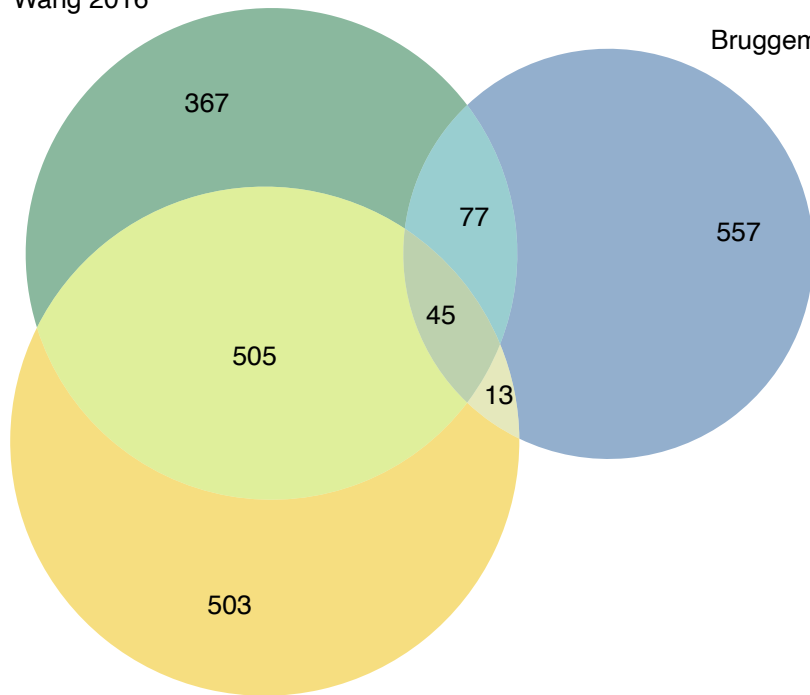


Published CT / germ-cell cancer sets
Mapped protein-coding nominations, before HPA filtering

