

# USDA RNAseq

*CHOP Microbiome Center*

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## Contents

<b>Reads breakdown</b>	<b>2</b>
<b>Genes that are associated with secondary bile acid biosynthesis (PathwayID: path:map00121)</b>	<b>3</b>
List of genes associated with secondary bile acid biosynthesis . . . . .	3
Difference in expression level . . . . .	4
<b>Pathway abundance</b>	<b>5</b>
Absolute abundance . . . . .	5
Relative abundance . . . . .	6
<b>Genes from Klebsiella</b>	<b>7</b>

## Reads breakdown

**N\_demux:** Number of reads after demultiplexing

**N\_GeneHit:** Number of reads that were mapped to KEGG database

**N\_KO\_avail:** Number of reads with K number available

RunSampleID	N_demux	N_GeneHit	N_KO_avail
USDA_RUN12_D12.BAF	11619799	3227414	2063224
USDA_RUN12_D13.BAF	11660175	3286867	2158529
USDA_RUN12_D14.BAF	10441139	3940189	2644173
USDA_RUN12_D25.BAF	8635146	5217940	3742637
USDA_RUN12_D27.BAF	9679037	5840159	4188877
USDA_RUN12_D28.BAF	8677862	5234306	3727330
USDA_RUN22_D12.BAF	29856924	7402276	4488794
USDA_RUN22_D13.BAF	30182774	8000536	4830753
USDA_RUN22_D14.BMF	33034334	11321082	7271823
USDA_RUN22_D25.BAF	25950552	6887160	4055104
USDA_RUN22_D27.BAF	26040156	6715962	3965754
USDA_RUN22_D28.BAF	30375471	9208802	5756164

## Genes that are associated with secondary bile acid biosynthesis (PathwayID: path:map00121)

### List of genes associated with secondary bile acid biosynthesis

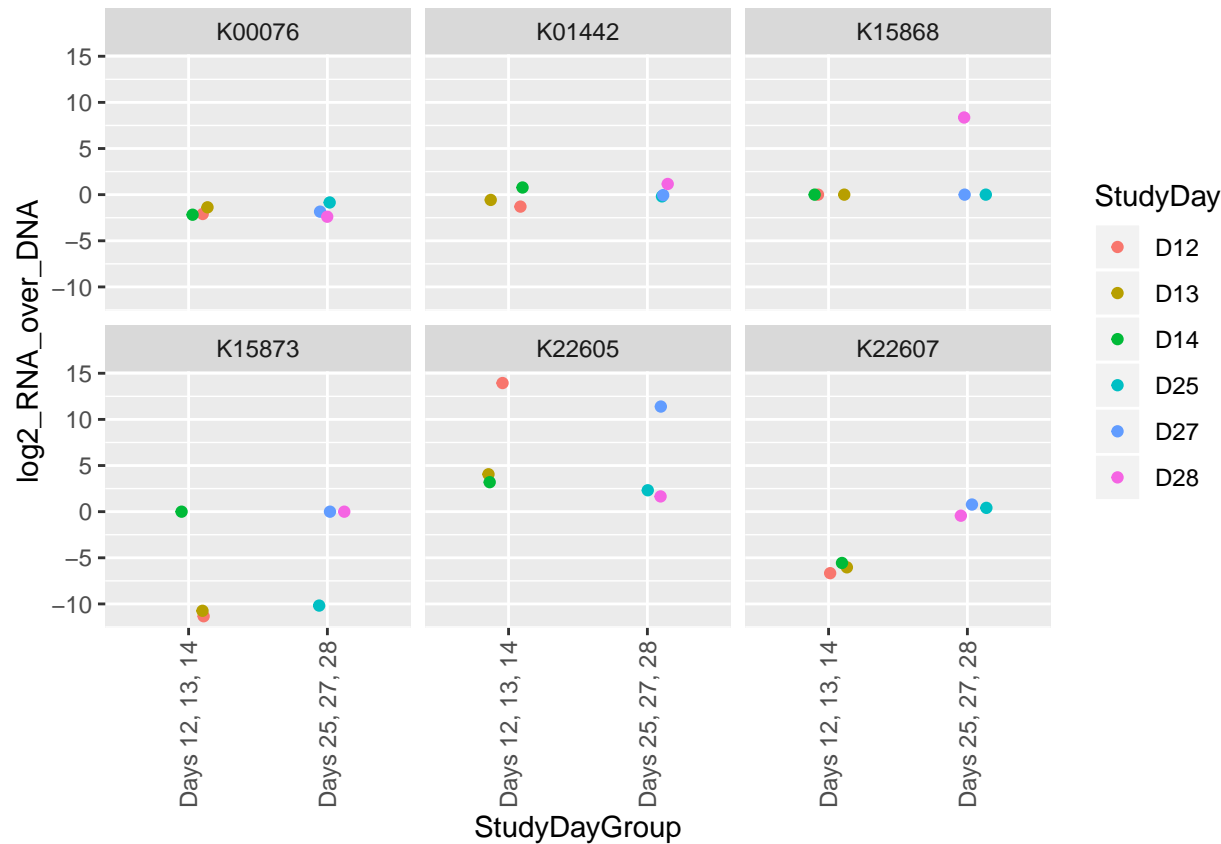
14 genes are associated with secondary bile acid biosynthesis

