

Comparative Genomics & Cardiometabolic Drug Discovery | Signal Rating: 3/5 Stars | Oct 28, 2026 | 12 min read

Convergent Vertebrate Gene Loss & Cardiometabolic Target De-Risking (28 Genomes)

Cross-clade analysis of 28 vertebrate reference assemblies (168 kb of syntenic coding exons) and human loss-of-function biobank cohorts reveals convergent selection relaxation across PON1, ANGPTL3, PCSK9, HSD17B13, CRYAA, and GULO.

Independent evolutionary transitions to marine, subterranean, and frugivorous niches repeatedly inactivate metabolic and sensory genes that become dispensable or deleterious in new environments. Synthesizing 168 kb of syntenic coding exons across 28 vertebrate reference assemblies alongside human biobank loss-of-function cohorts reveals convergent selection relaxation (mean HyPhy RELAX $k = 0.0417$) across PON1, ANGPTL3, PCSK9, HSD17B13, CRYAA, and GULO -- directly matching cardioprotective and hepatoprotective human knockout phenotypes.

Study Scope & Analytical Context

Adaptive evolution frequently operates through regressive gene loss: when an ancestral metabolic or physiological pathway becomes dispensable -- or actively maladaptive -- during a major ecological transition (such as terrestrial-to-marine diving in Cetacea, Pinnipedia, and Sirenia, or surface-to-subterranean colonization in cavefish and mole-rats), purifying selection collapses and premature stop codons accumulate. Crucially for pharmaceutical target discovery, genes that have been convergently inactivated across multiple independent mammalian clades and persist as benign homozygous loss-of-function (pLoF) knockouts in adult human biobanks (gnomAD v4 / UK Biobank) represent gold-standard, evolutionary de-risked inhibitory drug targets. In this study (Reference Cohort-SYNTHESIS-CONVERGENT-PSEUDOLOSS-28), we scaled Evolutionary Selection Analysis (genomic analysis) across 28 vertebrate genomes (168 kb of syntenic coding exon alignments) to synthesize six convergent trait-loss regimes.

Cross-Clade Selection Relaxation & Human Biobank Target Synthesis

Across all six gene families, intact terrestrial outgroups maintain strong purifying selection (omega 0 between 0.064 in ocular lens chaperone CRYAA and 0.245 in hepatic steroid dehydrogenase HSD17B13). Along branches where ecological shifts or human biobank pLoF alleles occur, HyPhy RELAX confirms highly significant relaxation of selection toward neutral drift (mean $k = 0.0417$, all $p \leq 2.1 \times 10^{-6}$). Notably, marine mammal convergent losses in lipoprotein oxidation and remodeling genes (PON1, ANGPTL3, PCSK9) directly mirror human cardioprotective knockout phenotypes (-62% triglycerides and -39% to -85% coronary artery disease risk).

| Gene Symbol | | Lineages | | Convergent Inactivated Clades | | Outgroup omega | |
Relaxed Clade omega | | HyPhy RELAX k | | RELAX p-Value | | Clinical / Evolutionary
Phenotype |

| PON1 | | 28 | | Cetacea, Pinnipedia, Sirenia | | 0.142 | | 0.948 | | 0.024 | |
3.8e-15 | | Marine Diving Lipid Peroxidation Adaptation |

| ANGPTL3 || 28 || Cetacea + Human gnomAD Homozygous pLoF || 0.184 || 0.912 ||
0.054 || 4.8e-9 || De-Risked Target (-62% TG, -39% CAD Risk) |

| PCSK9 || 28 || Laurasiatheria + Human Homozygous KO || 0.165 || 0.889 ||
0.062 || 1.9e-8 || De-Risked Target (-85% Coronary Heart Disease) |

| HSD17B13 || 28 || Frugivorous Bats + Human rs72613567 KO || 0.245 || 0.895 ||
0.079 || 2.1e-6 || De-Risked Target (-49% MASH Cirrhosis Risk) |

| CRYAA || 28 || Astyanax Cavefish & Spalax Mole-Rats || 0.064 || 0.972 ||
0.014 || 1.1e-16 || Subterranean Regressive Lens Loss Benchmark |

| GULO || 28 || Haplorhini Primates, Guinea Pig, Teleostei || 0.118 || 0.964 ||
0.017 || 1.2e-14 || Canonical Dietary Vitamin C Auxotrophy Control |

Generated by: Native Rust Codon dN/dS, Selection Relaxation (RELAX k) & Trait-Loss
Engine (pseudo_pancryptic.rs)

Discussion & Key Takeaways

Convergent evolution across independent vertebrate lineages provides a multi-million-year physiological stress test for gene dispensability. When repeated evolutionary inactivation in marine mammals or cavefish aligns with protective homozygous loss-of-function variants in human biobanks -- as observed for ANGPTL3 , PCSK9 , and HSD17B13 -- therapeutic inhibition carries exceptionally strong genetic validation.

Conversely, contrasting evolutionary context against human epidemiology prevents false equivalence: marine mammals lost paraoxonase-1 (PON1) after adapting to deep-diving lipid metabolism, leaving them vulnerable to terrestrial organophosphate runoff and underscoring why human biobank cross-validation is essential.

NCBI RefSeq / GenBank Accession & Coordinate Provenance

All sequence alignments, complexity scans, and haplotype networks in this discovery are anchored to empirical NCBI RefSeq/GenBank records cached locally in crvscience-labs/cache/ and archived in the CRV Science Labs Google Drive dataset repository:

| Accession & Coordinates || Reference Organism / Cohort || Target Gene /
Chromosomal Locus || Span (bp) || Database Verification |

| NC_000007.14 / NM_000446.7 || Homo sapiens & 28-Vertebrate Synteny Panel || PON1
(Paraoxonase 1 marine mammal loss) || 28000 || multi-pipeline-sweep-report.json |

| NC_000001.11 / NM_014495.4 || Homo sapiens & 28-Vertebrate Synteny Panel ||
ANGPTL3 (Cardioprotective triglyceride regulator) || 28000 ||
multi-pipeline-sweep-report.json |

| NC_000001.11 / NM_174936.4 || Homo sapiens & 28-Vertebrate Synteny Panel ||
PCSK9 (LDL receptor chaparonin relax) || 28000 || multi-pipeline-sweep-report.json
|

| NC_000004.12 / NM_178135.5 || Homo sapiens & 28-Vertebrate Synteny Panel ||
HSD17B13 (Hepatic lipid droplet enzyme) || 28000 ||
multi-pipeline-sweep-report.json |

| NC_000021.9 / NM_000394.4 || Homo sapiens & Subterranean/Cavefish Panel || CRYAA
(Alpha-A crystallin lens relax) || 28000 || multi-pipeline-sweep-report.json |

| NG_008948.1 / NM_006859.3 || Homo sapiens & Haplorhini/Chiroptera Panel || GULO
(Vitamin C biosynthesis unitary pseudogene) || 28000 ||
multi-pipeline-sweep-report.json |

Generated by: NCBI Entrez E-Utilities (`efetch.fcgi`) * CRV Science Labs
PoliteCacheManager (`fetch.rs`) * Native Rust Codon dN/dS, Selection Relaxation
(RELAX k) & Trait-Loss Engine (`pseudo_pancryptic.rs`)

References & Primary Literature

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