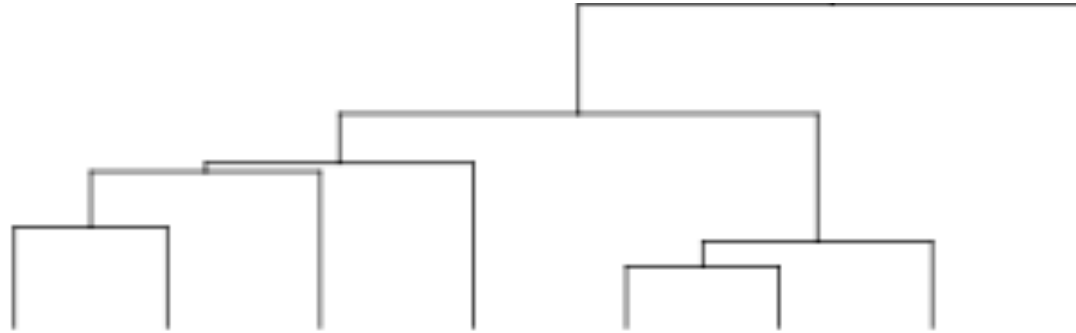


read NCBI taxonomy tree

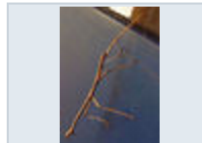
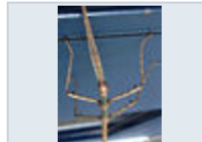


interesting NCBI taxonomic classifications...



Diaperomera femorata TRUSTED

 © Allen



[see all media](#)

Tribe recognized by [NCBI Taxonomy](#):

[Cellular organisms](#) +

[Eukaryota](#) +

[Opisthokonta](#) +

[Metazoa](#) +

[Eumetazoa](#) +

[Bilateria](#) +

[Protostomia](#) +

[Ecdysozoa](#) +

[Panarthropoda](#) +

[Arthropoda](#) +

[Mandibulata](#) +

[Pancrustacea](#) +

[Hexapoda](#) +

[Insecta](#) +

[Dicondylia](#) +

[Pterygota](#) +

[Neoptera](#) +

[Orthopteroidea](#) +

[Phasmatodea](#) +

[Verophasmatodea](#) +

[Anareolatae](#) +

[Diaperomeridae](#) +

[Diaperomerinae](#) +

[Diaperomerini](#)

[Bacteria](#) +

[Diaperomera](#) +

[Libethra](#) +

[Oncotophasma](#) +

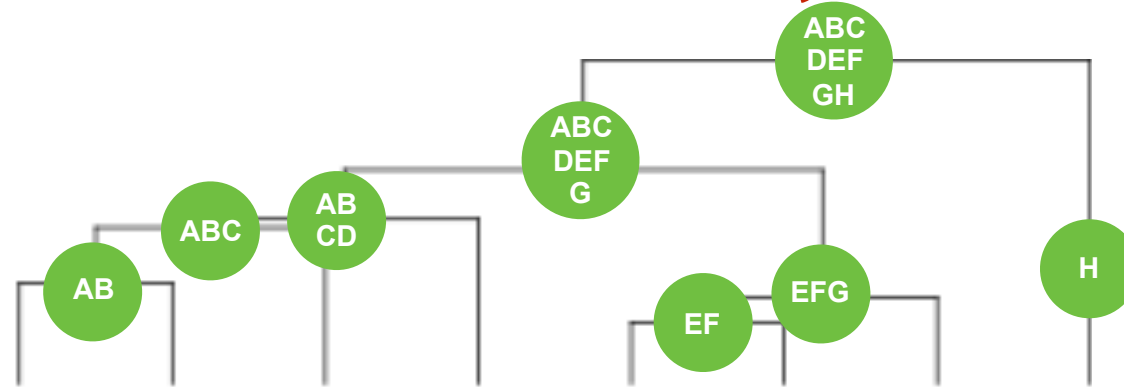
[Pseudosermyle](#) +

[Unclassified Diap](#)

