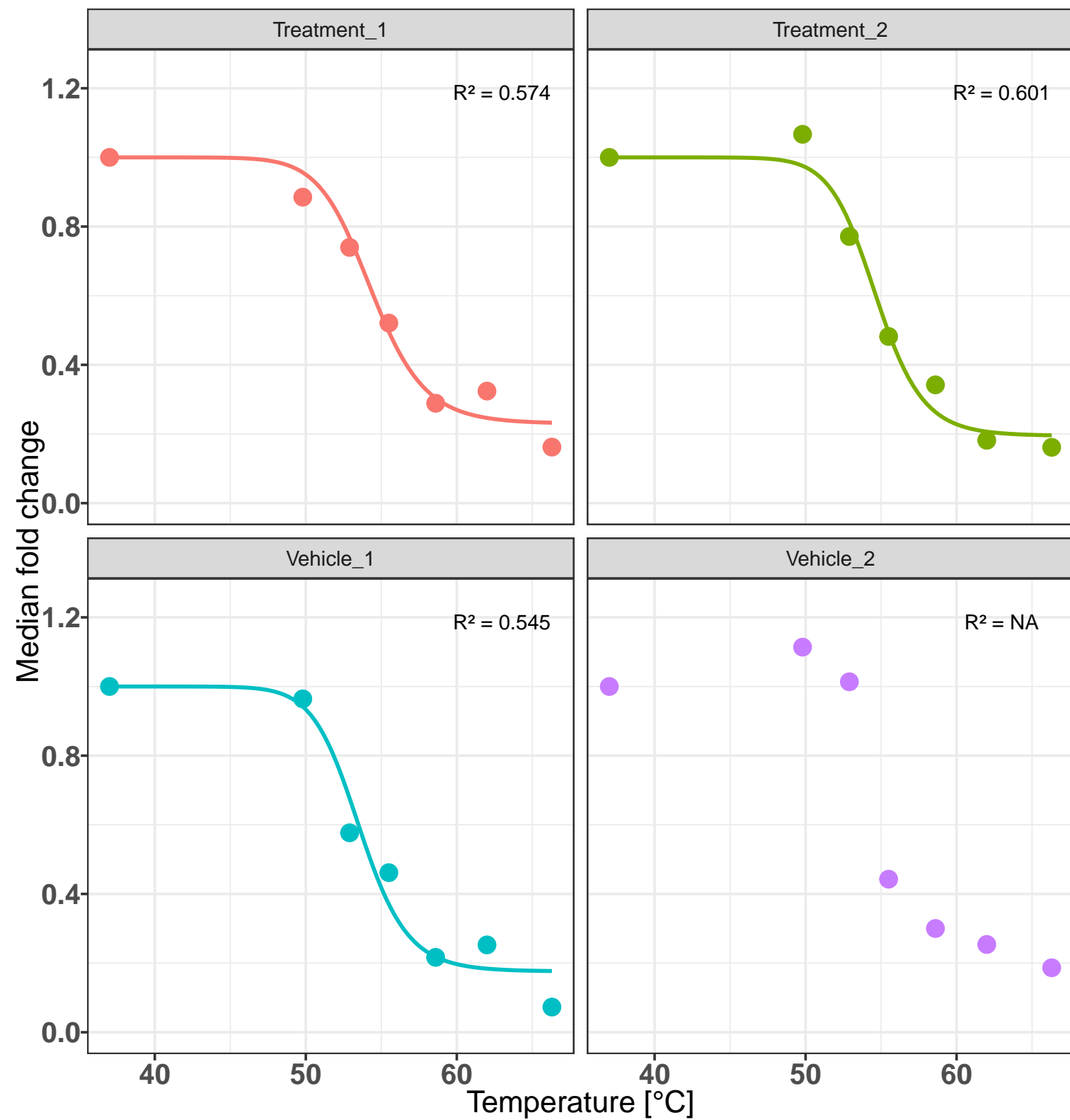
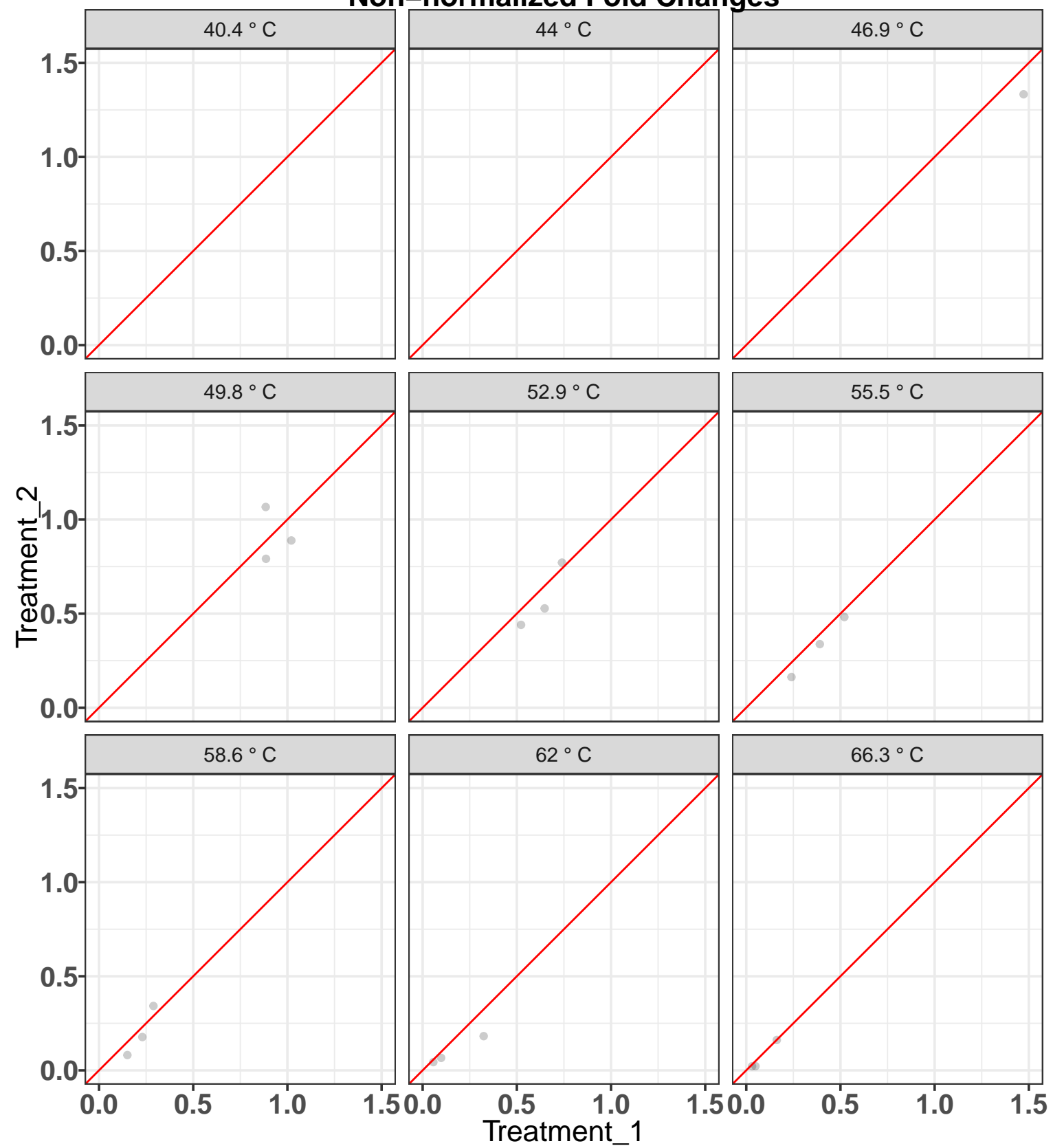


