

CTA screen: expanded permitted tissues

Human HPA v23 | vital RNA ≤ 1 nTPM; protected RNA ≤ 5 nTPM

Permitted: all reproductive organs, mammary, placenta/extraembryonic and explicit embryonic/fetal contexts; cutaneous melanocytes and hair follicles; plus whole skin, salivary glands and thymus. Whole-skin permission includes its mapped cellular compartments. Generic unsited cell types, eye, retina and inner ear do not become skin. This is an explicit project screening allowance.

Exact rules

All 2,537 protein-coding candidates from the 11 registered publication sources are screened. Each valid RNA measurement is compared with its tissue-specific ceiling using raw HPA v23 nTPM: vital ≤ 1 ; protected ≤ 5 . There is no averaging across tissues or subtraction of a noise floor. Any Low, Medium, High, Ascending or Descending IHC observation outside the permitted set blocks retention. At least one permitted RNA observation ≥ 1 nTPM or positive permitted IHC is required. All 50 routine bulk RNA contexts must be measured. Unmapped or tier-unresolved positive anatomy, unusable measurements and previously reviewed unreliable IHC prevent retention. Family exclusions and existing nomination/manual reviews also apply. Missing IHC is explicitly RNA-only observed compatibility; partial IHC remains partial. Neither establishes protein absence. Complete routine IHC means all 80 specified tissue/cell contexts. Routine contexts are those represented for at least half the genes in their source; the manifest lists them.

Vital roots: heart, lung, bronchus, brain, spinal cord, liver, kidney, bone marrow, blood, adrenal gland, pituitary gland, pancreas, small intestine, skeletal muscle, smooth muscle, peripheral nerve, endothelium. All mapped brain regions and organ descendants inherit these roots.

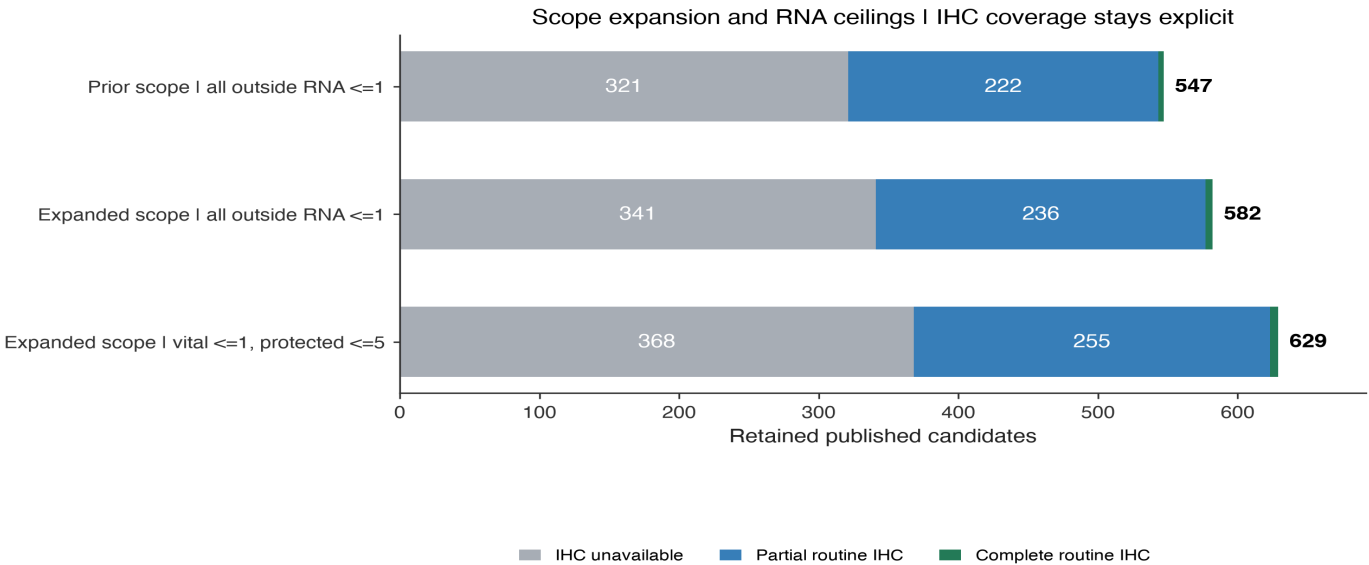
Protected roots: adipose tissue, retina, eye, inner ear, thyroid gland, parathyroid gland, lymph node, spleen, tonsil, appendix, esophagus, stomach, colon, rectum, gallbladder, urinary bladder, ureter, cartilage, oral mucosa, nasopharynx, tongue. Head, foot and generic soft tissue remain unresolved.

The tier assignment is a conservative project policy, not a clinically validated list of expendable organs. The clinical references motivate review of organ injury; they do not establish the 1/5 nTPM thresholds. The numerical analysis is human HPA v23 bulk RNA and normal IHC only. Anatomy transfers to dog and mouse; these human RNA thresholds and tolerability assumptions do not. Single-cell RNA, tumor expression and peptide-HLA presentation are not evaluated here. Developmental tissues absent from HPA remain unassessed.