[Ocnophilini](#) +

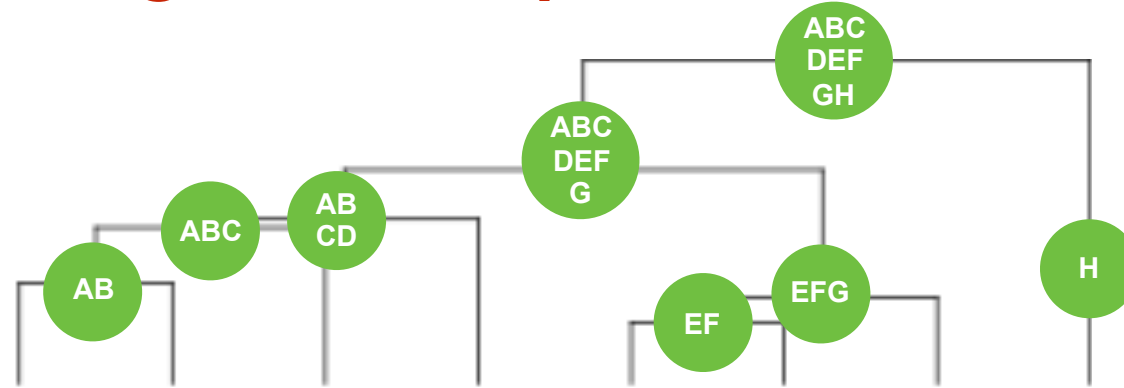
[Oreophoetini](#) +

read NCBI taxonomy tree



species

assign RNA-seq reads to leaves

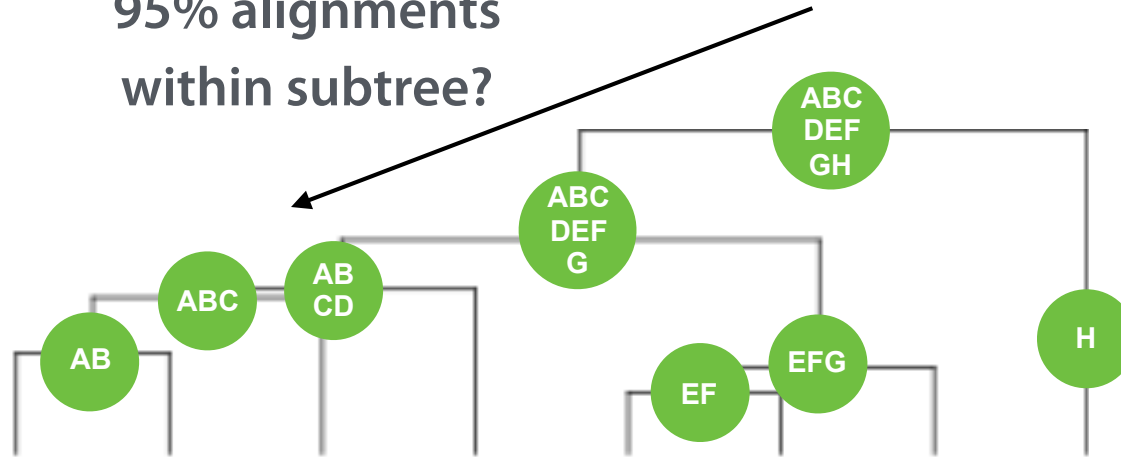


reads
1
2
3
4
5

	A	B	C	D	E	F	G	H
1	x	x	x	x				
2	x	x						
3					x	x	x	
4	x	x	x	x	x	x	x	
5	x	x	x		x	x		x

species

95% alignments
within subtree?



