

DART-ID Increases Single-Cell Proteome Coverage

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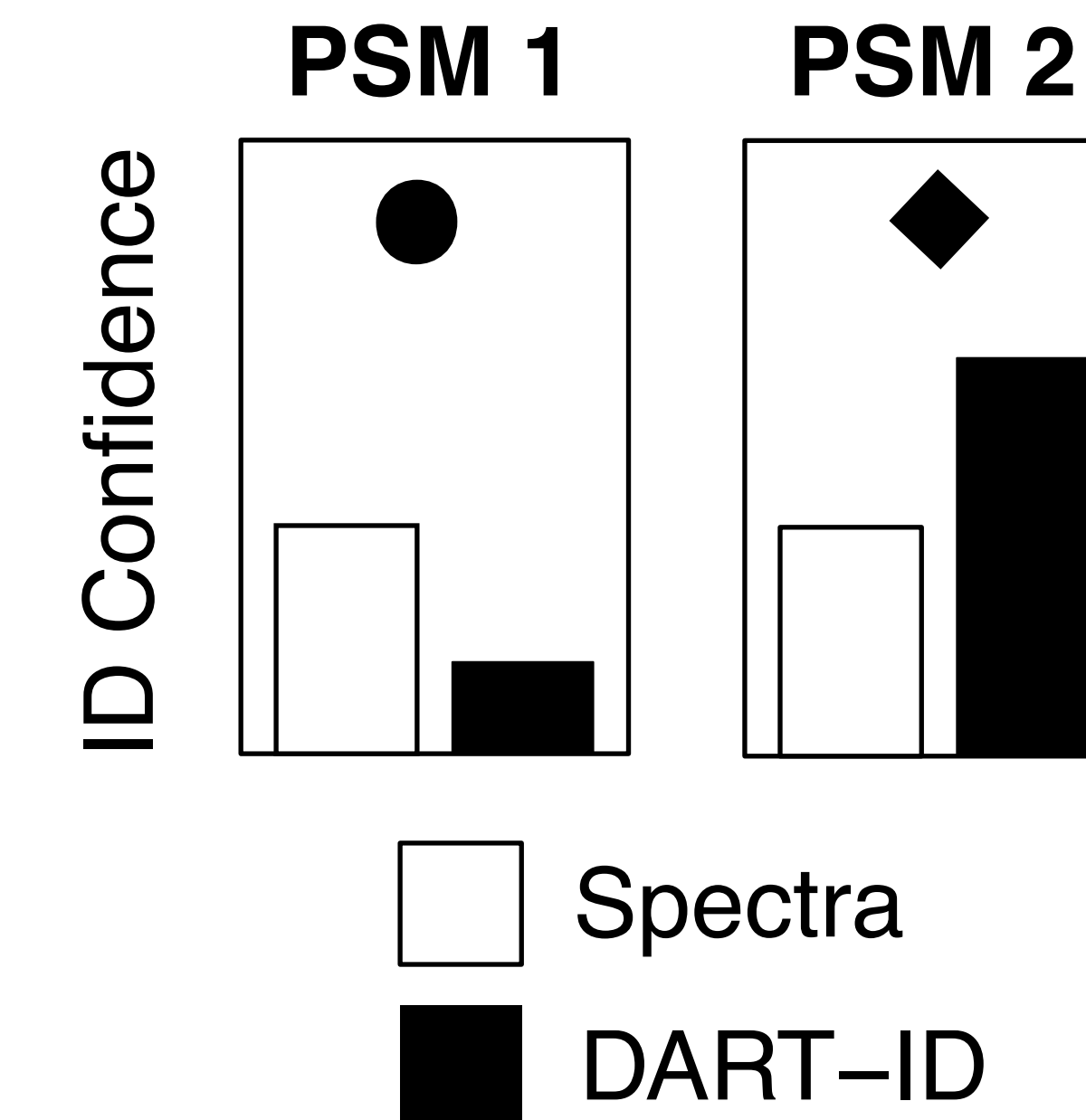
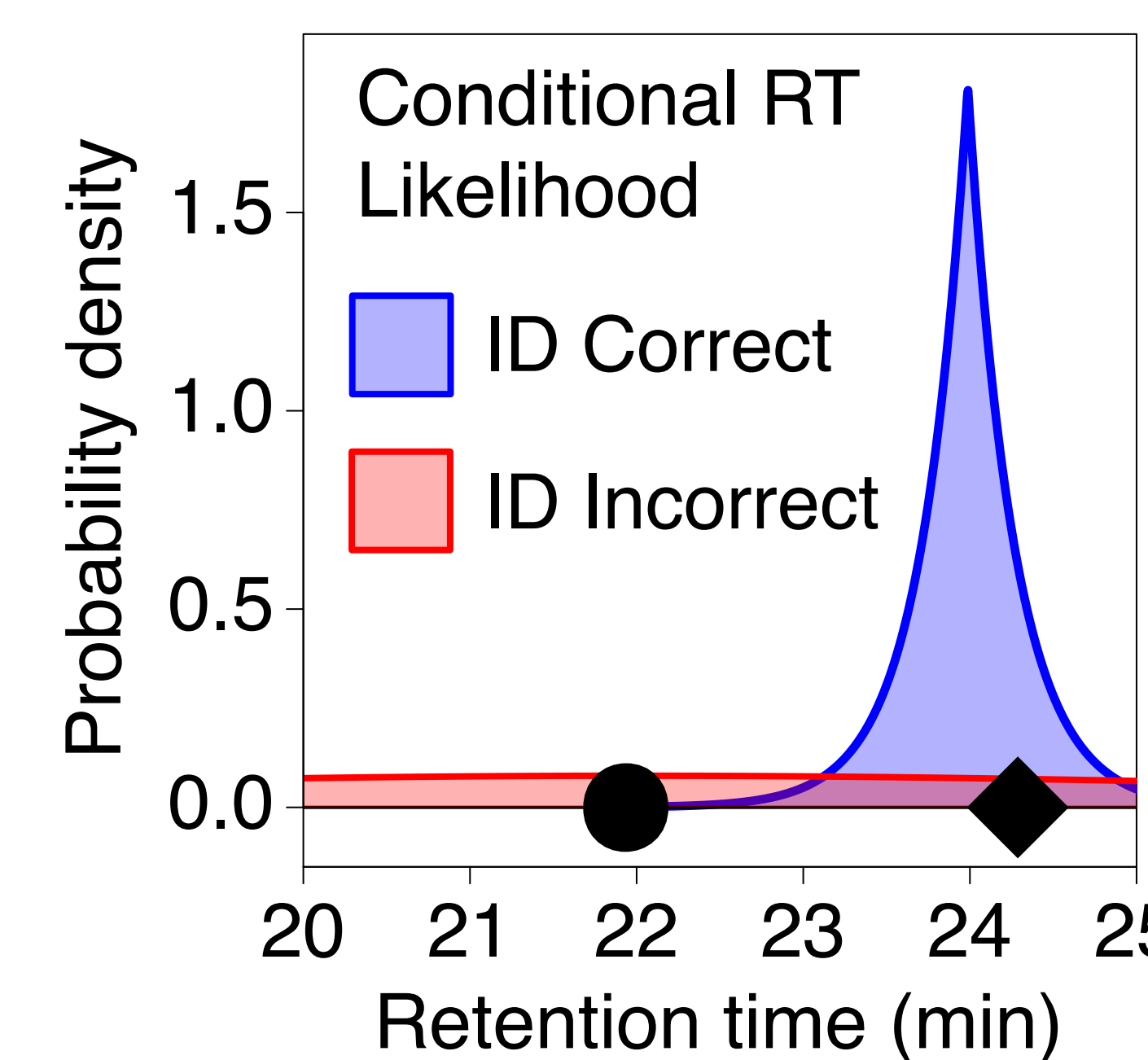
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Summary

- Global alignments of peptide RTs across experiments create robust inferences of peptide RTs.
- Applying inferred and observed RTs within a principled Bayesian framework greatly increases proteome coverage.
