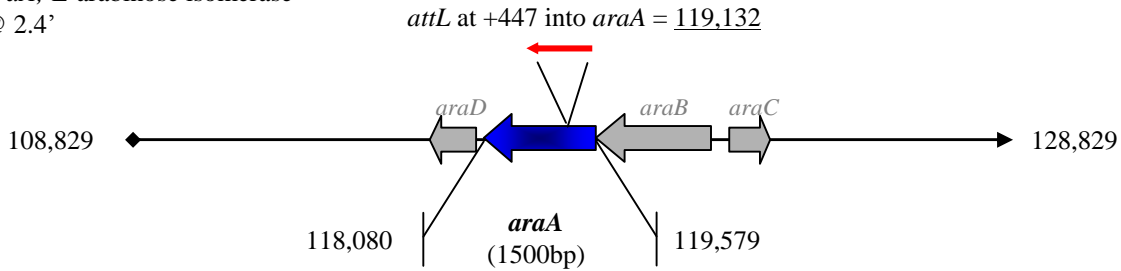


ORI @ 4,082,000 ~85'
Genome = 4,857,432

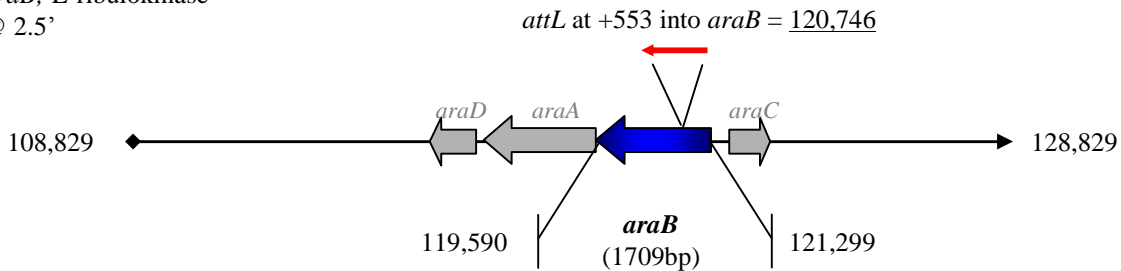
SDT1206, *araA::attL* (SDT1266 with pXis and *pattR*) - STM0102

araA; L-arabinose isomerase
@ 2.4'



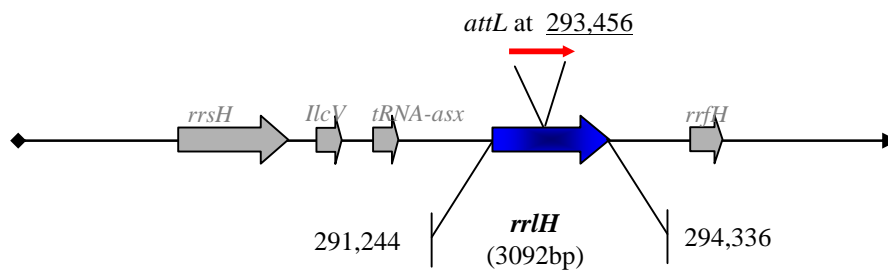
SDT1207, *araB::attL* (SDT1308 with pXis and *pattR*) - STM0103

araB; L-ribulokinase
@ 2.5'



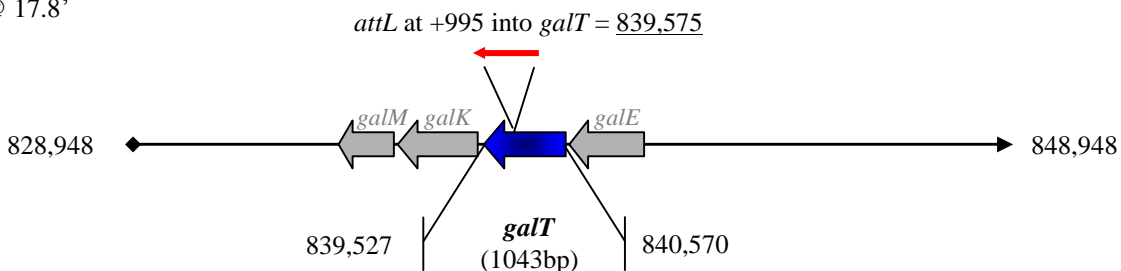
SDT1017, *rrlH::attL* (SDT1233 with pXis and *pattR*)