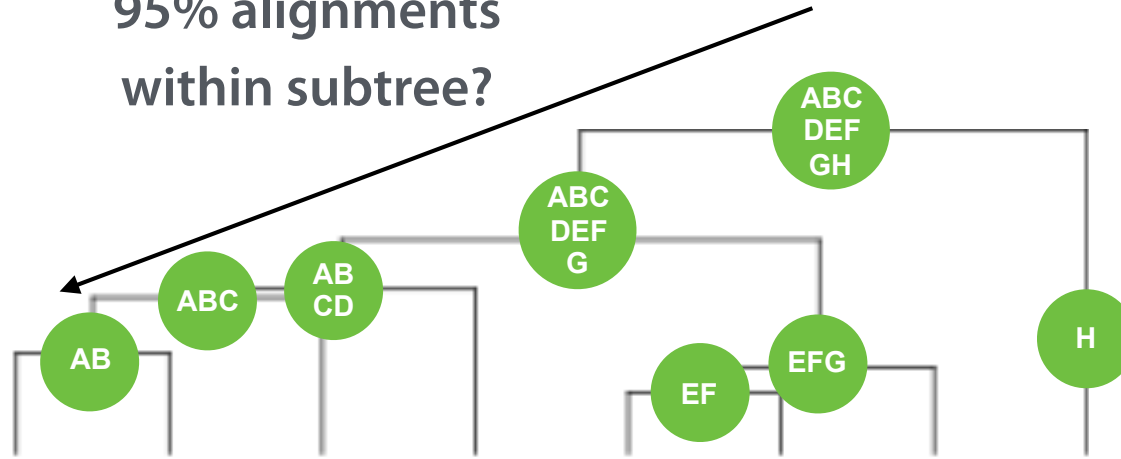
reads 1

A	B	C	D	E	F	G	H
x	x	x	x				
x	x						
				x	x	x	
x	x	x	x	x	x	x	
x	x	x		x	x		x

species

walk down from root until subtree no longer explains
x% of alignments

95% alignments
within subtree?



reads

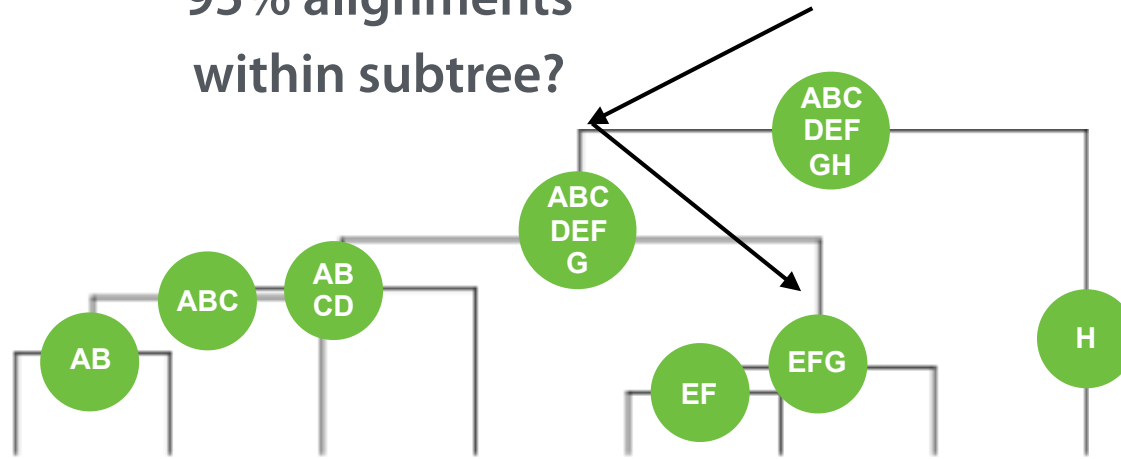
1
2
3
4
5

A	B	C	D	E	F	G	H
x	x	x	x				
x	x						
				x	x	x	
x	x	x	x	x	x	x	
x	x	x		x	x		x

species

do this for each read

95% alignments
within subtree?



