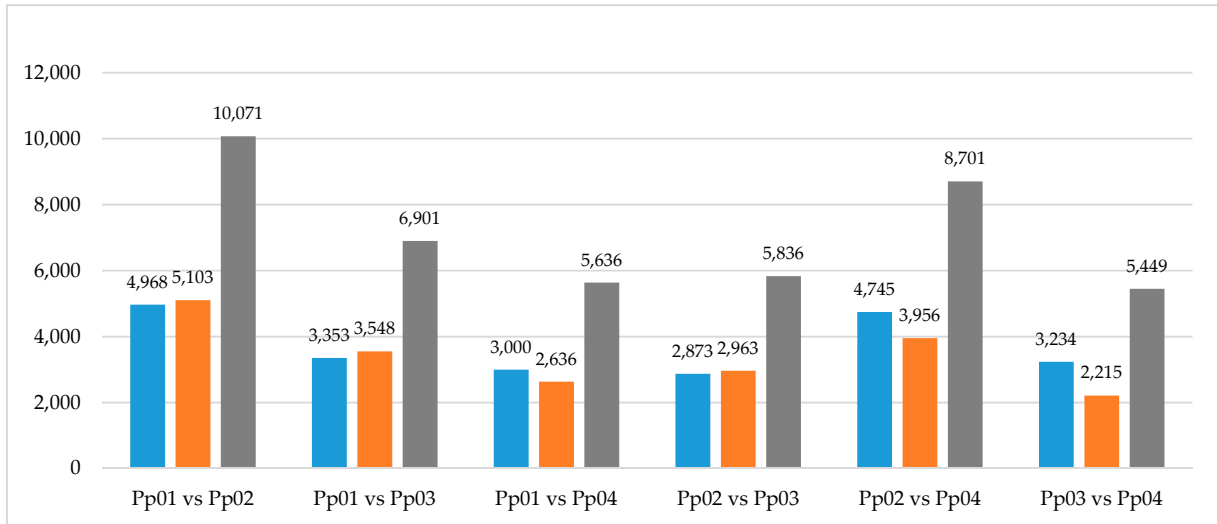


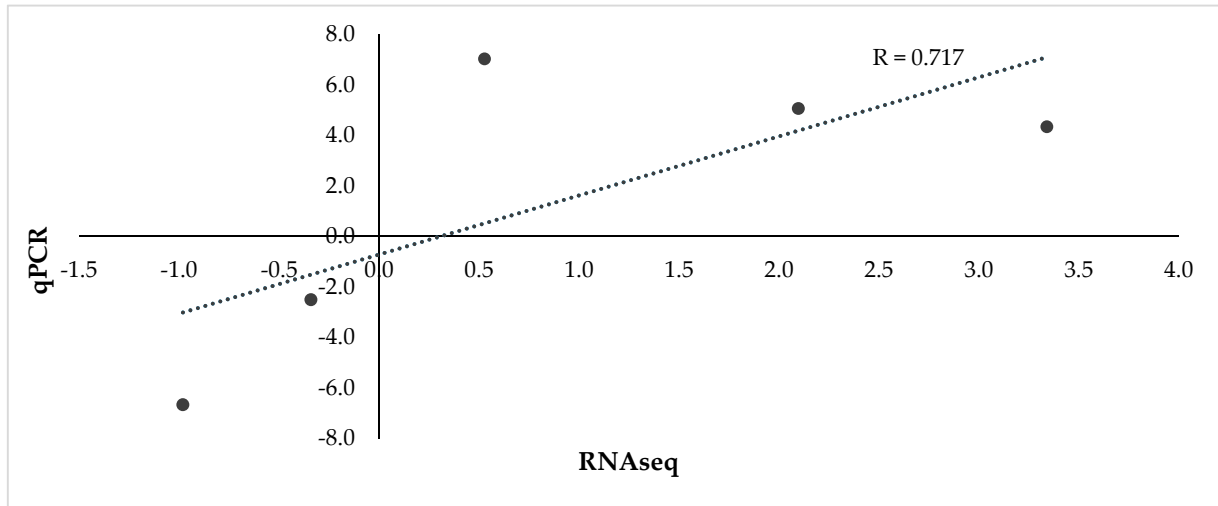
## Expression Profiling in *Pinus pinaster* in Response to Infection with the Pine Wood Nematode *Bursaphelenchus xylophilus*

