

<b>Significantly changed metabolites (SAM score (<i>d</i>) ≥ 1.0 (or) ≤ -1.0) in excess-nutrient adaptive evolutionary condition.</b>					
Over abundant metabolites in both the lines (MGAdp & DHAdp)			Less abundant metabolites in both the lines (MGAdp & DHAdp)		
Metabolites	Score( <i>d</i> )	Fold Change	Metabolites	Score( <i>d</i> )	Fold Change
5-Methyl-thioadenosine (236)	3.16	2.35	Erythrose-4-P (357)	-1.27	0.22
Adenine (264)	3.70	2.12	N-Acetyl_Aspartate (274)	-4.65	0.27
α-Glycerophosphate (357)	2.21	1.53	Oroticacid (254)	-1.80	0.36
α-Ketoglutarate(198)	1.57	5.03	Unknown30.70 (217)	-1.22	0.52
Alanine (116)	2.17	1.83			
Arginine (256)	2.22	1.91			
Asparagine (216)	2.55	3.03			
Cystathionine (128)	5.56	5.16			
Glucose-6-P (387)	1.44	1.34			
Glutamate (230,246)	2.31	2.01			
Glycerate-2-P (299,315,459)	2.81	1.72			
Glycine (174)	1.25	1.39			
Lysine (156)	1.42	2.77			
Malate (245,307)	3.33	1.96			
Methionine (176)	3.17	2.03			
o-acetyl_L_Homoserin3 (128)	1.50	1.41			
Ornithine (142)	3.91	2.08			
Proline (142)	1.75	1.88			
Ribose (217)	4.78	2.60			
Ribose-5-P (315,299)	2.77	1.81			
Salicylicacid (267)	2.34	2.31			
Succinate (247,409)	1.96	2.22			
Thymine (255)	2.08	1.57			
Tryptophane (202)	1.97	1.40			
Uracil (255,241)	3.32	2.16			
Urea (189)	1.14	16.14			
Valine (144)	1.35	1.52			

<b>Significantly changed metabolites (SAM score (<i>d</i>) ≥ 1.0 (or) ≤ -1.0) in environmental shift evolutionary condition.</b>					
Over abundant metabolites in both the lines (MGAdpGal & DHAdpGal)			Less abundant metabolites in both the lines (MGAdpGal & DHAdpGal)		
Metabolites	Score( <i>d</i> )	Fold Change	Metabolites	Score( <i>d</i> )	Fold Change
2-Isopropylmalate (275)	2.01	1.68	N-Acetyl_Aspartate (274)	-2.52	0.20
Agmatine (347)	2.13	1.60	Trehalose (361)	-1.90	0.36
Cystathionine (128)	2.25	3.23	Oroticacid (254)	-1.89	0.33
Malate (245,307)	1.41	1.34			
Panhotenic_acid (201)	3.10	2.35			
Putrescine (174)	2.27	1.79			
Urea (189)	0.98	3.43			

**Significantly changed metabolites (SAM score (*d*) ≥ 1.0 (or) ≤ -1.0) in prolonged stationary phase evolutionary condition.**

Over abundant metabolites in both the lines (MGStat & DHStat)			Less abundant metabolites in both the lines (MGStat & DHStat)		
Metabolites	Score( <i>d</i> )	Fold Change	Metabolites	Score( <i>d</i> )	Fold Change
Adenine (264)	1.76	2.42	Arabinose (217)	-1.74	0.64
α-Ketoglutarate (198)	1.62	6.46	Erythrose-4-P (357)	-1.30	0.21
Leucine (158)	1.64	3.93	Phenylalanine (192)	-1.02	0.53
Malate (245,307)	2.04	2.31	phosphate19.28 (299)	-2.22	0.17
Proline (142)	1.52	2.88	Trehalose (361)	-1.73	0.48
Salicylicacid (267)	1.76	2.50	Unknown32.96 (361)	-1.41	0.53
Shikimate (204)	1.00	8.82	Unknown44.66 (325)	-1.68	0.30
Thymine (255)	1.73	2.12			
Trehalose (361)	1.74	1.71			
Tryptophan (202)	1.17	1.50			
Urea (189)	1.15	16.34			
Valine (144)	1.60	1.88			