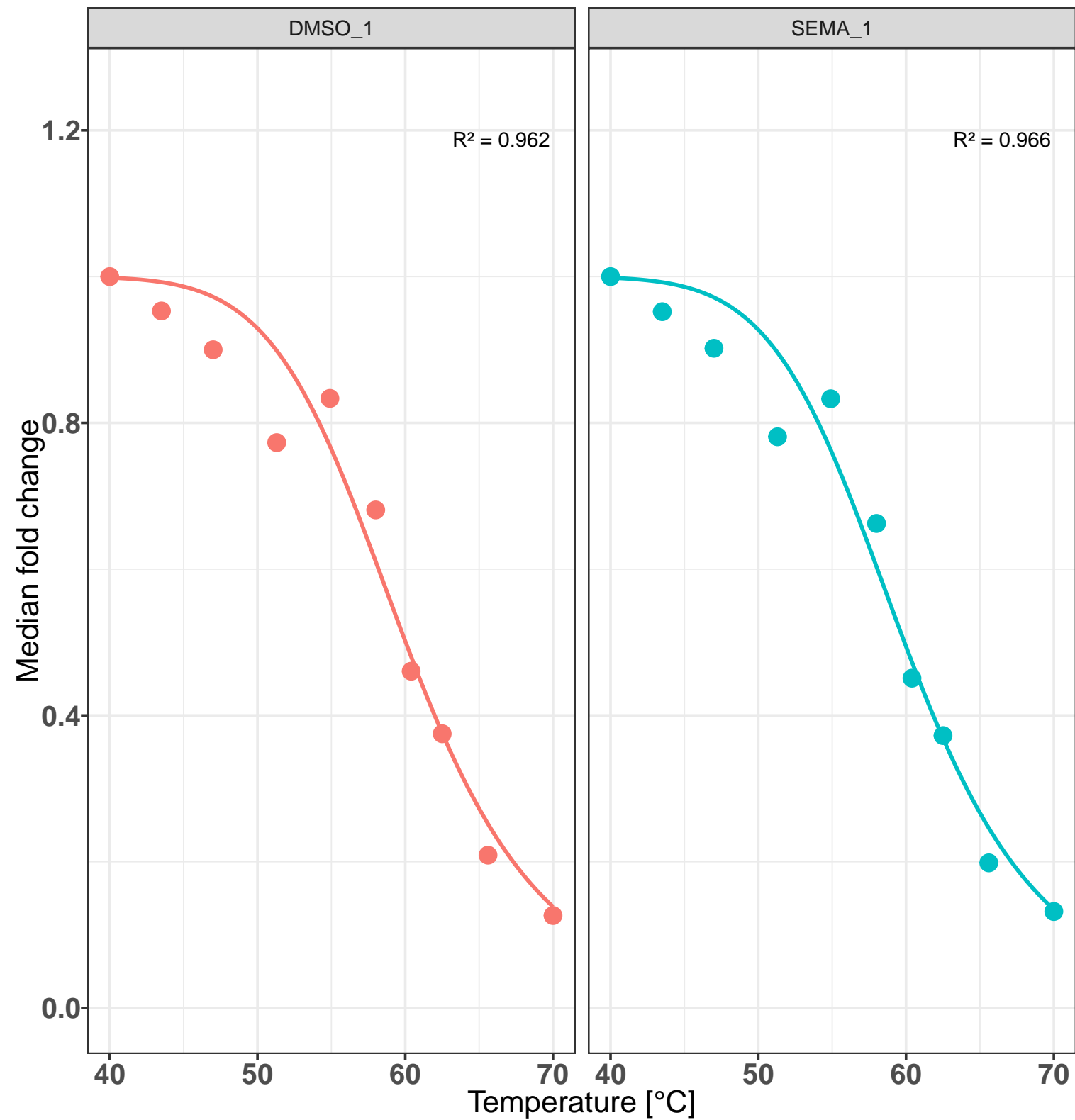
