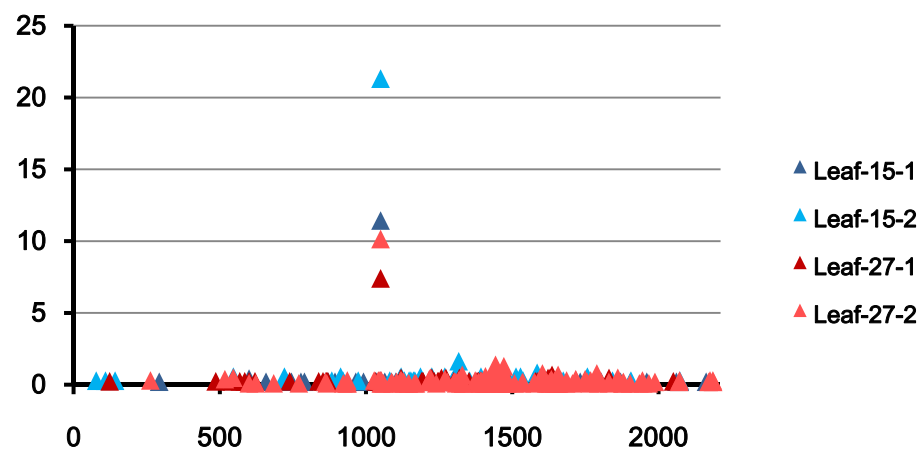
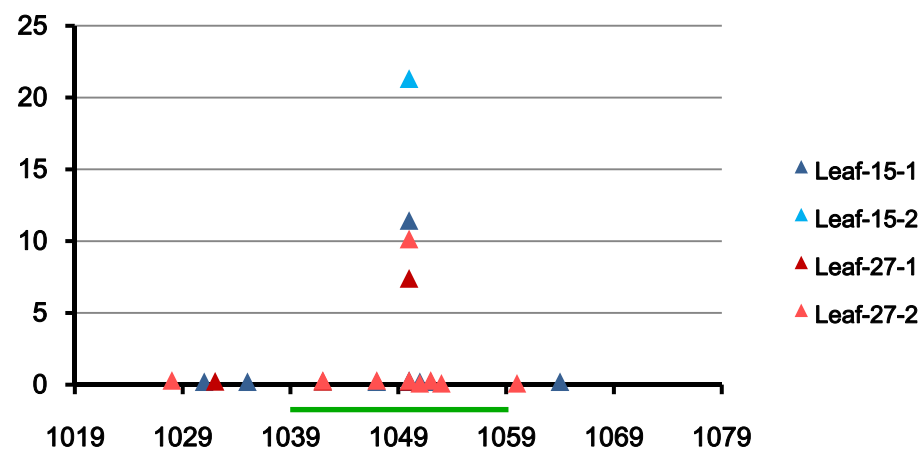


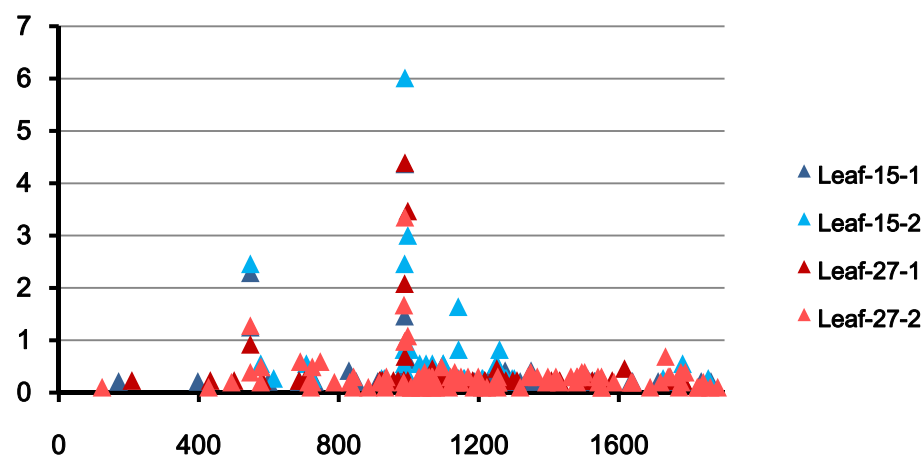
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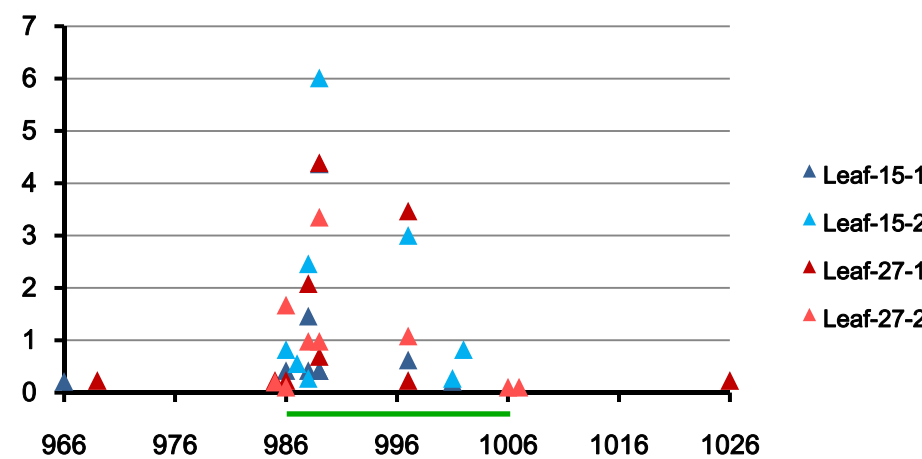
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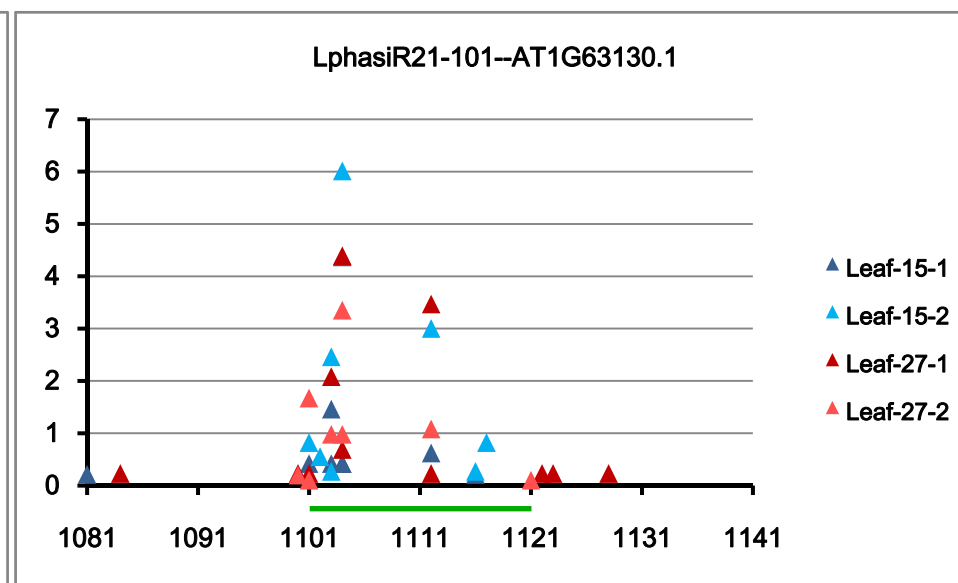
