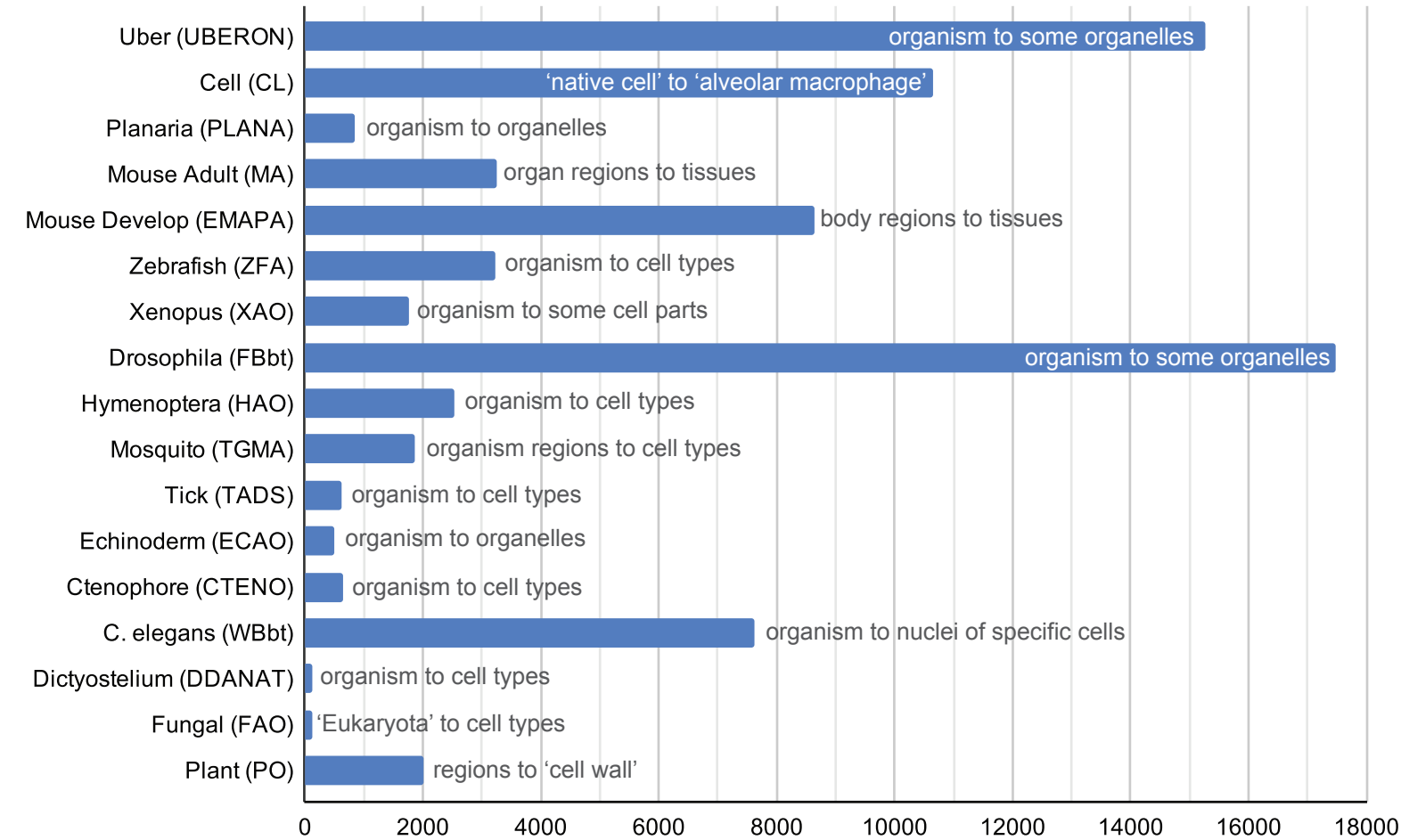
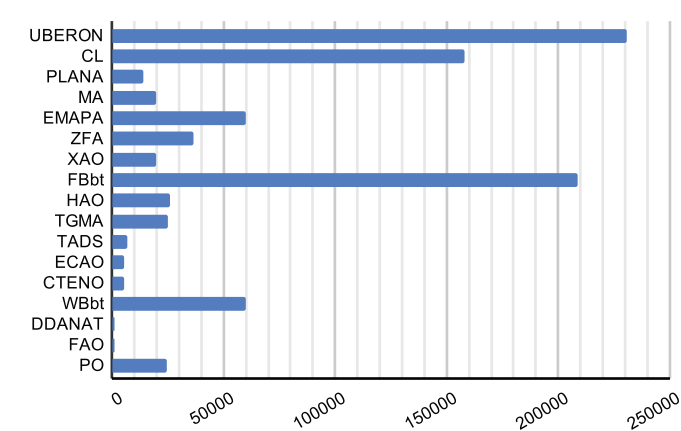


