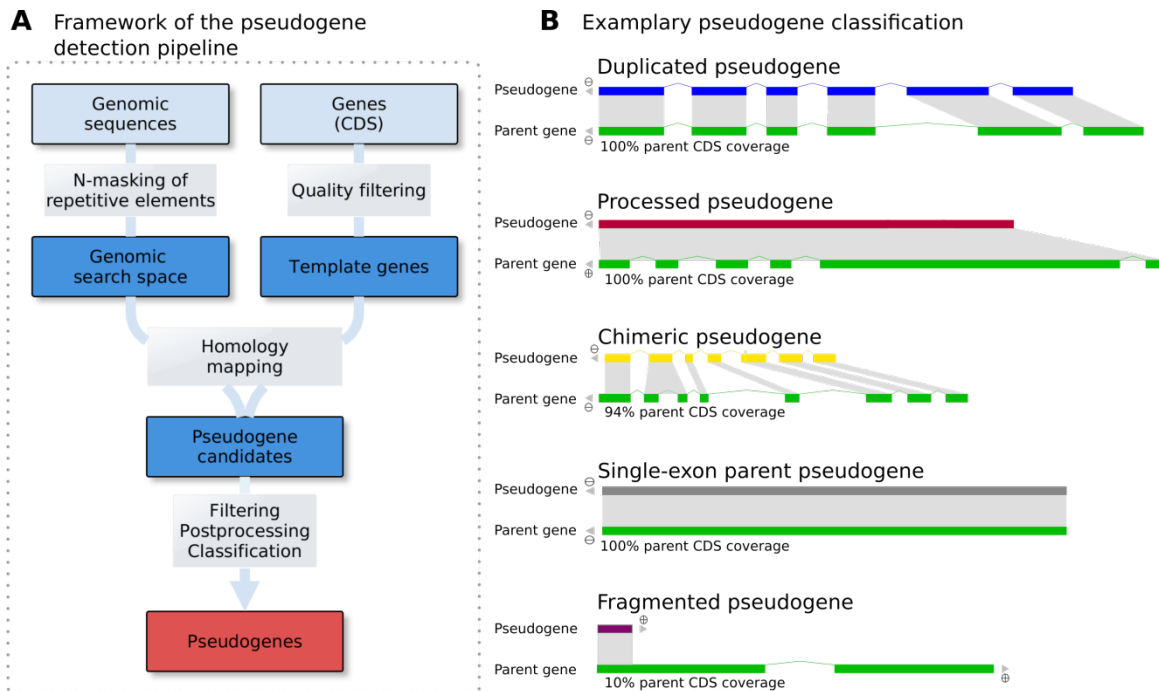
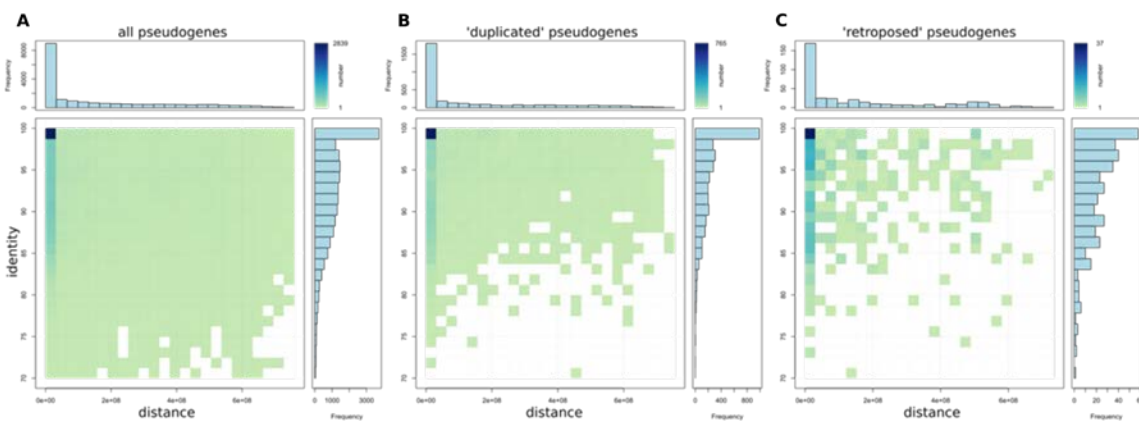


