Author: Kwon, Min Jin
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Supplemental material

The supplemental material of this thesis is comprises the following and available via each website:

Chapter 2: http://onlinelibrary.wiley.com/doi/10.1111/j.1365-2958.2010.07524.x/suppinfo

Fig. S1. Phylogenetic tree of fungal Rho GTPases.

Fig. S2. Deletion of *rhoD* causes loss of septation in *A. niger*.

Fig. S3. Phenotypes of wt, individual *rho* deletion and complemented strains.

Fig. S4. Phenotypes of wild-type, Δ*noxR* and Δ*noxA*.

Movie S1. Time-lapse movie of *A. niger* expressing eGFP::RacA.

Chapter 3:
http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0068946#s6

Table S1. Complete transcriptome data containing RMA expression values (log2 scale), mean expression values, p-values, q-values and fold changes

Table S2. Subset of the transcriptome data containing up-down-regulated gene sets.

Table S3. ZIP archive file containing FetGOat enrichment results for the up- and down-regulated gene sets of all six comparisons.

Table S4. Subset of the transcriptome data for selected intersection of the Venn diagram.

Table S5. Primers used in this study.

Chapter 4: http://www.biomedcentral.com/1471-2164/13/701/additional

Additional file 1. Differentially expressed genes between B36 and N402 maltose-limited chemostat cultures.

Additional file 2. Network map based on GO-enrichment analysis using the differentially expressed, induced and repressed gene sets in B36/N402 chemostat cultures.

Additional file 3. Enriched-GO terms using the differentially expressed, induced and repressed gene sets in B36/N402 chemostat cultures.

Additional file 4. Four higher-order categories of enriched-GO terms using the induced gene set in B36/N402 chemostat cultures.

Additional file 5. Expression values of iron uptake genes.

Additional file 6. Expression values of protease genes.

Additional file 7. Enriched-GO terms from the comparison between B36/N402 *versus* maltose/xylose.

Additional file 8. Primers used in qPCR and RT PCR.

Chapter 5: http://mic.sgmjournals.org/content/160/Pt_2/316/suppl/DC1

Supplemental Fig. 1. Schematic representations of the wild-type locus and disruptant locus and Southern blot analysis of the *sncA* (A and B) and *secB* (C and D).

Supplemental Fig. 2. Localization of GFP-tubulin (Kwon et al., 2011) and SlaB-YFP (Kwon et al. 2013b) reporter strains after treatment with respectively benomyl (5 µg/ml) or latrunculin B (2 µg/ml).

Supplemental video 1. Time lapse of *A. niger* expressing GFP-SncA.