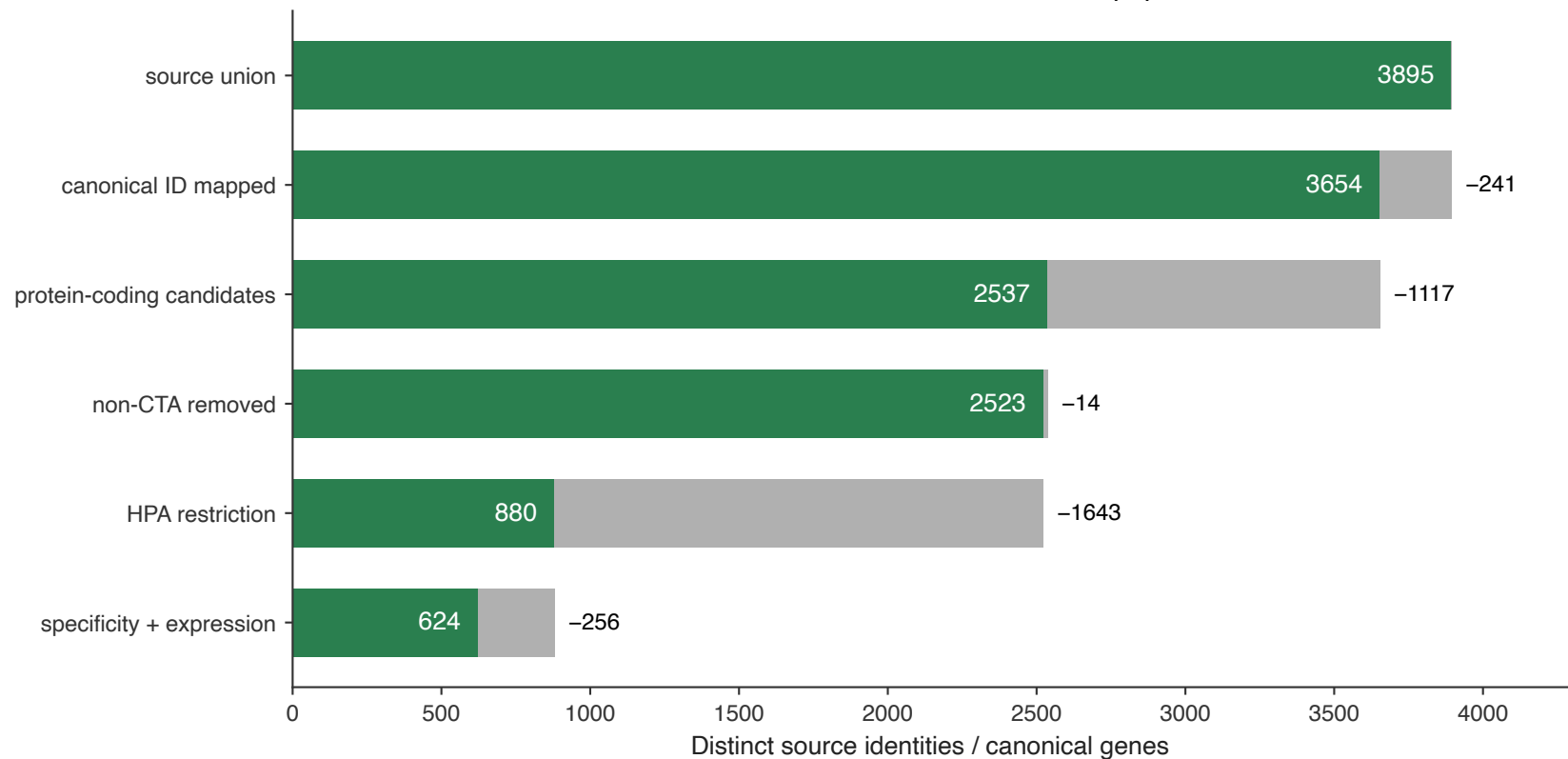
Wang 2016

Bruggeman 2018

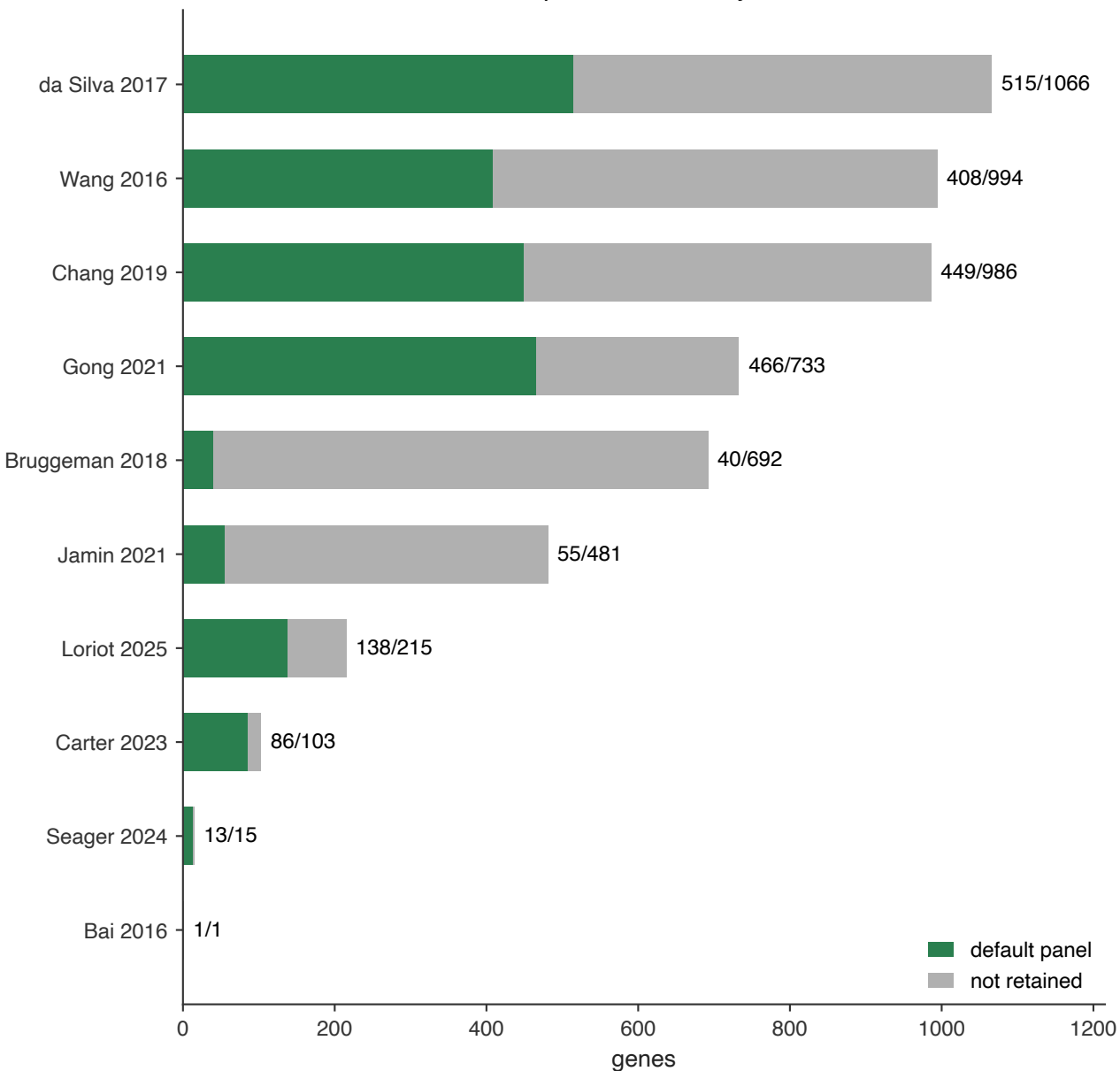