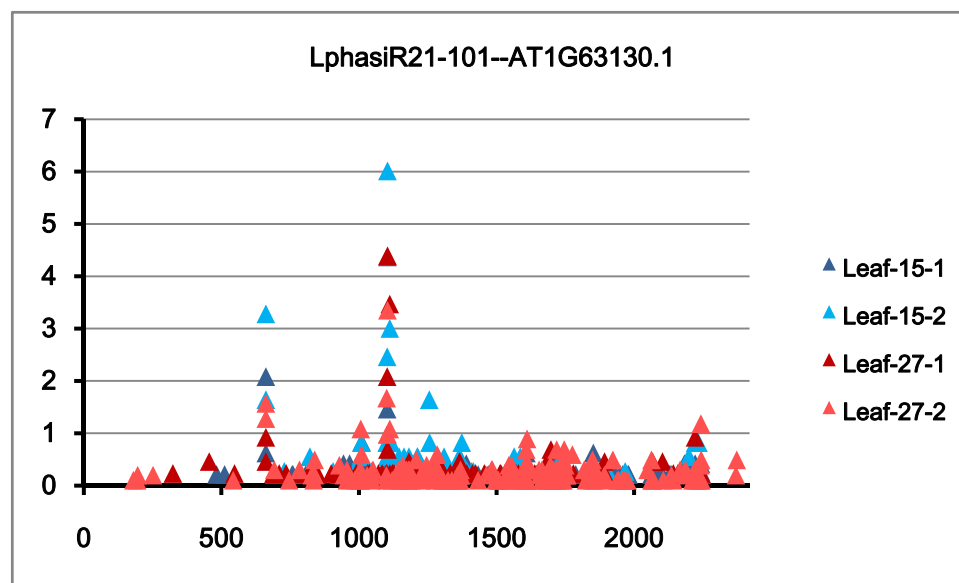
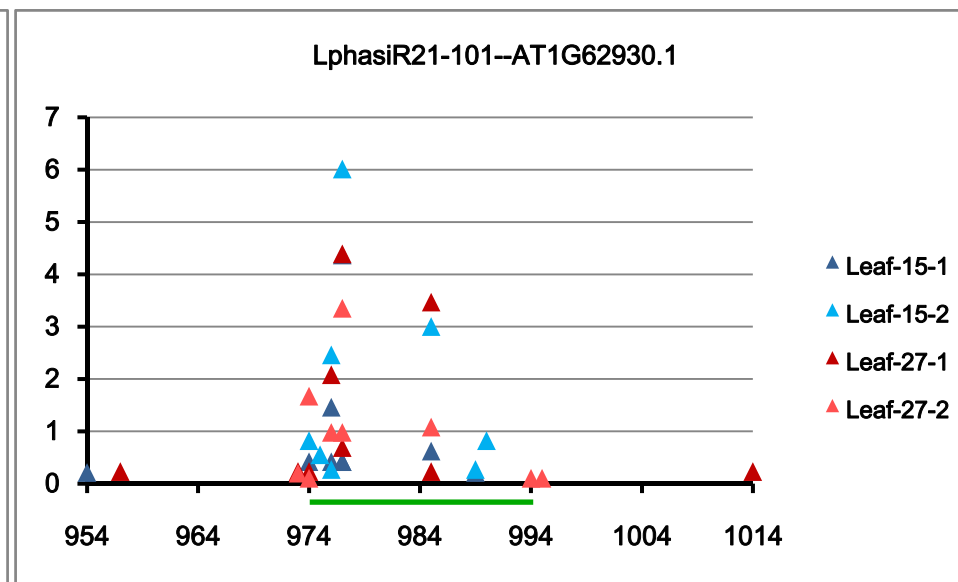
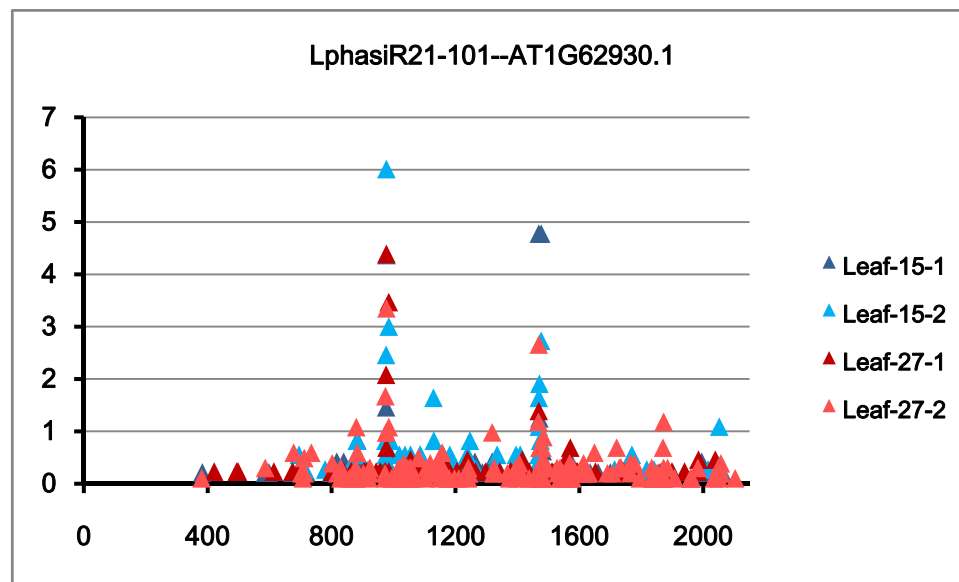


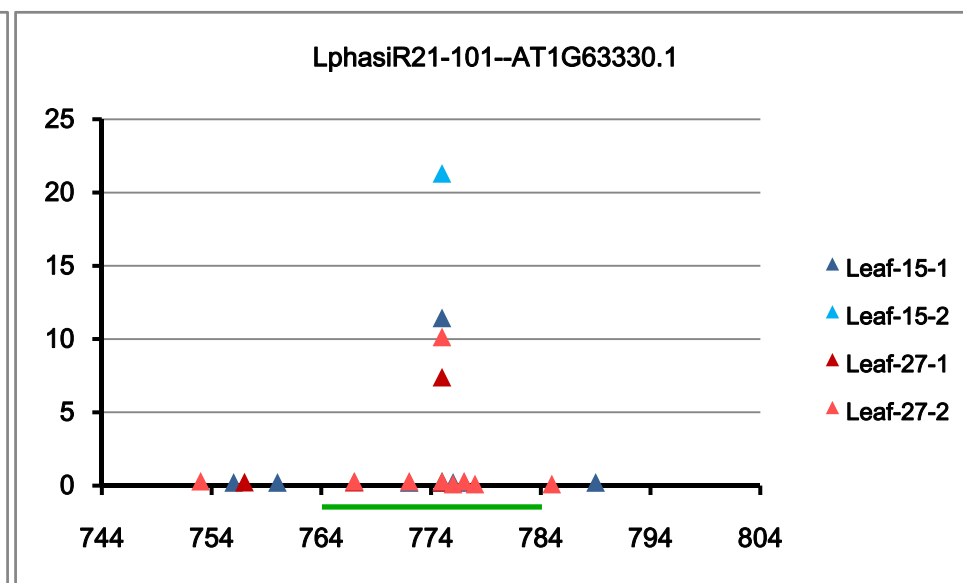
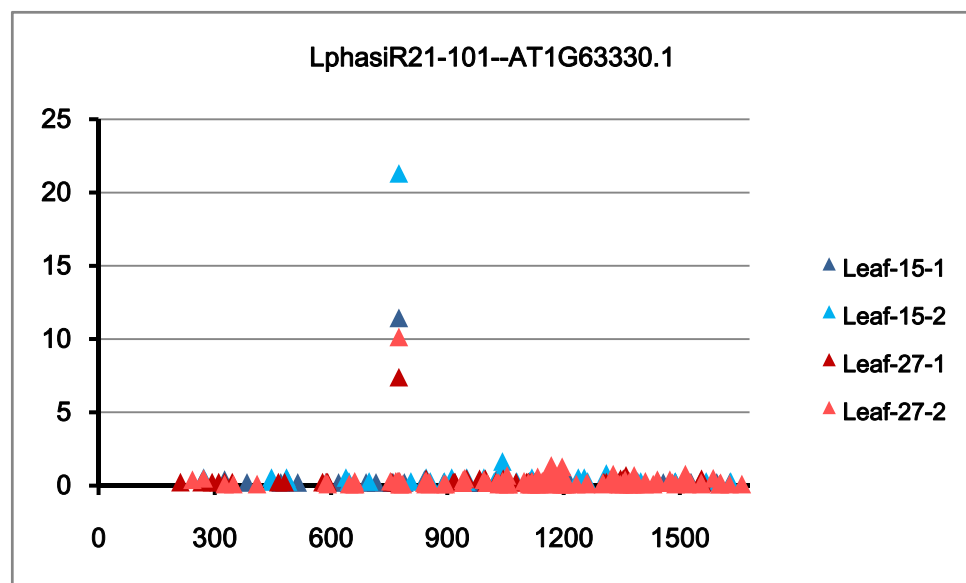
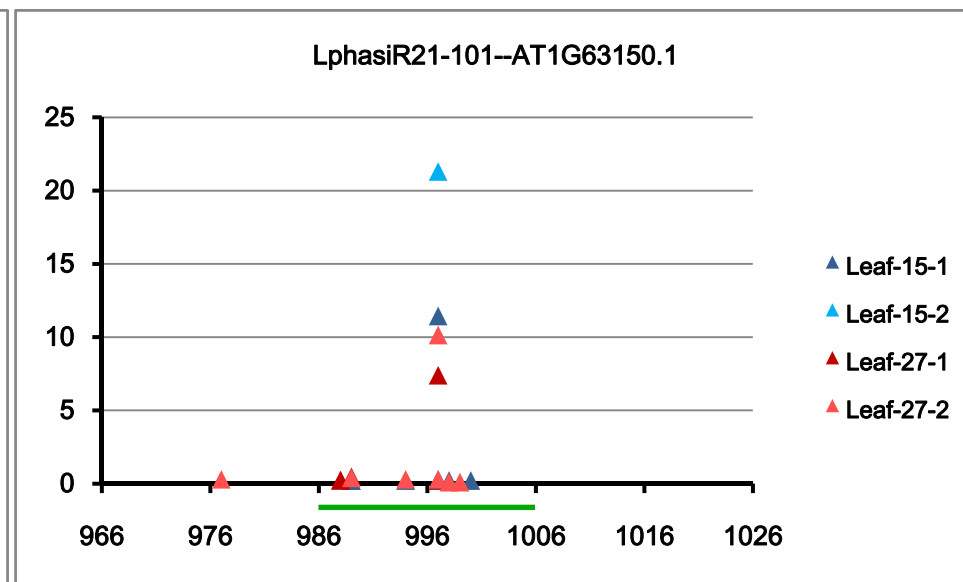