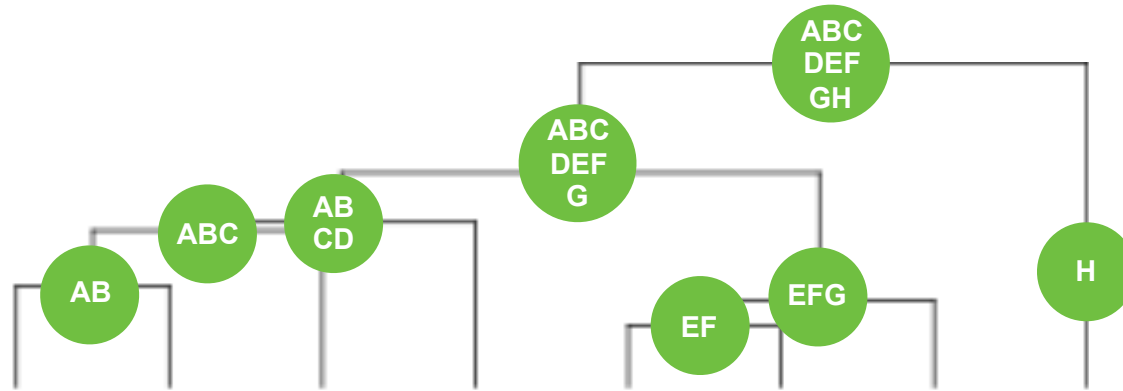
reads

1
2
3
4
5

A	B	C	D	E	F	G	H
x	x	x	x				
x	x						
				x	x	x	
x	x	x	x	x	x	x	
x	x	x		x	x		x

species

do this for each read



reads

1
2
3
4
5

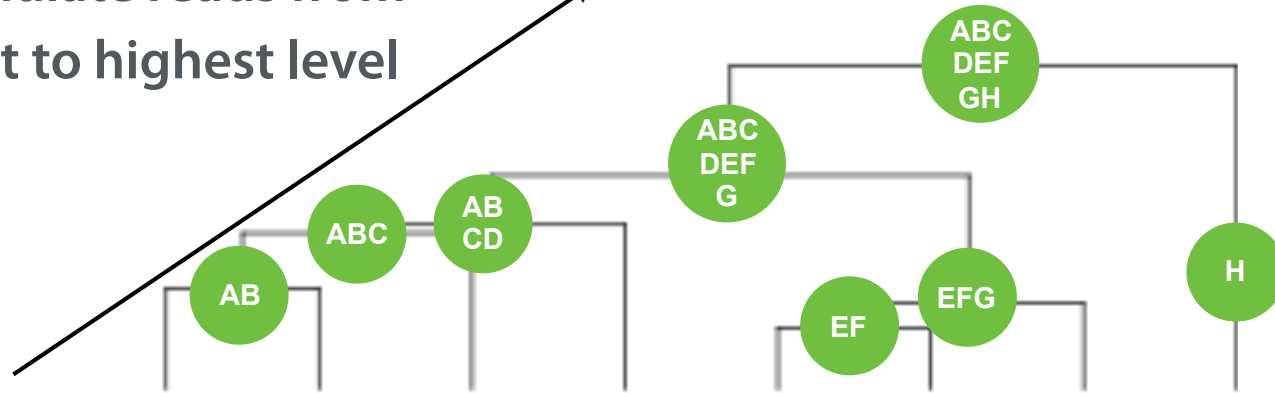
	A	B	C	D	E	F	G	H
1	x	x	x	x				
2	x	x						
3					x	x	x	
4	x	x	x	x	x	x	x	
5	x	x	x		x	x		x

species