da Silva 2017

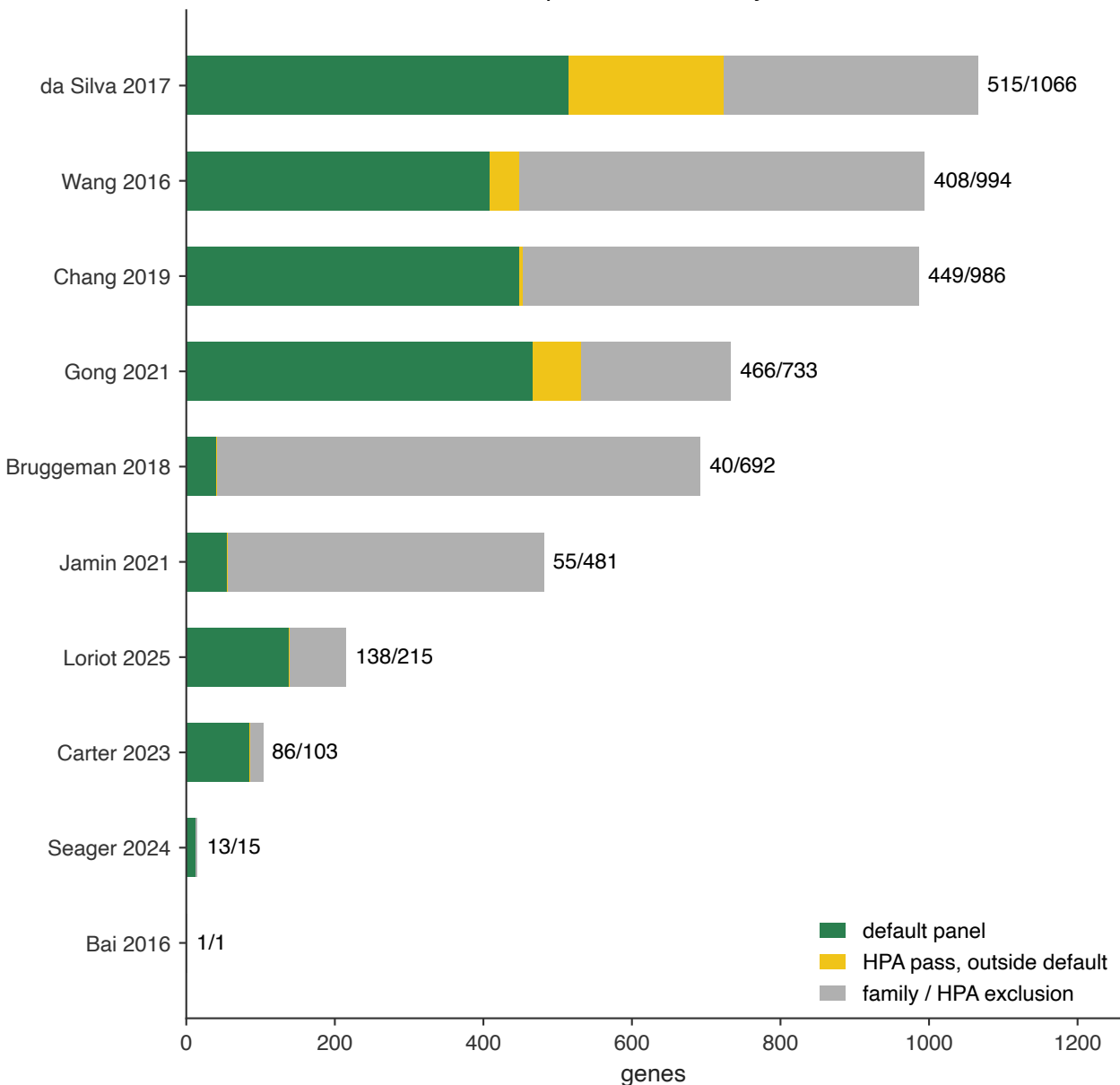
Full union of the ten minimum-cover papers



