Panaroo·····

·····Prokka·····Panaroo·····/·····clean-mode·····
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Panaroo·····
·····GFF3·····

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·····Panaroo···Prokka···GFF3·····
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···· | GFF3·····ID·· | ·····

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Panaroo··i·····GFF·····
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#!/usr/bin/env bash
set -euo pipefail
files=(/data/S1.gff /data/S2.gff /data/S3.gff)
for file in "${files[@]}"; do test -s "$file"; done
root="$PWD/panaroo-pilot-001"
test ! -e "$root" || { echo "output exists: $root" >&2; exit 2; }
mkdir -p "$root"
printf '%s
' "${files[@]}" > "$root/gff-paths.txt"
panaroo --version > "$root/version.txt"
panaroo --help > "$root/help.txt" 2>&1
/usr/bin/time -v -o "$root/resources.txt"   panaroo -i "$root/gff-paths.txt" -o "$root/results"   --clean-mode moderate -t 4 > "$root/run.log" 2>&1
test -s "$root/results/gene_presence_absence.csv"
test -s "$root/results/final_graph.gml"
printf 'Panaroo outputs checked in %s
' "$root/results"
```

···moderate·····strict·moderate·sensitive·····
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gene_presence_absence.csv·····final_graph.gml·····
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Panaroo·····CPU·····R
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Panaroo v1.8.1····· https://github.com/gtonkinhill/panaroo/blob/v1.8.1/panaroo/__main__.py

Panaroo····· https://github.com/gtonkinhill/panaroo