

My bins

From the anode's sample metagenomic work

Realtime taxonomy estimation for bins (whenever possible)

	Name	Splits	Len	Comp.	Red.
<input type="radio"/>	 bin_C45_R0	434	1.81M	45.1	0.0
<input type="radio"/>	 bin_C63_R6	903	3.63M	63.4	5.6
<input type="radio"/>	 bin_C67_R6	973	3.24M	67.6	5.6
<input type="radio"/>	 bin_C94_R11	723	3.72M	94.4	11.3
<input type="radio"/>	 bin_C94_R4	299	2.43M	94.4	4.2
<input type="radio"/>	 bin_C95_R11	629	3.80M	95.8	11.3
<input checked="" type="radio"/>	 bin_C97_R13	358	3.81M	97.2	12.7

 New bin

Load bin collection

Store bin collection

Generate a static summary page

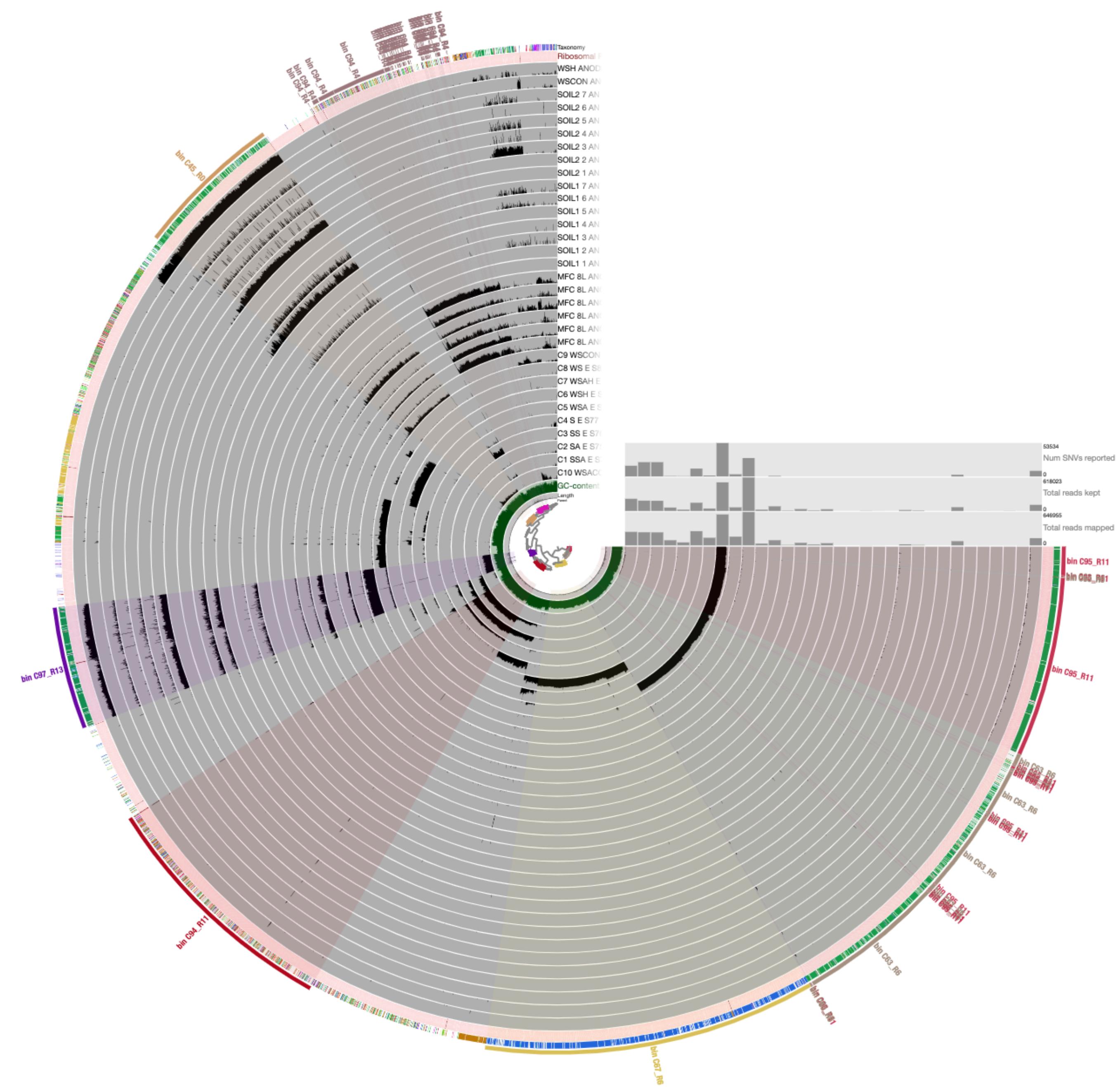
Recalculate / Show Taxonomy for Bins

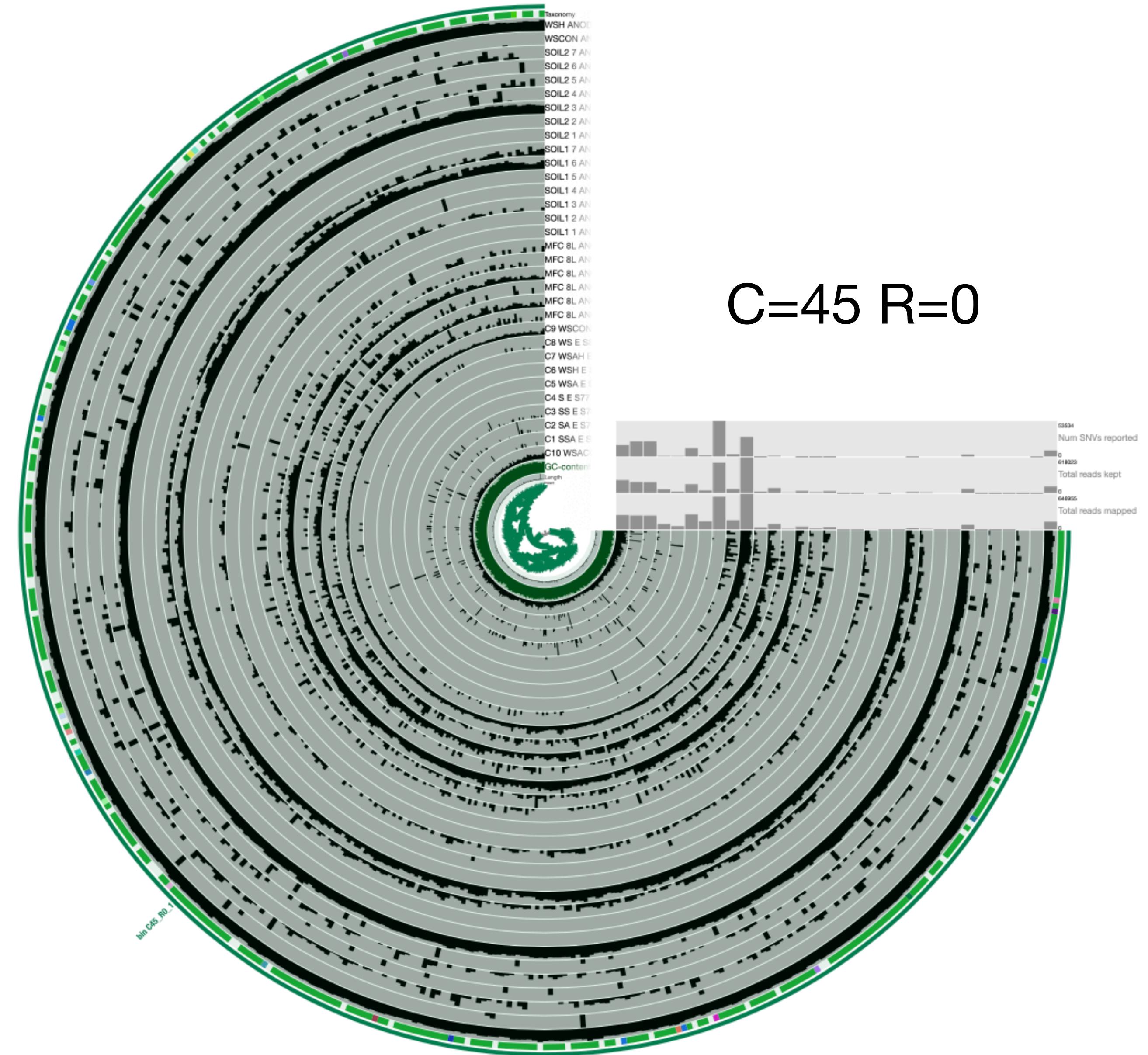