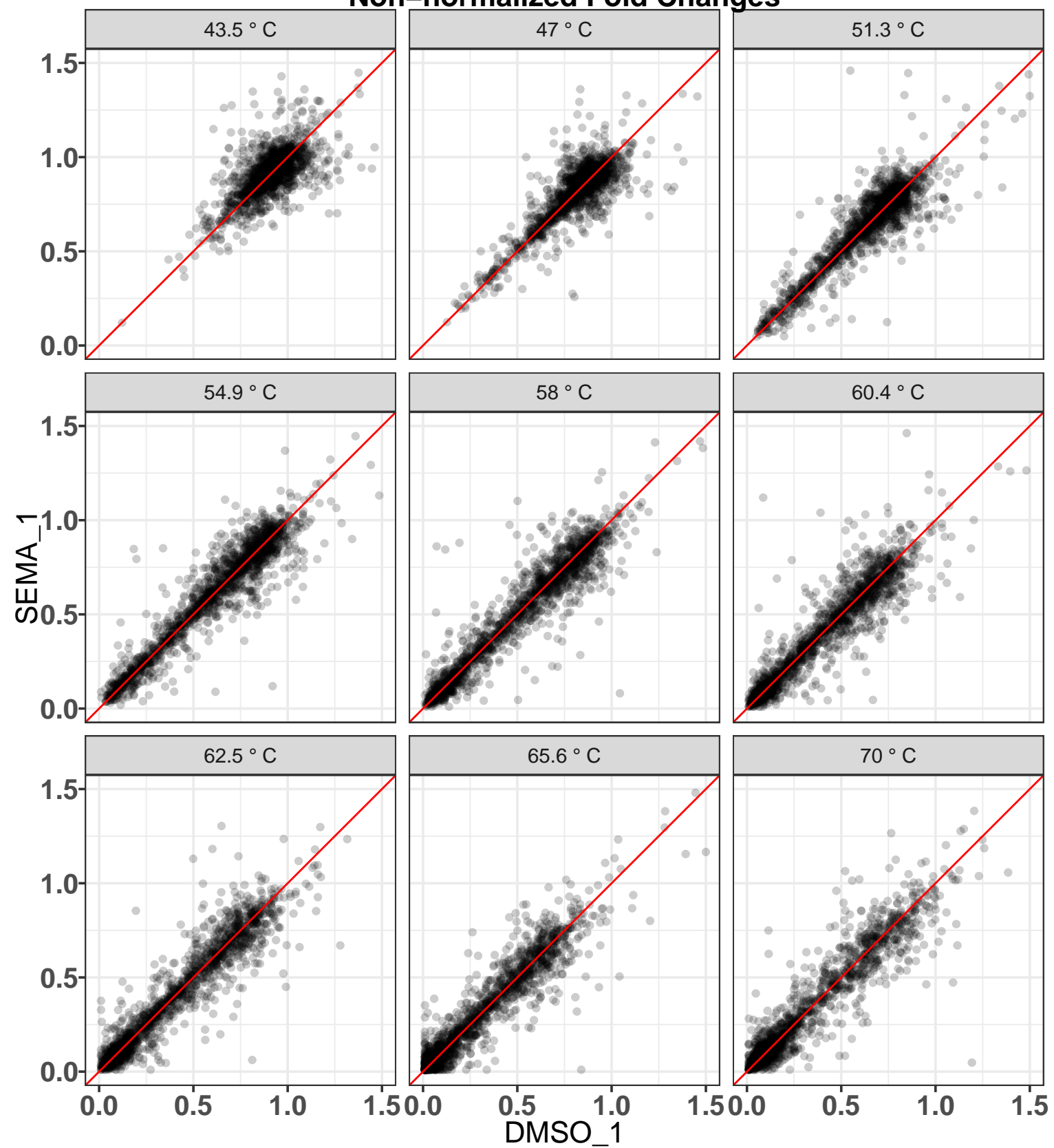