Normalization curves

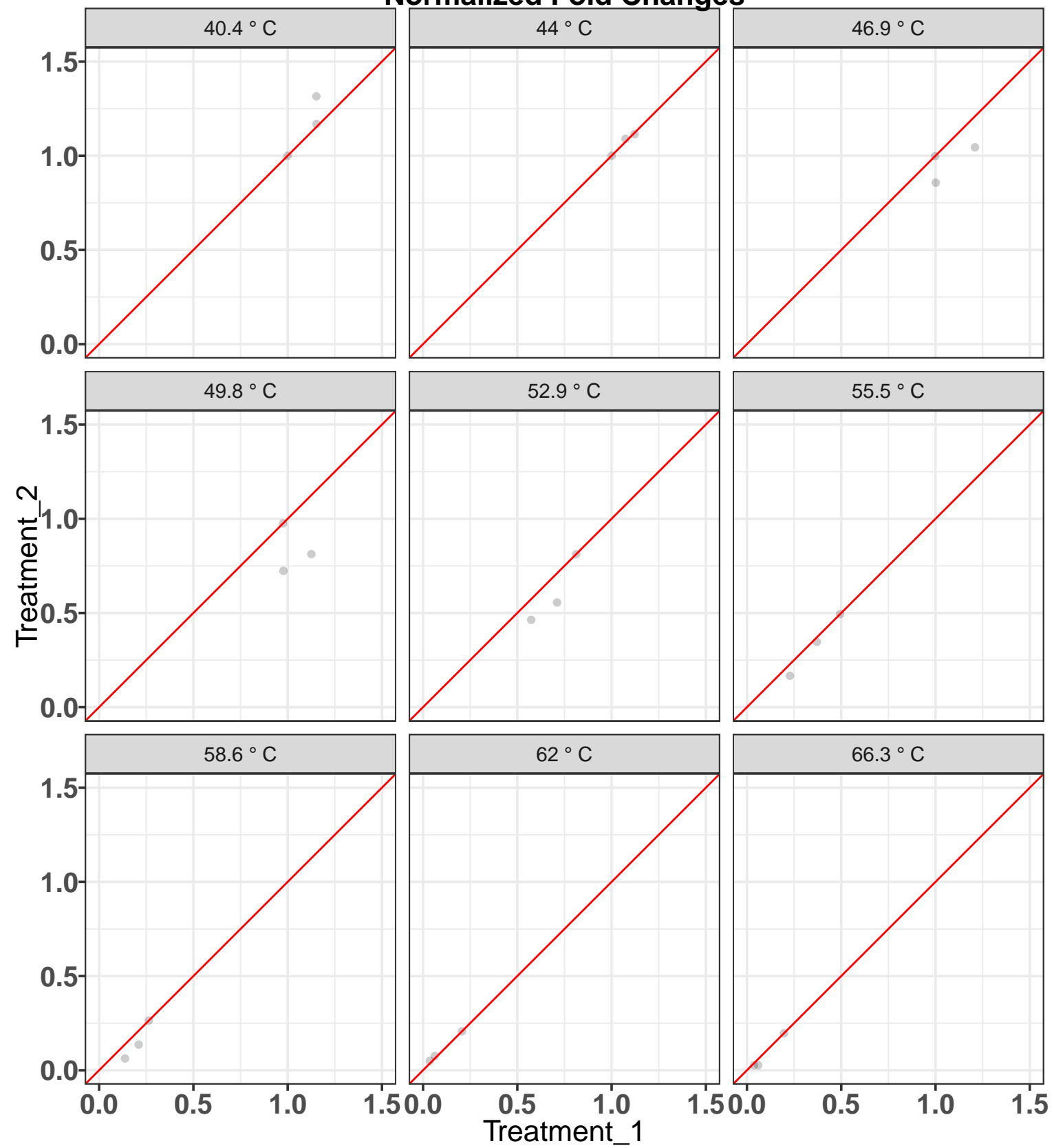
based on 1 proteins



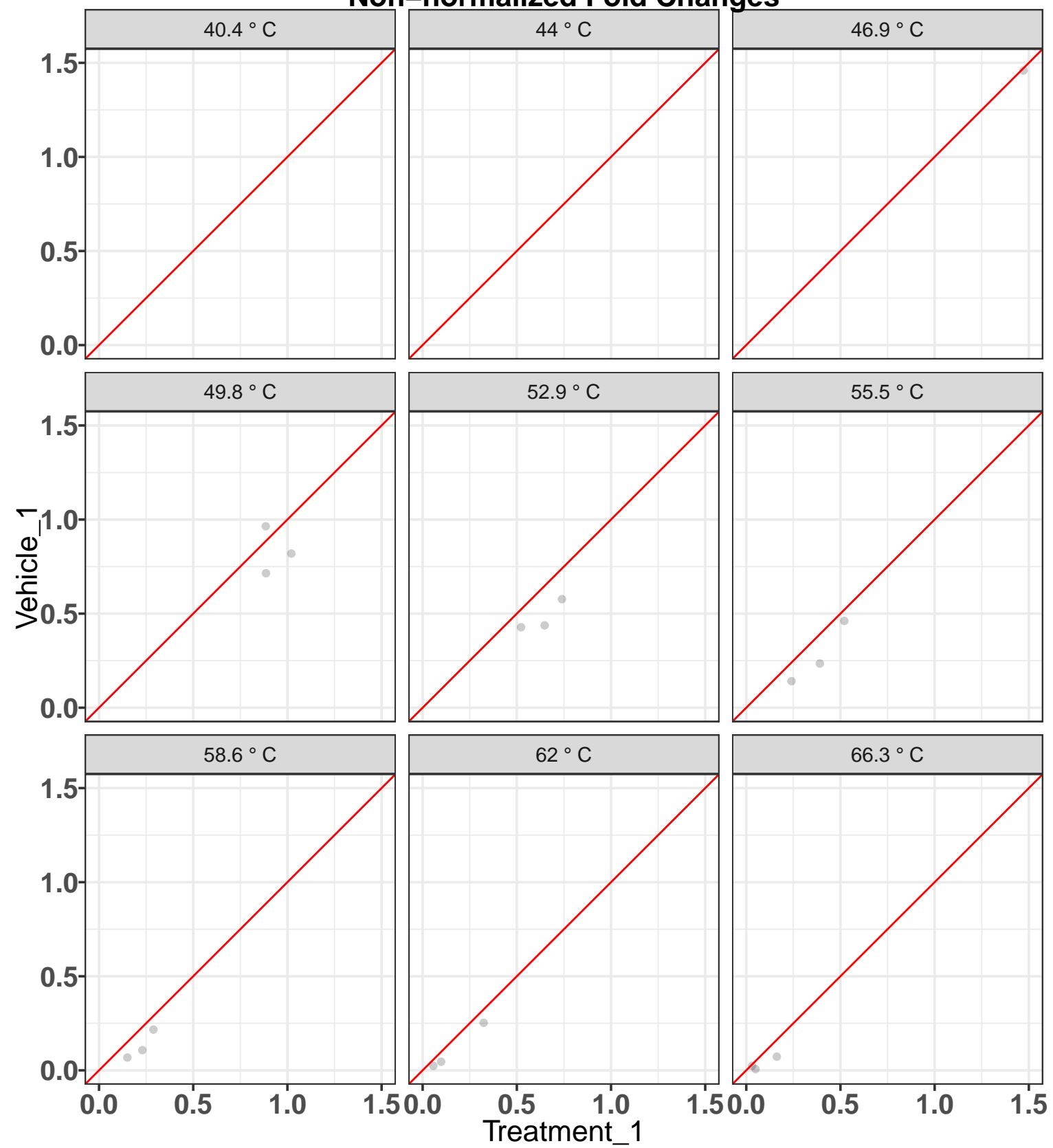
Non-normalized Fold Changes



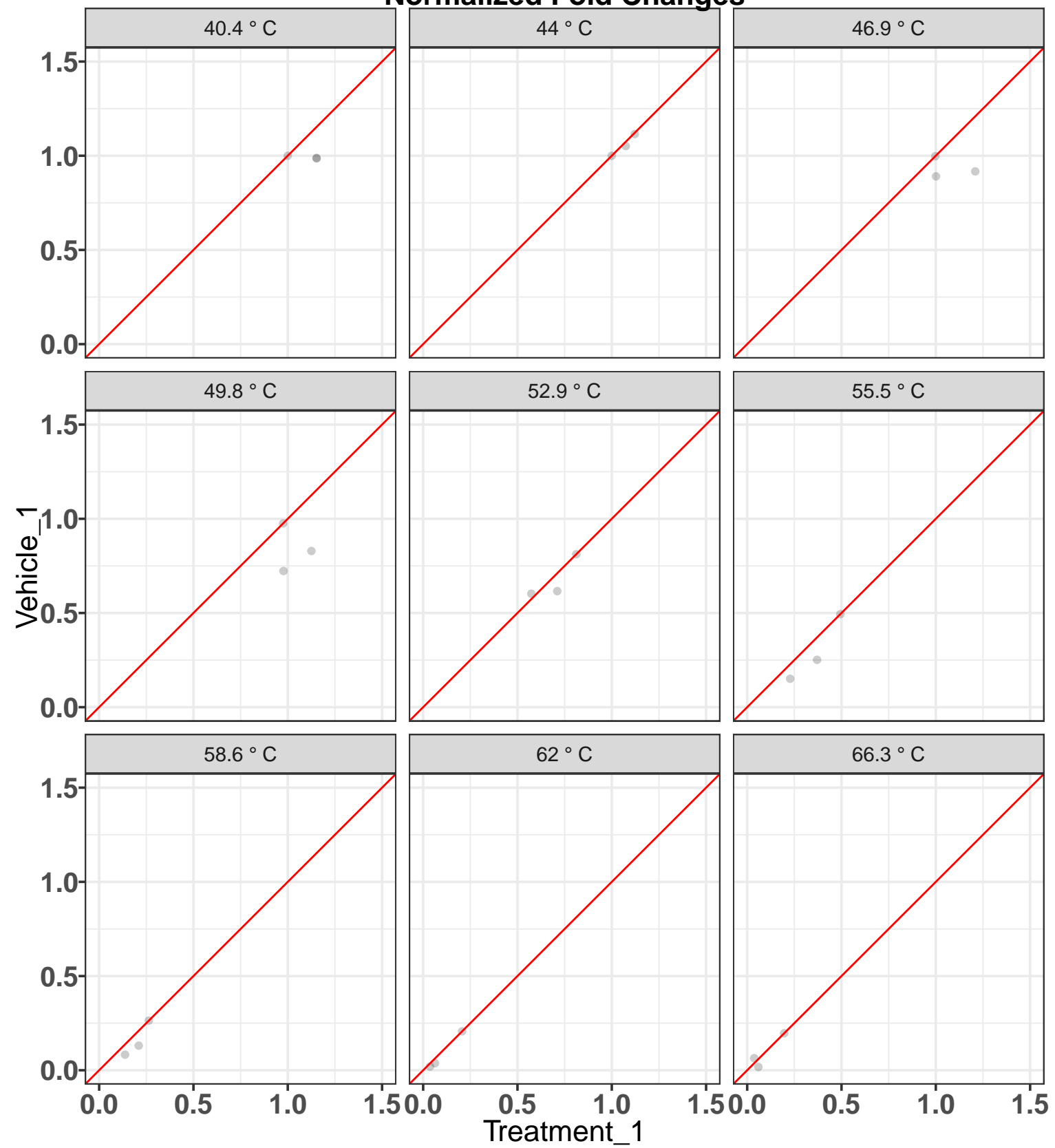
Normalized Fold Changes



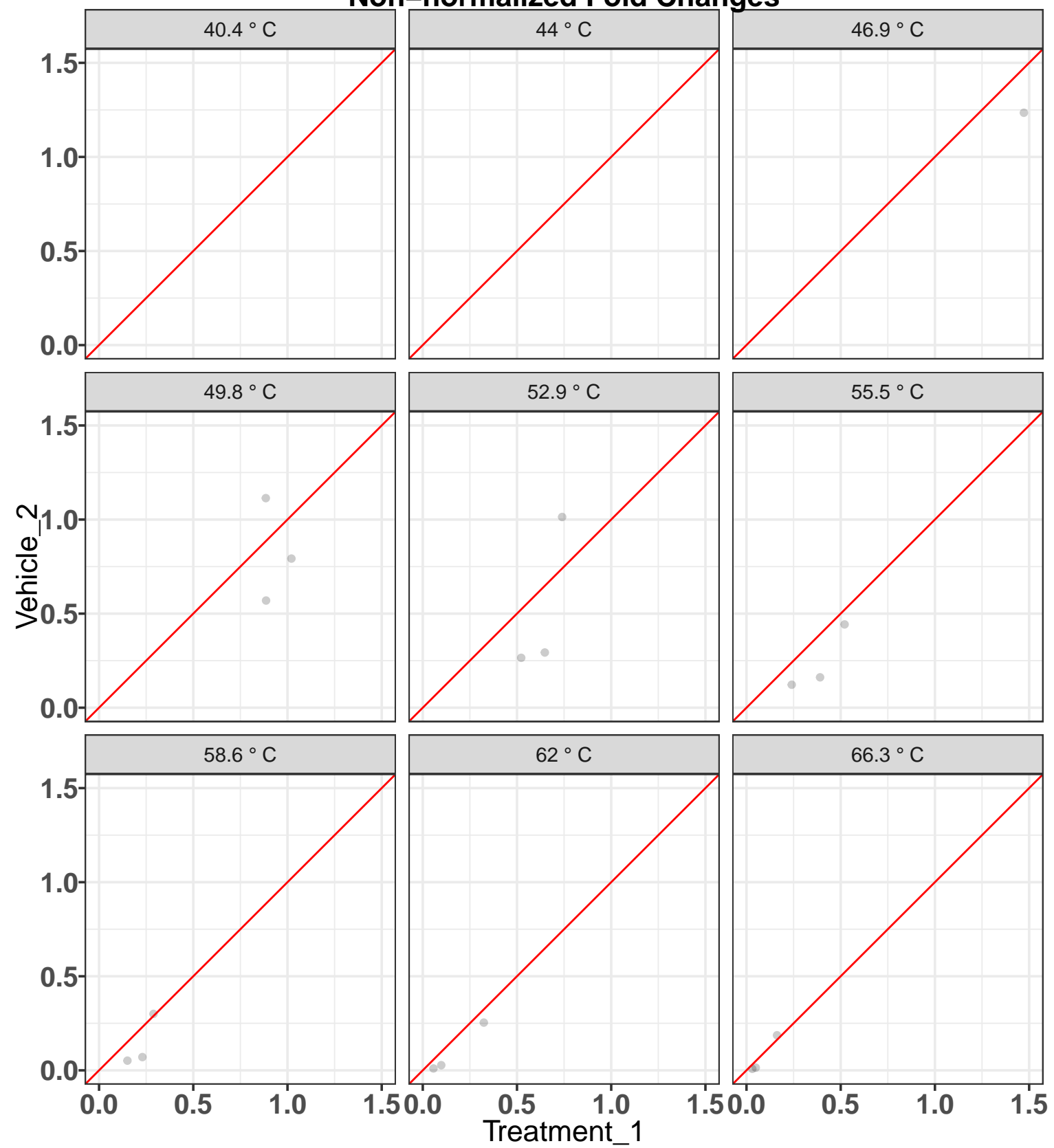
Non-normalized Fold Changes



