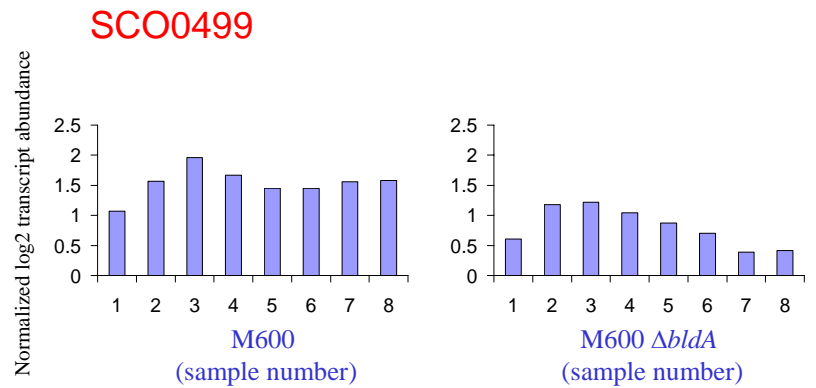
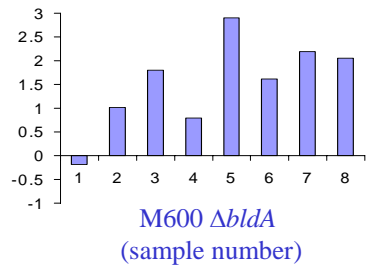
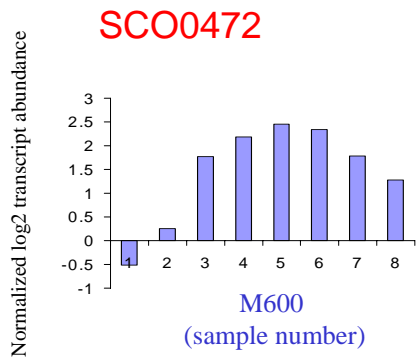
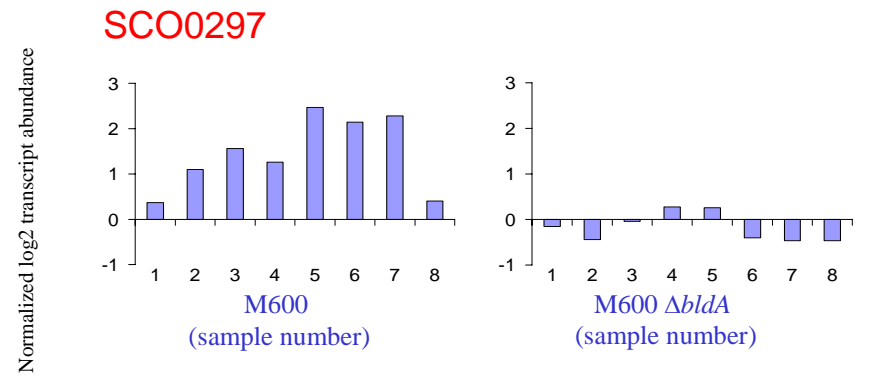
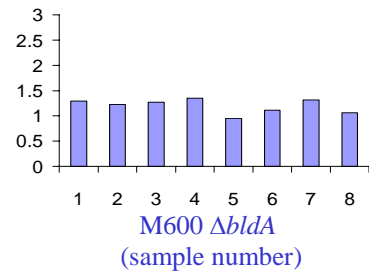
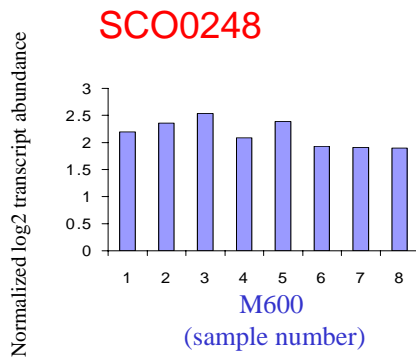
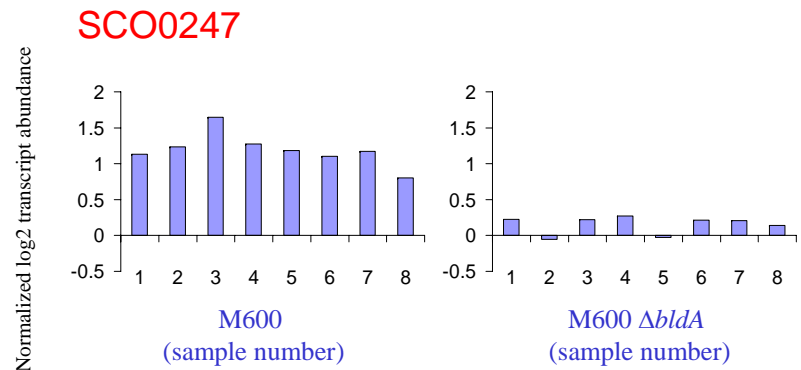
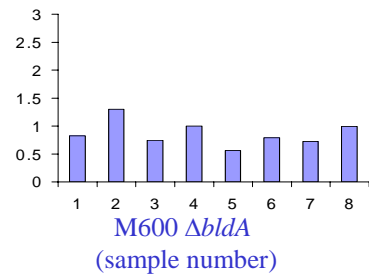
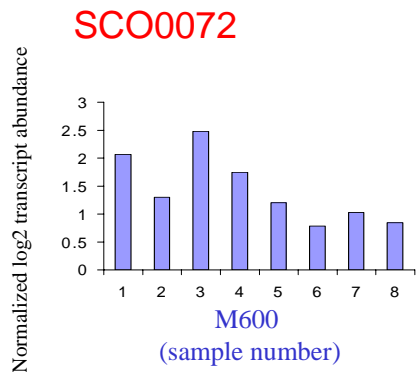
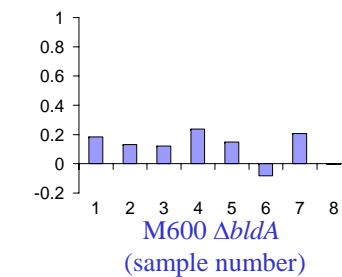
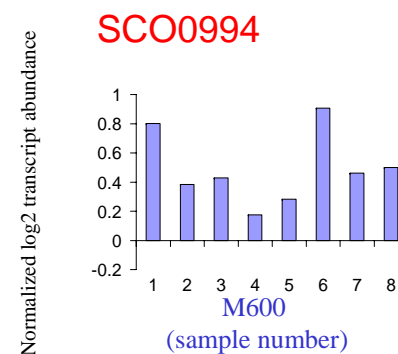
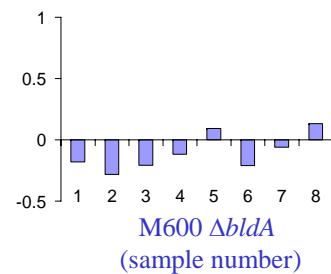
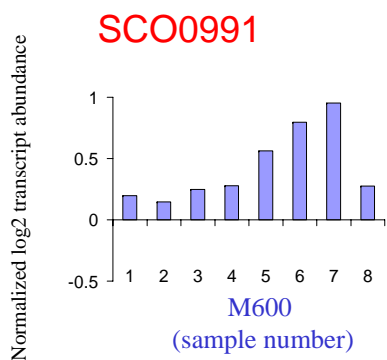
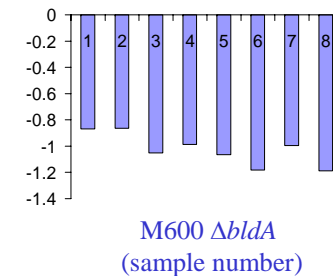
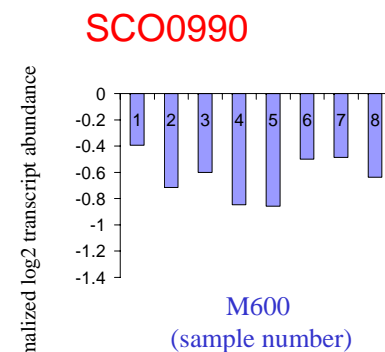
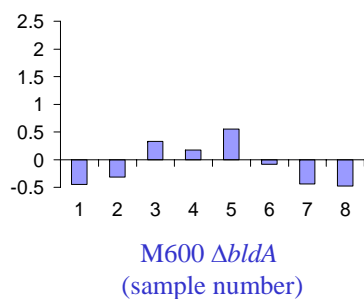
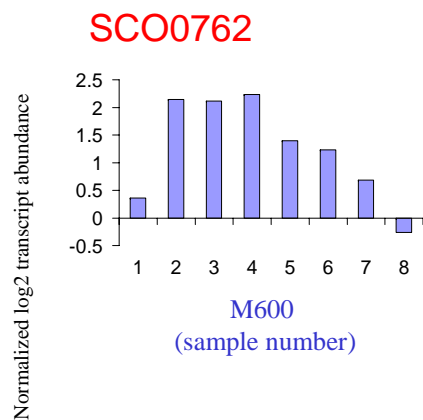
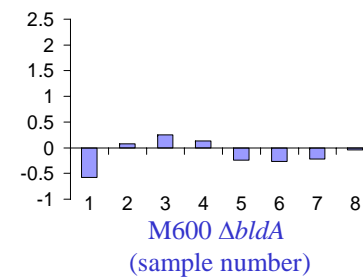
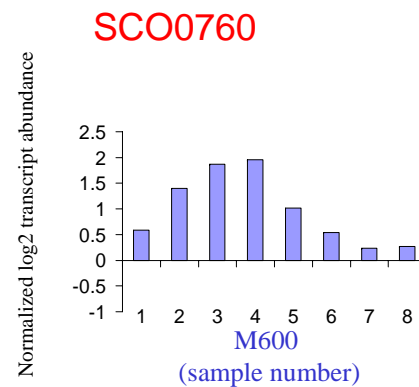
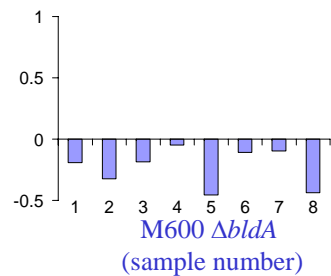
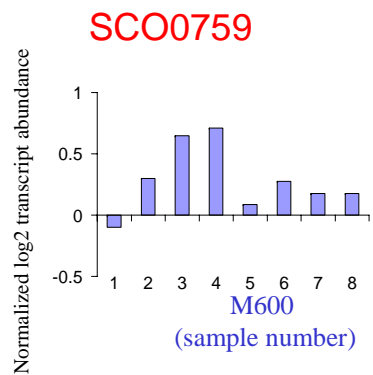