23S rRNA
@ 6.9'

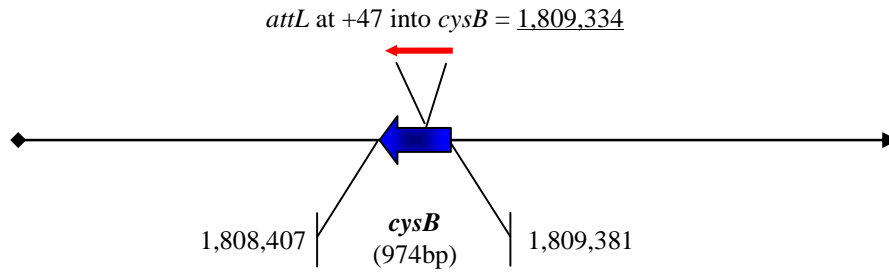


SDT1208, *galT::attL* (SDT1268 with pXis and *pattR*) - STM0775

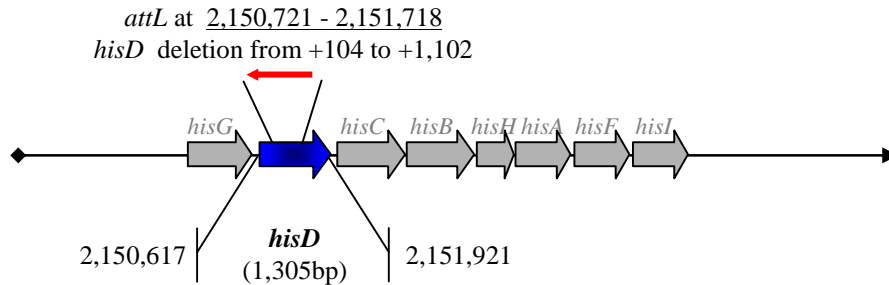
galT; galactose-1-phosphate uridylyltransferase
@ 17.8'



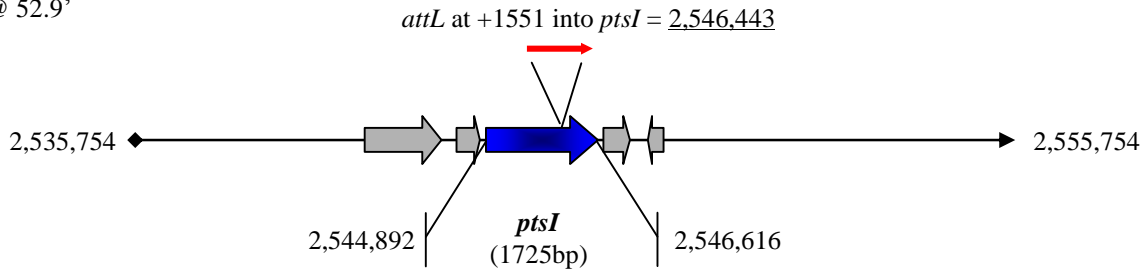
SDT1049, *cysB::attL* (SDT1060 with pXis and *pattR*) - STM1713
cysB; transcriptional regulator for cysteine regulon (LysR family)
 @ 37.7°



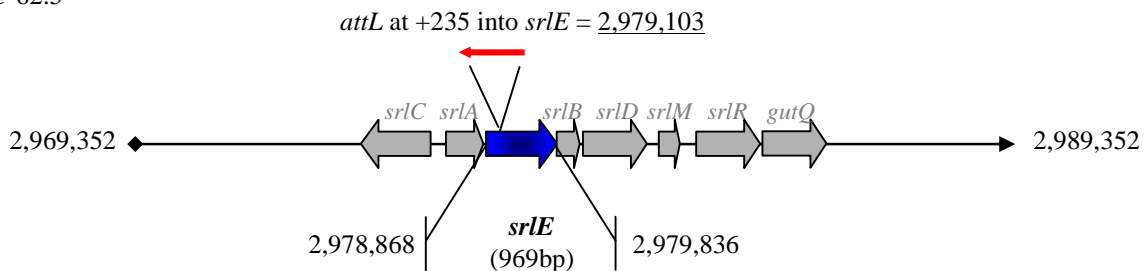
SDT1285, Δ *hisD::attL* (SDT1292 with pXis and *pattR*) - STM2072
hisD; histidinal dehydrogenase (also histidinol dehydrogenase activity)
 @ 44.7°