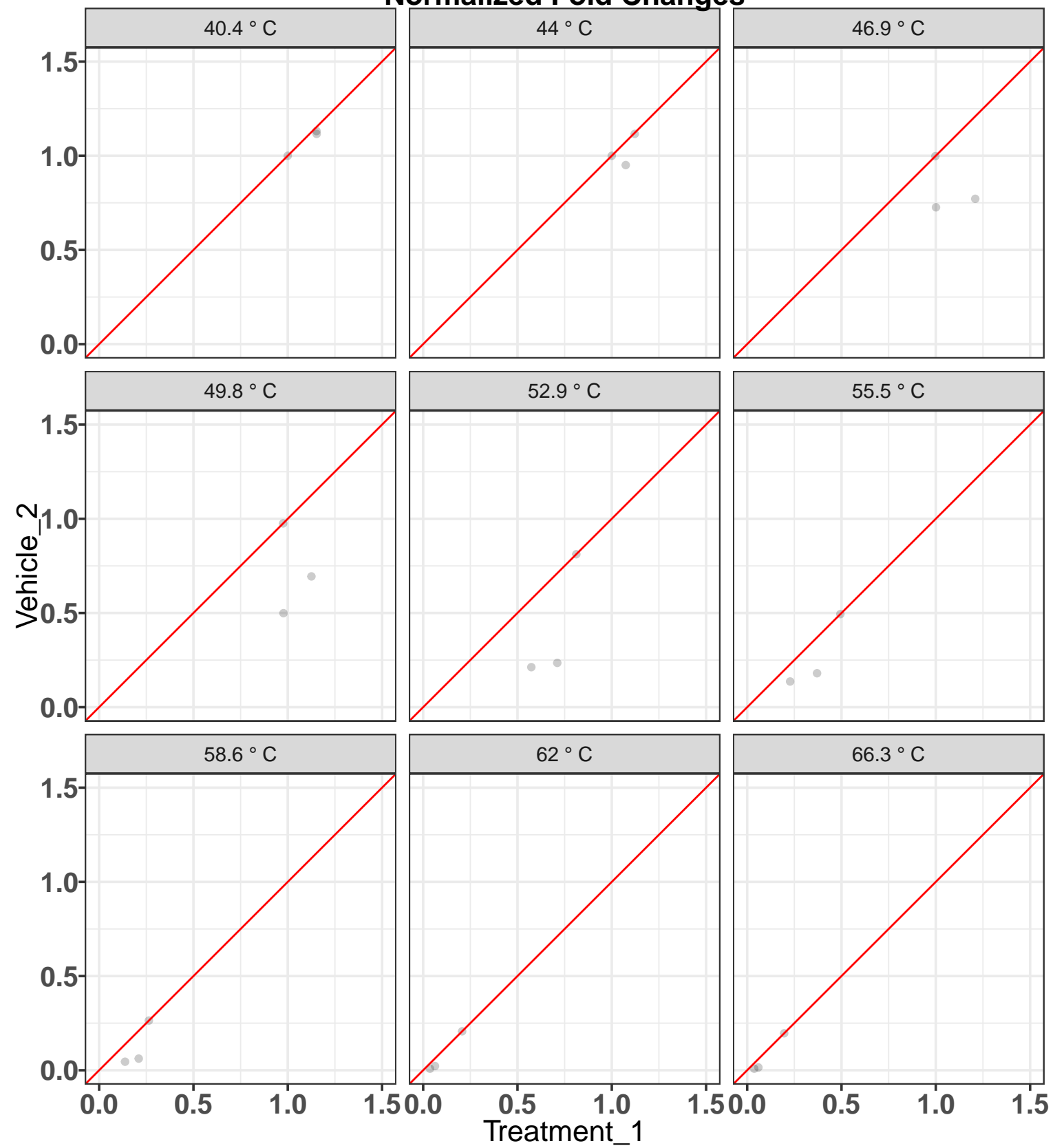
Normalized Fold Changes



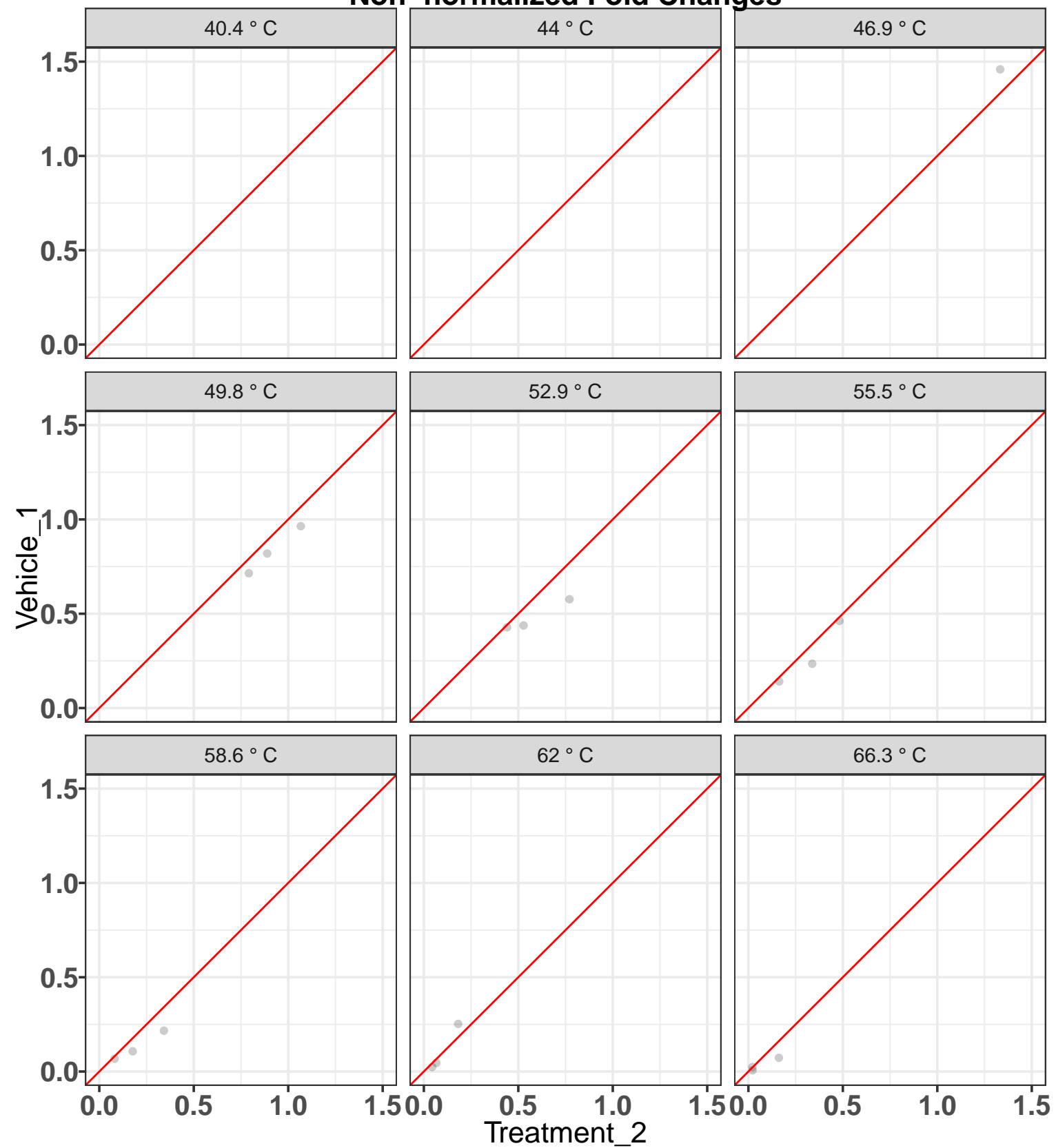
Non-normalized Fold Changes



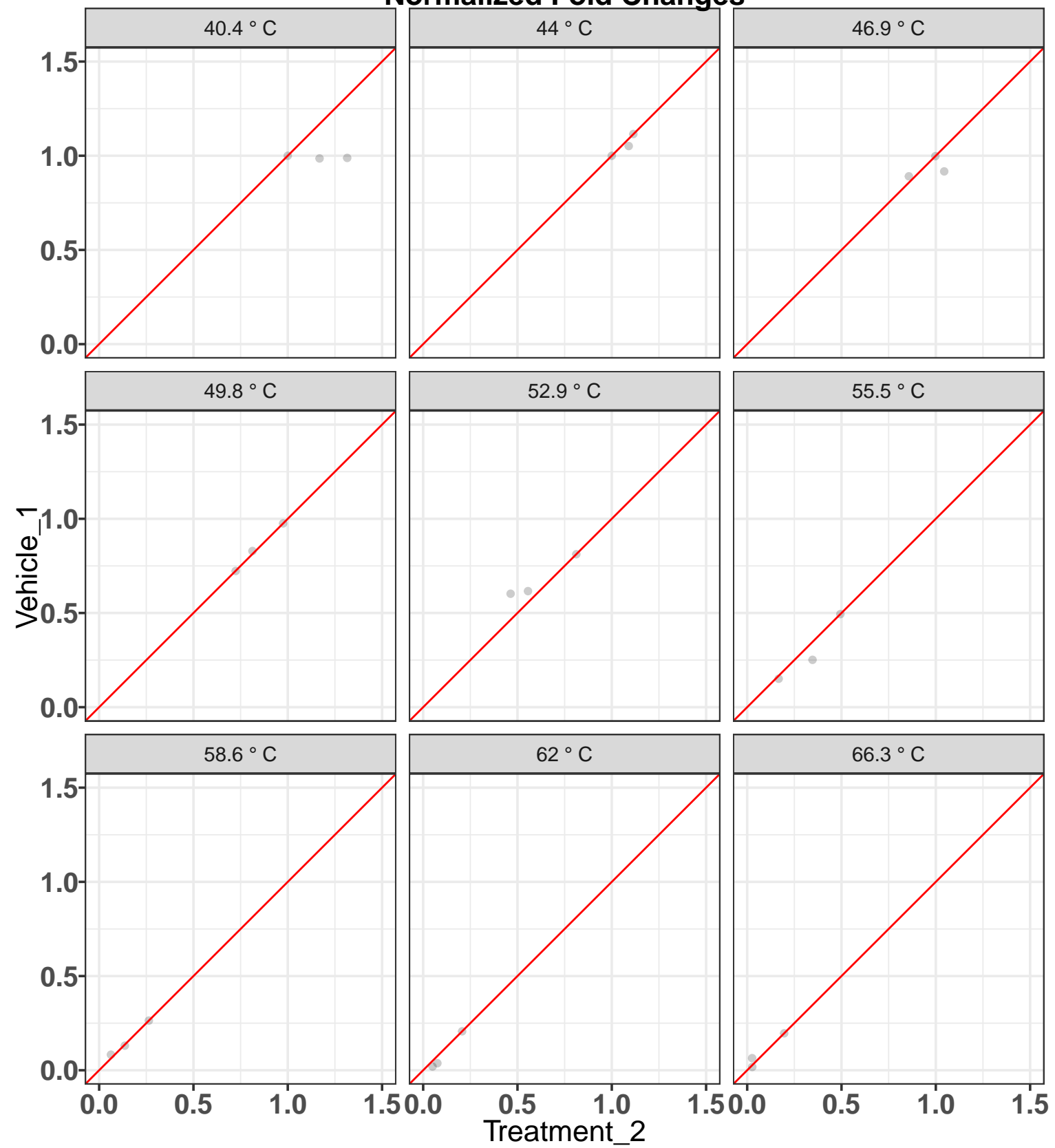
Normalized Fold Changes



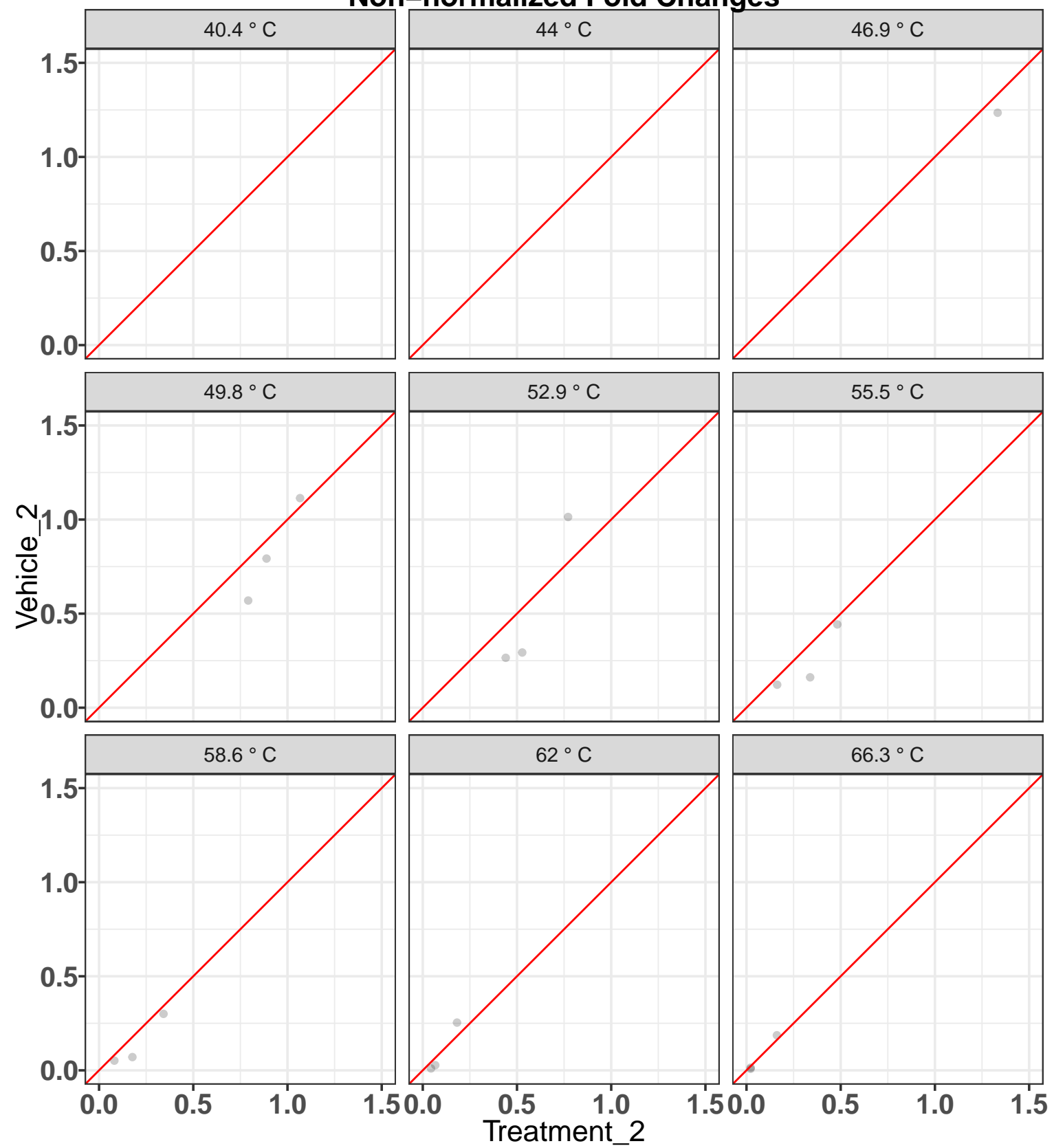
Non-normalized Fold Changes