Additional file 1.

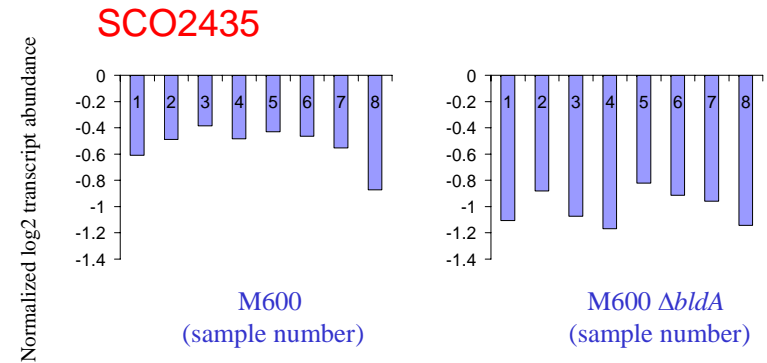
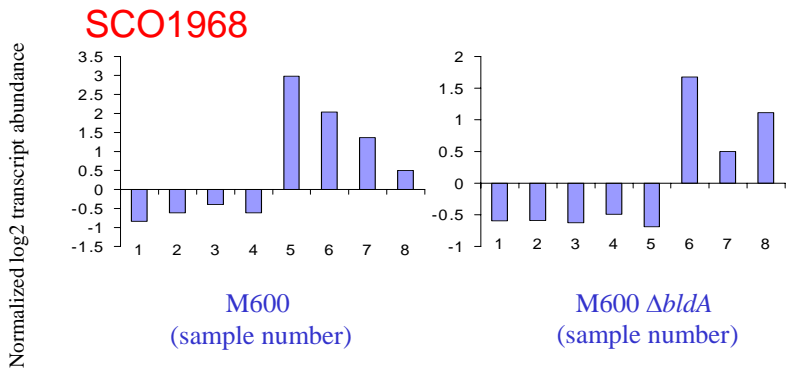
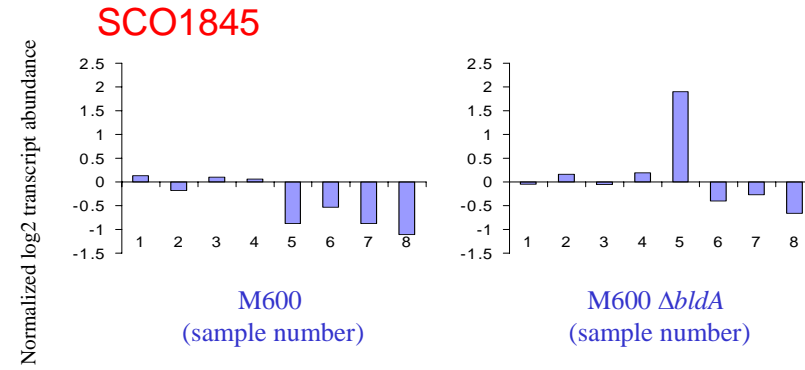
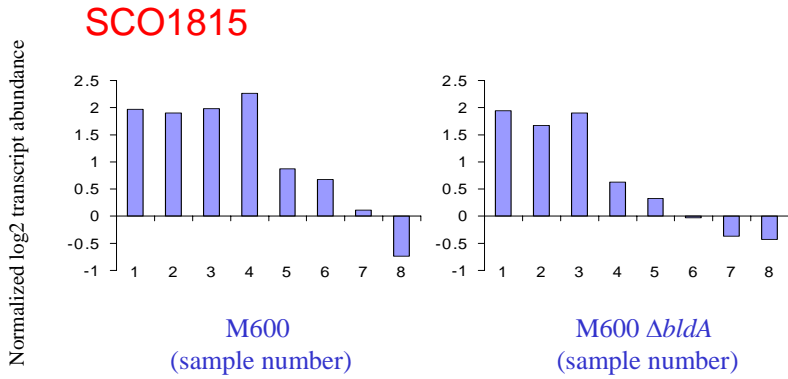
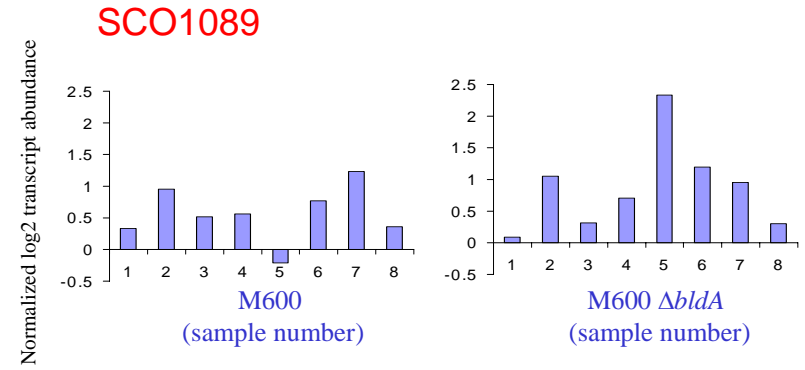
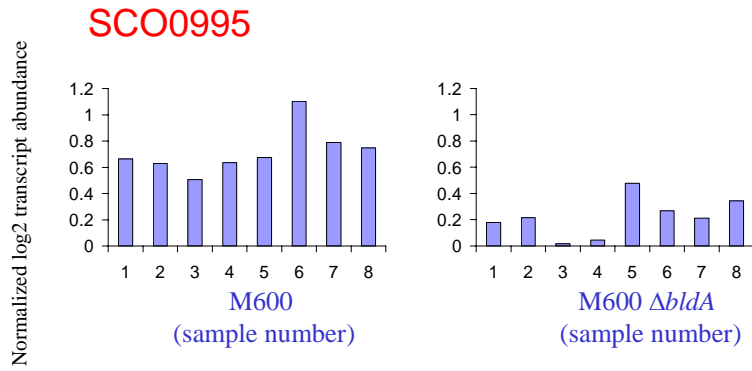
Transcript abundance profiles for all 74 genes identified as being differentially expressed between M600 and M600 $\Delta b/dA$ using DNA microarrays.