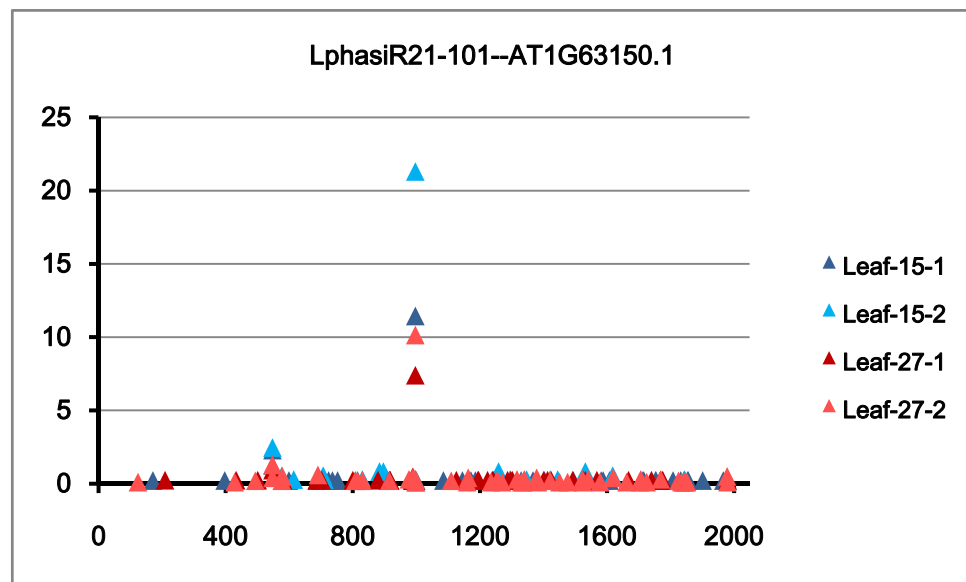
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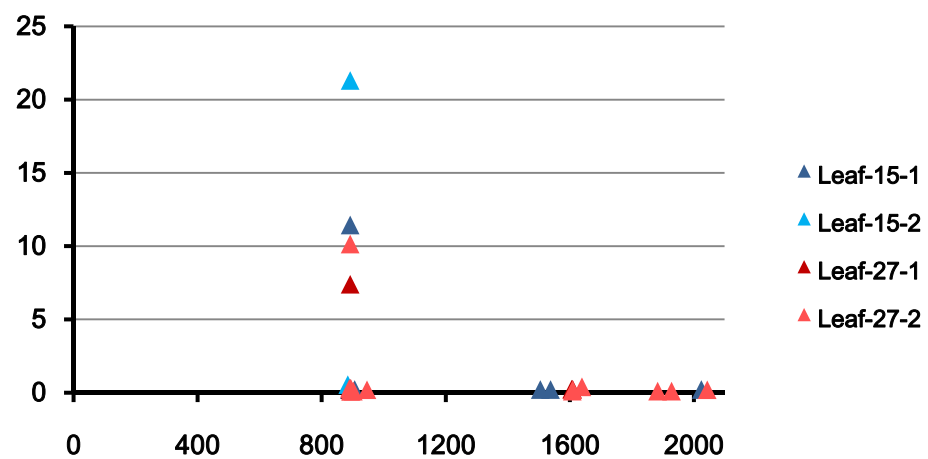
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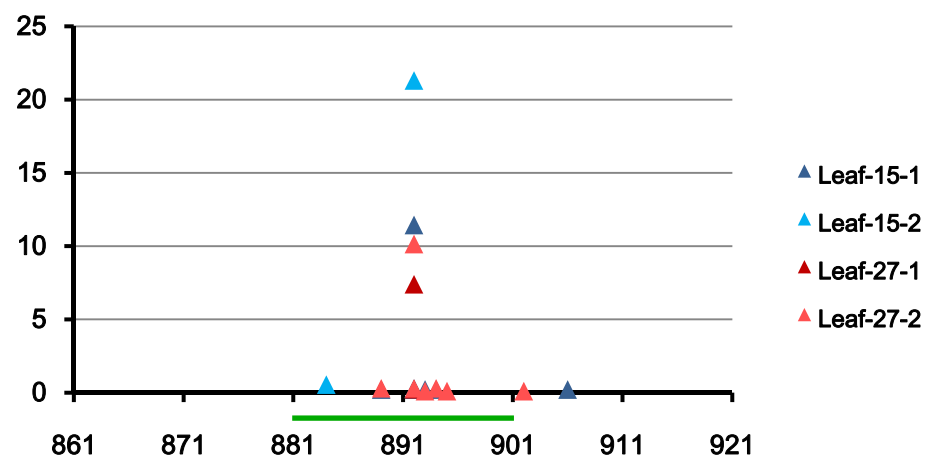




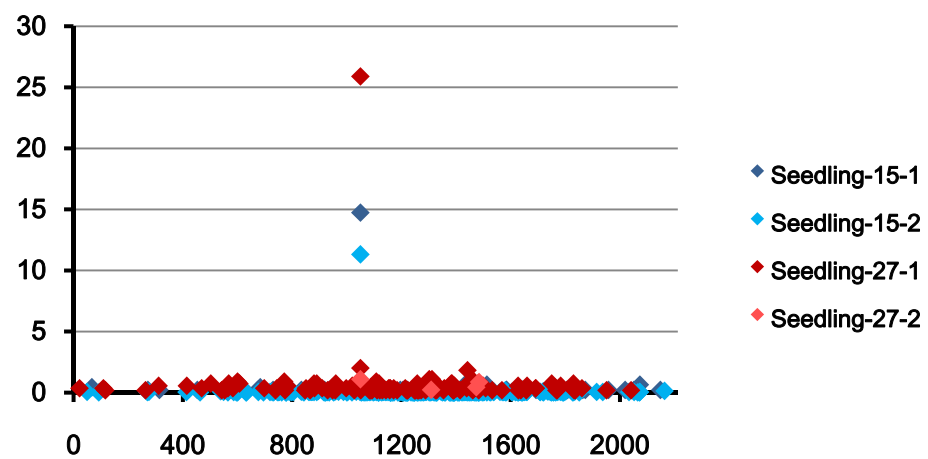