Draw

6892 splits and 44698 objects drawn in 3.61 seconds

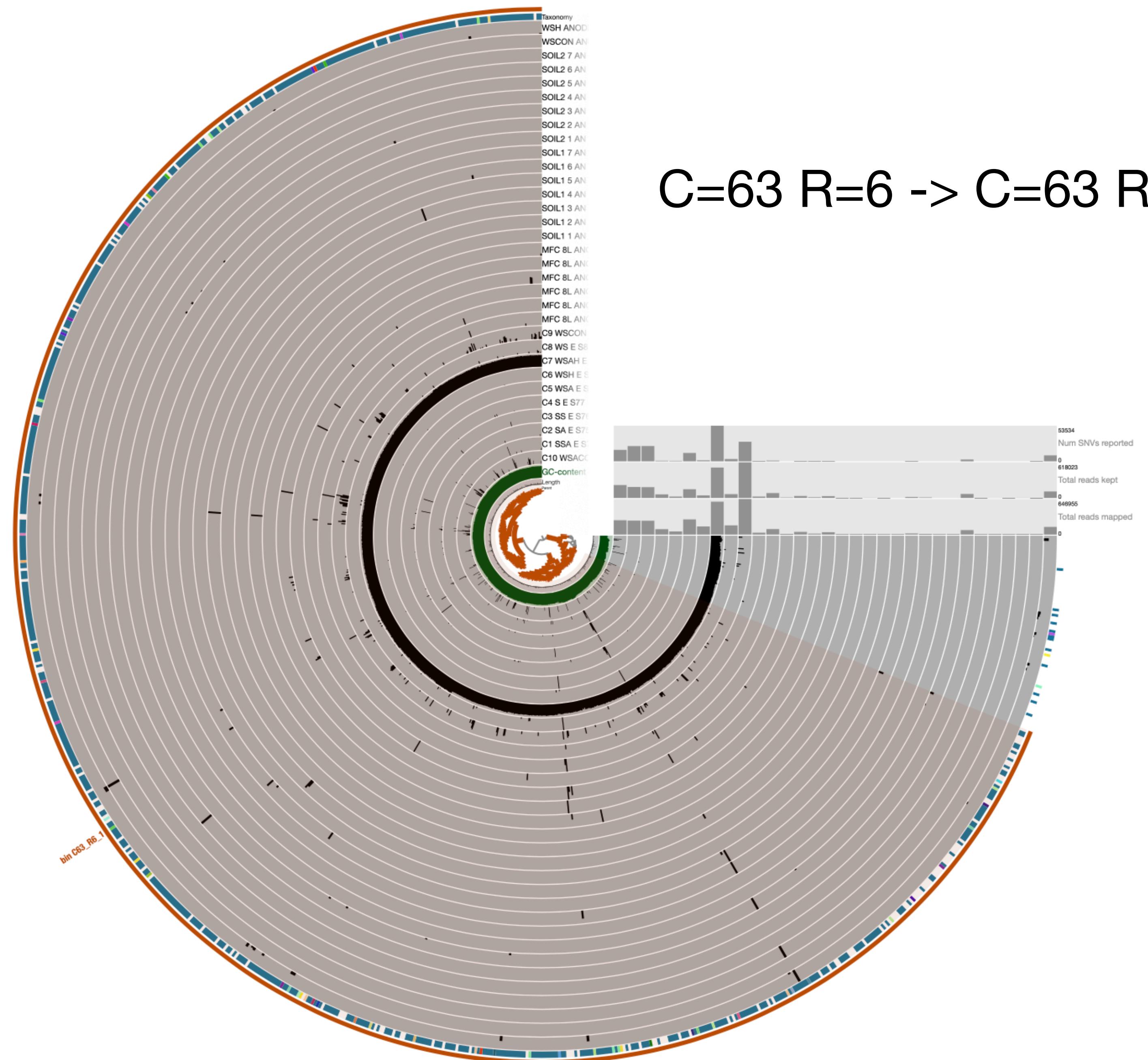
Load State

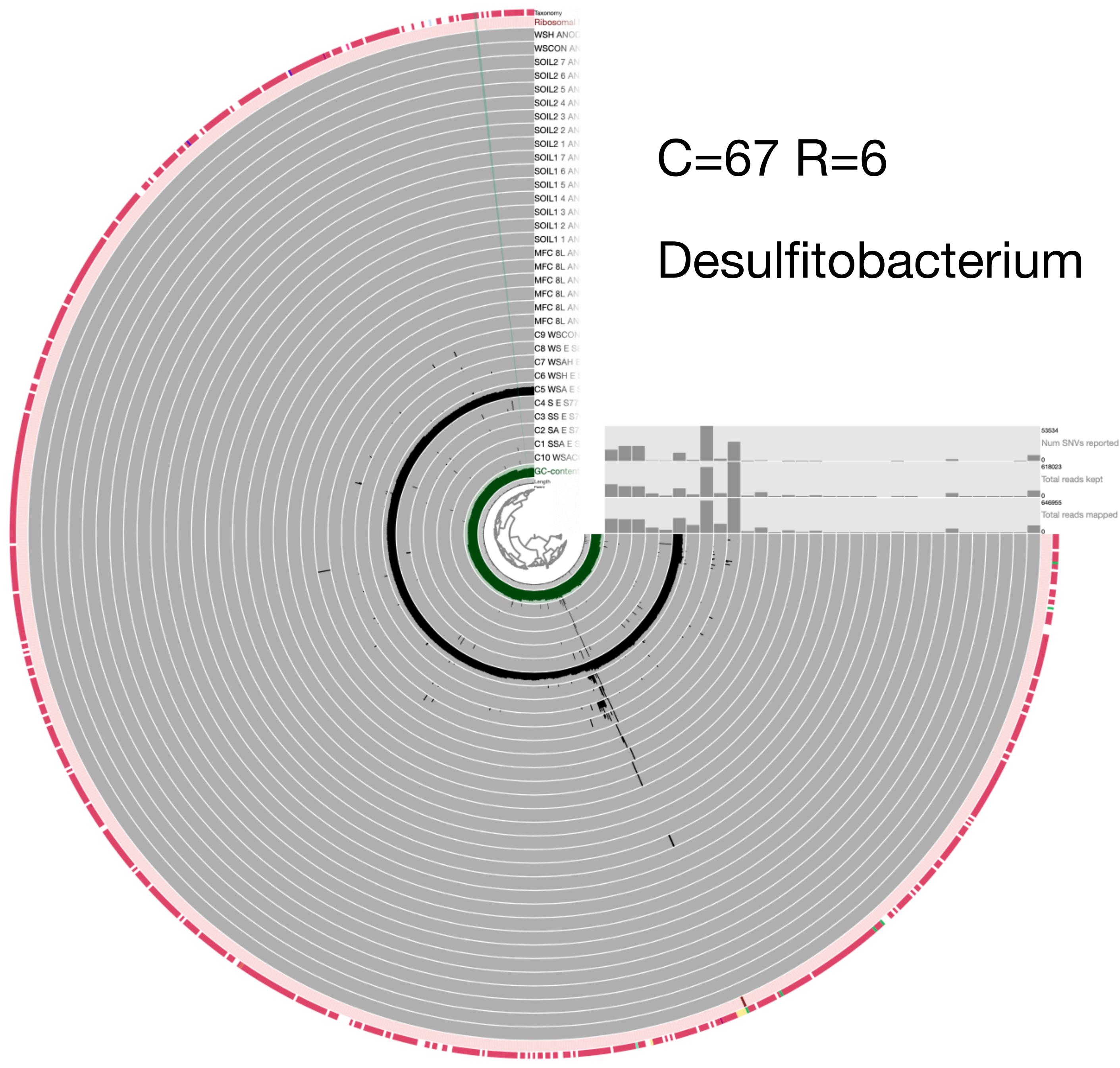
 Save State





C=63 R=6 → C=63 R=4





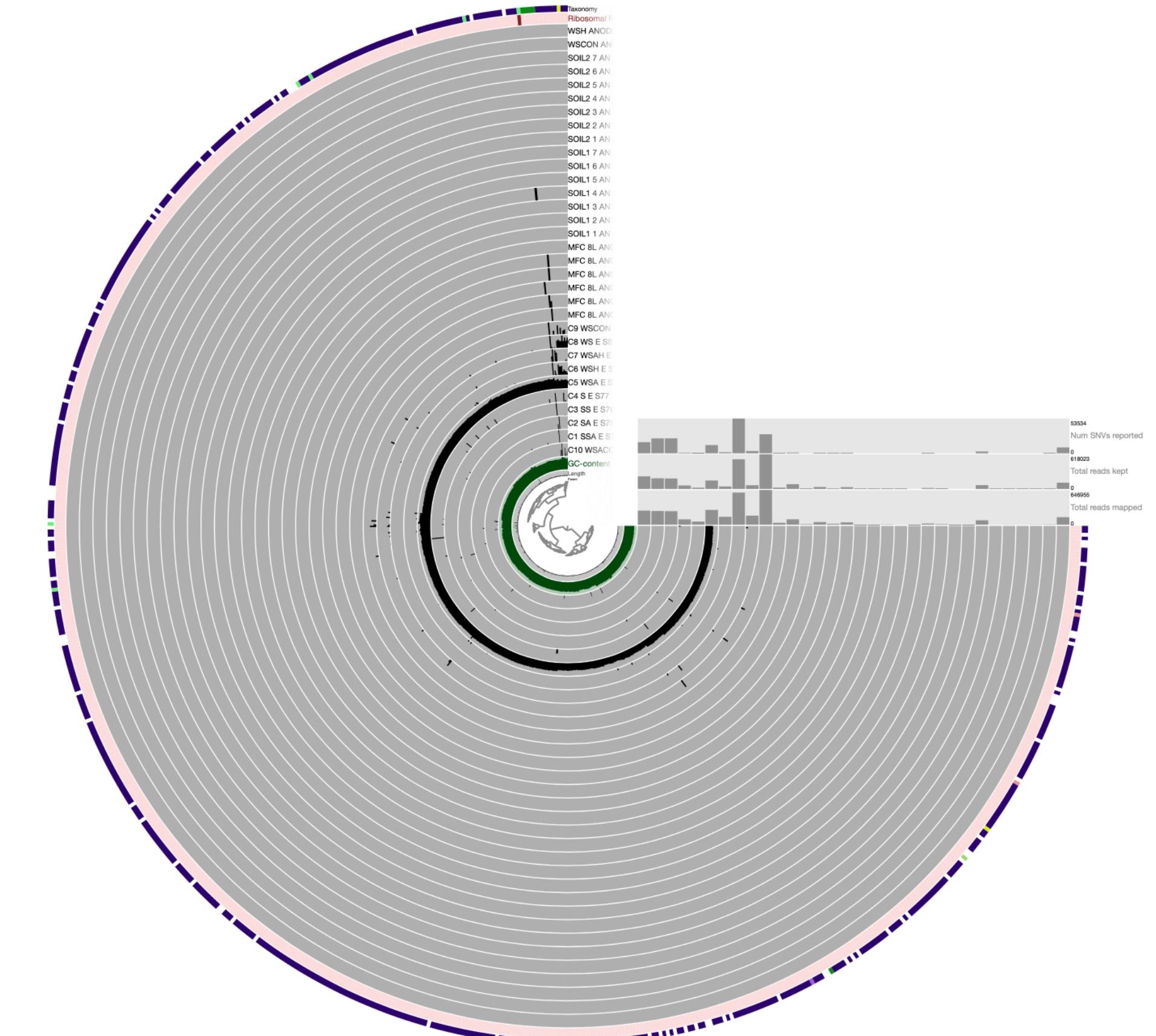
C=67 R=6

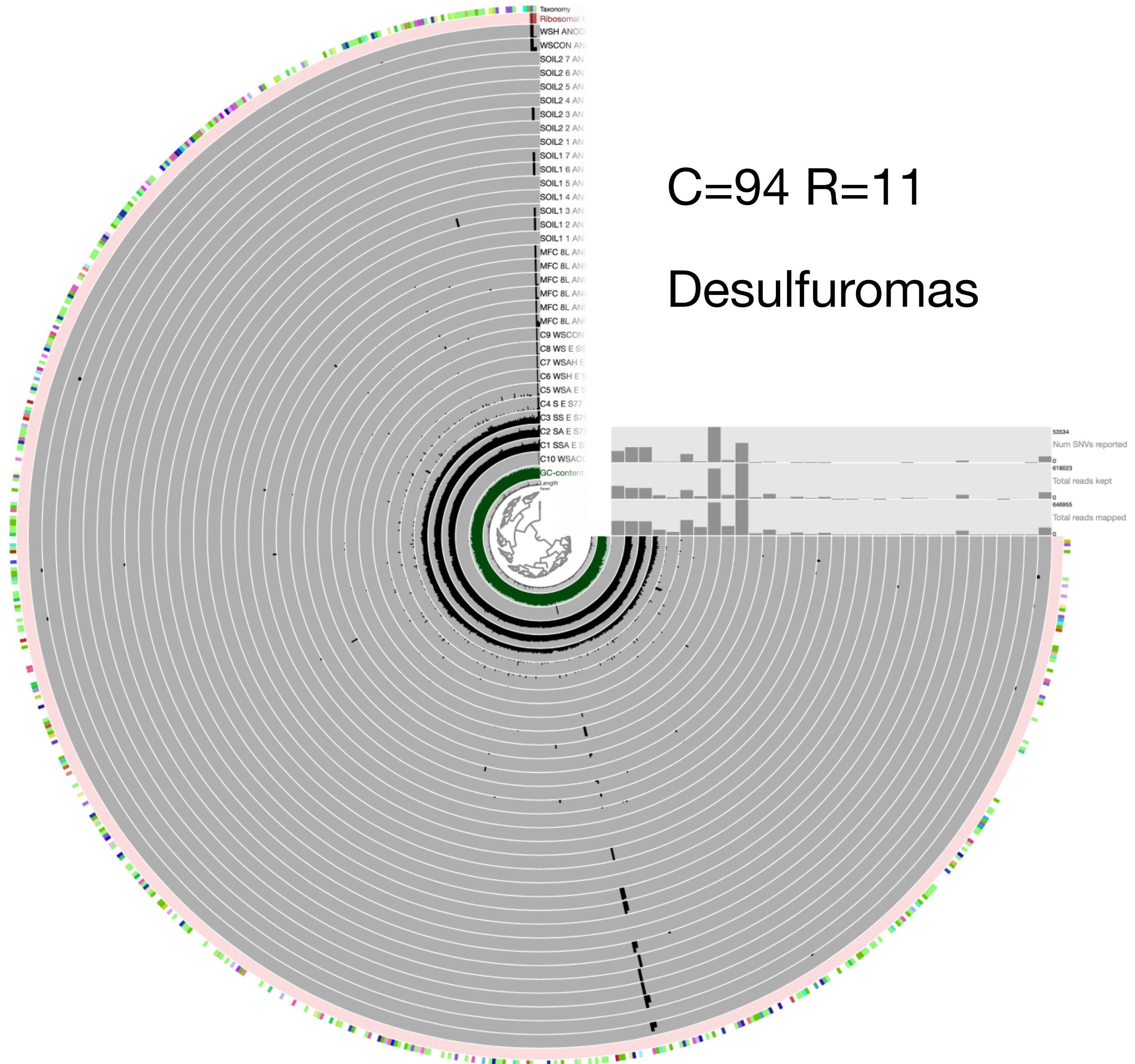
Desulfobacterium

C=56 R=4

Refining bin_C56_R4 from "collection_2"