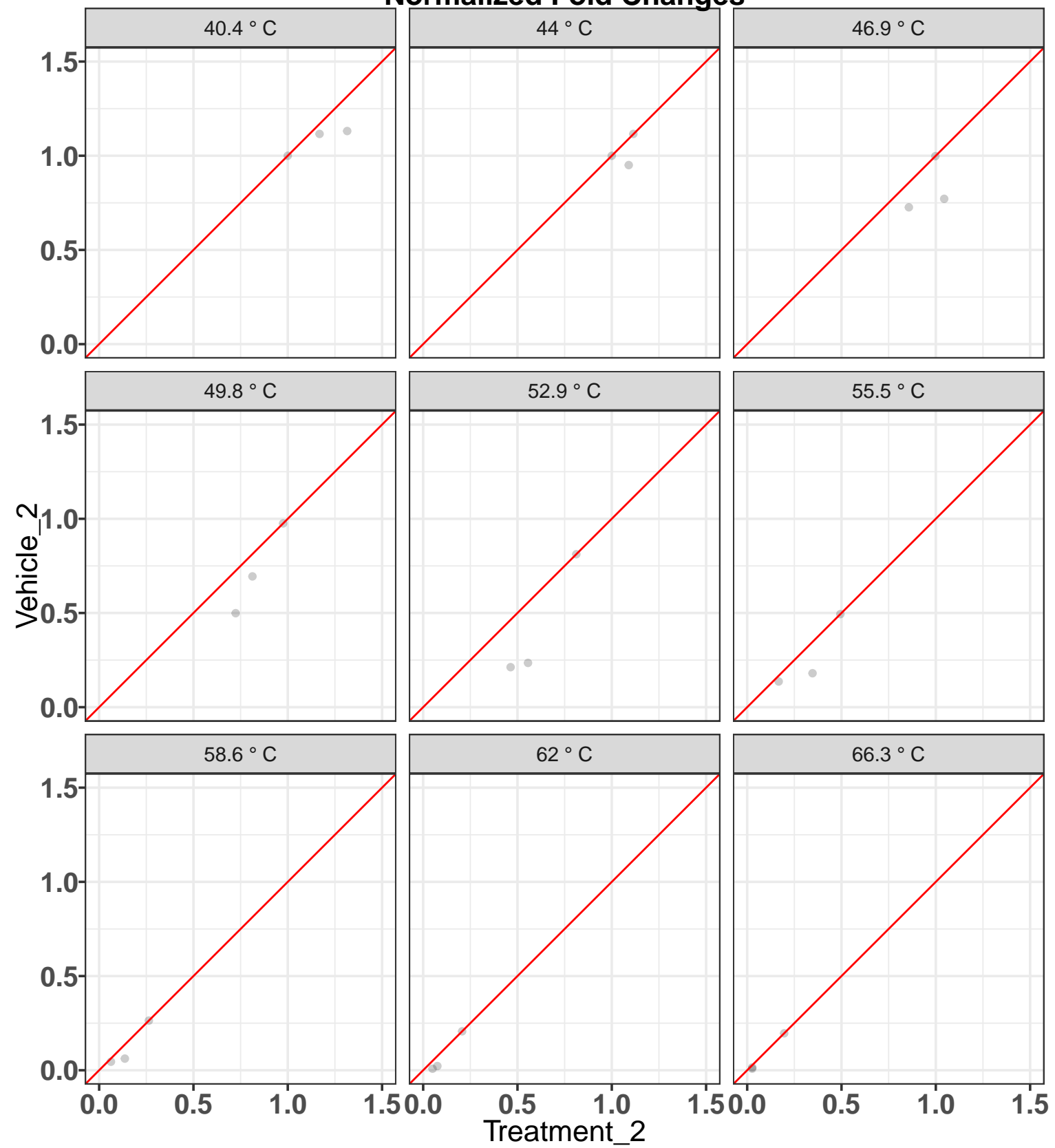
Normalized Fold Changes



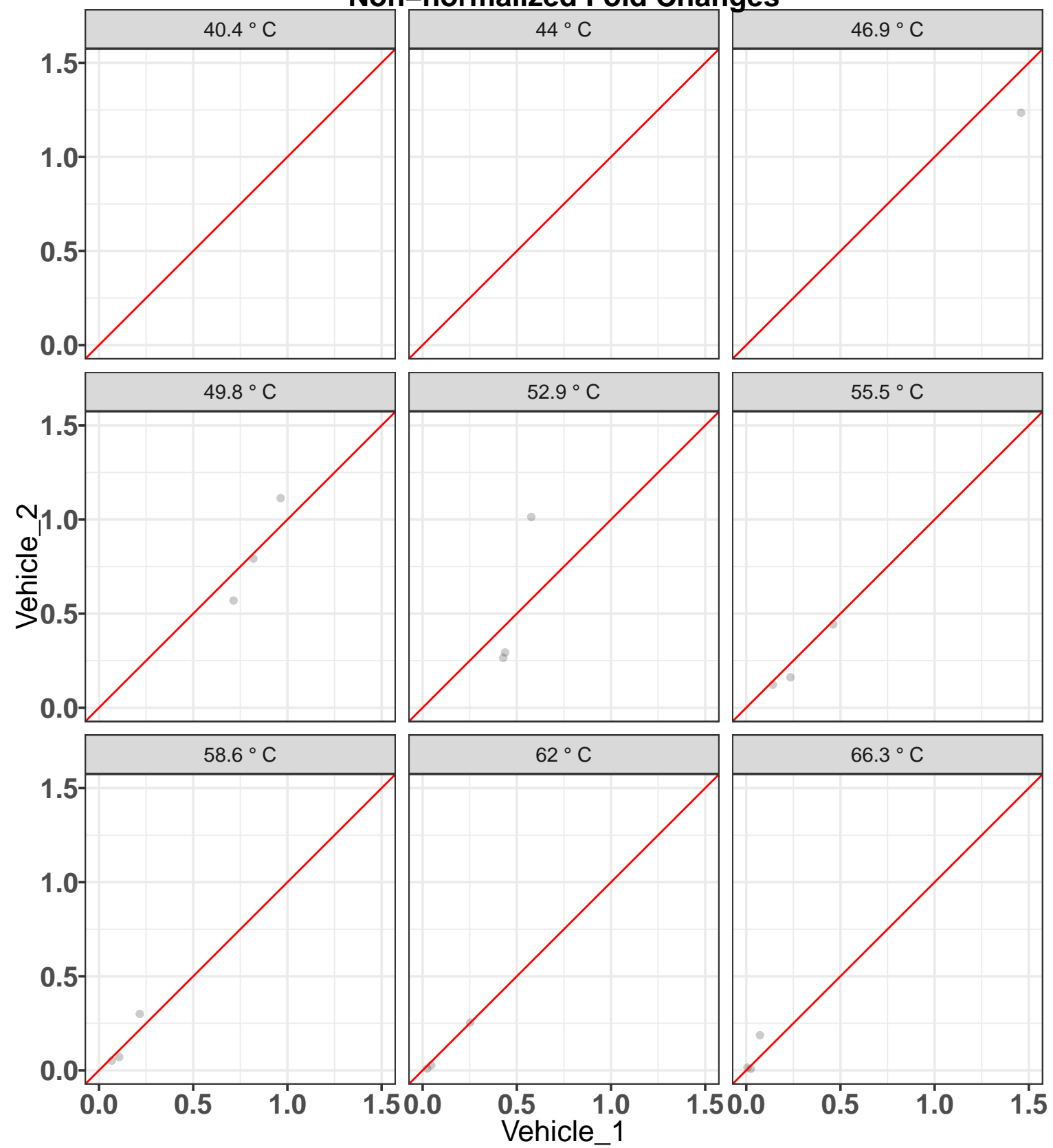
Non-normalized Fold Changes



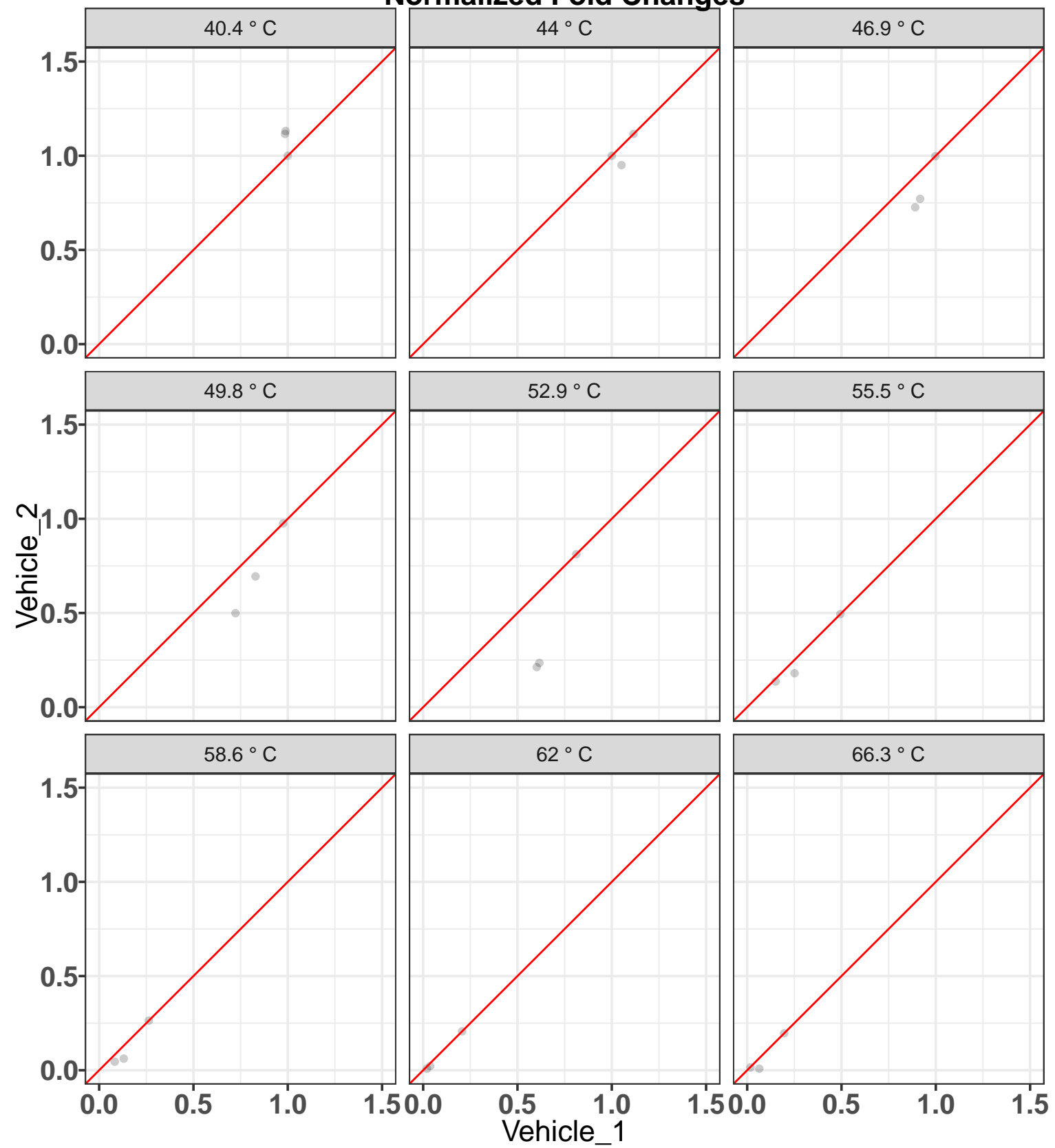
Normalized Fold Changes

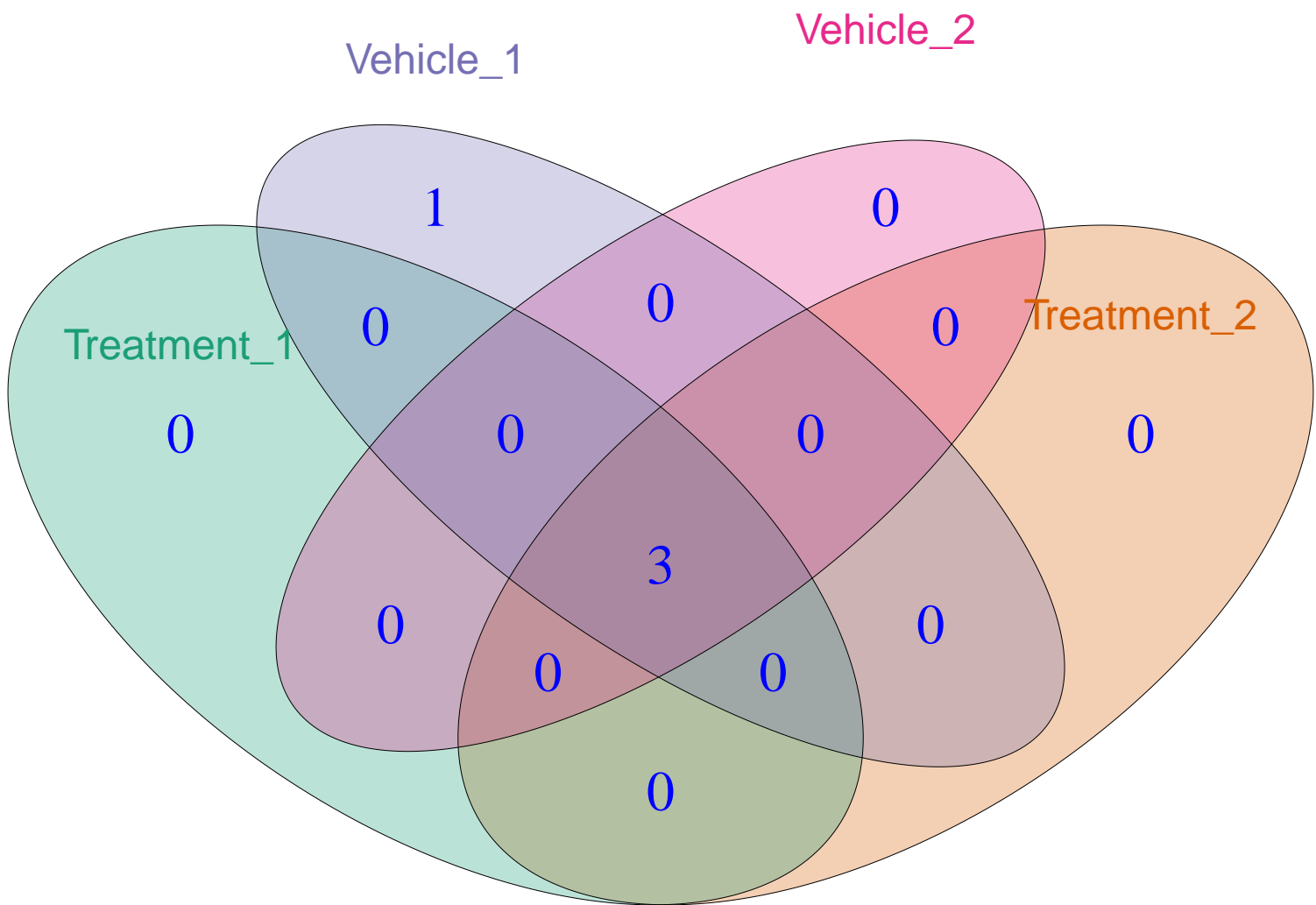


Non-normalized Fold Changes