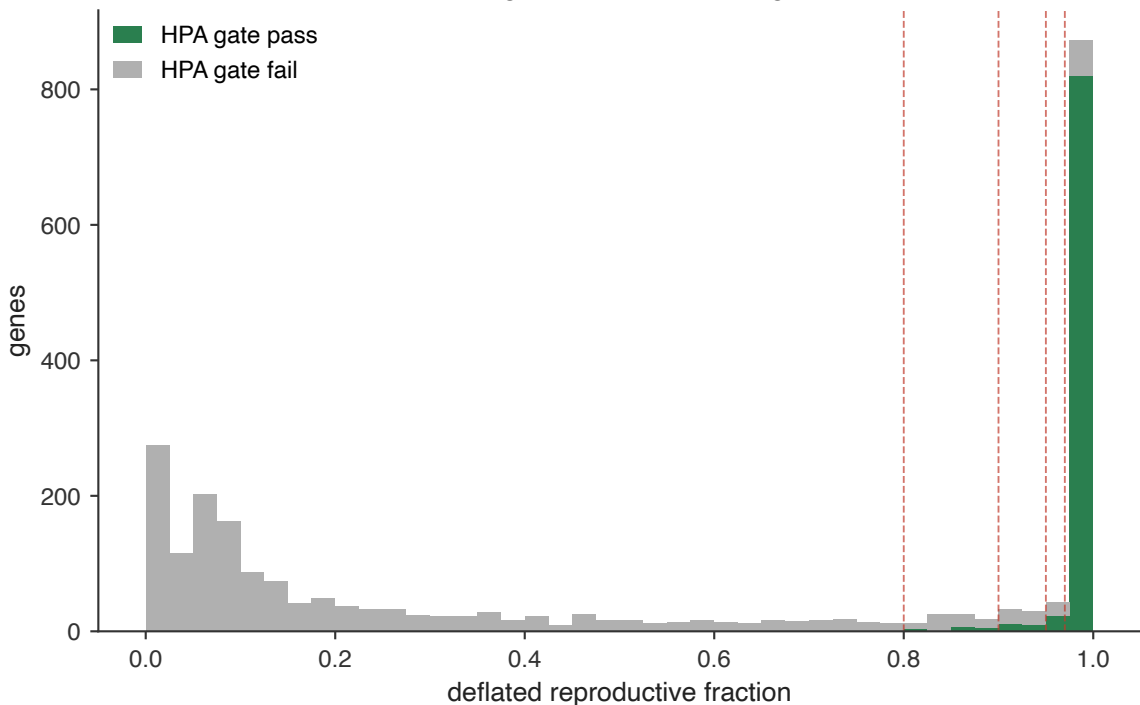
Default-panel retention by source



Default-panel outcomes by source

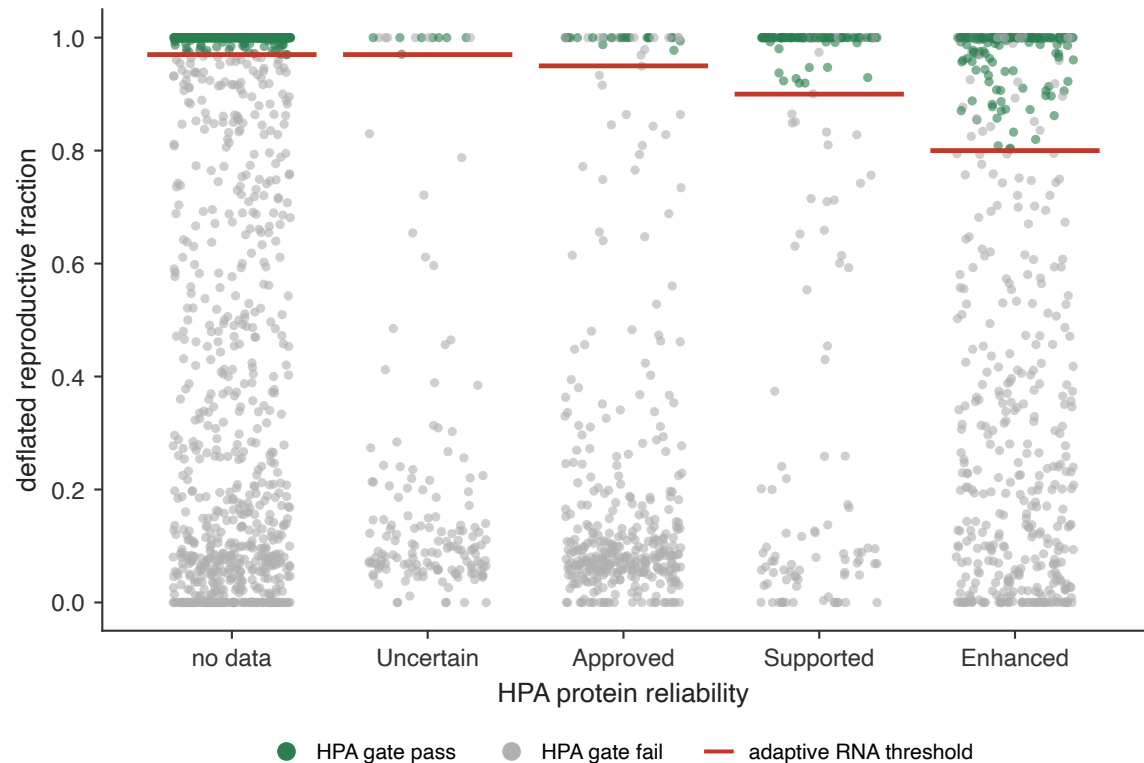


HPA restriction gate across all coding candidates



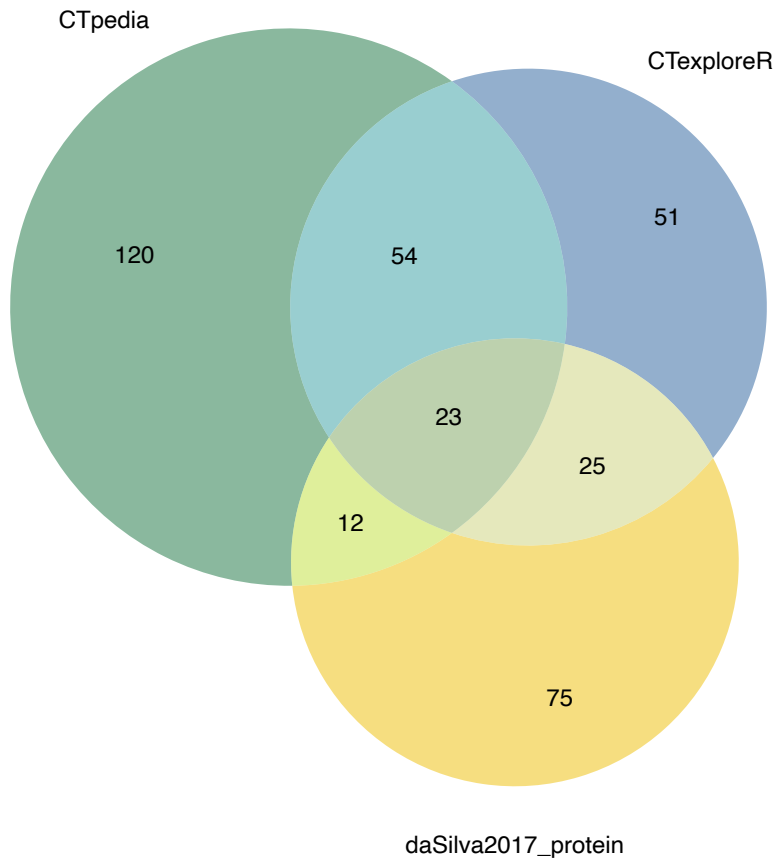
