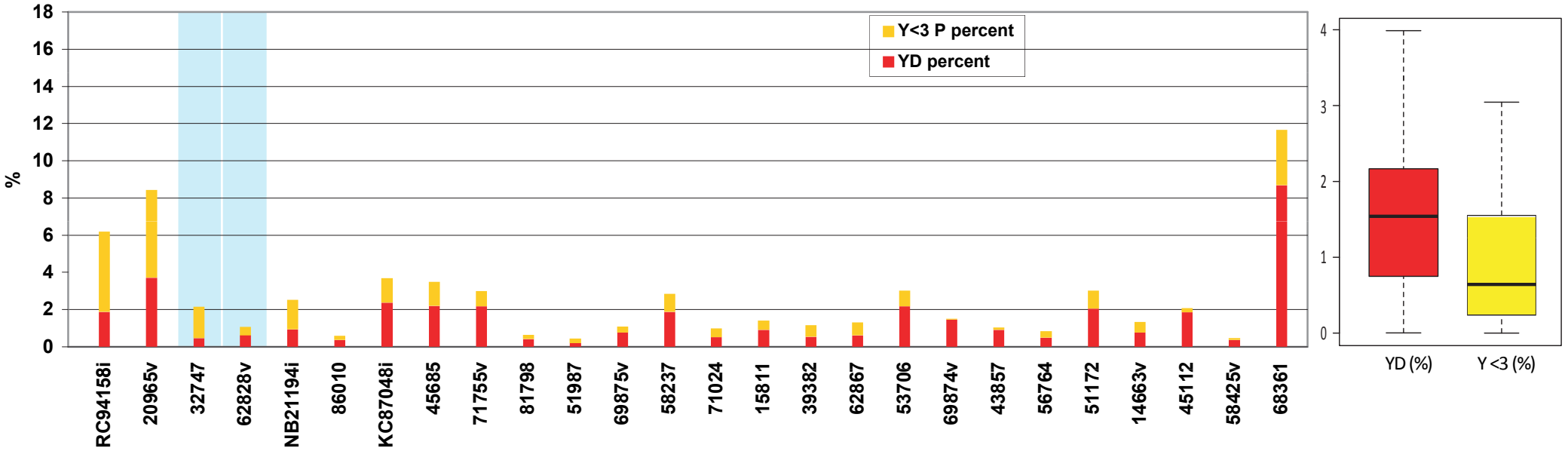
Protein Prospector = PP
Spectrum Mill = SM
X!Tandem = X!
Xcalibur = Xc

The iPRG study (via ABRF) allows researchers to benchmark against one another in their ability to accurately identify peptides. The regular study allows multiple search engines to be used to identify the maximum amount of peptides. While it is encouraged to utilize multiple engines for daily analysis, it makes identifying the contributions made by each database search engine unclear. The chart above is a streamlined version of the chart produced by the iPRG study (slide 26) with respect to cases where only researchers employed only one peptide identification method in order to give a clear view of indenpendent findings.

iPRG studies are not competitions. Leftmost is not meant to imply best, it just reflects the sorting criterion: total number of confident ids; this was chosen as a convenient means of sorting, and this sort is used throughout for consistency.

ESR or FDR

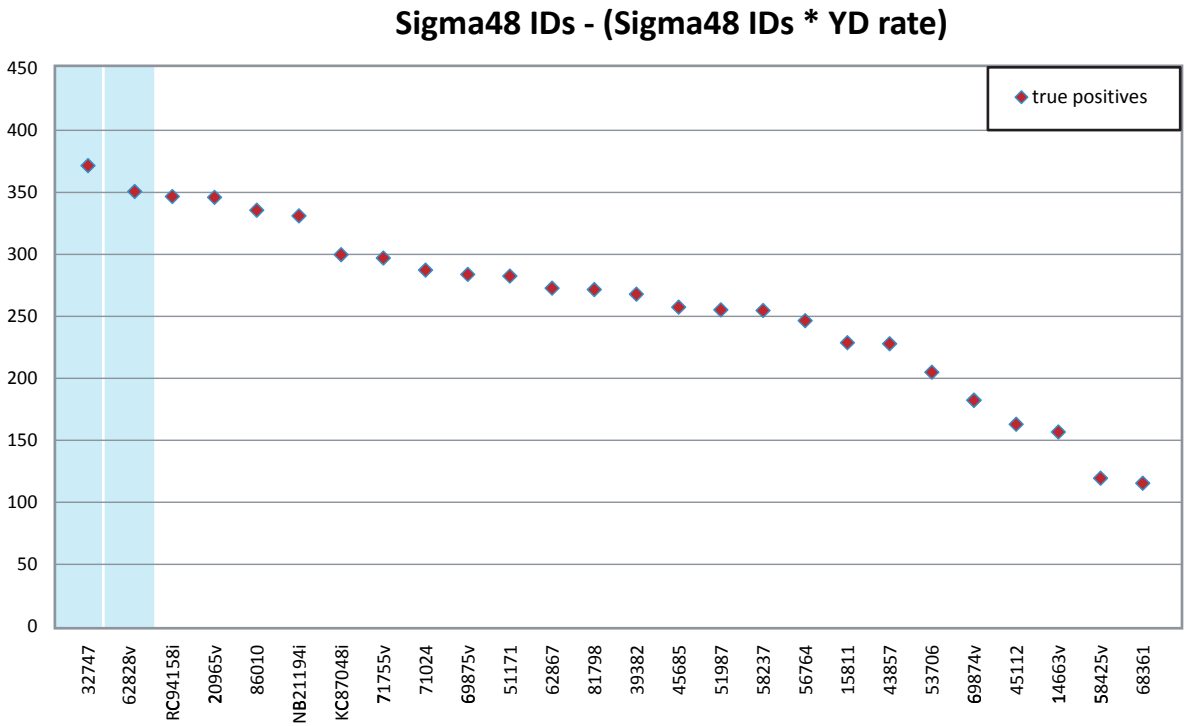
44 participants total
26 single engine participants (displayed)
3 for consensus



The ESR or FDR chart above demonstrates the "Extraordinary Skill Rate or High False Discovery Rate" of the user's methods involved in the study. The red bars represent results that differ from the consensus of other engines; yellow bars represent results without consensus. The red and yellow bars can be regarded as "soft" lower and upper bounds of the FDR. iPRG requested 1% FDR. This demonstrates each method's ability to accurately report low false positive rates.

Sigma 48 as TP Estimator

The sample was spiked with Sigma 48 proteins to act as the true positive estimator of each methodology. The ability to accurately identify the spike, along with overall performance indicates the user's true performance, as shown in the chart to the right.



ESR and FDR results were obtained from iPRG slide 32 and Sigma 48 as TP Estimator results were obtained from iPRG slide 36.