Red blotch disease alters grape berry development and metabolism by interfering with the transcriptional and hormonal regulation of ripening

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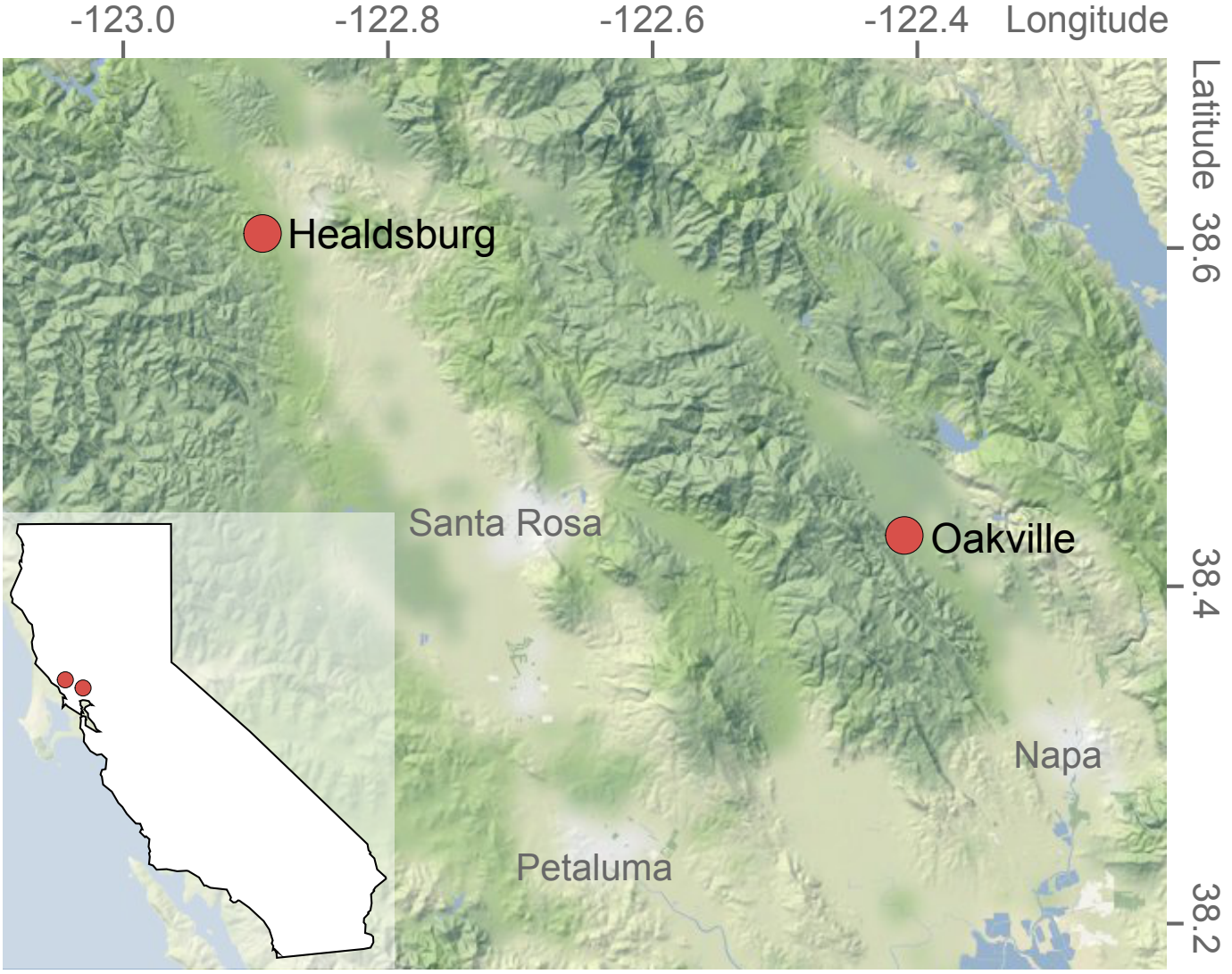
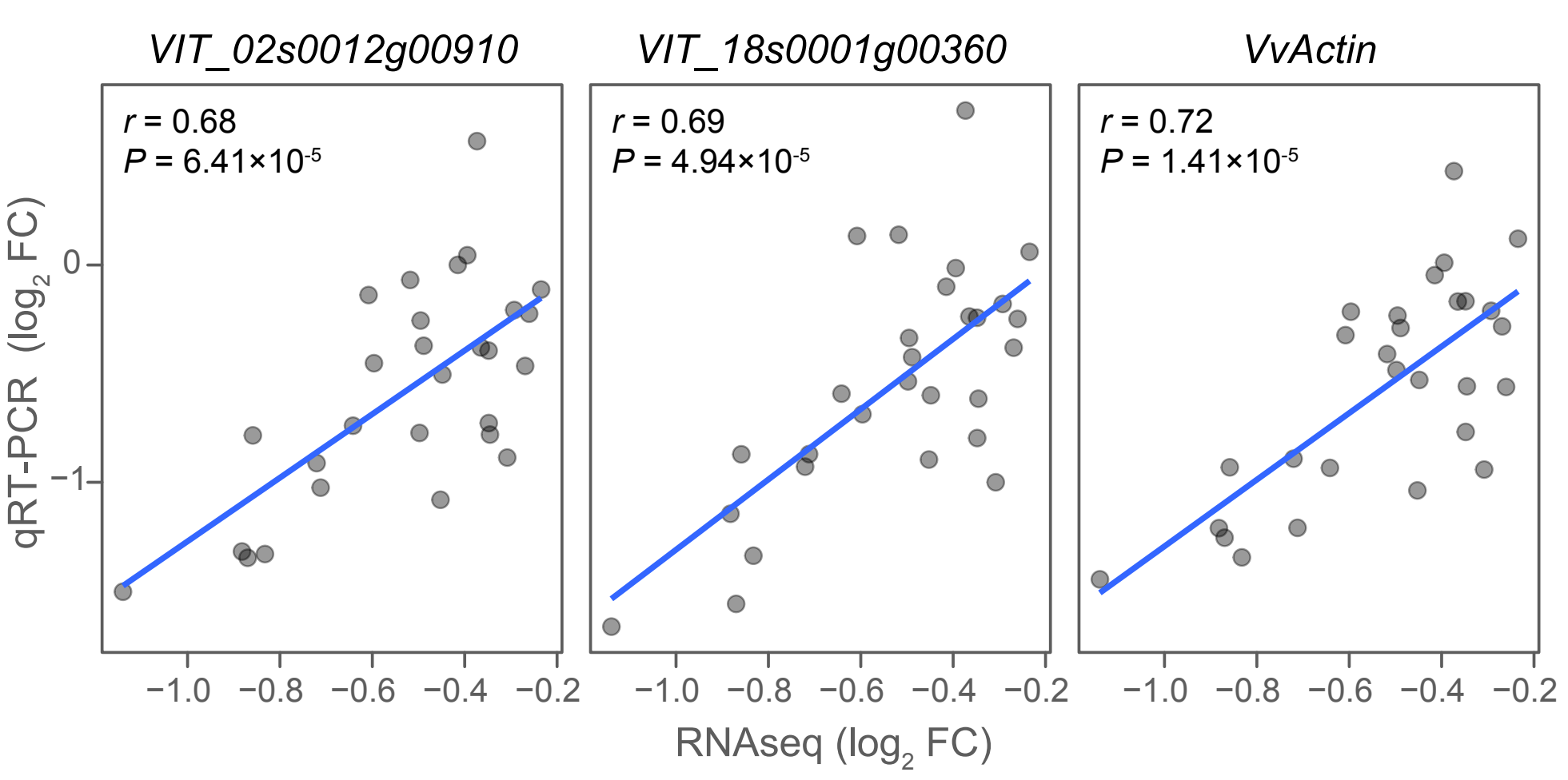
Supplementary Figures

