Supporting Information

Quantitative Characterization of the Neuropeptide Level Changes in Dorsal Horn and Dorsal Root Ganglia Regions of the Murine Itch Models

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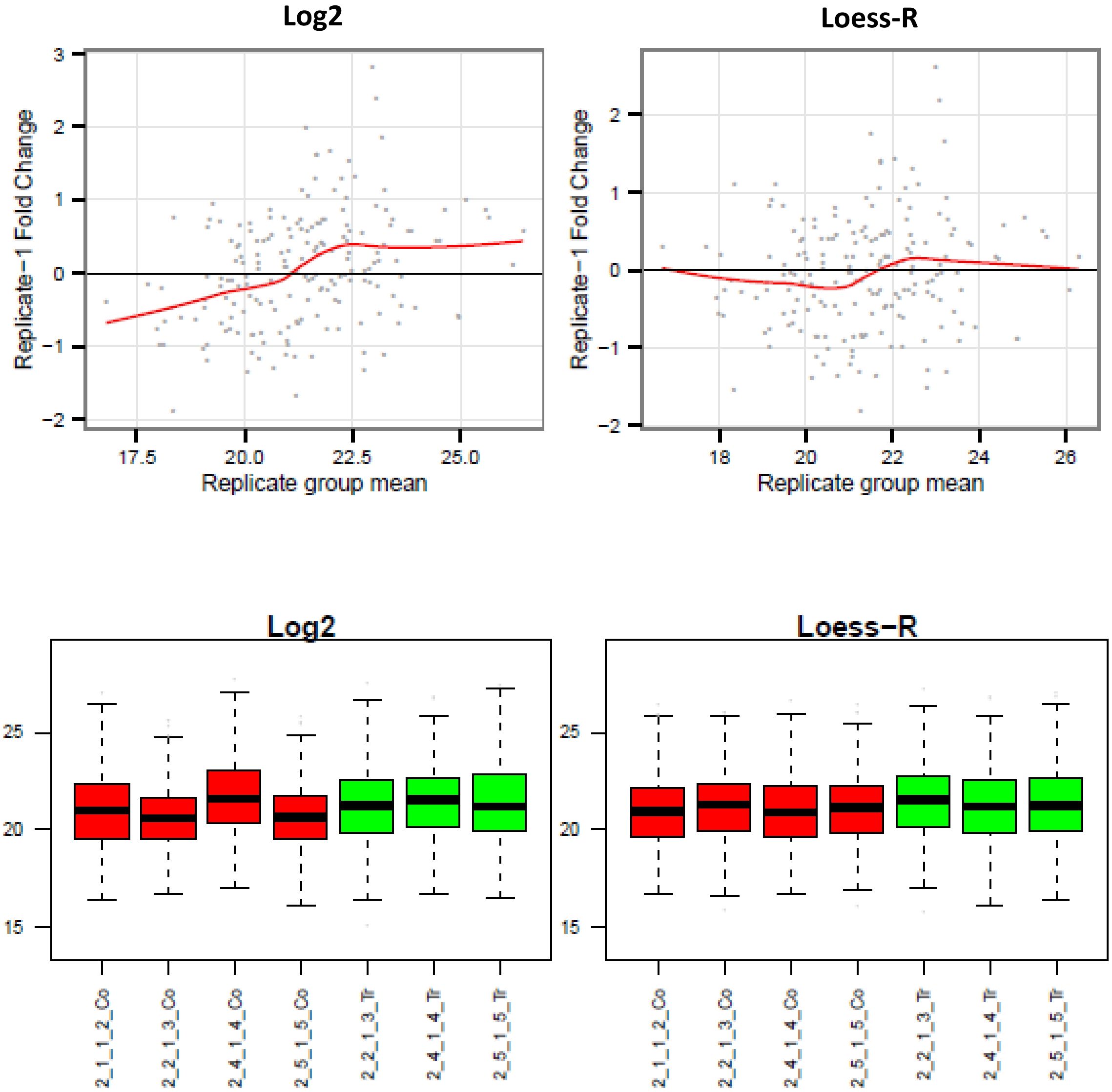
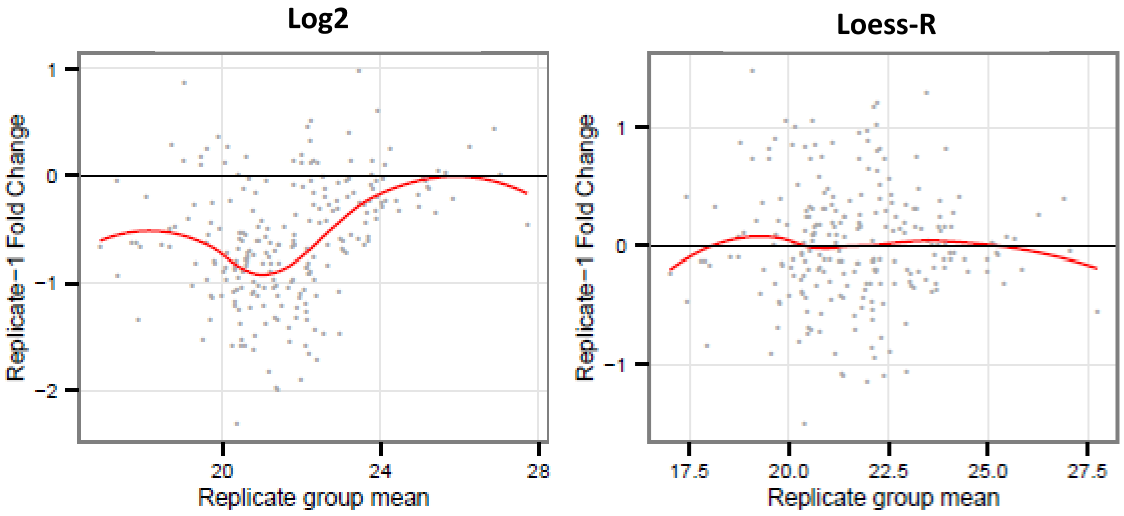
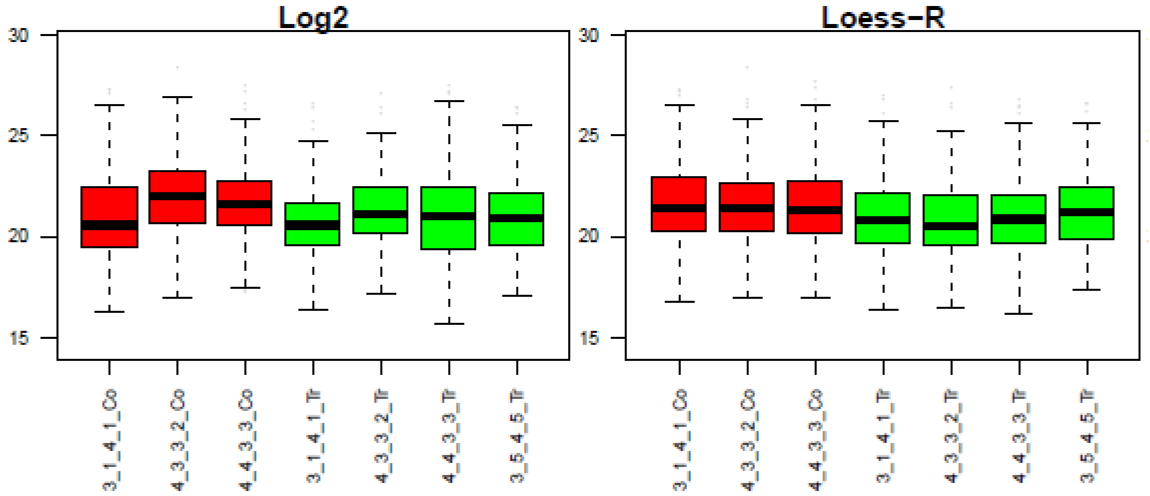
A. DRG AEW

