# **Resource Summary Report**

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# **VAAL**

RRID:SCR\_001184

Type: Tool

### **Proper Citation**

VAAL (RRID:SCR\_001184)

#### **Resource Information**

**URL:** <a href="http://www.broadinstitute.org/science/programs/genome-biology/computational-rd/vaal-manual">http://www.broadinstitute.org/science/programs/genome-biology/computational-rd/vaal-manual</a>

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**Description:** A polymorphism discovery algorithm for short reads. To run it, you provide reads (and quality scores) from a "sample genome" as input, along with a vector sequence to trim from the reads, and a reference sequence for a related genome to compare to. VAAL produces as output a an assembly for the sample genome, together with a mask showing which bases are "trusted". It then deduces from that a list of differences between the sample and related genomes. Alternatively, it can be provided as input read data for two sample genomes, together with a reference sequence for a related genome. In this case, VAAL produces assemblies for each of the sample genomes, and compares them to each other, thereby deducing a list of differences between them. VAAL has been tested on bacteria, using single lanes of 36 bp unpaired reads from the Illumina platform. Note: This software package is no longer supported and information on this page is provided for archival purposes only.

**Abbreviations:** VAAL

Resource Type: software resource

**Defining Citation: PMID:19079253** 

**Keywords:** dna sequence, polymorphism, parallel sequencing, bio.tools

Funding:

Resource Name: VAAL

Resource ID: SCR\_001184

Alternate IDs: biotools:vaal, OMICS\_02170

Alternate URLs: https://bio.tools/vaal

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20250420T014022+0000

### **Ratings and Alerts**

No rating or validation information has been found for VAAL.

No alerts have been found for VAAL.

### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We have not found any literature mentions for this resource.