TDB4	pabaA1, yA2; ΔstcK::trpC; veA1	no ST precursors
TDB2	methG1, ΔstcJ::argB; biA1; veA1	no ST precursors
TJH3.40*	biA1; veA1; ΔstcE::argB2, methG1; wA1	accumulates norsolorinic acid
	*incorrectly called TTS40 on the list	
TAHK45.44	pabaA1, yA2; ΔstcN::trpC; veA1	unknown block in ST pathway
TAHK54.11	veA1; ΔstcL::argB2; methG1, biA1	accumulates dehydrosterigmatocystin
TAHK64.42	biA1; veA1; ΔstcP::argB2	accumulates demethylsterigmatocystin
TAHK67.11	veA1; ΔstcQ::argB2, methG1; biA1	still produces ST
TAHK70.29	veA1; ΔstcV::argB2, methG1; biA1	still produces ST
TAHK78.36	veA1; ΔstcL::argB2, ΔstcU::hph; methG1, biA1	accumulates versicolorin B
	hygromycin phosphotransferase (*hph*) gene	
TAHK87.29	veA1; ΔstcB::argB2, methG1, biA1	accumulates averufin
TAHK68.44	veA1; ΔstcF::argB2, methG1, biA1	accumulates averantin
TAHK79.4	**veA1; ΔstcW::argB2, methG1, biA1**	**accumulates averufin**
TAHK72.25	veA1; ΔstcI::argB2, methG1, biA1	accumulates norsolorinic acid but is leaky and still produces ST
TMF4.12	veA1; ΔaflR::argB2, methG1, biA1	no ST precursors

I am including the papers from my lab that are pertinent. These include:

1. fadA, flbA mutants (Tom Adams' papers describe better):
   Hicks J K, Yu J-H, Keller N P, Adams T H. (1997) *Aspergillus* sporulation and mycotoxin production both require inactivation of the FadA Gα protein-dependent signaling pathway. EMBO J. 16:4916-4923.

2. stcL, stcU mutants:
   Kelkar H S, Schloss T W, Haw J, Keller N P, Adams T H. (1997) *Aspergillus nidulans stcL* encodes a putative P-450 monooxygenase required for bisfuran desaturation during aflatoxin/sterigmatocystin biosynthesis. J Biol Chem 272:1589-594.

3. stcJ, stcK, fasA, fasB mutants:
   Brown D W, Adams T H, Keller N P. (1996) A fatty acid synthase required for secondary metabolism. PNAS 93:14873-14877.

4. stcP mutant:
   Kelkar H S, Keller N P, Adams T H. (1996) *Aspergillus nidulans stcP* encodes an *O*-methyltransferase that is required for sterigmatocystin biosynthesis. Appl Environ Micro 62:4296-4298.