LINFOEXOMA

Análisis variantes puntuales en genes que han sido asociados con el desarrollo de leucemia linfoblástica aguda (ALL), leucemia linfática crónica (CLL), y linfoma no-Hodgkin (NHL)

Análisis de mutaciones somáticas adquiridas (linfoexoma somático)

Linfoexoma analiza simultáneamente las zonas codificantes de 76 genes*, utilizando tecnologías de secuenciación y protocolos de diseño propio.
Nuestro análisis bioinformático exclusivo nos permite detectar variantes puntuales (SNVs), deleciones e inserciones (INDELs) y variantes en el número de copias (CNVs). Las variantes detectadas son filtradas, priorizadas y clasificadas de acuerdo con las recomendaciones científicas internacionales.

*Para un listado completo de los genes, contacte con nosotros

76 genes
~200X germinal
~1000X somático
SNVs | INDELs | CNVs

Respuesta en 2-8 semanas

The characterization of tumour cells by genetic methods is now regarded as being important as the traditional morphological approach to diagnosis. This trend is being accelerated by the introduction of monoclonal antibody therapy and by novel drugs designed to target specifically the molecular abnormalities responsible for the development of the tumor.

Somatic genetic changes therefore increasingly define not just the diseases themselves, but the way in which an individual patient should best treated and monitored.

SabrinaTosi & Alistair G. Reid. The genetic basis of haematological cancers. John Wiley & Sons Ltd

With the introduction of NGS, it has become clear that, in addition to chromosomal rearrangements, CNVs such as sub-microscopic deletions and amplifications and sequence point mutations are common associated events in acute lymphoblastic leukemia"
"NGS technology have continued to deepen our understanding of the molecular pathogenesis of these diseases, improving patient management, and will ultimately fully catalogue all the biological relevant genomic lesions in these conditions, helping to provide curative strategies for these diseases"

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genome4

+ 34 646 684 540 | +34 629 636 029
amarmiesse@genome4care.com
www.genome4care.com