



Animal and Plant Re-sequencing



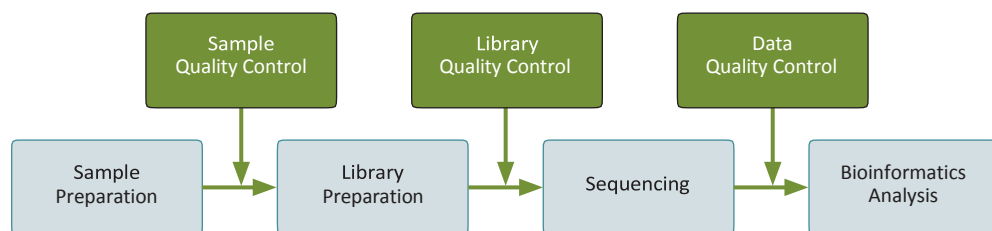
With advancements in next-generation sequencing technology, whole genome resequencing (WGS) has become the most rapid and effective method to unravel, at the genomic level, the underlying mechanisms of species origin, development, growth, and evolution. Using WGS, the complete genome data from one or more variants can be aligned to known genomic sequence(s) for the species. Applications of WGS include detection of genetic differences between variants, transposon fingerprinting for assessing germplasm diversity and lineages, and mapping loci associated with specific traits, such as disease resistance.

Medikonia is highly experienced in the applications of WGS for characterizing plant and animal variants. With cutting-edge Illumina HiSeq X™ Ten platform and our expert bioinformatics analysis, we provide researchers with high quality data in a highly cost-effective manner. Bioinformatics analysis includes but not limited to detecting SNPs, InDels, structure variations, and copy number variations with high accuracy and verification rates.

The Medikonia Advantage

- Extensive experience: We have completed over 1000 re-sequencing projects, and our data has been published in top-tier journals.
- Unsurpassed data quality: We guarantee a Q30 score $\geq 80\%$, exceeding Illumina's official guarantee of $\geq 75\%$.
- Cost-effective service: By employing state-of-the-art HiSeq X Ten platform that has enabled the \$1000 human genome, we provide higher data output, faster turnaround time, and lowest prices possible for plant and animal resequencing projects of any size.
- High verification rate: We promise that the verification rate of SNPs is higher than 95%.

Project Workflow



SEQUENCING STRATEGY

- 350 bp insert DNA library
- HiSeq X Ten platform, paired-end 150 bp

DATA QUALITY GUARANTEE

- Medikonia guarantees its data output. The quality of our data, as measured by the percentage of bases with a sequencing quality score above Q30 (PE150, $\geq 80\%$), exceeds Illumina's official guideline (PE150, $\geq 75\%$).

TURNAROUND TIME

- Within 15 working days from verification of sample quality (without data analysis)
- Additional 10 working days for data analysis

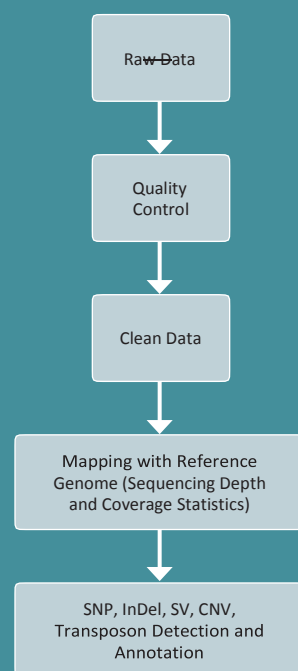
RECOMMENDED SEQUENCING DEPTH

- SNP and InDel: $\geq 10X$
- SV: $\geq 20X$
- CNV: $\geq 30X$

SAMPLE REQUIREMENTS

- DNA amount: $\geq 1.4 \mu\text{g}$ (for two libraries preparation, quantified by Qubit 2.0)
- Total volume: $\geq 10 \mu\text{l}$
- OD260/280 = 1.8-2.0 without degradation or RNA contamination