Results

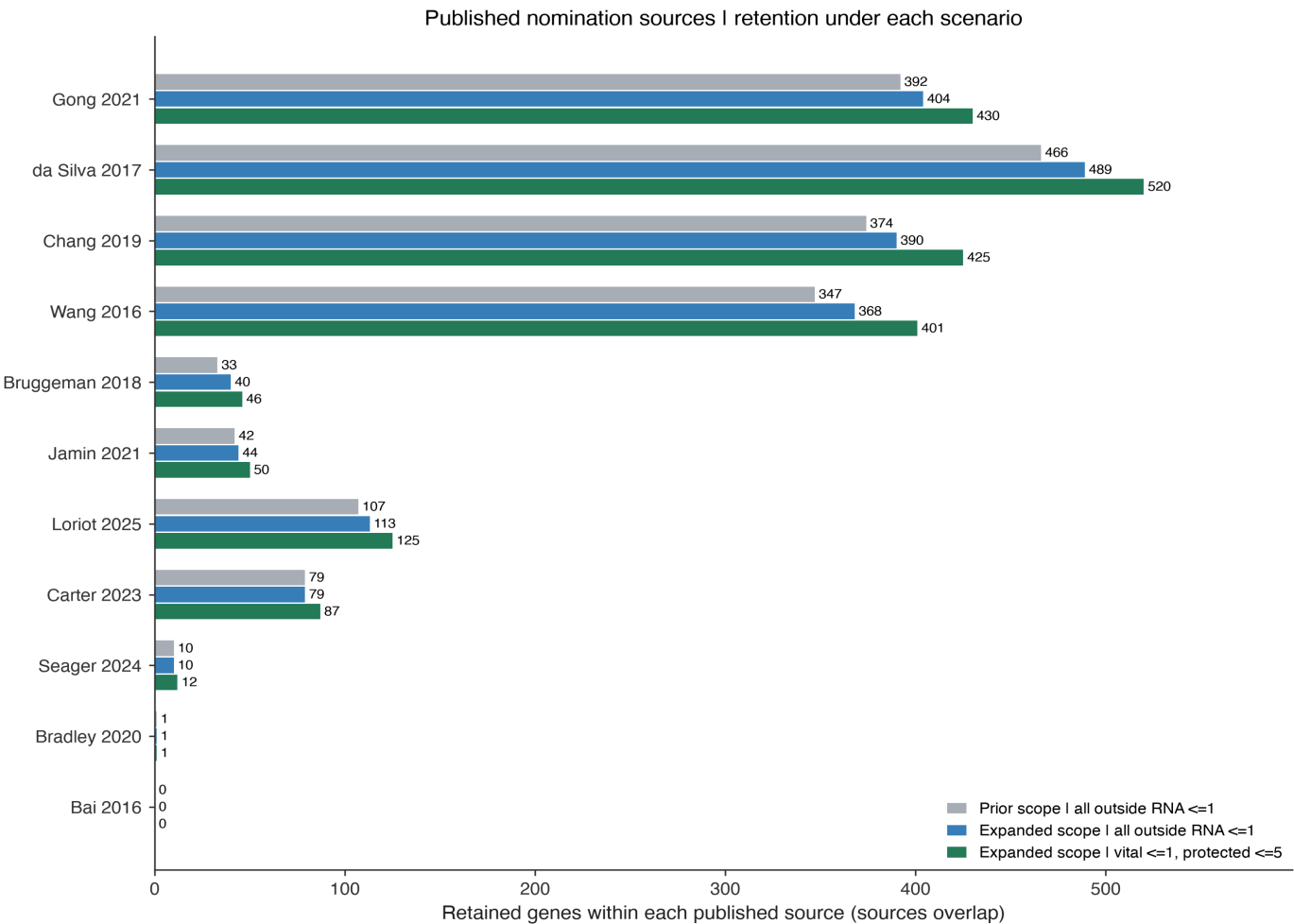
Scenario	Retained	No IHC	Partial IHC	Complete IHC
Prior scope all outside RNA ≤ 1	547	321	222	4
Expanded scope all outside RNA ≤ 1	582	341	236	5
Expanded scope vital ≤ 1 , protected ≤ 5	629	368	255	6

Policy comparison



Published source retention

All 11 registered sources enter the same 2,537-gene protein-coding universe. Sources overlap and cannot be summed.



Selected published targets

Green means retained under the stated evidence and curation gates. Missing IHC remains unassessed. All exact exclusion reasons follow in the table.