### SUPPLEMENTARY MATERIALS

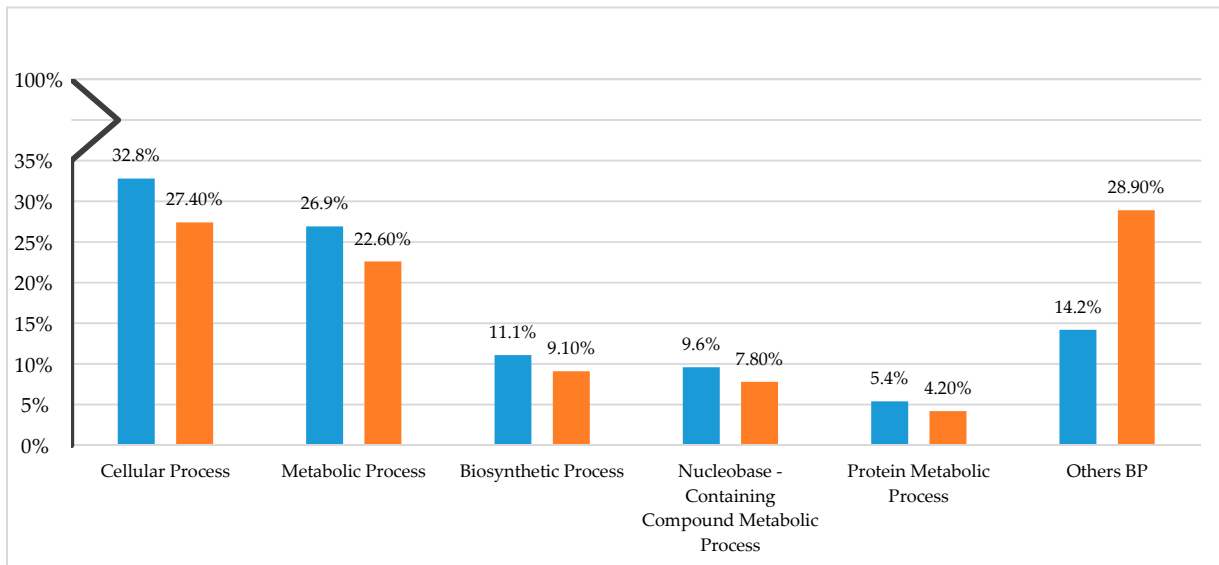
Daniel Gaspar, Cândida Trindade, Ana Usié, Brígida Meireles, Pedro Barbosa, Ana M. Fortes, Cátia Pesquita, Rita L. Costa and António M. Ramos



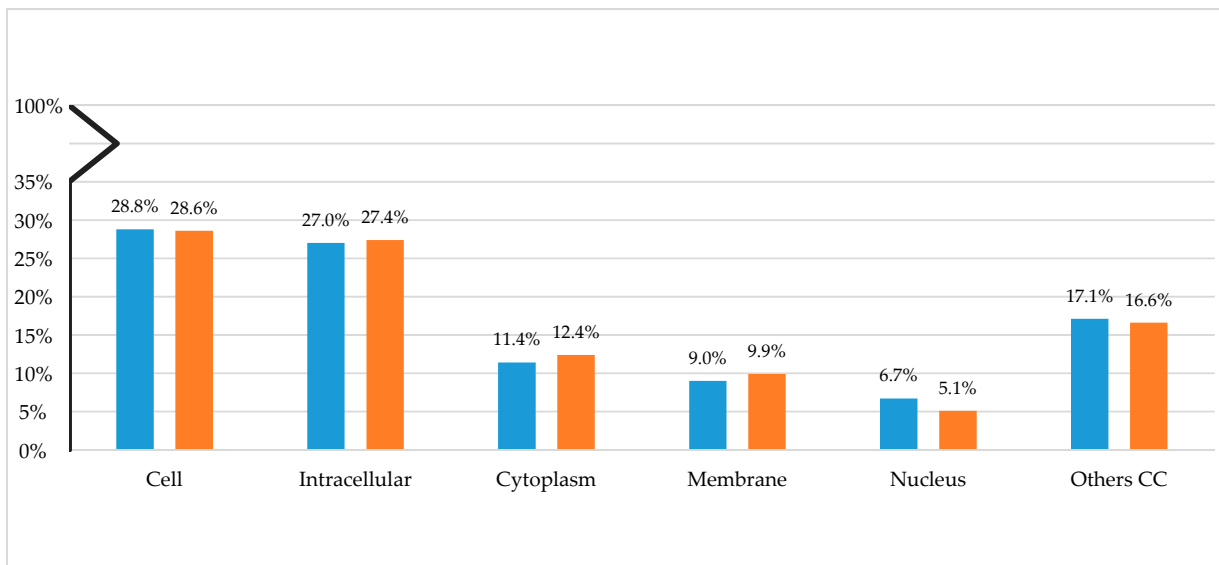
**Figure S1.** Total number of significant tests (up and down) between each comparison. Tests up-regulated are shown in blue, tests down regulated are shown in orange and the total number of tests is shown in gray