Normalized Fold Changes





4 proteins identified overall

Vehicle_2_2

3

1

4

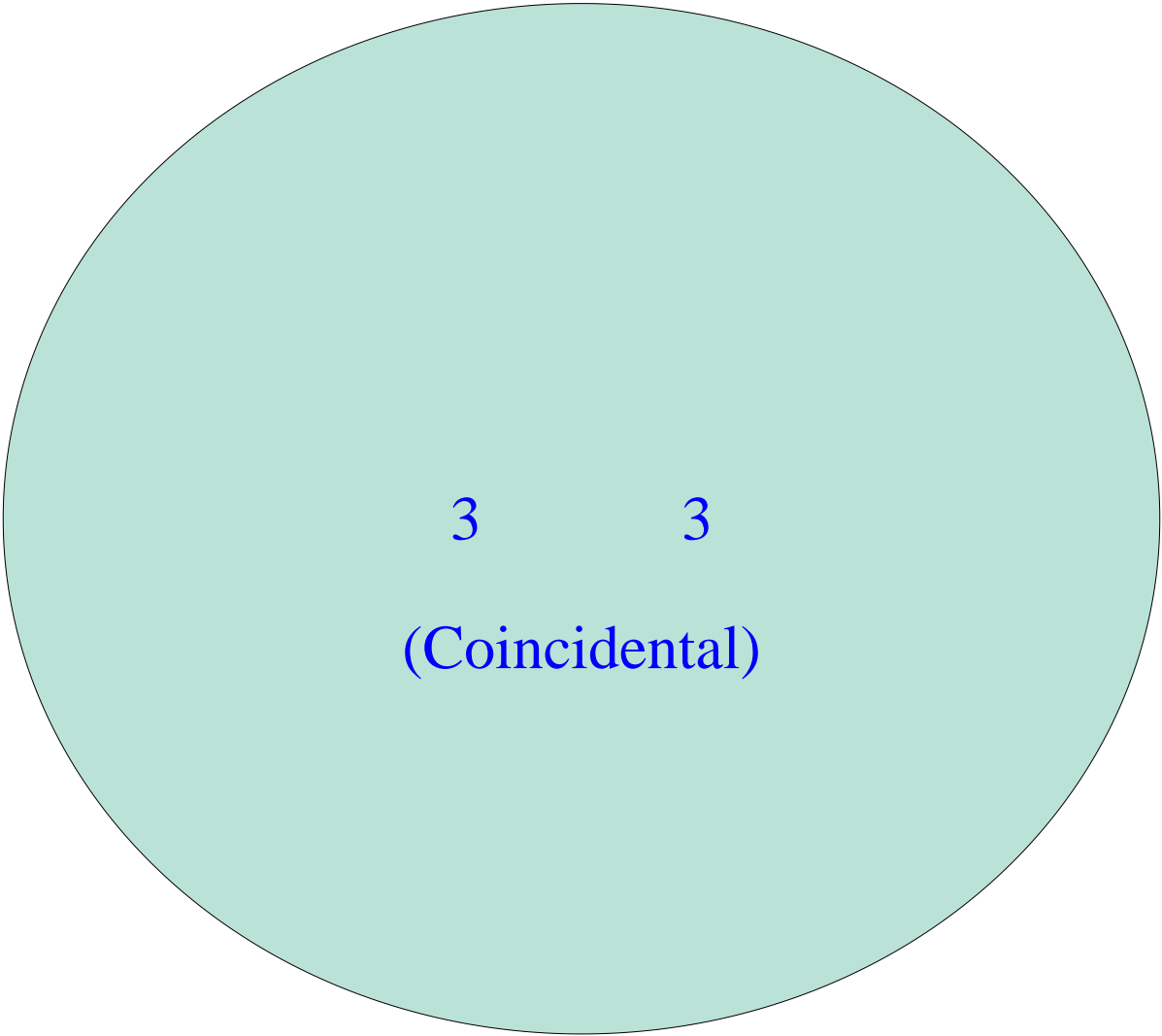
R2 >= 0.8

R2 < 0.8

Total

Treatment_2_vs_Vehicle_2

Treatment_1_vs_Vehicle_1



Treatment_2_vs_Vehicle_2

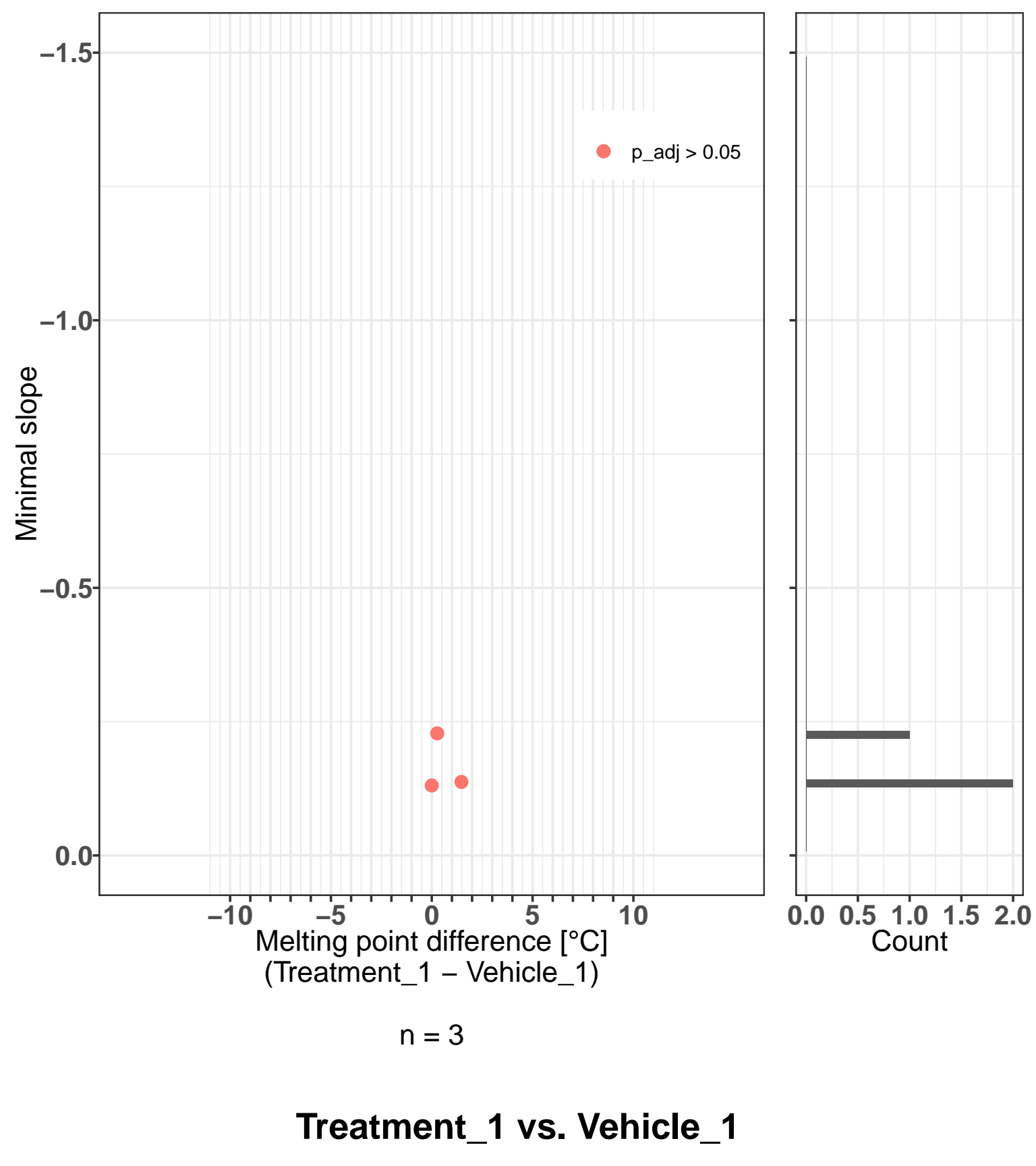
1

