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Describe in detail the calculation of FDRs at the PSM, peptide, and protein levels. Report the PSM-, peptide-, and protein-level FDR values along with the total number of expected true positives and false positives at each level. Present large-scale results thresholded at equal to or lower than 1% protein-level global FDR. If any large-scale datasets are individually thresholded and then combined, calculate the new, higher peptide- and protein-level FDRs for the combined result.

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