**Fig. S1: Genotyping for *pgip1-1* mutants.** Genomic DNA of Col-0 or knockout lines (*pgip1-1;* SALK_001662.33.10.x*)* was PCR amplified using Left primer (LP), Right Primer (RP), and border primer (BP or LB1.3). The presence or absence of intact wild-type allele is shown. Expected size for wild-type (LP+RP) was 1117bp and for *pgip1-1* (BP+RP) 511-811bp. Primer sequences are given in Table S1.

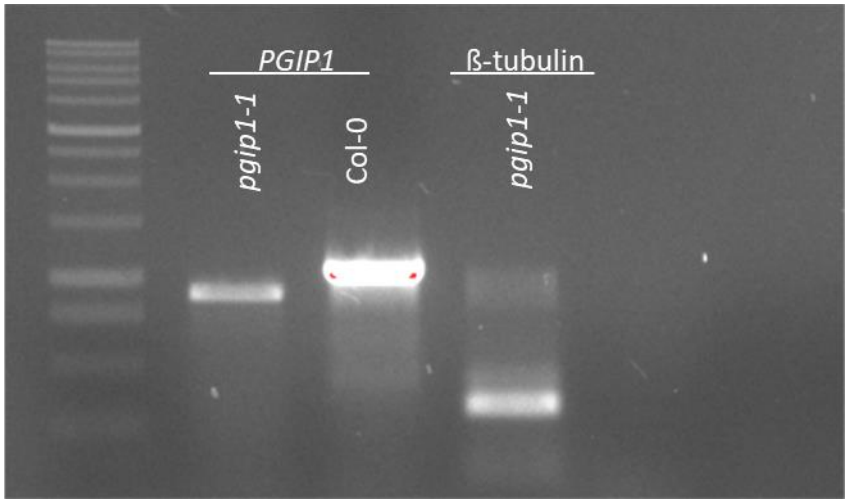

**Fig. S2**: **RT-PCR for presence or absence of gene expression in Col-0 or knockout mutants.** RNA from Col-0 or knockout lines (*pgip1-1*, *pgip1-2*, *pgip2-1*) was extracted to synthesize single stranded cDNA. The presence or absence of expression is shown using primers given in Table S2. UBQ5 was used as a positive control.

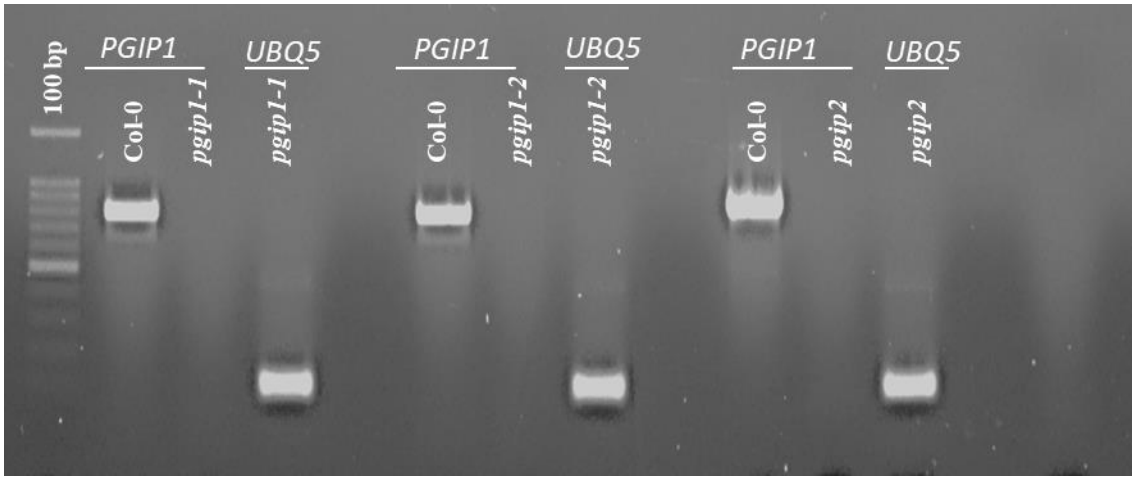

**Fig. S3**: **Cyst nematode infection assays in PGIP1 (*pgip1-2*) mutant lines**. (a) Average number of females and males per plant present in Col-0 and *pgip1-2* mutant lines at 12 dai. (b, c) Average sizes of female nematodes (b) and plant syncytia (c) in Col-0 and *pgip1-2* mutant lines. Bars represent mean ± SE for three independent experiments. Data were analysed using student's T-test ($P < 0.05$). Asterisks represent statistically significant difference to corresponding Col-0.