PathwayName	Ortholog	OrthologDefinition
Secondary bile acid biosynthesis	K00076	hdhA; 7-alpha-hydroxysteroid dehydrogenase [EC:1.1.1.159]
Secondary bile acid biosynthesis	K01442	E3.5.1.24; choloylglycine hydrolase [EC:3.5.1.24]
Secondary bile acid biosynthesis	K07007	baiN; 3-dehydro-bile acid Delta4,6-reductase [EC:1.3.1.114]
Secondary bile acid biosynthesis	K15868	baiB; bile acid-coenzyme A ligase [EC:6.2.1.7]
Secondary bile acid biosynthesis	K15869	baiA; 3alpha-hydroxy bile acid-CoA-ester 3-dehydrogenase [EC:1.1.1.395]
Secondary bile acid biosynthesis	K15870	baiCD; 3-oxocholoyl-CoA 4-desaturase [EC:1.3.1.115]
Secondary bile acid biosynthesis	K15871	baiF; bile acid CoA-transferase [EC:2.8.3.25]
Secondary bile acid biosynthesis	K15872	baiE; bile-acid 7alpha-dehydratase [EC:4.2.1.106]
Secondary bile acid biosynthesis	K15873	baiH; 7beta-hydroxy-3-oxochol-24-oyl-CoA 4-desaturase [EC:1.3.1.116]
Secondary bile acid biosynthesis	K15874	baiI; bile acid 7beta-dehydratase
Secondary bile acid biosynthesis	K22604	E1.1.1.52; 3alpha-hydroxycholanate dehydrogenase (NAD+) [EC:1.1.1.52]
Secondary bile acid biosynthesis	K22605	baiA; 3alpha-hydroxycholanate dehydrogenase (NADP+) [EC:1.1.1.392]
Secondary bile acid biosynthesis	K22606	E1.1.1.391; 3beta-hydroxycholanate 3-dehydrogenase (NAD+) [EC:1.1.1.391]
Secondary bile acid biosynthesis	K22607	E1.1.1.393; 3beta-hydroxycholanate 3-dehydrogenase (NADP+) [EC:1.1.1.393]

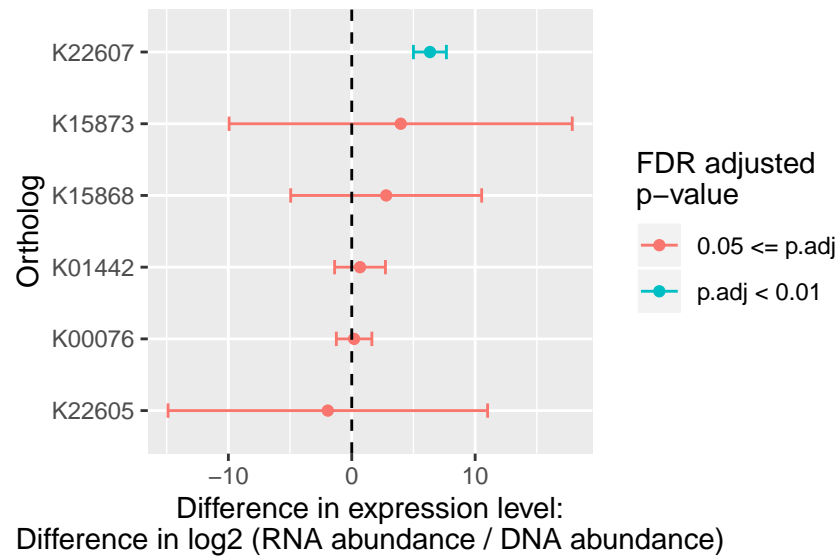
6 genes – K00076, K01442, K15868, K15873, K22605, K22607 – were detected in the data.