assign read to most specific node possible

accumulate reads from lowest to highest level



read counts
direct sum

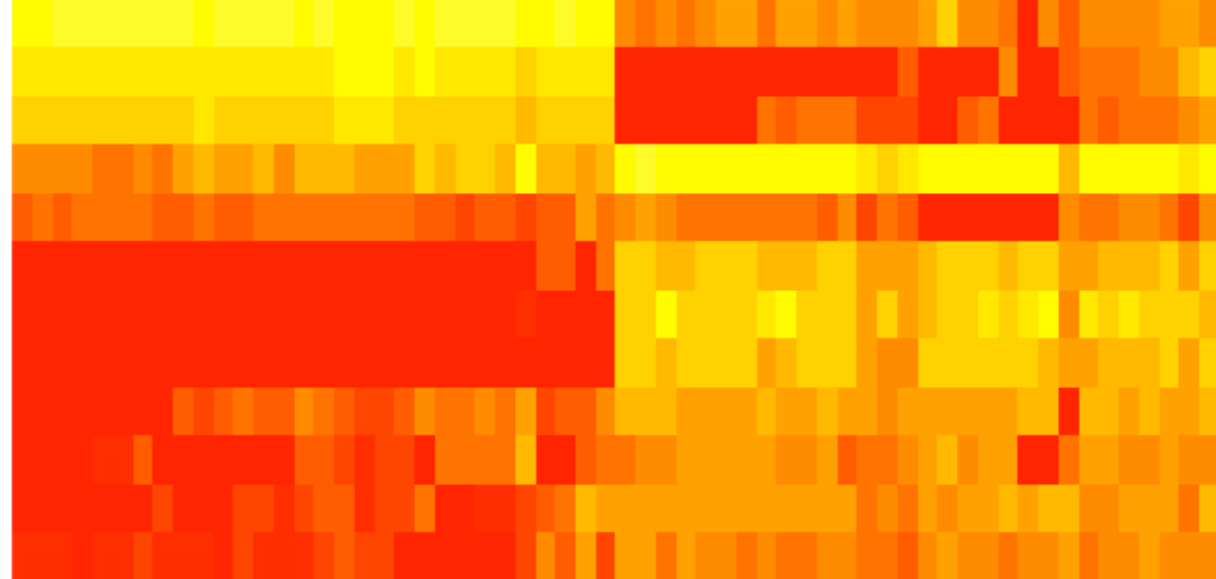
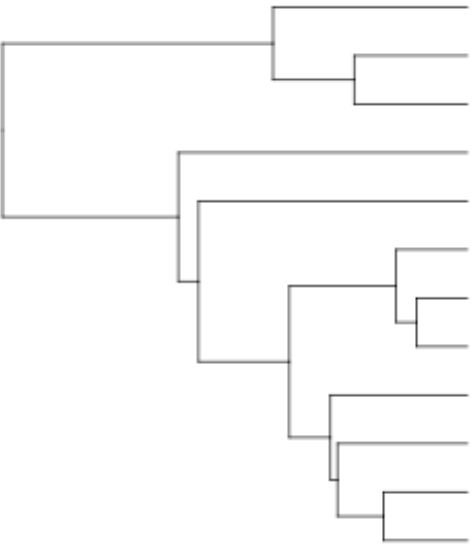
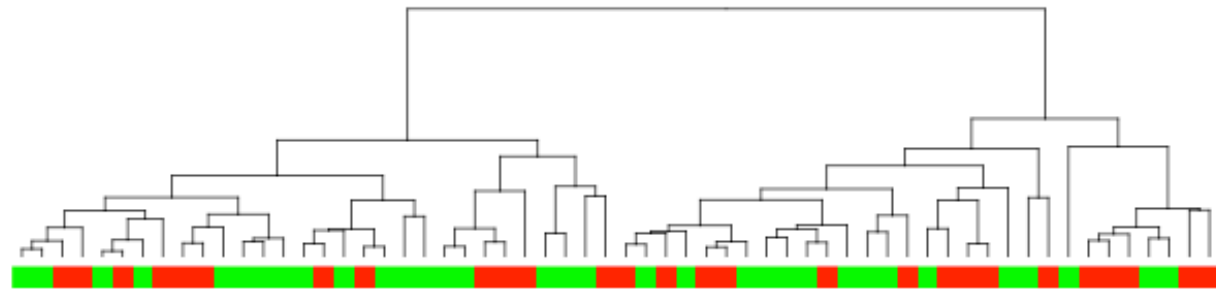
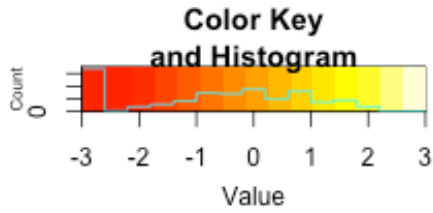
AB	1	1
ABC	0	1
AB CD	1	2
EF	1	1
EFG	0	1
ABC DEF G	1	4
ABC DEF GH	1	5