Profiles are the average of triplicate experiments

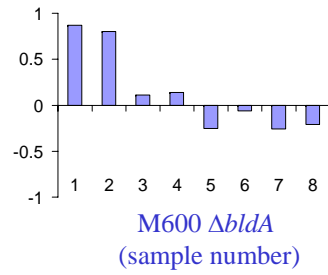
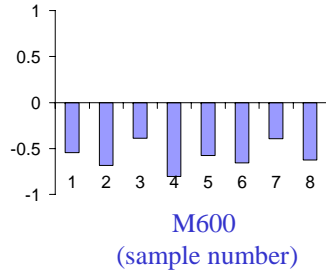


Profiles are the average of triplicate experiments

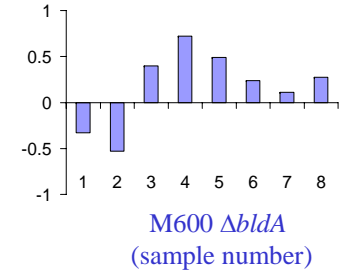
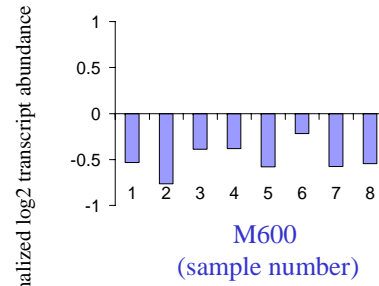


Profiles are the average of triplicate experiments

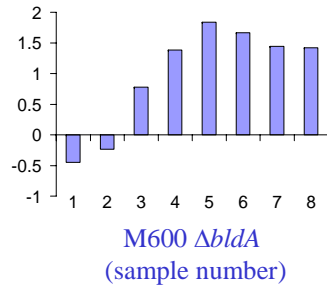
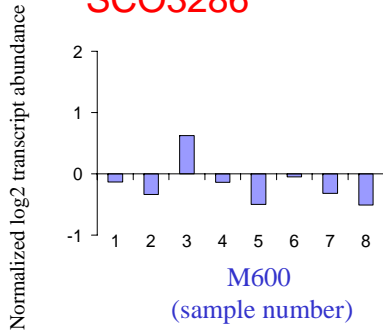
SCO3088



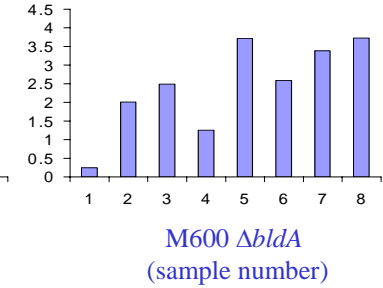
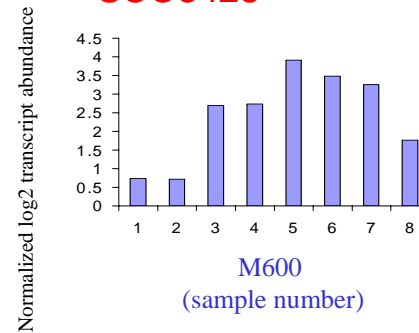
SCO3285



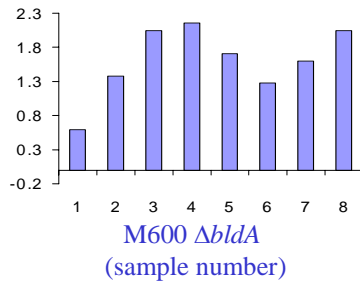
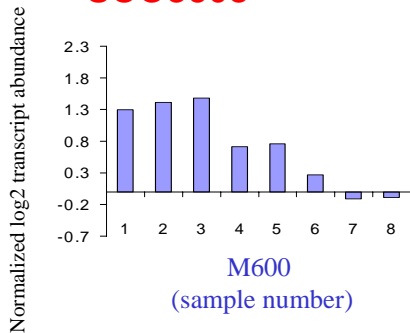
SCO3286



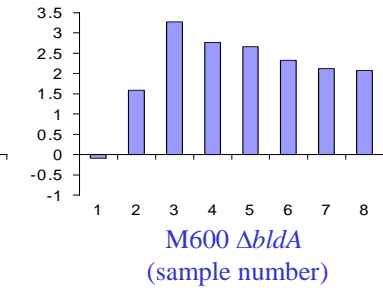
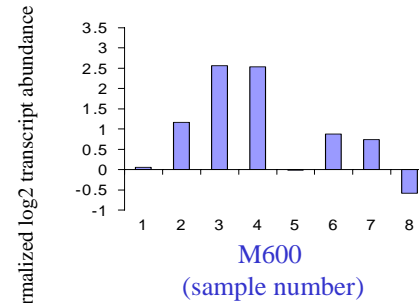
SCO3428



