

CTA screen: IHC-adaptive RNA ceilings

Human HPA v23 | approved project policy | 2026-10-20

Local negative IHC reliability	Vital maximum nTPM	Protected maximum nTPM
Missing	1	5
Uncertain	1	5
Approved	2	5
Supported	3	7.5
Enhanced	5	10

The same 2,537 published candidates and permitted tissue union are evaluated in both screens. The fixed screen uses vital ≤ 1 nTPM and protected ≤ 5 nTPM. The adaptive screen increases those ceilings only when all routine IHC tissue/cell contexts for the same anatomical tissue have valid Not detected results. The routine inventory is frozen from contexts measured for at least half of the source's measured genes. The weakest reliability among all IHC observations in that tissue determines the ceiling. Extra positive or invalid observations prevent relaxation. Missing contexts, unknown reliability, Uncertain reliability and reviewed-unreliable IHC cannot increase a ceiling. A narrow brain region cannot clear a broader RNA region. Negative evidence in another organ cannot supply support. These are tissue-specific observation rules, not claims of complete biological sampling.

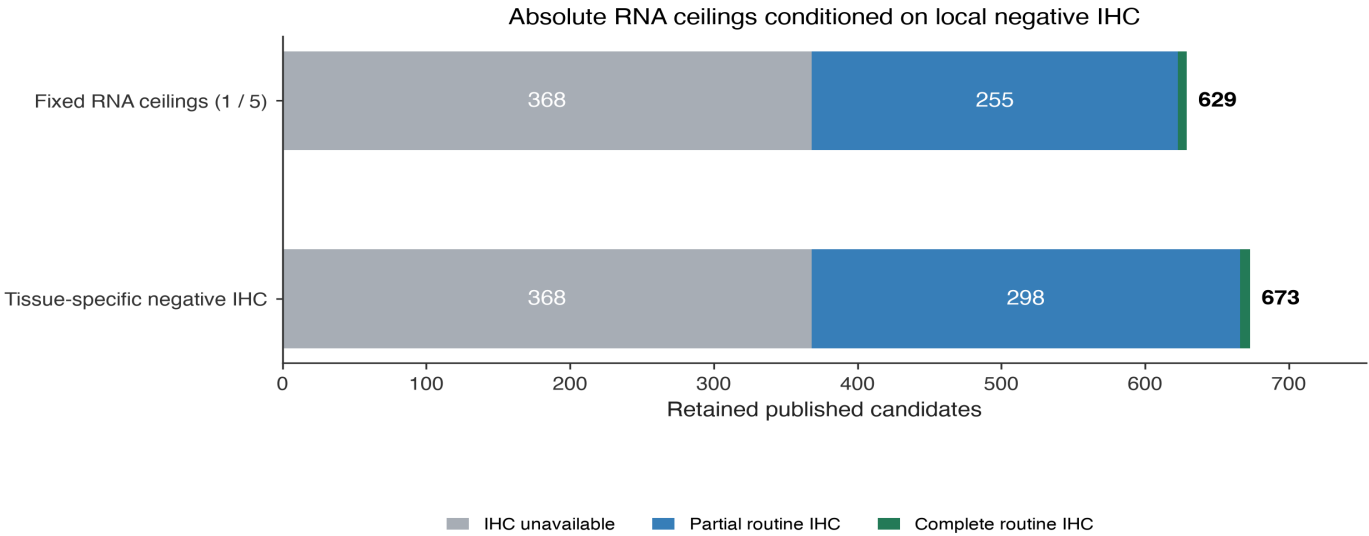
Any positive IHC outside the permitted set, including Low, remains an independent exclusion. Complete routine bulk RNA (50 contexts), positive evidence in the permitted set (RNA ≥ 1 nTPM or positive IHC), resolved positive anatomy and usable observations remain required. Existing family exclusions and manual nomination decisions remain separate gates. Complete routine IHC means 80 tissue/cell contexts; missing and partial coverage remain explicit. RNA is pinned human HPA v23 consensus nTPM with inclusive ceilings, no rounding to pass a cutoff, and no subtraction or averaging across organs.

