Supplementary Table 5. Pathway enrichments for signature genes for different comparisons between strains that contain the RM.EcoGIII system and strains that do not contain this system.

Up Regulated Pathways	**C227-11 vs. C227ΔRM Pathway Fold Enrichment (p value†)**	**C227-11 vs. 55989 Pathway Fold Enrichment (p value†)**	**K12 vs. K12+ ϕStx104 Pathway Fold Enrichment (p value†)**
Cation transport	2.4 (8.4x10e-10)	2.0 (1.2x10e-7)	8.5 (9.1x10e-16)
Iron ion transport	4.5 (4.0x10e-16	3.8 (3.1x10e-16)	116.9 (1.0x10e-40)
di-, tri-valent inorganic cation transport	4.2 (3.0x10e-15)	3.5 (5.1x10-15)	90.0 (4.5X10E-38)
Down Regulated Pathways			
Flagellum	3.6 (3.4x10e-14	3.0 (1.2x10e=19)	--
Cell projection	4.6 (4.6x10e-11)	3.2 (1.2x10e-9)	--
Flagellar motility	4.0 (7.4x10e-9)	3.5 (3.2x10e-12)	--
Organelle inner membrane	--	--	54.4 (2.0x10e-89)
Taxis	3.5 (7.8x10e-14)	3.2 (5.1x10e-20)	12.3 (7.8x10e-15)
Pathways Enriched for Genes in C227 Harboring CTGCAG Modifications			
Flagellum	1.9 (4.1x10e-5)		
Pathways Enriched for Genes in K12+ϕStx104 Harboring CTGCAG Modifications			
Organelle inner membrane	33.7 (1.2x10e-187)		
Taxis	4.9 (2.6x10e-11)		

† Nominal p-values represent the significance of the Fisher Exact Test statistic under the null hypothesis that the frequency of the indicated signature gene set is the same between a reference set of genes consisting of the intersection of the genes in each strain for the indicated comparison and the set of genes comprising the signature.

-- Indicates the p value was not < 5% FDR

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