Difference in expression level

$\log_2$  (RNA abundance / DNA abundance) of 6 genes was tested for association with aerobicity. Below is a summary of result for all 6 genes.

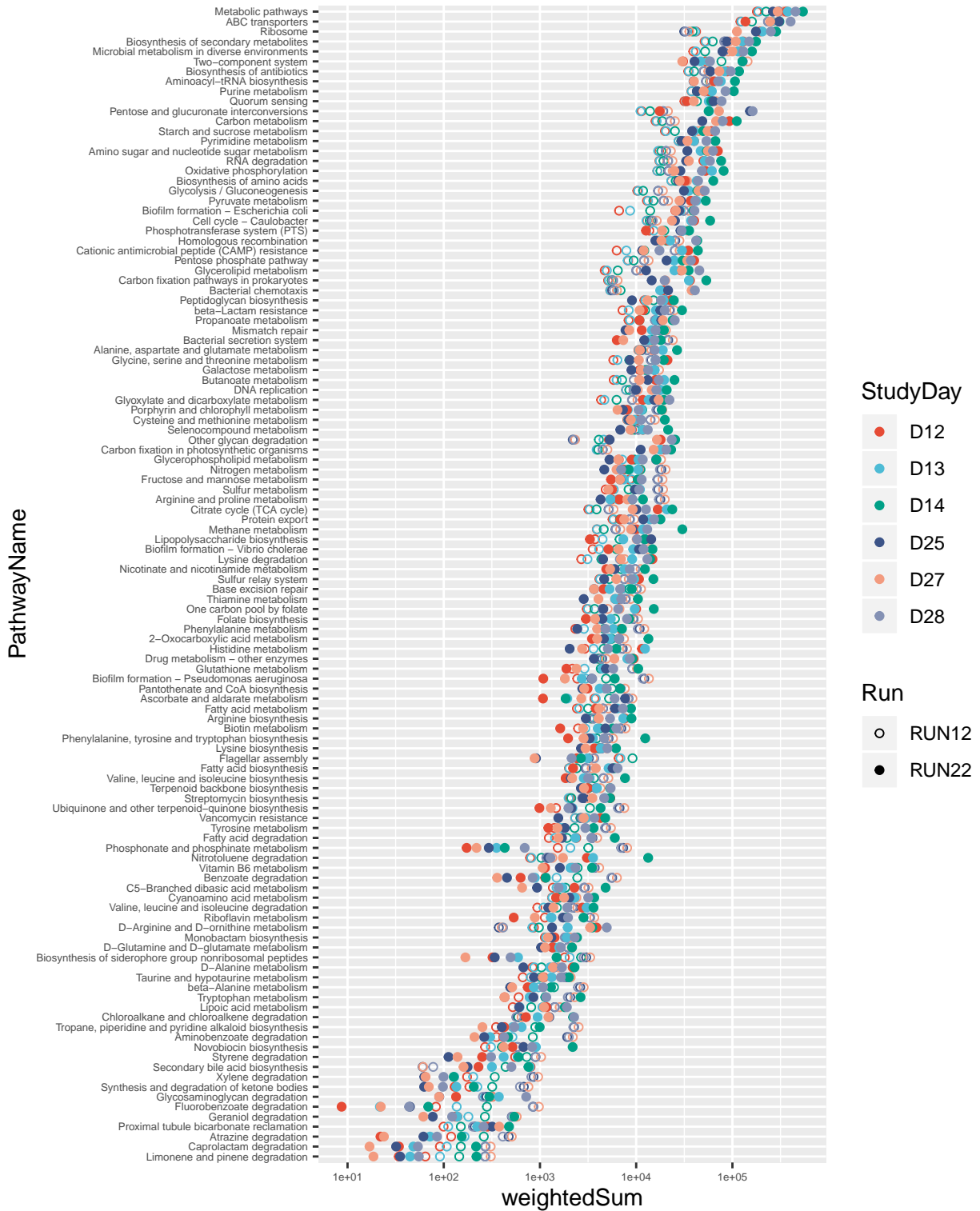


Difference below indicates change from Days 12, 13, 14 to Days 25, 27, 28.

