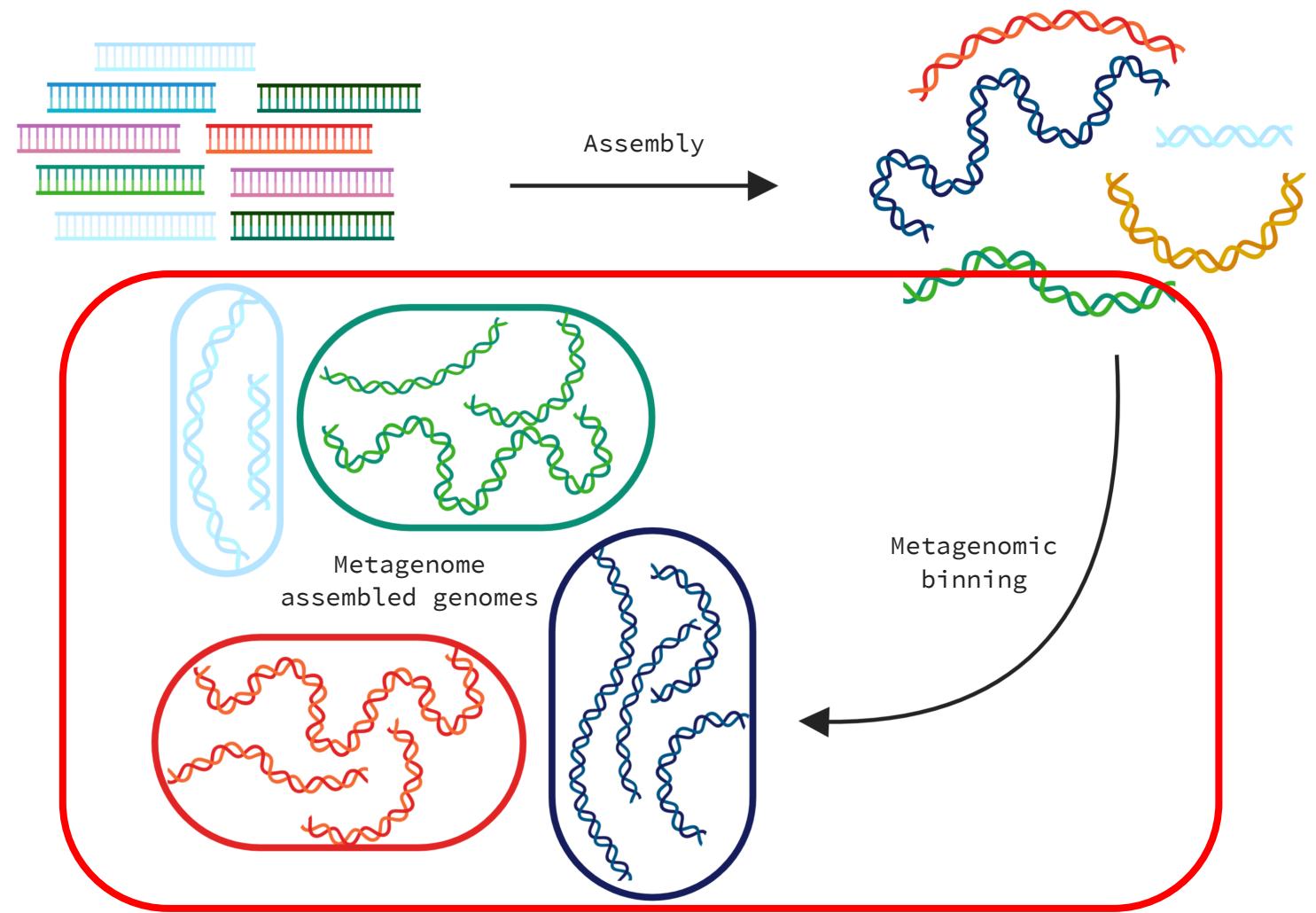
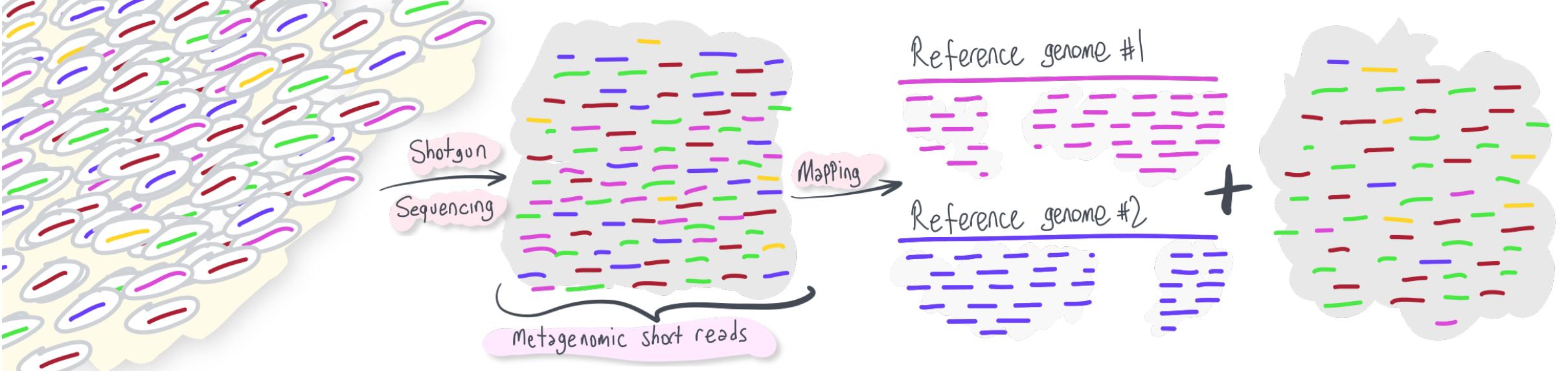


Environmental metagenomics

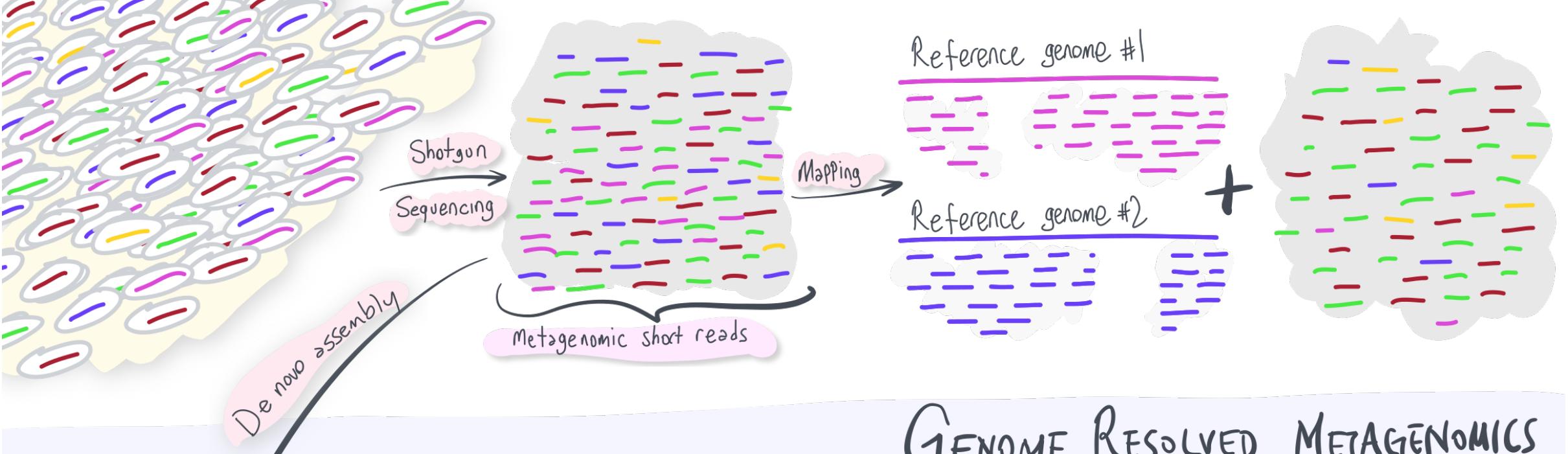
Genome-resolved metagenomics

What is genome-resolved metagenomics?