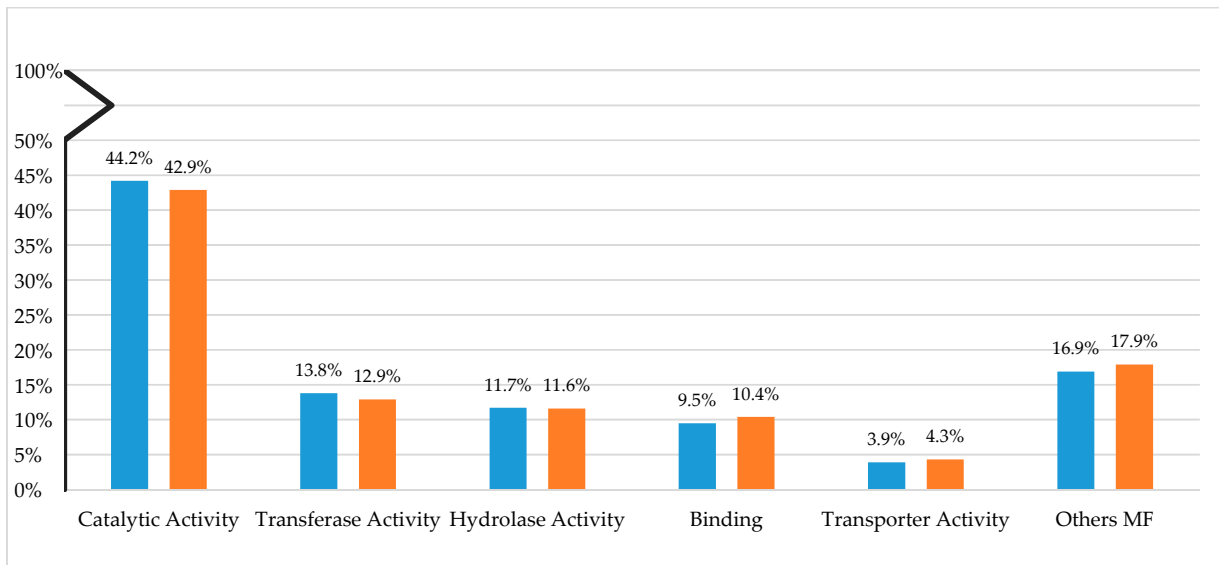
**Figure S2.** Correlation between the results from RNA-Seq and qPCR for the transcripts selected to perform validation, at time point Pp04



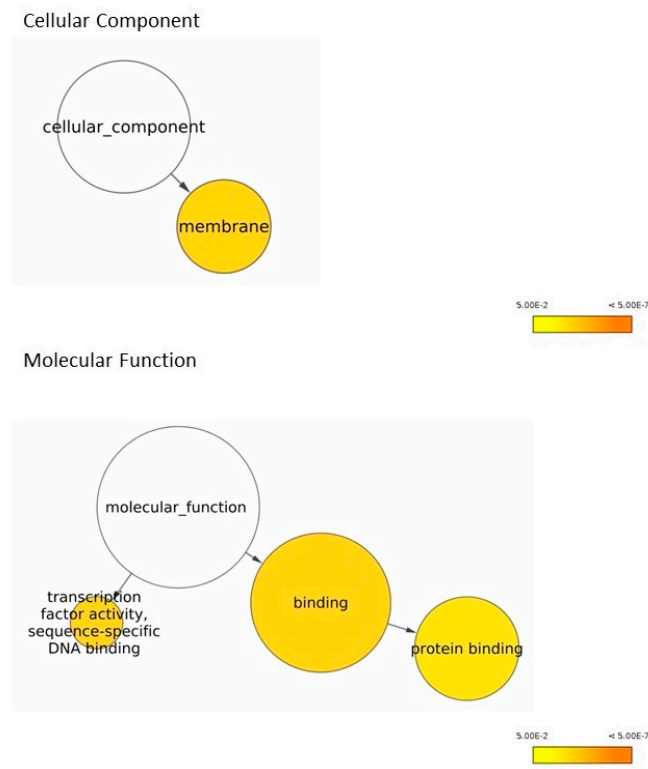
**Figure S3.** Distribution of the most representative biological process subcategories. The results for predicted genes are shown in blue and for DE genes in orange