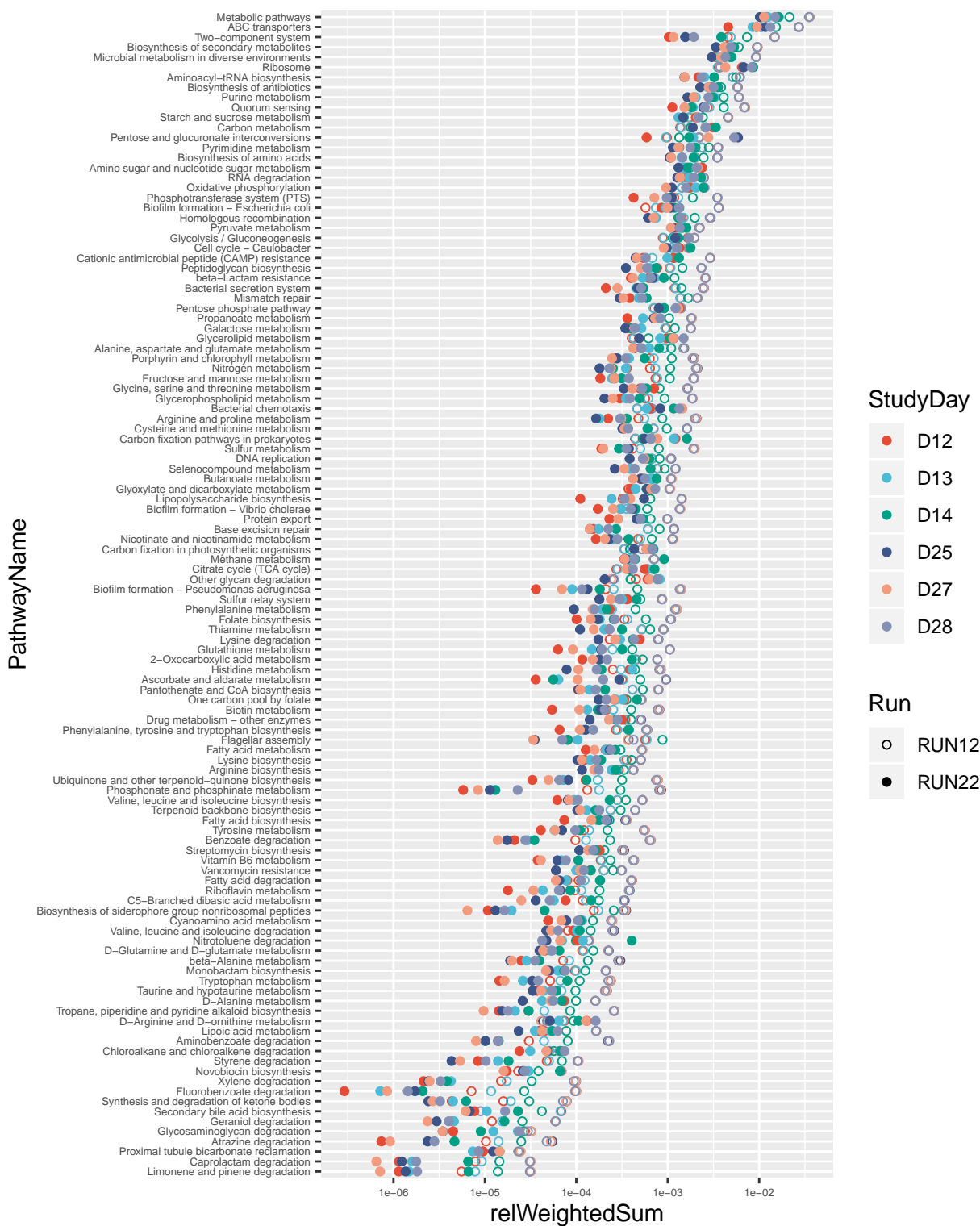


# Pathway abundance

## Absolute abundance



## Relative abundance



## Genes from Klebsiella

$\log_2$  (RNA abundance / DNA abundance) of pathways was tested for association with aerobic/anaerobic condition. Below is a summary of result for all 113 pathways. Difference below indicates change from Days 12, 13, 14 to Days 25, 27, 28.