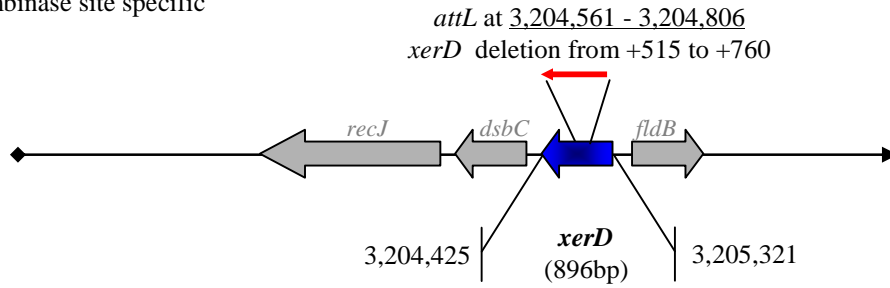
SDT1210, *ptsI::attL* (SDT1306 with pXis and *pattR*) - STM2432
ptsI; phosphoenolpyruvate-protein phosphotransferase
 @ 52.9°



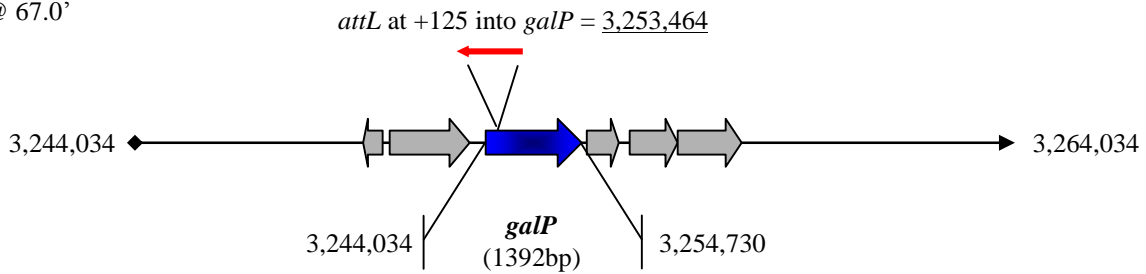
SDT1200 and SDT1201, *srlE::attL* (SDT1236 and SDT1249 with pXis and *pattR*) - STM2833
srlE; PTS system, glucitol/sorbitol-specific IIBC component
 @ 62.5°



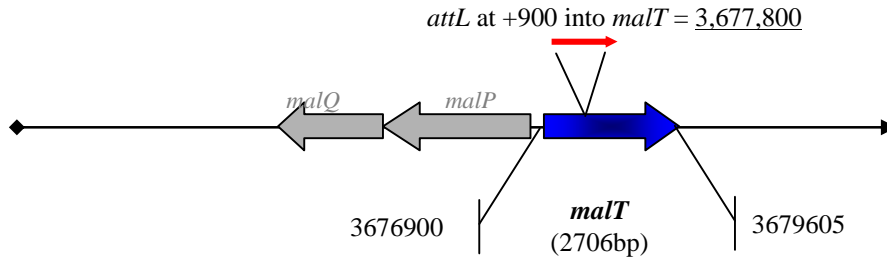
SDT1314, $\Delta xerD::attL$ (SDT1318 with pXis and *pattR*) - STM3044
xerD; recombinase site specific
 @ 66'