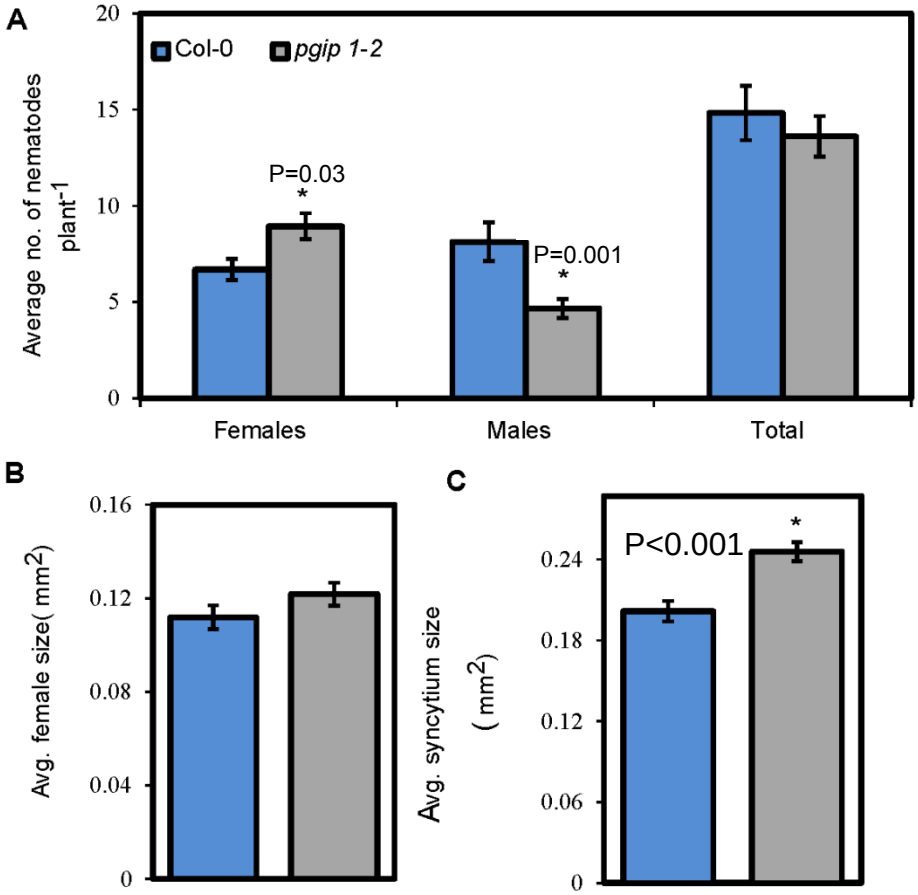

**Fig. S4: Cyst nematode infection assays in PGIP2 (*pgip2-1*) mutant lines**. (a) Average number of females and males per plant present in Col-0 and *pgip2-1* mutant lines at 12 dai. (b, c) Average sizes of female nematodes (b) and plant syncytia (c) in Col-0 and *pgip1-1* mutant lines. Bars represent mean ± SE for three independent experiments. Data were analysed using student's T-test ($P < 0.05$). Asterisks represent statistically significant difference to corresponding Col-0.

