Borrelia PeptideAtlas: A proteome resource of common *Borrelia burgdorferi* isolates for Lyme community

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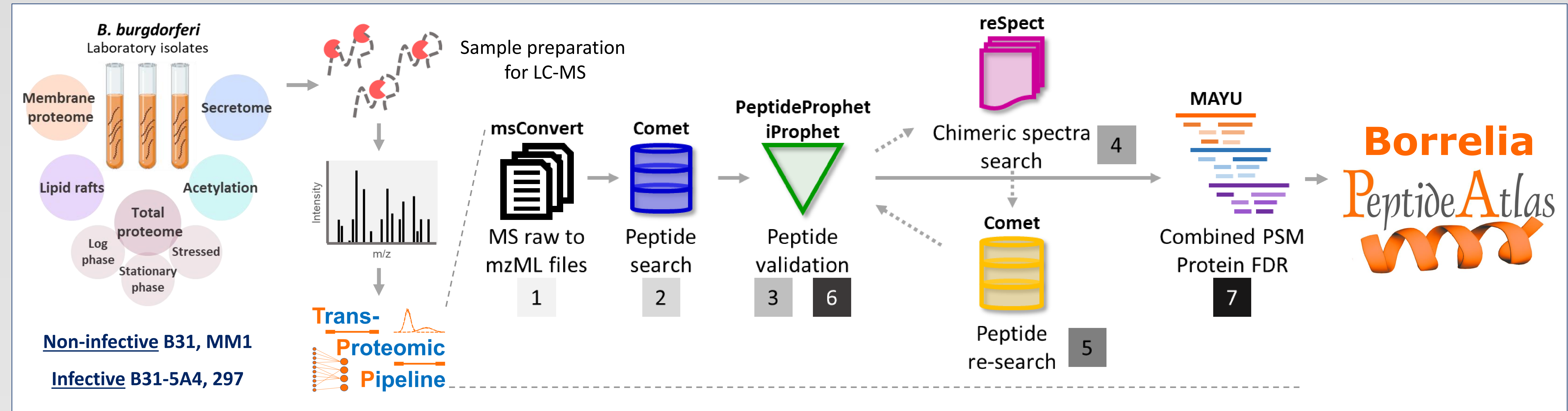The authors declare no competing financial interest.

Introduction

Lyme disease is a caused by the spirochete *B. burgdorferi*. Due to its genomic and proteomic variability, the study and further comparison of the isolates proteome is key to understand the biology and infectivity of this spirochete. In this study, mass spectrometry-based proteomics was used to assemble peptide datasets of laboratory isolates and is publicly available as the Borrelia PeptideAtlas. These datasets include information on total proteome, secretome, and membrane proteome of *B. burgdorferi*. Proteomic data provided identification of **1,221 canonical proteins (924 core and 297 non-core)** with protein-level FDR less than 1% - **86% of B31 proteome coverage**. The Borrelia PeptideAtlas is readily available as an important resource for the Lyme disease research community.

PeptideAtlas workflow

B. burgdorferi Laboratory isolates — Membrane proteome, Secretome, Lipid rafts, Acetylation, Total proteome, Log phase, Stationary phase, Stressed

Non-infective B31, MM1
Infective B31-5A4, 297

Sample preparation for LC-MS

Trans-Proteomic Pipeline

msConvert — MS raw to mzML files [1]
Comet — Peptide search [2]
PeptideProphet iProphet — Peptide validation [3] [6]
reSpect — Chimeric spectra search [4]
Comet — Peptide re-search [5]
MAYU — Combined PSM Protein FDR [7]
Borrelia PeptideAtlas