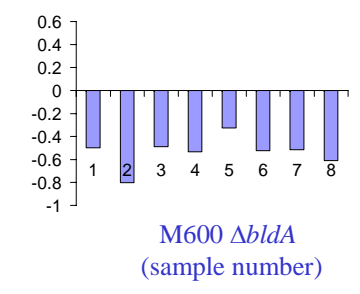
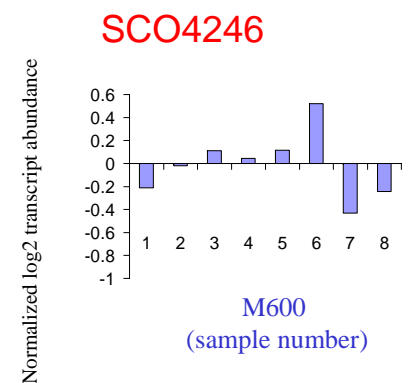
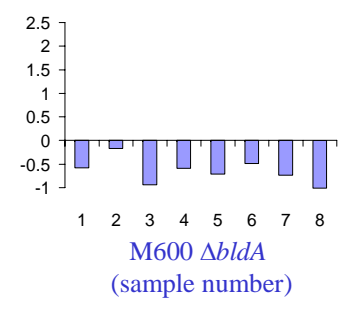
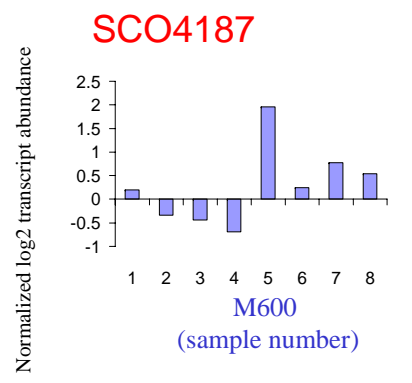
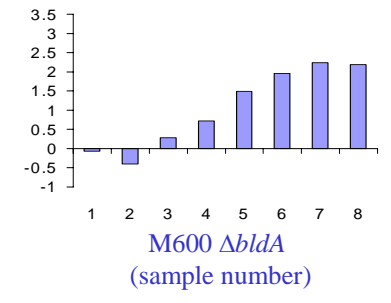
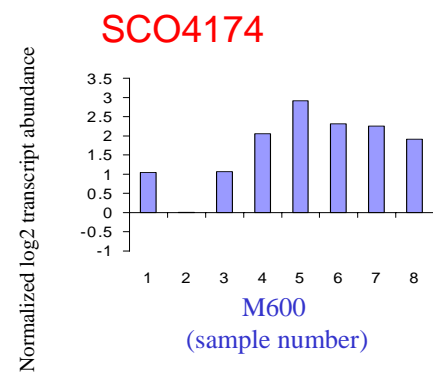
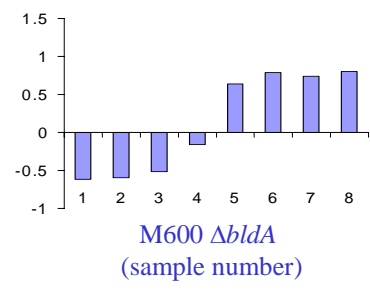
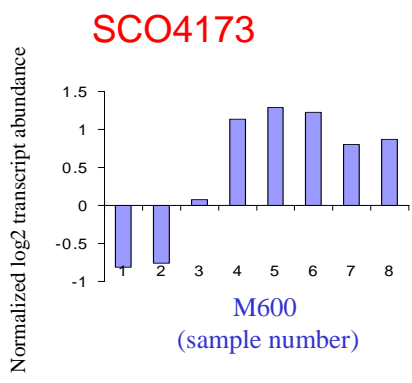
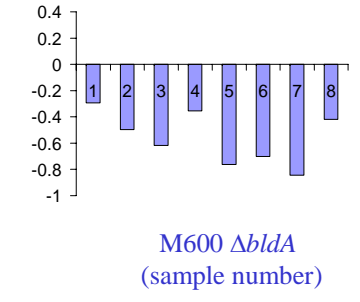
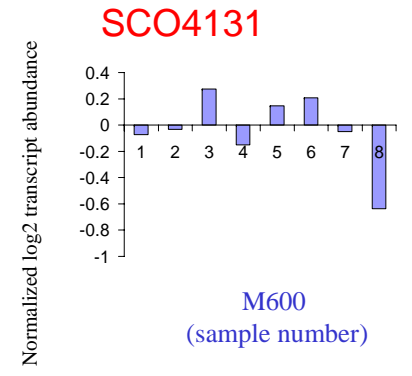
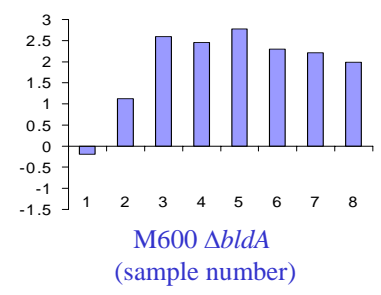
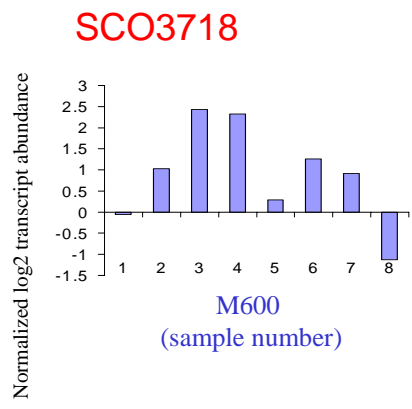
SCO3608



SCO3717



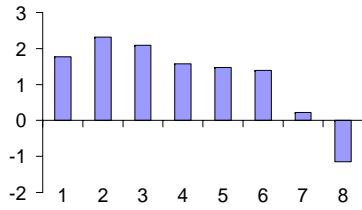
Profiles are the average of triplicate experiments



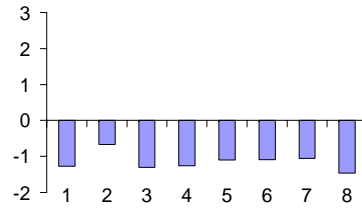
Profiles are the average of triplicate experiments

Normalized log₂ transcript abundance

SCO4252



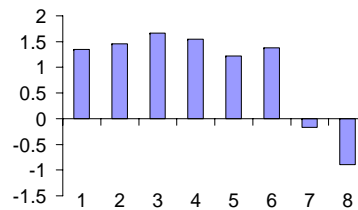
M600
(sample number)



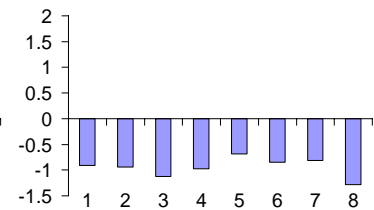
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO4253



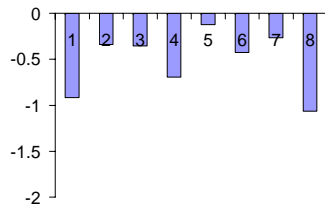
M600
(sample number)



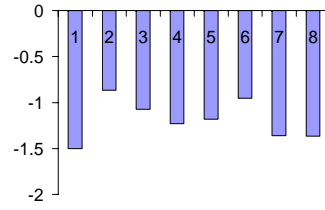
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO4256



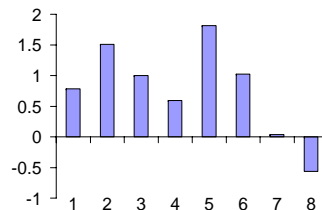
M600
(sample number)



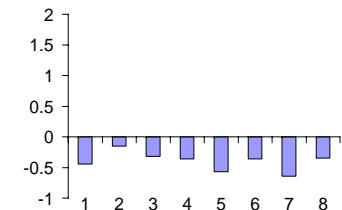
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO4262



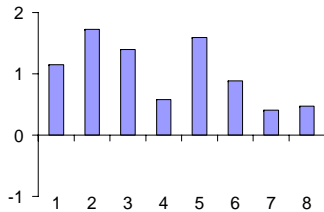
M600
(sample number)



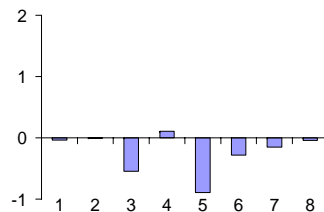
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO4295