- Manuscript: <https://doi.org/10.1101/399121>
- GitHub: <https://github.com/SlavovLab/DART-ID>

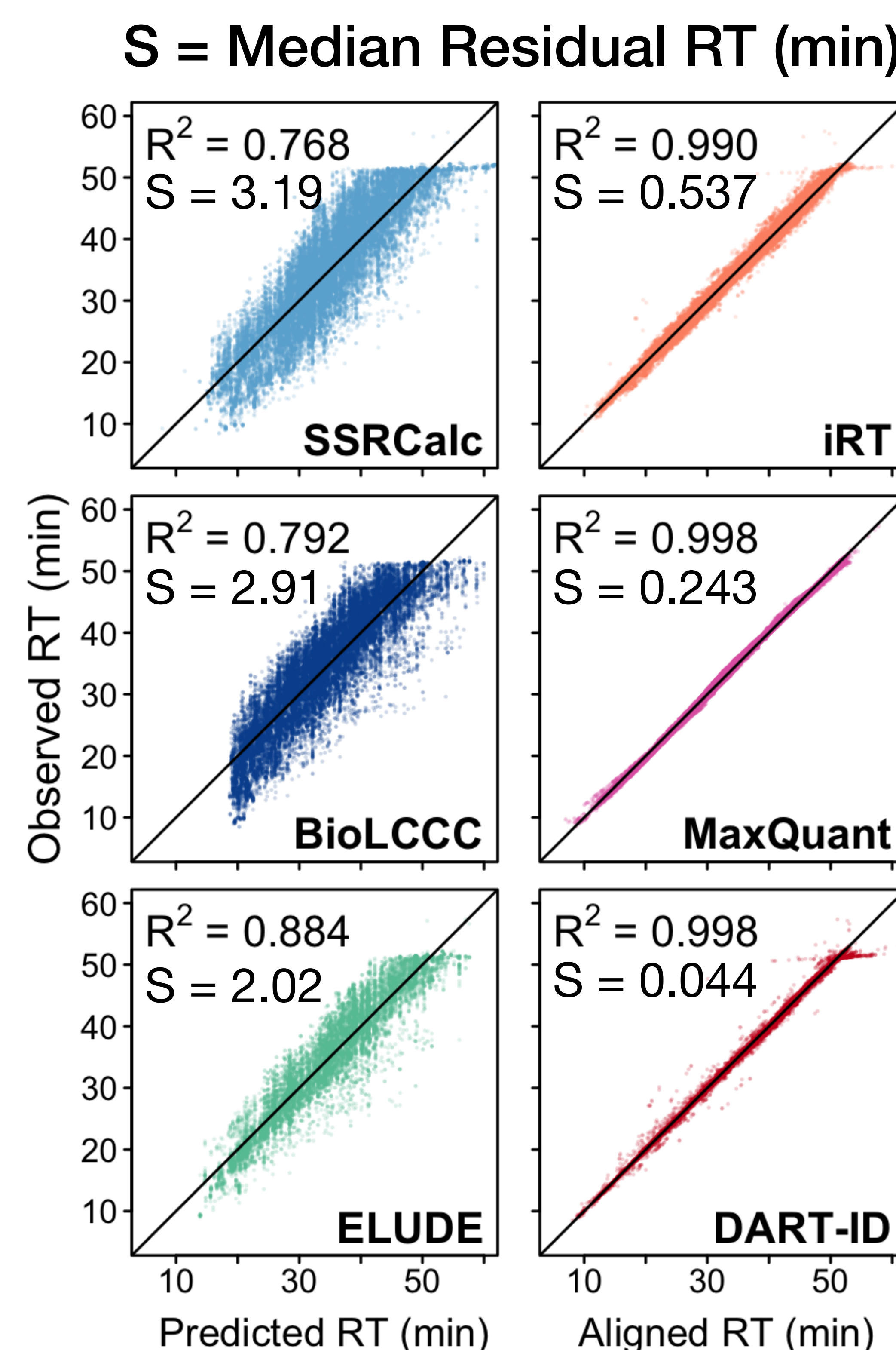
Bayesian Framework for Updating ID Confidence



