ALLERGY, GENETICS

INDELLIGENT

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I am detailing in a forthcoming paper in “Allergy”, that the contradicting results found with ADAM33 (the first positionally cloned asthma gene) probably results from a rather poor design of all follow-up studies.
It does not make so much sense to repeat over and over the same few SNP marker; instead a full resquencing of the linkage region would be necessary. From the analysis of public LD maps it is even possible that neighboring genes may be responsible for the observed associations.
I have also doubts if the SNP-centric view is always leading to success. BTW there is a new database of over 400,000 non-reduandt indels of which 280,000 are validated by comparison with other human or chimpanzee genomes (see Mills et al., the indels are available in dbSNP under the “Devine_lab” handle).