

Supplementary Information

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Combining transcriptomics and genetic linkage based information to identify candidate genes associated with *Heterobasidion*-resistance in Norway spruce

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Supplementary table 1: Primer sequence used for qPCR

Genes	Forward Primer	Reverse primer	Annotation
MA_103386g0010	ACCTTCTCCAAC AAGCCACAC	ACTGGAGCCTTG AGGGTAGTGG	NAC-Transcription factor
MA_264971g0010	GGACCTTCGACC ACAAGCTATAG	ACTGGAGTCTTAA GGGTACTGC	NAC-Transcription factor (<i>PaNAC04</i>)
eIF4A	AGTAAGCCCGTG AGGATTC	AGTCAGCCAGTC AACCTTTC	Reference gene
ELF1 α	TGGCAAGGAACT GGAGAAGGAA	TAGTCCCTCACAG CAAAACGA	Reference gene

Supplementary table 2: Differential expressed genes in inoculation or wounding at proximal and distal site.

Conditions	DEGs	Up-regulated in inoculation	Down-regulated in inoculation
3A_I vs 3A_W	6999	4562	2437
7A_I vs 7A_W	8767	4976	3791
7C_I vs 7C_W	4401	1723	2678

Supplementary table 3: Distribution of expressed and differential expressed candidate genes in QTL regions of Norway spruce associated with *H. parviporum* resistance

LG ^a	Trait ^b	CCG ^c	CCG ^c	PCG ^d	PCG ^d
		Expressed genes	DEGs	Expressed genes	DEGs
LG1	IP	12	6	0	0
	E	3	2	13	3
LG2	IP	12	4	3	0
	E	3	1	36	15
	SWG	1	0	11	4
LG3	E	1	0	16	3
LG6	SWG1	1	1	22	5
	E	19	10	72	32
	SWG2	13	10	3	0
LG8	LL	1	1	12	7
LG9	SWG	8	3	7	2
LG11	IP1	5	3	23	12
	IP2	1	0	0	0
Total		80	41	218	83

^a Linkage groups are numbered according to the Lind et al 2014; ^b QTL regions for traits controlling resistance to *H. parviporum* as described in Lind et al 2014: exclusion (E), infection prevention (IP), lesion length (LL), sapwood growth of fungus (SWG); ^c the number expressed and DEGs of confidence interval (CCG) in the QTL regions ^d, the number of expressed and DEGs putative candidate genes (PCG) outside confidence interval by de Miguel et al 2015.