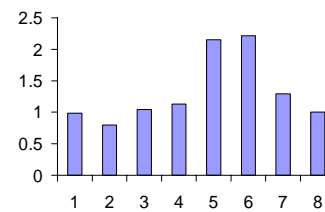
M600
(sample number)



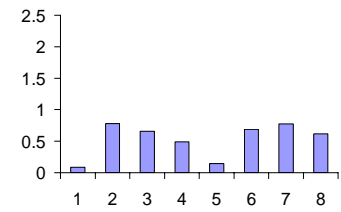
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO4442

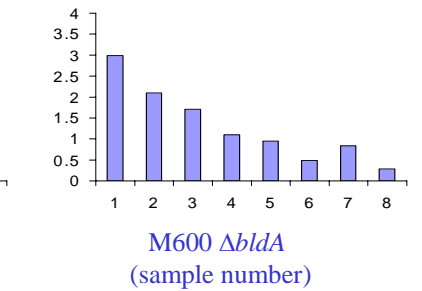
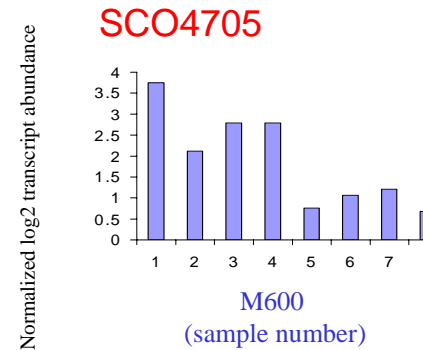
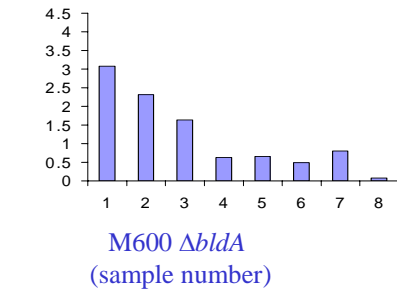
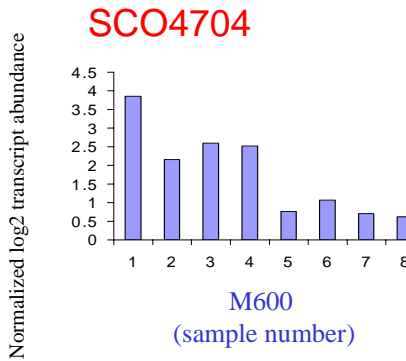
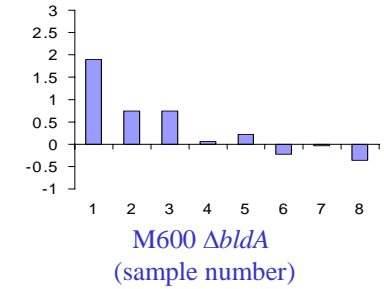
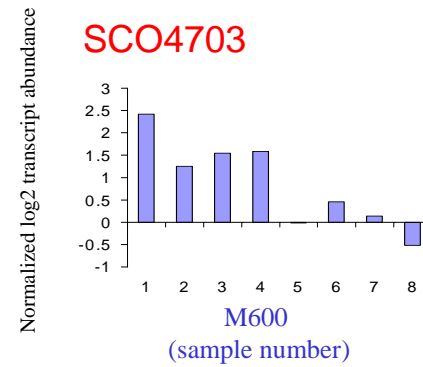
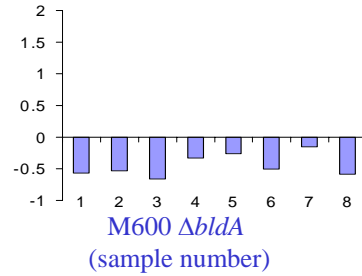
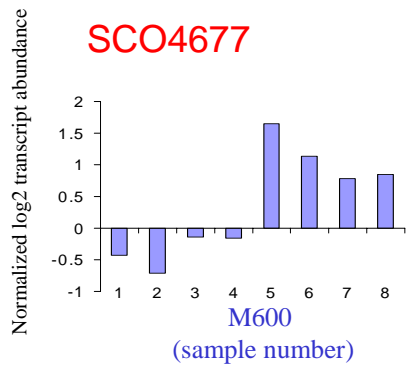
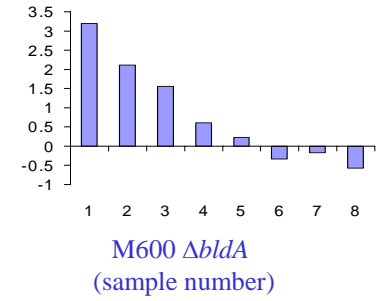
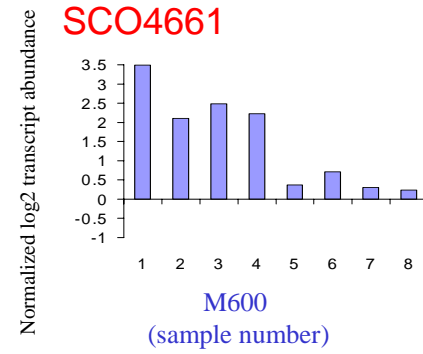
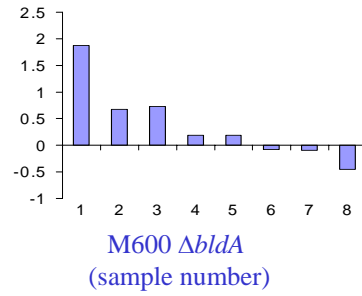
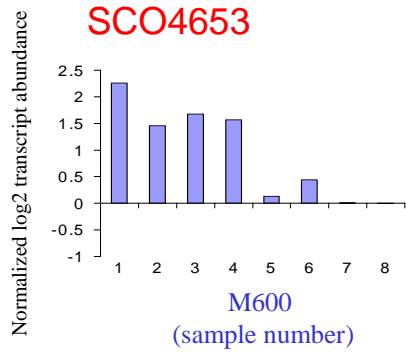


M600
(sample number)

