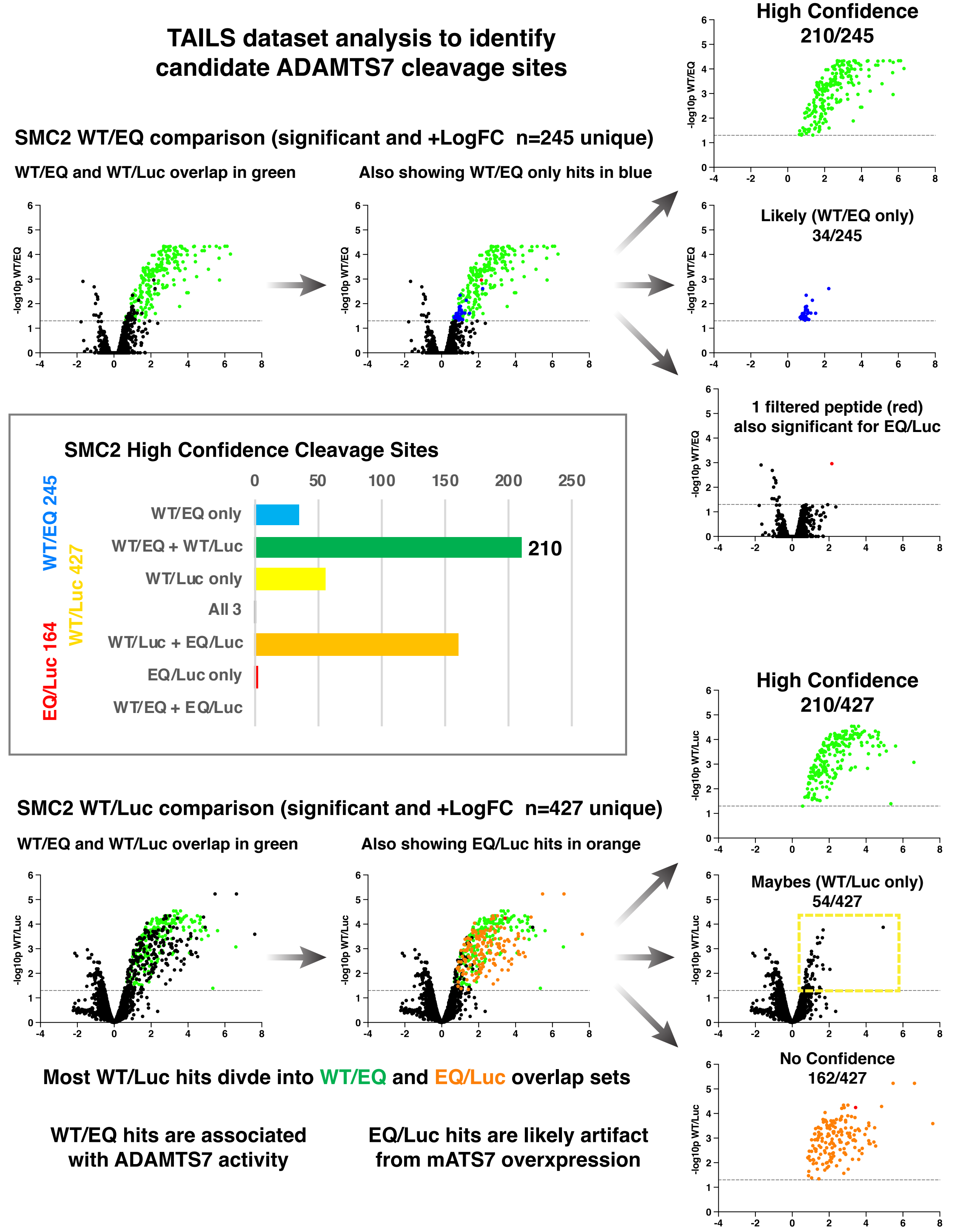
Figure S6



TAILS dataset analysis to identify candidate ADAMTS7 cleavage sites

SMC2 WT/EQ comparison (significant and +LogFC n=245 unique)

WT/EQ and WT/Luc overlap in green

Also showing WT/EQ only hits in blue

High Confidence 210/245

Likely (WT/EQ only) 34/245

1 filtered peptide (red) also significant for EQ/Luc

SMC2 High Confidence Cleavage Sites

SMC2 WT/Luc comparison (significant and +LogFC n=427 unique)

WT/EQ and WT/Luc overlap in green

Also showing EQ/Luc hits in orange

High Confidence 210/427

Maybes (WT/Luc only) 54/427

No Confidence 162/427

Most WT/Luc hits divde into WT/EQ and EQ/Luc overlap sets

WT/EQ hits are associated with ADAMTS7 activity

EQ/Luc hits are likely artifact from mATS7 overexpression

Figure S6 Candidate assessment from SMC2 WT/EQ and SMC2 WT/Luc TAILS comparisons after removal of auto-cleavage sites. Detailed breakdown of candidates from volcano plots shown in Figure 4B to illustrate the 210 high confidence substrate cleavage sites and remaining unqualified regulated peptides. Panel from Figure 5C is included to show the distribution of SMC2 regulated peptides. A majority of WT/EQ regulated peptides met all the criteria for high confidence substrate cleavage sites, while roughly half of the WT/Luc regulated peptides were categorized as high confidence. In the case of the SMC2 TAILS dataset, the WT/EQ only average logFC was 1.0 versus the WT/EQ high confidence average of logFC of 2.5. While a predominance of high confidence hits were present in the WT/EQ regulated peptides, the WT/Luc regulated peptides contained a mixture of overlap with the activity associated WT/EQ comparison and the EQ/Luc regulated peptides likely associated with artifact from ADAMTS7 overexpression. For simplicity numbers reflect unique substrate cleavage sites, however the volcano plots contain all regulated peptides including multiple identifications for ADAM9_69 and COL1A2_113 within the SMC2 TAILS dataset.