



De Novo Genome Sequencing



With *de novo* genome sequencing, the first genome map for a species is generated, providing a valuable reference sequence for phylogenetic studies, analysis of species diversity, mapping of specific traits and genetic markers, and other genomics research.

With the development of next-generation sequencing technology, *de novo* genome sequencing has become more rapid and affordable, and Medikonia is based on the forefront of this technology with SOAP Denovo software package for genome assembly. Medikonia team have contributed to several important publications on novel genome sequences, and we can provide you with the high level of expertise required for your *de novo* genome sequencing project.

The Advantages

- Highly experienced: We have completed major *de novo* genome sequencing projects, and our data has been published in top-tier journals.
- Leader in NGS services: We provide high-quality sequencing, an efficient

standard workflow, fast turnaround time, and bioinformatics analyses at a cost-effective price.

- Bioinformatics expertise: The SOAPdenovo software and the NovoHeter software, developed by Medikonia scientists, are used for complex genome assembly.

Project Types

Simple Genome

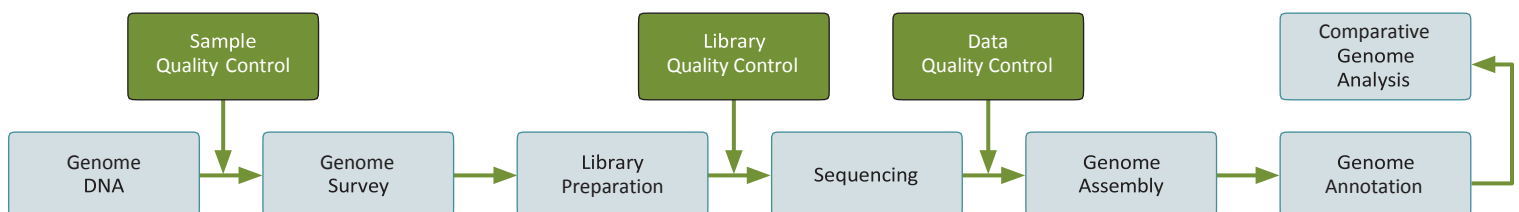
Simple genome refers to a haploid genome with a low repeat content (less than 50%), or a diploid genome with a low rate of heterozygosity (less than 0.5%), such as most mammals, birds, and cultivated crops.

Complex Genome

Complex genome refers to a diploid or polyploid genome with a high repeat content (higher than 50%) or a high rate of heterozygosity (higher than 0.5%), such as many species of plants, aquatics, and insects.

- Moderately heterozygous genome (diploid)
- Highly heterozygous genome (diploid)
- Highly repetitive genome (diploid)

Project Workflow



SEQUENCING STRATEGY

- HiSeq platform, paired-end 150 bp

SAMPLE REQUIREMENTS

- DNA amount for survey: $\geq 10 \mu\text{g}$ (quantified by Qubit 2.0)
- DNA amount for RAD-seq: $\geq 3 \mu\text{g}$ (quantified by Qubit 2.0)
- DNA amount for genome de novo sequencing: $\geq 500 \mu\text{g}$ (quantified by Qubit 2.0)
- DNA concentration: $\geq 50 \text{ ng}/\mu\text{l}$
- Purity: $\text{OD}_{260/280} = 1.8 - 2.0$ without degradation and RNA contamination

DATA QUALITY GUARANTEE

- Simple genome: Contig N50 $\geq 30 \text{ Kb}$, Scaffold N50 $\geq 1 \text{ Mb}$
- Mammal or bird genome: Contig N50 $\geq 40 \text{ Kb}$, Scaffold N50 $\geq 4 \text{ Mb}$
- Complex genome: Contig N50 $\geq 20 \text{ Kb}$, Scaffold N50 $\geq 500 \text{ Kb}$

TECHNICAL PARAMETERS

Procedures	Library Preparation	Sequencing Depth	Turnaround Time
Survey Analysis	350 bp insertion	50X	40 Days
Simple Genome Sequencing	350 bp/ 2 kb/ 5 kb/10 kb insertion	100X	12 Months
Complex Genome Sequencing	350 bp/ 450 bp/ 2 kb/ 5 kb/ 10 kb/ 20 kb insertion	200X	15 Months
Pan-Genome Sequencing	350 bp/ 2 kb/ 5 kb insertion	80X (simple genome) 100X (complex genome)	Depending on the number of samples