A	B	C	D	E	F	G	H
x	x	x	x				
x	x						
				x	x	x	
x	x	x	x	x	x	x	
x	x	x		x	x		x

species

sum reads going up the tree

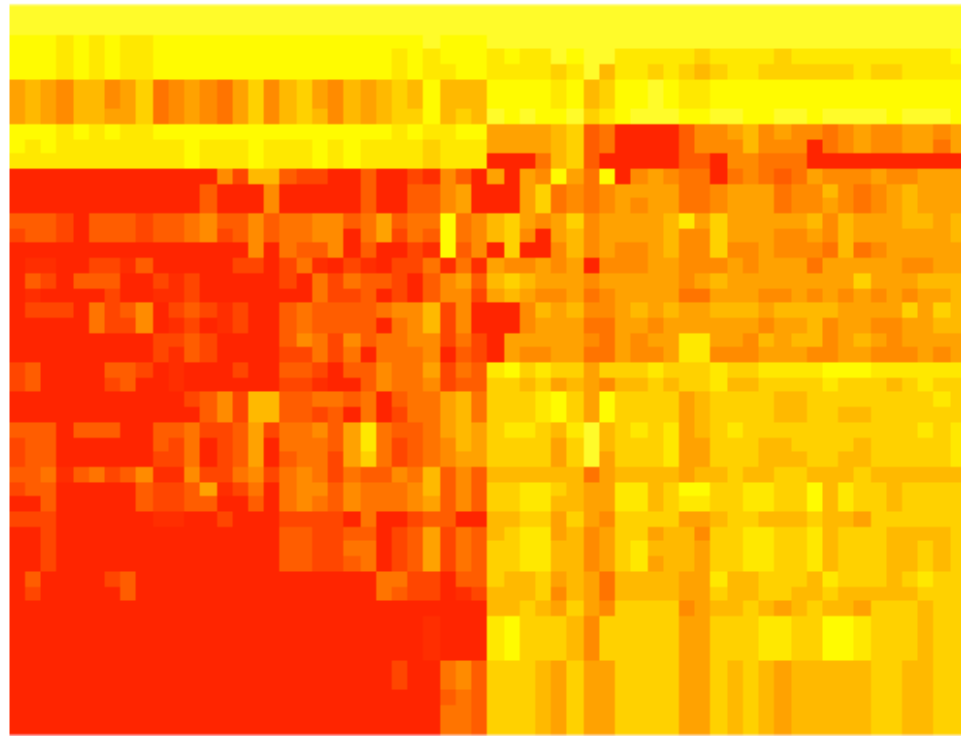
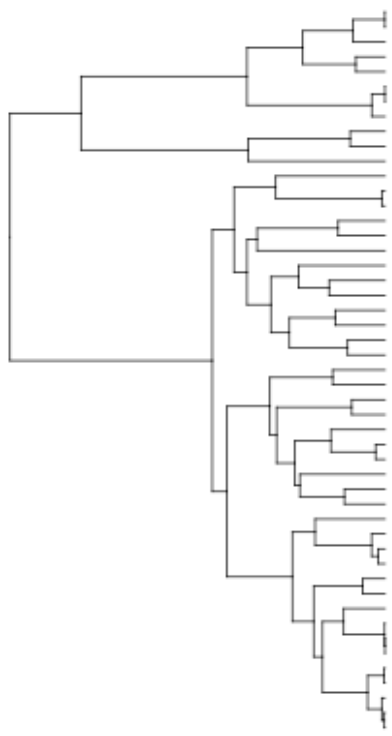
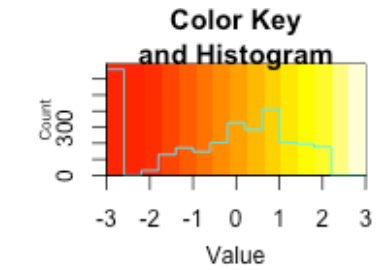
indent	distFromRoot	level	name	uniqueReads	allSumReads
>	1	no rank	root	0	5964
>>	2	no rank	cellular organisms	70	5894
>>>	3	superkingdom	Bacteria	22	5080
>>>>	4	phylum	Proteobacteria	9	4039
>>>>>	5	class	Gammaproteobacteria	6	226
>>>>>>	6	order	Pseudomonadales	0	201
>>>>>>>	7	family	Moraxellaceae	5	80
>>>>>>>>	8	genus	Acinetobacter	11	24
>>>>>>>>>	9	species	Acinetobacter johnsonii	3	0
>>>>>>>>>>	9	species group	Acinetobacter calcoaceticus/baumannii complex	1	12
>>>>>>>>>>>	10	species	Acinetobacter baumannii	11	1
>>>>>>>>	8	genus	Enhydrobacter	0	43
>>>>>>>>>	9	species	Enhydrobacter aerosaccus	0	43
>>>>>>>>>>>	10	no rank	Enhydrobacter aerosaccus SK60	43	0
>>>>>>>>	7	family	Pseudomonadaceae	0	116
>>>>>>>>>	8	genus	Pseudomonas	33	83
>>>>>>>>>>	9	species group	Pseudomonas aeruginosa group	0	37
>>>>>>>>>>>	10	species	Pseudomonas mendocina	1	34
>>>>>>>>>>>>	11	no rank	Pseudomonas mendocina EGD-AQ5	34	0
>>>>>>>>>>>	9	species group	Pseudomonas fluorescens group	0	3
>>>>>>>>>>>	9	species group	Pseudomonas putida group	0	36
>>>>>>>>>>>>	10	species	Pseudomonas putida	28	8
>>>>>>>>>>>>>	11	no rank	Pseudomonas putida H8234	6	0
>>>>>>>>>>>	9	species group	Pseudomonas stutzeri group	0	3
>>>>>>>>>>>>>	10	species subgroup	Pseudomonas stutzeri subgroup	0	3
>>>>>>>>	6	order	Enterobacteriales	0	9
>>>>>>>>>	7	family	Enterobacteriaceae	1	8
>>>>>>>>>>	8	genus	Serratia	0	3
>>>>>>>>>>>	9	species	Serratia marcescens	0	3
>>>>>>>>>>>>	10	subspecies	Serratia marcescens subsp. marcescens	0	3
>>>>>>>>>>>>>	11	no rank	Serratia marcescens subsp. marcescens Db11	3	0
>>>>>>>>	6	order	Xanthomonadales	0	12
>>>>>>>>>	7	family	Xanthomonadaceae	0	12
>>>>>>>>>>	8	genus	Stenotrophomonas	8	4
>>>>>	5	class	Alphaproteobacteria	13	3739
>>>>>>	6	order	Rhizobiales	10	3679
>>>>>>>	7	family	Bradyrhizobiaceae	36	3563
>>>>>>>>	8	genus	Bradyrhizobium	14	3500
>>>>>>>>>	9	species	Bradyrhizobium sp. BTAil	3141	0
>>>>>>>>>>	9	species	Bradyrhizobium sp. DFCI-1	356	0
>>>>>>>>	8	genus	Nitrobacter	0	10