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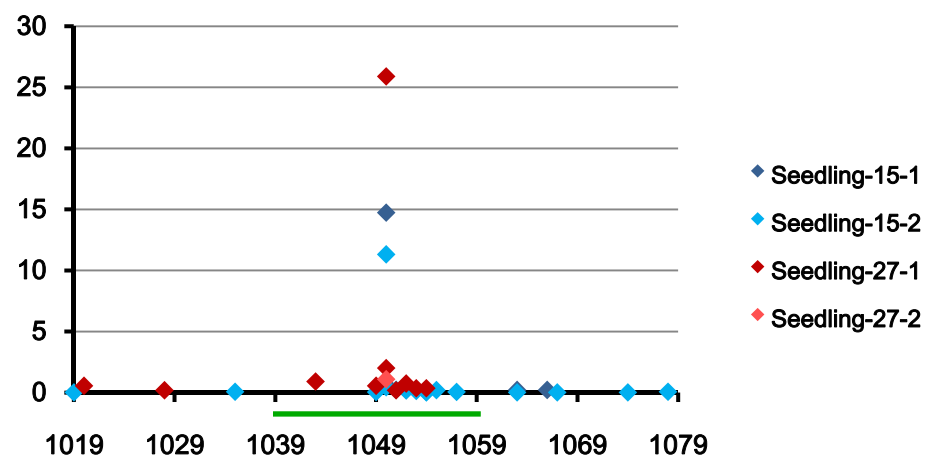
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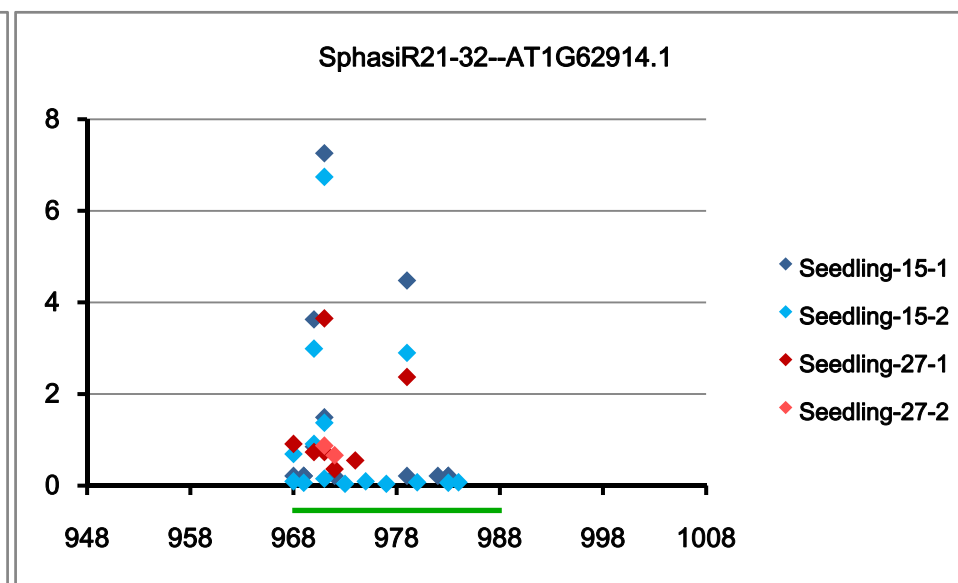
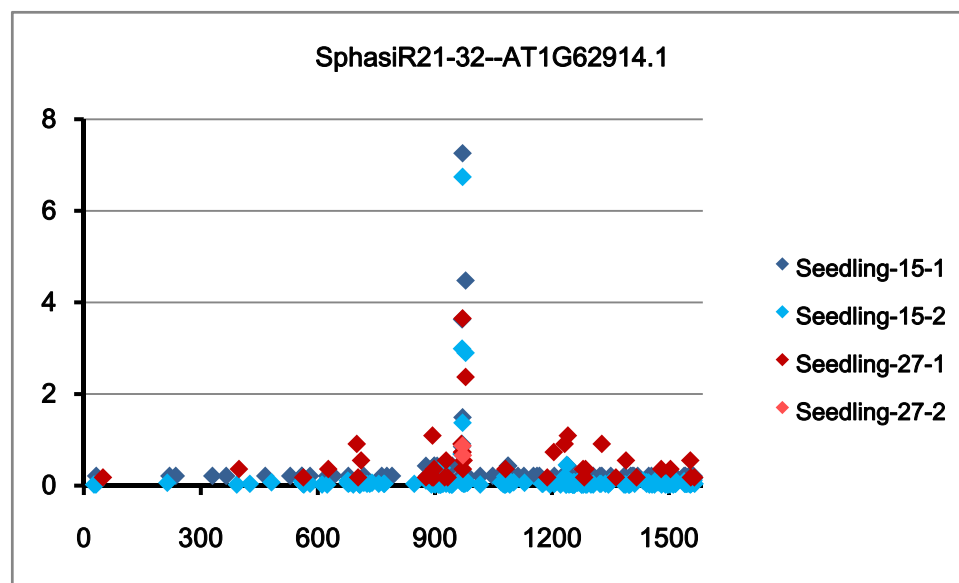
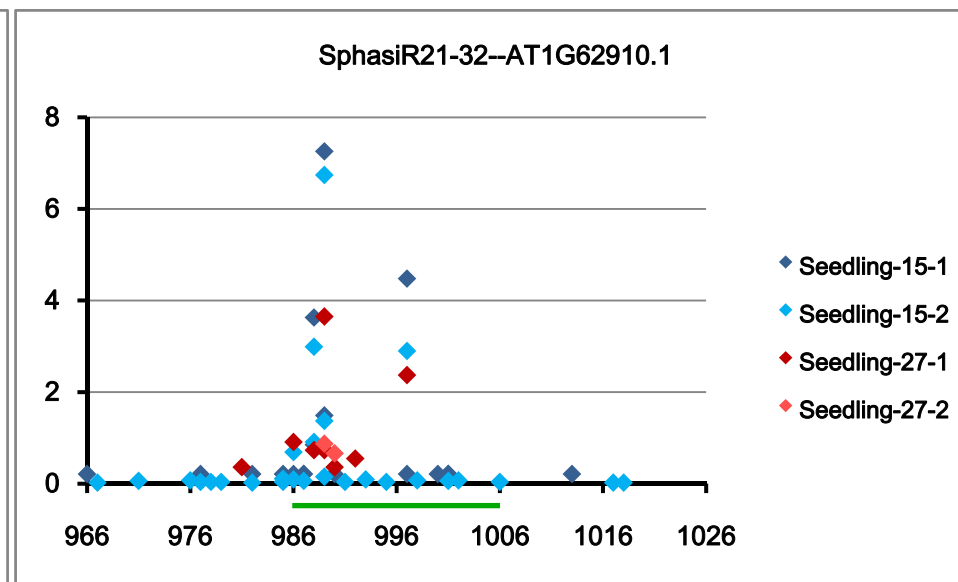