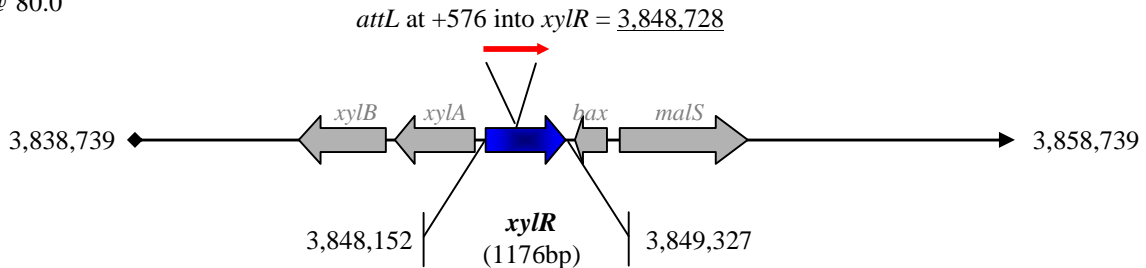
SDT1209, *galP::attL* (SDT1305 with pXis and *pattR*) - STM3091
galP; glucose/galactose transporter
 @ 67.0'



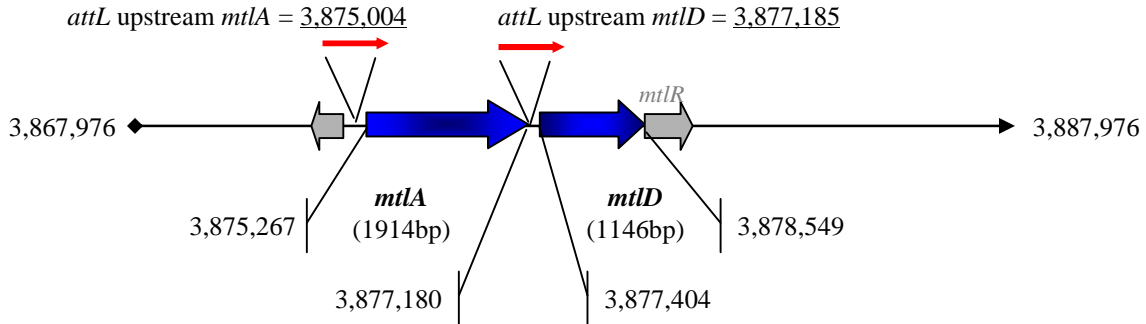
SDT1262, *malT::attL* (SDT1309 with pXis and *pattL*) - STM3515
malT; transcriptional activator of the *mal* genes; binds inducer (maltotriose) and ATP (LysR family).
 @ 76.8'



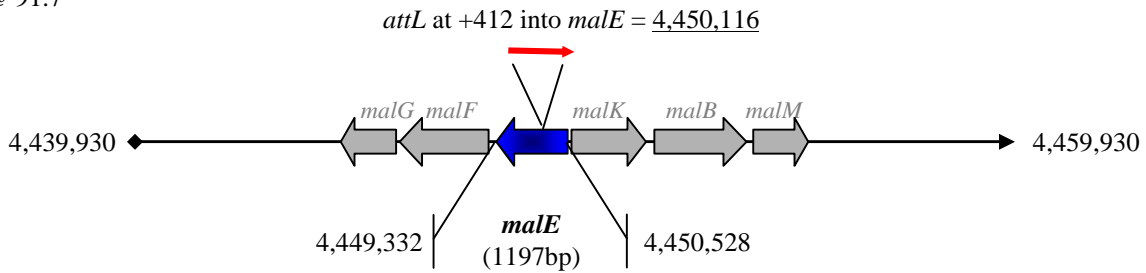
SDT1205, *xyIR::attL* (SDT1250 with pXis and *pattR*) - STM3662
xyIR; xylose operon regulatory protein
 @ 80.0'



SDT1199 (mtl-), upstream *mtlA*::*attL* (SDT1235 with pXis and *pattR*) - STM3685
SDT1202 (mtl+), upstream *mtlD*::*attL* (SDT1361 with pXis and *pattR*) - STM3686
mtlA; PTS system, mannitol-specific IIBC component/PTS system, mannitol-specific IIA component
mtlD; mannitol-1-phosphate 5-dehydrogenase
 @ 80.4'