# Normalization curves

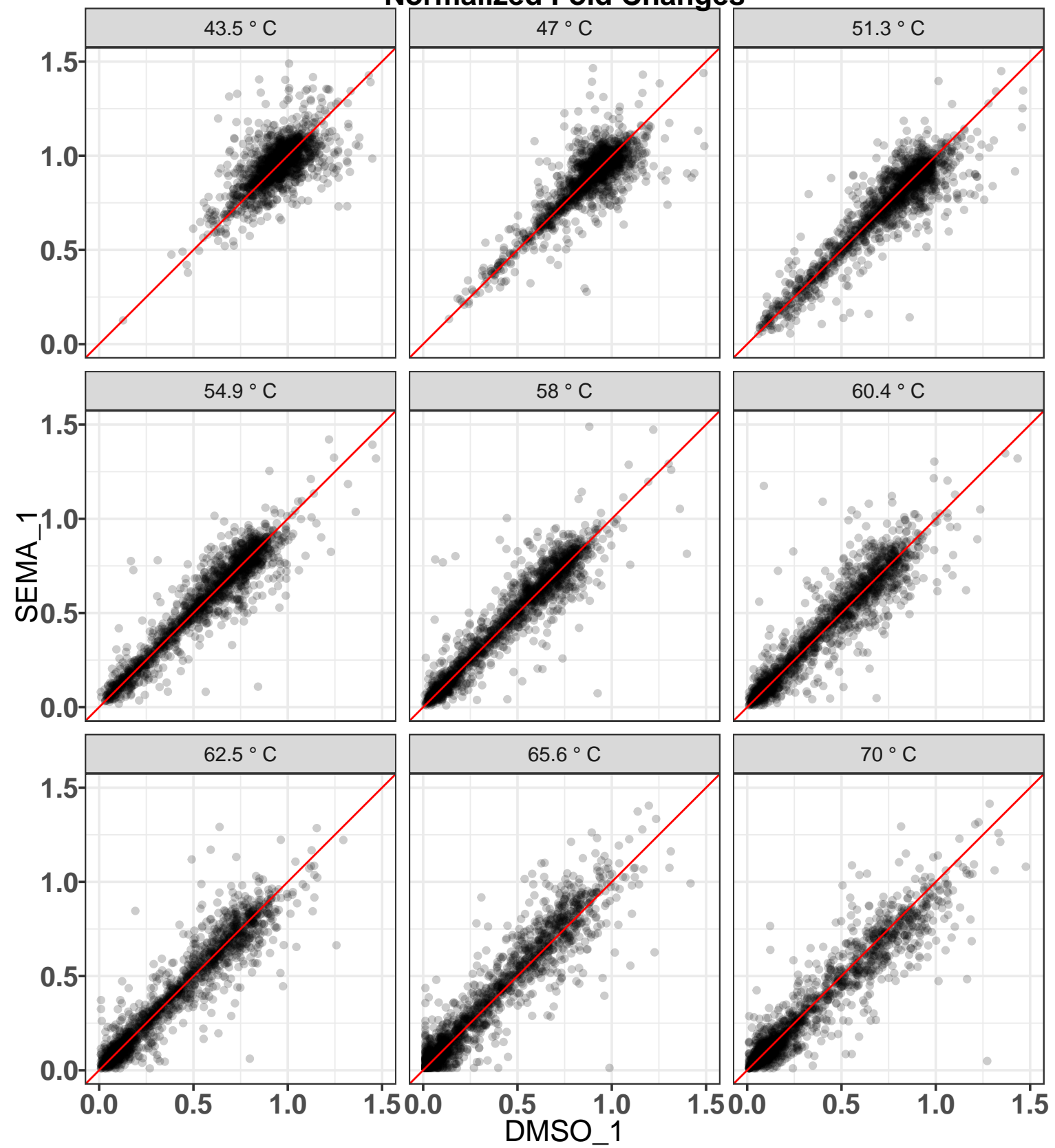
based on 104 proteins

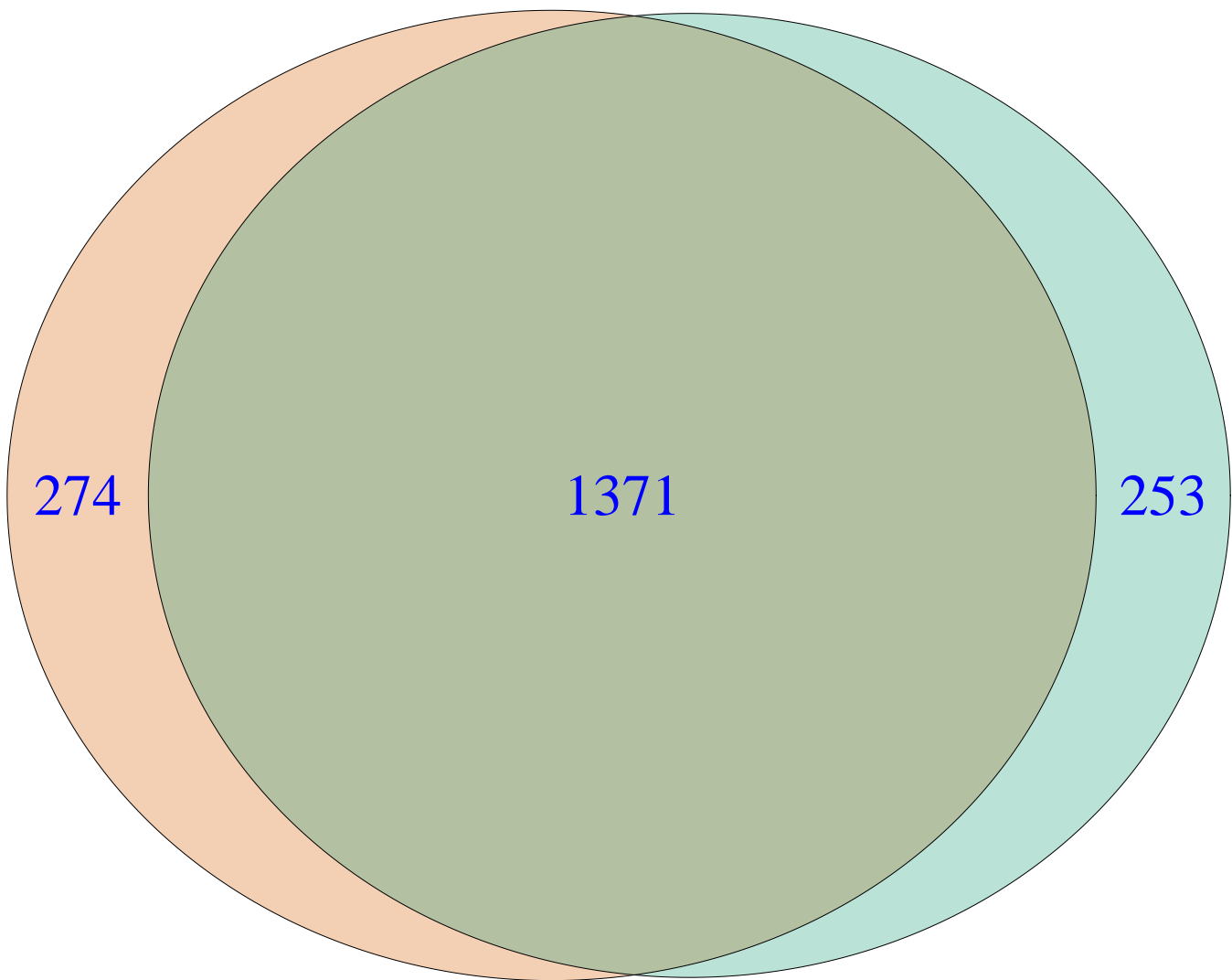