A Classes per Ontology



B Axioms per Ontology



C Axioms per Class

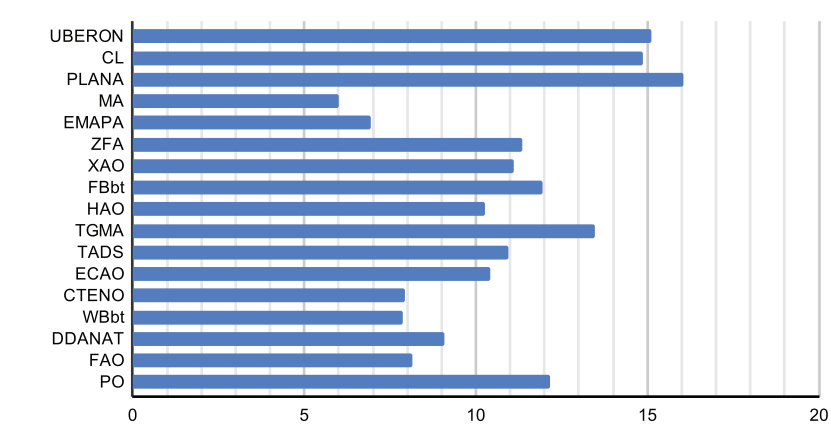
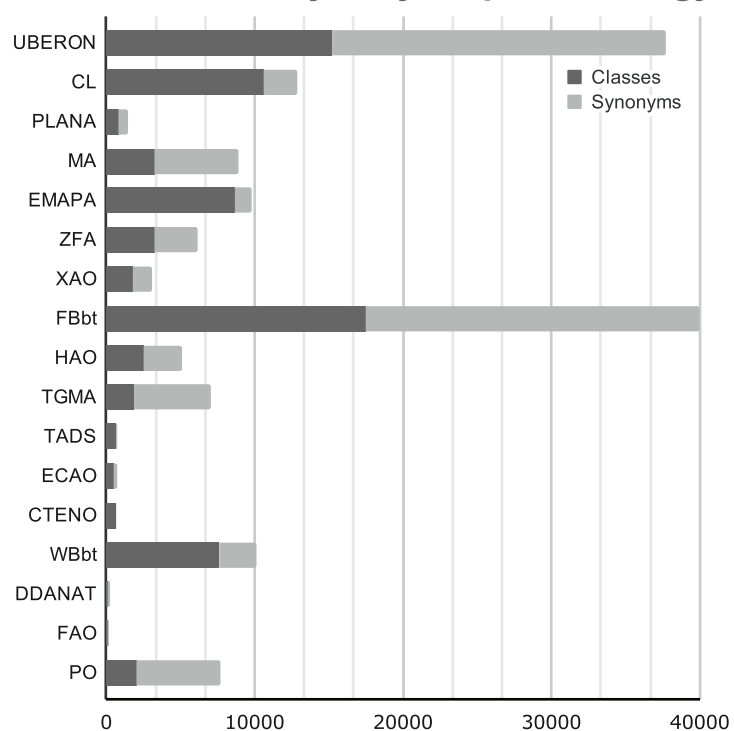


Fig. S1. Benchmark-driven comparisons of PLANA and other anatomy ontologies A) Total classes per anatomy ontology with the range of classes annotated to the right (largest scale classes/categories to smallest scale classes/categories). B) Number of axioms per ontology. C) Axioms per Class as a metric of average relational complexity. PLANA's complexity is comparable to other commonly used anatomy ontologies.