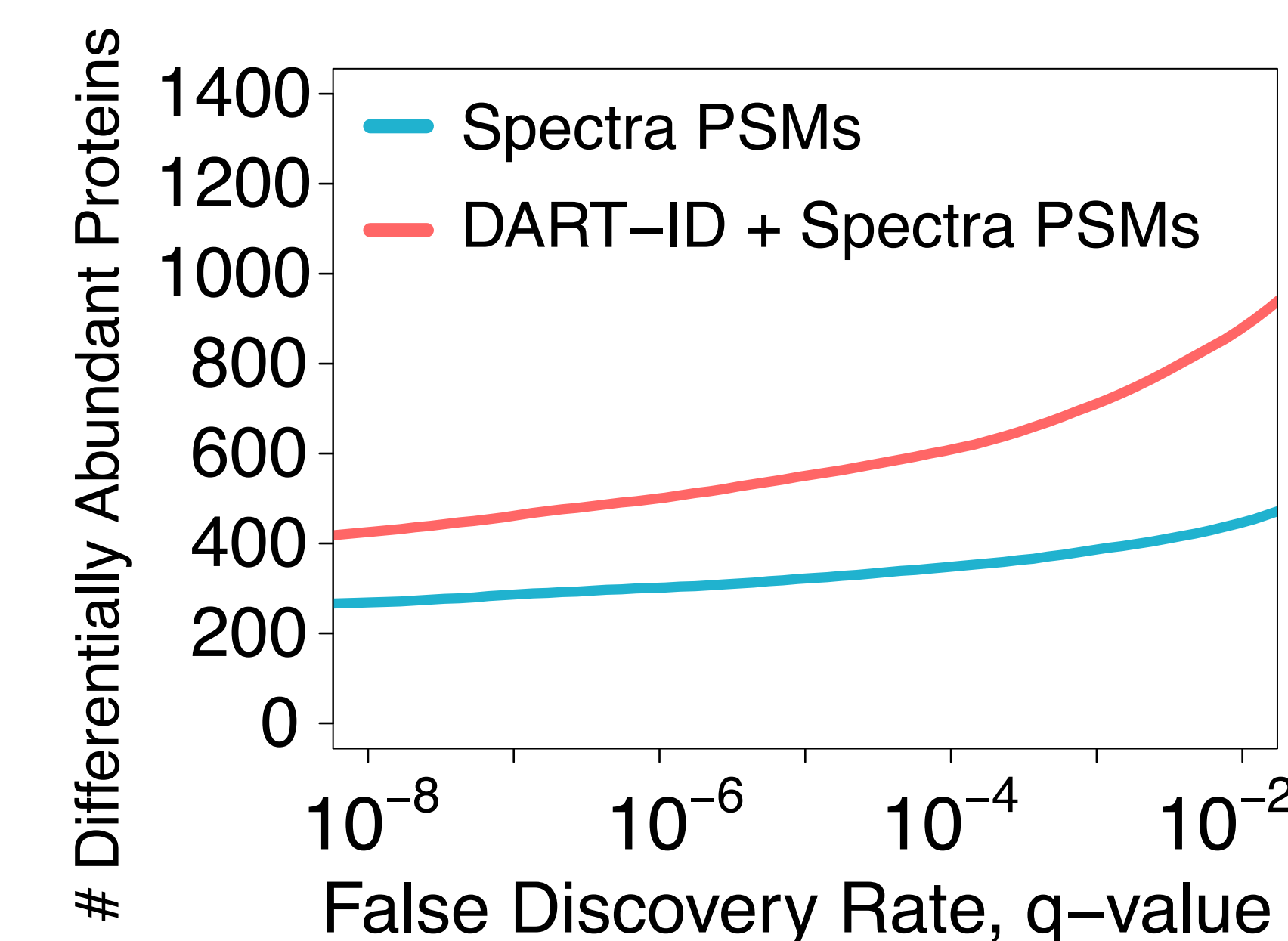
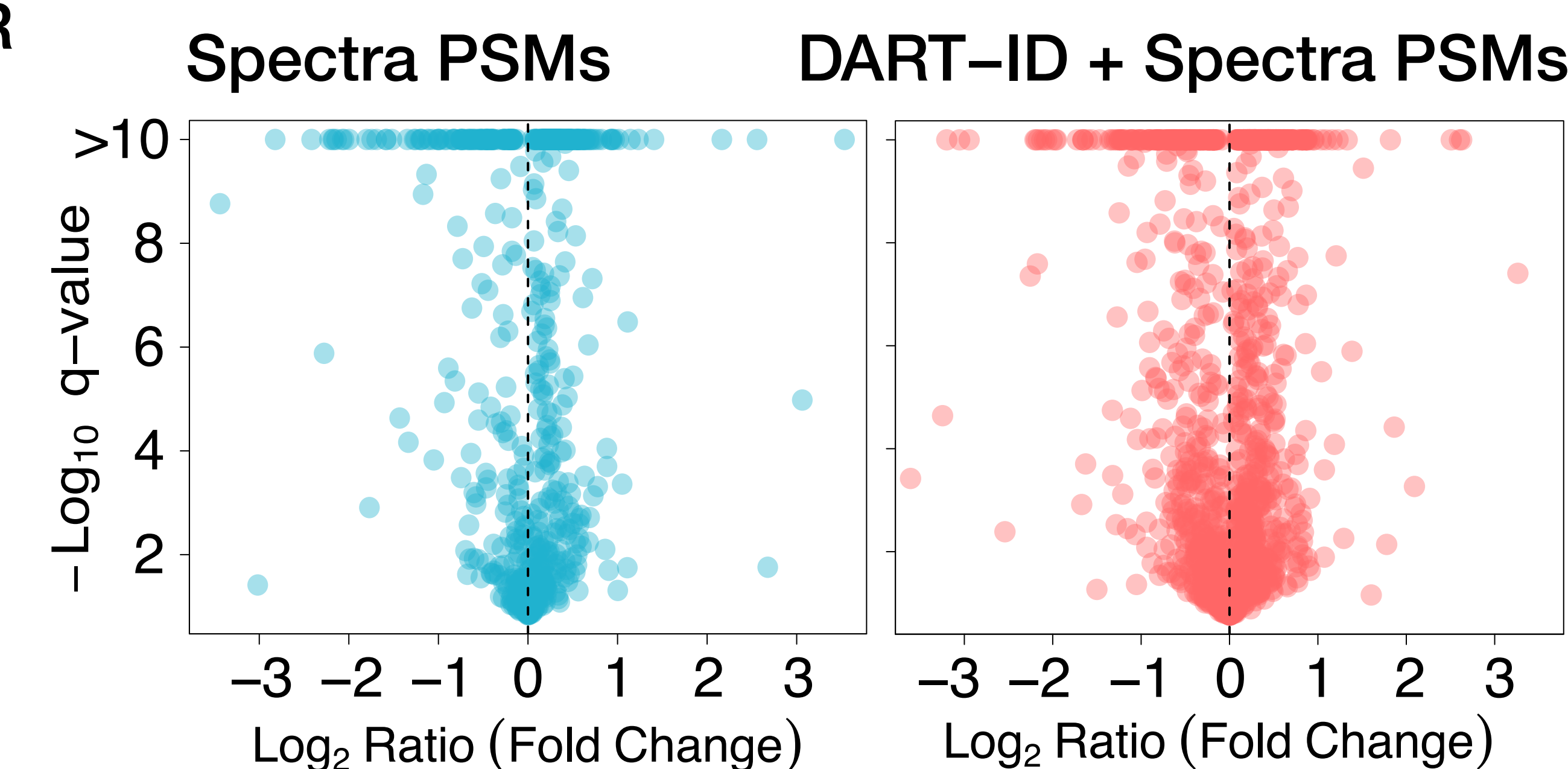
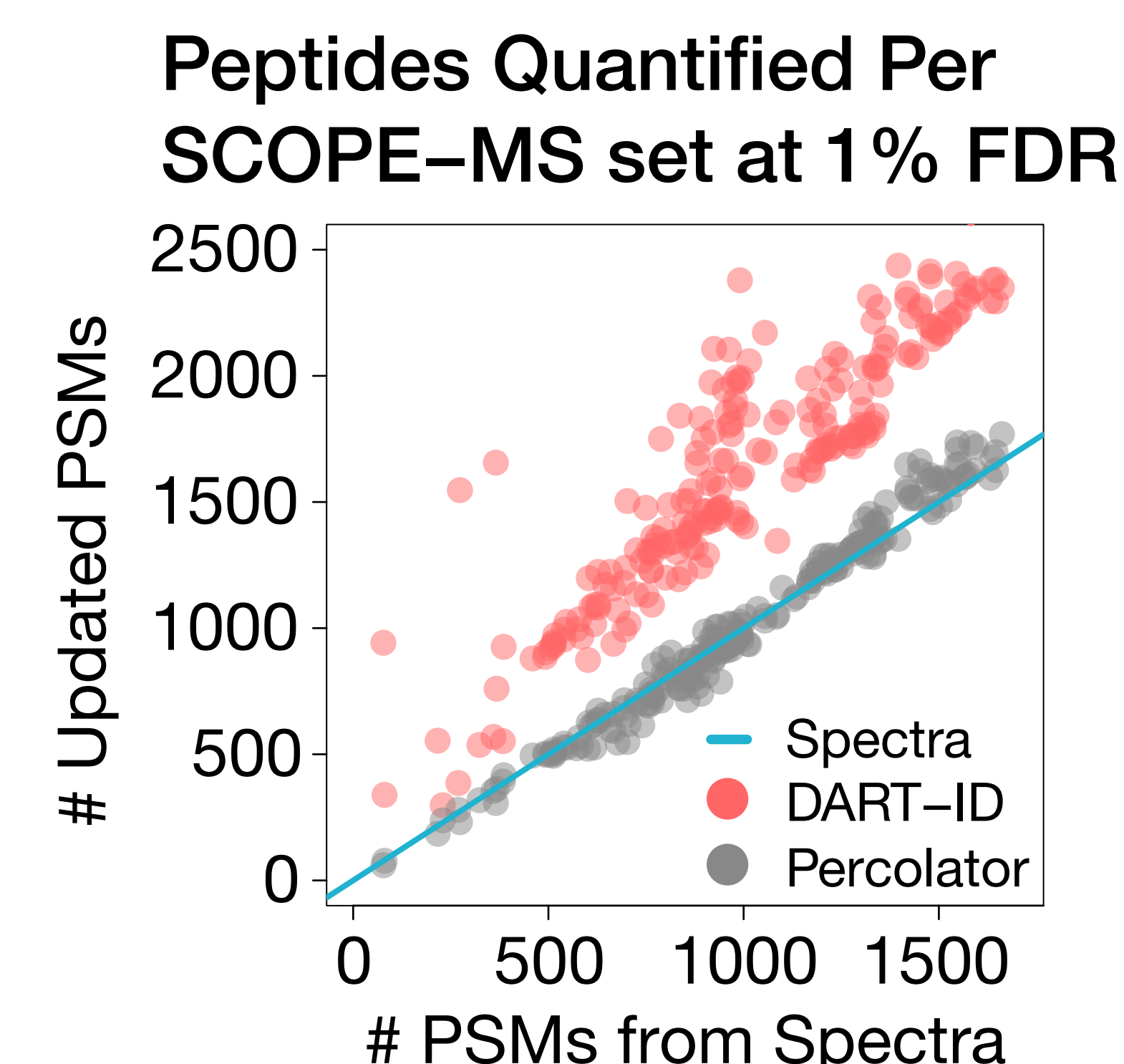
$$P(\text{ID correct} \mid \text{RT}) = \frac{P(\text{RT} \mid \text{ID correct}) \times P(\text{ID correct})}{P(\text{RT})}$$

- Distributions generated from a mixture model
- PSM 1 - confidence downgraded
- PSM 2 - confidence upgraded

Global RT Alignment: Residuals < 1 min for 60 min LC Runs



Identify More Peptides and Differentially Abundant Proteins



New IDs are Consistent and Separate Cell Types

