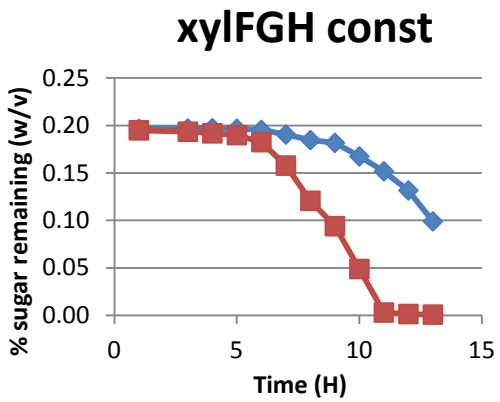
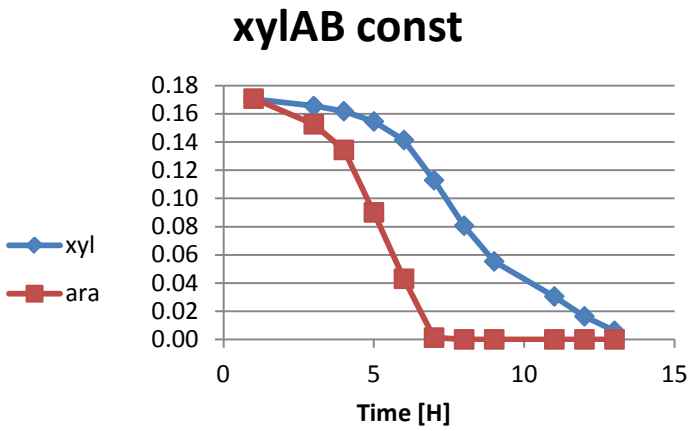




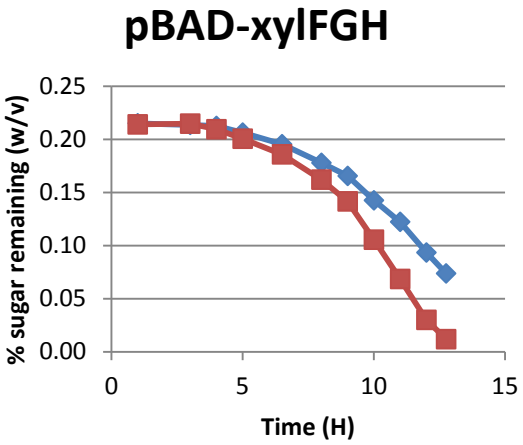
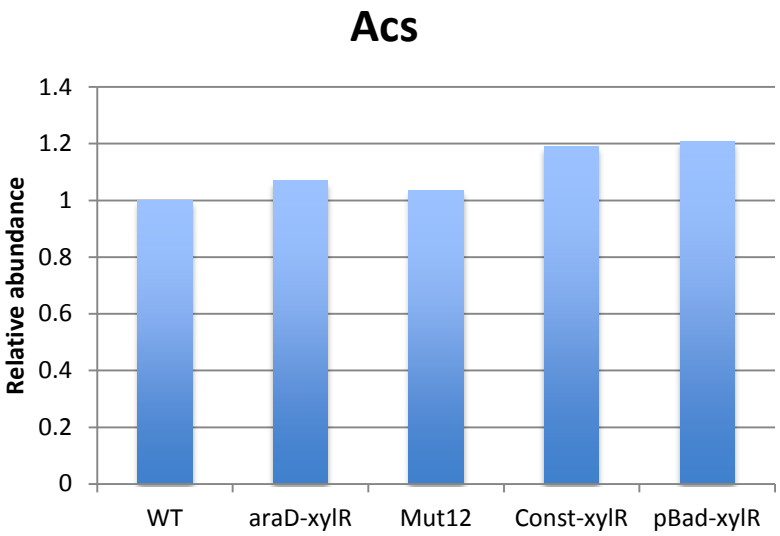


Figure S1: Neither low-level supplementation with xylAB nor xylFGH is sufficient to eliminate ara/xyl diauxie. Strain MG1655 transformed with the indicated plasmids were grown overnight and then diluted 1:20 into fresh MMM supplemented with 0.4% total sugars and appropriate antibiotics. Cultures were grown at 37° with 200 RPM agitation. Samples were withdrawn at indicated time points, the OD_{600} was measured and the sugar was analyzed using liquid chromatography with refractive index detection.

Q1	Q3	Protein	Sequence
506.303	702.393	araA1	araA.LPVANALWK.y6
617.288	705.336	araA2	araA.WNEVYYGFR.y5
670.882	986.531	araB	araB.QLLPALTEAWAK.y9
527.798	629.325	xylB2	xylB.LAQIAANPEK.y6
506.806	685.388	xylF1	xylF.LLTPIDVNK.y6
523.777	759.436	xylF2	xylF.ADTTLNNGLK.y7
535.316	730.373	xylG	xylG.ILILDEPTR.y6
529.801	775.406	xylR1	xylR.VALSSVAQGAR.y8
517.306	819.472	xylR2	xylR.ITLLFNANK.y7
574.78	870.45	XylA1	xylA.FMQMVVEHK.y7
678.33	1023.51	XylA2	XylA.AGGFTTGGLNFDAK.y10
643.864	1158.663	araC1	araC.QQLGISVLSWR.y10
643.864	1030.604	araC2	araC.QQLGISVLSWR.y9
643.864	917.52	araC3	araC.QQLGISVLSWR.y8
643.864	860.499	araC4	araC.QQLGISVLSWR.y7
643.864	747.415	araC5	araC.QQLGISVLSWR.y6
643.864	660.383	araC6	araC.QQLGISVLSWR.y5
643.864	561.314	araC6	araC.QQLGISVLSWR.y4
563.286	997.47	araD1	araD.KPSSDTPTHR.y9
563.286	900.417	araD2	araD.KPSSDTPTHR.y8
563.286	813.385	araD3	araD.KPSSDTPTHR.y7
563.286	726.353	araD1	araD.KPSSDTPTHR.y6
563.286	611.326	araD2	araD.KPSSDTPTHR.y5
563.286	510.278	araD3	araD.KPSSDTPTHR.y4

Table S2: Protein transitions used for measuring relative concentrations of xyl and ara proteins.



