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Methodology

**Using
GWAS
Data to
Identify
Copy
Number
Variants
Contributing**

to Common Complex Diseases

Sebastian

Zöllner, Tanya M.

Teslovich

*(Submitted on 25
Oct 2010)*

Copy
number
variants
(CNVs)
account
for more
polymorphic
base
pairs in
the
human
genome
than do
single
nucleotide
polymorphisms
(SNPs).
CNVs
encompass