CTA and oncofetal selection

463

selected protein-equivalence groups

481 gene loci · 17,388 Unsafe · 2,012 Neither

Versioned evidence, uniform rules and explicit coverage for human, dog and mouse.

The selection rules

Gate	Rule
Association	Reproductive ≥5 nTPM and > adult bulk; OR embryonic mean ≥5 TPM
Tumor	≥2 TPM / pTPM in at least one compatible tumor sample
Coverage	Required bulk / cell / immune panels; DICE and cornea optional
Normal RNA	Tissue / IHC ceiling; > ceiling is a hold, ≥2× is Unsafe evidence
Normal protein	Low stays flagged; stronger / unquantified accepted positives exclude
Final category	CTA passes all gates; Unsafe dominates; other failures are Neither

Thresholds express research preferences. No named gene or clinical product bypasses a gate.

One linked threshold grid

Candidate ceiling	Missing / unusable	Approved –	Supported –	Enhanced –
Vital	4	8	16	32
Protected	8	16	32	64
Manageable	16	32	64	128
Specified bowel cells	32	64	128	256

Stronger RNA boundary = 2 × candidate ceiling

Bulk keeps its organ tier. Mapped adult HPA fibroblasts use Manageable; specified colon/rectum epithelial cells use 32. Positive Low gives no negative-IHC credit.

Published lists and current assignments

Paper	Mapped groups	CTA	Unsafe	Neither
da Silva 2017	1,017	356	276	385
Wang2016	988	264	521	203
Chang2019	985	311	519	155
Gong2021	729	360	201	168
Bruggeman2018	692	25	622	45
Jamin2021	469	32	412	25
Loriot2025	202	79	67	56
Carter2023	103	58	20	25
Seager2024	15	8	3	4
Bradley2020	9	1	8	0
Bai2016	1	0	1	0
Garg2007	1	0	1	0
Boel1995	0	0	0	0

13 papers · 2,482 unique mapped groups. List membership annotates selection; it does not grant admission.

Overlaps and biological association

Shared selected	da Silva 2017	Wang 2016	Chang 2019	Gong 2021	Bruggeman 2018	Jamin 2021
da Silva 2017	356	237	282	316	15	28
Wang 2016	237	264	247	233	18	25
Chang 2019	282	247	311	286	18	20
Gong 2021	316	233	286	360	22	24
Bruggeman 2018	15	18	18	22	25	6
Jamin 2021	28	25	20	24	6	32

Association: 1,231 reproductive only · 9,481 embryonic only · 1,427 both

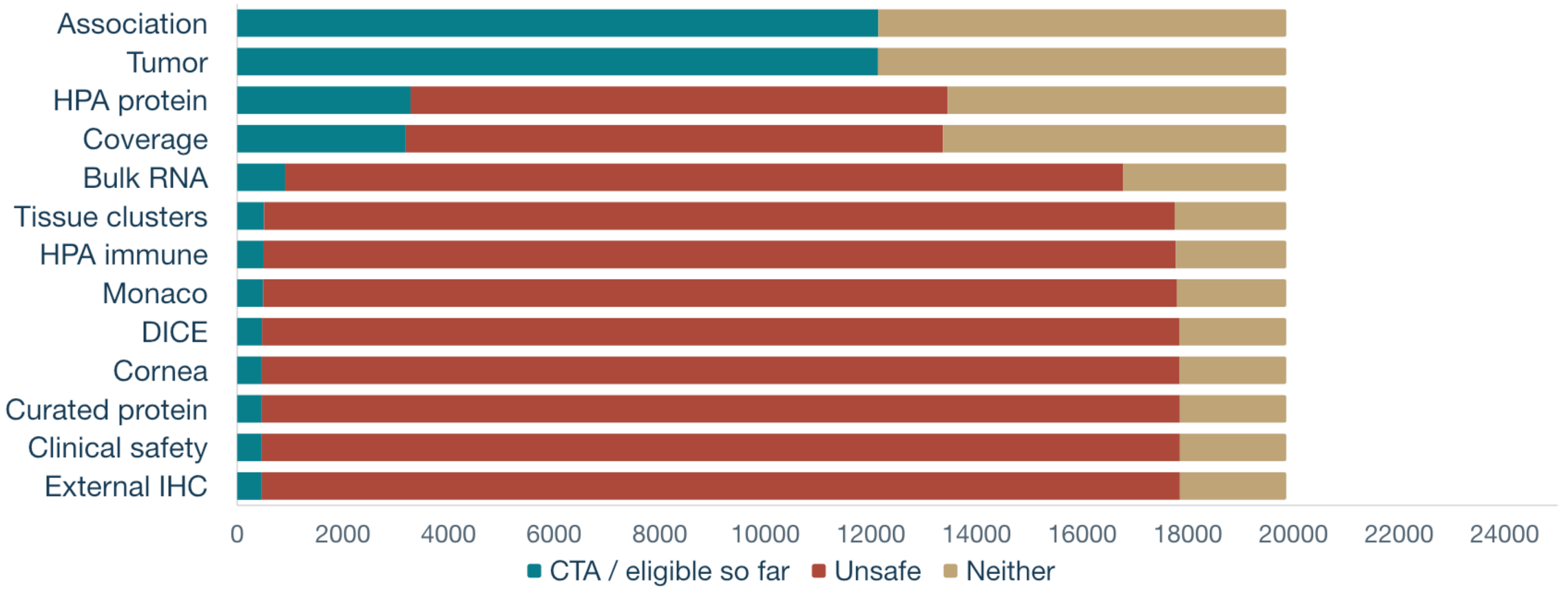
Embryonic admission uses one gastrulation embryo. Later fetal atlases remain outside this release.