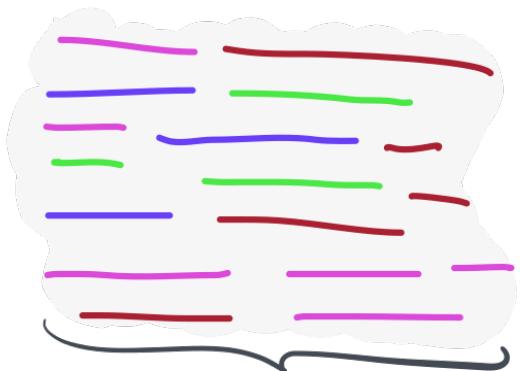


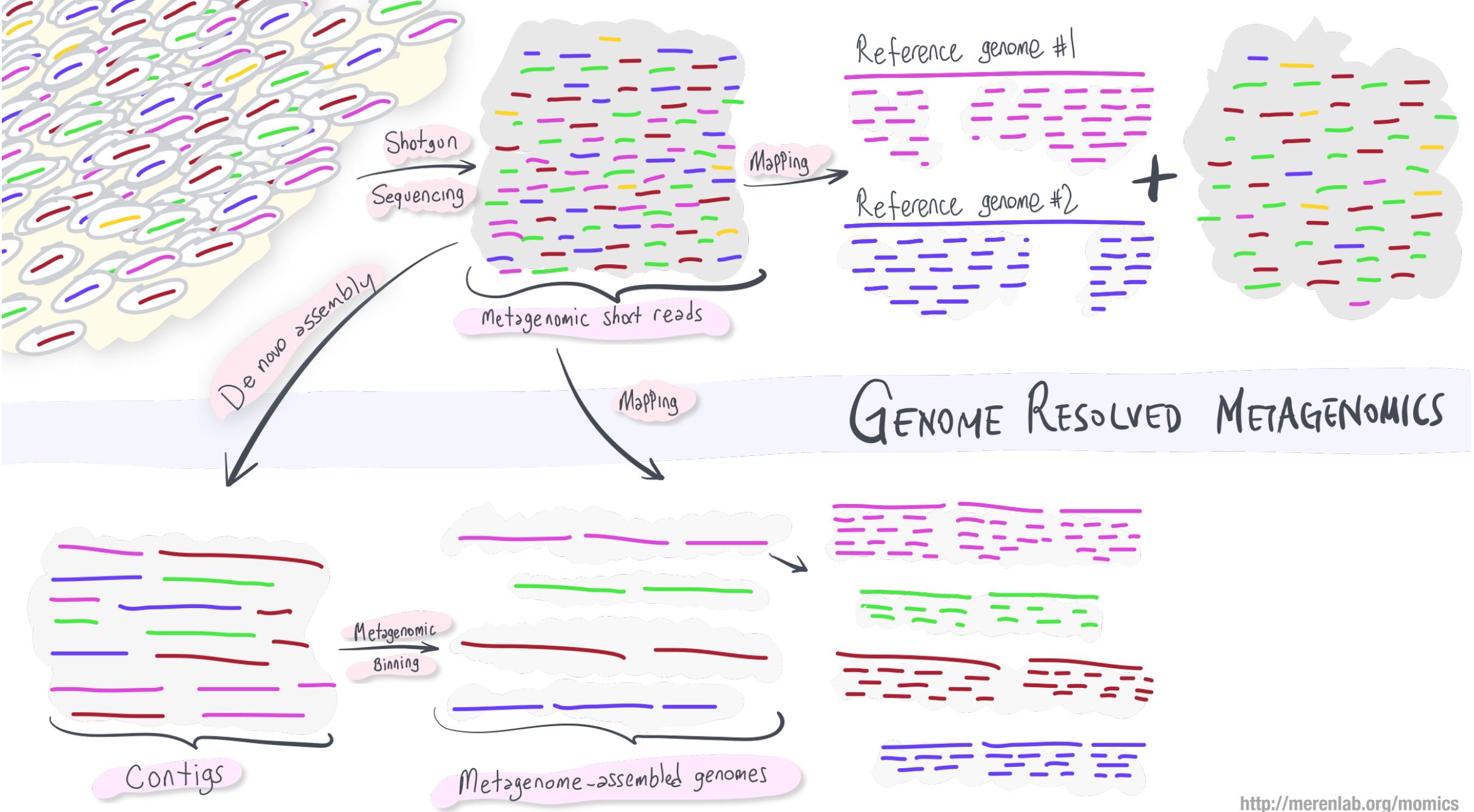


GENOME RESOLVED METAGENOMICS



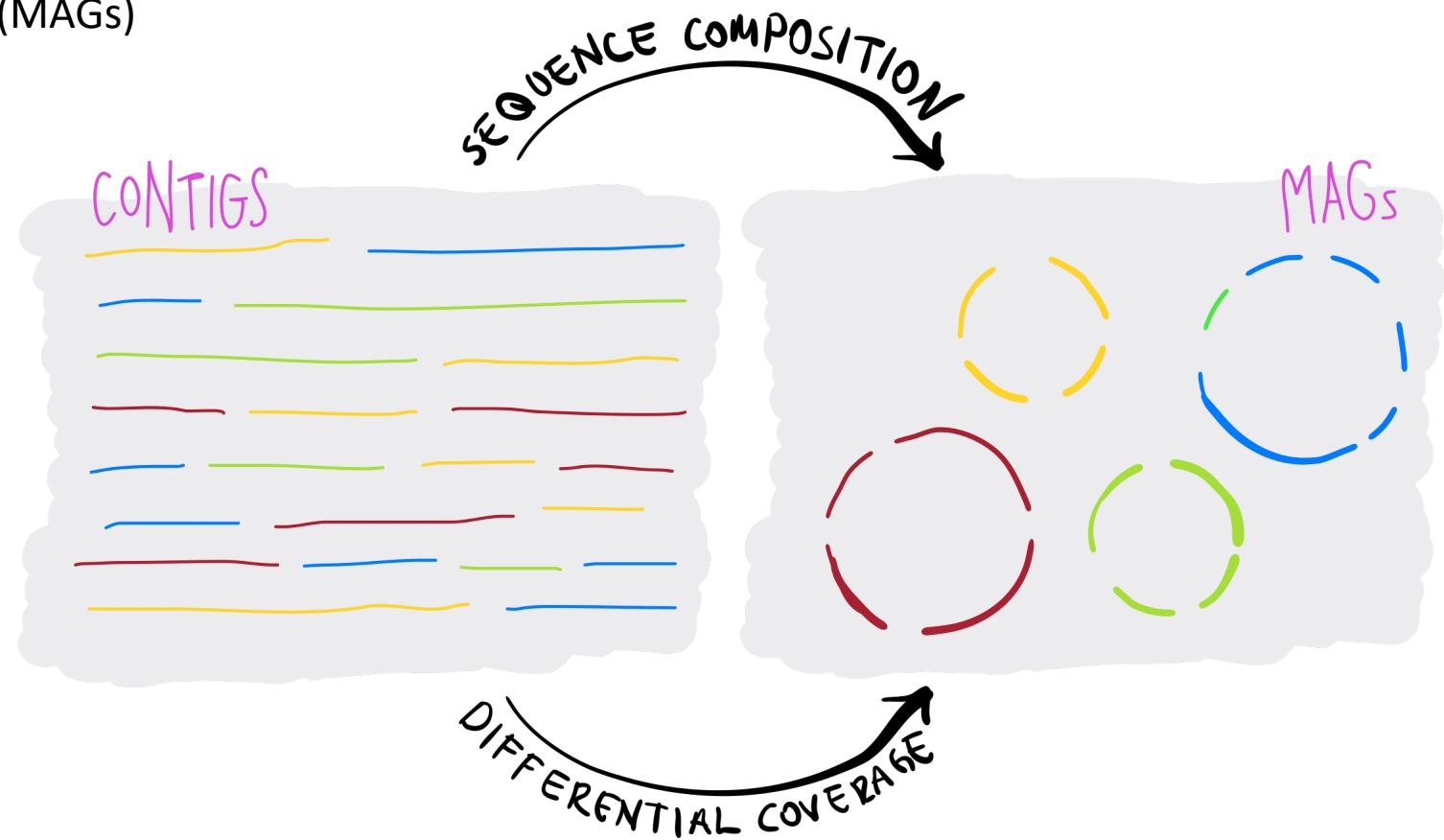
GENOME RESOLVED METAGENOMICS



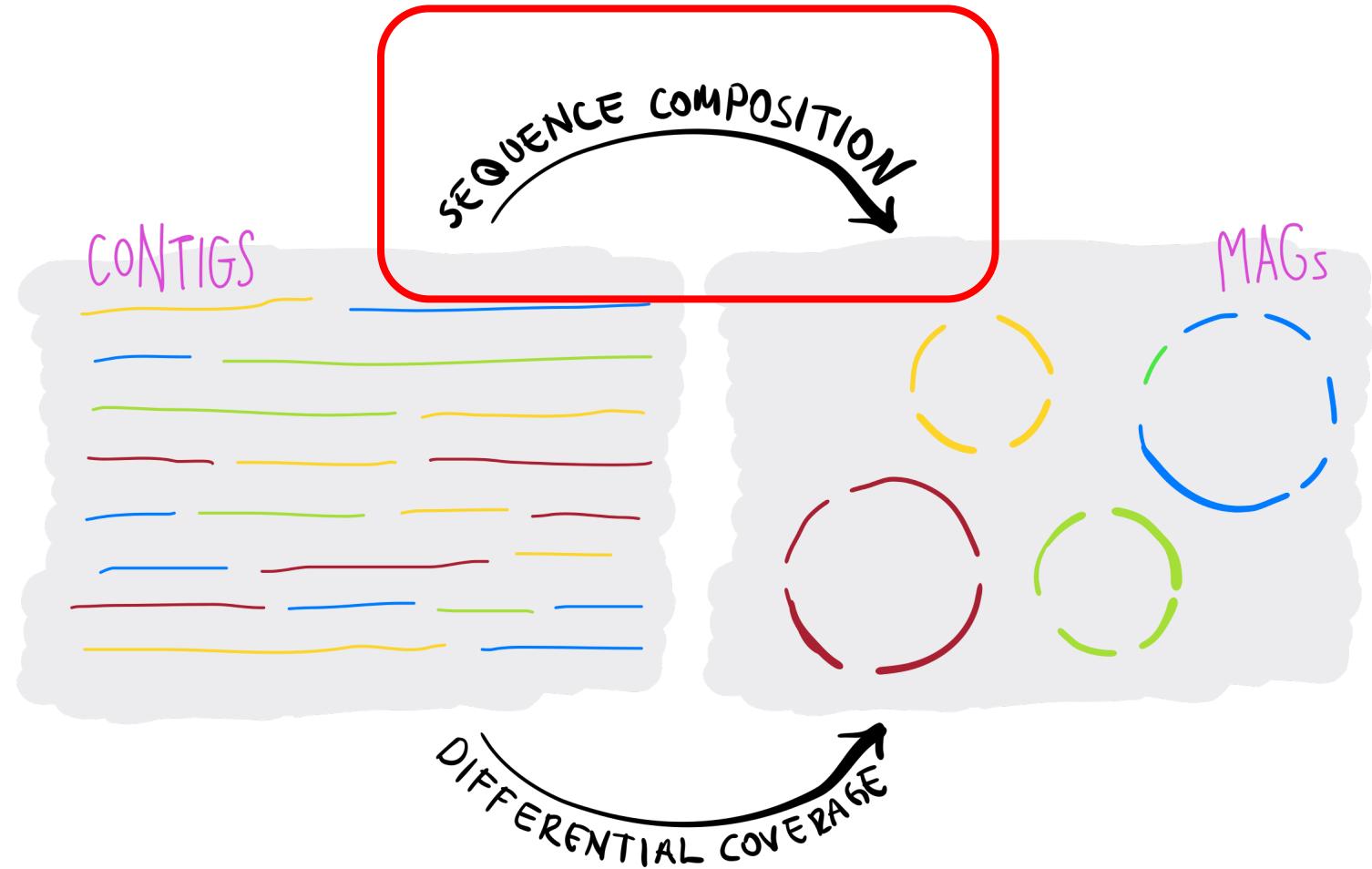


Metagenomic binning

From contigs to
metagenome assembled genomes (MAGs)



Sequence composition – kmers



GTTTGCGCATGATTAAGGGAGTTCTTTGTGCTTC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

k=2

GT

TTGGCATGATTAAGGGAGTTCTTGTGCTTC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0

k=2

TT	TGGCATGATTAAGGGAGTTCTTGTGCTTC
AA	AC AG AT CA CC CG CT GA GC GG GT TA TC TG TT
0	0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1

k=2

GT	TT	GGCATGATTAAGGGAGTTCTTGTGCTTC													
AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2

k=2

GTTTGCGCATGATTAAGGGAGTTCTTGTGCTTC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
1	0	2	2	1	0	0	2	2	2	2	3	1	2	4	10

k=2

GTTTGCGATGATTAAAGGGAGTTCTTGTGCTTC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
1	0	2	2	1	0	0	2	2	2	2	3	1	2	4	10

9

GAAGCACAAAAGAAACTCCTTAATCATGCCAAAAAC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
10	3	2	2	4	2	0	2	2	2	5	0	1	2	1	1

k=2

