

GENETICS

# HOW DEEP IS DEEP ENOUGH?

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In case that the common disease / common variant is leading to *nirvana*, we urgently need to resequence common genes in large populations. 2kb long CRP is a particular good candidate which might be a reason why [Crawford from Uwash](#) resequenced ~500 individuals. They found indeed potentially relevant codings SNPs – of course rare (<1%) but they are there! There is a greater number in African-Americans than other populations and more than half are private to a single population (BTW more than half in dbSNP can not be validated). Of course tag SNPs would not discover them. Yea, yea.

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