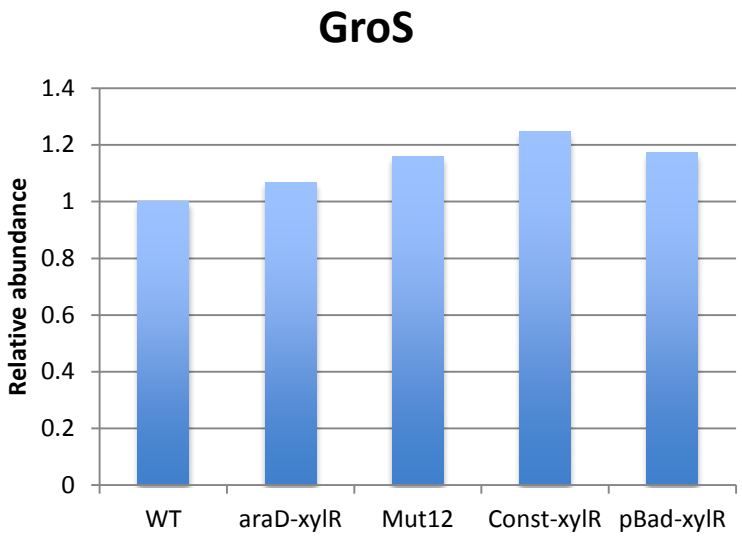


Figure S3: Housekeeping genes Acs and GroS have consistent concentrations for all treatments. See text for details.

Primer name	Sequence
S8A-xylR xylR Gib F	gatcttttaagaaggagatatacatATGTTTACTAAACGTCACCGCATC
S8A-xylR xylR Gib R	ggagatccttactcgagtttggatccCTACAACATGACCTCGCTATTTACATCGCG
S8A-xylR S8A Gib F	CGCGATGTAAATAGCGAGGTCATGTTGTAGggatccaaactcgagtaaggatctcc
S8A-xylR S8A Gib R	GATGCGGTGACGTTTAGTAAACATatgtatatctccttcttaaaagatc
pUA66 PxylA F	AGCATctcgagCATGGTGTAGGGCCTTCTGTAGTTAG
pUA66 PxylA R	AGCATggatccTAATATTGGGCACTCCCTTTCAGTTG
xylR SD OPT F	GTAATTTTAAGAAGGAGGAATACATATGTTTACTAAACGTCAC
xylR SD OPT R	GTTTAGTAAACATATGTATTCCTCCTTCTTAAAATTACTGCCC
BB xylAB EcoRI F	agcatGAATTCttaagaaggaggtatacatATGCAAGCCTATTTTGACC
BB xylAB BamHI R	ATGCTggatccTTACGCCATTAATGGCAGAAGTTGCTGATAG
BB xylFGH EcoRI F	agcatGAATTCttaagaaggaggtatacatATGAAAATAAAGAACATTCTACTCACCC
BB xylFGH BamHI R	ATGCTggatccTCAAGAACGGCGTTTGGTTGCGGAG
PxylF const R	GATAAAAATCTGTAATTGTTTTCCCCTGTTTAGTTGCTAAAAA
PxylF const F	AGCATggatccATTTTAGCAACTgAACAGGGcttgtCAATTACAGATTTTTATC
xylAB BamHI F	TATTAGGATCCTCTAGATTTAAGAAGGAGATATACATATGCAAGCCTATTTTGACC
xylAB KpnI R	ATGCTggtaccTTACGCCATTAATGGCAGAAGTTGCTGATAG
pUA66 const R	GTATATCTCCTTCTTAAATCTAGAGG
pUA66 const F	AGCATggtaCCTGAATTGTACAAATAAATGTCC
xylFGH Con HindIII F	CTCTAGATTTAAGAAGGAGATaagcttATGAAAATAAAGAACATTCTAC
xylFGH Con KpnI R	CATGCCTGCAGGTCTGGACATggtaccTCAAGAACGGCGTTTGGTTG
xylR Con HindIII F	GAGATaagcttATGTTTACTAAACGTCACCGC
xylR Con KpnI F	GACATggtaccCTACAACATGACCTCGCTATTTAC
pUA66 con KpnI F	CAACCAAACGCCGTTCTTGAggtaccATGTCCAGACCTGCAGGCATG
pUA66 con HindIII R	GTAGAATGTTCTTTATTTTCATaagcttATCTCCTTCTTAAATCTAGAG
araD-xylR F	GAAGGCATATTACGGGCAGTAAttttaagaaggagatatacatATG
araD-xylR R	GGCGTTTGAGATCTTCTAACATgatcttttgaattcccaaaaaaacgg
araD KO F	GCGCGGCGTCTTTGTGATCAAACCTTCCGGCGTCGATTACgtgtaggctggagctgcttc
araD KO R	AGCCTGGTTTCGTTTGATTGGCTGTGGTTTTATACAGTCAatccggggatccgtcgacc
araD KI FI	GGTATTAGAAGCCAACCTGG
xylR KI R	agcctGGTTTCGTTTGATTGGCTGTGGTTTTATACAGTCAcCTACAACATGACCTCGC

Table S4: Primers used for all constructs and mutagenesis.