INPUTS	FEATURES	ENCODER	CLUSTERING	OUTPUT

INPUTS

Contigs
FASTA · TNF · length

Alignments
BAM · coverage · damage

SCG Markers
HMM · 206 profiles

FEATURES

Encoder Input
TNF (136d) + coverage (2d)
138 dim

aDNA Features
damage (10d) · decay (2d)
fragment (2d) · CGR (9d)
29 dim

ENCODER

SCG-supervised
InfoNCE

MLP 138→512→256→128

6 augmented views

3 encoder restarts

128 dim

157 dim
128 + 29 concat

CLUSTERING

k-NN Graph
HNSW · k=10 · cosine

Quality Leiden
Phase 1: SCG-guided CPM
Phase 2: Contamination split
Phase 3: SCG rescue
75 runs (3 enc × 25 seeds)

amber resolve
co-binning consensus

OUTPUT

HQ Bins
≥90% comp · <5% cont

MQ Bins
≥50% comp · <10% cont

Per-bin QC
SCG · completeness · cont

Damage Profile
C→T · G→A · decay λ

aDNA-aware components (novel)   Standard components

AMBER
Ancient Metagenomic Binning with aDNA-aware Encoder and Refinement