Analysis Pipeline



Project Example

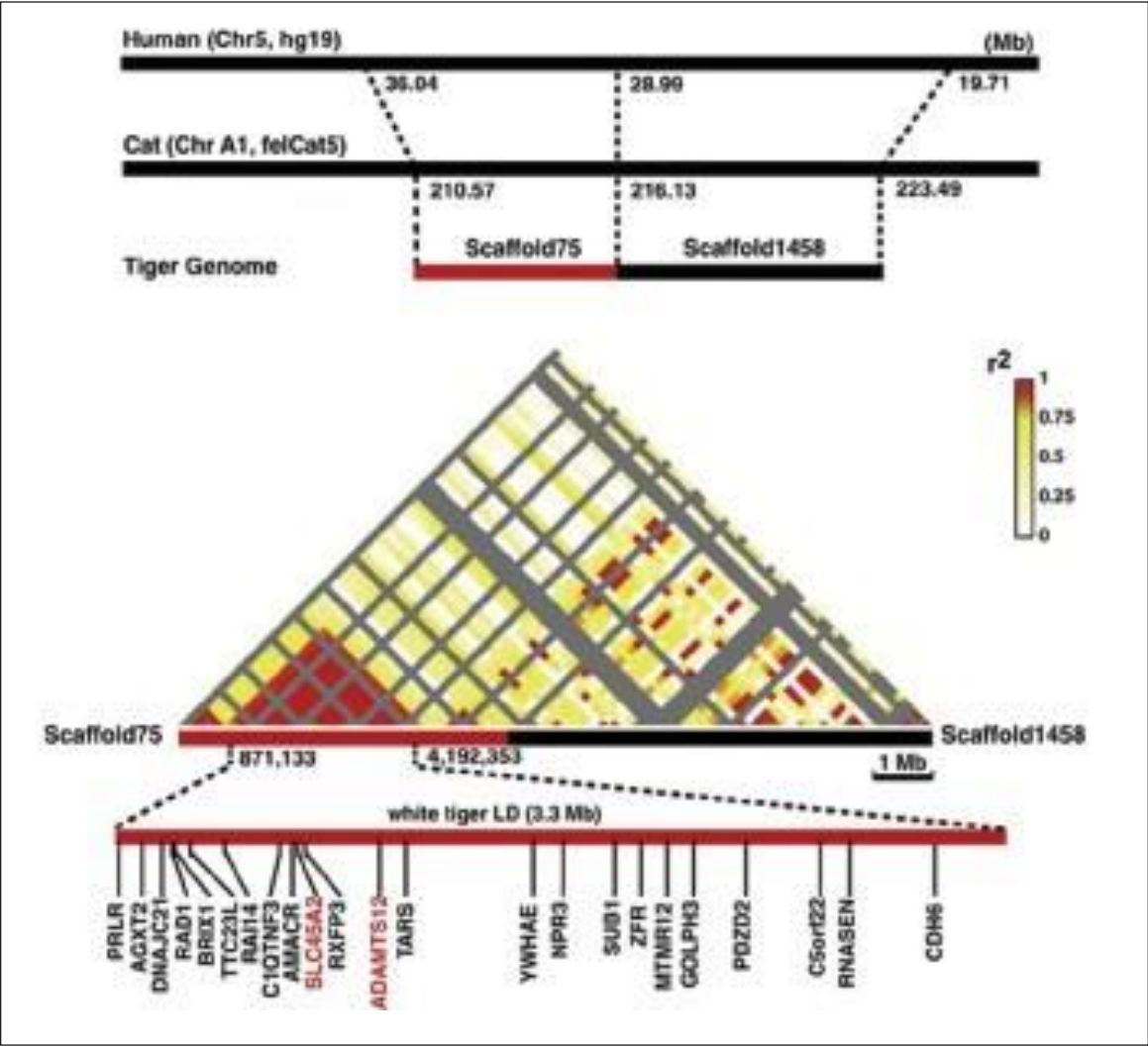
The following study utilized Medikonia’s sequencing services.

The Genetic Basis of White Tigers

Current Biology, 23:1031–1035 (2013)

In this study on tiger variants, researchers examined the genetic basis for white fur, an autosomal recessive trait that is often selected in tiger breeding programs. Using WGS, restriction-site-associated DNA sequencing (RAD-seq), and a genome-wide association study (GWAS), the genomes of 16 captive tigers

Were analyzed. The white fur trait was mapped to a missense mutation in a transporter protein gene potentially associated with melanogenesis, furthering our understanding of the natural diversity in tiger populations and the factors that contribute to mammalian pigmentation.



Genetic Mapping of the White Tiger Mutation Based on RAD-Seq and Whole Genome Sequencing

EXAMPLES OF PUBLICATIONS

Journal	Title
Mol Biol Evol, 33:1337 (2016)	History and temperate adaptation of the honey bee subspecies <i>Apis mellifera sinisxinyuan</i> n. ssp.
Scientific Reports, 5:14256 (2015)	Genetic responses to seasonal variation in altitudinal stress: whole-genome resequencing of great tit in eastern Himalayas.
Scientific Reports, 4:4678 (2014)	Whole-genome sequencing of Berkshire (European native pig) provides insights into its origin and domestication.
Nature Genetics, 46:1303 (2014)	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history.
Nature Genetics, 45:1431 (2013)	Genomic analysis identifies distinct patterns of selection in domesticated pigs and Tibetan wild boars.
Nature Genetics, 45:51 (2012)	The draft genome of watermelon (<i>Citrullus lanatus</i>) and re-sequencing of 20 diverse accessions.