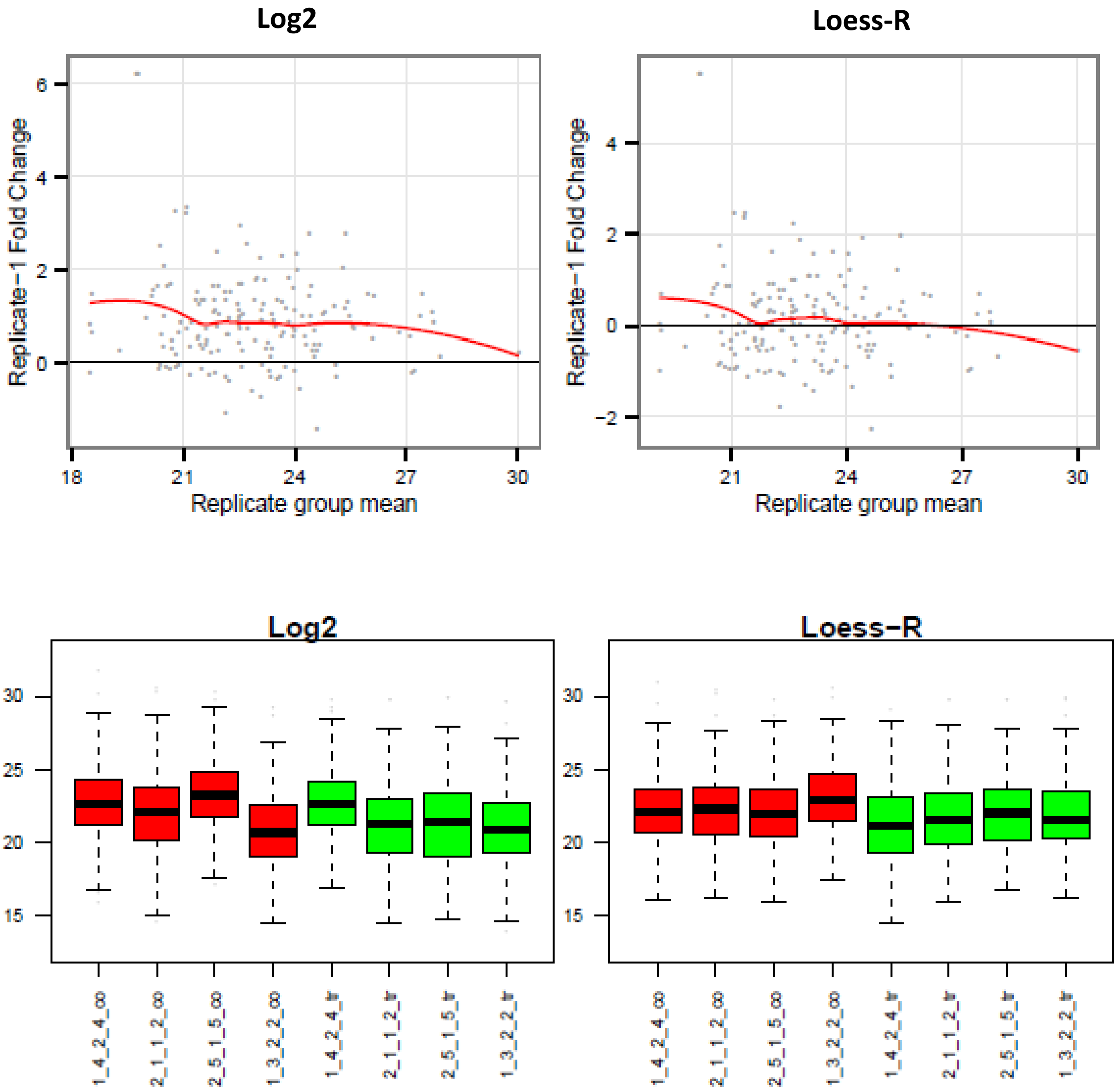

Log2
Loess-R
Replicate−1 Fold Change
3
2
1
0
−1
−2
17.5
20.0
22.5
25.0
Replicate group mean
18
20
22
24
26
Replicate group mean
Log2
Loess−R
25
20
15
2_1_1_2_Co
2_2_1_3_Co
2_4_1_4_Co
2_5_1_5_Co
2_2_1_3_Tr
2_4_1_4_Tr
2_5_1_5_Tr

