

Resource Summary Report

Generated by [RRID](#) on Aug 5, 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: data processing software, source code, data analysis software, software resource, software application

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: 20260805T044543+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 73 mentions in open access literature.

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

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

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

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

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

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

Chen SY, et al. (2025) Chromosome-level reference genome assembly for the protected resource plant, *Zenia insignis*. *Scientific data*, 12(1), 459.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Li D, et al. (2025) Assembly and comparative analysis of the first complete mitochondrial genome of *Camellia sinensis* var. *assamica* 'Hainan Dayezhong', endemic to Hainan Province, China. *BMC plant biology*, 25(1), 1304.

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

Shen R, et al. (2025) Chromosome-level genome of the shining chafer *Kibakoganea tamdaoensis* (Coleoptera: Scarabaeidae: Rutelinae). *Scientific data*, 12(1), 1345.

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.

Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. *GigaScience*, 14.

Dotsuta Y, et al. (2025) Complete genome sequences of *Micrococcus luteus* isolated from the radioactive element-containing water in Fukushima Daiichi nuclear power station unit 2. *Microbiology resource announcements*, 14(10), e0076925.

Yoshioka I, et al. (2025) Itraconazole resistance in *Madurella fahalii* linked to a distinct homolog of the gene encoding cytochrome P450 14- α sterol demethylase (CYP51). *PLoS neglected tropical diseases*, 19(3), e0012623.

Ren L, et al. (2025) Genomes reveal pervasive distant hybridization in nature among cyprinid fishes. *GigaScience*, 14.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Huang T, et al. (2025) Chromosome-level genome assembly of the aphid *Megoura crassicauda*. *Scientific data*, 12(1), 994.

Dong Z, et al. (2025) Near telomere-to-telomere genome assembly of the blackspot tuskfish (*Choerodon schoenleinii*). *Scientific data*, 12(1), 537.

Song L, et al. (2025) Biological and Genomic Insights into *Fusarium acuminatum* Causing Needle Blight in *Pinus tabulaeformis*. *Journal of fungi* (Basel, Switzerland), 11(9).

Yang G, et al. (2025) Chromosome-level genome assembly of *Megachile sculpturalis* Smith (Hymenoptera, Apoidea, Megachilidae). *Scientific data*, 12(1), 46.