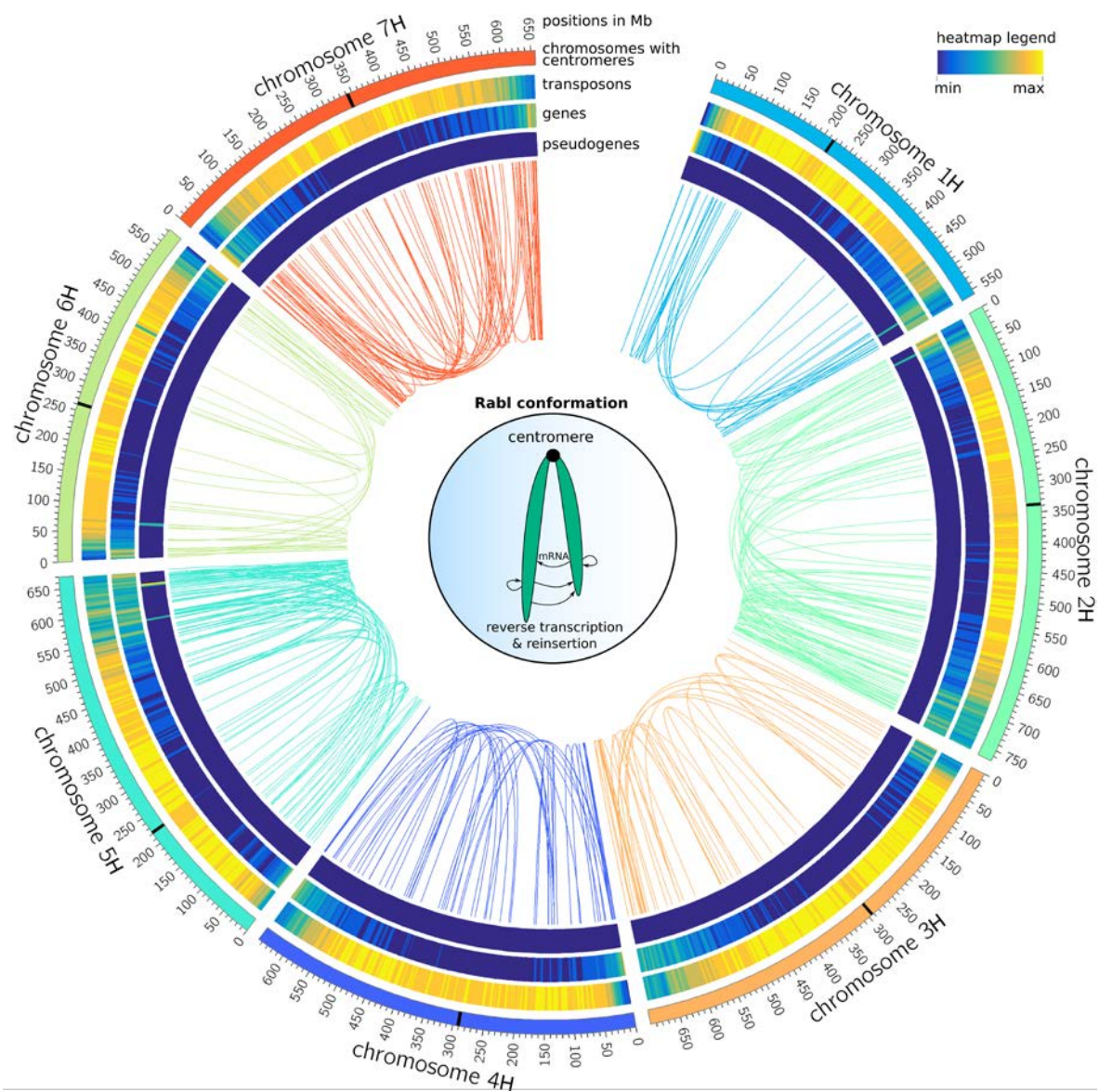
## Supplementary Figures – The Pseudogenes of Barley