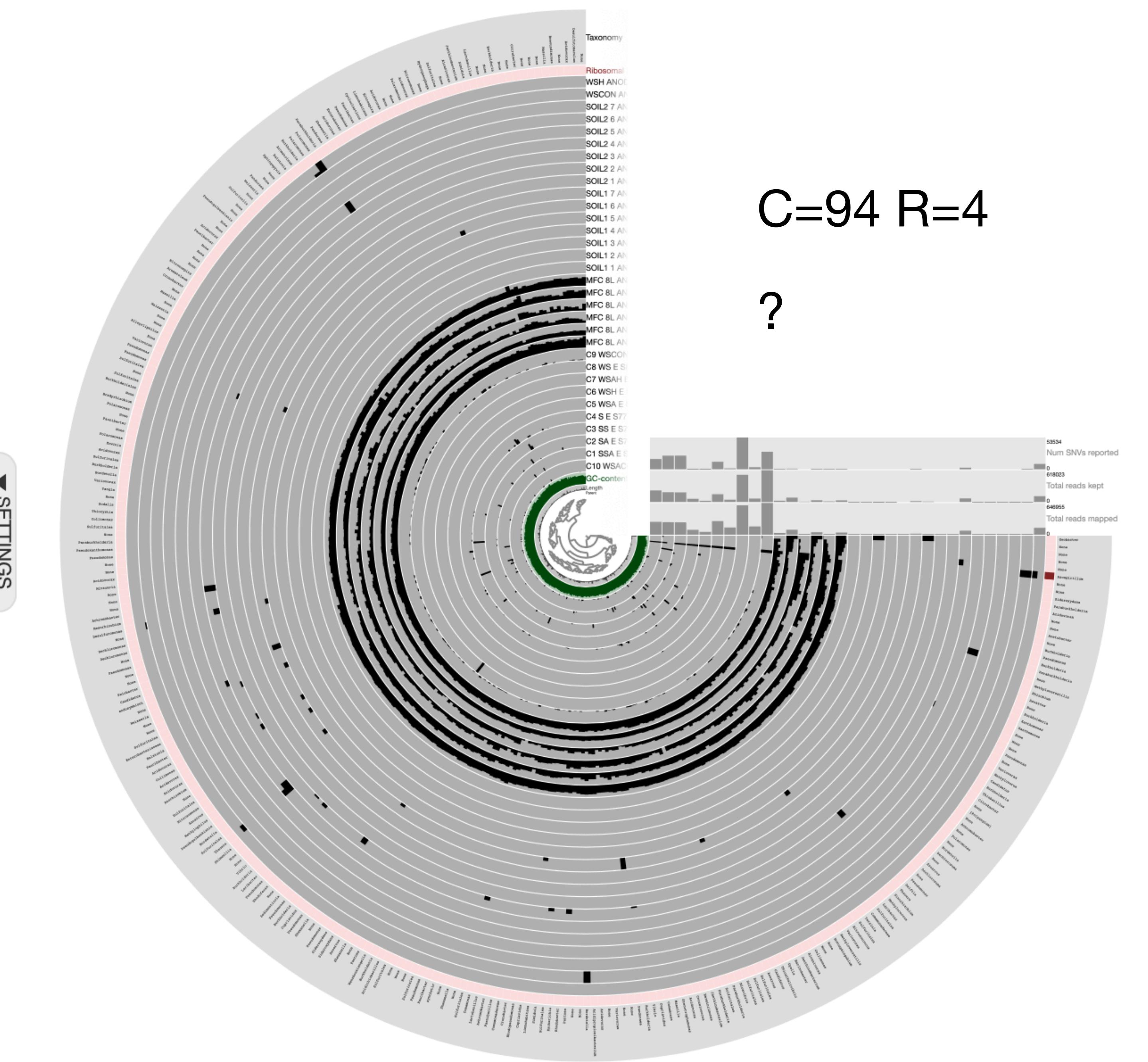
Items order: Seq. Composition + Diff. Coverage (D: Euclidean; L: Ward) | Current view: mean_coverage | Sample order: custom