# Non-normalized Fold Changes



# Normalized Fold Changes





2411 proteins identified overall

**SEMA\_1**

**1645**

**766**

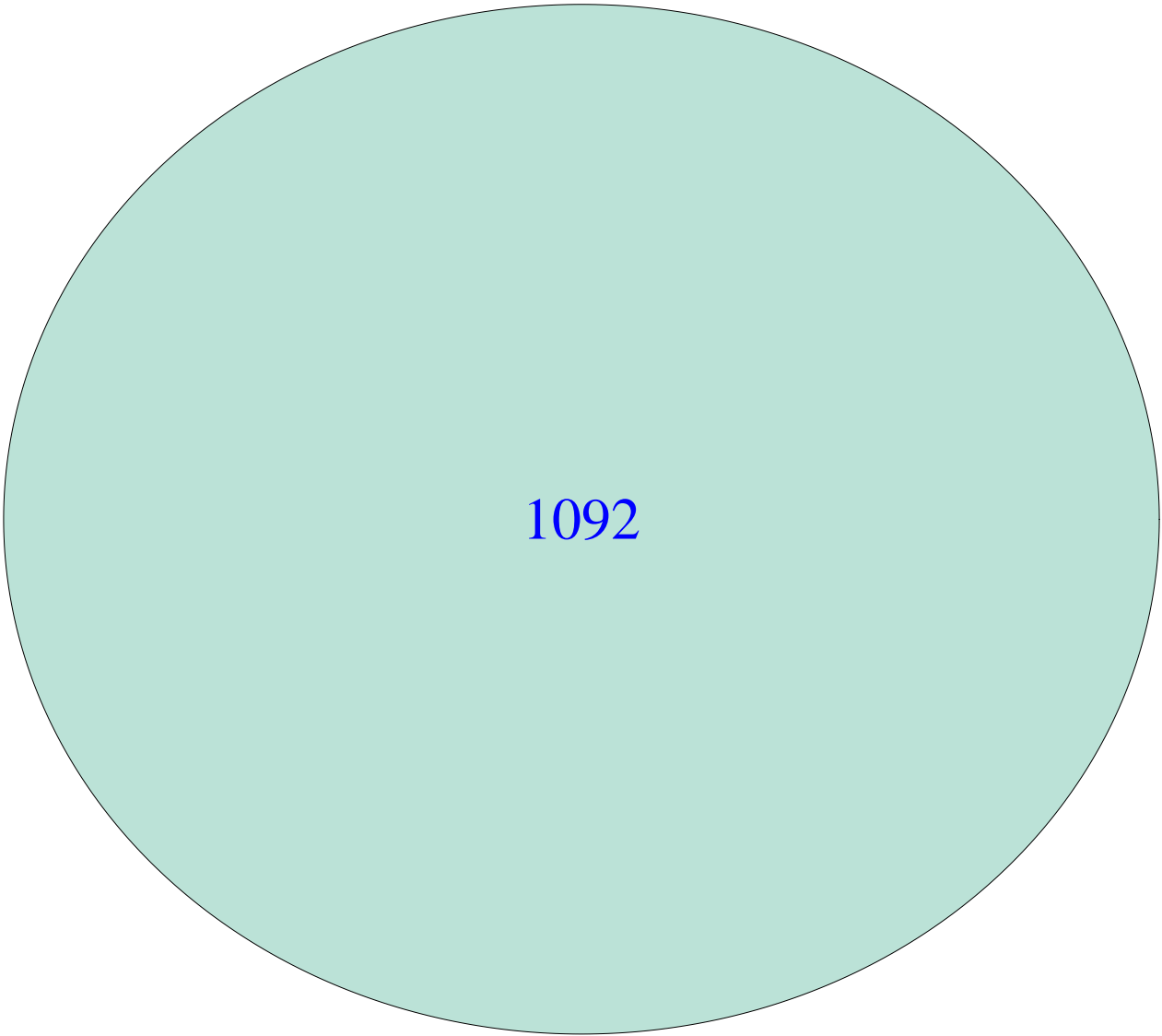
**2411**

**R2 >= 0.8**

**R2 < 0.8**

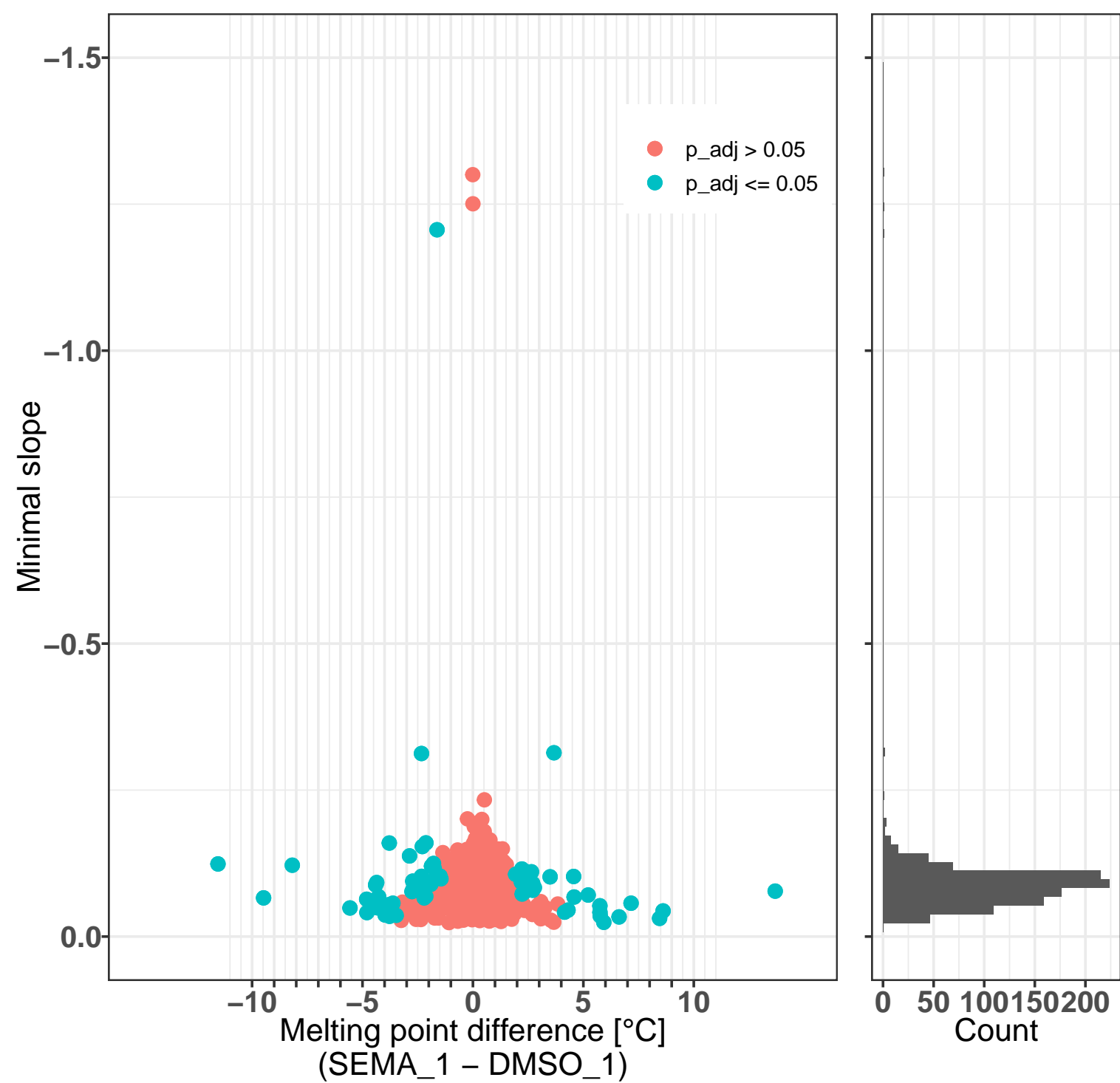