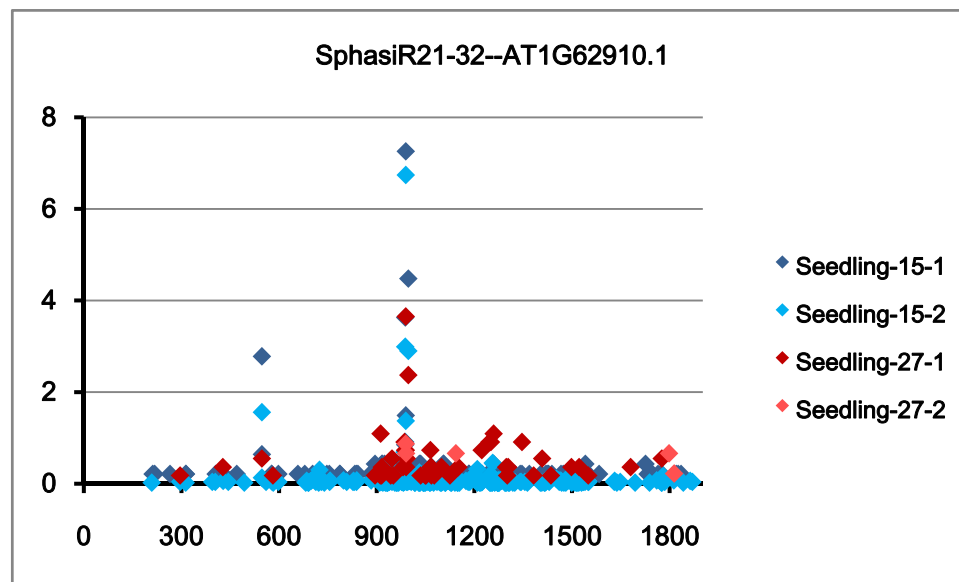


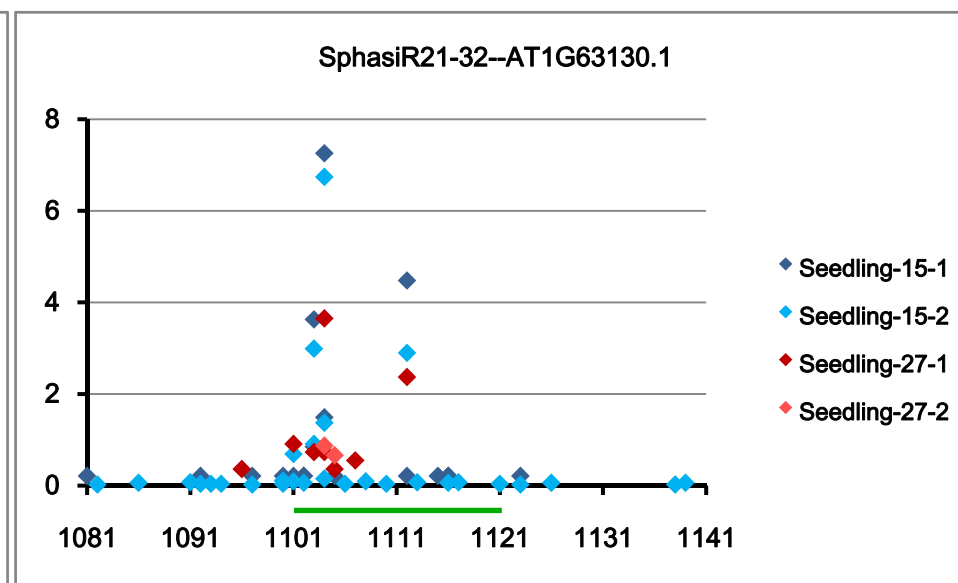
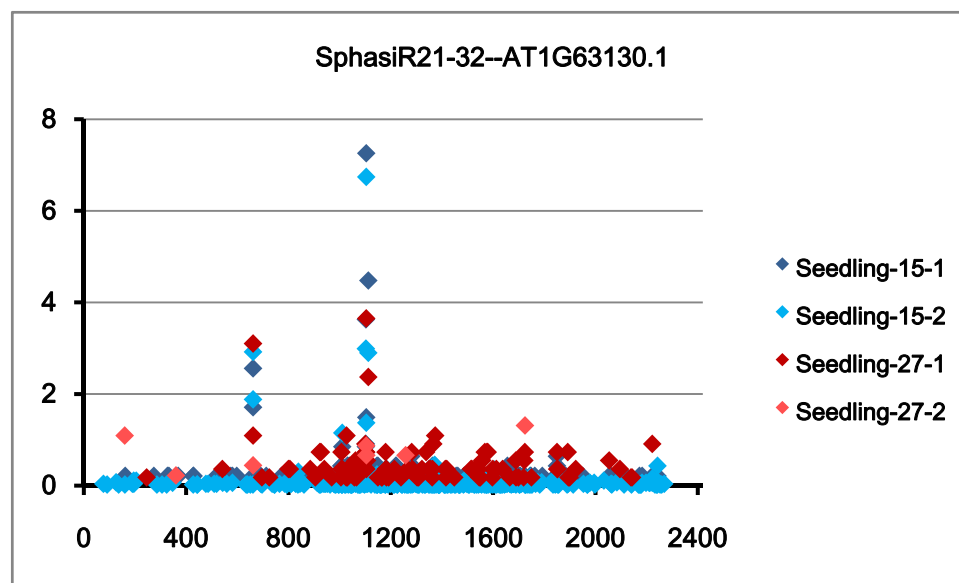
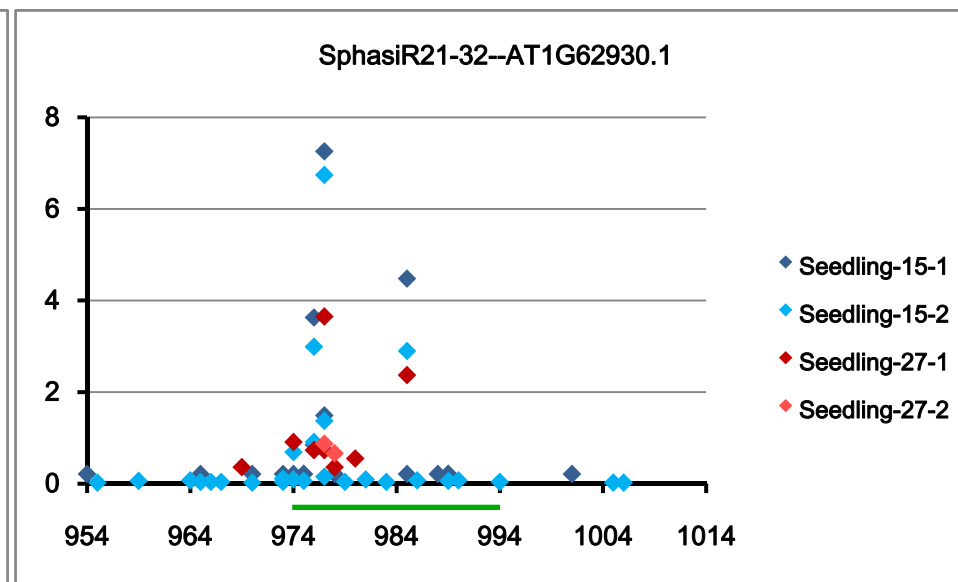
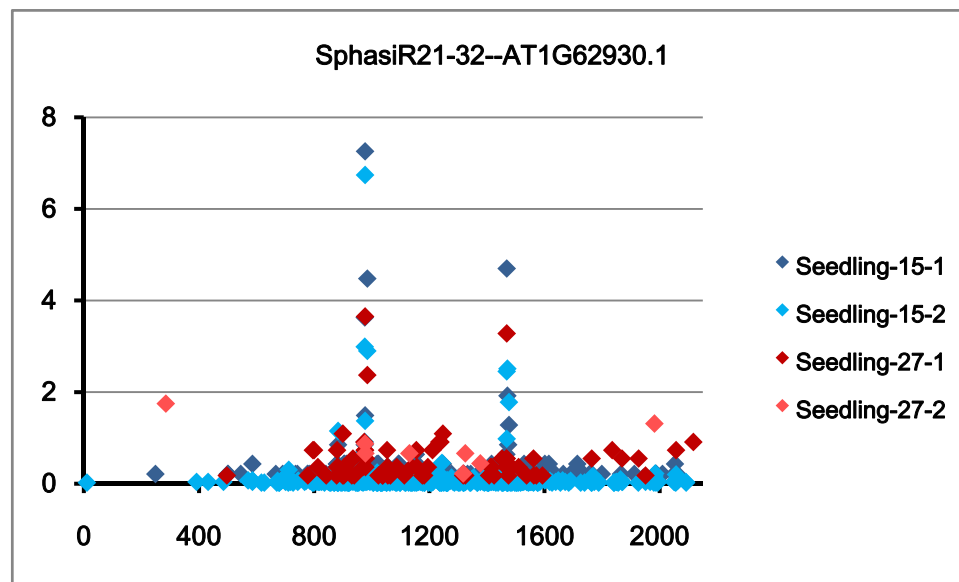
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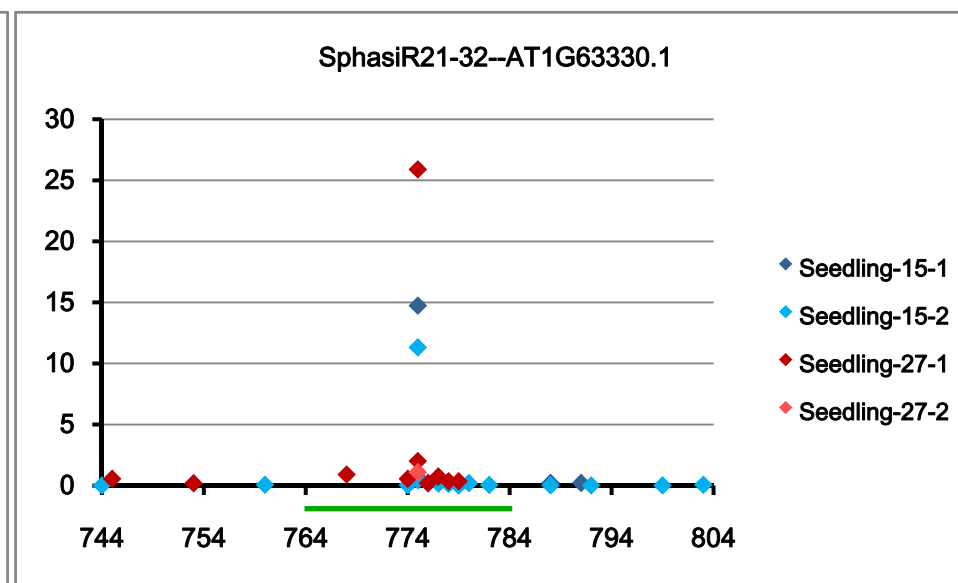