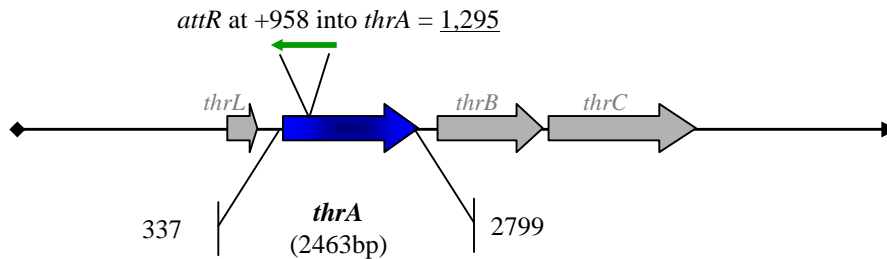
SDT1264, *malE*::*attL* (SDT1355 with pXis and *pattR*) - STM4229
malE; maltose uptake; periplasmic maltose-binding protein
 @ 91.7'



SDT1151, *thrA::attR* (SDT1239 with pXis and *pattL*) - STM0002

thrA; aspartokinase I; bifunctional enzyme: N-terminal is aspartokinase I and C-terminal is homoserine dehydrogenase I.

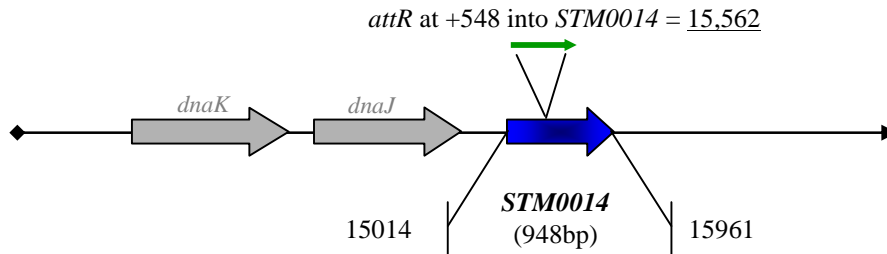
@ 0'



SDT1253, *STM0014::attR* (not made with pXis and *pattL*)

Putative LysR family transcriptional regulator

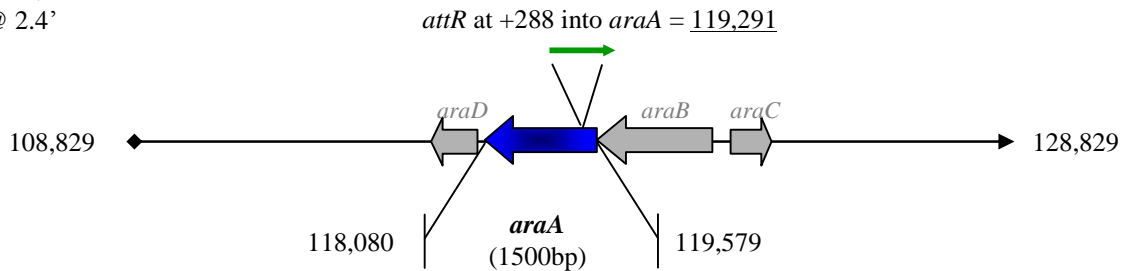
@ 0.3'



SDT1183, *araA::attR* (SDT1276 with pXis and *pattL*) - STM0102

araA; L-arabinose isomerase

@ 2.4'

