

LOH AND GENE CONVERSION

Most tumor-suppressor (TS) genes have been identified through Loss of Heterozygosity (LOH) in cancer cells. SNP-microarrays is the ideal technique to detect LOH, confirmed by Comparative Genome Hybridization (CGH). Occasionally, however, copy neutral loss of heterozygosity are detected, resulting from different mechanisms, such as mitotic recombination. The homozygosity of a mutation in a TS gene can also result from [gene conversion](#) (Wikipedia).

In a recent paper in Genome Research, [Takahashi and Innan](#)¹ report the development of an algorithm to detect somatic gene conversion from short-read sequencing data. They analyzed 6,285 cancer patient samples and found 4,978 instances in which the homozygosity of the mutation of the TS gene had resulted from gene conversion. This figure represents the 14.8% of the total LOH mutations detected in their samples.

1 <https://genome.cshlp.org/content/32/6/1017>