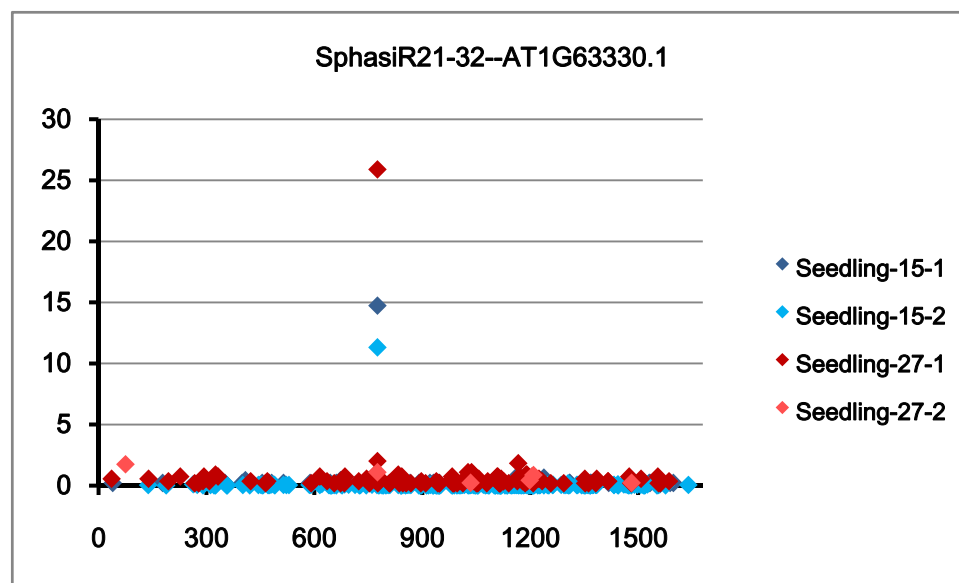
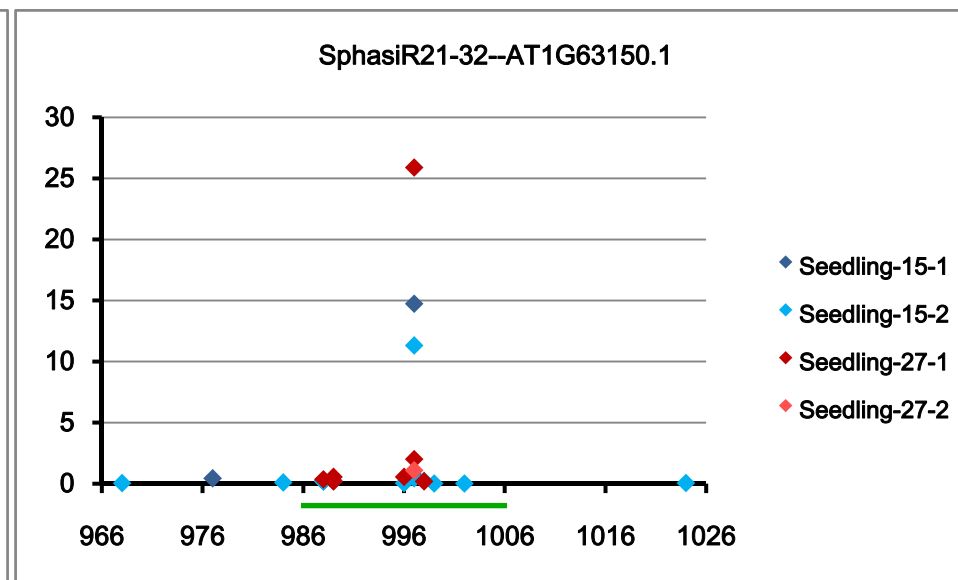
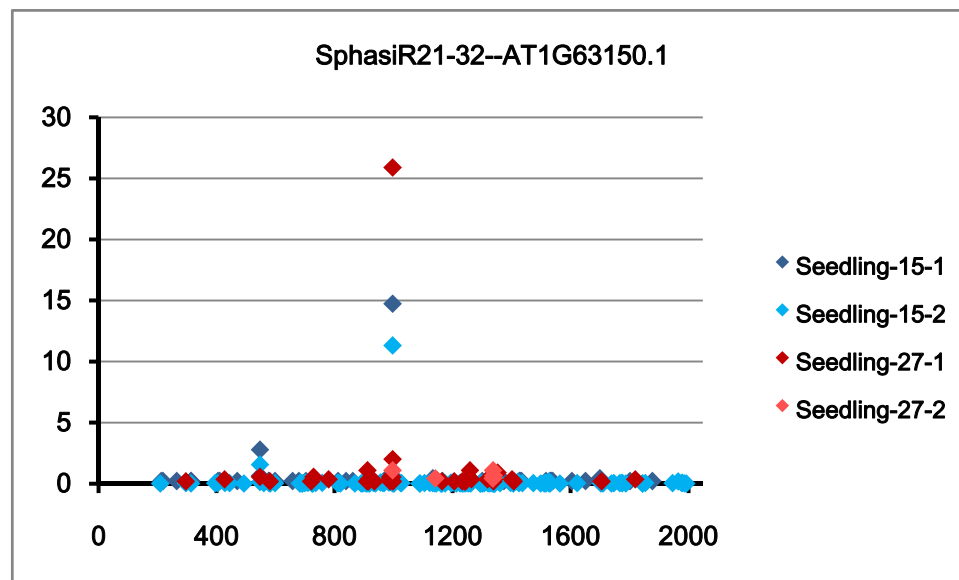


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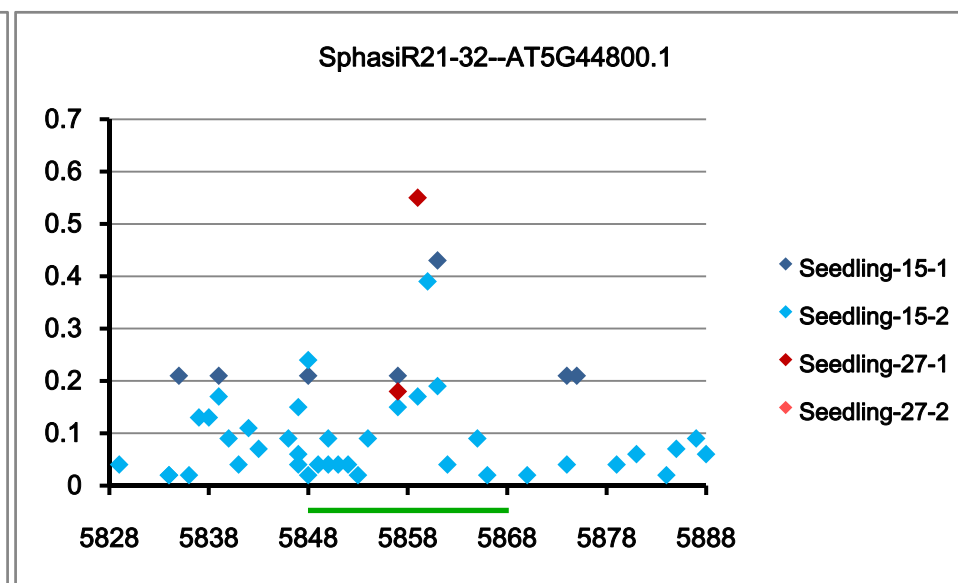
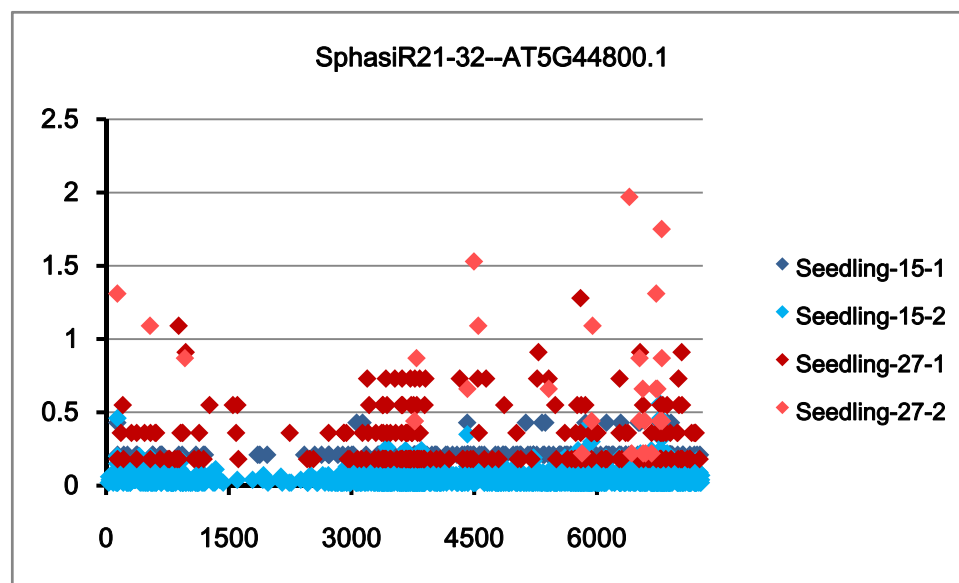
