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Sample preparation for shotgun proteomics: comparison of stacking gel, tube-gel, FASP, S-TRAP, SPE and liquid methods

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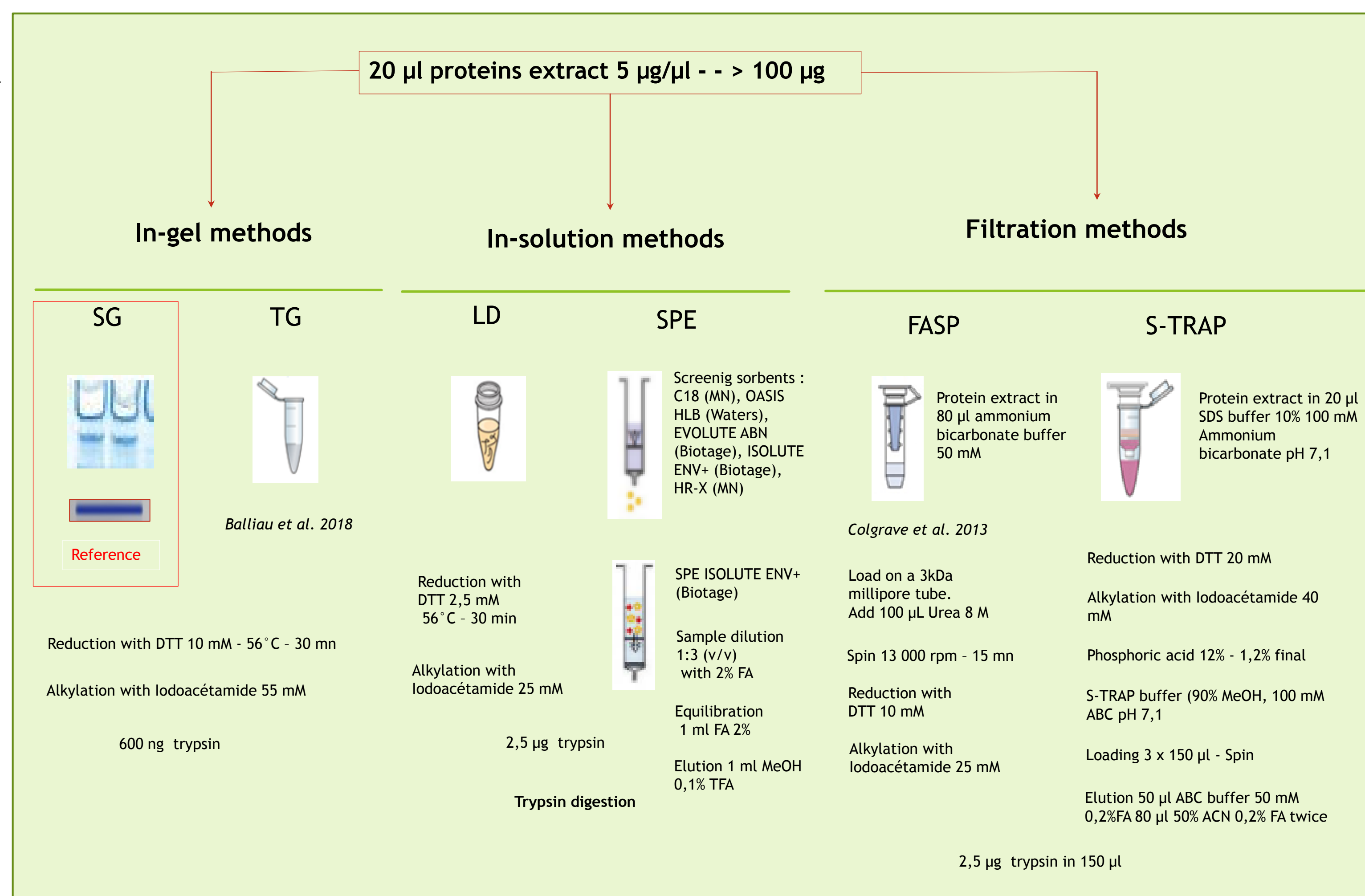
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Objective