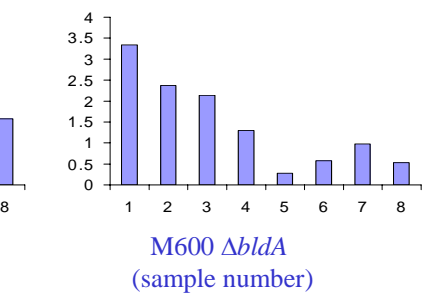
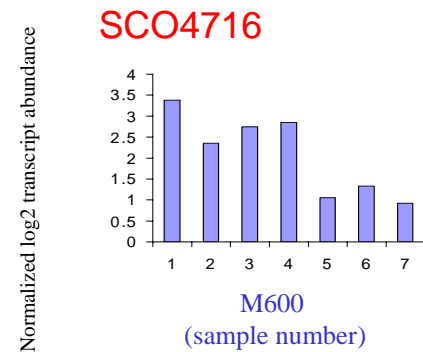
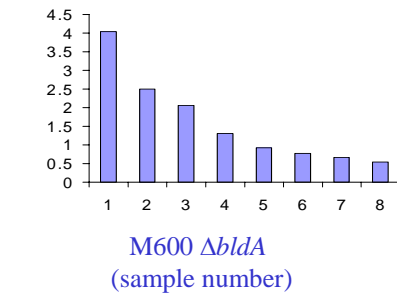
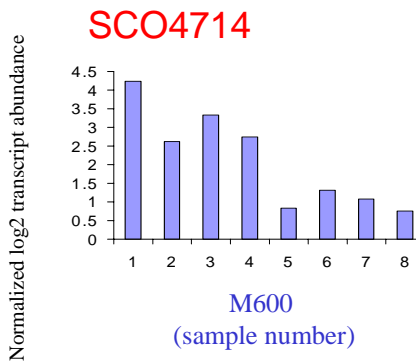
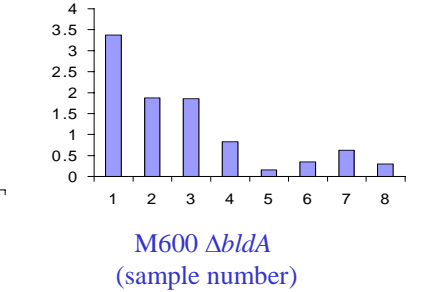
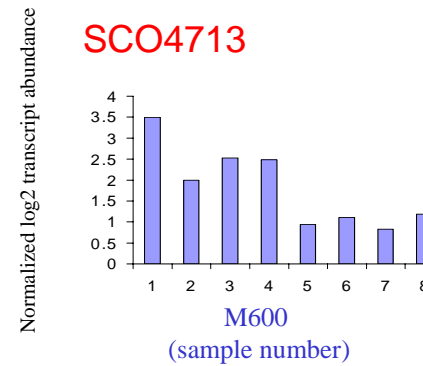
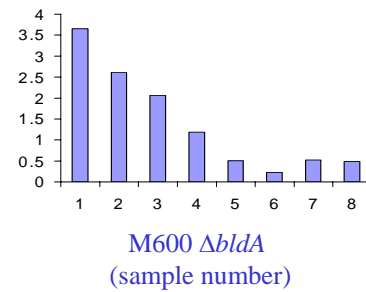
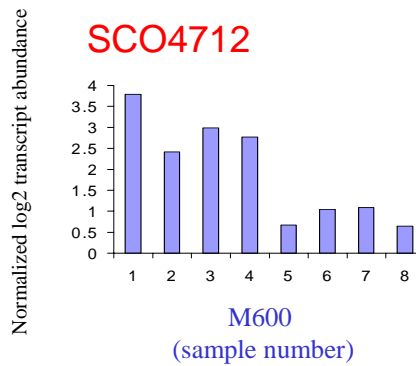
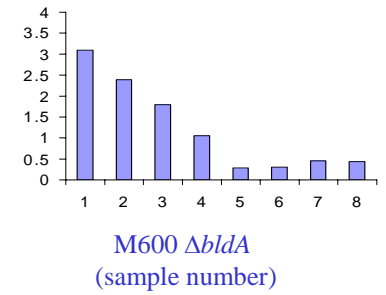
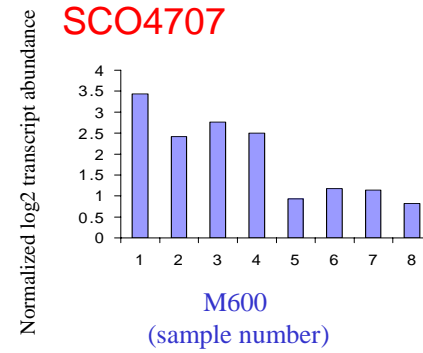
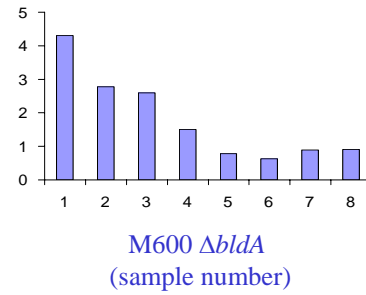
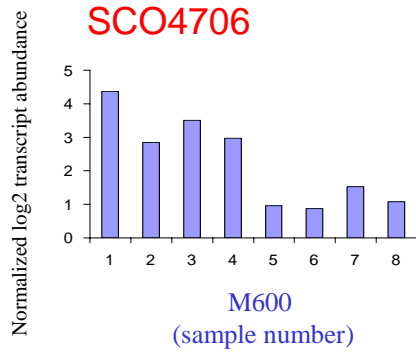


M600 $\Delta bldA$
(sample number)

Profiles are the average of triplicate experiments



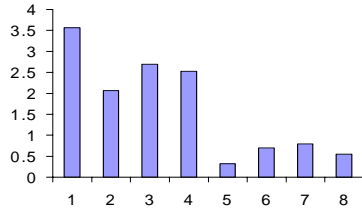
Profiles are the average of triplicate experiments



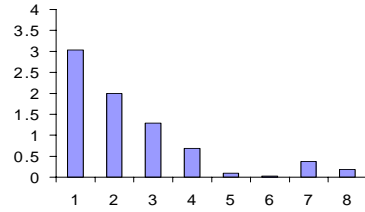
Profiles are the average of triplicate experiments

Normalized log₂ transcript abundance

SCO4717



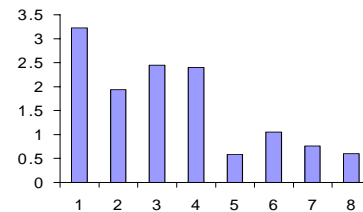
M600
(sample number)



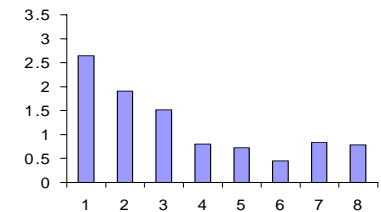
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO4718



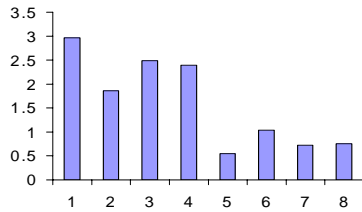
M600
(sample number)



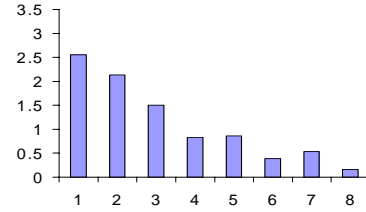
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO4719



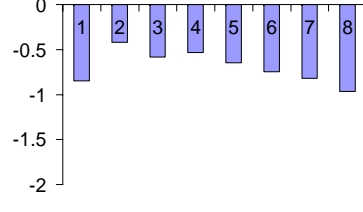
M600
(sample number)



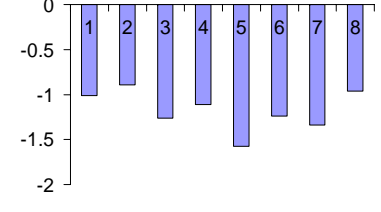
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO4994



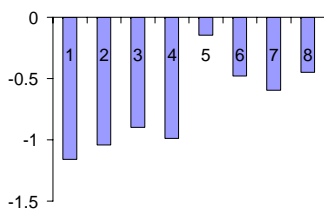
M600
(sample number)



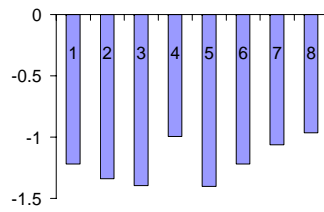
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO5013



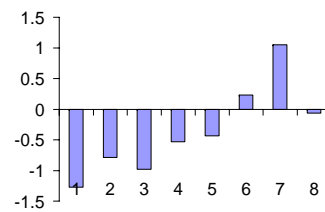
M600
(sample number)