6 candidates lack RNA fractions and are omitted here. HPA pass precedes final-panel curation.

HPA protein reliability and reproductive RNA



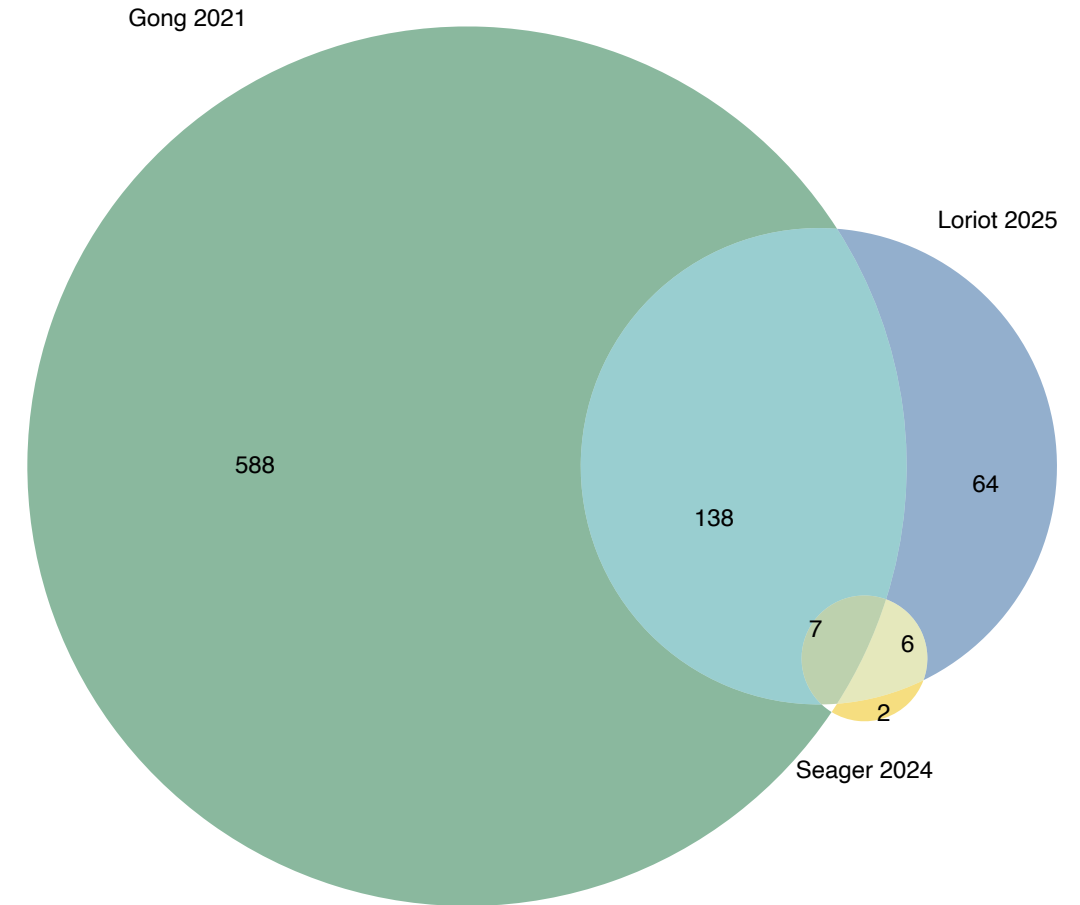
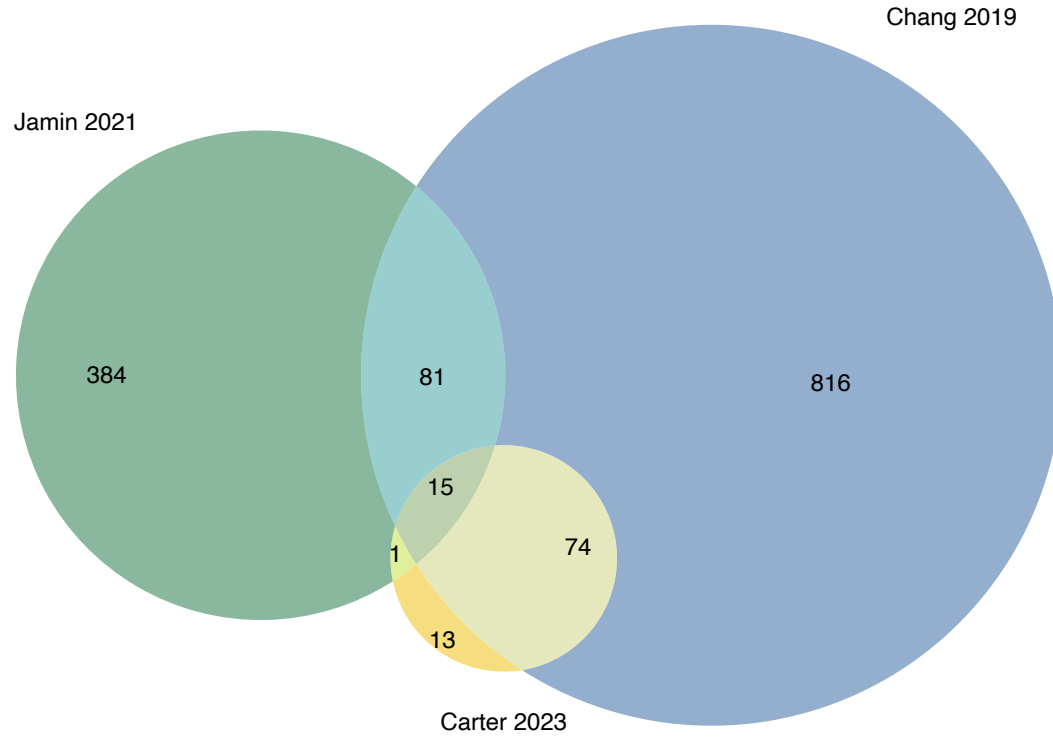
6 candidates lack RNA fractions and are omitted here. HPA pass precedes final-panel curation.