GTTTGCGATGATTAAAGGGAGTTCTTGTGCTTC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
1	0	2	2	1	0	0	2	2	2	2	3	1	2	4	10

9

GAAGCACAAAAGAAAACCTCCTTAATCATGCCAAAAAC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
10	3	2	2	4	2	0	2	2	2	5	0	1	2	1	1

GTTTGCGATGATTAAAGGGAGTTCTTGTGCTTC
GAAGCACAAAAGAAAACCTCCTTAATCATGCCAAAAAC

AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
11	3	4	4	5	2	0	2	2	1

k=2

GTTTGCGCATGATTAAGGGAGTTCTTTGTGCTTC

	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
X	11	3	4	4	5	2	0	2	2	1
Y										
Z										
L										
K										
M										

k=2

ACTTCCGCAGTCGGGCATTACGCGTTGTGGAATGA

	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
X	11	3	4	4	5	2	0	2	2	1
Y	4	5	2	4	5	4	4	3	2	1
Z										
L										
K										
M										

k=2

AC TTGCGCAGTCGCGCATTACGCGTAGTGGAAATAA

	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
X	11	3	4	4	5	2	0	2	2	1
Y	4	5	2	4	5	4	4	3	2	1
Z	4	5	3	2	4	1	5	5	2	3
L										
K										
M										

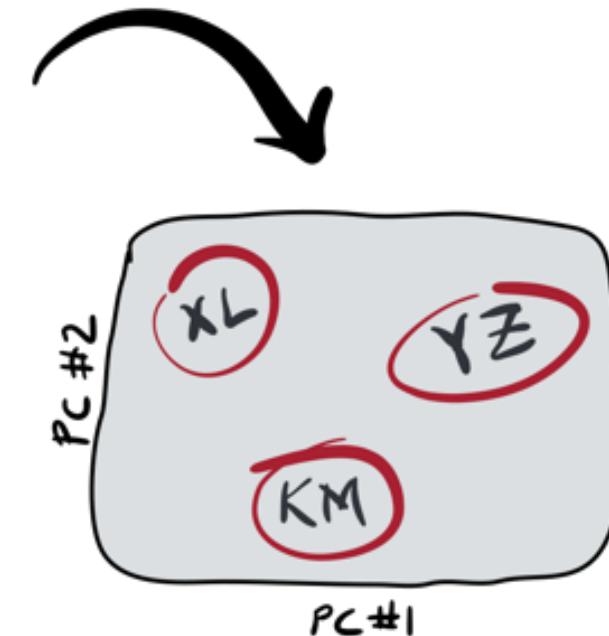
k=2

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Y	4	5	2	4	5	4	4	3	2	1
Z	4	5	3	2	4	1	5	5	2	3
L	11	6	3	2	2	3	2	1	1	4
K	1	1	2	2	1	8	9	10	0	0
M	0	4	4	3	4	10	4	5	0	0

