Barriere et al.

Table S2. Summary of genome-wide computational search for putative heterozygous loci in the *C. remanei* WGS assembly.

C. elegans query chromosome	*C. remanei* dimorphic genes	Dimorphic genes after identity filter (% total)	Dimorphic genes after identity, tandem duplication, and overlap filters (% total)	Mean read depth for all dimorphic genes	Mean read depth for dimorphic genes after identity, tandem duplication, and overlap filters
I	88	25 (28.4)	17 (19.3)	9.13	7.14
II	94	19 (20.2)	12 (12.8)	9.63	11.01
III	76	9 (11.8)	9 (11.8)	9.17	9.75
IV	561	443 (79.0)	414 (73.8)	6.11	5.84
V	191	43 (22.5)	29 (15.2)	8.89	5.58
X	70	9 (12.9)	6 (8.6)	8.25	6.17
TOTAL	1080	548 (50.7)	487 (45.1)	7.51	6.07