Results Report

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A New DNA isolation technique was developed at HSapiens.inc. We evaluated the 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:

Gene Name	Breadth of coverage	Mean depth of coverage
GOLDEN_GENE1	82%	3.7X
UNWANTED_REGION1	100%	53.1X
GOLDEN_GENE2	91%	4.3X
UNWANTED_REGION2	97.5%	72.7X
GOLDEN_GENE3	64.6%	2.5X

Sequencing Coverage for the target panel

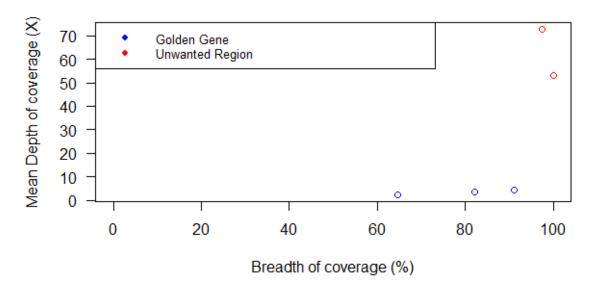


Figure 1 Comparison of the coverage values for the targeted genes and the surrounding unwanted regions.

In average, the panel of golden genes was 79.2% covered, at 3.5X; in respect to unwanted regions the average values were 98.75% covered, at 62.9X.

Conclusions

• According to our observations, the proposed DNA isolation technique is not appropriate. There is a significant bias towards the unwanted regions.