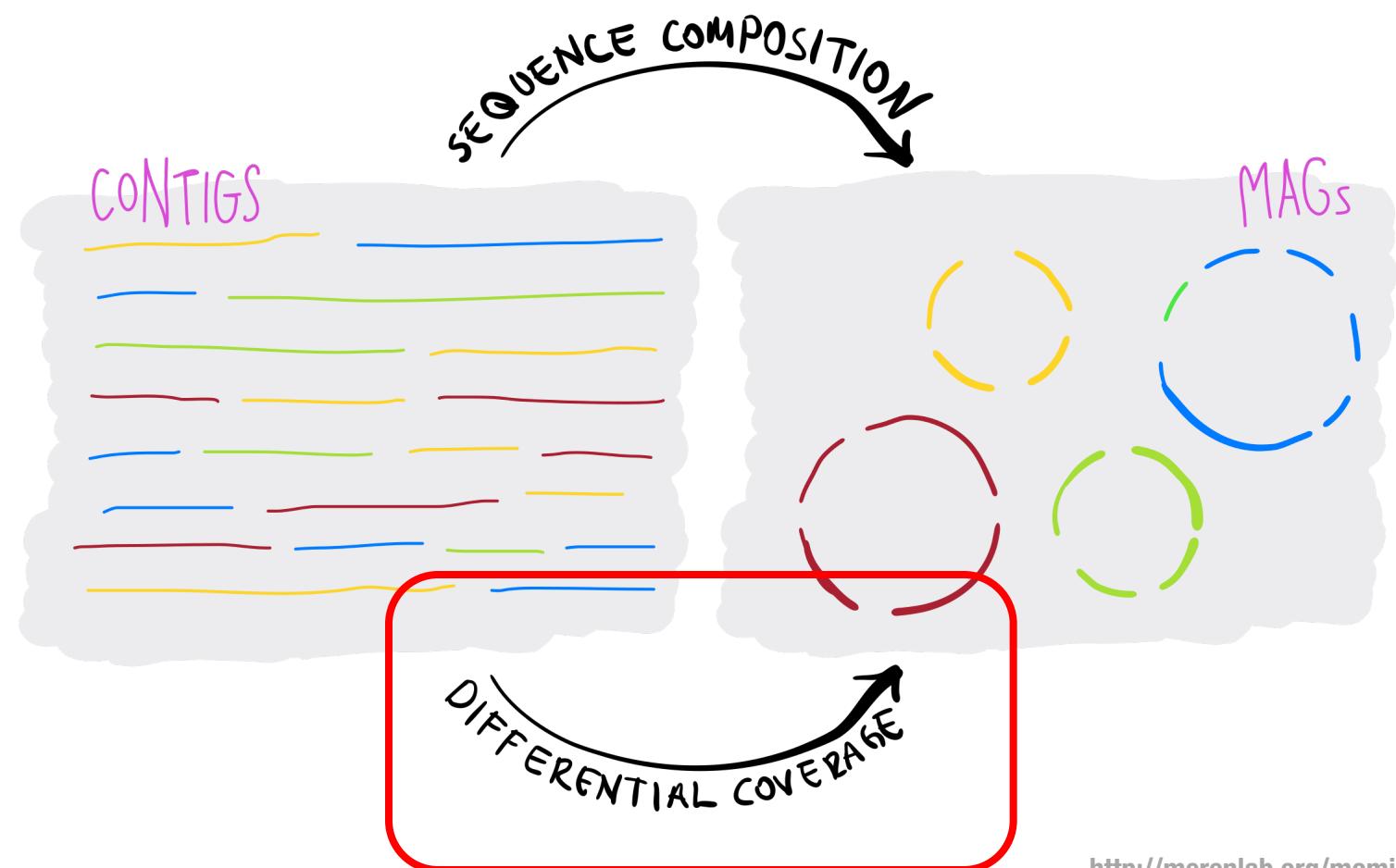
k=2

	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
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Y	4	5	2	4	5	4	4	3	2	1
Z	4	5	3	2	4	1	5	5	2	3
L	11	6	3	2	2	3	2	1	1	4
K	1	1	2	2	1	8	9	10	0	0
M	0	4	4	3	4	10	4	5	0	0

k=2



Differential coverage

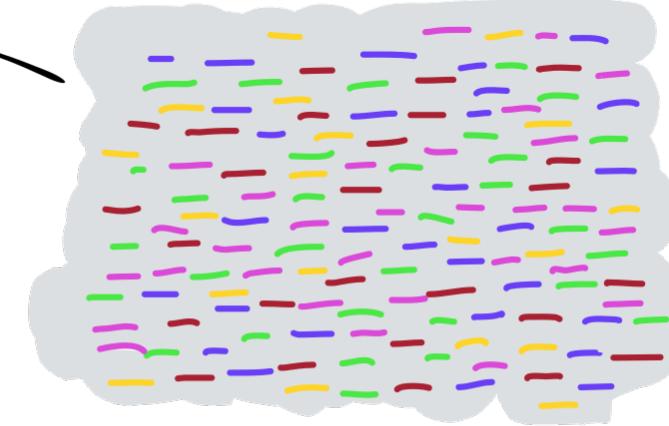


<http://merenlab.org/momics>

CONTIG #1

CONTIG #2

CONTIG #1

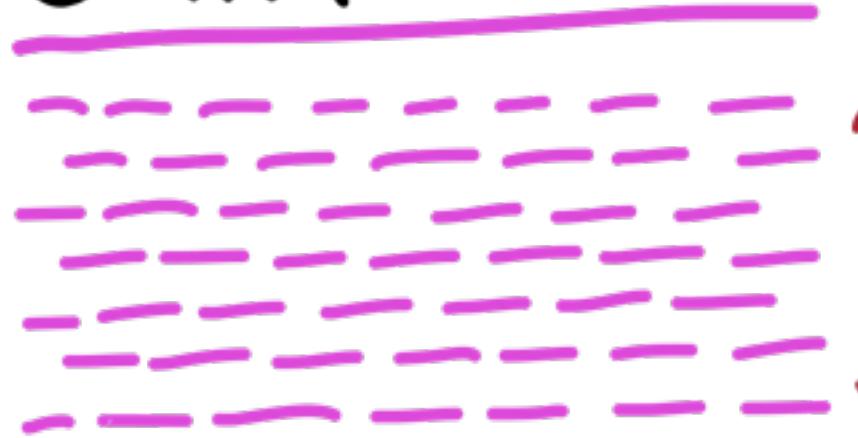


METAGENOMIC READS

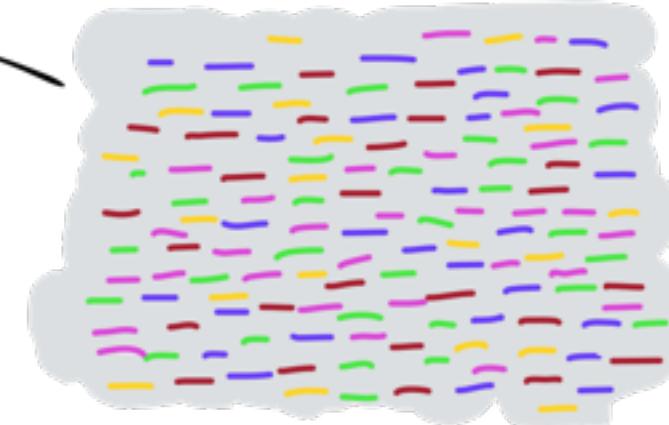
CONTIG #2



CONTIG #1



MAPPING



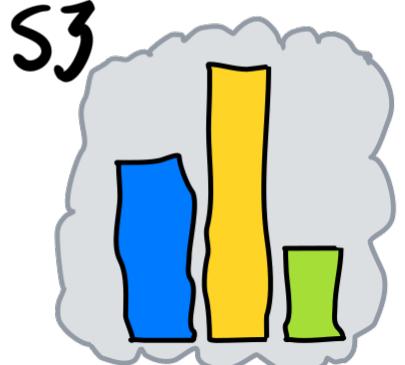
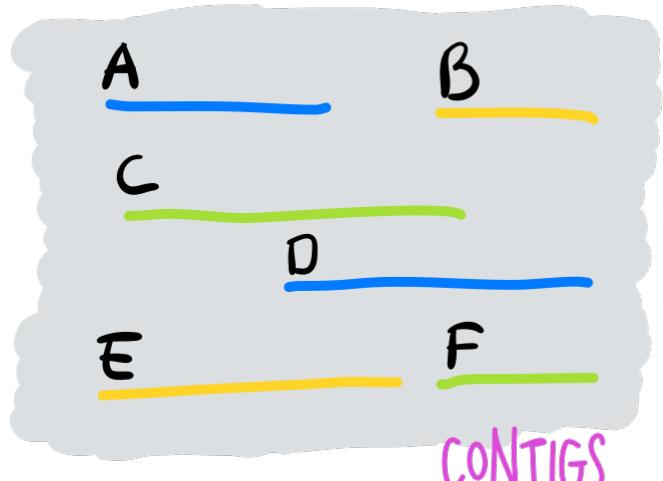
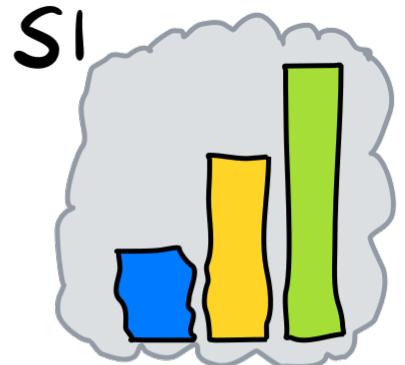
METAGENOMIC READS