Borrelia PeptideAtlas

1. Overview of the Borrelia PeptideAtlas characteristics, including (a) cumulative number of peptides and (b) proteins per experiment. (c,d) Frequency of tryptic peptides and peptide charge, with majority of 2+ and 3+ peptides. (e) Total MS/MS spectra observed for each isolate. (f) Percentage of protein sequence coverage for canonical proteins. (g) Number of phosphorylated serine (S), threonine (T), and tyrosine (Y) sites in all experiments, with PTMProphet probabilities (nP) ranging from 0.8 to 1. No-choice shows PSMs with only one possible phosphorylation site available, hence nP = 1.
2. Visualization of post-translational modifications (PTMs) within the Borrelia PeptideAtlas interface. Includes (a) sequence coverage, (b) detected peptides, (c) phosphorylated STY-sites, and (d) information on peptides.
3. Proteome coverage for laboratory isolates (a) B31, (b) B31-5A4, and (c) MM1, with chromosome coverage higher than 95% for all isolates, and plasmid coverage ranging from 35-85%.
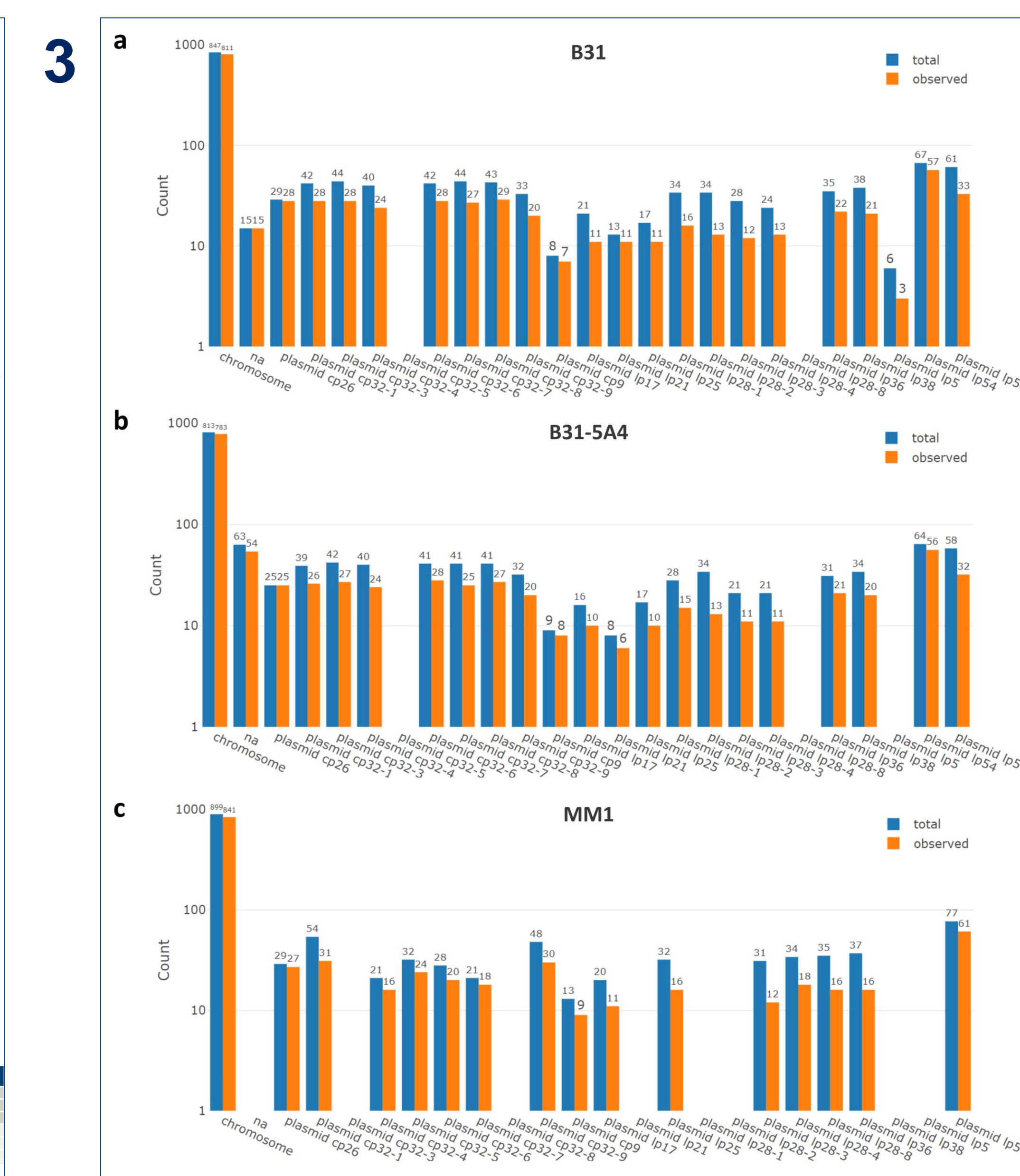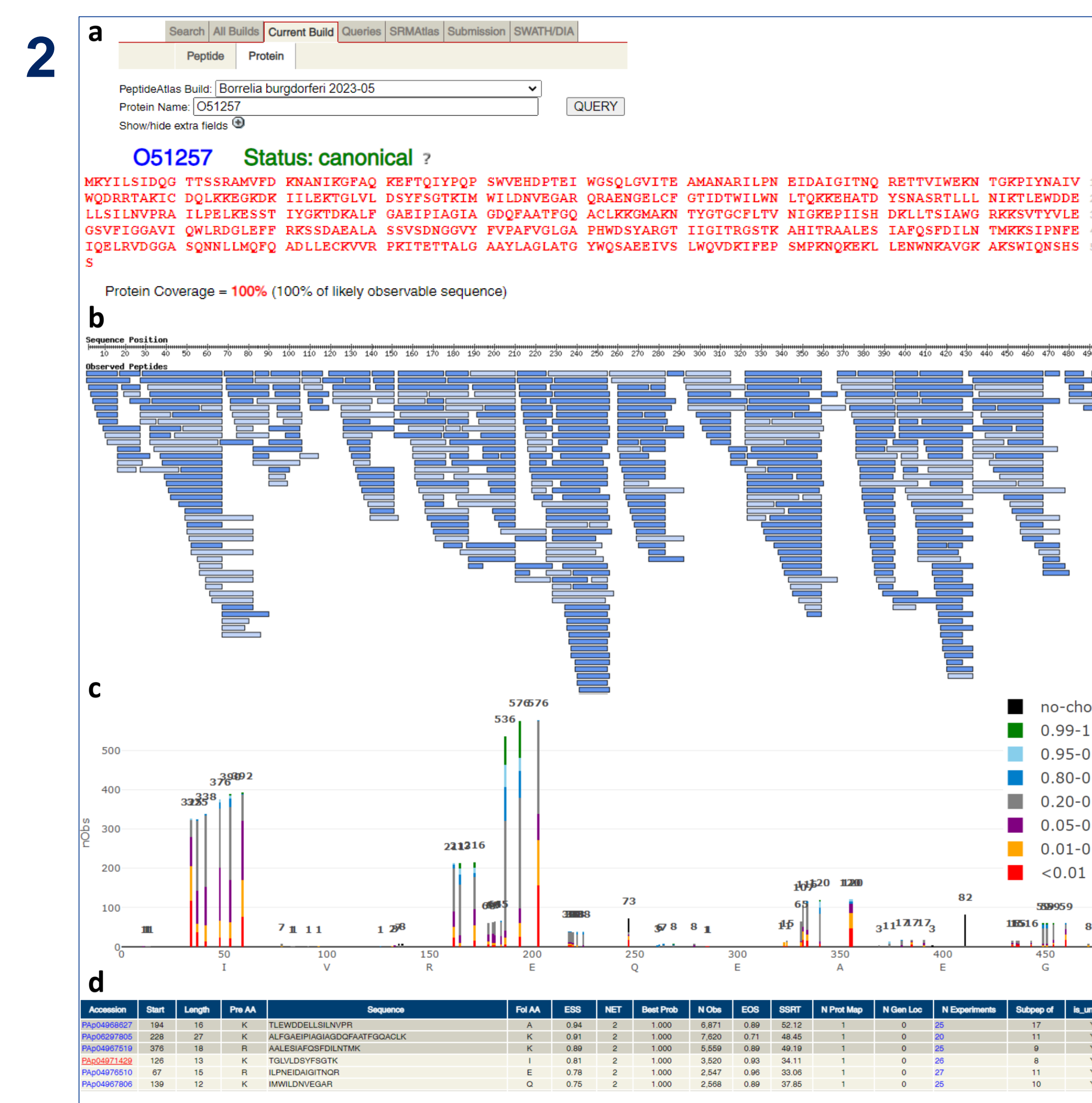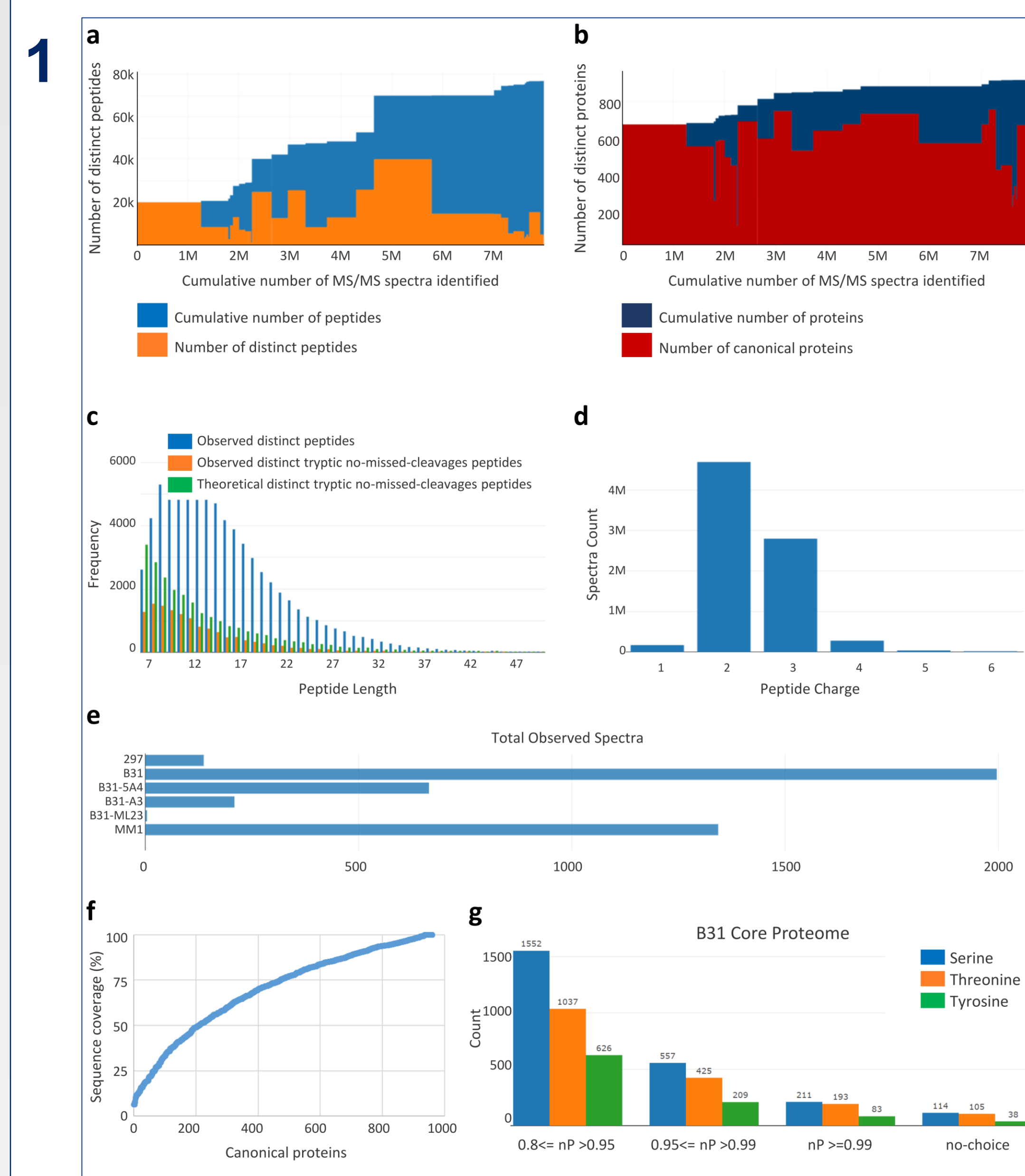
Resource highlights

- A *B. burgdorferi* **MS-based peptide repository** for the Lyme research community
- Different experimental conditions
- 855 high-res mass spectrometry runs
- 30 ISB experiments & 10 public datasets
- 57 M MS/MS spectra searched
- 8 M PSMs w/ FDR levels ≤ 0.0005
- 76,936 peptides w/ FDR ≤ 1%
- 1,221 canonical proteins w/ FDR ≤ 1%
- 85% of isolate BB-B31 proteome coverage
- Publicly available at:

http://www.peptideatlas.org/builds/borrelia