B. DRG MC903


Log2
Replicate−1 Fold Change
1
0
−1
−2
20
24
28
Replicate group mean
Loess-R
Replicate−1 Fold Change
1
0
−1
17.5
20.0
22.5
25.0
27.5
Replicate group mean


Log2
30
25
20
15
3_1_4_1_Co
4_3_3_2_Co
4_4_3_3_Co
3_1_4_1_Tr
4_3_3_2_Tr
4_4_3_3_Tr
3_5_4_5_Tr
Loess−R
30
25
20
15
3_1_4_1_Co
4_3_3_2_Co
4_4_3_3_Co
3_1_4_1_Tr
4_3_3_2_Tr
4_4_3_3_Tr
3_5_4_5_Tr

C. DH AEW


Log2
Loess-R
Replicate−1 Fold Change
6
4
2
0
18
21
24
27
30
Replicate group mean
Replicate−1 Fold Change
4
2
0
−2
21
24
27
30
Replicate group mean
Log2
Loess−R
30
25
20
15
1_4_2_4_co
2_1_1_2_co
2_5_1_5_co
1_3_2_2_co
1_4_2_4_tr
2_1_1_2_tr
2_5_1_5_tr
1_3_2_2_tr
30
25
20
15
1_4_2_4_co
2_1_1_2_co
2_5_1_5_co
1_3_2_2_co
1_4_2_4_tr
2_1_1_2_tr
2_5_1_5_tr
1_3_2_2_tr