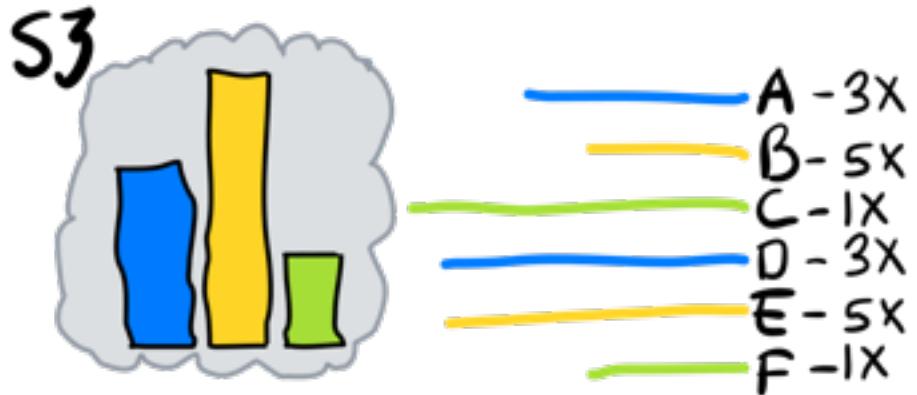
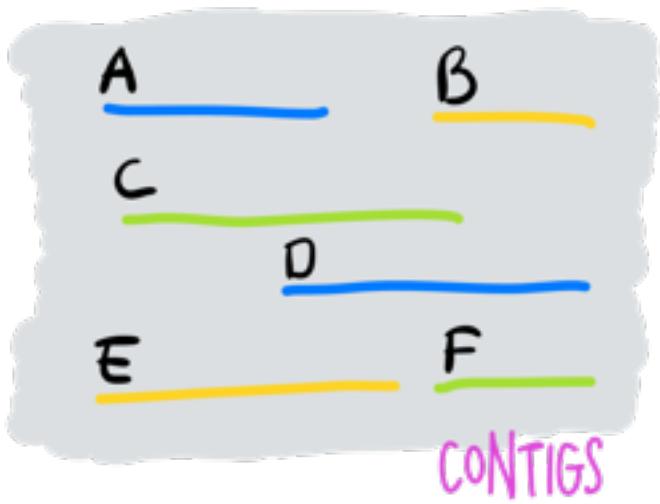
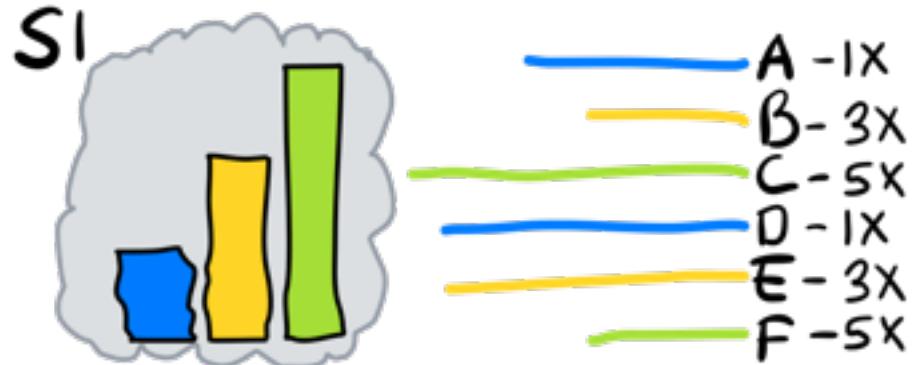
COVERAGE: ~7X

