



SECOND GENOME
THE MICROBIOME COMPANY

Metagenomics at Second Genome

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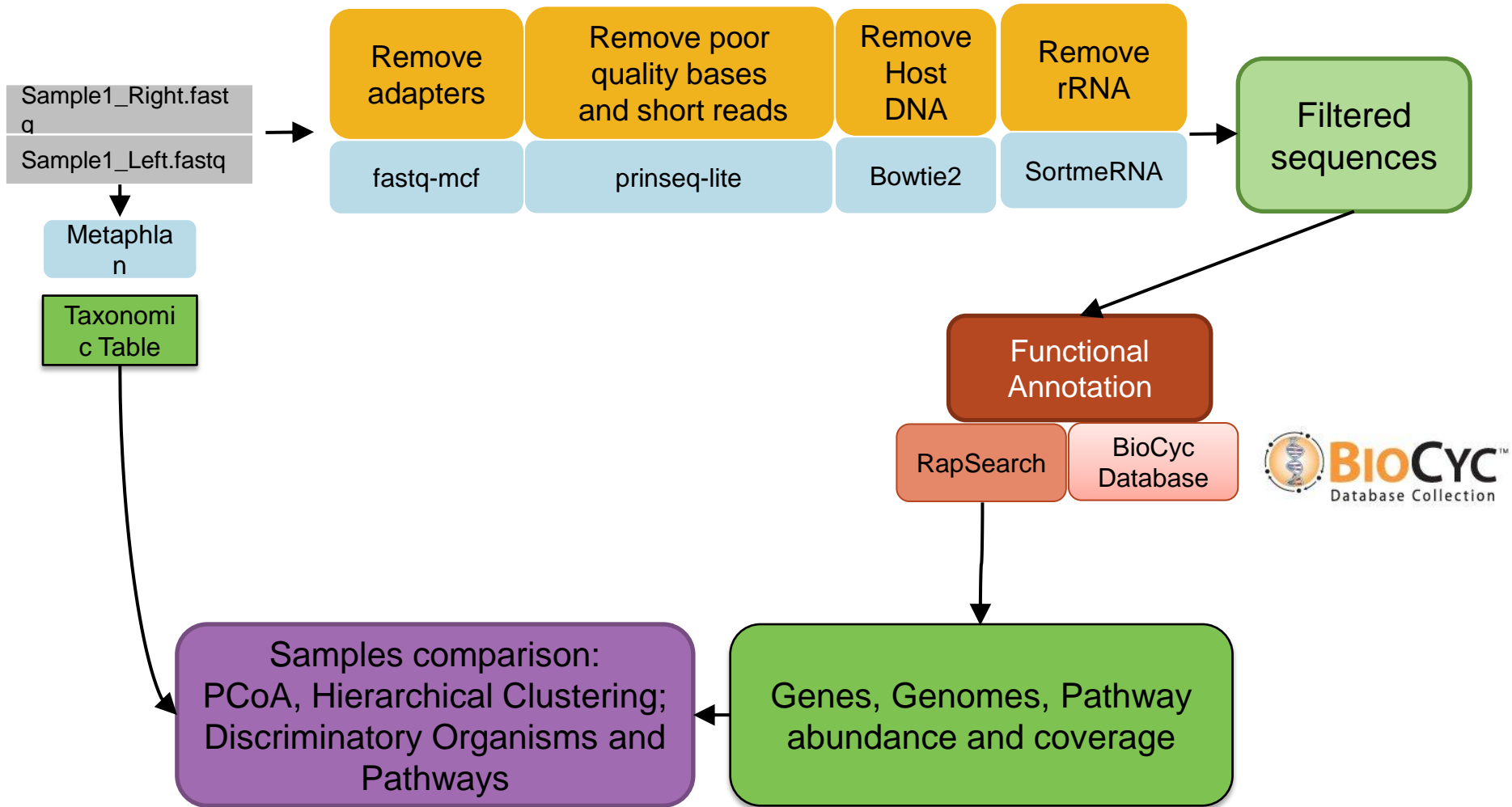


