GENETICS

HOW TO GET CLOSER TO THE TARGET

27.11.2007 1 COMMENT

Attending last week another Illumina sequencer course, I still have the question how to enrich the target sequence. A colleague calling me this morning (thanks TB!) had a pointer to a new nature methods editorial covering three different methods- a 100-mer capture probe for each exon sized segment with the need of extremely deep resequencing and two other methods using direct hybridization of segments onto commercially oligo arrays. ArenÂ´t there any other protocols?

NACHTRAG

admin

20.02.2008 AT 11:46

Laborwelt 2008;9:6 has the description by a Roche employee how high density capture arrays by NimbleGen were used to enrich some 6726 exon carrying fragments of 0.5-2 Mb length that covered 660 genes. More on http://www.nature.com/nmeth/journal/v4/n11/abs/nmeth1109.html and http://bioinformatics.oxfordjournals.org/cgi/content/full/22/2/134 This lead to an 400--fold enrichment of target sites.

COMMENTS ARE CLOSED.