- Bacteria
- Escherichia coli
- Enterobacteriaceae
- Propionibacterium
- Gamma proteobacteria
- Agrobacterium tumefaciens F2
- Janibacter hoylei PVAS-1
- Pseudomonas mendocina EGD-A
- Propionibacterium acnes
- Corynebacterium
- Pseudomonas
- Proteobacteria

TCGA-E9-A1NH.normal.unmapped_nonIBC_TCGA-E9-A1NH
 TCGA-AN-A04D.normal.unmapped_nonIBC_TCGA-AN-A04D
 TCGA-EW-A1PH.tumor.unmapped_nonIBC_TCGA-EW-A1PH
 TCGA-AN-A04D.tumor.unmapped_nonIBC_TCGA-AN-A04D
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 TCGA-AN-A0AT.tumor.unmapped_nonIBC_TCGA-AN-A0AT
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 TCGA-AD-A03N.normal.unmapped_nonIBC_TCGA-AD-A03N
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 TCGA-EW-A1J5.normal.unmapped_nonIBC_TCGA-EW-A1J5
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 TCGA-BH-A0EA.tumor.unmapped_nonIBC_TCGA-BH-A0EA
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 Sample_Yale-IBC-311.normal.unmapped
 Sample_Yale-IBC-300.tumor.unmapped
 Sample_Yale-IBC-300.normal.unmapped
 Sample_Yale-IBC-208.tumor.unmapped
 Sample_Yale-IBC-312.tumor.unmapped
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 Sample_Yale-IBC-311.tumor.unmapped
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 IBC_228_tumorSample_ibc_228_tumor.unmapped
 Sample_Yale-IBC-220.normal.unmapped
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 Sample_Yale-IBC-333.tumor.unmapped

direct read counts



- root
- cellular organisms
- Bacteria
- Proteobacteria
- Gammaproteobacteria
- Propionibacteriales
- Propionibacteriaceae
- Actinobacteria
- Enterobacteriales
- Enterobacteriaceae
- Escherichia
- Bradyrhizobiaceae
- Methylobacteriaceae
- Methylobacterium
- Betaproteobacteria
- Burkholderiales
- Burkholderiaceae
- Propionibacterium acnes
- Moraxellaceae
- Acinetobacter
- Corynebacteriales
- Corynebacteriaceae
- Lactobacillales
- Streptococcaceae
- Micrococcales
- Micrococcaceae
- Alphaproteobacteria
- Rhizobiales
- Pseudomonadales
- Pseudomonadaceae
- Pseudomonas
- Propionibacterium
- Firmicutes
- Bacilli
- Pseudomonas aeruginosa group
- Staphylococcus
- Bacillales
- Staphylococcaceae
- Micrococcus
- Micrococcus luteus
- Pseudomonas mendocina
- Intrasporangiaceae
- Janibacter hoylei
- Janibacter
- Rhizobiaceae
- Rhizobium/Agrobacterium group
- Agrobacterium tumefaciens
- Agrobacterium
- Agrobacterium tumefaciens complex