SECOND GENOME

THE MICROBIOME COMPANY

- San Francisco based company leveraging microbiome science to enable the discovery and development of human health products through services, collaborations and internal R&D
- Taking a **mechanistic** approach to discovery
 - First-of-kind microbiome drug discovery platform with pharma partner validation
 - **Not Dx, not nutrition, not fecal transplant, not strains as drugs**
- Curator of Greengenes™ database (Todd DeSantis)
- Qiime developer (Justin Kuczynski from Rob Knight Lab)
- Over 200 microbiome studies completed to date across industry, government, academic researchers, nutrition companies, and pharma

Metagenomic (and RNA-seq) Pipeline at SG



Open source software
Cloud = Amazon AWS spot

Functional annotation

Genes -> Enzymes -> Pathways and Strains

1 Query Sequence from Sample1: KDYDTAQRVLGNVVLNIIIGLAFTVLTILFLD

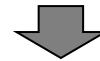


Functional assignments

Genes	1	2
GJXV-1205, GTP cyclohydrolase	1	0
GJXV-2161, Na ⁺ -driven multidrug pump	0	10

Enzymes	1	2
ENZRXNJXV-1763	1	0
ENZRXNJXV-1765	0	10

Pathways	1	2
NAGLIPASYN-PWY	1	0
PWY-5687	0	10



Bacterial strain assignments

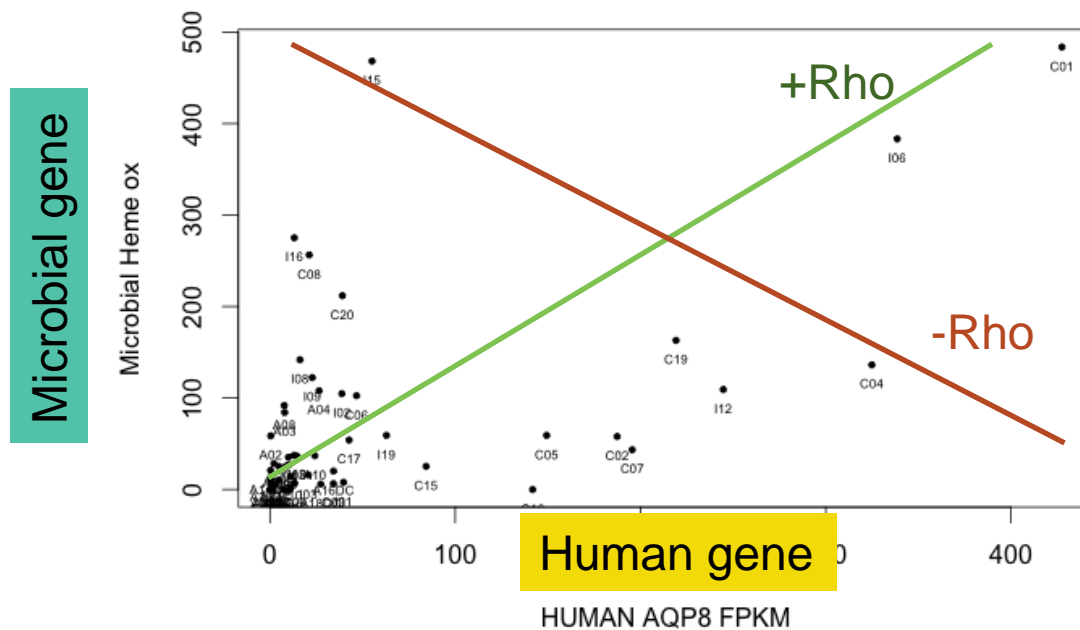
Strains	1	2
Faecalibacterium prausnitzii M-65	1	100
Acidovorax sp.JS42	0	1

