Results Report

Autor: Everardo Gutiérrez

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A New DNA isolation technique was developed at Hsapiens.inc. We evaluated to specificity to capture a set of Golden Genes without capturing the surrounding unwanted regions.

Sequencing depth was evaluated for a given set of 5 genomic loci. The following coverage values were found:

CHROMOSOME	START	END	LOCUS_NAME	BREADTH OF COVERAGE	MEAN DEPTH OF COVERAGE
22	147620	147719	GOLDEN_GENE1	82%	3.70X
22	147970	148069	GOLDEN_GENE2	91%	4.27X
22	148490	148639	GOLDEN_GENE3	64.6%	2.47X
22	147820	147889	UNWANTED_REGION1	100%	53.14X
22	148190	148389	UNWANTED_REGION2	97.5%	72.66X

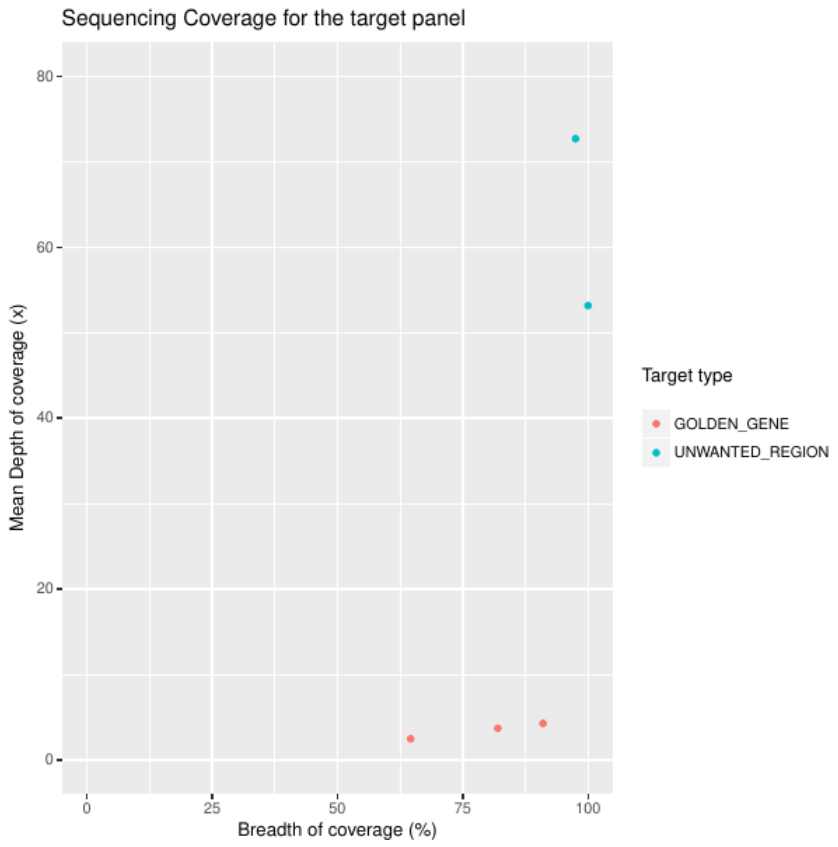

Figure 1. Comparison of coverage values for the targeted genes and the surrounding unwanted regions.

In average, the panel of Golden Genes was 79.2% covered, at 3.4X; for the unwanted regions the average values were 98.75% covered, at 62.9X.

Conclusions

- According to the results obtained, the new method to isolate DNA regions has a low specificity. Although the coverage percentage is high in the regions of interest, the average depth per base is very low with respect to the unwanted regions.
- The average depth of readings per base is 18 times greater in the unwanted regions with respect to the Golden gene regions.
- The quality of the sequencing is good in both regions, since the average coverage percentage is high. However, the amount of DNA extracted is very low in the regions of interest compared to the unwanted regions.
- Due to the high values obtained in the two parameters measured in the unwanted regions, it is possible that the marking of the samples was erroneous. That is, they were marked upside down.