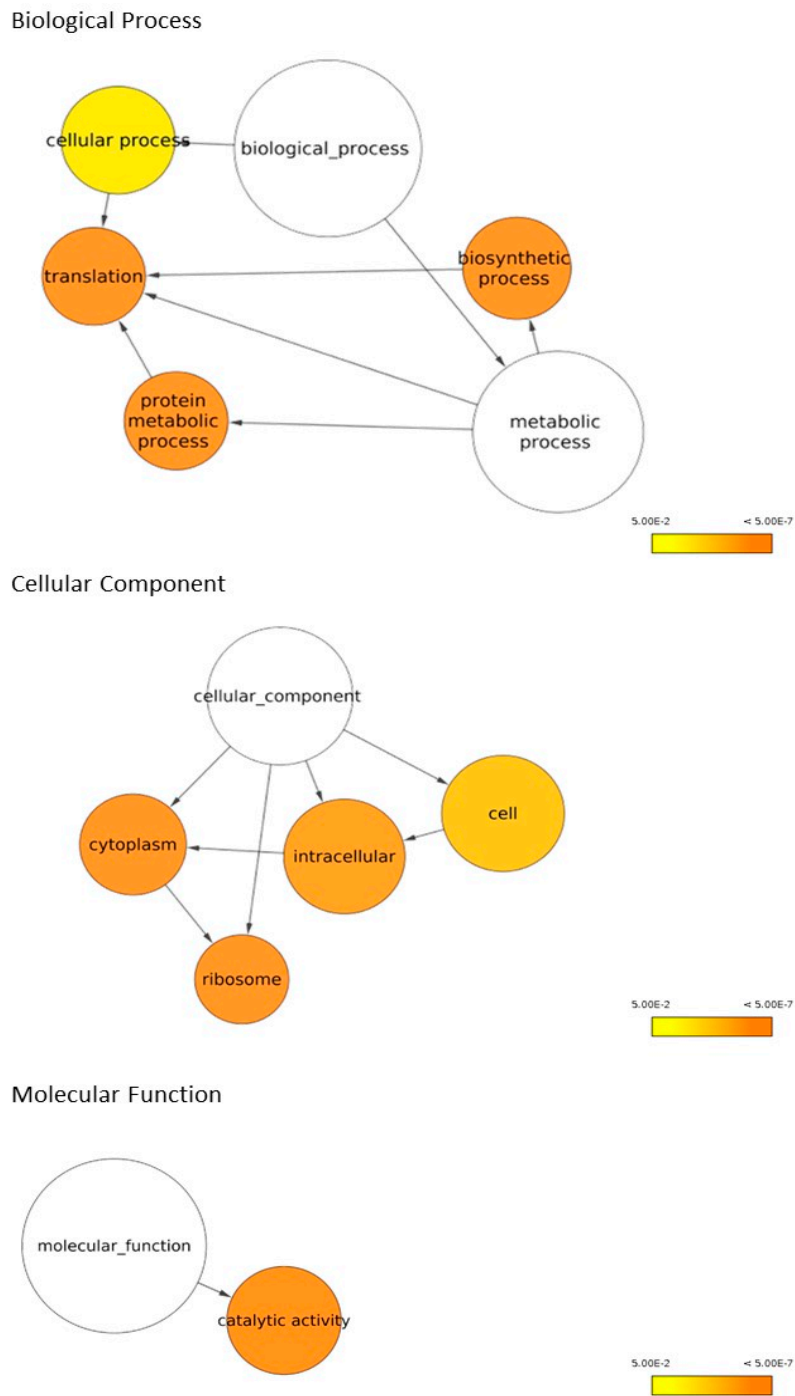
**Figure S4.** Distribution of the most representative cellular component subcategories. The results for predicted genes are shown in blue and for DE genes in orange



**Figure S5.** Distribution of the most representative molecular function subcategories. The results for predicted genes are shown in blue and for DE genes in orange



**Figure S6.** Overrepresentation of cellular component and molecular function terms in control, obtained by BINGO. Color bar in the right lower quadrant indicates level of significance from low (yellow) to high (orange). The size of the nodes is proportional to the number of genes in GO category. Statistical analysis was performed with a hypergeometrical test and a p-value of < 0.05.