Connecting
genes/enzymes to
bacterial genomes

Challenges

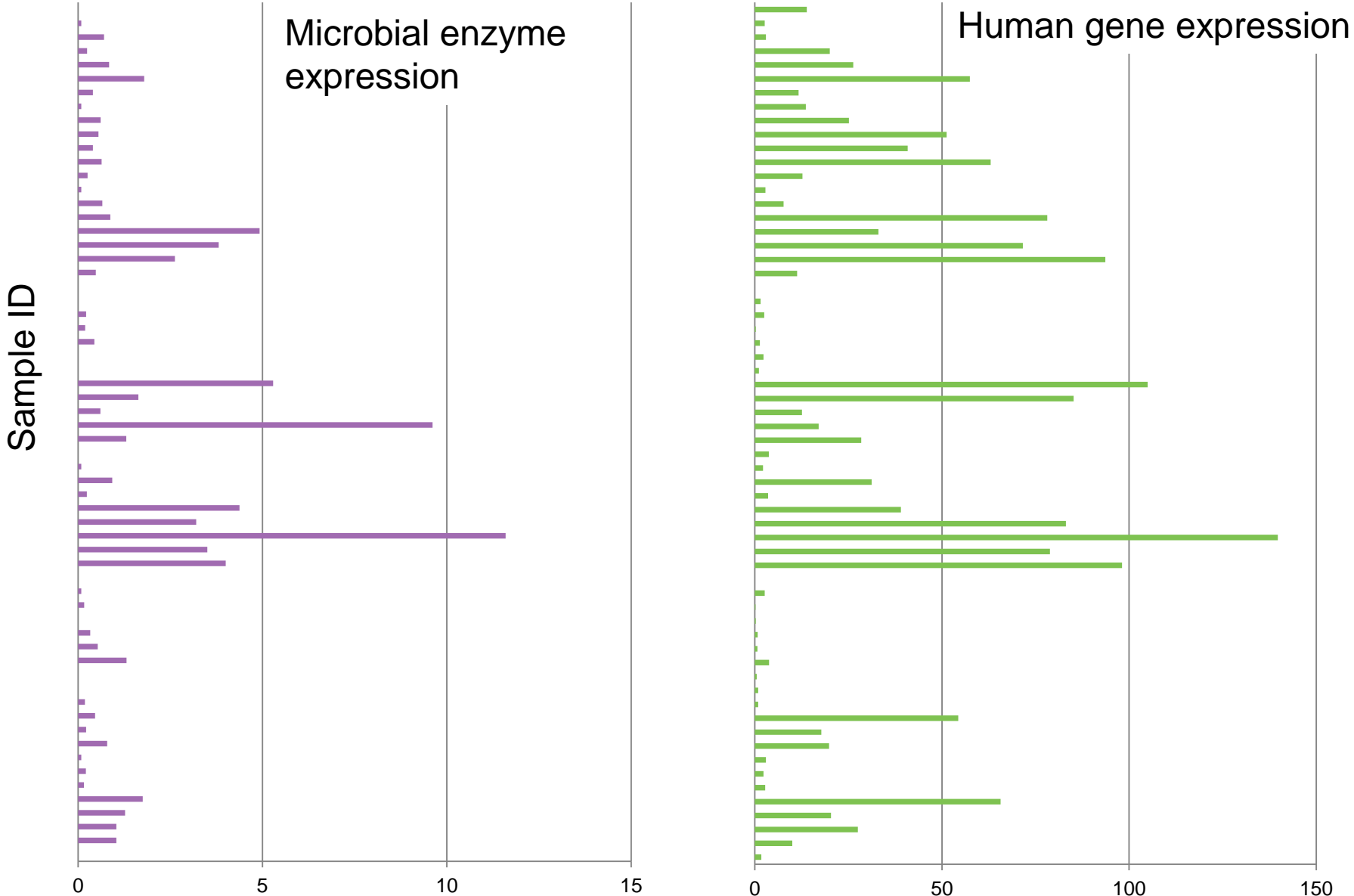
- ~1% filtered sequences with a significant hit to BioCyc database
- Assembly with complex microbiota?
- Paired-end sequences are treated independently (for hi-seq)
- Confidence in identification of strains hits from metagenomic and transcriptomic datasets
- Database: KEGG vs BioCyc vs others
- Some samples forward and reverse reads result in different microbiome profiles