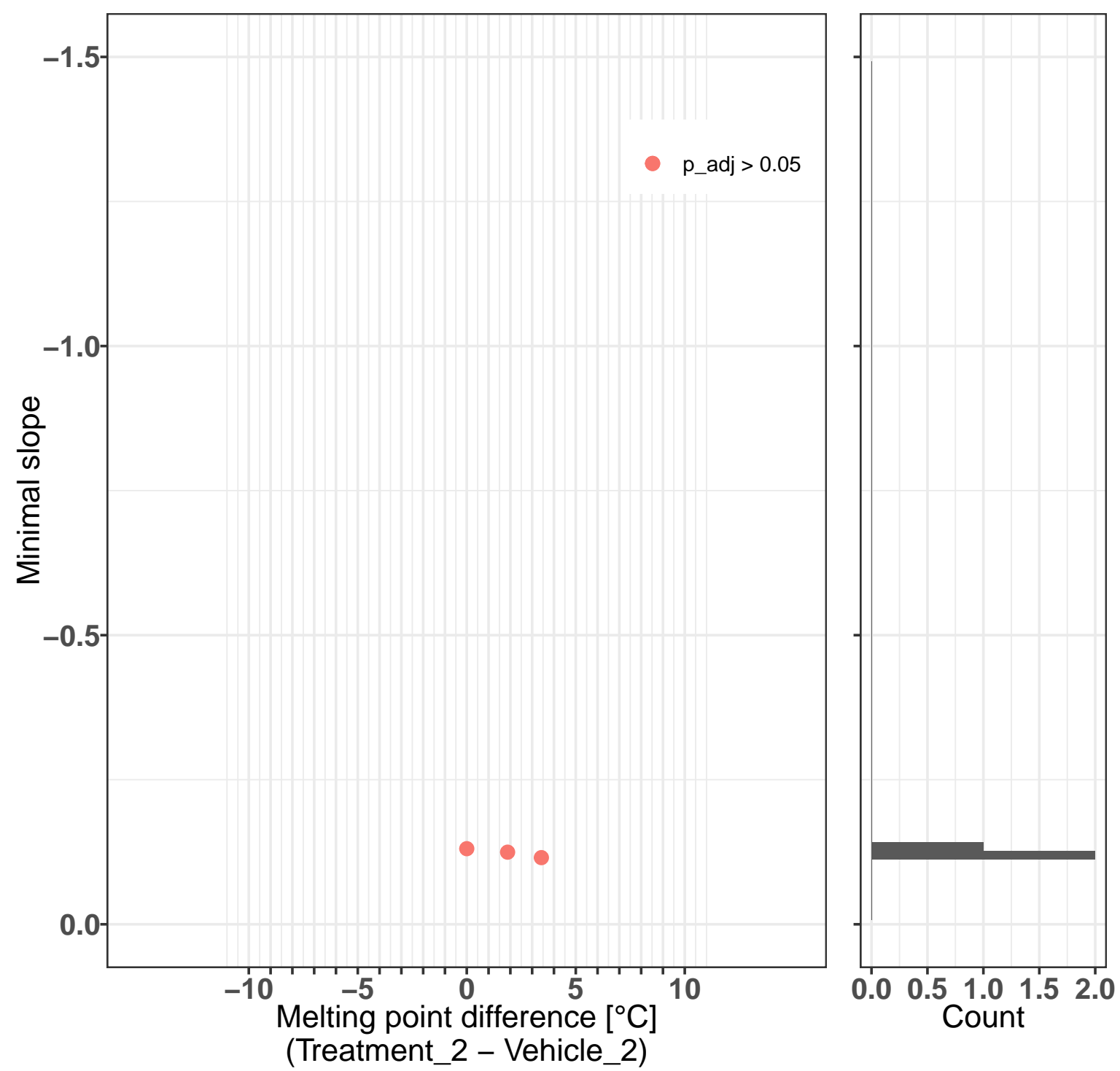
4

passed_filter

filtered_out

Total

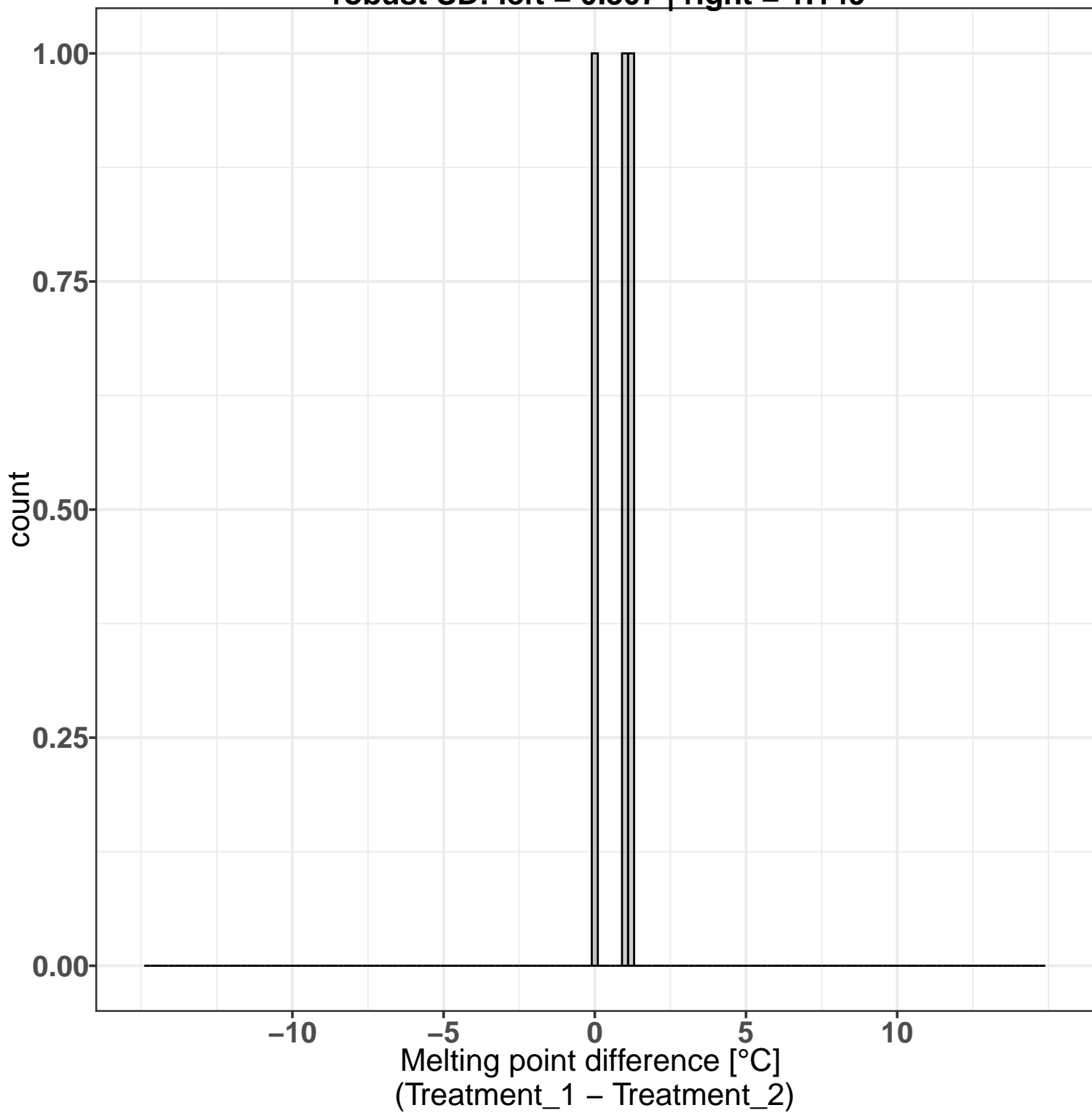




n = 3

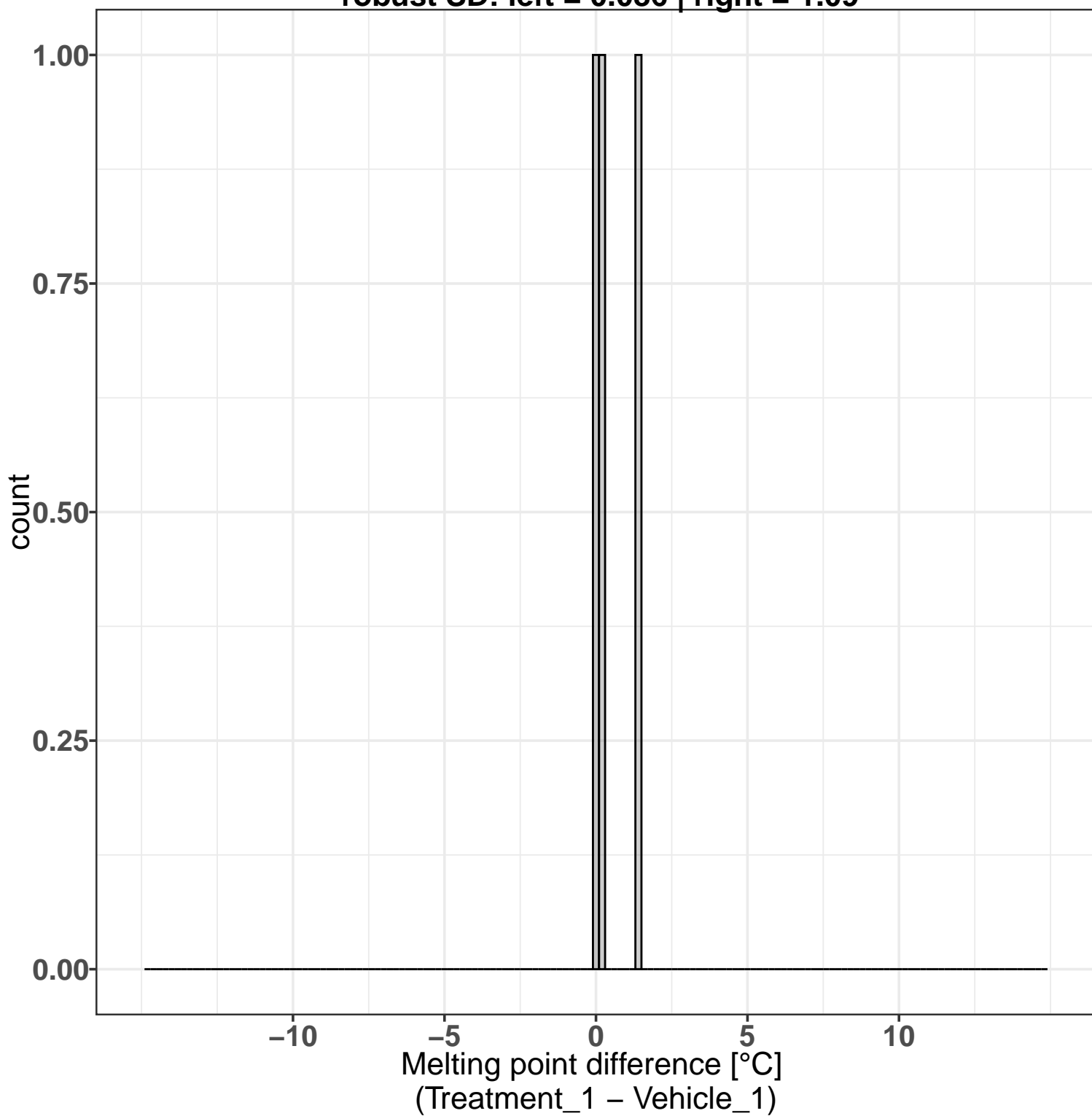
Treatment_2 vs. Vehicle_2

median = 0.967 ,
robust SD: left = 0.307 | right = 1.149



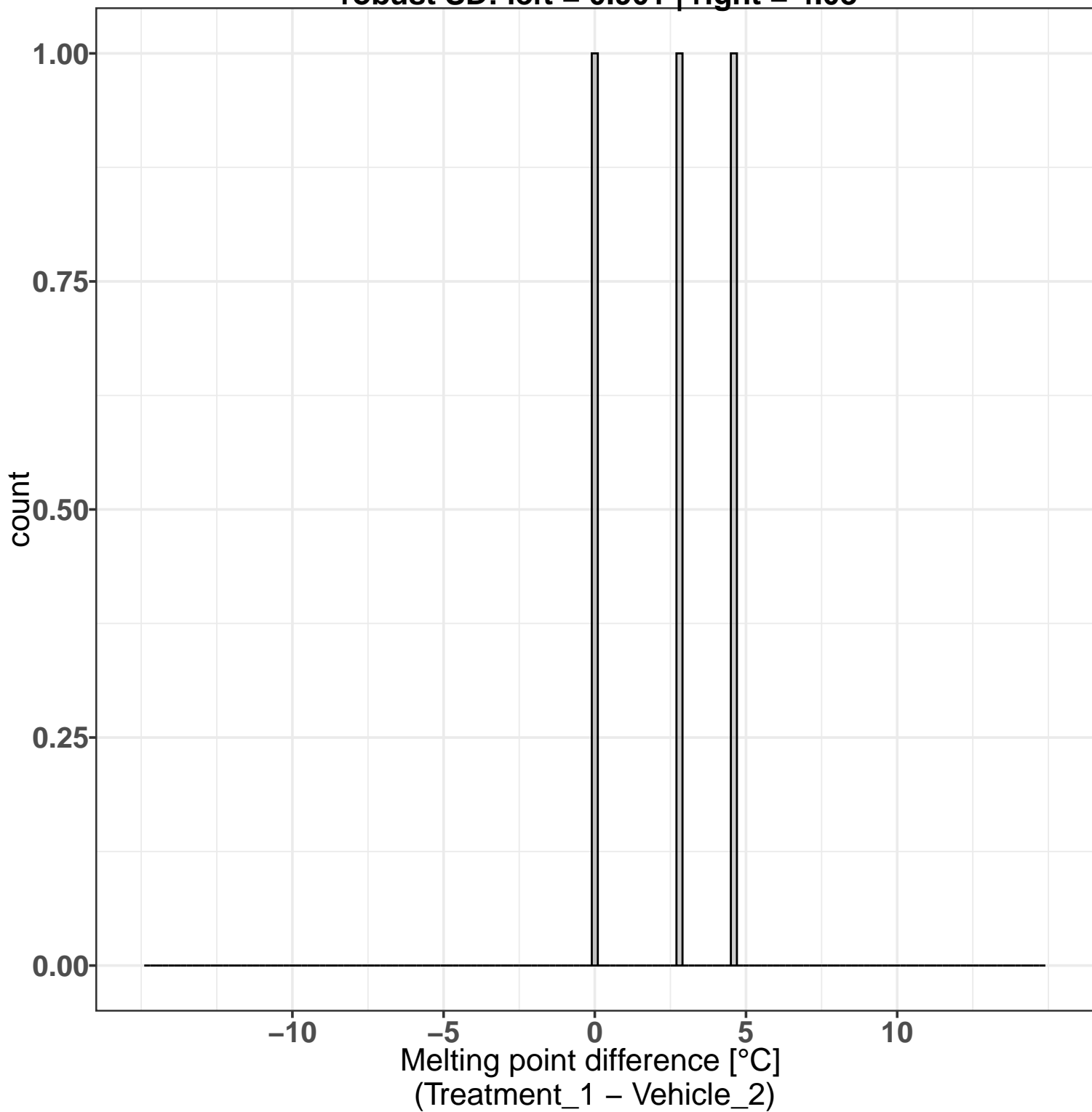