Data used to filter normal expression

Source	Measured quantity	Use
HPA consensus	Bulk nTPM	Organ tier, association and coverage
HPA tissue clusters	Cell-cluster nTPM; ≥20 reads	Cell compartments and rare-cell signals
HPA / Monaco immune	Native nTPM / TPM	Protected unless explicitly classified otherwise
Original DICE	TPM; third-highest reported value	Recurring immune RNA; coverage optional
Collin adult cornea	CP10K; support in ≥2 sample groups	Ocular signals; coverage optional
HPA + external IHC	Staining, confidence, tissue / cell	Positive findings and matched negative credit
Curated protein / clinical	Categorical findings + source evidence	Independent exclusions and retained flags

Missing measurements remain unknown. These adult panels do not establish pediatric safety.

Every layer can contribute



19,863 groups at every step. Final: 463 CTA / 17,388 Unsafe / 2,012 Neither.

Counts at each filtering choice

Layer	New removals	CTA*	Unsafe	Neither
Association	7,724	12,139	0	7,724
Tumor ≥2	7	12,132	0	7,731
HPA protein	8,850	3,282	10,172	6,409
Required coverage	90	3,192	10,172	6,499
Normal bulk	2,288	904	15,870	3,089
HPA tissue clusters	396	508	17,242	2,113
HPA immune	8	500	17,273	2,090
Monaco immune	11	489	17,308	2,066
DICE immune	21	468	17,369	2,026
Adult cornea	4	464	17,383	2,016
Curated protein	1	463	17,387	2,013
Clinical safety	0	463	17,388	2,012
External IHC	0	463	17,388	2,012

*Eligible so far until the final row. A later layer can change Neither to Unsafe.

Effect of the policy choices

Cumulative rule	CTA	Added
Previous policy	343	0
Double the linked RNA grid	445	102
Classify fibroblasts as Manageable	446	1
Allow specified large-bowel cells	448	2
Flag Low HPA protein	462	14
Flag explicitly Low imported protein	463	1

