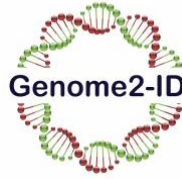


Genetic Analysis Sample Report

Customer ID: EXAMPLE
 Customer Sample number: 123456
 DNA4 Tracking ID: 1419
 Date submitted: Jan 10 2018
 Date sequenced: Jan 20, 2018



DNA Isolation Method: Promega Maxwell with Plant LEV Extraction kit using standard 2 gram small fragment protocol
 DNA quantitation: 12.2 ng/ul in 60 ul (via Qubit 2.0 Fluorometer Broad Sensitivity)
 Library Preparation: Whole Genome Shotgun
 Kapa Hyperprep (cat# : 07962312001)
 Primers: n/a
 Sequencing platform: Illumina MiSeq
 Sequencing chemistry: MiSeq Reagent Kit v3 150 cycle (Illumina cat #: MS-102-3001)

Data Analysis Platform: Genome2-ID™
 Reference Sequence Database: Complete Chloroplast Genomes (n=1500)

Assignment:

Matching Reference	ID Score	Variance	Coverage	Depth	Proportion In Sample	p_value
Panax_ginseng_KM067390.1	17015.42	25.74	97.33	4.78	>0.98	1.46E-23
Rhodiola_rosea_NYBG02609584	96.17	4.86	0.62	0.01	<0.01	1.46E-23
Panax_quinquefolius_NC027456.1	89.25	2.28	0.51	0.02	<0.01	1.46E-23
Gonystylus_bancanus_EU849490.1	80.08	4.31	0.43	0.01	<0.01	1.46E-23
Triticum_monococcum_NC021760.1	65.58	10.83	0.43	0.00	<0.01	1.46E-23

Definitions

Score: A summed value for all the sequences from the sample that match a reference sequence. The fraction of the coverage of the reference sequence and the depth of the matches contribute to the score. The higher the score the greater the confidence.

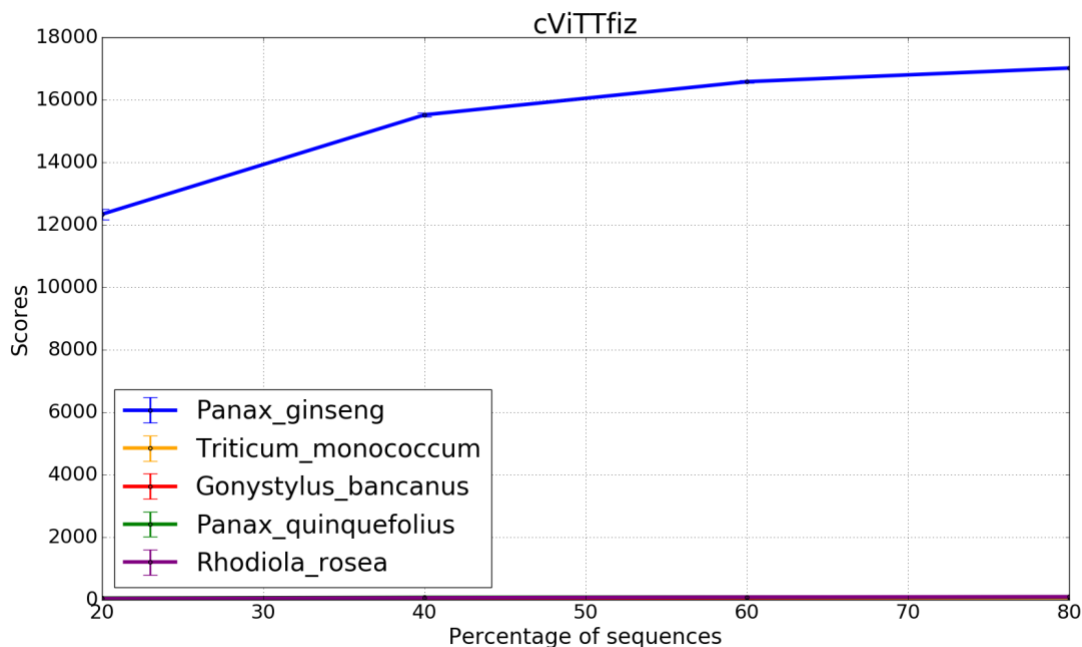
Variance: Each Genome2-ID analysis is repeated via a Jackknife, that resamples the raw data 100 times using a random draw of 30% of the data and recalculating the score. A mean and variance of the score are then calculated. When the variance value is greater than or equal to the score, there is no statistical confidence for presence of that species in the sample. A score of n/a means that the sample had below a threshold error probability and was not reported in the jackknife analysis.

Coverage: Percent of the reference sequence matched by input sequences. Greater coverage reflects greater proportion of the species in the sample. When the entire reference is matched, the calculation of the score will asymptote.

Depth: The average number of sequences from a sample that match a reference.

Proportion: The proportion of each observed reference species in the sample is inferred from the ratio of the scores where the score is asymptotic for the most abundant reference species.

Rarefaction Graph of Assignment to Reference Species:



METADATA

Raw Data output

Data availability: raw data files available upon request at: info@dna4tech.com
Sequencing output: 582,729 sequence reads
Median sequence quality: Q 29 (>99% accuracy)
Read length: 75 x 2 (paired end)
Sequence filtering: Usearch10.0 (program used to filter and clean raw sequences)
Filtering parameters: No ambiguous bases, minimum Q20, minimum length 50 bases.

Data Analysis Portal: <http://www.dna4tech.com/portal/genome2-id/>
(portal provides Genome2-ID analysis software for customer use with original data)

Sample processed in accordance with standard operating procedures at DNA4 Technologies, as certified by:

David L. Erickson, Ph.D.

On this date: January 21, 2018