

The “junk” in your genetic trunk isn’t junk at all

[W]hen the human genome project began it was assumed that, due to the complexity of human beings we would have a lot of genes, certainly many more than a lowly worm. No offence to round worms but we are way more complex. I mean they only have 970 cells, compared to our 60 trillion. So how come we only have 30% more protein-coding genes than a simple roundworm and why is so much of our DNA junk?

The non-coding or ‘junk’ regions can help switch genes on or off which, in turn, influences whether a cell makes a certain protein or not. Non-coding DNA can recruit machinery in the cell which can either promote or hinder the process of turning a gene into a protein. The non-coding DNA can also be actively modified by a process called methylation, which switches off genes. Methylation can occur at any point in your life and may represent a way by which our environment and lifestyle can actually change our DNA. This is one of many ways our underlying genetic code can be modulated and is called an ‘epigenetic’ alteration. Such epigenetic changes might go some way to explaining why genetically identical twins, who have lived quite separate lives, often become less alike as they age.

View the original article here: [The Junk in Your Genetic Trunk](#)