Correlating human with microbial transcriptome

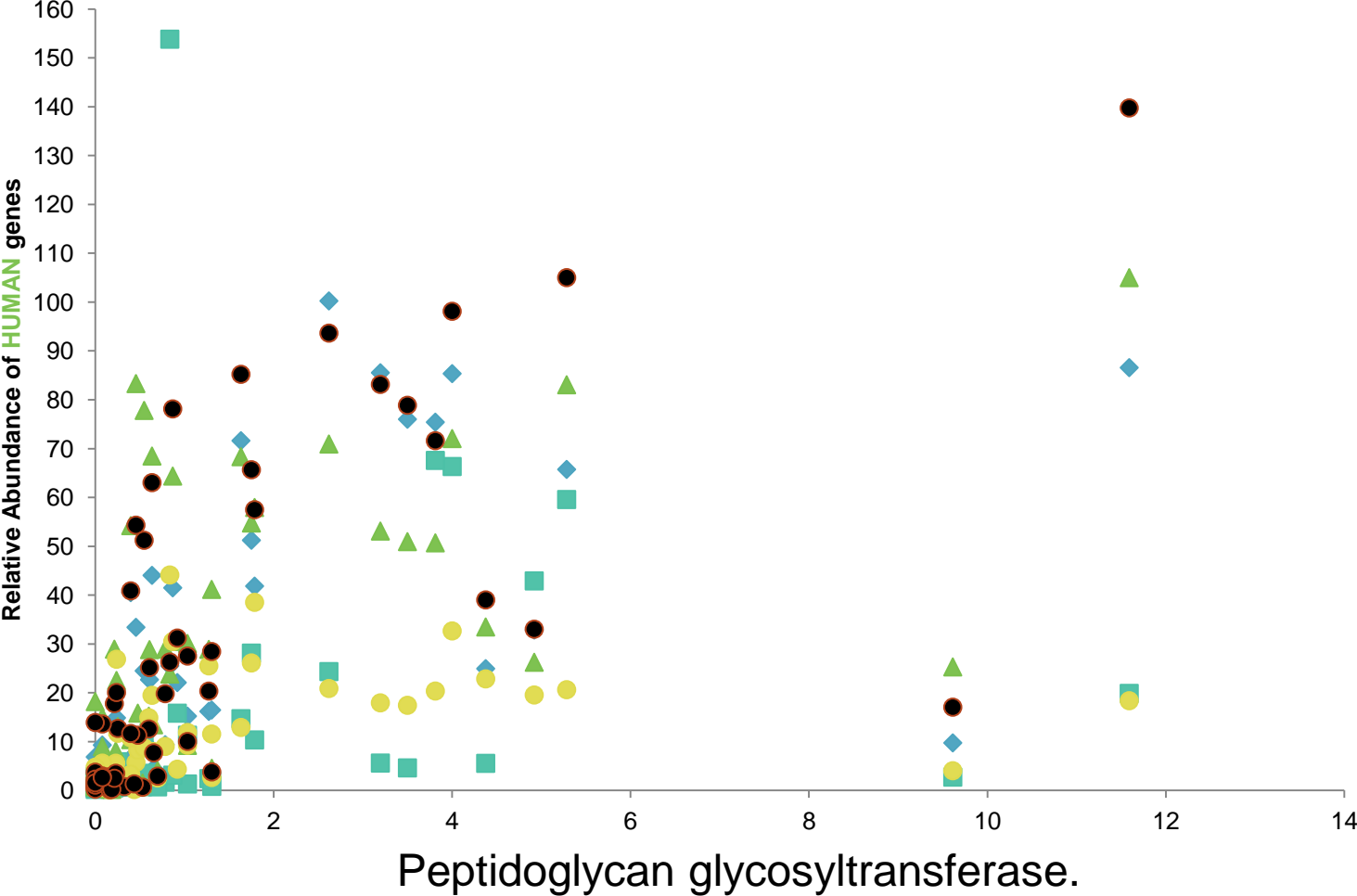


Get correlation coefficient (Rho) and p value
23 mln correlations, 400 after bonferroni correction

Best correlation: Peptidoglycan glycosyltransferase vs Human gene (inflammasome related)



Best correlation: microbial enzyme vs 5 human genes



Summary

- Will be happy to discuss our methods and some of the findings
- Currently working on relating human and microbiome functions in disease states

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