TCGA-AN-A0XR:normal,unmapped_nonIBC_TCGA_AN-A0XR
TCGA-E9-A1NH:tumor,unmapped_nonIBC_TCGA_E9-A1NH
TCGA-BH-A0D1:normal,unmapped_nonIBC_TCGA_BH-A0D1
TCGA-EW-A1PH:tumor,unmapped_nonIBC_TCGA-EW-A1PH
TCGA-AN-A0A1:tumor,unmapped_nonIBC_TCGA-AN-A0A1
TCGA-AN-A0A1:normal,unmapped_nonIBC_TCGA-AN-A0A1
TCGA-AN-A0A0:tumor,unmapped_nonIBC_TCGA-AN-A0A0
TCGA-AN-A0A0:normal,unmapped_nonIBC_TCGA-AN-A0A0
TCGA-EW-A1PH:normal,unmapped_nonIBC_TCGA-EW-A1PH
TCGA-BE-A0F0:tumor,unmapped_nonIBC_TCGA-BE-A0F0
TCGA-EZ-A1B6:tumor,unmapped_nonIBC_TCGA-EZ-A1B6
TCGA-BH-A0B3:tumor,unmapped_nonIBC_TCGA-BH-A0B3
TCGA-E9-A1NH:normal,unmapped_nonIBC_TCGA-E9-A1NH
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TCGA-EZ-A1B5:normal,unmapped_nonIBC_TCGA-EZ-A1B5
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TCGA-AN-A0G3:tumor,unmapped_nonIBC_TCGA-AN-A0G3
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TCGA-EW-A1A5:tumor,unmapped_nonIBC_TCGA-EW-A1A5
TCGA-EW-A1A5:normal,unmapped_nonIBC_TCGA-EW-A1A5
TCGA-AB-A0B2:normal,unmapped_nonIBC_TCGA-AB-A0B2
TCGA-BH-A0EA:tumor,unmapped_nonIBC_TCGA-BH-A0EA
TCGA-A2-A0EY:normal,unmapped_nonIBC_TCGA-A2-A0EY
Sample_Yale-IBC-315:normal,unmapped
IBC_228_tumor,unmapped
Sample_Yale-IBC-278:tumor,unmapped
Sample_Yale-IBC-266:tumor,unmapped
Sample_Yale-IBC-328:tumor,unmapped
Sample_Yale-IBC-298:normal,unmapped
Sample_Yale-IBC-333:tumor,unmapped
Sample_Yale-IBC-270:normal,unmapped
Sample_Yale-IBC-232:normal,unmapped
Sample_Yale-IBC-208:normal,unmapped
Sample_Yale-IBC-314:tumor,unmapped
Sample_Yale-IBC-312:normal,unmapped
Sample_Yale-IBC-287:tumor,unmapped
Sample_Yale-IBC-305:tumor,unmapped
Sample_Yale-IBC-232:tumor,unmapped
Sample_Yale-IBC-343:normal,unmapped
Sample_Yale-IBC-328:tumor,unmapped
Sample_Yale-IBC-208:normal,unmapped
Sample_Yale-IBC-305:tumor,unmapped
Sample_Yale-IBC-300:normal,unmapped
Sample_Yale-IBC-235:normal,unmapped
Sample_Yale-IBC-300:tumor,unmapped
Sample_Yale-IBC-298:normal,unmapped
Sample_Yale-IBC-235:tumor,unmapped
Sample_Yale-IBC-267:tumor,unmapped
Sample_Yale-IBC-333:normal,unmapped
Sample_Yale-IBC-266:normal,unmapped
Sample_Yale-IBC-311:tumor,unmapped
Sample_Yale-IBC-220:tumor,unmapped

cumulative read counts

Zimmerome

indent	distFromRoot	level	name	uniqueReads	allSumReads
>	0	no rank	root	0	419163
>>	1	no rank	cellular organisms	0	419163
>>>	2	superkingdom	Bacteria	320159	99004
>>>>	3	phylum	Proteobacteria	28057	70938
>>>>>	4	class	Gammaproteobacteria	2321	68607
>>>>>>	5	order	Pseudomonadales	0	68509
>>>>>>>	6	family	Moraxellaceae	0	68488
>>>>>>>>	7	genus	Acinetobacter	0	68488
>>>>>>>>>	8	species	Acinetobacter sp. MII	68486	0
>>>>>>>	6	family	Pseudomonadaceae	0	21
>>>>>>>>	7	genus	Pseudomonas	2	19
>>>>	5	order	Enterobacteriales	0	6
>>>>>	6	family	Enterobacteriaceae	12	6
>>>>>>	7	genus	Escherichia	4	0
>>>>>>>	8	species	Escherichia coli	8	0
>>>>>>>>	9	no rank	Escherichia coli O104:H4	0	3
>>>>>>>>>	10	no rank	Escherichia coli O104:H4 str. 2011EL-1675A	3	0
>>>>>>>	7	genus	Klebsiella	0	60
>>>>>>>>	8	species	Klebsiella pneumoniae	0	60
>>>>>>>>>	9	subspecies	Klebsiella pneumoniae subsp. pneumoniae	0	59
>>>>>>>>>>	10	no rank	Klebsiella pneumoniae subsp. pneumoniae BJ1-GA	59	0

In healthy individuals, Acinetobacter colonies on the skin correlate with low incidence of allergies. Acinetobacter is thought to be allergy-protective.

Klebsiella pneumoniae ...found in the normal flora of the mouth, skin, and intestines