Selected published targets | all evidence and curation gates

	Prior scope 1 nTPM	Expanded scope 1 nTPM	Expanded scope 1 / 5 nTPM
PRAME	Out	Out	Out
KK-LC-1	Out	Keep	Keep
NY-ESO-1	Keep	Keep	Keep
LAGE-1	Out	Out	Out
MAGE-A1	Keep	Keep	Keep
MAGE-A3	Keep	Keep	Keep
MAGE-A4	Keep	Keep	Keep
MAGE-A10	Keep	Keep	Keep
MAGE-A11	Out	Out	Out
MAGE-C1 / CT7	Keep	Keep	Keep
MAGE-C2	Keep	Keep	Keep
XAGE1B	Out	Out	Out
XAGE1A	Keep	Keep	Keep
SSX1	Keep	Keep	Keep
SSX2	Keep	Keep	Keep
ROPN1	Out	Keep	Keep
ROPN1B	Out	Out	Out
LDHC	Out	Out	Out
HORMAD1	Out	Out	Keep
HORMAD2	Out	Out	Out
PAGE4	Out	Out	Out
PAGE2B	Out	Out	Out
FATE1	Out	Keep	Keep
LIN28B	Out	Out	Keep
PIWIL1	Out	Out	Keep

■ Retained
 ■ Excluded or unresolved

Known and published targets: decisions

Selected clinical and research targets. Exclusions summarize up to two observations per assay; the CSV contains every failing context. Existing manual reviews remain separate from the new expression gates.

Target	Result	Evidence / reason
PRAME	Out / unresolved	adrenal gland: 3.6 nTPM (vital, limit 1); kidney: 1.8 nTPM (vital, limit 1)
KK-LC-1	Included	Included; IHC unavailable
NY-ESO-1	Included	Included; IHC partial
LAGE-1	Out / unresolved	heart muscle: 5.1 nTPM (vital, limit 1); kidney: 3.4 nTPM (vital, limit 1); +2 more; existing nomination or manual review
MAGE-A1	Included	Included; IHC partial
MAGE-A3	Included	Included; IHC unavailable
MAGE-A4	Included	Included; IHC partial
MAGE-A10	Included	Included; IHC partial
MAGE-A11	Out / unresolved	existing nomination or manual review
MAGE-C1 / CT7	Included	Included; IHC partial
MAGE-C2	Included	Included; IHC partial
XAGE1B	Out / unresolved	liver: 1.5 nTPM (vital, limit 1); lung: 1.2 nTPM (vital, limit 1)
XAGE1A	Included	Included; IHC unavailable
SSX1	Included	Included; IHC partial
SSX2	Included	Included; IHC partial
ROPN1	Included	Included; IHC partial
ROPN1B	Out / unresolved	basal ganglia: 2.9 nTPM (vital, limit 1); heart muscle: 2.9 nTPM (vital, limit 1); +5 more
LDHC	Out / unresolved	liver: 1.4 nTPM (vital, limit 1); pancreas: 1.3 nTPM (vital, limit 1)
HORMAD1	Included	Included; IHC partial
HORMAD2	Out / unresolved	liver: 2.8 nTPM (vital, limit 1)
PAGE4	Out / unresolved	smooth muscle: 23.3 nTPM (vital, limit 1); adrenal gland: 5.5 nTPM (vital, limit 1); +5 more
PAGE2B	Out / unresolved	bone marrow: 4 nTPM (vital, limit 1)
FATE1	Included	Included; IHC partial
LIN28B	Included	Included; IHC partial
PIWIL1	Included	Included; IHC partial
TDRD1	Out / unresolved	kidney: 1.6 nTPM (vital, limit 1)
BRDT	Out / unresolved	bone marrow: 2.6 nTPM (vital, limit 1)
CABYR	Out / unresolved	choroid plexus: 12.7 nTPM (vital, limit 1); pituitary gland: 8 nTPM (vital, limit 1); +13 more

Target	Result	Evidence / reason
EGFL6	Out / unresolved	lung: 24.8 nTPM (vital, limit 1); adipose tissue: 19.5 nTPM (protected, limit 5); +3 more
GAGE12F	Out / unresolved	stomach: 8.3 nTPM (protected, limit 5)
GAGE12G	Out / unresolved	stomach: 5.9 nTPM (protected, limit 5)
GAGE12J	Included	Included; IHC partial
GAGE13	Included	Included; IHC partial
MAGEB6	Out / unresolved	kidney / proximal tubules (microvilli): Medium (Enhanced); reviewed unreliable ihc
CT45A8	Out / unresolved	heart muscle / cardiomyocytes: Low (Supported); reviewed unreliable ihc
CT45A10	Out / unresolved	hippocampal formation: 1.4 nTPM (vital, limit 1); amygdala: 1.2 nTPM (vital, limit 1); +1 more
HAGE	Out / unresolved	duodenum: 1.2 nTPM (vital, limit 1); pancreas: 1.2 nTPM (vital, limit 1); lung / macrophages: Medium (Enhanced)
BORIS	Included	Included; IHC partial
AKAP4	Included	Included; IHC partial
PLAC1	Included	Included; IHC partial
PASD1	Included	Included; IHC partial
LY6K	Out / unresolved	esophagus: 12.1 nTPM (protected, limit 5); adipose tissue: 5.2 nTPM (protected, limit 5); +11 more

Evidence and citations

[HPA v23 bulk RNA](#)

[HPA v23 normal IHC](#)

[NCI organ inflammation](#)

[NIDDK adrenal insufficiency](#)

[PRAME clinical TCR study](#)

[KK-LC-1 clinical trial](#)

[ROPN1 preclinical TCR study](#)

[Original source-intake audit and publication citations](#)