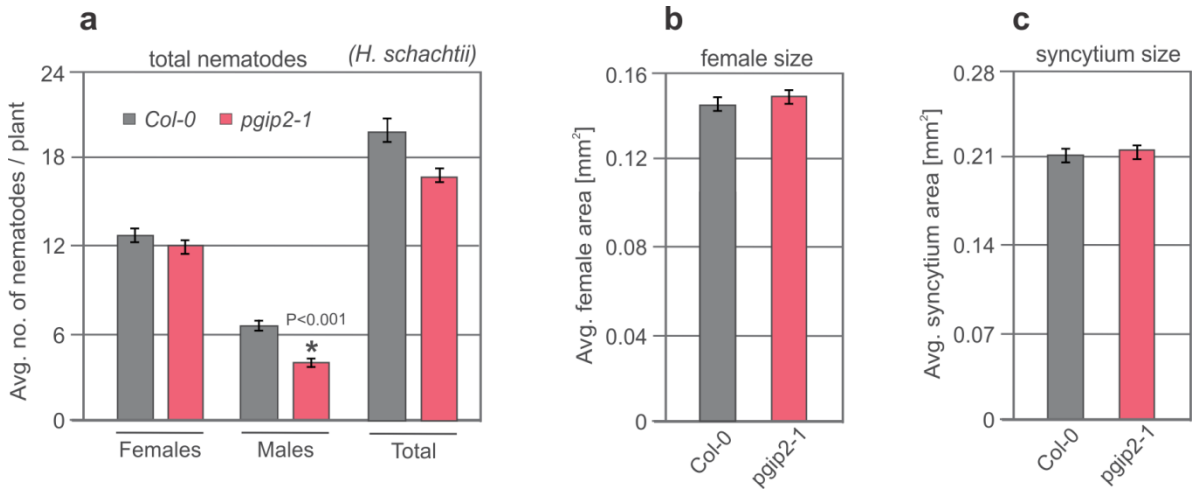

**Fig. S5: Cyst nematode infection assays in complementation lines for *PGIP1* (*35S::PGIP1/pgip1-1*) mutant lines**. Two independent homozygous lines overexpressing *PGIP1* in *pgip1-1* background (*35S::PGIP1/pgip1-1-L1*, *35S::PGIP1/pgip1-1-L2*) were selected and analysed for changes in transcript abundance of PGIP. *UBQ5* and *β-tubulin* were used as housekeeping genes to normalize the data. The values represent relative fold change in roots of transgenic lines with the value in uninfected Col-0 root set to one. (b, d) Average area of female nematodes (b) and plant syncytia (d) in Col-0 and PGIP1 overexpression lines at 14 dai. (c) Average number of females and males per plant present in Col-0 and PGIP1 overexpression lines at 12 dai. (b-d) Bars represent mean ± SE for three independent experiments. Data were analysed using student's T-test ($p < 0.05$). Asterisks represent statistically significant difference to corresponding Col-0.