n = 3 , R_sq >= 0.8

median = 0.269 ,
robust SD: left = 0.086 | right = 1.09



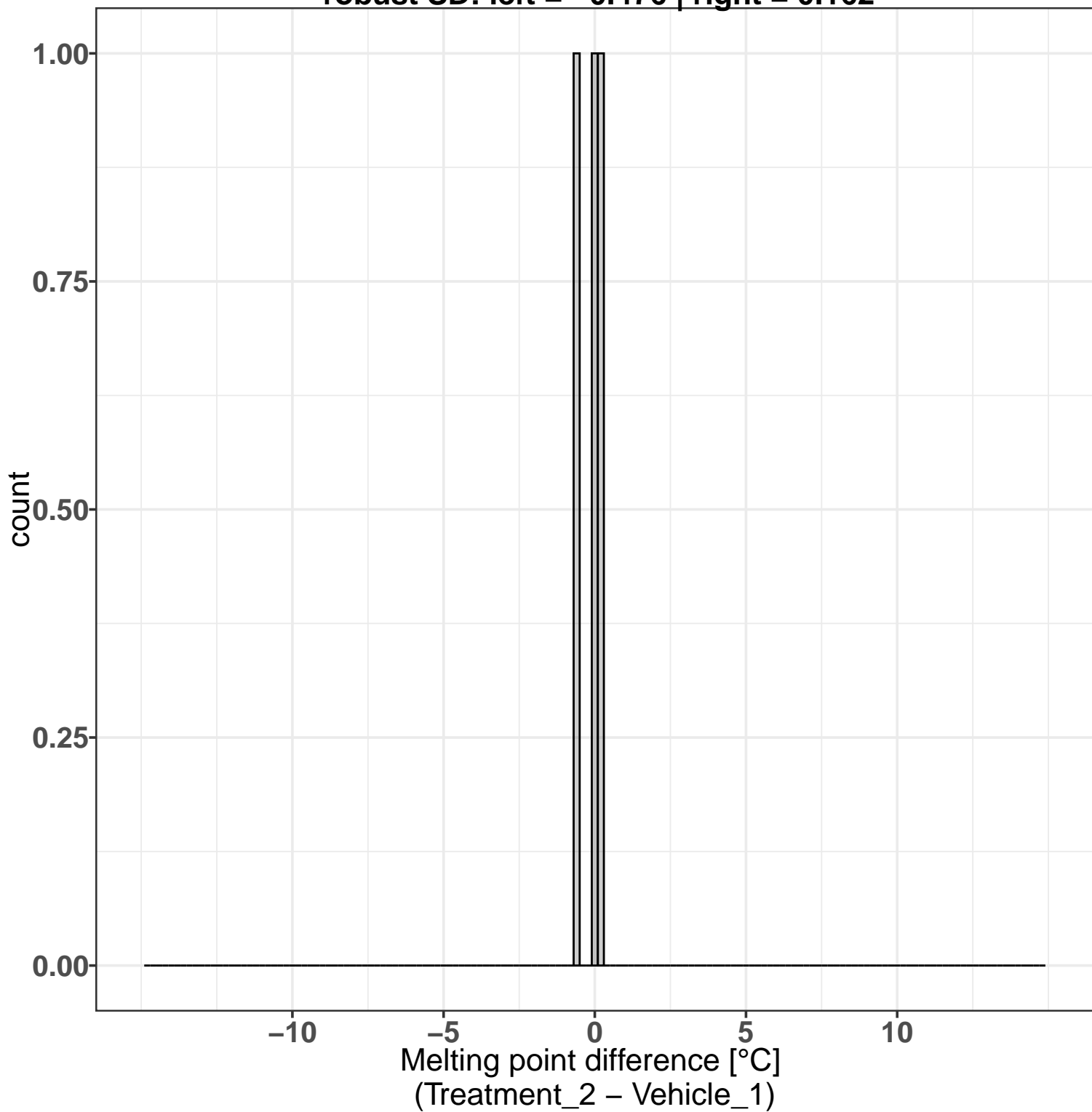
n = 3 , R_sq >= 0.8

median = 2.84 ,
robust SD: left = 0.901 | right = 4.08



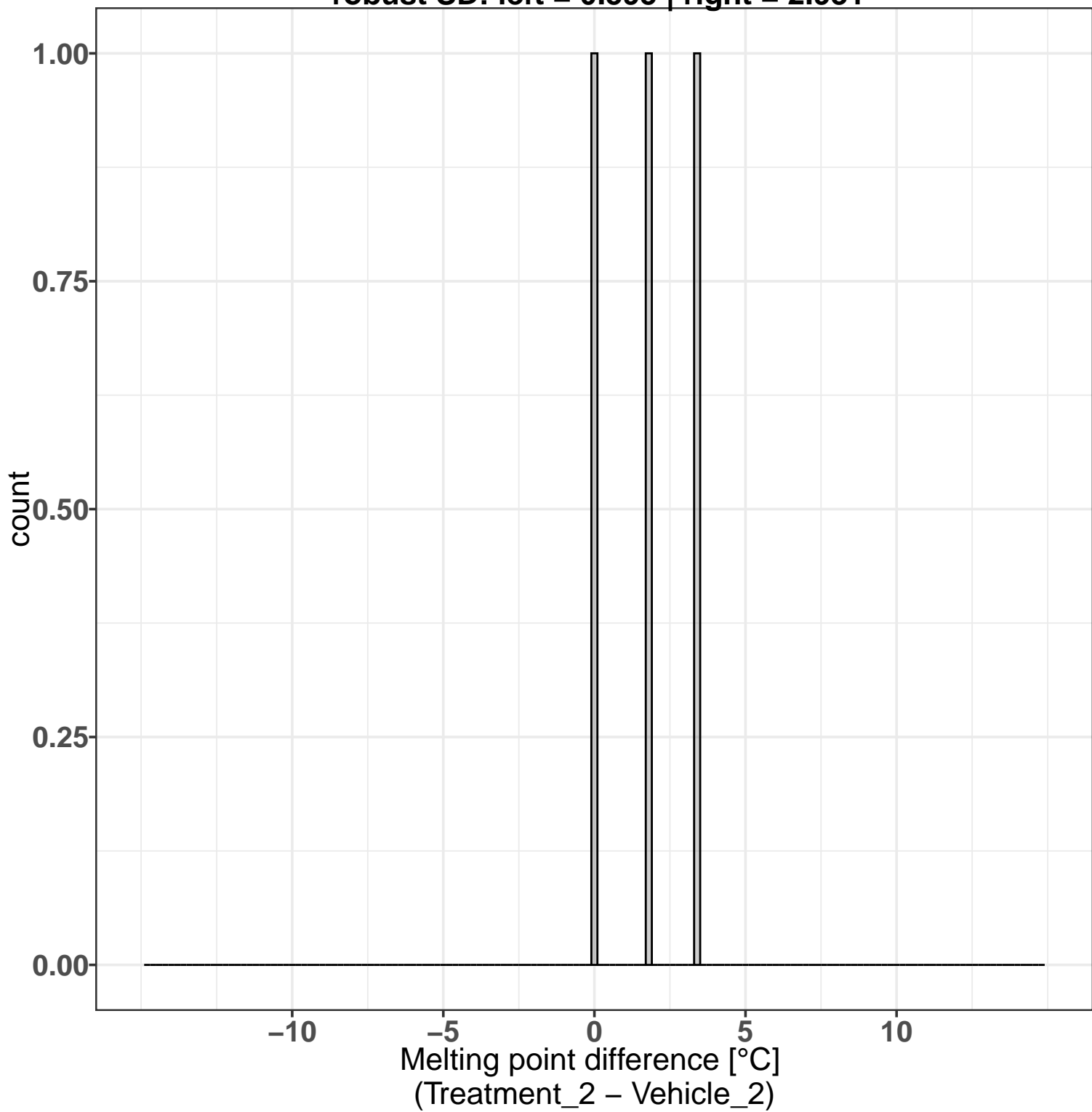
n = 3 , R_sq >= 0.8