The 1/5, 2/5, 3/7.5 and 5/10 nTPM values are user-approved starting project parameters, not clinically validated safety limits. Enhanced is an HPA validation label, not a guaranteed detection limit for a negative stain. Routine negative IHC does not establish absence of protein or peptide-HLA presentation. Anatomical definitions apply across human, dog and mouse; these numerical rules apply only to human HPA v23. The existing core/extended CTA API panels retain their separately documented selection rules.

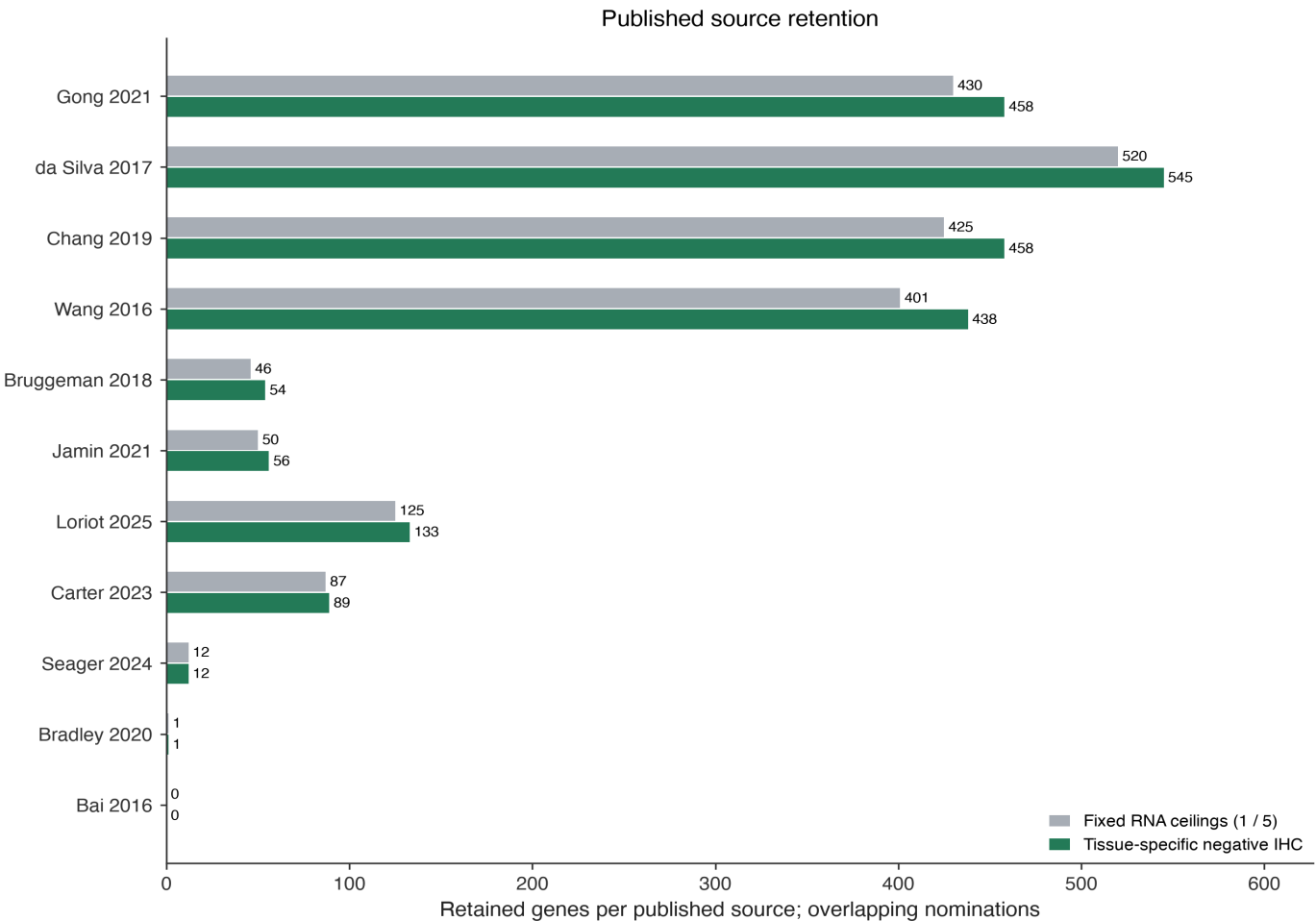
Results and coverage

Scenario	Retained	No IHC	Partial IHC	Complete IHC
Fixed RNA ceilings (1 / 5)	629	368	255	6
Tissue-specific negative IHC	673	368	298	7

Policy comparison



Published source retention



Sources overlap and cannot be summed. The complete audit includes all 2,537 published candidates.