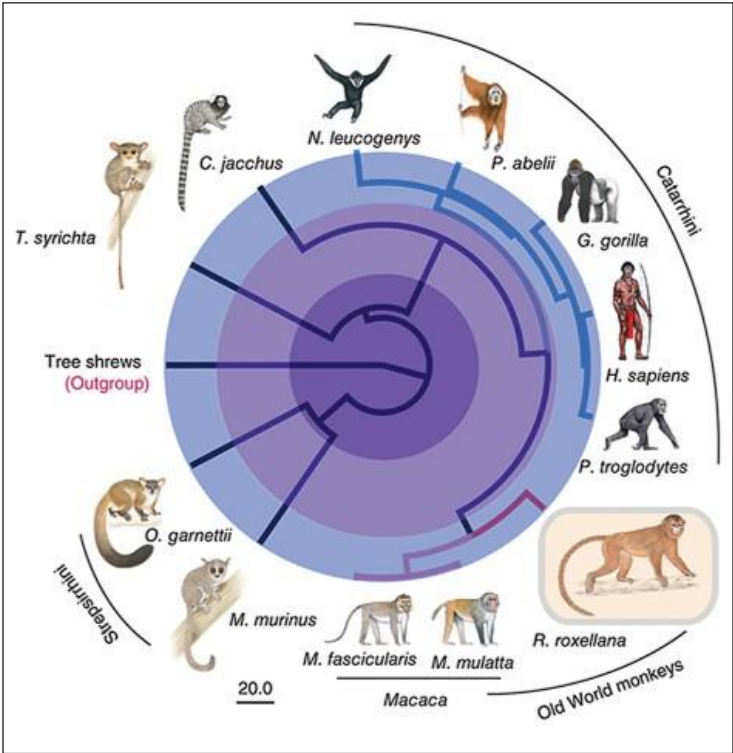
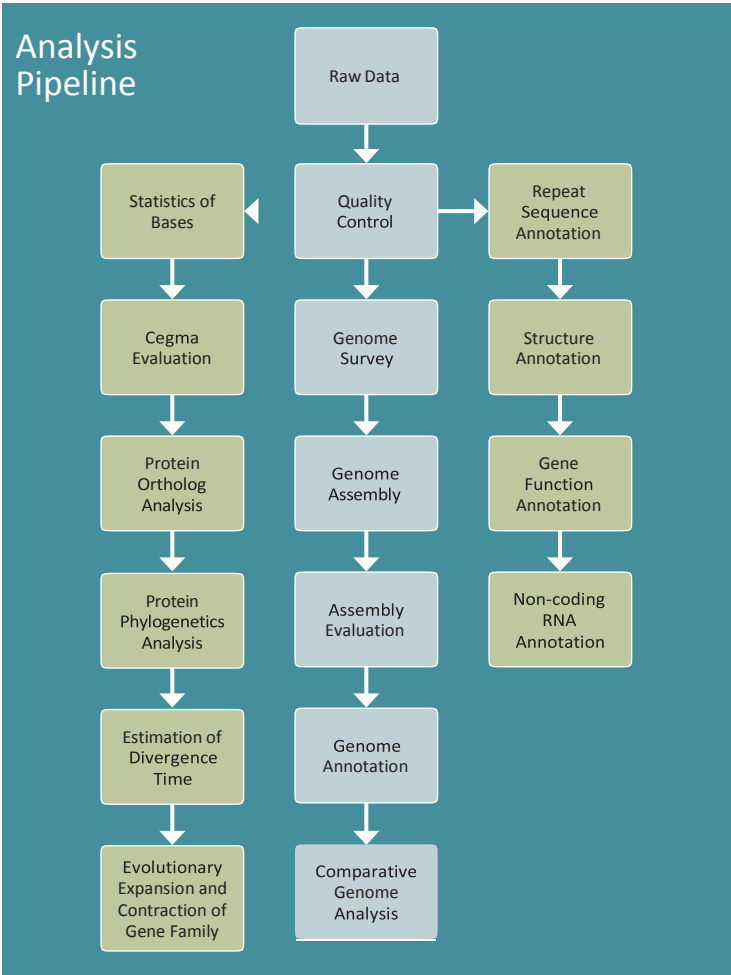
Project Example

The following study utilized Medikonia’s sequencing expertise.

Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history.

Nature Genetics, 46:1303–1310 (2014)

Researchers from Medikonia and the Chinese Academy of Science collaborated on the whole-genome sequencing of the golden snub-nosed monkey, a species of Old World monkey. The de novo genome sequencing data were compared with genome resequencing data from three other related species, and provided insights into the evolutionary adaptations associated with the unique diets of these primates.



Phylogenetic tree and estimated divergence times for GSM and other mammals.

RELATED’S PUBLICATIONS

Journal	Title
Nature Biotechnology 33:531 (2015)	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement.
Nature Genetics, 46:1303 (2014)	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history.
Nature Biotechnology, 32:1045 (2014)	De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits.
Nature Genetics, 45:1431 (2013)	Genomic analyses identify distinct patterns of selection in domesticated pigs and Tibetan wild boars.
Nature Communications, 4:2071 (2013)	Ground tit genome reveals avian adaptation to living at high altitudes in the Tibetan plateau.