



**FIGURE 5** Phenotypic analysis of Arabidopsis WT, *s3h* knockout mutants and *s3h* transgenic plants expressing *ZmS5H* (2). a) Arabidopsis WT, *s3h* mutant and *s3h* transgenic plant expressing *ZmS5H* (T3.10 line) at 35 DAG. b) Altered duration of senescence in leaves of *s3h* mutants compared with that of WT and *s3h ZmS5H* transgenic plants. Values indicate the time period (days) it takes for senescence to progress from the first visible yellowing at the leaf tip to the leaf petiole in leaf #5 used as a model. c and d) Chlorophyll a (c) and b (d) content in leaf #5 from WT, *s3h* mutants and *s3h* transgenic plants expressing *ZmS5H*. Results represent the average of at least 6 biological replicates from one experiment  $\pm$  S.E. Three independent experiments were performed with similar results. e and f) Expression analysis of *SAG13* (e) and *NAP* (f) by RT-qPCR. Transcript levels were analyzed in rosette leaves at 35 DAG from WT, *s3h* and *s3h ZmS5H* transgenic plants. Each reaction was normalized using the cycle threshold values corresponding to the *ACTIN2* mRNA. Data are represented as the means  $\pm$  S.E. of 3 biological replicates from three different experiments. Different letters indicate statistically significant differences applying one-way ANOVA ( $P < 0.05$ ).