

Resource Summary Report

Generated by [dkNET](#) on Aug 17, 2026

NextPolish

RRID:SCR_025232

Type: Tool

Proper Citation

NextPolish (RRID:SCR_025232)

Resource Information

URL: <https://github.com/Nextomics/NextPolish>

Proper Citation: NextPolish (RRID:SCR_025232)

Description: Software tool to fix base errors SNV/Indel in genome generated by noisy reads. Used to correct error bases in reference genome.

Resource Type: software application, data processing software, software resource, source code, data analysis software

Keywords: fix base errors, SNV/Indel, genome, noisy reads, correct error bases, reference genome,

Availability: Free, Available for download, Freely available

Resource Name: NextPolish

Resource ID: SCR_025232

License: GNU GPL v3.0

Record Creation Time: 20240409T053245+0000

Record Last Update: 20260817T040714+0000

Ratings and Alerts

No rating or validation information has been found for NextPolish.

No alerts have been found for NextPolish.

Data and Source Information

Usage and Citation Metrics

We found 105 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Zhang K, et al. (2026) De novo assembly of the first mitochondrial genome in Benincasa reveals structural dynamics and evolutionary insights in Cucurbitaceae. BMC plant biology, 26(1).

Jia S, et al. (2026) Multipartite mitochondrial genome evolution in Halophila seagrasses: repeat-driven structural plasticity and selection signatures of marine adaptation. BMC plant biology, 26(1).

Li F, et al. (2026) Transition From Land to Sea: Comparative Genomics Illuminates the Adaptive Evolution of the Intertidal Spider. Molecular ecology resources, 26(4), e70147.

Chen H, et al. (2026) A telomere-to-telomere genome assembly of Nymphaea minima provides details into the developmental transcriptome atlas and adaptive regulatory mechanisms. Horticulture research, 13(6), uhag085.

Zhou Y, et al. (2026) Comparative analysis of complete mitochondrial genomes from Curcuma longa and Curcuma kwangsiensis reveals structural plasticity, conserved core genes, and species-specific evolutionary dynamics. Frontiers in plant science, 17, 1782424.

Wei C, et al. (2026) Complete telomere-to-telomere genomes of cowpea reveal insights into centromere evolution in Phaseoleae. Horticulture research, 13(4), uhaf359.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect Cryptophyllum westwoodii provide insights into the evolution of leaf-like masquerade. GigaScience, 15.

Oubassou EZ, et al. (2026) Genome sequencing and comparative analysis of Nocardiosis moroccensis sp. nov., a halotolerant Actinomycetota from Moroccan hypersaline ecosystem. BMC microbiology, 26(1).

Zhou J, et al. (2026) Chromosome-Scale Genome Architecture and Historical Demography of the Southern White Rhinoceros. Biology, 15(12).

Zhou P, et al. (2026) Chromosome-Level Genome Assembly of the Allotetraploid Gynostemma pentaphyllum Provides Novel Insights Into the Biosynthesis of Ginsenoside and Gypenoside LVI. Plant biotechnology journal, 24(6), 4204.

Loo EPI, et al. (2026) Removal of Transgenes and Evaluation of Yield Penalties in Genome Edited Bacterial Blight Resistant Rice Varieties. Plant biotechnology journal, 24(2), 939.

Liu T, et al. (2026) Chromosome-level genome assembly and annotation of the endangered plant *Primula kwangtungensis* (Primulaceae). *Scientific data*, 13(1), 212.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Wang ZL, et al. (2026) Centromeric tandem repeats expansions in plateau zokor enhance chromosome stability for high-altitude adaptation. *Genome biology*, 27(1).

Lu Y, et al. (2025) Comparative genomics of *Nocardia tsunamensis* IFM 10818, a new source of the antibacterial macrolide nargenicin A1. *Microbiology spectrum*, 13(12), e0122025.

Ryan AP, et al. (2025) Small pangenome of *Candida parapsilosis* reflects overall low intraspecific diversity. *mBio*, 16(10), e0132025.

Dong WY, et al. (2025) Chromosome-level genome assembly of the parasitoid wasp *Aenasius arizonensis*. *Scientific data*, 12(1), 809.

Huang C, et al. (2025) A comparative genomic analysis at the chromosomal-level reveals evolutionary patterns of aphid chromosomes. *Communications biology*, 8(1), 427.

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phylllobates terribilis*. *GigaByte* (Hong Kong, China), 2025, gigabyte157.

Park H, et al. (2025) Chromosome-level Genome Assembly of the Halophytic Turfgrass *Zoysia macrostachya*. *Scientific data*, 12(1), 1335.