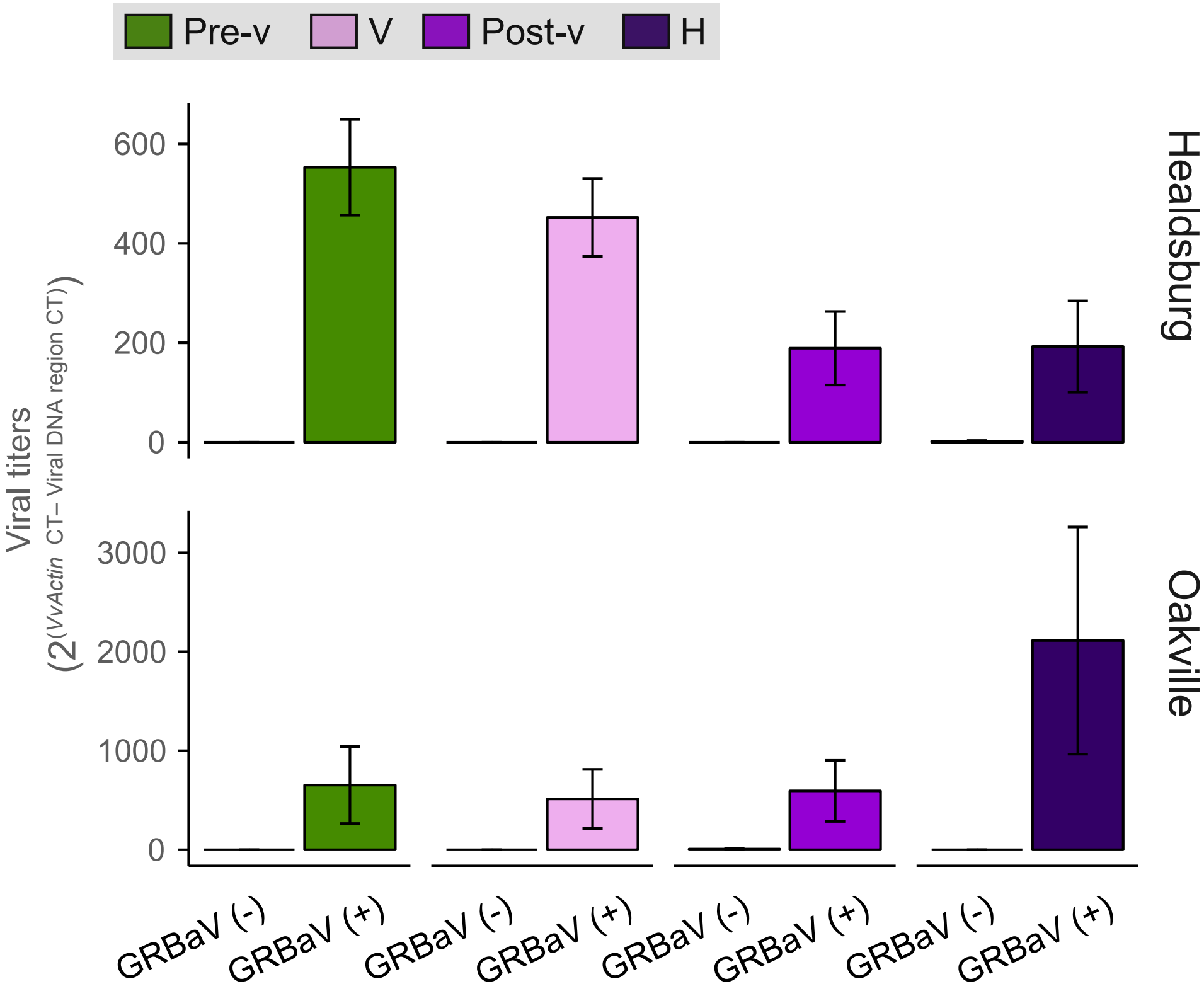
Figure S1. Geographic location of the two vineyards in California where berry sampling was performed.

