

CORRECTION

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# Correction: RNA-Seq and secondary metabolite analyses reveal a putative defence-transcriptome in Norway spruce (*Picea abies*) against needle bladder rust (*Chrysomyxa Rhododendri*) infection

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**Correction:** *BMC Genomics* 21, 336 (2020)  
<https://doi.org/10.1186/s12864-020-6587-z>

Following publication of the original article the following errors were reported for Additional files 13–15:

- The content of additional file 15 should have been the content of additional file 13.
- The content of additional file 13 were a duplicate of those of additional file 14.
- The correct content of additional file 15 was missing.

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The online version of the original article can be found at <https://doi.org/10.1186/s12864-020-6587-z>.

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The correct additional files 13 and 15 are given in this Correction and the original article has been updated.

## Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12864-024-10831-z>.

**Additional file 13:** Table S7. Sequence datasets of plant species applied for KEGG Orthology (KO) assignment using the KEGG Automatic Annotation Server (KAAS). KEGG Orthology (KO) assignment was applied using the Bi-directional Best Hit (BBH) method and all datasets of dicot plants (excluding *Camelina sativa*, *Lupinus angustifolius* and *Cucurbita moschata*), monocot plants and a basal magnoliophyta (*Amborella* family) were selected as reference organisms. (XLS 1108 kb)

**Additional file 15:** Figure S6. RT-qPCR assay details. Primer sequences of RT-qPCR assays.

Published online: 07 October 2024

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