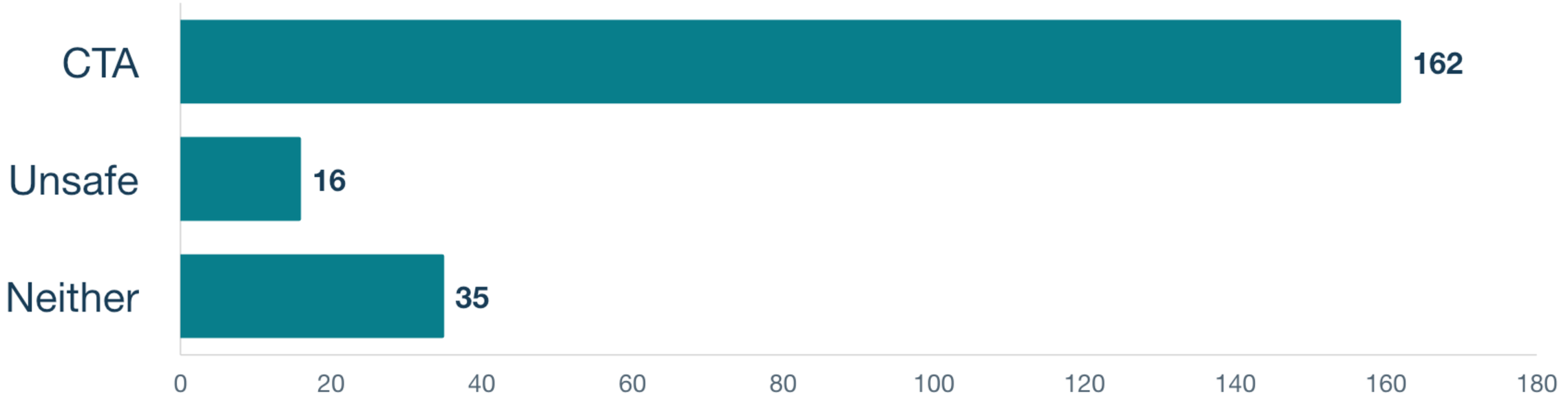
2,902 grouped IHC labels corrected; 11 intermediate decisions changed; 0 final category changes versus the prior 463-group proposal.

Named targets in the current set

Target / group	Category	Retained context
PAGE1	CTA	All gates pass
SMC1B	CTA	All gates pass
CTAG2	Unsafe	Bronchial basal RNA; other findings
MAGEA4	CTA	All gates pass
TBXT	CTA	External review; adult disc
PRAME	CTA	Low protein; progenitor expression
CT83	CTA	External-IHC review
NY-ESO-1	CTA	All gates pass
SSX2/B	CTA	All gates pass
XAGE1A/B	CTA	All gates pass

No gene-name exemptions. Other MAGE genes enter only through the same rules.