Historical tags (audit only)
Not the paper-union intake or independent validation



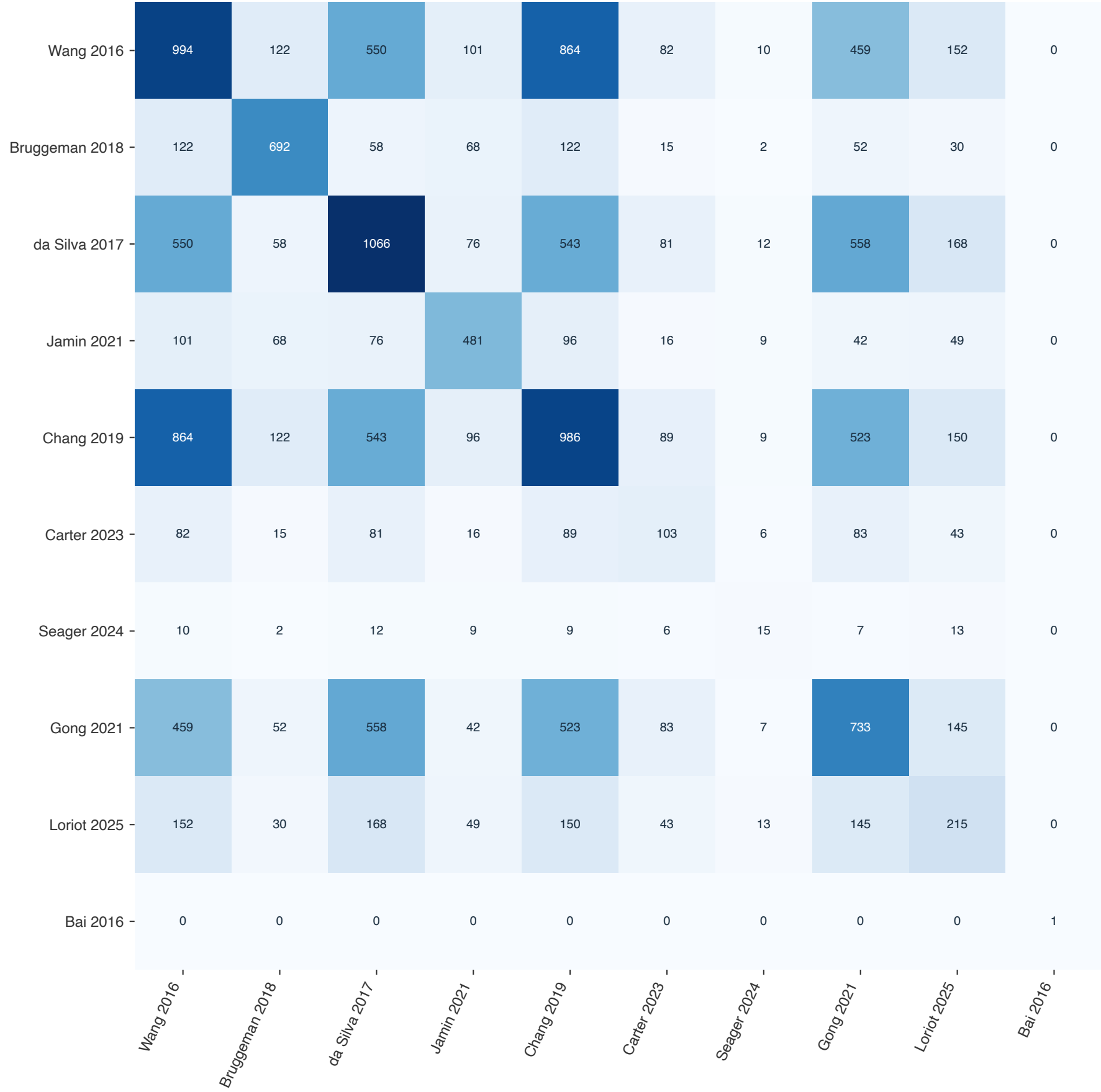
Reproductive enrichment and cancer-germline lists