**Figure S7.** Overrepresentation of biological processes, cellular component and molecular function terms in first stage (pp01), obtained by BINGO. Color bar in the right lower quadrant indicates level of significance from low (yellow) to high (orange). The size of the nodes is proportional to the number of genes in GO category. Statistical analysis was performed with a hypergeometrical test and a p-value of < 0.05

**Table S1.** List of proteins with "unknown" annotation associated to flavonoid biosynthesis, terpenoid backbone biosynthesis and phenylpropanoid biosynthesis pathways. GI: Gene Identifier; GB: Gene Bank identifier.

Annotation	Sequence ID	GI	GB
<b>Flavonoid biosynthesis</b>			
unknown	Contig6427 m.4857	294461446	ADE76284.1
<b>Terpenoid backbone biosynthesis</b>			
unknown	TR848 c0_g2_i1 m.23879	294462020	ADE76565.1
unknown	TR62191 c0_g1_i1 m.102063	224285512	ACN40476.1
unknown	TR40753 c0_g2_i1 m.81358	224286774	ACN41090.1
unknown	TR7839 c1_g6_i1 m.32299	224285512	ACN40476.1
unknown	TR34290 c4_g3_i1 m.71383	224286575	ACN40993.1
unknown	TR14892 c6_g2_i2 m.44264	294462020	ADE76565.1
unknown	TR20398 c0_g9_i1 m.50638	294462020	ADE76565.1
unknown	TR7839 c1_g2_i2 m.32296	224285512	ACN40476.1
unknown	TR50718 c0_g2_i1 m.93996	294462020	ADE76565.1
unknown	TR35413 c30_g34_i1 m.73743	224284456	ACN39962.1
unknown	TR35413 c30_g79_i1 m.73747	224284456	ACN39962.1
<b>Phenylpropanoid biosynthesis</b>			
unknown	TR64144 c0_g1_i1 m.103213	116793602	ABK26805.1
unknown	TR8848 c0_g1_i1 m.34958	116784653	ABK23423.1
unknown	TR20162 c0_g1_i1 m.50168	116791388	ABK25962.1
unknown	TR25209 c5_g3_i2 m.58347	148908746	ABR17480.1
unknown	TR52891 c0_g13_i4 m.96632	116786481	ABK24123.1
unknown	TR27155 c0_g6_i1 m.60824	116785793	ABK23862.1
unknown	TR3197 c3_g2_i1 m.26681	116781273	ABK22032.1
unknown	TR10130 c1_g9_i1 m.36498	116794018	ABK26974.1
unknown	TR13667 c1_g1_i1 m.42023	116785375	ABK23698.1
unknown	TR10130 c1_g5_i6 m.36496	116794018	ABK26974.1
unknown	TR42016 c3_g53_i1 m.82745	116781273	ABK22032.1
unknown	TR42016 c3_g78_i1 m.82747	116781273	ABK22032.1
unknown	TR25209 c5_g3_i1 m.58346	148908746	ABR17480.1
unknown	Contig3439 m.2653	116781273	ABK22032.1
unknown	TR52891 c0_g13_i1 m.96631	116786481	ABK24123.1
unknown	TR12470 c0_g2_i1 m.40478	116785793	ABK23862.1
unknown	TR4476 c0_g4_i2 m.29395	116782301	ABK22453.1
unknown	TR31657 c0_g4_i1 m.67142	294462186	ADE76645.1
unknown	TR10130 c1_g9_i2 m.36499	148908746	ABR17480.1
unknown	TR10130 c1_g11_i2 m.36501	116794018	ABK26974.1
unknown	TR43775 c0_g1_i1 m.84610	116791388	ABK25962.1
unknown	TR56075 c2_g25_i1 m.98861	294461169	ADE76148.1
unknown	TR4476 c0_g4_i1 m.29394	116782301	ABK22453.1
unknown	TR598 c0_g3_i1 m.23602	294461169	ADE76148.1
unknown	TR52892 c2_g19_i1 m.96636	116781149	ABK21983.1
unknown	TR59477 c0_g2_i1 m.100843	294461169	ADE76148.1