**median = 0 ,
robust SD: left = -0.476 | right = 0.162**



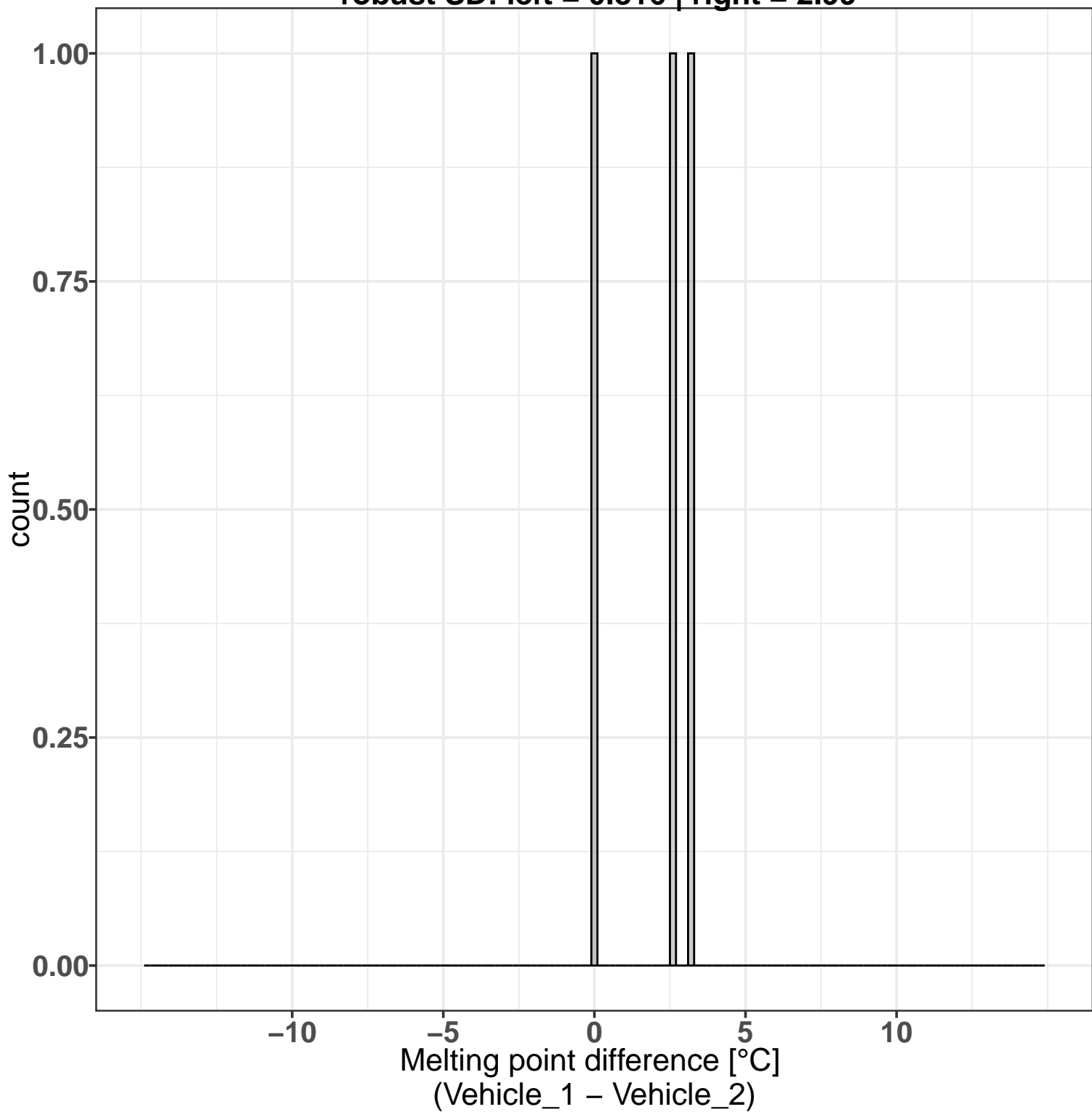
n = 3 , R_sq >= 0.8

median = 1.873 ,
robust SD: left = 0.595 | right = 2.931



n = 3 , R_sq >= 0.8

**median = 2.57 ,
robust SD: left = 0.816 | right = 2.99**



n = 3 , R_sq >= 0.8