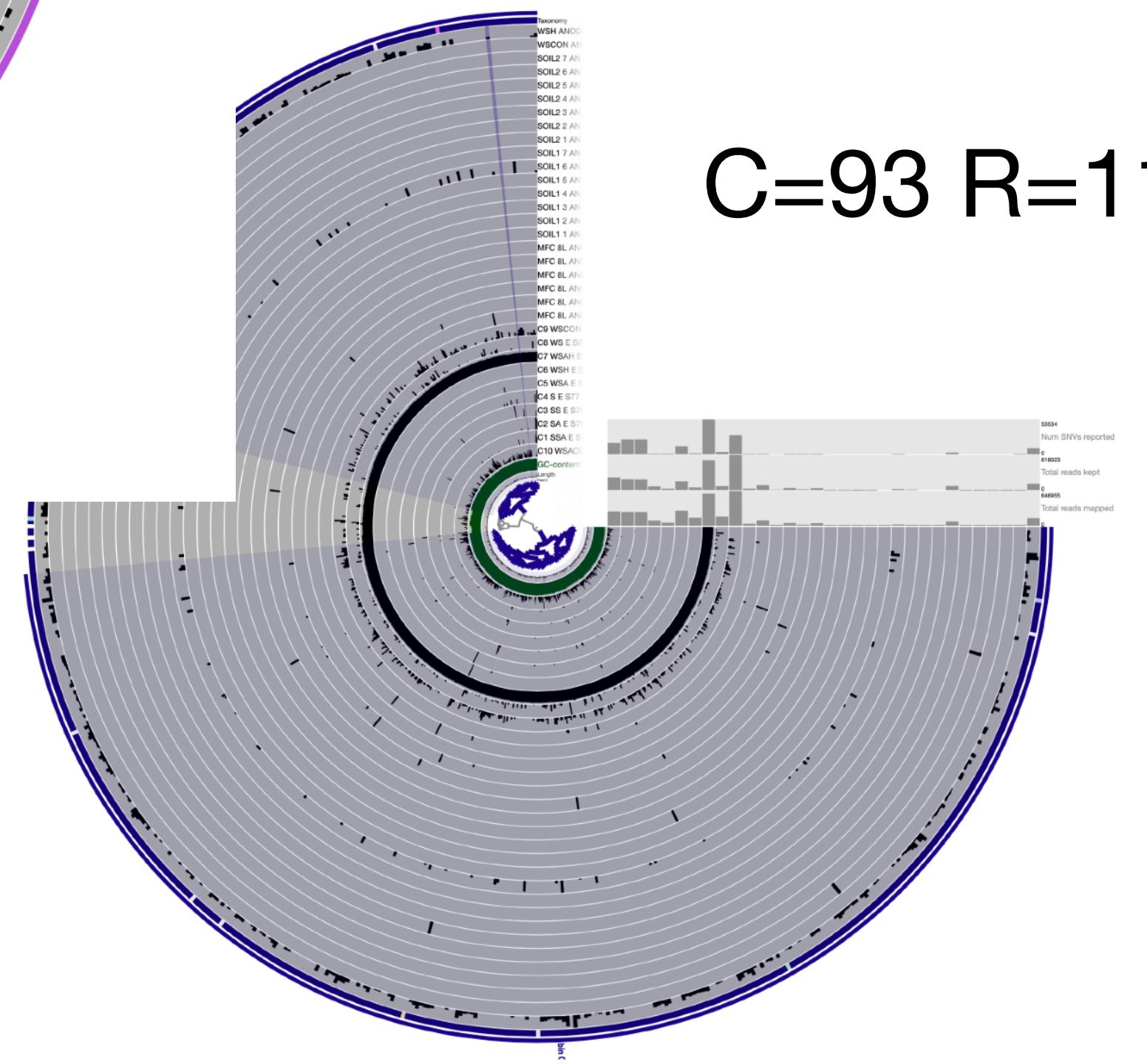
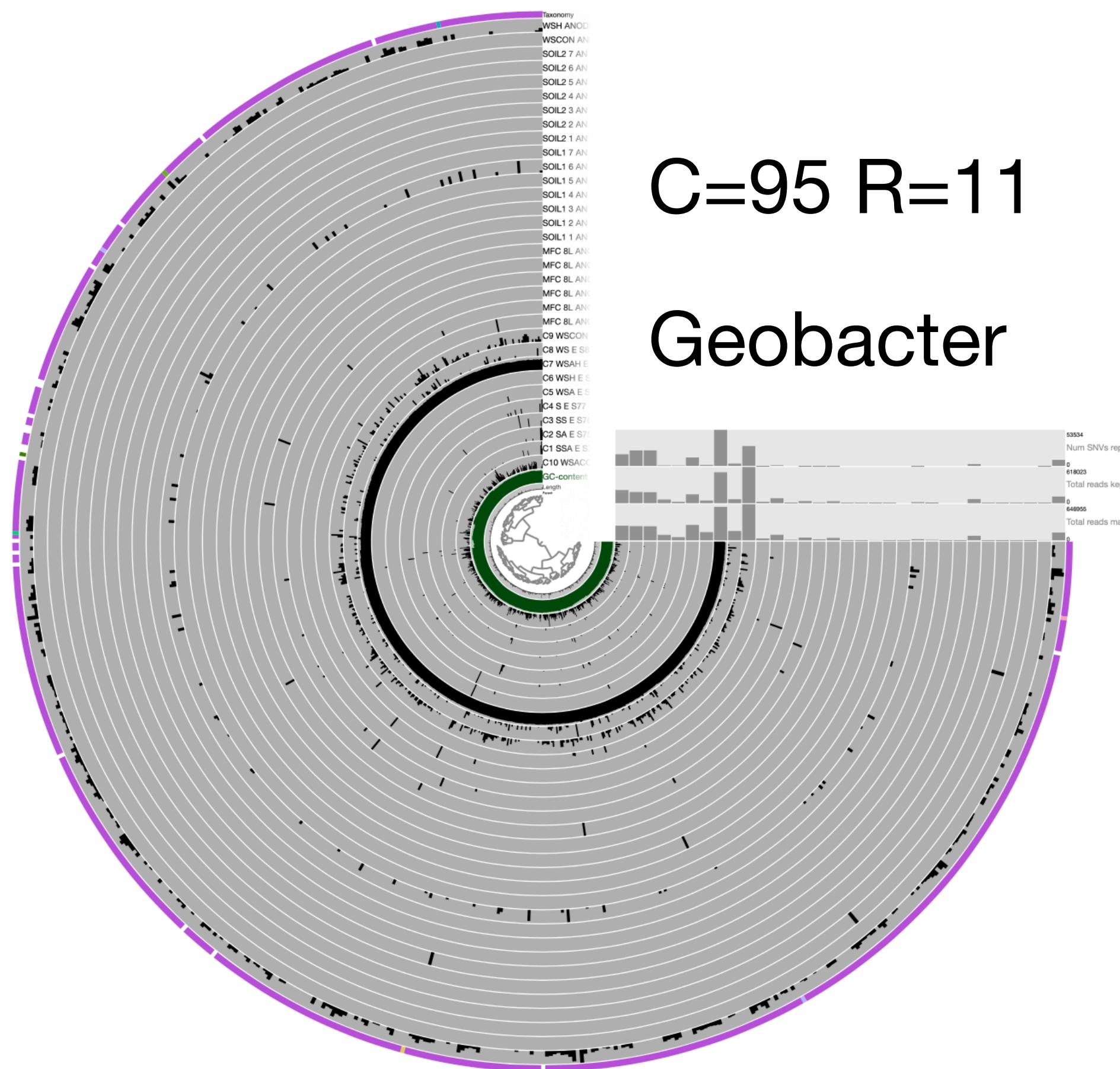
C=94 R=11

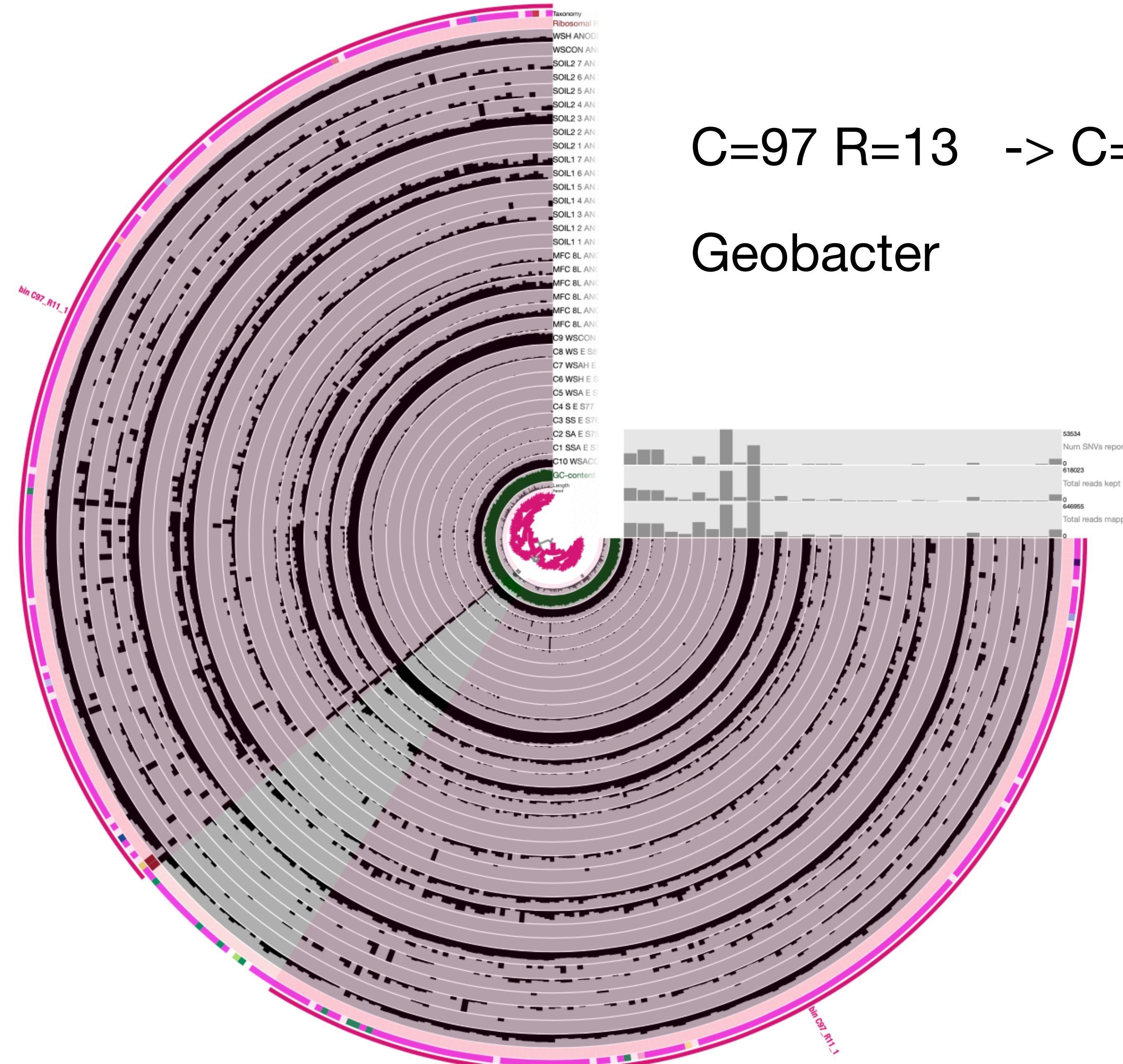
Desulfuromas



C=94 R=4

?





