Discovery points to explanation for “missing” genetic risk

Susceptibility to common diseases is believed to arise through a combination of many common genetic variants that individually slightly increase the risk of disease, plus a smaller number of rare mutations that often carry far greater risk.

However, even when their effects are added together, the genetic variants so far linked to common diseases account for only a relatively small proportion of the risk we know is conveyed by genetics through studies of family history.

But the major new study, published in the journal PLOS Genetics, shows for the first time in cancer that some common genetic variants could actually be indicators of the presence of much more influential rare mutations that have yet to be found.

Read the full, original story: Discovery may help to explain mystery of ‘missing’ genetic risk