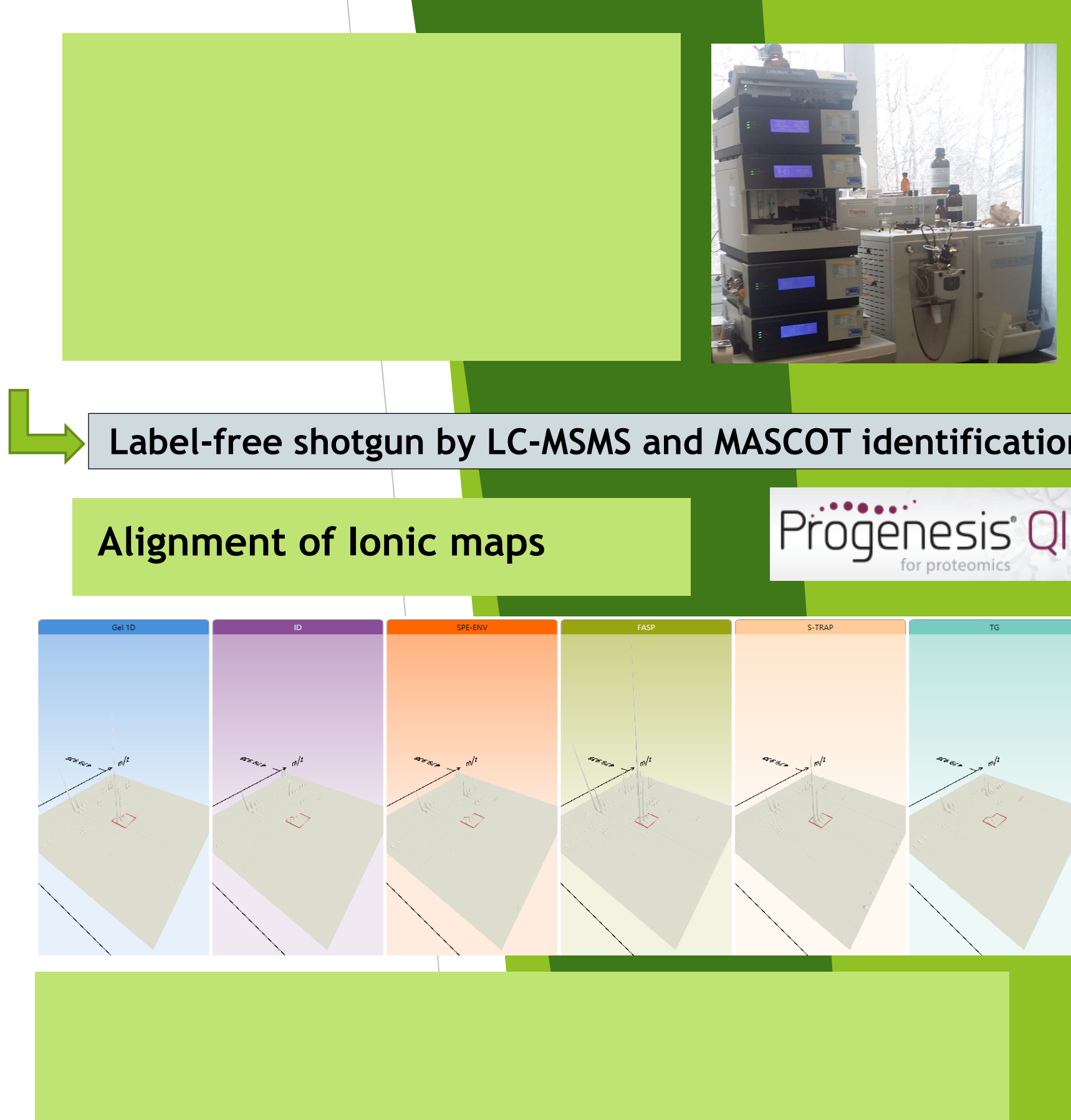
- Sample preparation is a crucial step in high-throughput shotgun proteomics, challenged with detergent incompatibility that has a strong influence on the accuracy and robustness of MS analyses. Classical approaches using stacking-gel (SG), Solid Phase Extraction (SPE) or liquid digestion (LD) have been developed but show limitations due to the time-consuming and repetitive sample processing, their recovery efficiency and overall yield. In recent years, strategies by filtration such as filter-aided sample preparation (FASP) based on a molecular weight cut-off (MWCO), and its new alternative, the suspension traps (S-TRAP) confining particulate protein suspensions with the subsequent depletion of interfering substances, have tried to overcome these drawbacks.
- The objective of this work was to compare for the first time all these preparation methods, *i.e.* FASP, S-TRAP, SPE, SG, TG (tube-gel) and LD before subjecting the samples to a label-free semi-quantitative proteomic analysis (shotgun proteomics). A soluble fraction of muscle proteins (100 µg), spiked with 1.5 µg of casein, was used to assess sample preparation methods. Ten replicates were prepared for each method.