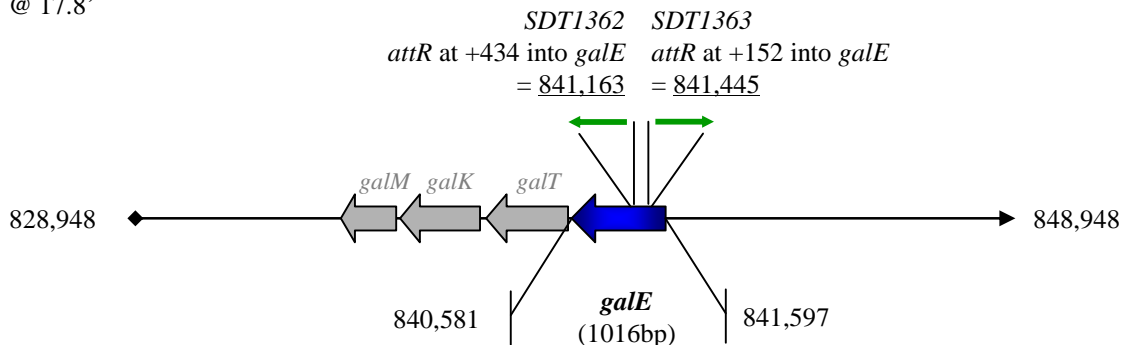


SDT1362, *galE::attR* (SDT1366 with pXis and *pattL*) - STM0776

SDT1363, *galE::attR* (SDT1367 with pXis and *pattL*) - STM0776

galE; galD, UDP-galactose 4-epimerase

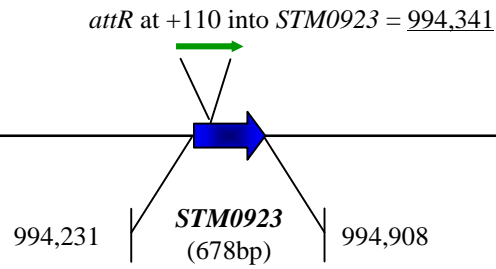
@ 17.8'



SDT1155, *STM0923::attR* (not made with pXis and *pattL*)

Putative Fels-1 prophage tail assembly protein

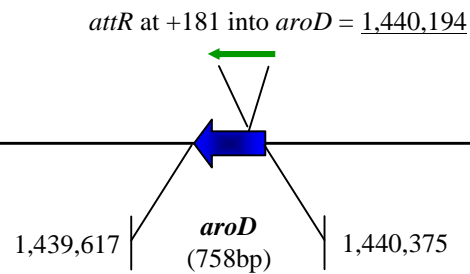
@ 19.0'



SDT1058, *aroD::attR* (SDT1258 with pXis and *pattL*) - STM1358

aroD; 3-dehydroquinate dehydratase

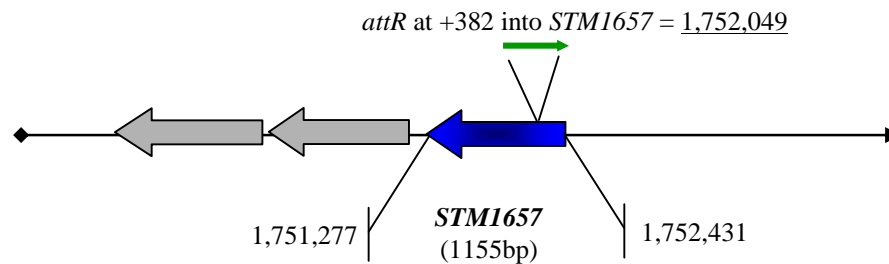
@ 30.5'



SDT1163, *STM1657::attR* (not made with pXis and *pattL*)

Putative methyl-accepting chemotaxis protein

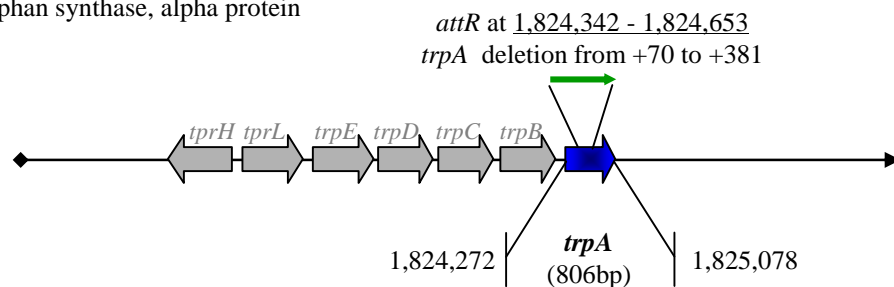
@ 36.5'



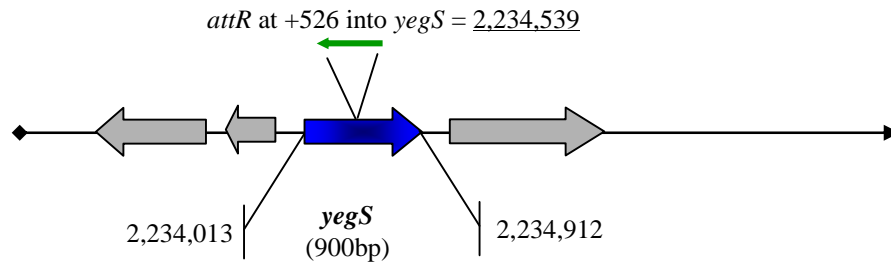
SDT1337, Δ *trpA::attR* (SDT1344 with pXis and *pattL*) - STM1727