Figure S2. Scatterplots showing the correlation between the fold changes (log2) in expression obtained by processing the RNAseq data with DESeq2 and the fold changes (log2) measured by qRT-PCR. Relative expression was calculated using VIT_02s0012g00910, VIT_18s0001g00360 and VIT_04s0044g00580 (VvActin to choose the best performing reference gene. Linear trends, correlation coefficients (r) and P-values are provided.

Figure S3. Viral titers in grape berries based on qPCR amplification of GRBaV DNA. Pre-v, Pre-véraison; V, véraison; Post-v, post-véraison; H, harvest. Error bars correspond to the standard error.


-123.0
-122.8
-122.6
-122.4
Longitude
Latitude
38.6
38.4
38.2
Healdsburg
Santa Rosa
Oakville
Napa
Petaluma


VIT_02s0012g00910
VIT_18s0001g00360
VvActin
r = 0.68
P = 6.41×10-5
r = 0.69
P = 4.94×10-5
r = 0.72
P = 1.41×10-5
qRT-PCR (log2 FC)
0
−1
−1.0
−0.8
−0.6
−0.4
−0.2
RNAseq (log2 FC)


Pre-v
V
Post-v
H
Viral titers
(2(VvActin CT– Viral DNA region CT))
600
400
200
0
3000
2000
1000
0
Healdsburg
Oakville
GRBaV (-)
GRBaV (+)
GRBaV (-)
GRBaV (+)
GRBaV (-)
GRBaV (+)
GRBaV (-)
GRBaV (+)