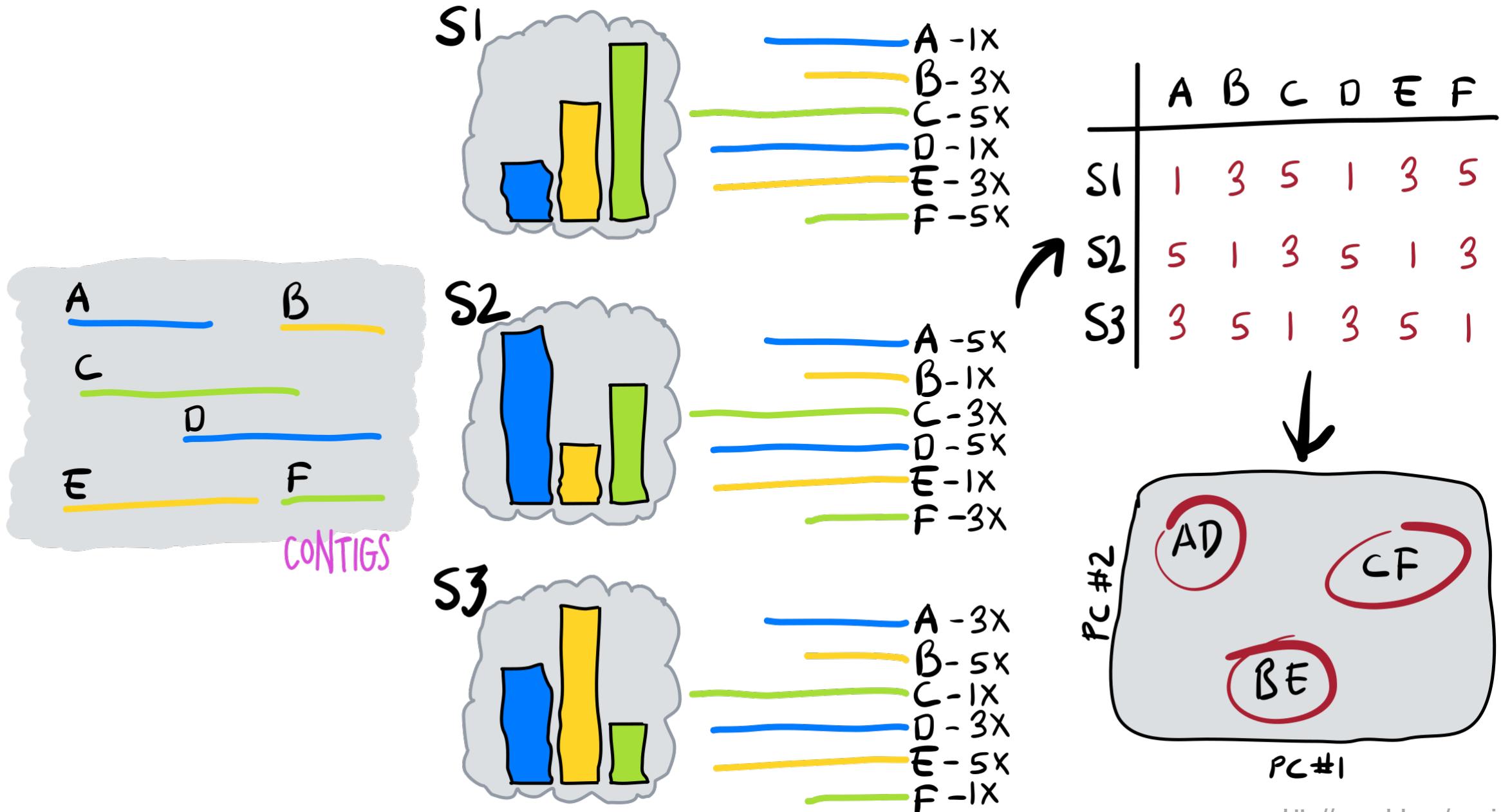
CONTIG #2



COVERAGE: ~4X



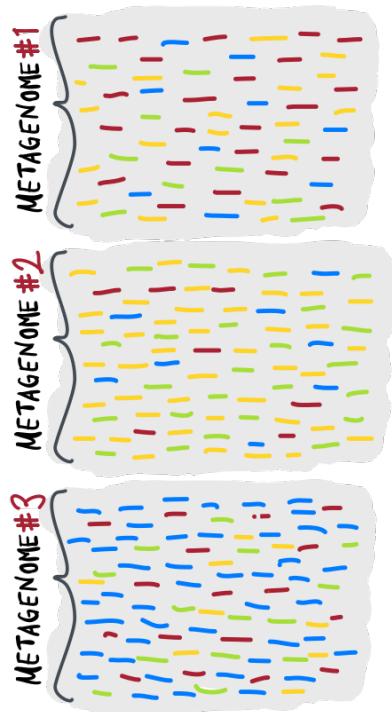


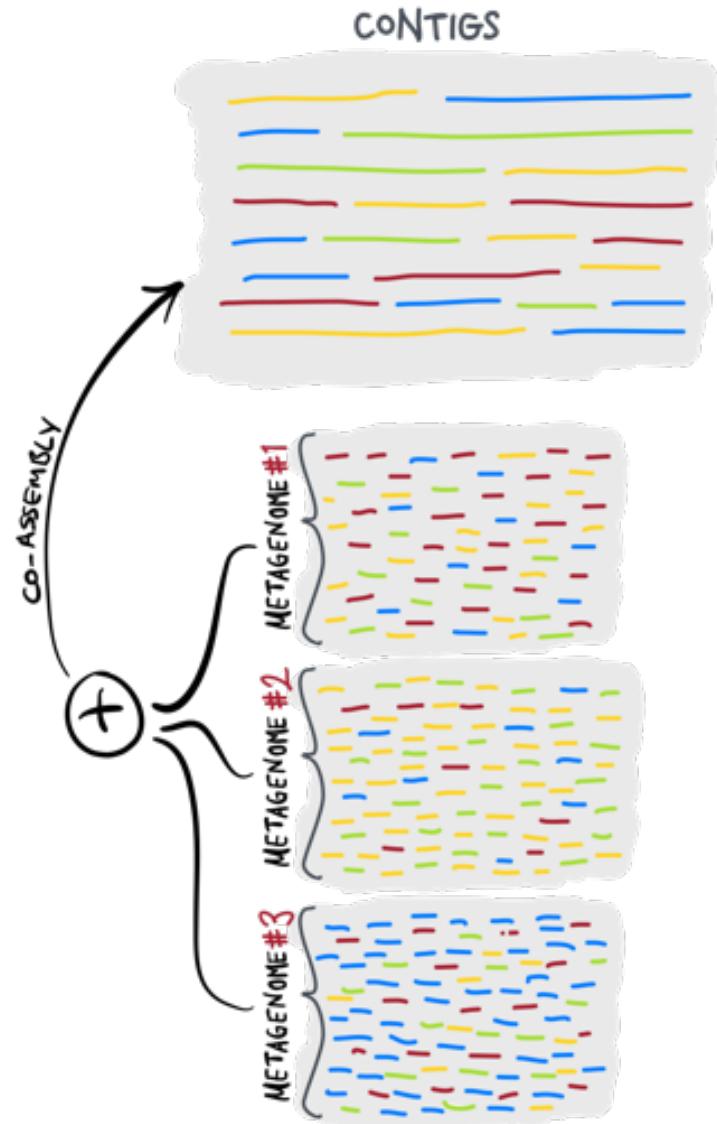


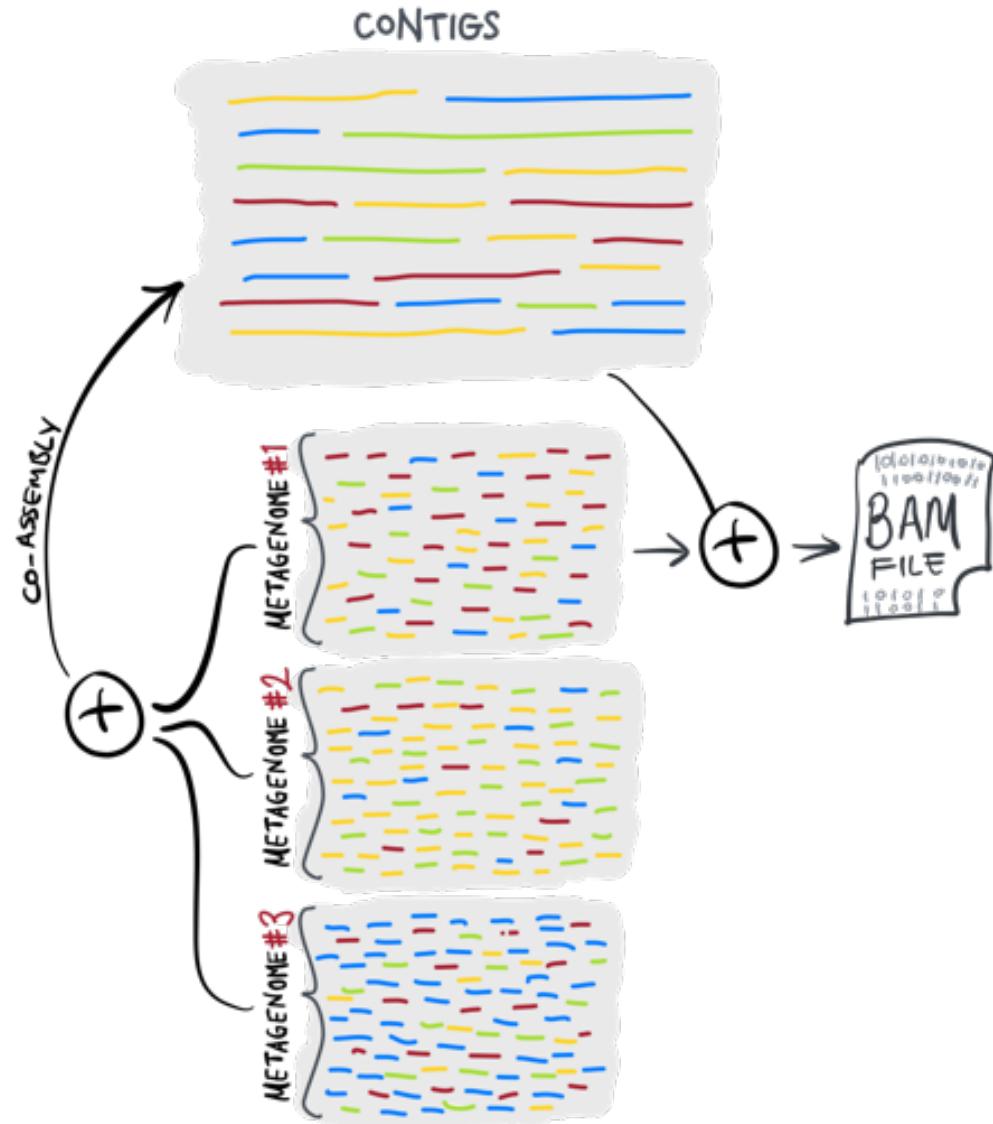
Genome-resolved metagenomics *in action*

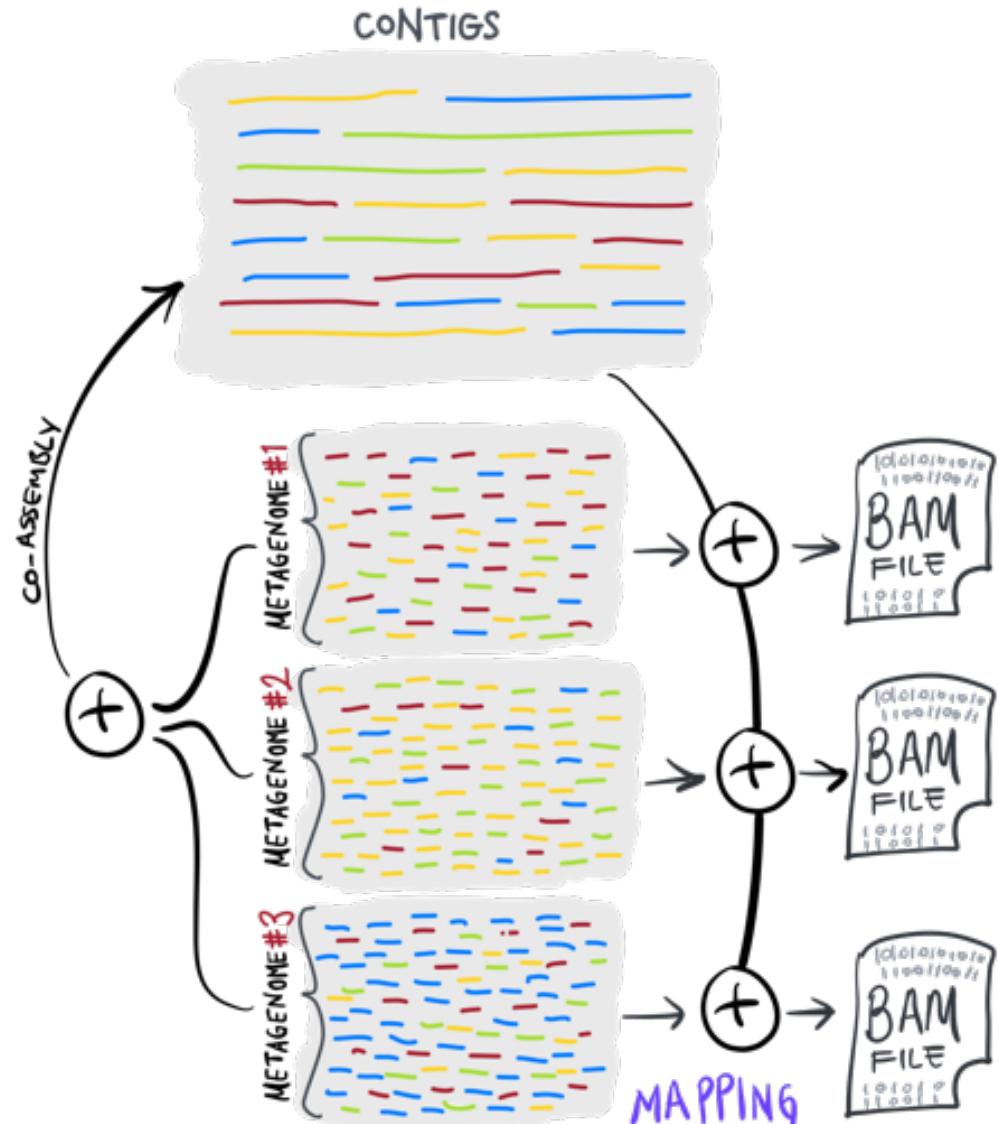
Genome-resolved metagenomics *in action*