trpA; tryptophan synthase, alpha protein

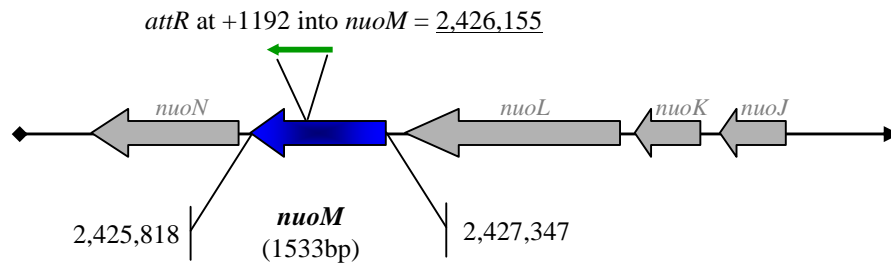
@ 38.1'



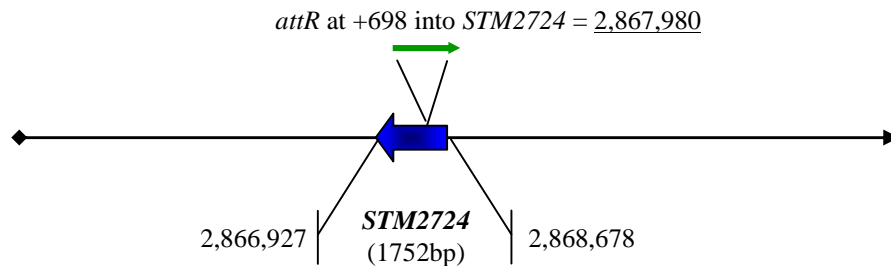
SDT1158, *yegS::attR* (not made with pXis and *pattL*)
 Putative diacylglycerol kinase catalytic domain
 @ 46.5'



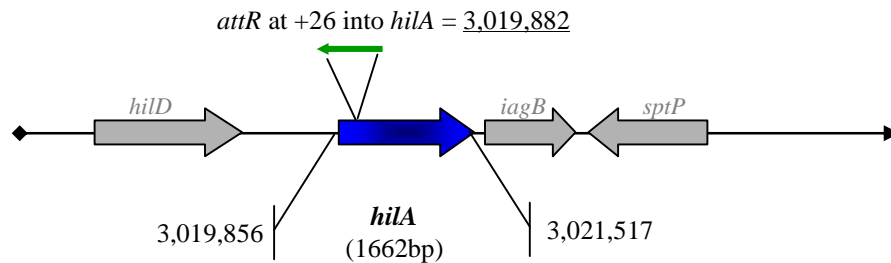
SDT1162, *nuoM::attR* (not made with pXis and *pattL*) - STM2317
nuoM; NADH dehydrogenase I chain M
 @ 50'



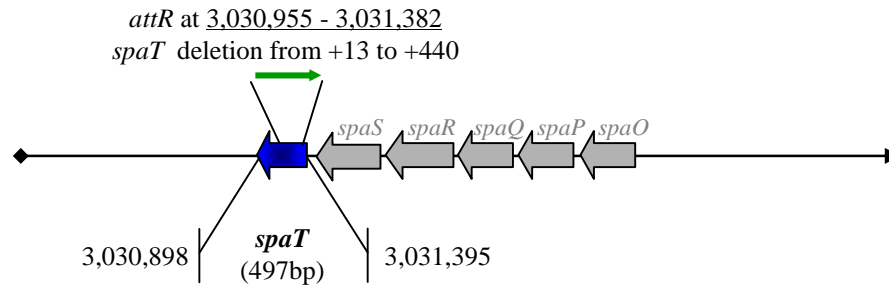
SDT1156, *STM2724::attR* (not made with pXis and *pattL*)
 Fels-2 prophage hypothetical protein
 @ 59.5'