Known and published targets

42 published targets | all evidence and curation gates

	Fixed 1 / 5 nTPM	IHC-adaptive ceilings
PRAME	Out	Keep
KK-LC-1	Keep	Keep
NY-ESO-1	Keep	Keep
LAGE-1	Out	Out
MAGE-A1	Keep	Keep
MAGE-A3	Keep	Keep
MAGE-A4	Keep	Keep
MAGE-A10	Keep	Keep
MAGE-A11	Out	Out
MAGE-C1 / CT7	Keep	Keep
MAGE-C2	Keep	Keep
XAGE1B	Out	Out
XAGE1A	Keep	Keep
SSX1	Keep	Keep
SSX2	Keep	Keep
ROPN1	Keep	Keep
ROPN1B	Out	Out
LDHC	Out	Keep
HORMAD1	Keep	Keep
HORMAD2	Out	Keep
PAGE4	Out	Out
PAGE2B	Out	Out
FATE1	Keep	Keep
LIN28B	Keep	Keep
PIWIL1	Keep	Keep
TDRD1	Out	Keep
BRDT	Out	Out
CABYR	Out	Out
EGFL6	Out	Out
GAGE12F	Out	Out
GAGE12G	Out	Keep
GAGE12J	Keep	Keep
GAGE13	Keep	Keep
MAGEB6	Out	Out
CT45A8	Out	Out
CT45A10	Out	Out
HAGE	Out	Out
BORIS	Keep	Keep
AKAP4	Keep	Keep
PLAC1	Keep	Keep
PASD1	Keep	Keep
LY6K	Out	Out

Decisions and supporting evidence

Selected clinical and research targets. The CSV preserves all failing and rescued contexts; summaries below are abbreviated.

Target	Fixed	Adaptive	Evidence / reason
PRAME (PRAME)	Out	Keep	Recovered: adrenal gland: 3.6 <= 5 nTPM; negative_enhanced; kidney: 1.8 <= 5 nTPM; negative_enhanced
KK-LC-1 (CT83)	Keep	Keep	Retained; IHC unavailable
NY-ESO-1 (CTAG1B)	Keep	Keep	Retained; IHC partial
LAGE-1 (CTAG2)	Out	Out	heart muscle: 5.1 nTPM (vital, limit 5); Existing review: LAGE-1 / NY-ESO family target with source-database CTA evidence; excluded from the strict default because HPA RNA has a low-level heart signal.
MAGE-A1 (MAGEA1)	Keep	Keep	Retained; IHC partial
MAGE-A3 (MAGEA3)	Keep	Keep	Retained; IHC unavailable
MAGE-A4 (MAGEA4)	Keep	Keep	Retained; IHC partial
MAGE-A10 (MAGEA10)	Keep	Keep	Retained; IHC partial
MAGE-A11 (MAGEA11)	Out	Out	Existing review: MAGE-A family target with trace non-reproductive HPA RNA; keep clinical discoverability but do not silently promote into the default strict CTA set.
MAGE-C1 / CT7 (MAGEC1)	Keep	Keep	Retained; IHC partial
MAGE-C2 (MAGEC2)	Keep	Keep	Retained; IHC partial
XAGE1B (XAGE1B)	Out	Out	liver: 1.5 nTPM (vital, limit 1); lung: 1.2 nTPM (vital, limit 1)
XAGE1A (XAGE1A)	Keep	Keep	Retained; IHC unavailable
SSX1 (SSX1)	Keep	Keep	Retained; IHC partial
SSX2 (SSX2)	Keep	Keep	Retained; IHC partial
ROPN1 (ROPN1)	Keep	Keep	Retained; IHC partial
ROPN1B (ROPN1B)	Out	Out	basal ganglia: 2.9 nTPM (vital, limit 1); pituitary gland: 2.9 nTPM (vital, limit 1); +2 more
LDHC (LDHC)	Out	Keep	Recovered: liver: 1.4 <= 5 nTPM; negative_enhanced; pancreas: 1.3 <= 5 nTPM; negative_enhanced
HORMAD1 (HORMAD1)	Keep	Keep	Retained; IHC partial
HORMAD2 (HORMAD2)	Out	Keep	Recovered: liver: 2.8 <= 5 nTPM; negative_enhanced
PAGE4 (PAGE4)	Out	Out	smooth muscle: 23.3 nTPM (vital, limit 5); adrenal gland: 5.5 nTPM (vital, limit 5); +2 more
PAGE2B (PAGE2B)	Out	Out	bone marrow: 4 nTPM (vital, limit 3)
FATE1 (FATE1)	Keep	Keep	Retained; IHC partial
LIN28B (LIN28B)	Keep	Keep	Retained; IHC partial
PIWIL1 (PIWIL1)	Keep	Keep	Retained; IHC partial
TDRD1 (TDRD1)	Out	Keep	Recovered: kidney: 1.6 <= 5 nTPM; negative_enhanced
BRDT (BRDT)	Out	Out	bone marrow: 2.6 nTPM (vital, limit 2)
CABYR (CABYR)	Out	Out	choroid plexus: 12.7 nTPM (vital, limit 1); pituitary gland: 8 nTPM (vital, limit 1); +8 more
EGFL6 (EGFL6)	Out	Out	lung: 24.8 nTPM (vital, limit 5); adipose tissue: 19.5 nTPM (protected, limit 10); +2 more