**Total**

SEMA\_1\_vs\_DMSO\_1



SEMA_1_vs_DMSO_1	1092	1319	2411
------------------	------	------	------

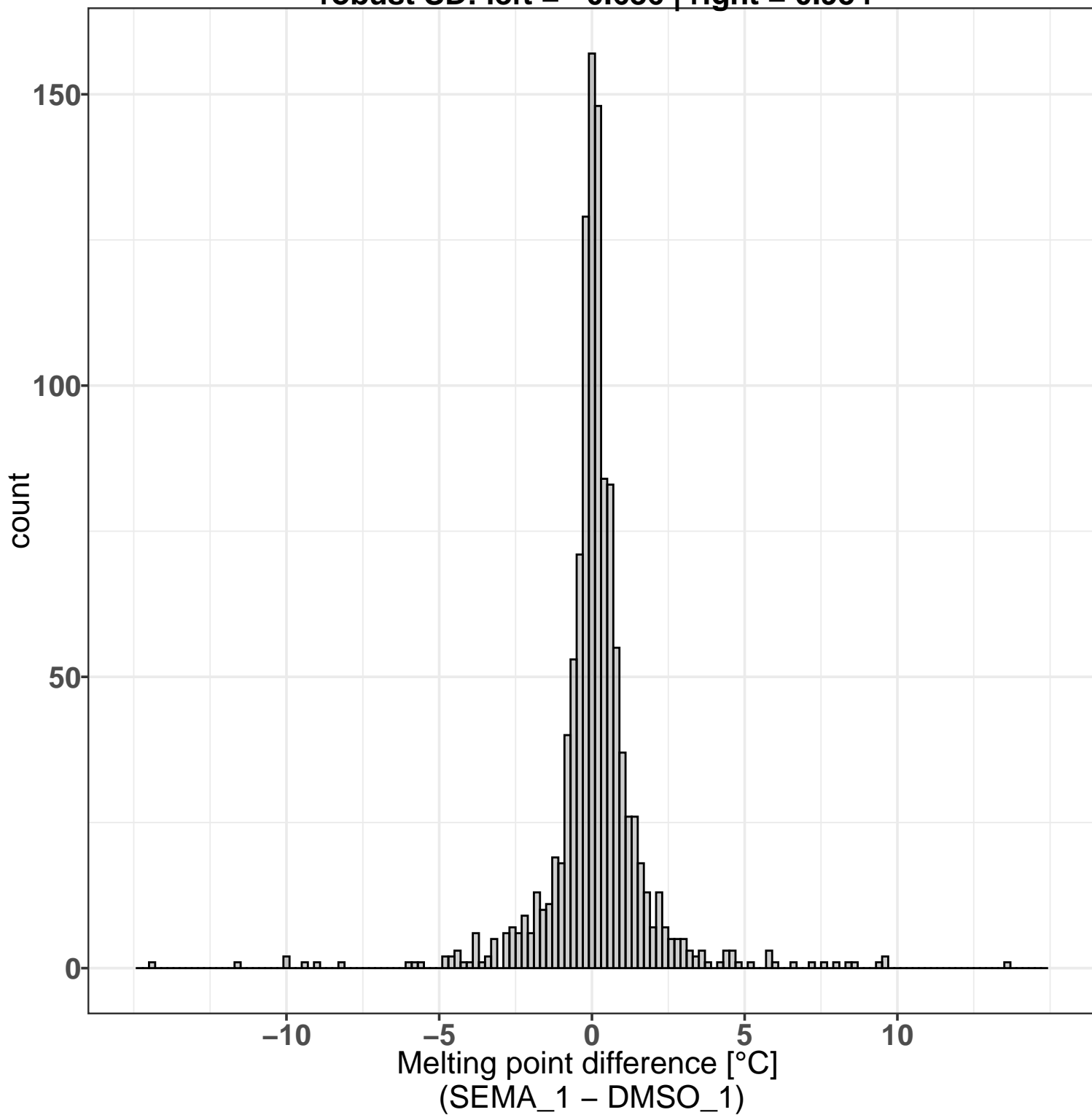
passed_filter	filtered_out	Total
---------------	--------------	-------



