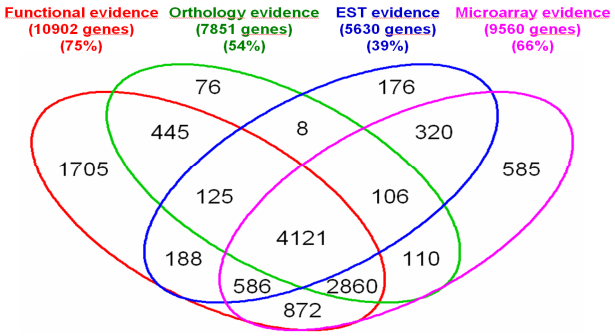
Figure S3

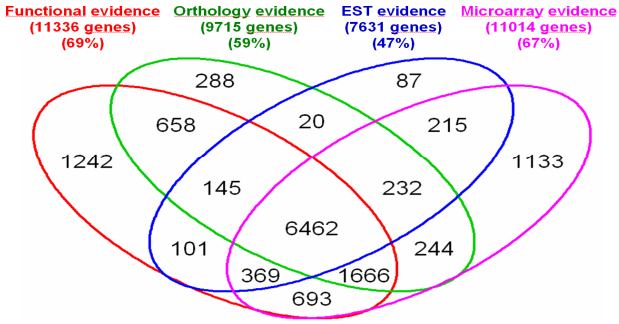
Evidence for accuracy of gene prediction in *S. sclerotiorum* (A), *B. cinerea* T4 (B) and *B. cinerea* B05.10 (C).

Four types of evidence were combined: (i) Functional annotation (at least one domain/motif), (ii) Orthology between *S. sclerotiorum*, *B. cinerea* and other fungi, (iii) EST support, (iv) Nimblegen Microarrays support.

A. Evidence for the 14522 *S. sclerotiorum* predicted genes:



B. Evidence for the 16360 *B. cinerea* T4 predicted genes :



C. Evidence for the 16448 *B. cinerea* B05.10 predicted genes :