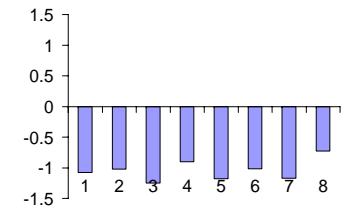
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO5073

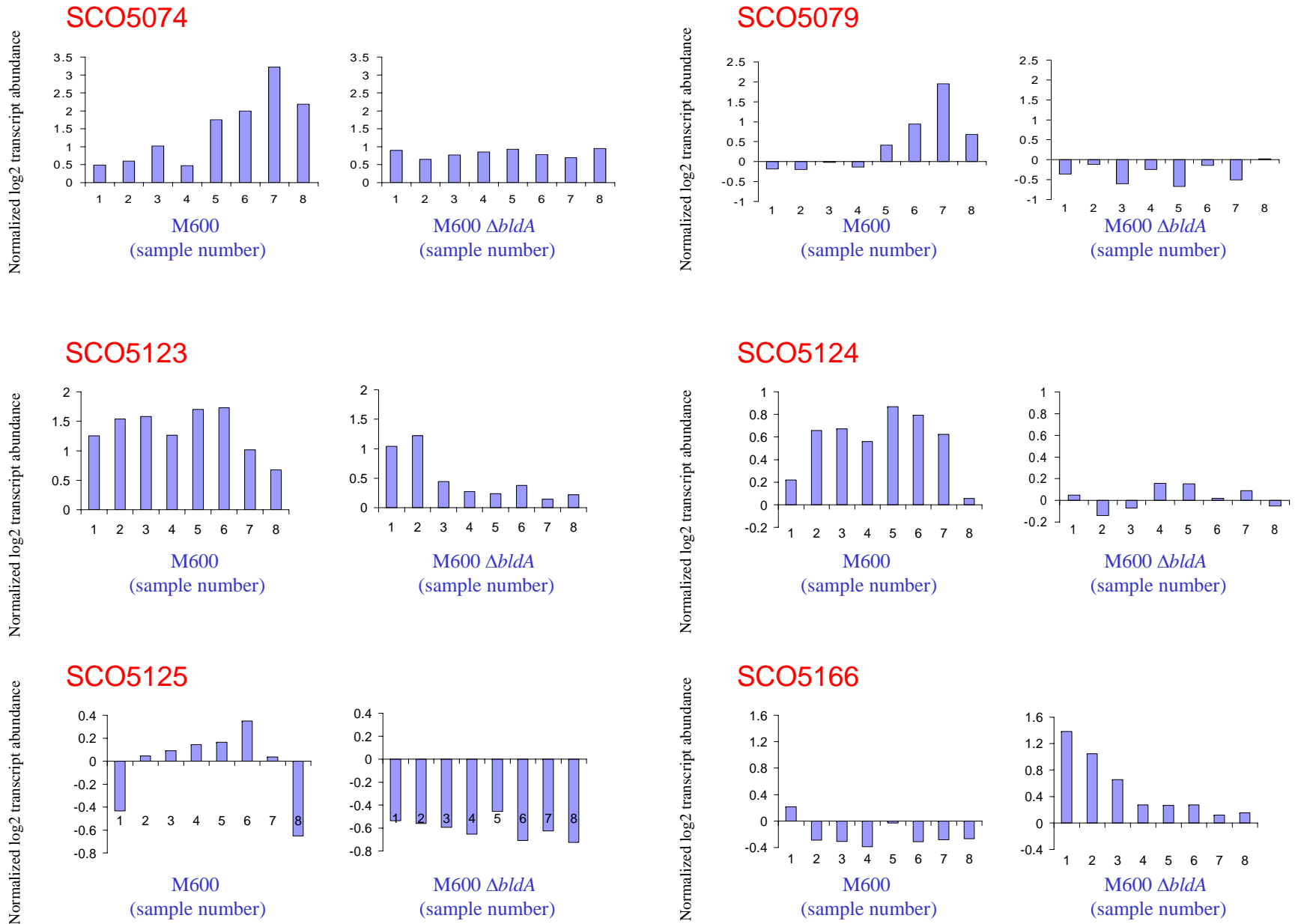


M600
(sample number)

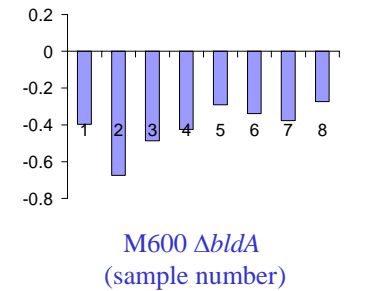
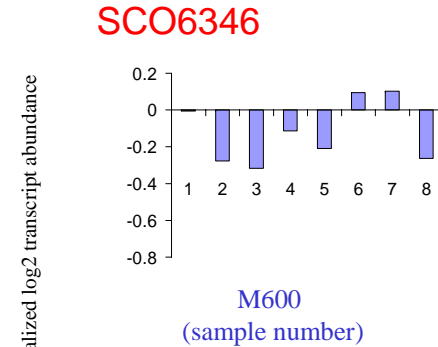
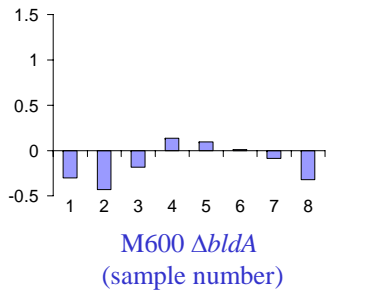
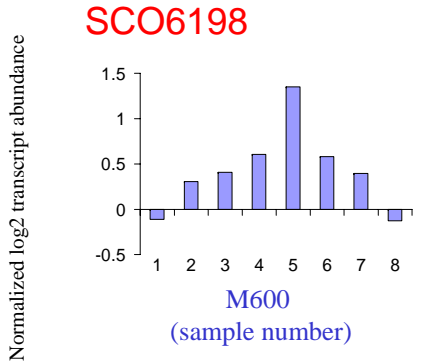
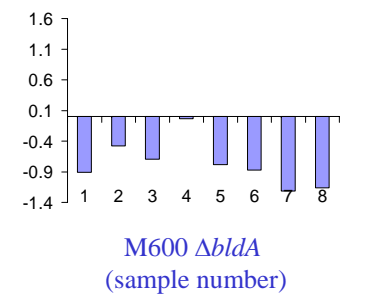
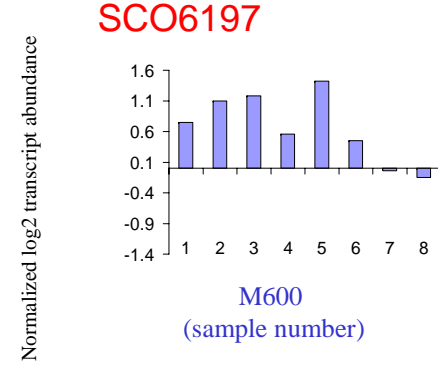
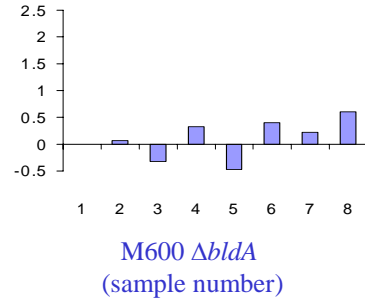
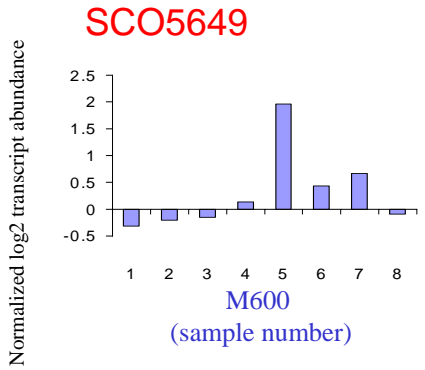
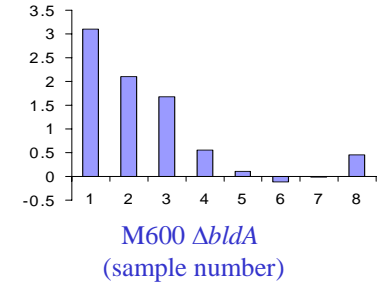
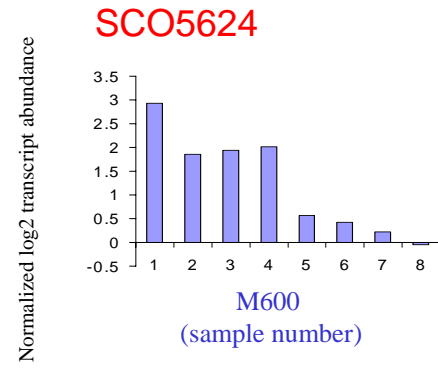
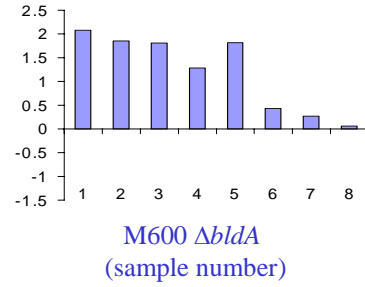
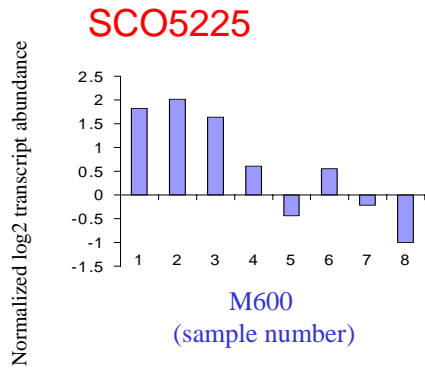


