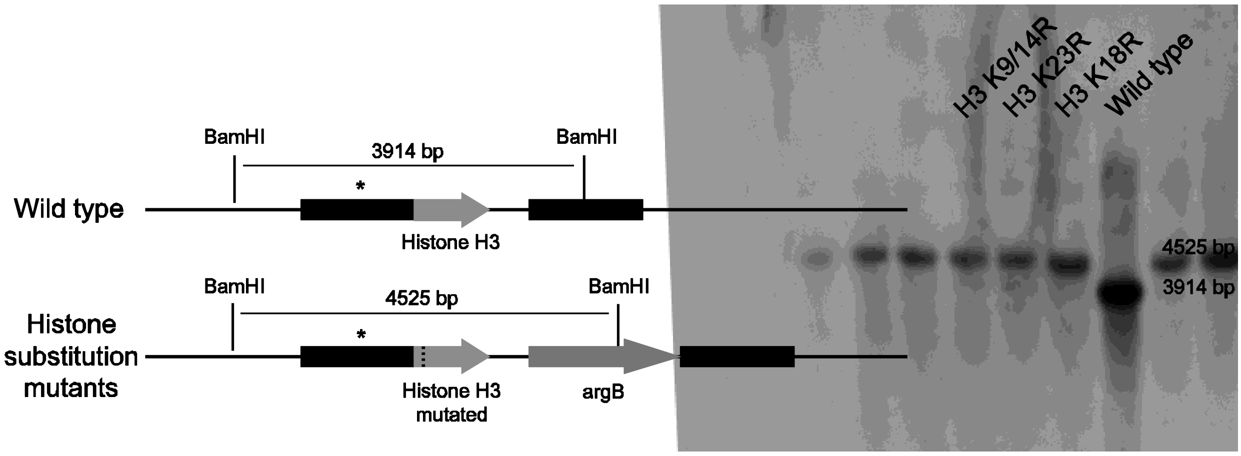
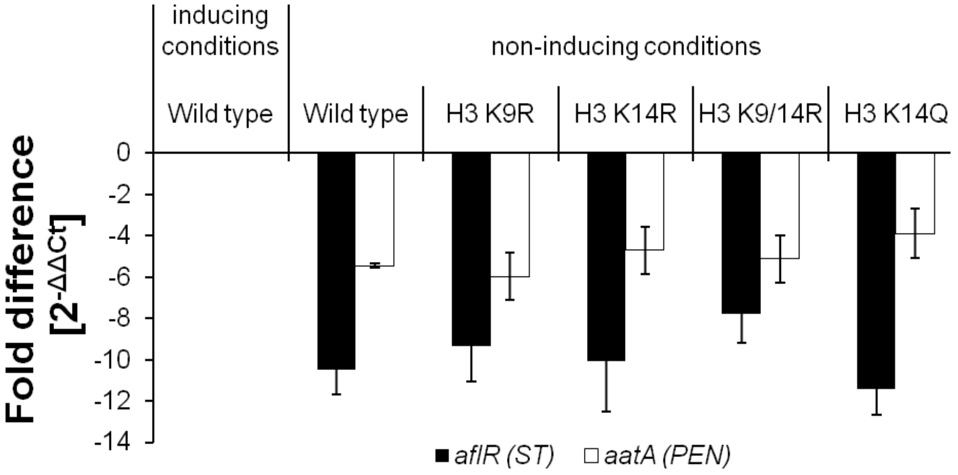
Supplementary Figure 1. Generation of strains of histone substitution strains. Schematic representation of genomic arrangements of Wild type and histone substitution strains. Arrows indicate genes, black boxes mark ~1,000-bp–long regions serving for homologous recombination. Restriction sites used for Southern blot analyses are indicated. As probes for Southern blot, the DNA regions marked by a black box with a star were used. Southern blot analyses show the expected restriction patterns for Wild type and histone substitution strains (not all are shown).



Supplementary Figure 1. Generation of histone substitution strains.

Supplementary Figure 2. Expression of penicillin and sterigmatocystin biosynthesis genes of histone H3 mutant strains under non-inducing conditions. Wild type and histone mutant strains were grown in AMM and mycelia were harvested after 3 h of incubation. As a control, the wild-type strain was grown for 36 h in AMM media for comparison under inducing conditions. Given are fold difference of the mRNA steady-state level of penicillin and sterigmatocystin biosynthesis genes *aatA* and *aflR*. The *β*-actin gene of *A. nidulans* was used as an internal standard.



Supplementary Figure 2. Penicillin and sterigmatocystin biosynthesis cluster genes mRNA steady state level in histone H3 mutant strains under non-inducing conditions.