C=97 R=13 → C=97 R=11

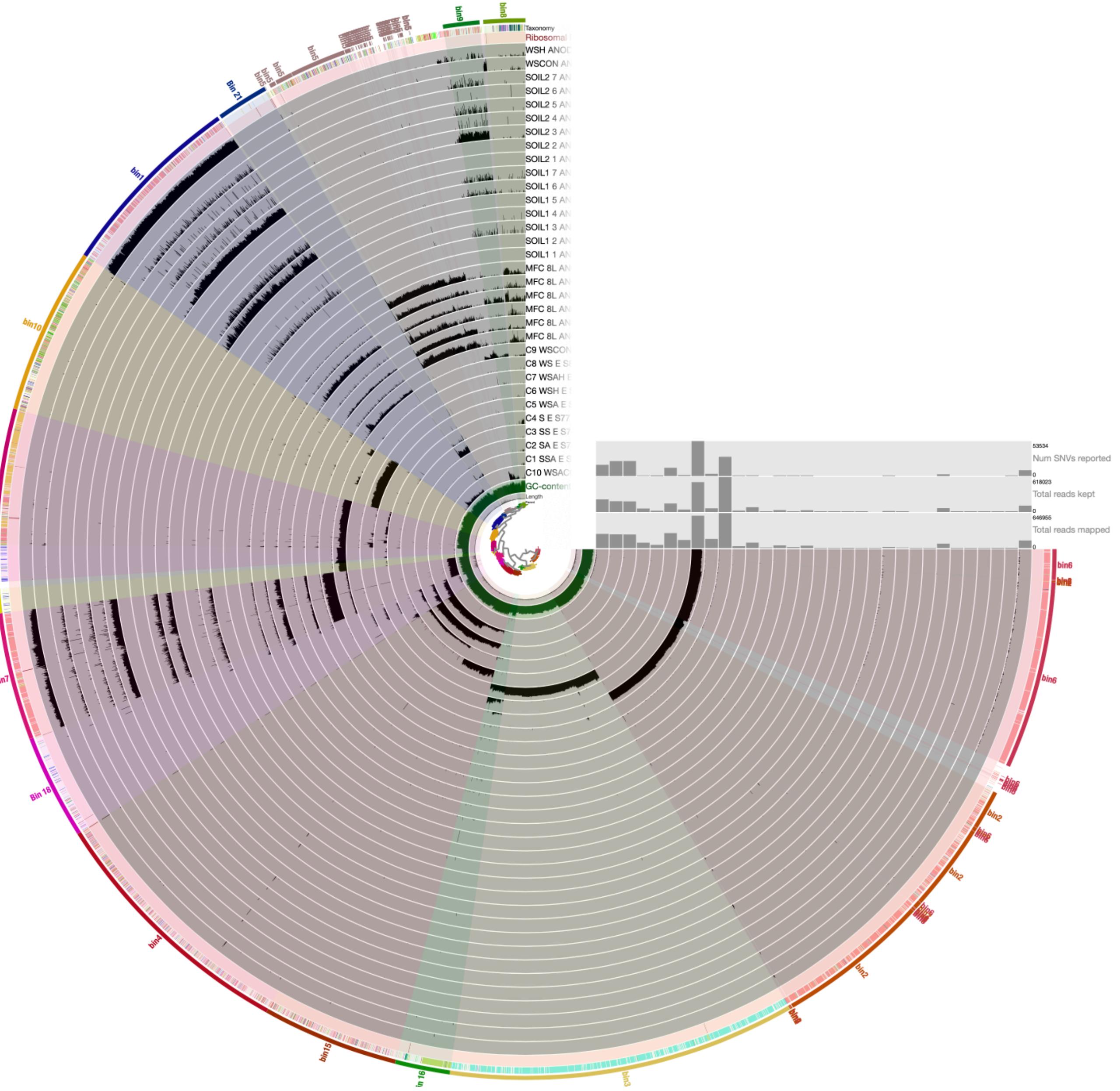
Geobacter

Test2

SAMPLES MERGED

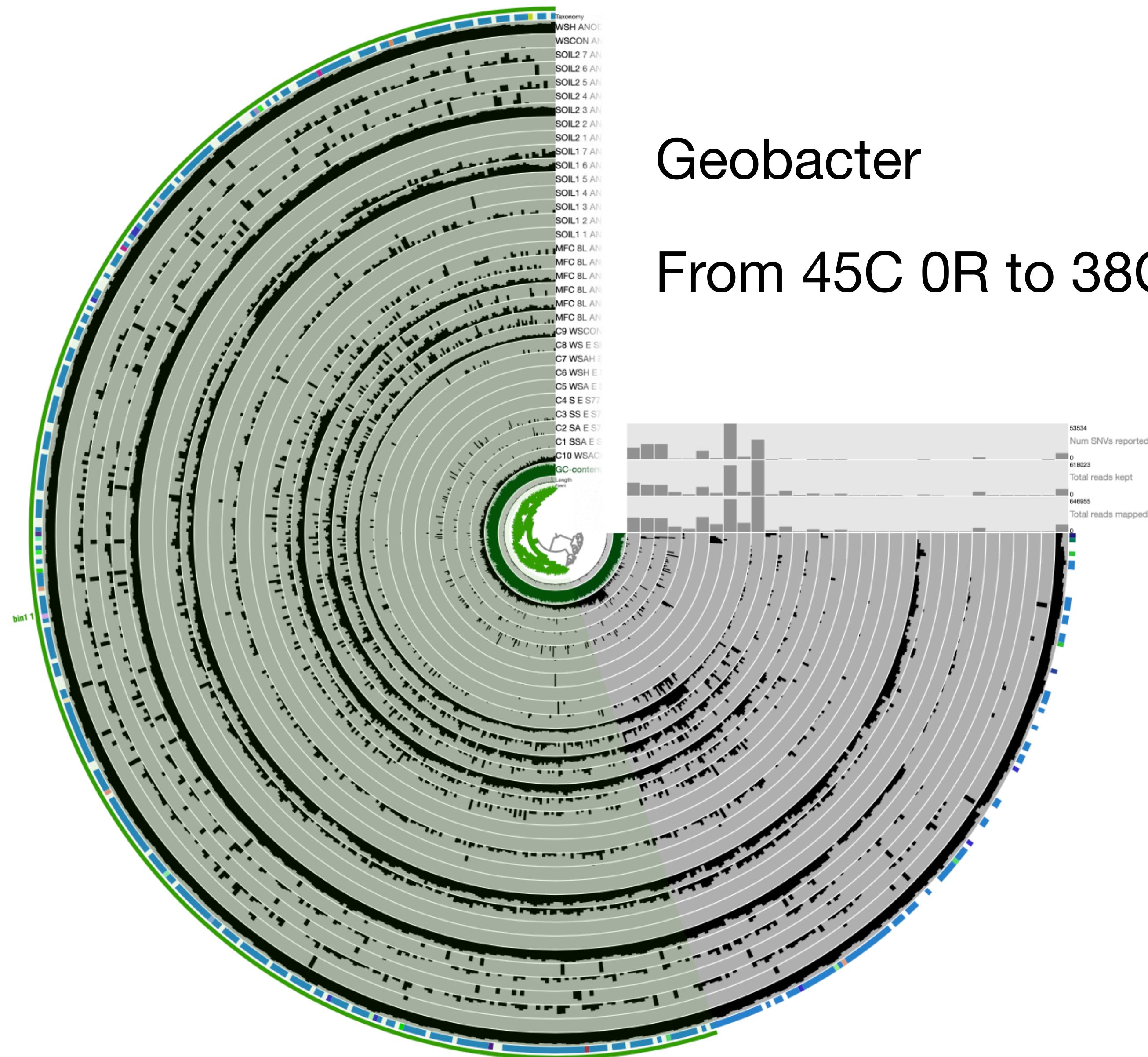
Items order: Seq. Composition + Diff. Coverage (D: Euclidean; L: Ward) | Current view: mean_coverage | Sample order: custom