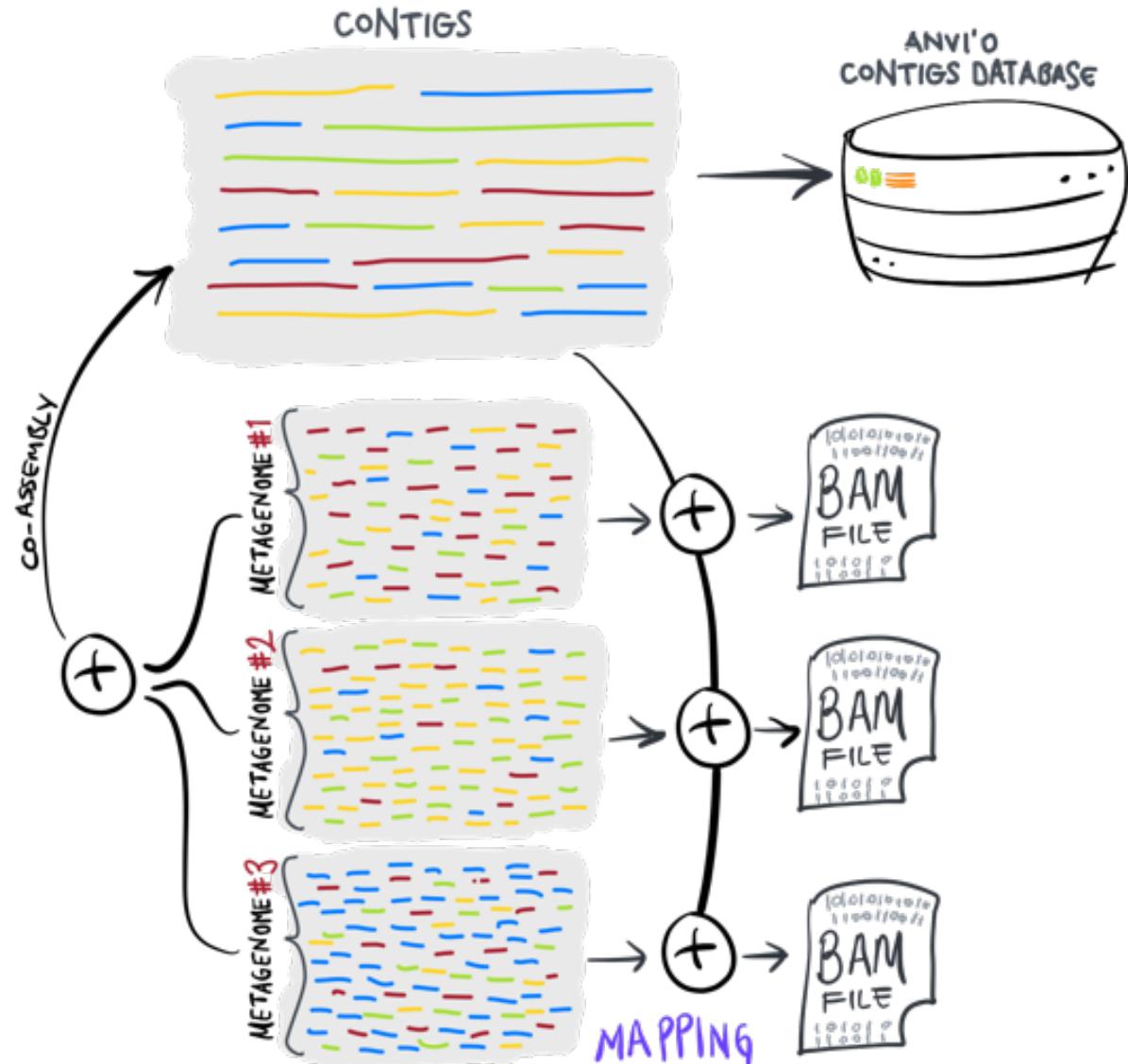
- Several automatic binning algorithms available
 - CONCOCT, MetaBat, MaxBin, BinSanity, Autometa, DAS Tool, ...
 - Various algorithms, but most rely on kmers and coverage
- Manual binning in anvi'o
 - Tetranucleotide frequency ***and/or*** differential coverage
 - Also, automatic binning results can be visualised