A Classes and Synonyms per Ontology



B Overlap of Classes and Synonyms

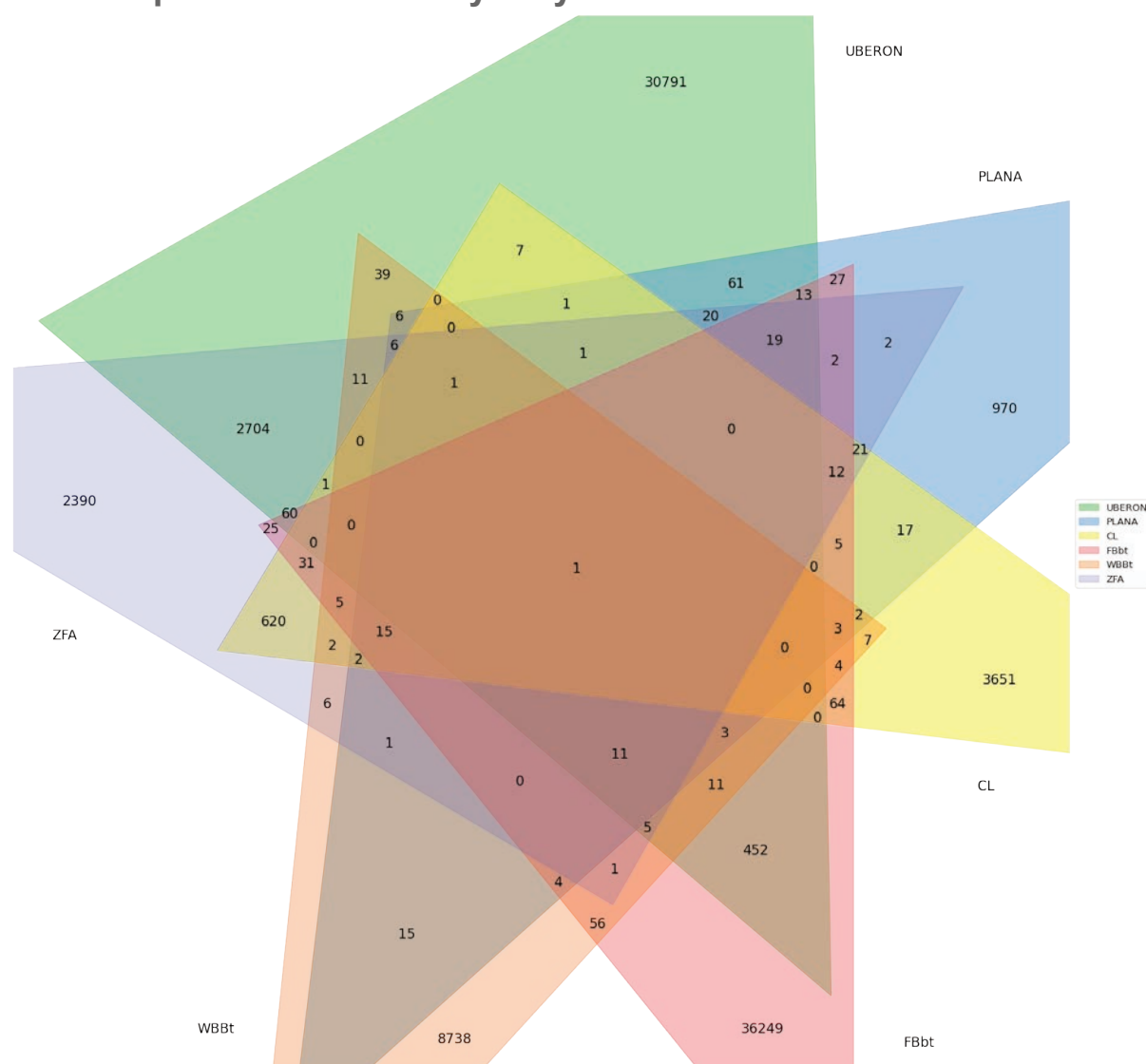


Fig. S2. Classes and synonyms between ontologies

A) Ratio of number of classes to synonyms for common anatomy ontologies. B) Overlap between ontologies by their classes and synonym.

A

basal lamina of epidermis
PLANA:0001005

homologous dbxref annotations:

basal lamina of epithelium
UMLS:C0085872

basal lamina
ZFA:0001485

basal lamina
EHDAA2:0003065

basal lamina
BILA:0000065

basal lamina of epithelium
VHOG:0001592

basal lamina
CARO:0000065

basal lamina
HAO:0000065

basal lamina
TAO:0001485

basement membrane
MESH:D001485

basal lamina
TGMA:0001850

basal lamina
XAO:0003163

basal lamina
FMA:62918

basal lamina
NIF_Subcellular:sao1397492660

basal lamina
WBbt:0005756

basal lamina
AEO:0000065

B

Ontologies in PLANA's dbxref fields

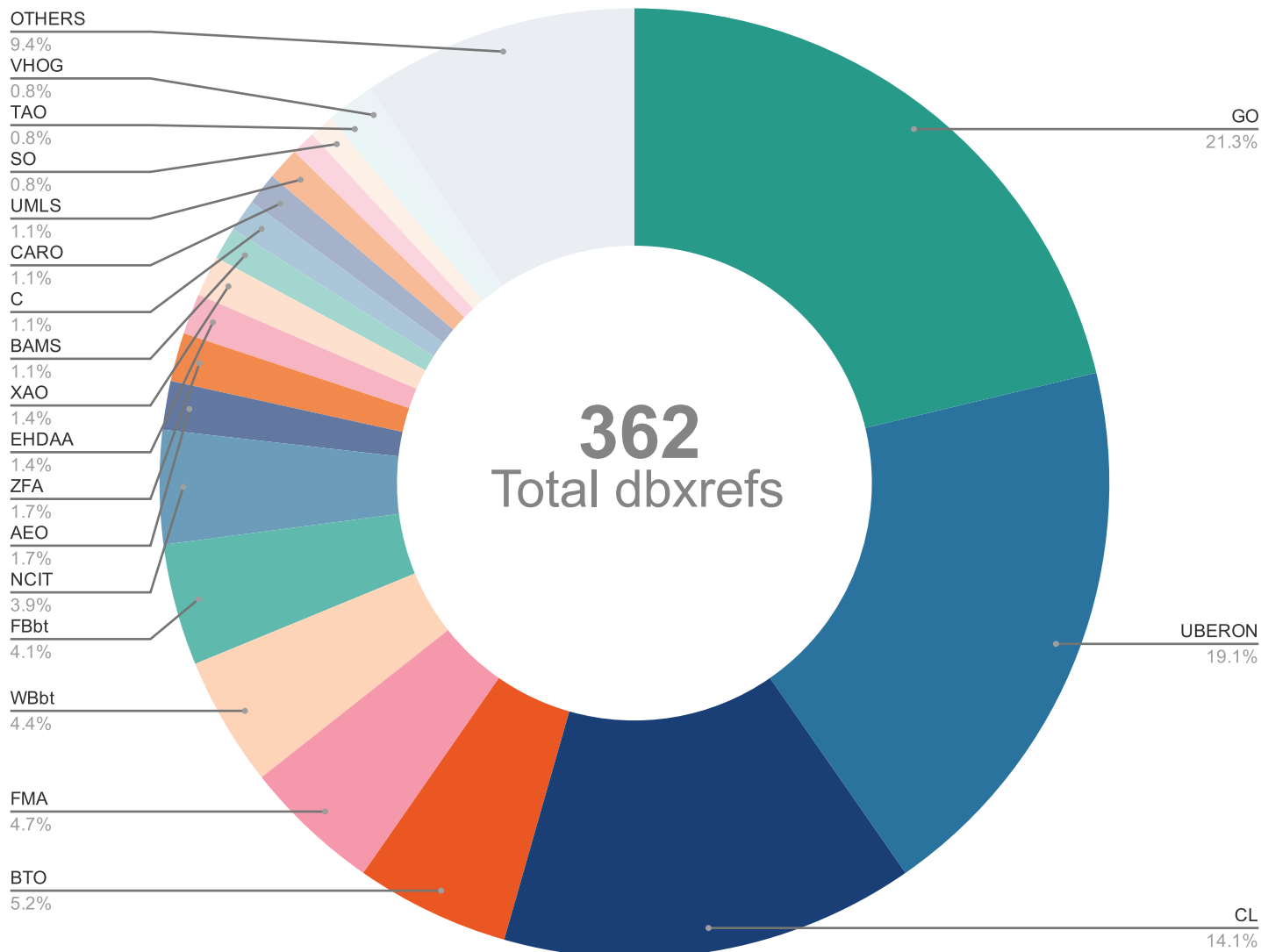


Fig. S3. Interoperability metrics

A) The dbxref annotation field confers interoperability through linkages to other anatomy ontologies, via “homologous” classes. For example, the PLANA class ‘basal lamina of epidermis’ has 15 “homologous” classes in 15 other ontologies. Class color reflects ontology as it is displayed in B. B) Breakdown of dbxref field by ontology referenced.