Target	Fixed	Adaptive	Evidence / reason
GAGE12F (GAGE12F)	Out	Out	stomach: 8.3 nTPM (protected, limit 7.5)
GAGE12G (GAGE12G)	Out	Keep	Recovered: stomach: 5.9 <= 7.5 nTPM; negative_supported
GAGE12J (GAGE12J)	Keep	Keep	Retained; IHC partial
GAGE13 (GAGE13)	Keep	Keep	Retained; IHC partial
MAGEB6 (MAGEB6)	Out	Out	kidney / proximal tubules (microvilli): Medium (Enhanced); reviewed unreliable ihc
CT45A8 (CT45A8)	Out	Out	heart muscle / cardiomyocytes: Low (Supported); reviewed unreliable ihc
CT45A10 (CT45A10)	Out	Out	hippocampal formation: 1.4 nTPM (vital, limit 1); amygdala: 1.2 nTPM (vital, limit 1); +1 more
HAGE (DDX43)	Out	Out	lung / macrophages: Medium (Enhanced)
BORIS (CTCF)	Keep	Keep	Retained; IHC partial
AKAP4 (AKAP4)	Keep	Keep	Retained; IHC partial
PLAC1 (PLAC1)	Keep	Keep	Retained; IHC partial
PASD1 (PASD1)	Keep	Keep	Retained; IHC partial
LY6K (LY6K)	Out	Out	esophagus: 12.1 nTPM (protected, limit 10); skeletal muscle: 5.2 nTPM (vital, limit 5); +6 more

Source interpretation: CTAG2 and PRAME

HPA is both a study and a portal that displays other studies. HPA consensus selects the maximum tissue estimate from HPA and GTEx; it is not evidence that both datasets agree. The pinned v23 CTAG2 heart value used here is 5.1 nTPM. The previously reviewed v23 HPA donors were 13.5, 7.1, 0 and 0 nTPM. The current HPA page, checked 2026-10-20, reports its own cohort at 5.0, versus HPA-normalized GTEx at 0.4 (atrial appendage) and 0.9 (left ventricle). These are different datasets and release-specific estimates. Current page values do not replace the pinned input. CTAG2 heart IHC is Not detected with Enhanced reliability, so the new ceiling is 5; pinned 5.1 still fails. PRAME adrenal RNA is 3.6 in the pinned consensus and its IHC is Not detected, Enhanced. The current adrenal page separates HPA 0.5 from GTEx 3.6.

RNA and IHC donors differ. Neither a low central RNA estimate nor negative IHC establishes absence of protein or peptide-HLA. Existing core/extended API membership is separate from these comparative screens.

References

[HPA v23 consensus RNA input](#)

[HPA v23 normal IHC input](#)

[HPA normalization and maximum-source consensus](#)

[CTAG2 current HPA and GTEx heart data](#)

[PRAME current adrenal data](#)

[IMA203 phase 1 primary report](#)

[Full web report, source citations and downloadable audit](#)