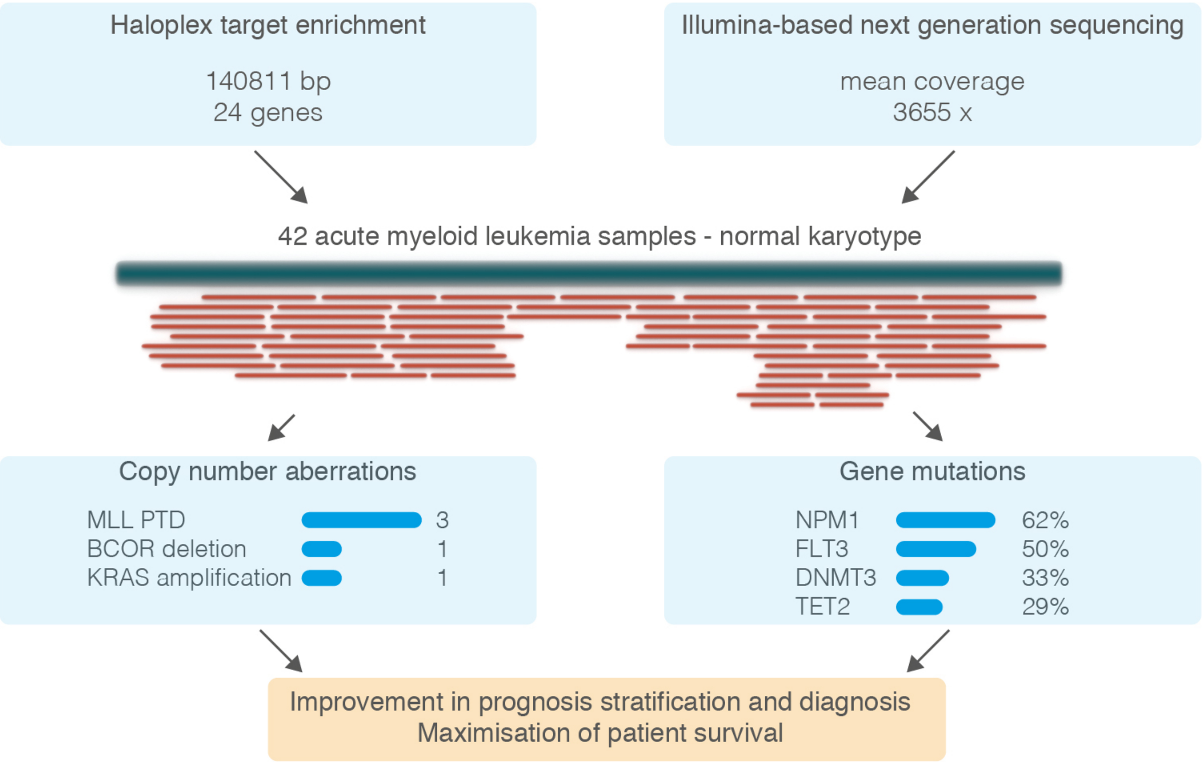
Characterization of Gene Mutations and Copy Number Changes in Acute Myeloid Leukemia Using a Rapid Target Enrichment Protocol



Haloplex target enrichment

140811 bp
24 genes

Illumina-based next generation sequencing

mean coverage
3655 x

42 acute myeloid leukemia samples - normal karyotype

Copy number aberrations

MLL PTD	3
BCOR deletion	1
KRAS amplification	1

Gene mutations

NPM1	62%
FLT3	50%
DNMT3	33%
TET2	29%

Improvement in prognosis stratification and diagnosis
Maximisation of patient survival

Bolli et al., Haematologica, 2015