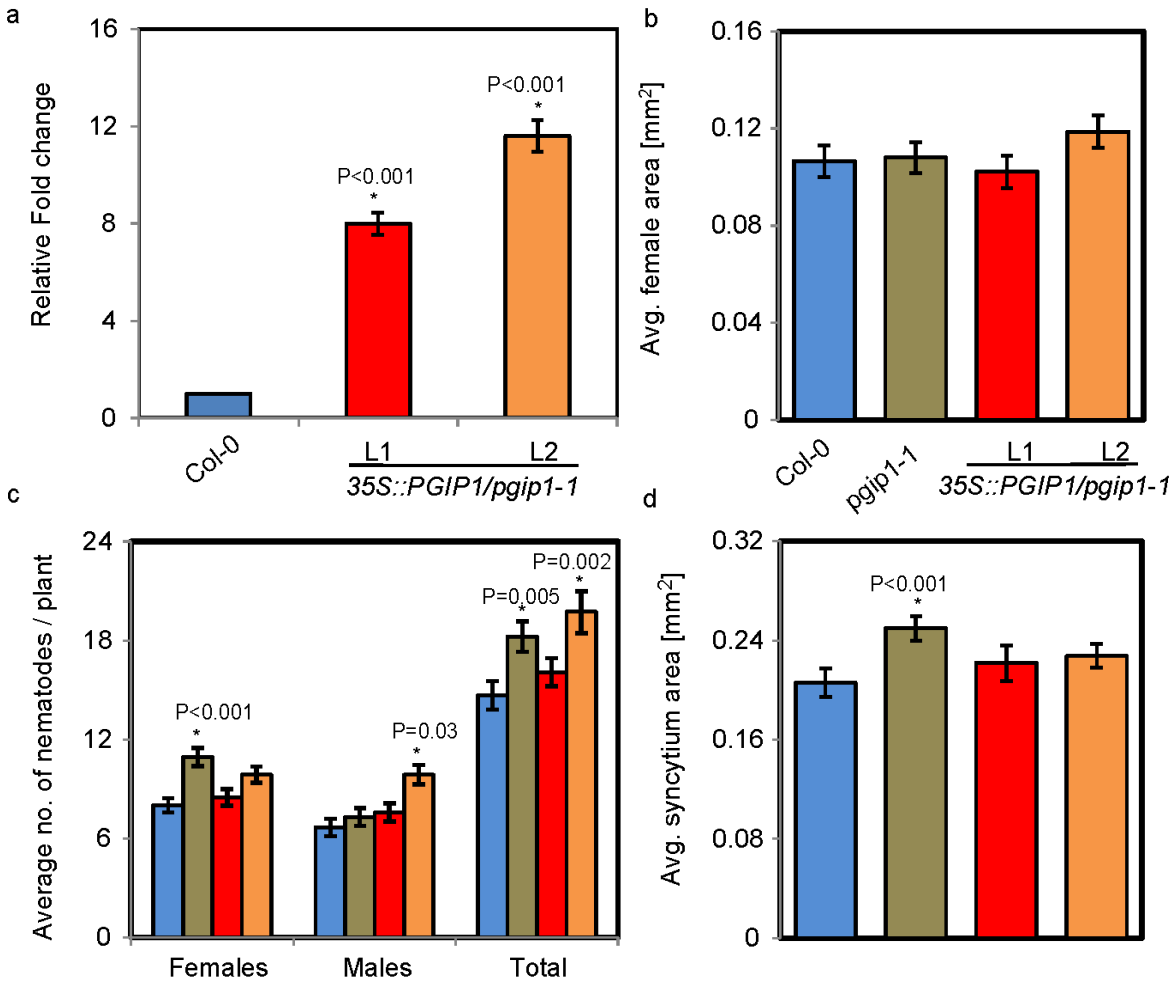

**Fig. S6: Cyst nematode infection assays in *PGIP2* overexpression lines**. (a) Two independent homozygous lines (L1, L2) overexpressing PGIP2 (*35S::PGIP2*) were selected and analysed for changes in transcript abundance of PGIP. *UBQ5* and *β-tubulin* were used as housekeeping genes to normalize the data. The values represent relative fold change in roots of transgenic lines with the value in uninfected Col-0 root set to one. (b) Average number of females and males per plant present in Col-0 and *PGIP2* overexpression lines at 12 dai. (c, d) Average sizes of female nematodes (b) and plant syncytia (d) in Col-0 and *PGIP2* overexpression lines at 14 dai. (b-d) Bars represent mean ± SE for three independent experiments. Data were analysed using student's T-test ($p < 0.05$). Asterisks represent statistically significant difference to corresponding Col-0.

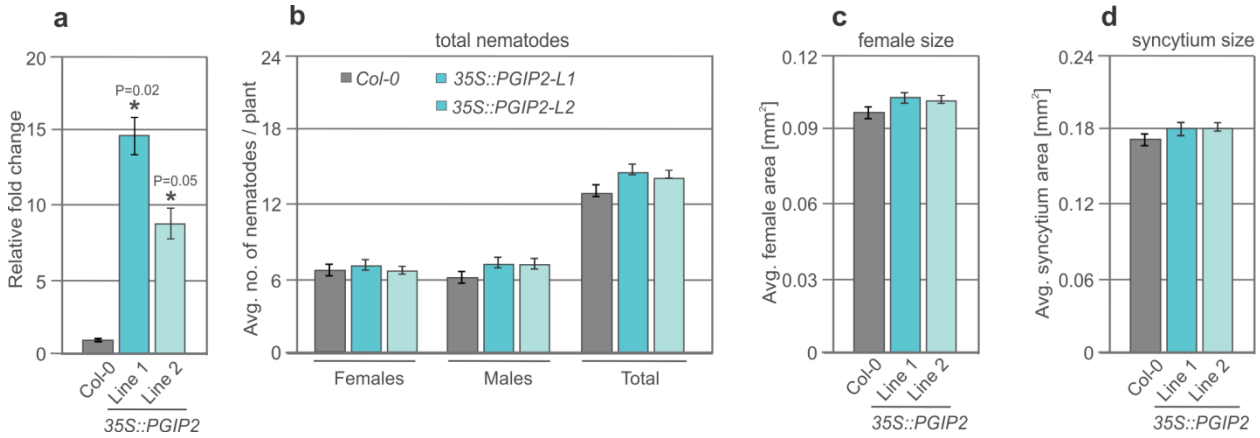

**Fig. S7**: **Root-knot nematode infection assays in *PGIP1* and *PGIP2* overexpression lines**. (a) Average number of galls per plant present in Col-0, and *PGIP* overexpression lines at 21 dai. (b) Average size of galls per plant present in Col-0 *PGIP* overexpression lines at 21 dai. Data were analysed using student's T-test ($P < 0.05$).