Additional complete candidate lists

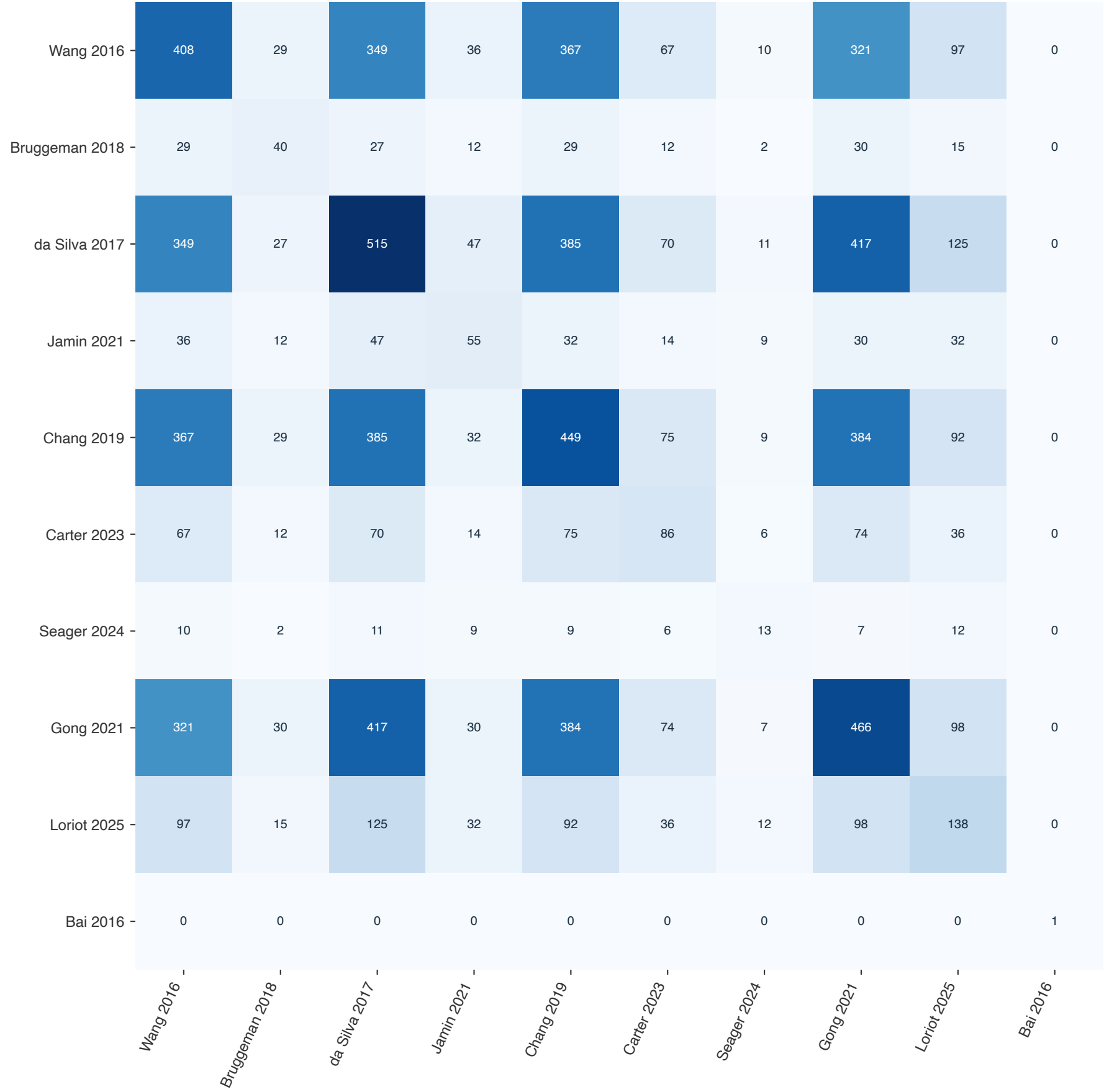


Unique mapped coding genes before HPA filtering. Bai's single EGFL6 nomination is shown in the all-paper matrix. Normal-only reproductive nominations remain candidates; shared probes do not establish locus-specific validation.