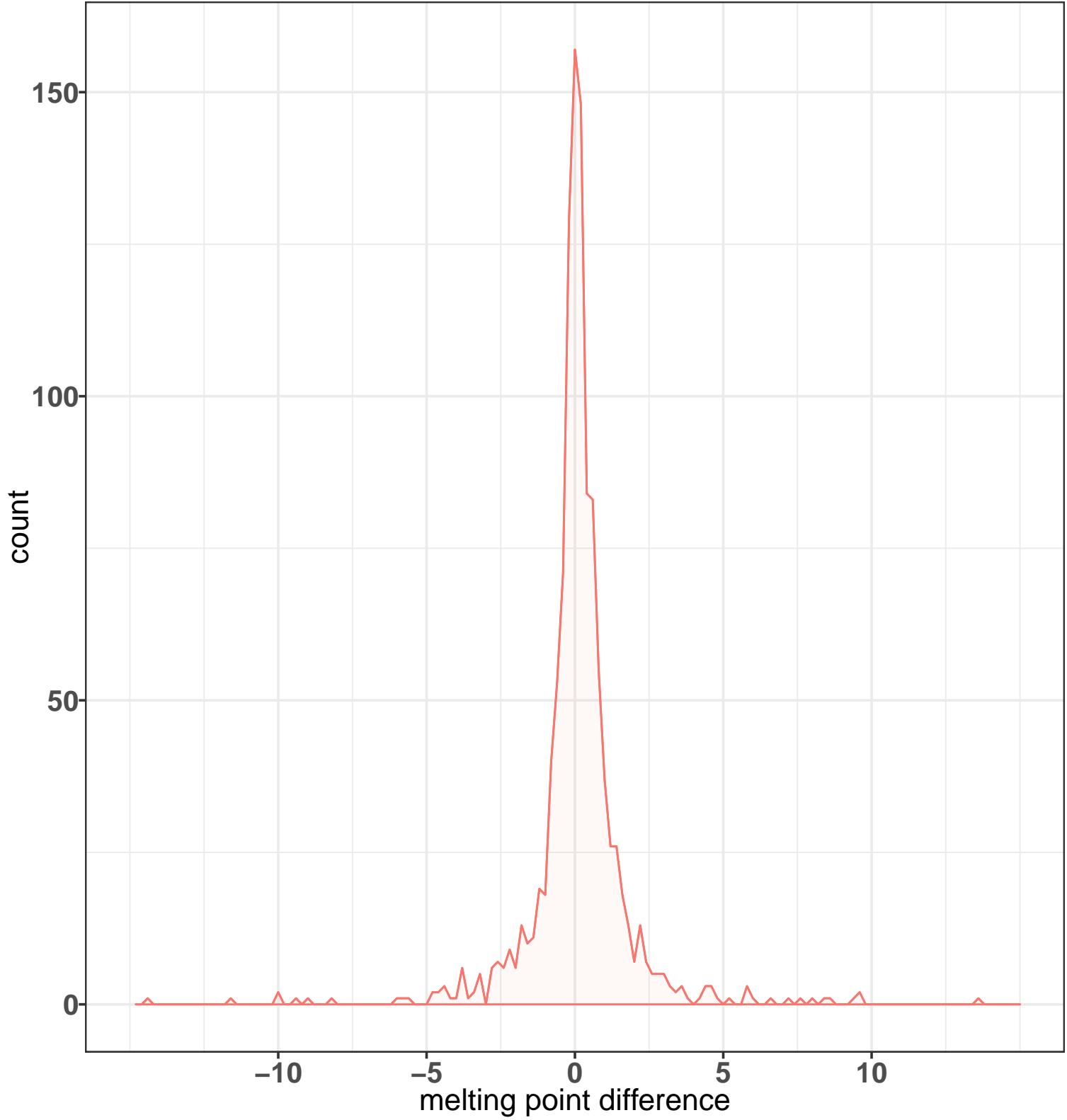
n = 1077

**SEMA\_1 vs. DMSO\_1**

median = 0.082 ,  
robust SD: left = -0.686 | right = 0.954



n = 1371 , R\_sq >= 0.8



comparison  SEMA\_1 - DMSO\_1