<input checked="" type="radio"/>	■	bin1	532	2.18M	45.1	0.0	
<input type="radio"/>	■	bin2	830	3.32M	63.4	4.2	
<input type="radio"/>	■	bin3	973	3.24M	67.6	5.6	
<input type="radio"/>	■	bin4	723	3.72M	94.4	11.3	
<input type="radio"/>	■	bin5	299	2.43M	94.4	4.2	
<input type="radio"/>	■	bin6	629	3.80M	95.8	11.3	
<input type="radio"/>	■	bin7	358	3.81M	97.2	12.7	
<input type="radio"/>	■	bin8	117	285K	??	??	
<input type="radio"/>	■	bin9	102	380K	??	??	
<input type="radio"/>	■	bin10	468	1.23M	??	??	
<input type="radio"/>	■	bin11	381	1.02M	31.0	5.6	
<input type="radio"/>	■	bin12	103	274K	??	??	
<input type="radio"/>	■	bin15	382	1.15M	42.3	2.8	
<input type="radio"/>	■	Bin_16	154	389K	??	??	
<input type="radio"/>	■	Bin_18	293	783K	32.4	4.2	
<input type="radio"/>	■	Bin_19	68	174K	??	??	
<input type="radio"/>	■	Bin_21	146	541K	??	??	



Refining bin1 from "test2"

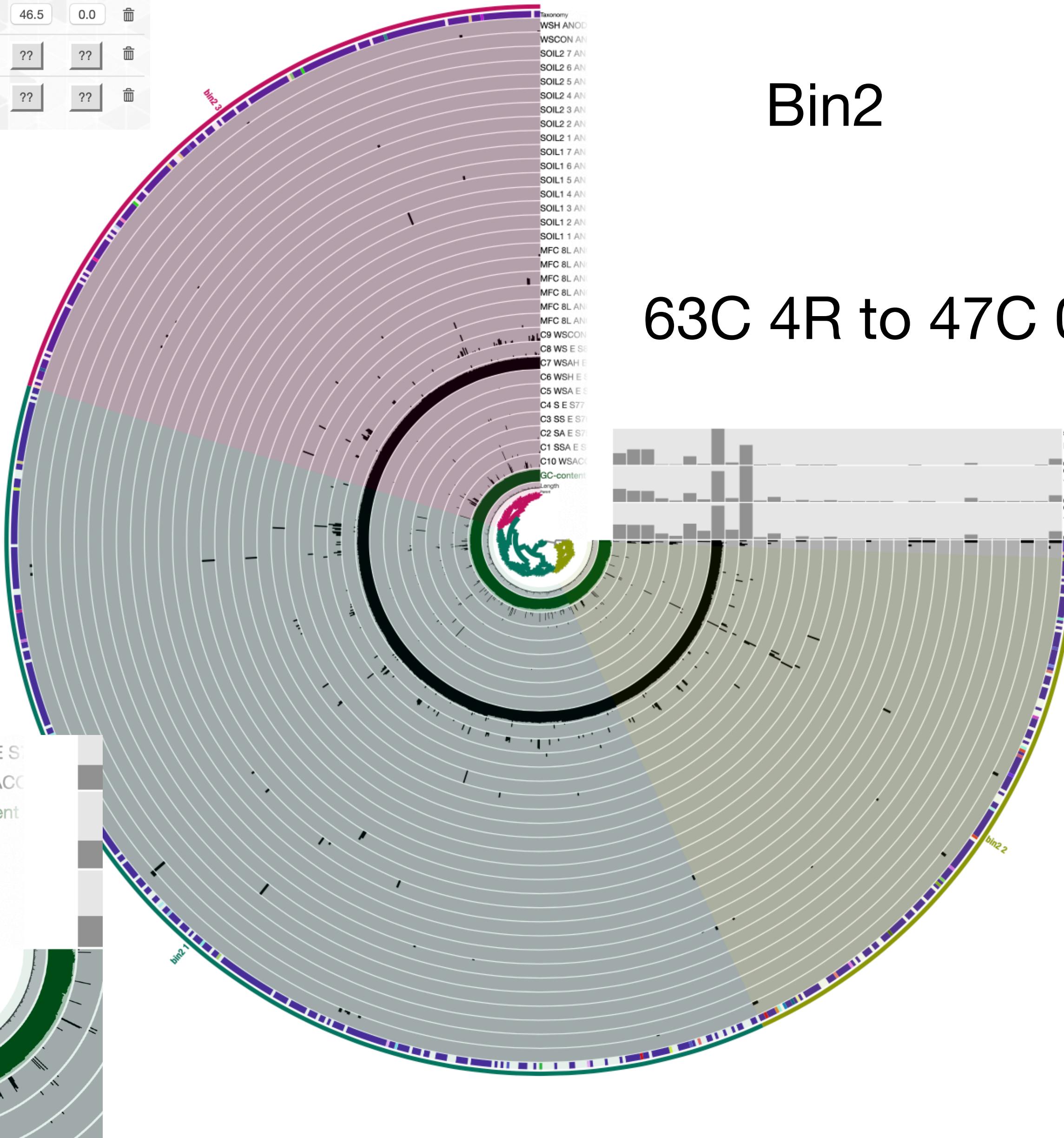
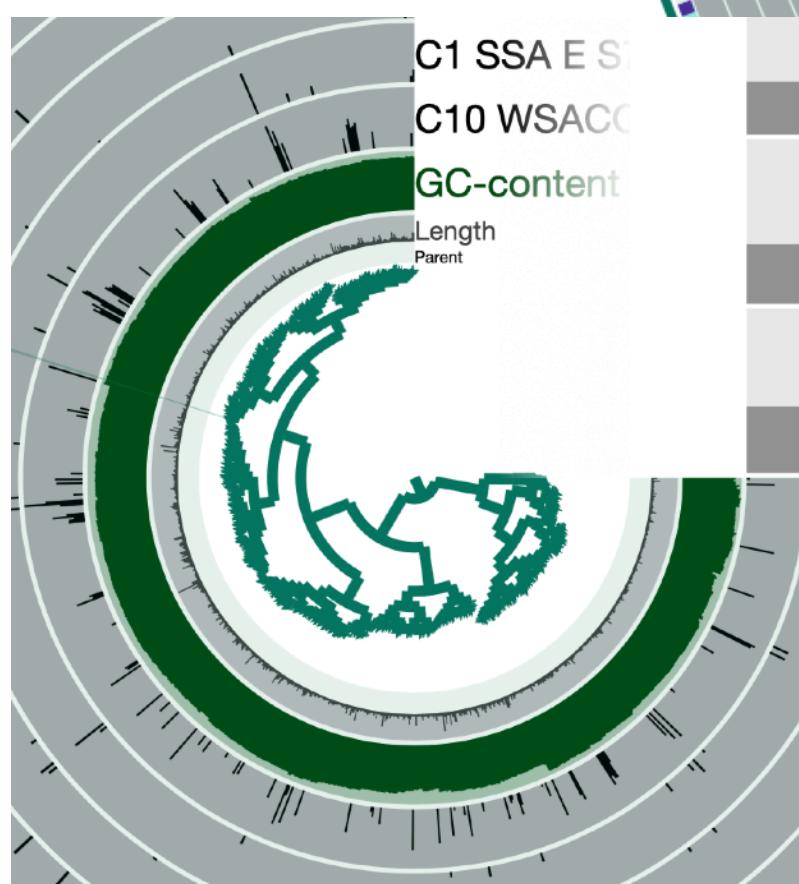
Items order: Seq. Composition + Diff. Coverage (D: Euclidean; L: Ward) | Current view: mean_coverage | Sample order: custom



Geobacter

From 45C 0R to 38C 0R

<input type="radio"/>		bin2_1	404	1.77M	46.5	0.0	
<input type="radio"/>		bin2_2	195	633K	??	??	
<input checked="" type="radio"/>		bin2_3	225	894K	??	??	