Complete coding candidate pool

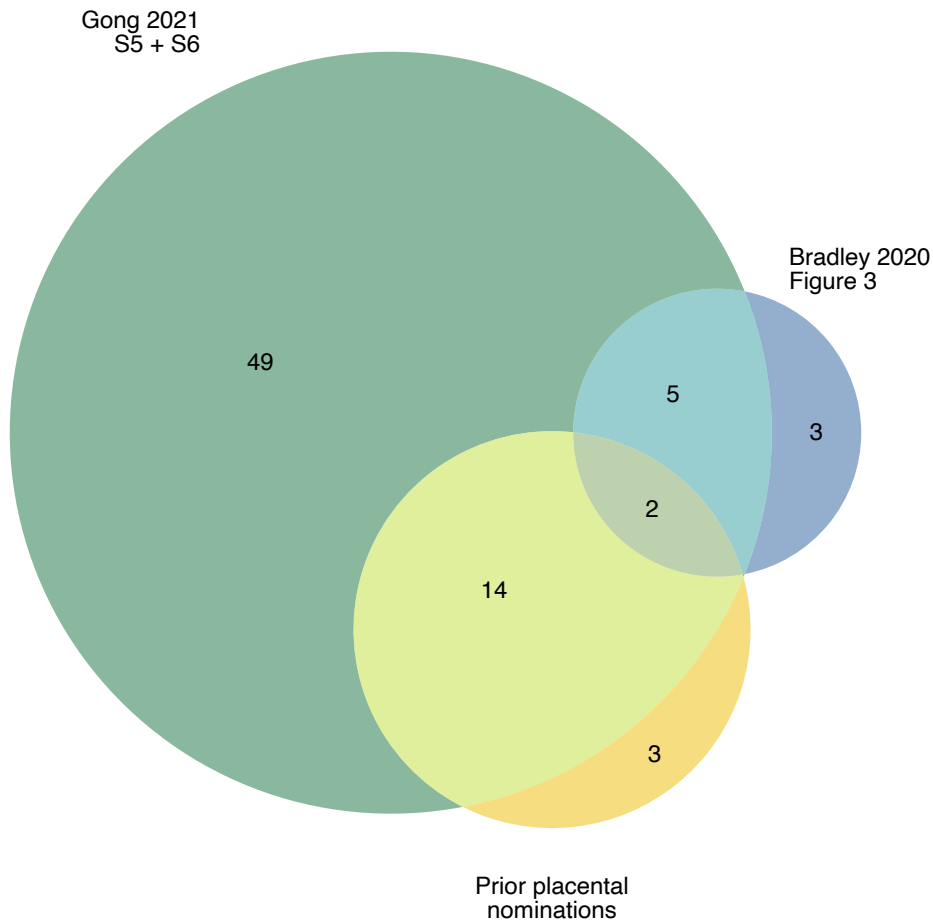


Retained by current default rules



Cells count unique shared genes; diagonals are source totals. Nested and overlapping sources must not be summed.

Placental source audit (includes unselected Bradley)
Mapped coding candidates before HPA filtering



Ten selected papers: full lists through curation

Jamin 2021	605	498	481	481	56	55
Chang 2019	1,036	1,031	986	979	453	449
Wang 2016	1,019	1,018	994	987	449	408
Bruggeman 2018	756	734	692	692	42	40
Gong 2021	1,809	1,704	733	727	532	466
Carter 2023	103	103	103	102	86	86
Bai 2016	1	1	1	1	1	1
Seager 2024	17	15	15	15	13	13
Loriot 2025	280	280	215	213	139	138
da Silva 2017	1,104	1,100	1,066	1,055	724	515
	Unique source identities	Unique IDs mapped	Protein coding	Family filter	HPA restriction	Default rules

Counts after each stage; shading is the fraction retained within that source

Source identities collapse mapped aliases and repeated entries across tables within each paper; unresolved probes remain upstream.
 Paper lists overlap and must not be summed. RNA/protein nomination does not establish HLA presentation.

All 19 earlier placental nominations now have publication provenance

	Gong 2021	Bradley 2020	Rull 2005	Rull 2008*	Kubiczak 2013*	Bialas 2020	McKellar 2025†
CGB1			•	•	•	•	
CGB2 [D]			•	•	•	•	
CGB3	•	•					
CGB5	•	•					
CGB7			•				•
CSH1	•						
ERVFRD-1	•						
ERVH48-1 [D]	•						
ERVV-1	•						
ERVV-2 [D]	•						
ERVW-1	•						
GH2	•						
LGALS13 [D]	•						
LGALS14 [D]	•						
LGALS16 [D]	•						
PSG2 [D]	•						
PSG4	•						
PSG6 [D]	•						
PSG7 [D]	•						

[D] Retained in default CTA panel (9/19). Blank cells mean no record in these curated source rows.

* Combined CGB1/CGB2 assays, not separate positives. † Preprint.

Expression / nomination evidence is distinct from gene-specific antigen validation.