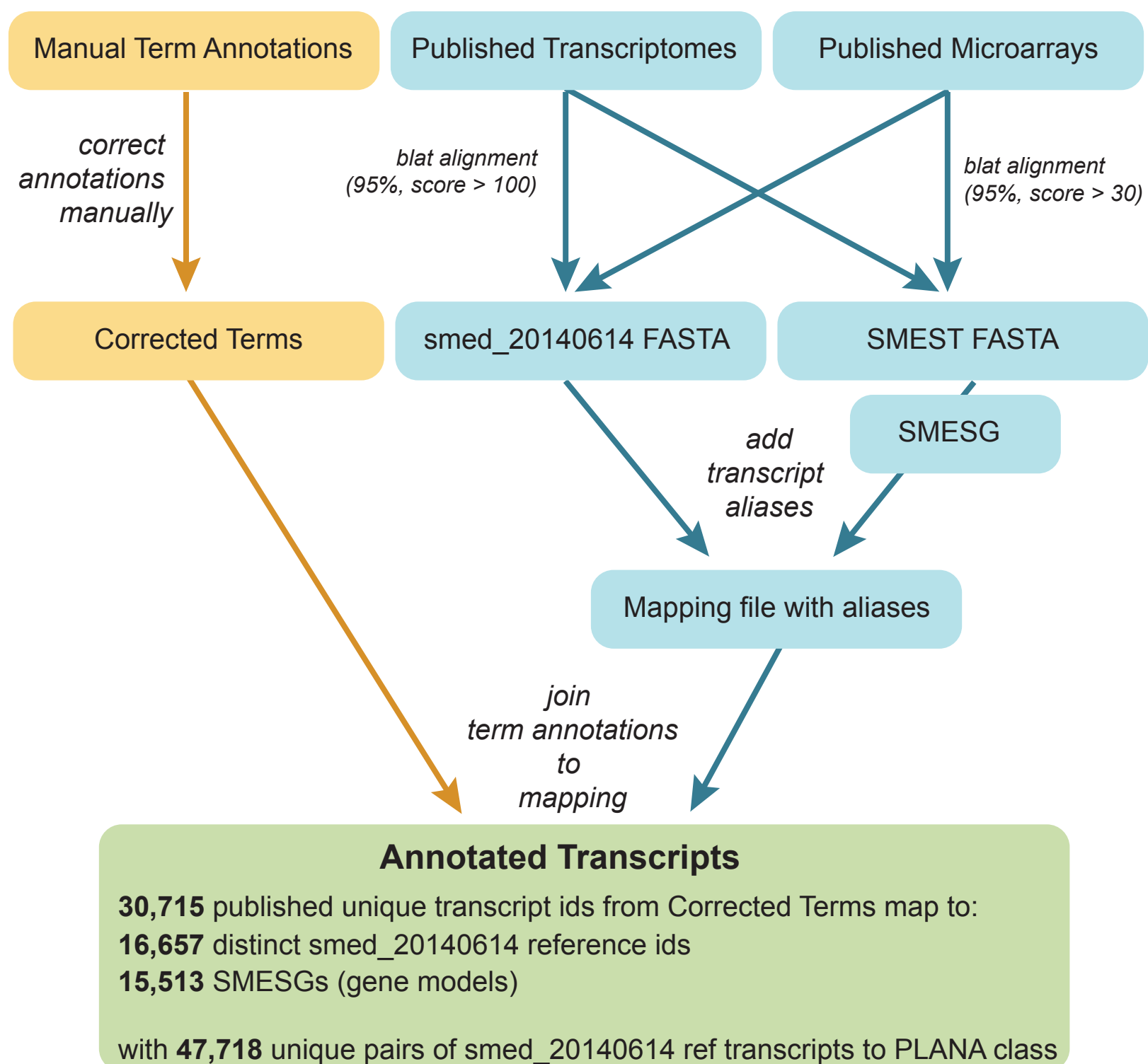


Fig. S4. Mapping workflow for PAGE

Manual term annotations were reviewed for proper accession names and fields to make a Corrected Terms set (right side, yellow). Published transcriptomes and microarrays were aligned with the reference smed_20140614 transcriptome and dd_Smes_v2 transcriptome; transcript aliases were added to create a Mapping File (left side, blue). The transcript IDs in the Corrected Terms file were then mapped to the reference transcriptome and ultimately gene models using the Mapping File.

Table S1. List of 200 publications comprising the literature review for Smed anatomical terms

[Click here to download Table S1](#)

Table S2. PLANA Classes and IDs used in the manuscript

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Table S3. Composite Patterns

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Table S4. Competency questions for DL queries

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Table S5. GO Terms used in PLANA

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Table S6. PAGE PLANA Term Coverage

[Click here to download Table S6](#)

Table S7. PAGE Transcript Search

[Click here to download Table S7](#)

Table S8

[Click here to download Table S8](#)

Table S9

[Click here to download Table S9](#)

Table S10

[Click here to download Table S10](#)

Table S11

[Click here to download Table S11](#)

Table S12. MIRO Reporting for PLANA

[Click here to download Table S12](#)

Table S13. All repositories referenced in manuscript

[Click here to download Table S13](#)

Table S14. Transcriptome Mapping for PAGE

[Click here to download Table S14](#)

Table S15. Regular Expressions used to parse transcriptome ids

[Click here to download Table S15](#)

Table S16. PAGE Curation Rules

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