Current assignments of known CTAs

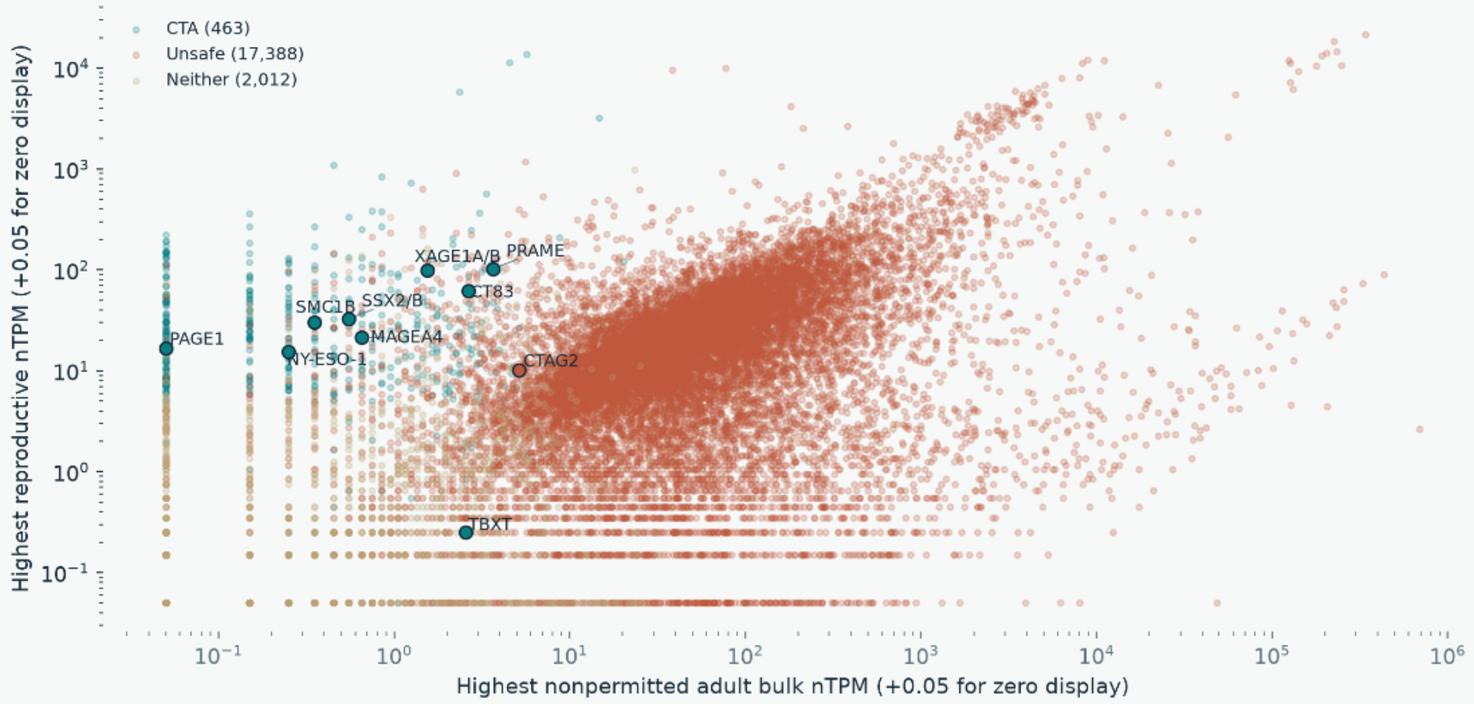


162 retained · 16 Unsafe · 35 Neither

Expression distributions and named targets

Where the named antigens land

Maximum nonpermitted adult bulk versus reproductive RNA · HPA native nTPM



Color uses the complete evidence cascade, not these two RNA values alone. TBXT can enter through embryonic expression.
CTAG1A/B and XAGE1A/B are summed within matched source contexts before filtering; named genes have no automatic admission.

PRAME, CTAG2 and TBXT

Target	Measured normal finding	Current treatment
PRAME	Adrenal 3.6 / ceiling 4; Low protein	CTA; protein observation retained
PRAME	Heart fibroblasts 12 / 16	CTA; stromal tolerance assumption
PRAME	Colon undifferentiated cells 20.3 / 32	CTA; progenitor caution retained
CTAG2	Bronchial basal respiratory cells 24.9 / 4	Unsafe; stronger boundary is 8
TBXT	External antibody disagreement; adult disc	CTA; tissue-specific review retained

RNA values are nTPM. Clinical targeting supports product-specific evidence; it does not validate these thresholds or prove gene-wide safety.

The same evidence categories across species

Evidence role	Human: used / annotated	Dog: available / registered	Mouse: identified only
Nomination	Published lists	14 native nominations	No curated snapshot
Reproductive / developmental	HPA / Tyser	Bgee / BarkBase / DoGA*	MOCA / gastrulation / GXD
Tumor	132 cohorts + HPA	Study assays; cohort blocked	Native cohort needed
Normal bulk	HPA consensus	Bgee / BarkBase / Pfizer*	GXD assay resource
Normal cell / immune	HPA / Monaco / DICE / cornea	No equivalent integrated panel	Tabula Muris/Senis
Normal protein	HPA / external evidence	Pfizer iBAQ / native IHC	GXD assay resource

*Metadata only for DoGA and Pfizer RNA. No mouse atlas is integrated; human thresholds and safety do not transfer by orthology.

A simple API with explicit coverage

```
cta_selection.results(species="human", category="CTA")
cta_selection.coverage(species="dog")
cta_selection.sources(species="mouse")
```

Species	Result entities	Assessment
Human	19,863 groups	Current research-policy decisions
Dog	14 native nominations	Neither / unassessed; policy unavailable
Mouse	0 rows; stable schema	Curation unavailable, not biological absence

IDs, reasons and flags stay attached. Missing history is unknown; ambiguous names never silently collapse.

What the release establishes

463 groups under one reproducible human policy

Complete decisions, named-target evidence and source overlaps
Consistent species schema with honest missing-data states
Protein observations, donor uncertainty and native units preserved

Still unvalidated: numerical toxicity cutoffs, mucosal tolerance, pediatric use and cross-assay equivalence. One early embryo does not provide comprehensive fetal coverage.