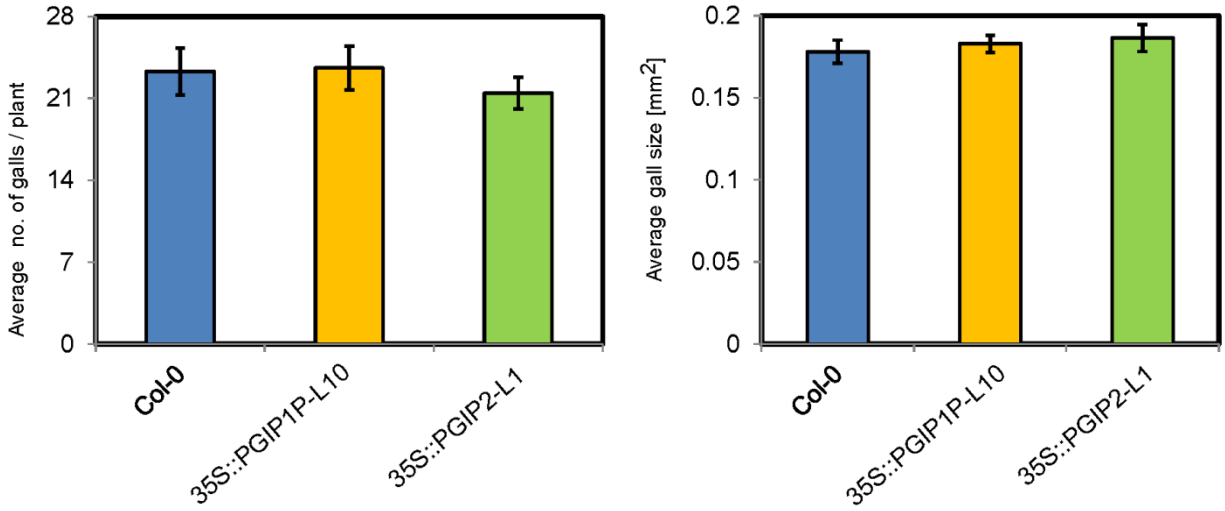

**Fig. 8: Cyst nematode infection assays upon OG treatment**. (a) Average number of females and males per plant present in water- or OG-treated Col-0 plants at 12 dai. (b, c) Average area of female nematodes (b) and plant syncytia (c) in water- or OG-treated Col-0 plants at 14 dai. (a-c) Bars represent mean ± SE for three independent experiments. All data were analysed using student's T-test ($p < 0.05$). Asterisks represent statistically significant difference to corresponding $H_2O$ treated Col-0.

