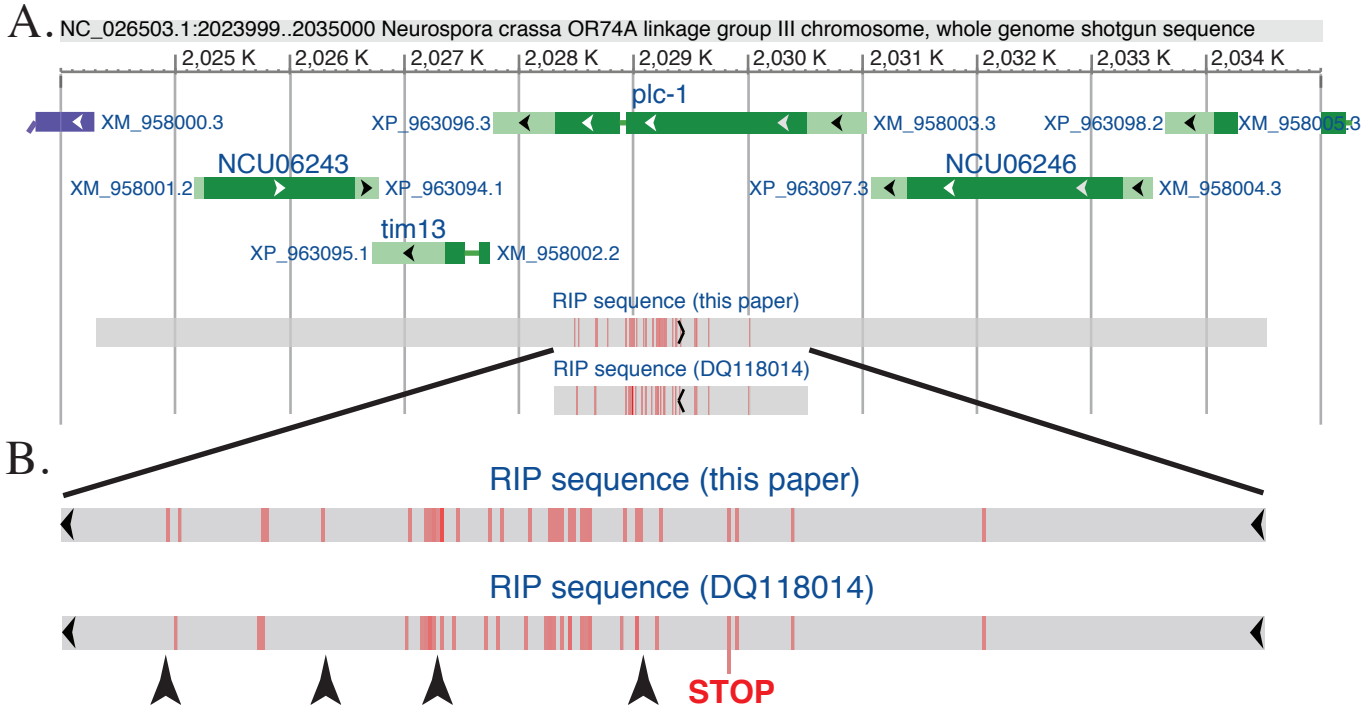
Supplemental Figure 1. A. The plc–1 gene and flanking regions from NCBI. To determine whether nearby genes were affected by the RIP mutation (and causing the RIP phenotype), regions flanking the plc–1 gene in the RIP plc–1 mutant were sequenced on linkage group III chromosome from position 2024319 to 2034513. The 4 kb flanking regions were identical to the wildtype sequence. The RIP mutations were localized to the plc–1 gene. B. There were four differences compared to the original DQ118014 RIP sequence: 1) a base substitution C —> T at position 2028490; 2) a base substitution C —> T at position 2028781; 3) a base substitution C —> T at position 2029004; and 4) no base substitution (C —> T) at position 2029007. Otherwise, all missense and nonsense mutations were confirmed, including the stop at amino acid 412 that results in expression of a dysfunctional plc–1 protein. C. Complete sequence of the RIP sequence (this paper).



C.

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