Supplementary Material

Supplementary Table S1. Properties of the RNA and RNA sample libraries used in wheat root-*Pratylenchus* transcriptomics.[1]

Treatment	RNA sample	RNA (ng/µL)[2]	RIN[3]	Library (ng/µL)[4]	Library size (bp)[5]
P. neglectus	Pn	368.7 ± 61.3	4.07 ± 0.21	30.87 ± 0.42	514.7 ± 20.2
P. thornei	Pt	328.7 ± 169.3	5.43 ± 1.08	32.47 ± 0.47	499.7 ± 55.9
P. neglectus+*P. thornei* (1:1)	PnPt	441.3 ± 42.8	4.20 ± 0.26	30.60 ± 5.03	485.3 ± 9.6
No nematode control	Cont	374.3 ± 263.2	3.93 ± 0.25	32.27 ± 2.21	494.3 ± 29.0

[1] Values are the averages ± S.D. of three biological replicates.

[2] Concentration of total RNA prior to library preparation.

[3] RNA Integrity Number, a quality parameter based on the 28S/16S RNA ratio [108].

[4] RNA concentration of the prepared library prior to sequencing.

[5] Mean size of RNA fragments in the prepared library.

Supplementary Table S2. Candidate IWGSC wheat *DORN1* orthologues of brassica GenBank accessions

GenBank query	Host spp.	Highest % identity	IWGSC Accession
NM_001085304.1	*A. thaliana*	62.9	Traes_2B_80806CA5F.1
XR_002332231.1	*A. lyrata*	66.2	Traes_2AS_DE7DCB2941.1
XM_019237557.1	*C. sativa*	61.9	Traes_1BS_A999A190E.3