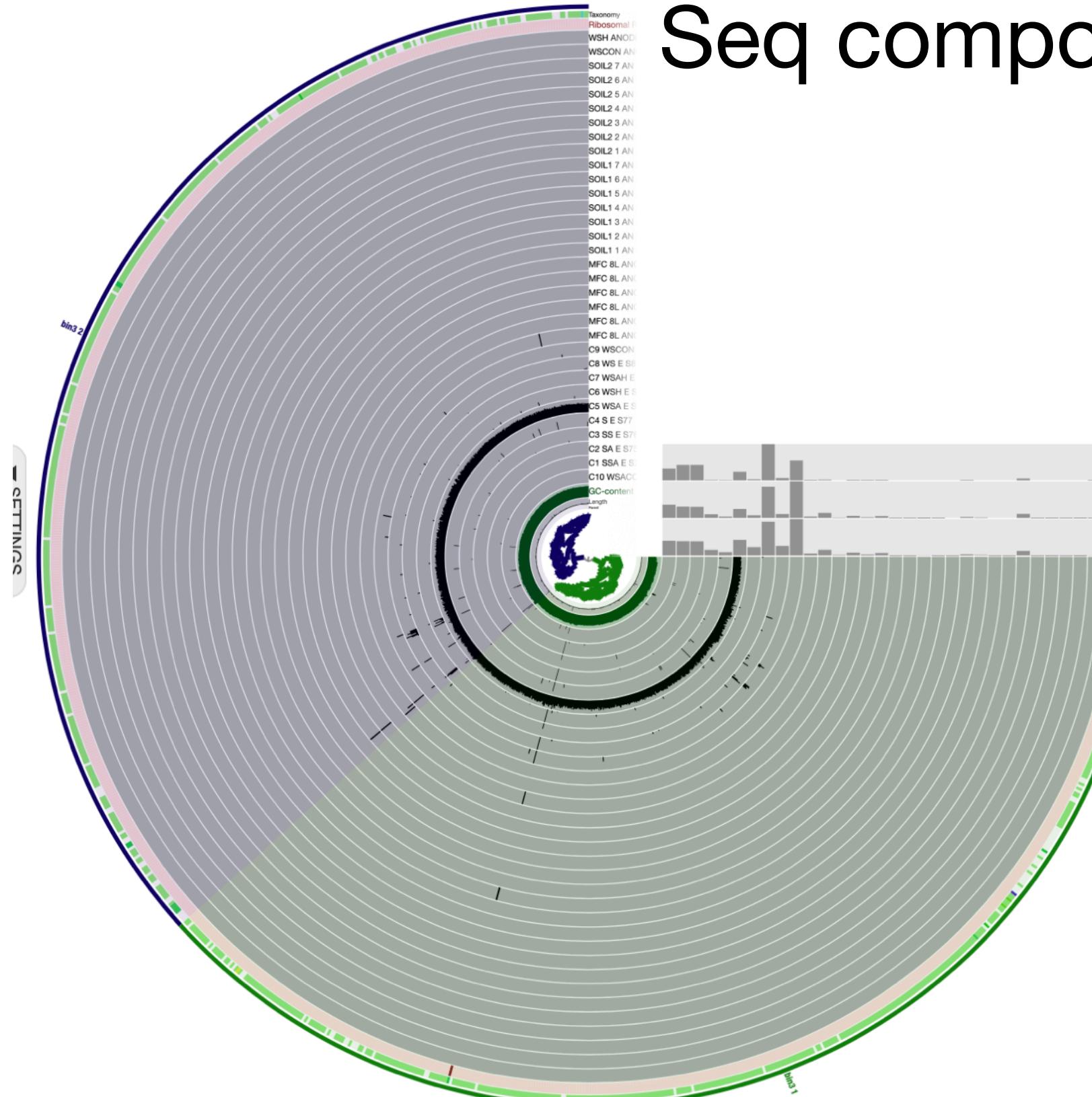


Bin2

63C 4R to 47C 0R

Refining bin3 from "test2"

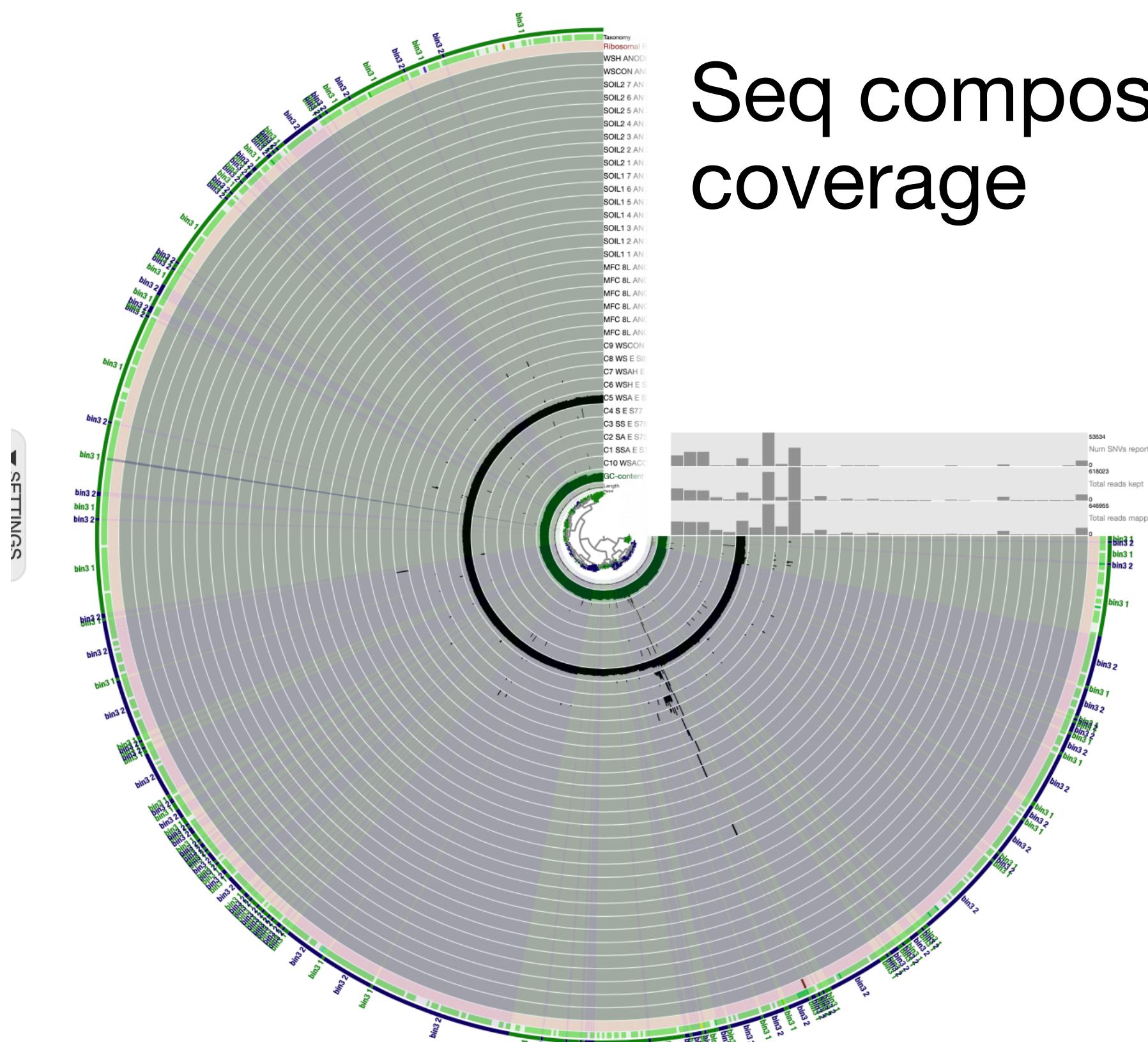
Items order: Sequence composition (D: Euclidean; L: Ward) | Current view: mean_coverage | Sample order: custom



Seq composition

Refining bin3 from "test2"

Items order: Seq. Composition + Diff. Coverage (D: Euclidean; L: Ward) | Current view: mean_coverage | Sample order: custom



Seq composition+Diff coverage