

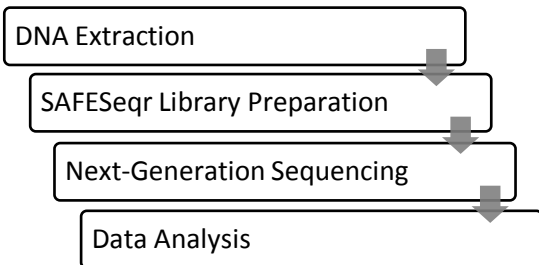
## Highlights

- ✓ Minimal starting input of 2 ng.
- ✓ Able to detect mixture components in sample.
- ✓ Ability to identify < 0.05 % minor contributor.
- ✓ Limit of detection as low as 0.0001 ng / 0.1 pg.
- ✓ Streamlined workflow with sample-to-report in < 1 day.
- ✓ User-friendly analysis software with targeted database.

## Overview

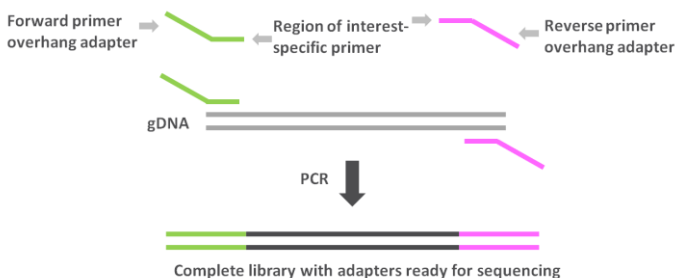
The SAFESeqr solution includes the SAFESeqr Kit and SAFESeqr Suite. SAFESeqr delivers a very robust and fast method in the identification of up to 1842 eukaryotic species (1161 genus) using high output massively parallel sequencing. Combining SAFESeqr one-step PCR library preparation workflow and the Illumina MiSeq Next-Generation Sequencing platform, it is capable of detecting resolving complex and low level sample mixtures requiring just 2ng of input DNA. Sequence data can be easily visualized and reports generated using the SAFESeqr Suite Analysis software.

## Streamlined Workflow (< 1 day)



## One-step library prep workflow

PCR amplify template out of genomic DNA using region of interest-specific primers with overhang adapters\*.



\* Overhang adapter includes P5/P7 sequencing primer with specific index sequence.

## Product Information

The SAFESeqr Kit contains both forward and reverse primers. It provides the user with the greatest flexibility in preparing up to 96 multiplexed sequencing libraries with 96 index combinations.

Features	Description
Technology	Massively Parallel Sequencing
Assay	Amplicon Sequencing
Instrument	Illumina MiSeq System
DNA input	2 ng
Amplicon size	73 - 110 bp
Sensitivity (LOD)	0.0001 ng or 0.1 pg
Kit Support	MiSeq Micro Kit v2
Number of Samples per Kit	96
Workflow	< 1 day

## SAFESeqr Kit



## SAFESeqr Suite



## Features

- ✓ User-friendly.
- ✓ Comprehensive database.
- ✓ Ready to print report.

**SAFESeqr Suite** is a point-and-click software that is easy to use. The software automatically analyzes the data with as little as four clicks. Report is ready to be printed as soon as the analysis is completed.

## System Requirement

The software is recommended to be installed on Ubuntu 12.04 with a minimum of 24 threads and 16Gb of RAM.

For more information on SAFESeqr, please contact us at:

[support@bioeasy.com.my](mailto:support@bioeasy.com.my) or visit our website [www.sciencevision.com.my/safeseqr/](http://www.sciencevision.com.my/safeseqr/)

## Benchmark

Reagent	Million reads (M)	Computer Specification	Analysis Time
MiSeq Reagent Micro Kit v2	4 M	24 threads	~2hours*

\*Analysis speed at 40K reads per minute.

## Software Interface and features

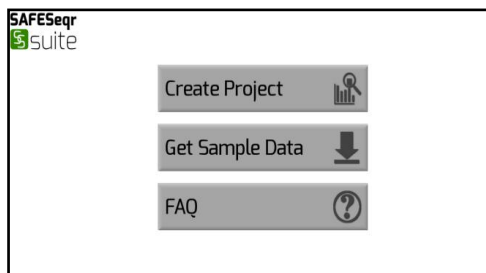


Figure 1: Easy to use and simple workflow

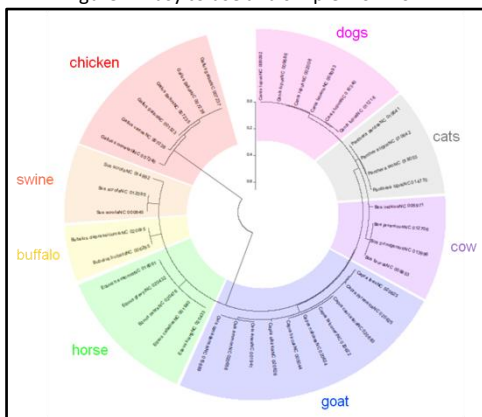


Figure 2: A representative database of 1161 eukaryotic genus

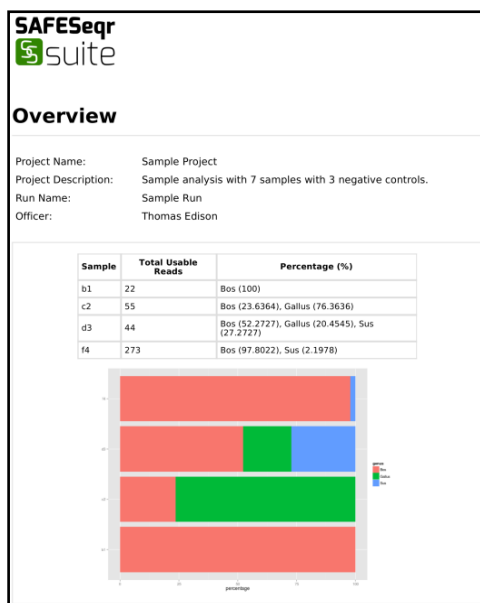


Figure 3: Report

## Options for SAFESeqr Suite

### (A) SAFESeqr Suite

### (B) SAFESeqr Suite Box

#### Specification

Processor	Dual Intel Xeon Processor E5-2620 v2 (Six Core HT, 2.1GHz Turbo, 15 MB)
Memory	16 GB RAM (4x4GB)
Operating System	Based on Ubuntu Linux Version 12.04
Hard drive	6Tb

#### Ordering Information

Cat no.	Item	Description
SQ-4896-11	SAFESeqr Kit	One kit with 96 index combinations for 96 reactions
SS-011	SAFESeqr Suite	Annual License for One computer
SS-021	SAFESeqr Suite Box	Annual License for One computer with hardware

## References

1. Shehzad W, McCarthy TM, Pompanon F et al (2012) Prey preference of snow leopard (*Panthera uncia*) in South Gobi, Mongolia. *PLoS One*. 7(2):e32104.
2. Ficetola GF, Coissac E, Zundel S et al (2010) An in silico approach for the evaluation of DNA barcodes. *BMC Genomics*. 11:434.
3. Humair PF, Douet V, Morán Cadenas F (2007) Molecular identification of bloodmeal source in *Ixodes ricinus* ticks using 12S rDNA as a genetic marker. *J Med Entomol*. 44(5):869-80.

For more information on SAFESeqr, please contact us at:

[support@bioeasy.com.my](mailto:support@bioeasy.com.my) or visit our website [www.sciencevision.com.my/safeseqr/](http://www.sciencevision.com.my/safeseqr/)