Materials & methods

Sample preparation

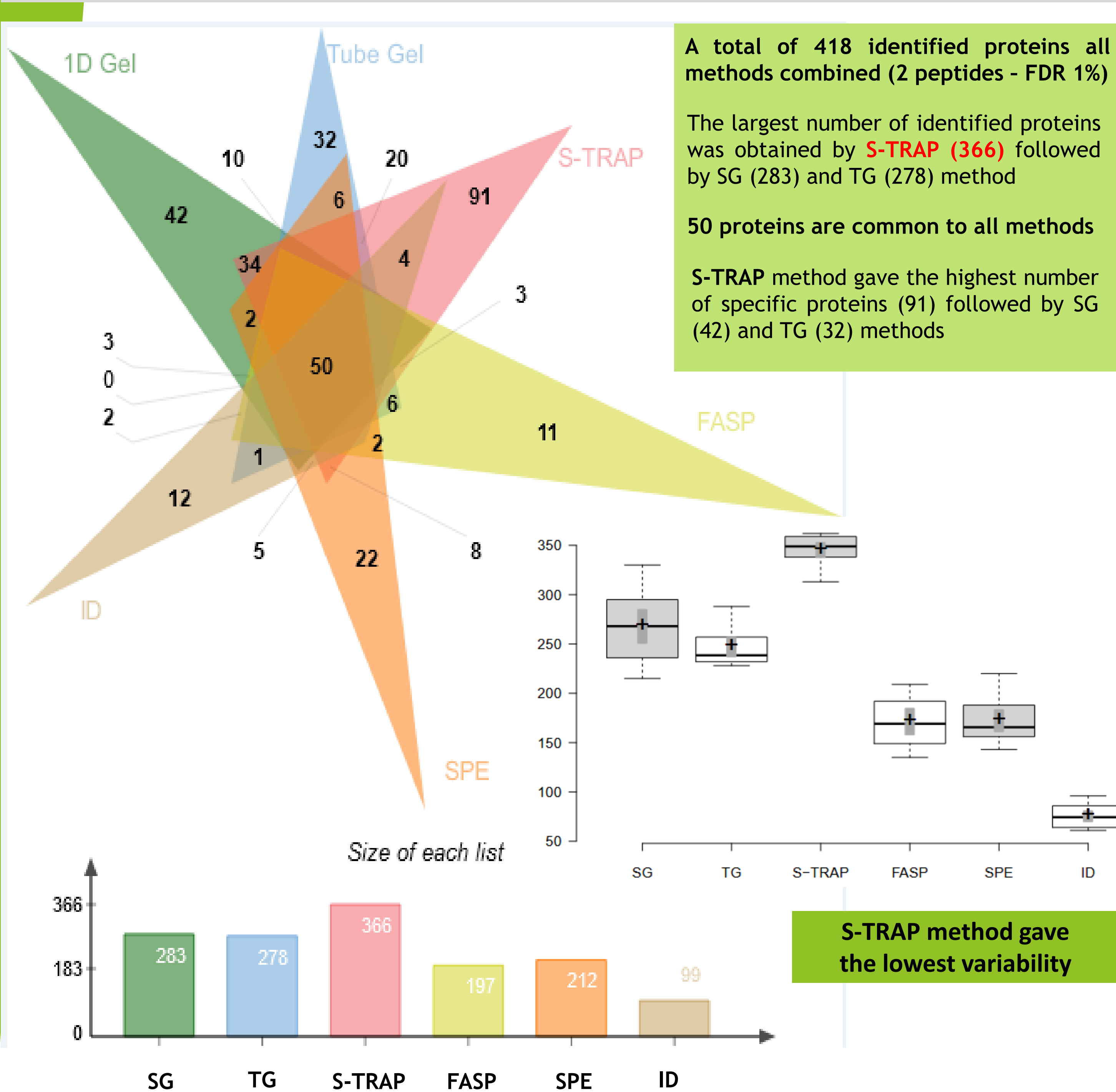


Quantitative analysis

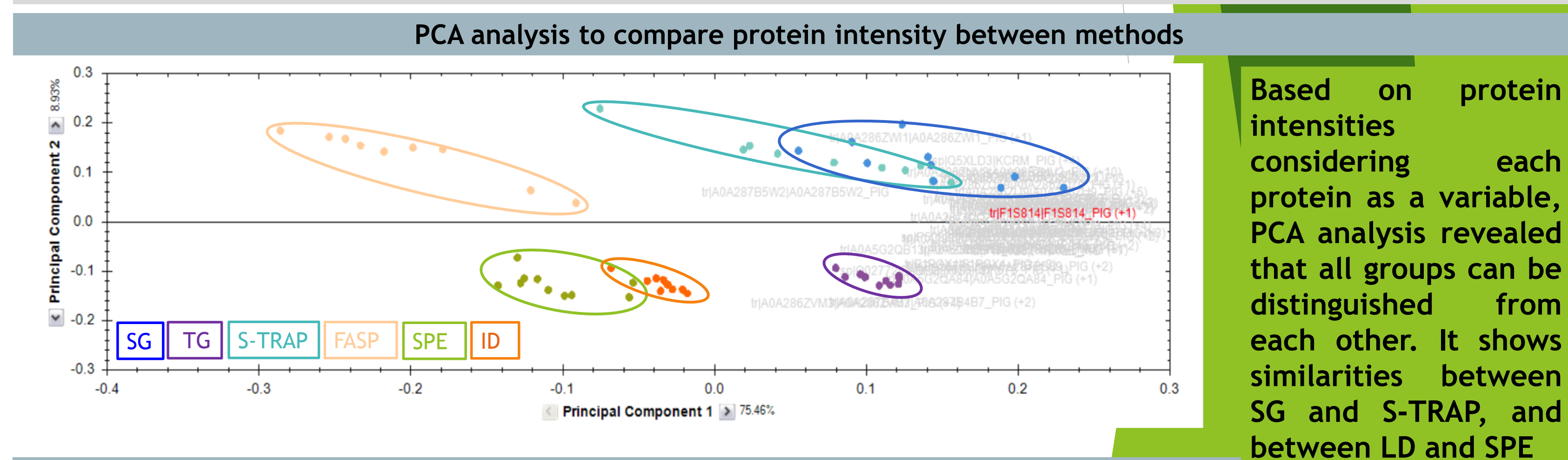


Results

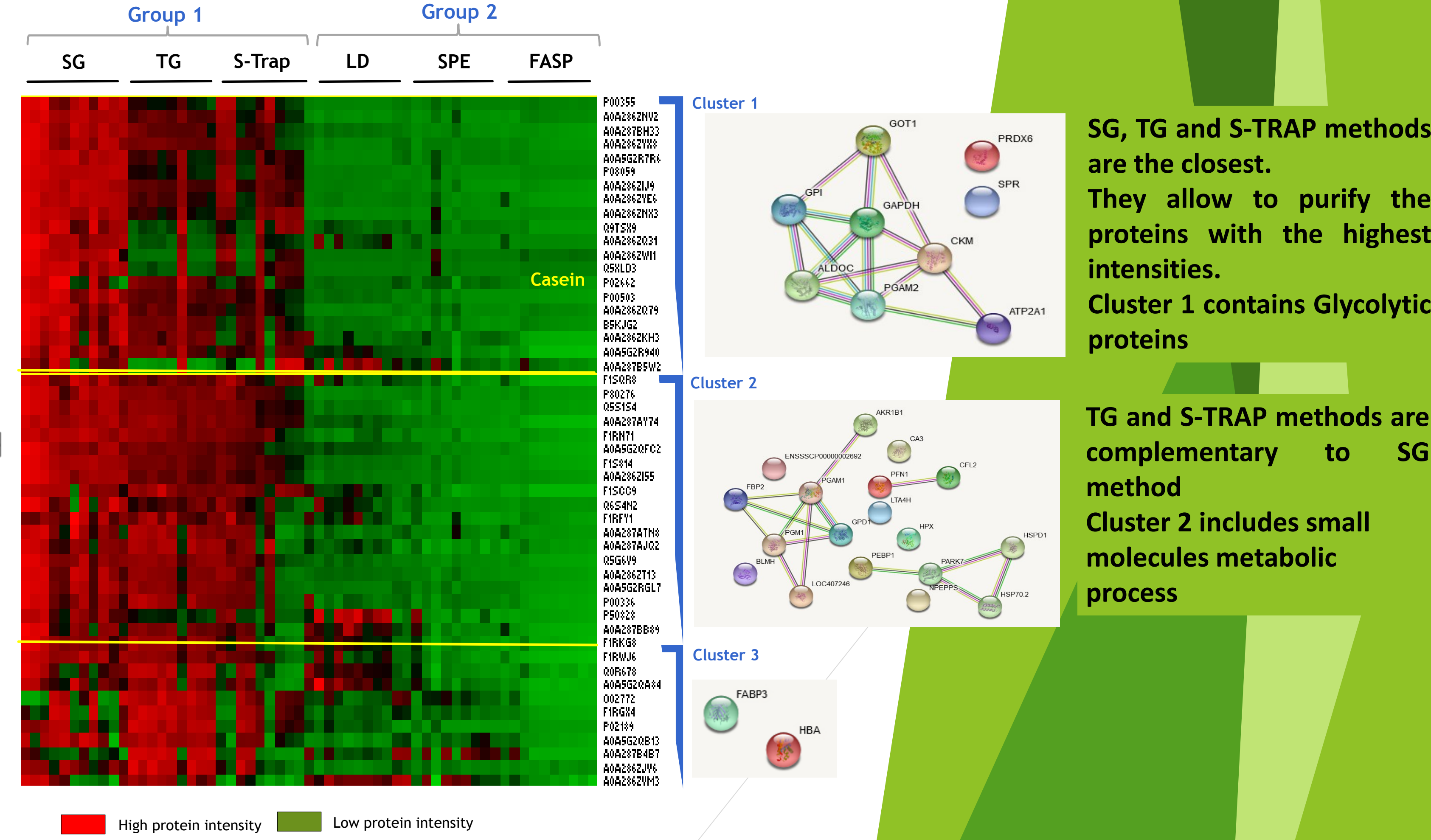
Identifications



Statistical analysis : multivariate analysis of the 50 common proteins



Hierarchical clustering method (HCA) to group methods



Conclusion

- The originality of this study lay in the comparison of proteins identified by LC-MS/MS from the same sample by implementing several preparation methods based on different principles: gel, liquid and filtration.
- The analysis of the results by Venn diagram, principal-component analysis, hierarchical clustering and the abundance ranking of quantitative proteins highlights significant differences in identified proteins, according to the sample preparation method. Moreover, there is a specificity in the nature of extracted proteins according to the method.
- A total of 418 proteins were identified combining all the methods and the largest number of identified proteins was obtained by S-TRAP (366), followed by SG (283) and TG (278) methods.
- Statistical results and the qualitative analyses of significant proteins indicate that S-TRAP method outperforms SG method.
- S-TRAP would purify the majority of the proteins in a sample rapidly and with the greatest intensity.
- The faster and easier S-TRAP method turns out to be the best alternative to replace classical in-gel and in-solution methods, resulting in an ultrafast sample-preparation approach for shotgun proteomics.