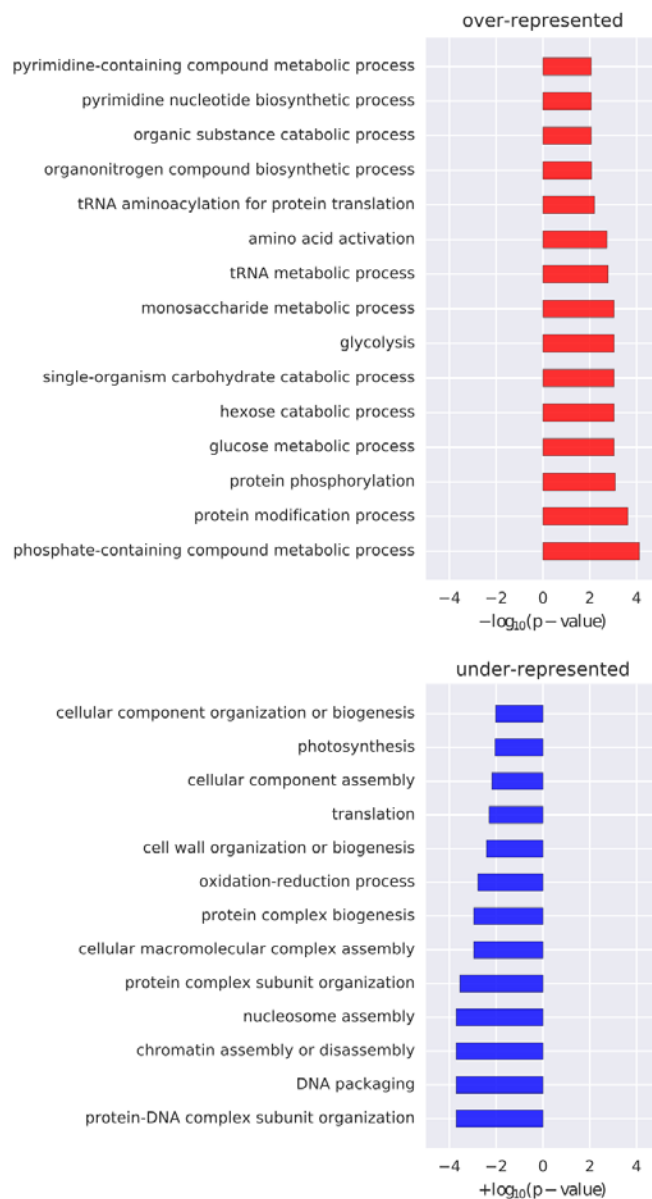
**Figure S1** : Computational pseudogene detection and classification pipeline. **A**: Framework of the pipeline; **B**: Exemplary pseudogene classification.



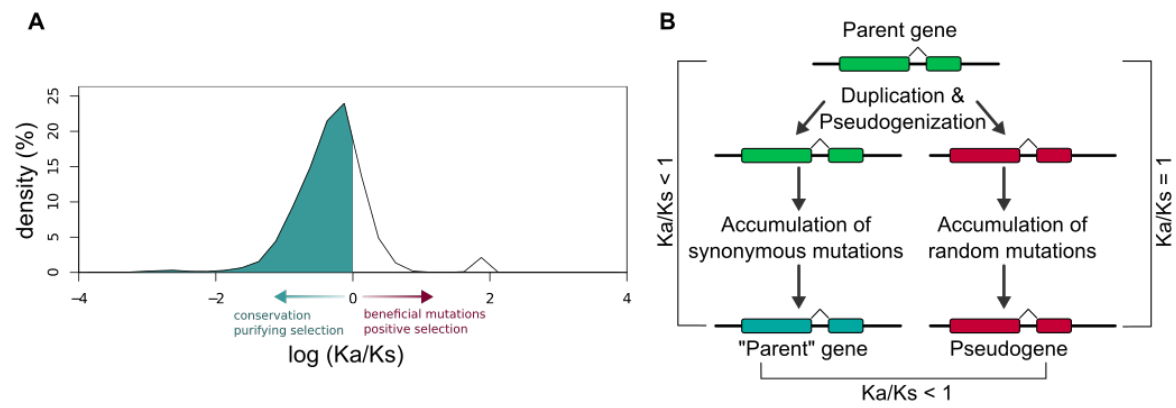
**Figure S2** : Sequence identity vs. distance of pseudogenes compared to their parent genes. **A** all pseudogenes; **B** duplicated pseudogenes; **C** retroposed pseudogenes.



**Figure S3 :** Distribution of transposable elements, genes and intrachromosomally retroposed pseudogenes on the seven chromosomes of barley. The first (outer) track shows the seven barley chromosomes with positions in Mb and highlighted centromeres. The second to fourth track show densities of transposable element sequences (min. 47% to max. 85% sequence coverage), genes (min. 0% to max. 5% sequence coverage) and intrachromosomally retroposed pseudogenes (min. 0% to max. 0.2% sequence coverage), respectively. Densities have been calculated using a sliding window of 5 Mb shifted by 1 Mb. Links connect parent genes with their pseudogene ‘descendants’ and are colored in the chromosome of the parent gene. In the center is a schematic representation of the Rab1 conformation of chromosomes and the small distances between opposing chromosome arms, which might facilitate retrotransposition.



**Figure S4** : Over- and under-represented Gene Ontology (GO) terms for the parent gene set of transcribed pseudogenes compared to the complete gene set of the barley genome.



**Figure S5 :** Analysis of the relative rates of synonymous and non-synonymous substitutions between pseudogenes and their parent genes. **A** Log10 Ka/Ks analysis of pseudogenes and their parent genes. **B** Schematic representation of the concurrent accumulation of substitutions in pseudogenes and their parent genes and the effect on the Ka/Ks ratio.