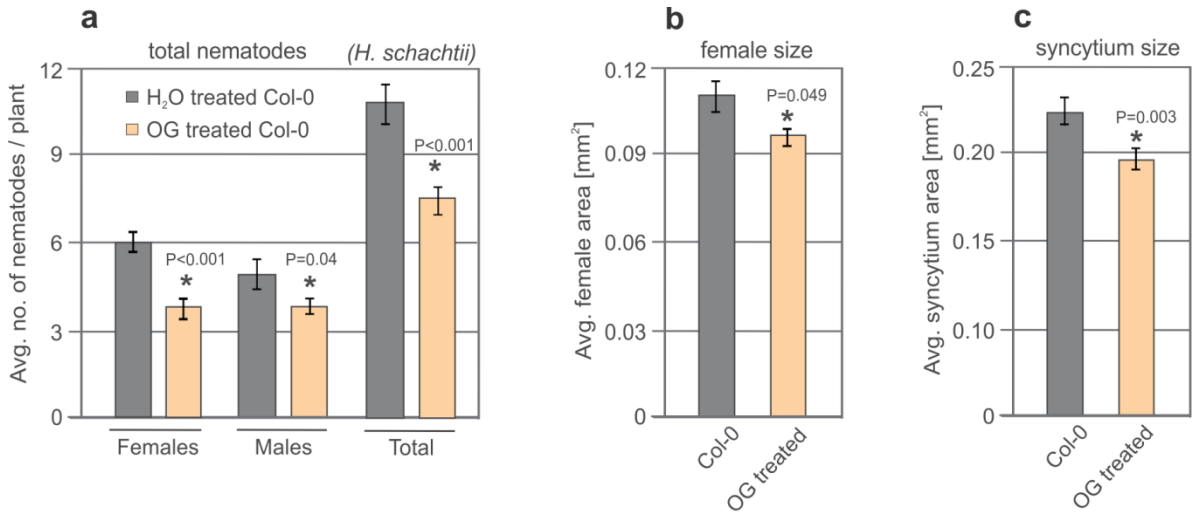

**Table S1** Primer sequences used in this work.

| Gene | Locus | Forward Primer | Reverse Primer | Efficiency |
|---|---|---|---|---|
| **UBQ5** | At3g62250 | GTTAAGCTCGCTGTTCTTCAGT | TCAAGCTTCAACTCCTTCTTTC | 98 |
| **JAZ8** | At1g30135 | TGTGTTTTTCTTCAGATGTTACCC | TCTCTGCTTGCGATCGATATT | 98 |
| **PROPEP1** | At5g64900 | ACGAAGCGAAGAAAGTCACC | TTCGGCTGTTTCGAAGTTCC | 102 |
| **NPR2** | At4g26120 | AAACCGAGTTGCACTTGCTC | AGTGATGTCCGCTTTTCACC | 106 |
| **PAD3** | At3g26830 | TTAAGCTCGTGGTCAAGGAGAC | GACCCATCGCATAAACGTTGAC | 106 |
| **CYP81F2** | At5g57220 | ATCGTGCTAGTGAACGCTTG | TTCGTCCGTTACCAAACACC | 95 |
| **CYP71A12** | At2g30750 | GCTTCTTGAGATCCCTTGCG | GTGATGTGGTGTTTGGTCCC | 98 |
| **PGIP1-qPCR** | At5g06860 | AGTCCCTGACCTTCGCCTAT | AGCATCACCTTGGAGCTTGT | 93 |
| **PGIP2-qPCR** | At5g06870 | AACAAGCTTCAAGGCGATGC | AACCTTGGAGAGATCGAACTGG | 95 |
| **PGIP-RTPCR** | At5g06860 | CTGACAGGTCCAATTCCTGAC | AATCCATCAAATAAAACATTTTGAA | |
| **PGIP2-RTPCR** | At5g06870 | TCTTGTCCACTCTCCTCCTCA | CCGGAATACTCCCTGTGATG | |
| **GWpPGIP1:GUS** | At5g06860 | GGGGACAAGTTTGTACAAAAAAGCA GGCTGCAAAAGGGCAGGCTAGGCTAA | GGGGACCACTTTGTACAAGAAAGCT GGGTCCTGAGGCAATGTCTTCACCA | |
| **GWpPGIP2:GUS** | At5g06870 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGC ACCAAGCTTATCTCTAGGAT | GGGGACCACTTGACAAGAAAGCT GGGTCGAGTTTTTATGGAAACTATGATTG | |
| **35S::PGIP1** | At5g06860 | ATGGATAAGACAGCGACATTGTGTC | TTACTTGCAAATTTCAAGAGGAGCAC | |
| **35S::PGIP2** | At5g06870 | ATGGATAAGACAATGACACTGTTC | TCACTTGCAACTAGGAAGAGG | |
| **Left primer** | | CTGACAGGTCCAATTCCTGAC | | |
| **Right primer** | | TATGAATGCATGGTGCGATAC | | |
| **Border primer** | | ATTTTGCCGATTTCGGAAC | | |

**Table S2:** An overview of PGIP1 and PGIP2 expression in published and unpublished transcriptomic data. Values are relative fold change. Asterisks indicate significant difference to control.

| Locus | Gene Name | Root vs Sync (5+15 dpi) Szakasits et al., 2009 | Root vs migratory stage (10 hpi) Mendy et al., (2017) |
|---|---|---|---|
| At5g06860 | PGIP1 | 3.40 * | 3.98 * |
| At5g06870 | PGIP2 | 0.70 | 1.07 |