D. DH MC903

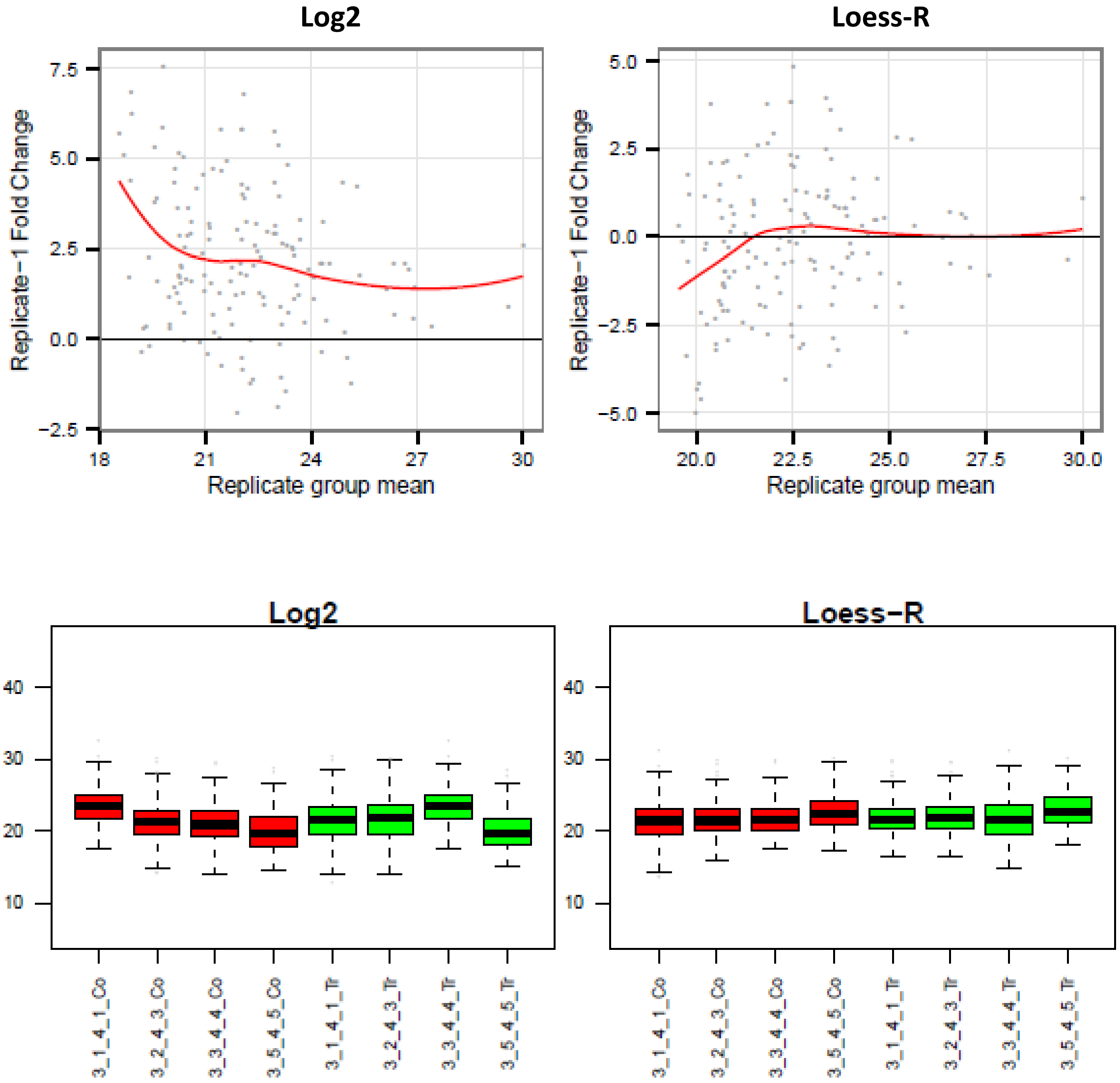


Figure S1. A–D. Fold-change (M) vs. average (A) plots for the quantified peptides and box plots corresponding to all quantified peptides before and after normalization. **Top rows:** MA plots where the y-axis represents the fold change (M) and the x-axis represents the group average (A). These plots illustrate the change introduced due to normalization via LOESS compared to un-normalized (Log2) peptide peak areas. Although each row depicts only 1 replicate, the two plots are representative of the whole sample. **Bottom rows:** Box plots that depict the first quartile, median, third quartile, and the interquartile range of the peptide quantitation data before and after normalization for all the replicates.

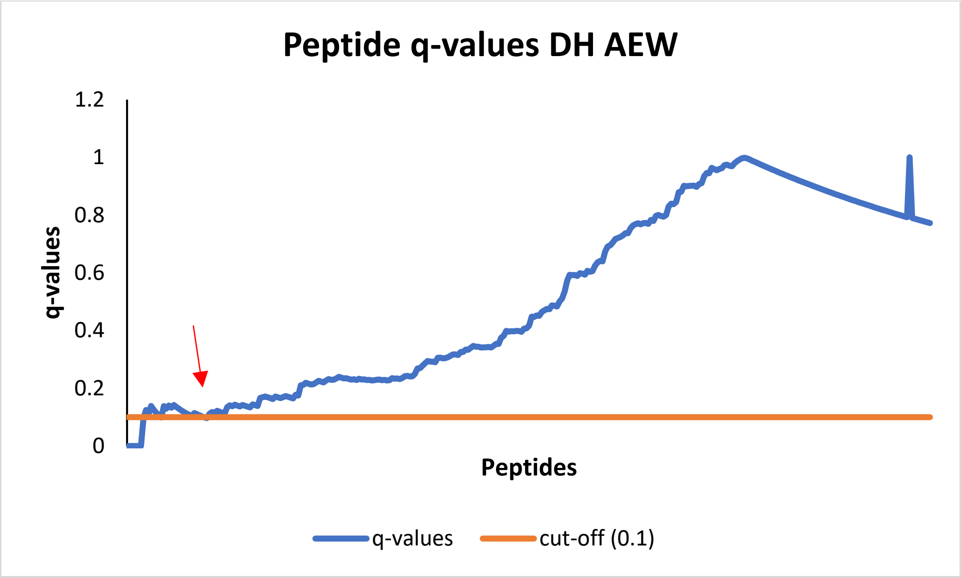


Figure S2. Due to the non-monotonic increase of q-values, we considered all of the peptides that fall under the farthest occurrence of q≤0.1 (i.e., to the left of the red arrow).