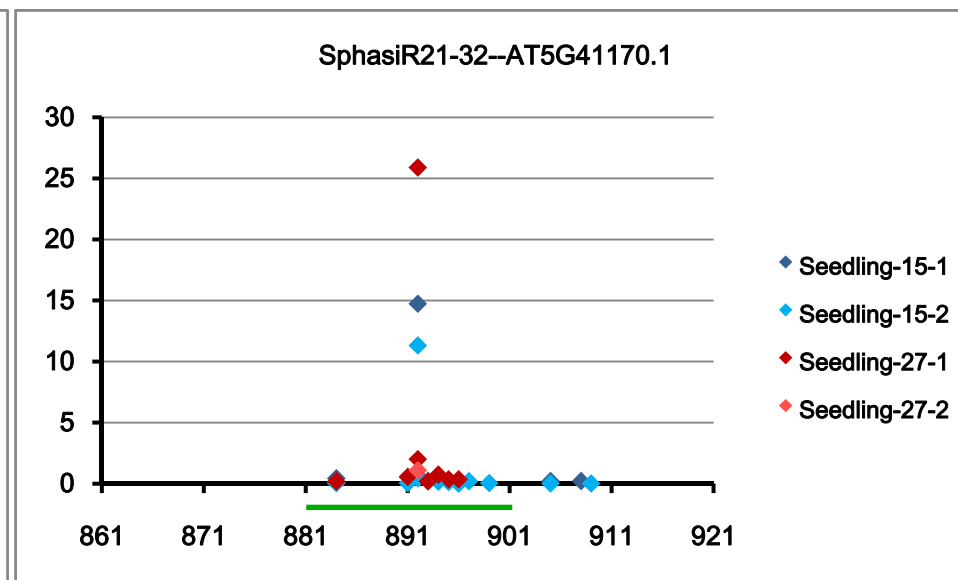
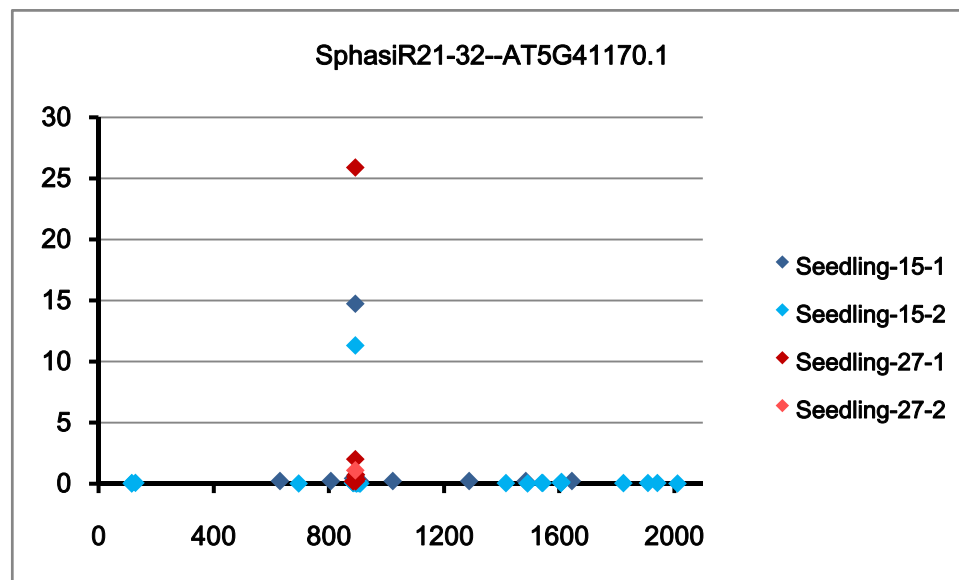


Figure S5 Target plots showing the degradome-validated target transcripts of the ta-siRNAs encoded by a *TAS* candidate. For each phasiRNA—target pair, the left plot shows the global distribution of the degradome signatures along the full-length target transcript, and the right plot shows the local degradome signals surrounding the target binding site (marked by a green horizontal line). The *y* axes measure the degradome signal levels in RPM (reads per million).