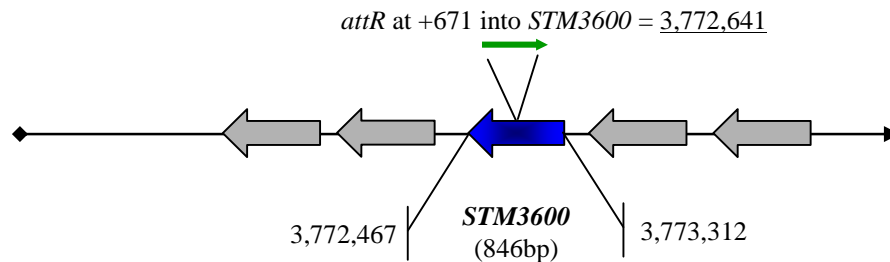
SDT1364, *hilA::attR* (SDT1368 with pXis and *pattL*) - STM2876
hilA; invasion genes transcription activator
 @ 62.8'



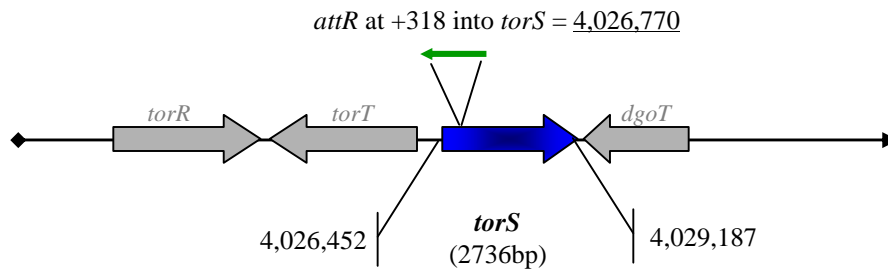
SDT1313, $\Delta spaT::attR$ (SDT1327 with pXis and *pattL*) - STM2886
spaT; surface presentation of antigens; secretory proteins
 @ 62.9'



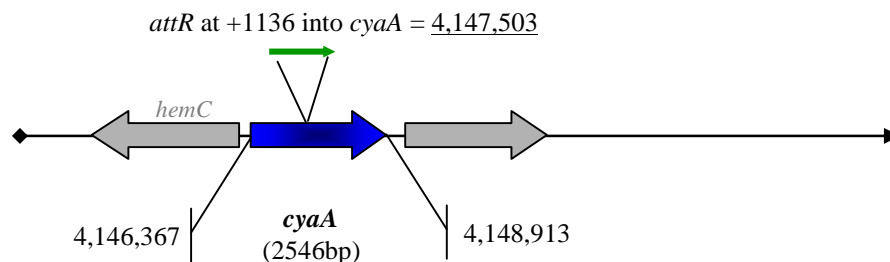
SDT1159, *STM360::attR* (not made with pXis and *pattL*)
 Putative sugar kinases, ribokinase family
 @ 78.5'



SDT1365, *torS::attR* (SDT1369 with pXis and *pattL*) - STM3826
torS; sensory kinase in multi-component regulatory system with TorR (regulator) and TorT (periplasmic sensor); regulates *tor* operon
 @ 82.5'



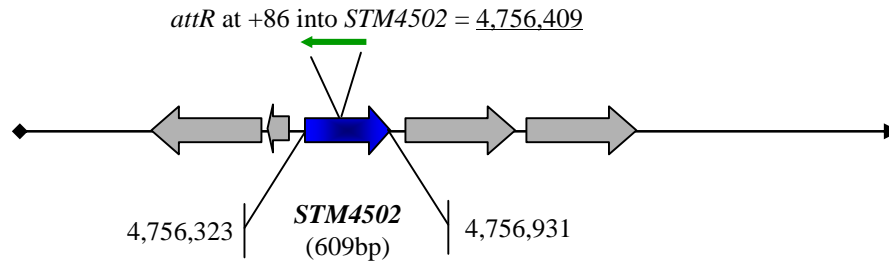
SDT1400, *cyaA::attR* (not made with pXis and *pattL*) - STM3939
 Adenylate cyclase
 @ 85.7'



SDT1161, *STM4502::attR* (not made with pXis and *pattL*)

Putative cytoplasmic protein

@ 98'



SDT1160, *STM4534::attR* (not made with pXis and *pattL*)

Putative NtrC family transcriptional regulators, ATPase domain

@ 98.5'

