Table S2. Transcription factors are significantly enriched among genes associated with wCNEs. We have used two high-quality transcription factor prediction databases to annotate wCNE-associated genes. DBD is a database of transcription factors predicted through homology to domains of known sequence-specific DNA-binding transcription factors [1]. The *C. elegans* genes analysed in DBD correspond to WormBase release WS150. wTF2.0 is a compendium of computationally predicted and manually curated transcription factors [2]. The *C. elegans* genes analysed in wTF2.0 correspond to WormBase release WS140. Using both databases we have found that the set of genes associated with wCNEs contains a significantly higher proportion of predicted transcription factors than the rest of the genes in the genome. The total number of genes associated with wCNEs is 1,241.

Database of predicted transcription factors	DBD [1]	wTF2.0[2]
Number of genes coding for transcription factors associated with wCNEs	108	137
Number of genes coding for transcription factors in the *C. elegans* genome	723	934
Total number of genes considered in the *C. elegans* genome	20,053	19,735
Log odds ratio	1.037 (±0.213)	1.014 (±0.191)
P-value	< 2.2e-16	< 2.2e-16

References

1. Kummerfeld SK, Teichmann SA: **DBD: a transcription factor prediction database**. *Nucleic Acids Res* 2006, **34**(Database issue):D74-81.
2. Reece-Hoyes JS, Deplancke B, Shingles J, Grove CA, Hope IA, Walhout AJ: **A compendium of Caenorhabditis elegans regulatory transcription factors: a resource for mapping transcription regulatory networks**. *Genome Biol* 2005, **6**(13):R110.