M600 $\Delta bldA$
(sample number)

Profiles are the average of triplicate experiments



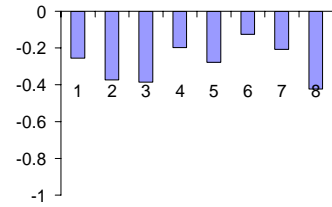
Profiles are the average of triplicate experiments



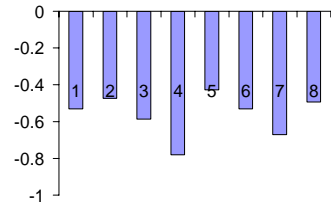
Profiles are the average of triplicate experiments

Normalized log₂ transcript abundance

SCO6362



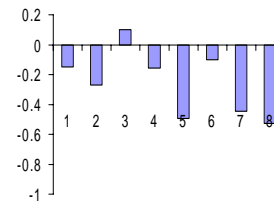
M600
(sample number)



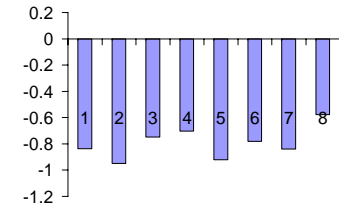
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO6637



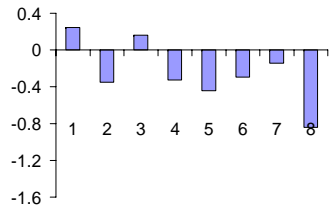
M600
(sample number)



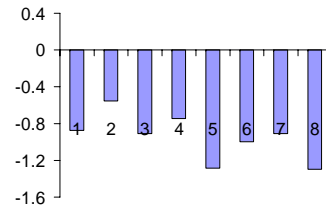
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO6638



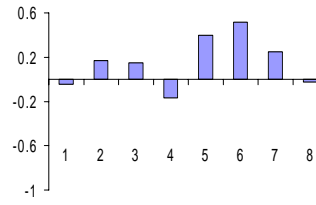
M600
(sample number)



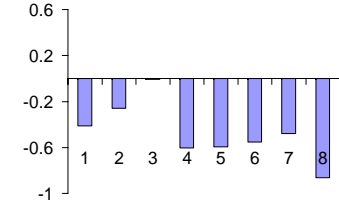
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO6808



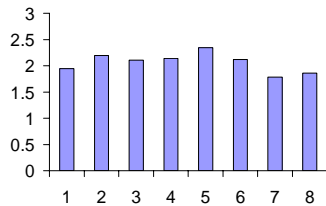
M600
(sample number)



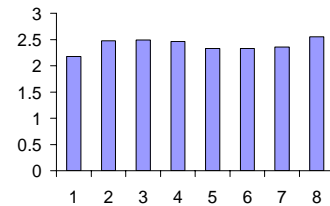
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO6958



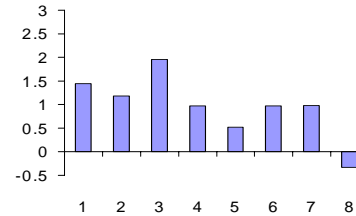
M600
(sample number)



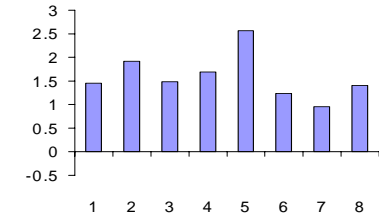
M600 $\Delta bldA$
(sample number)

Normalized log₂ transcript abundance

SCO7510



M600
(sample number)

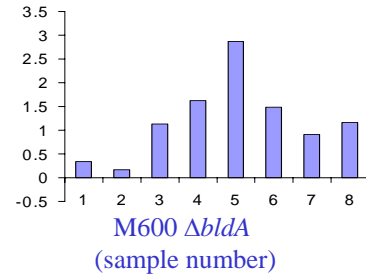
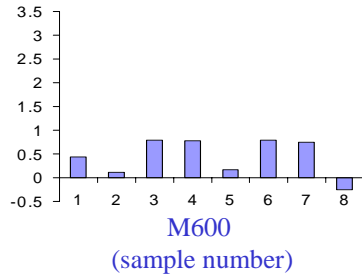


M600 $\Delta bldA$
(sample number)

Profiles are the average of triplicate experiments

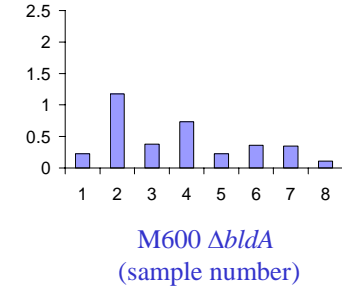
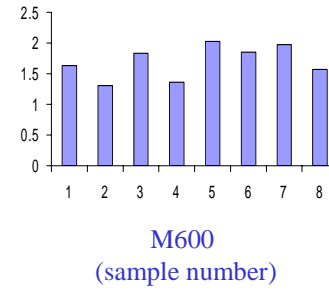
SCO7511

Normalized log₂ transcript abundance



SCO7657

Normalized log₂ transcript abundance



Profiles are the average of triplicate experiments