# Resource Summary Report

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## Anchored Assembly

RRID:SCR_001188
Type: Tool

### Proper Citation

Anchored Assembly (RRID:SCR_001188)

### Resource Information

**URL:** http://www.spiralgenetics.com/products/

**Proper Citation:** Anchored Assembly (RRID:SCR_001188)

**Description:** Analysis pipeline that accurately detects and maps variations that are often missed by standard analysis algorithms. It uses direct de novo read overlap assembly to accurately detect and characterize SNPs (single nucleotide polymorphisms), indels, and SVs (structural variations). The pipeline uses existing Illumina HiSeq data and does not require additional library preparation. The algorithm is optimized for projects with at least 20x coverage per chromosome set (i.e. 40x for diploid).

**Abbreviations:** Anchored Assembly

**Resource Type:** commercial organization, software resource

**Keywords:** variation, structural variation, single nucleotide polymorphism

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Anchored Assembly

**Resource ID:** SCR_001188

**Alternate IDs:** OMICS_02167

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

**Record Last Update:** 20260905T133320+0000

### Ratings and Alerts

No rating or validation information has been found for Anchored Assembly.

No alerts have been found for Anchored Assembly.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We have not found any literature mentions for this resource.