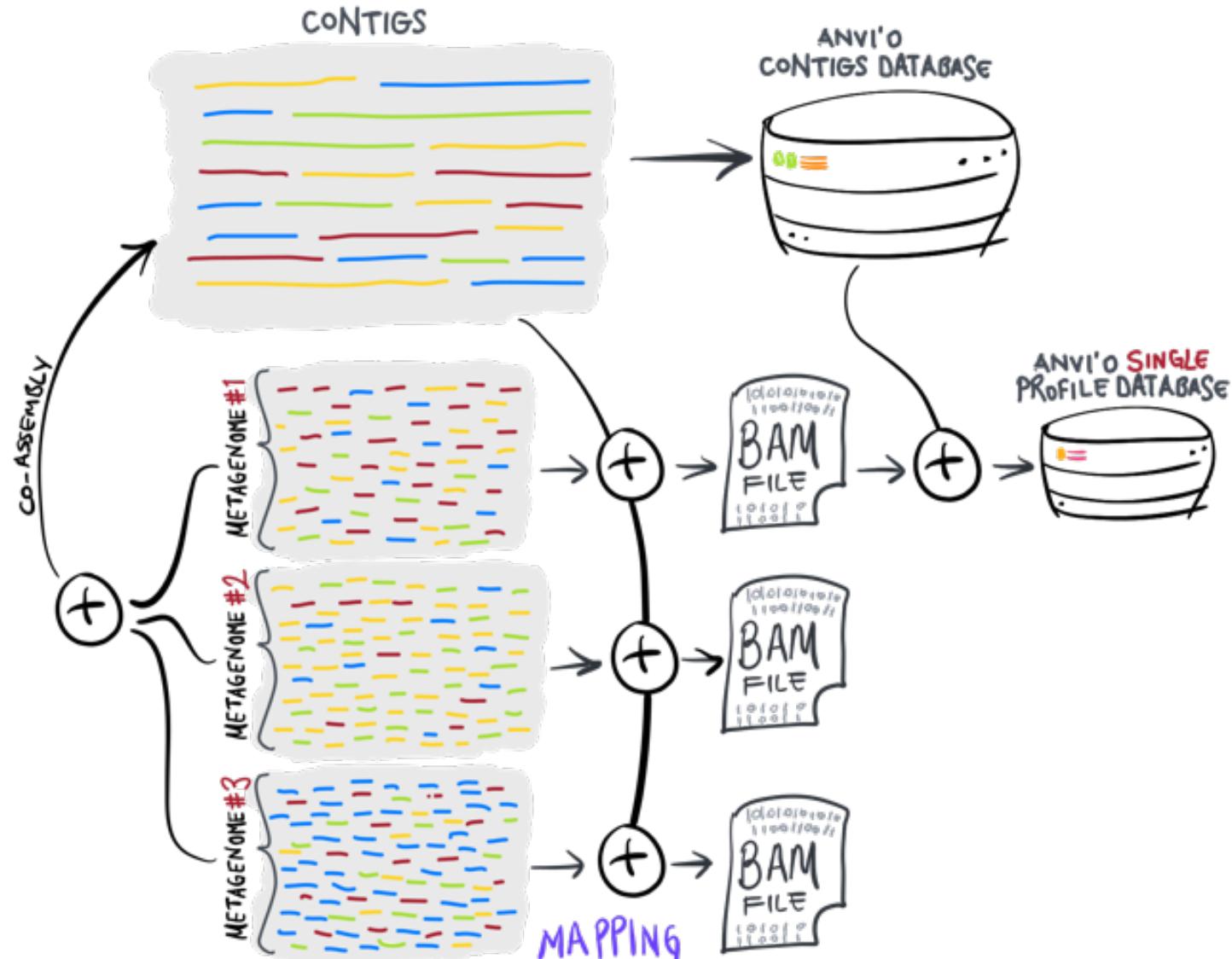


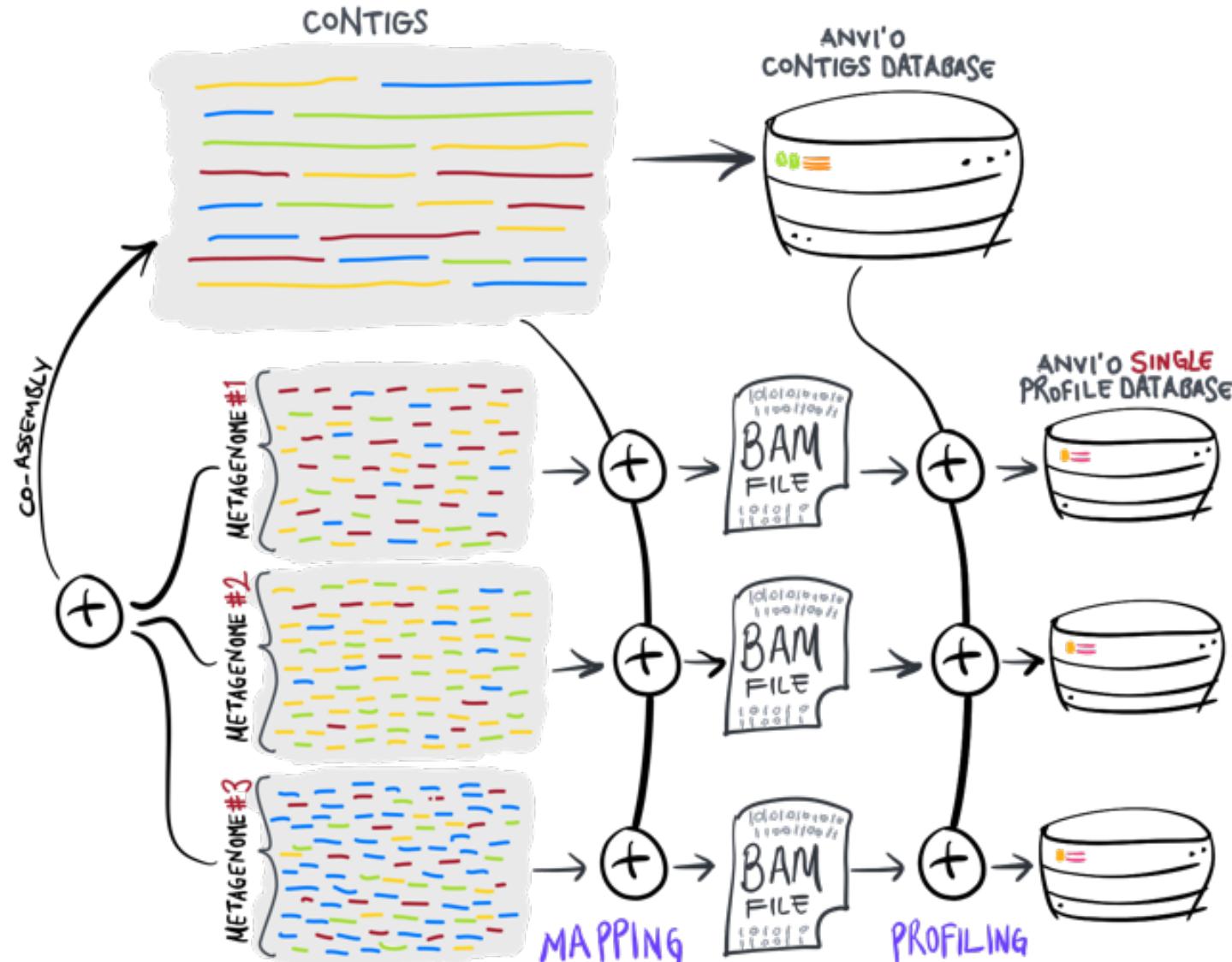


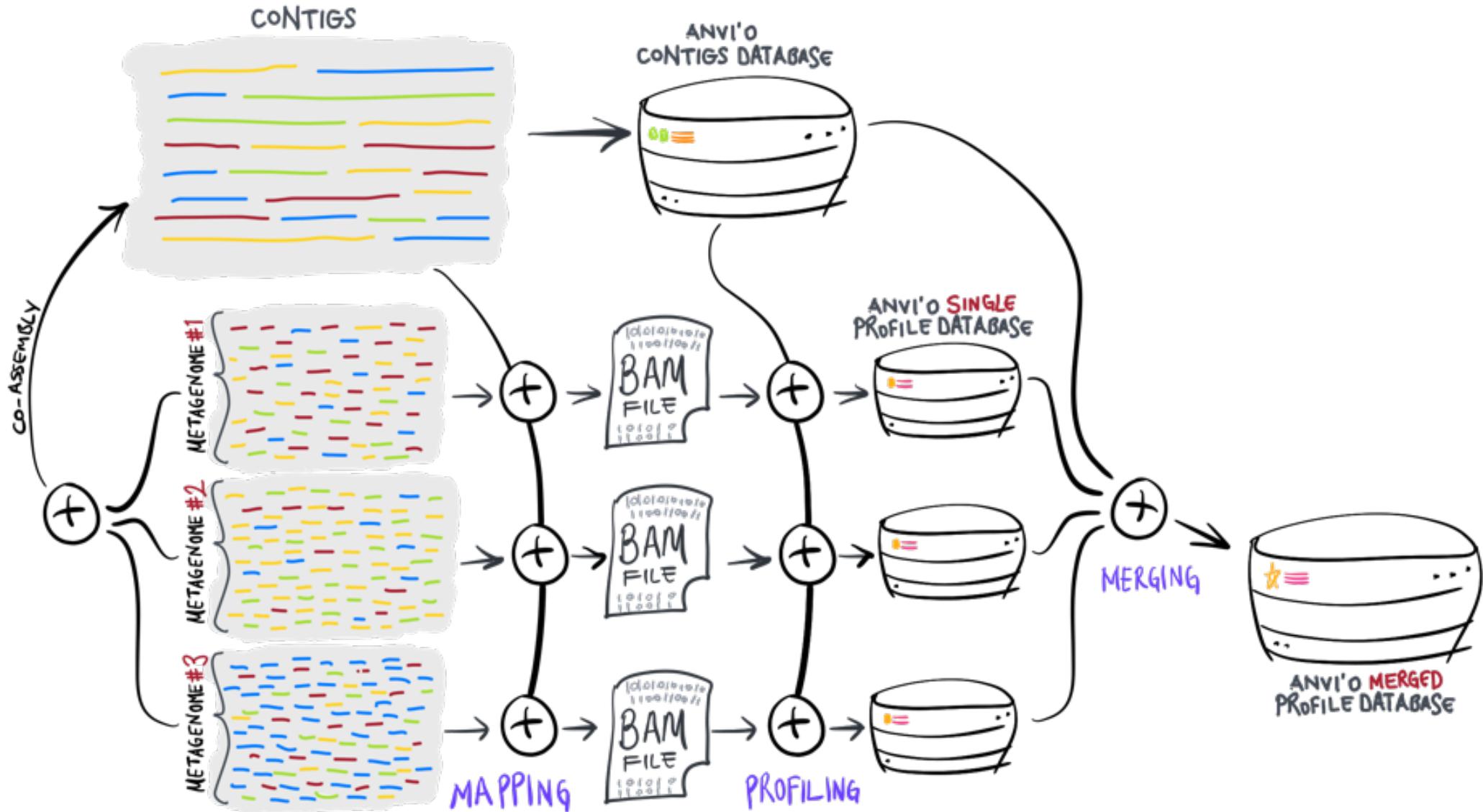


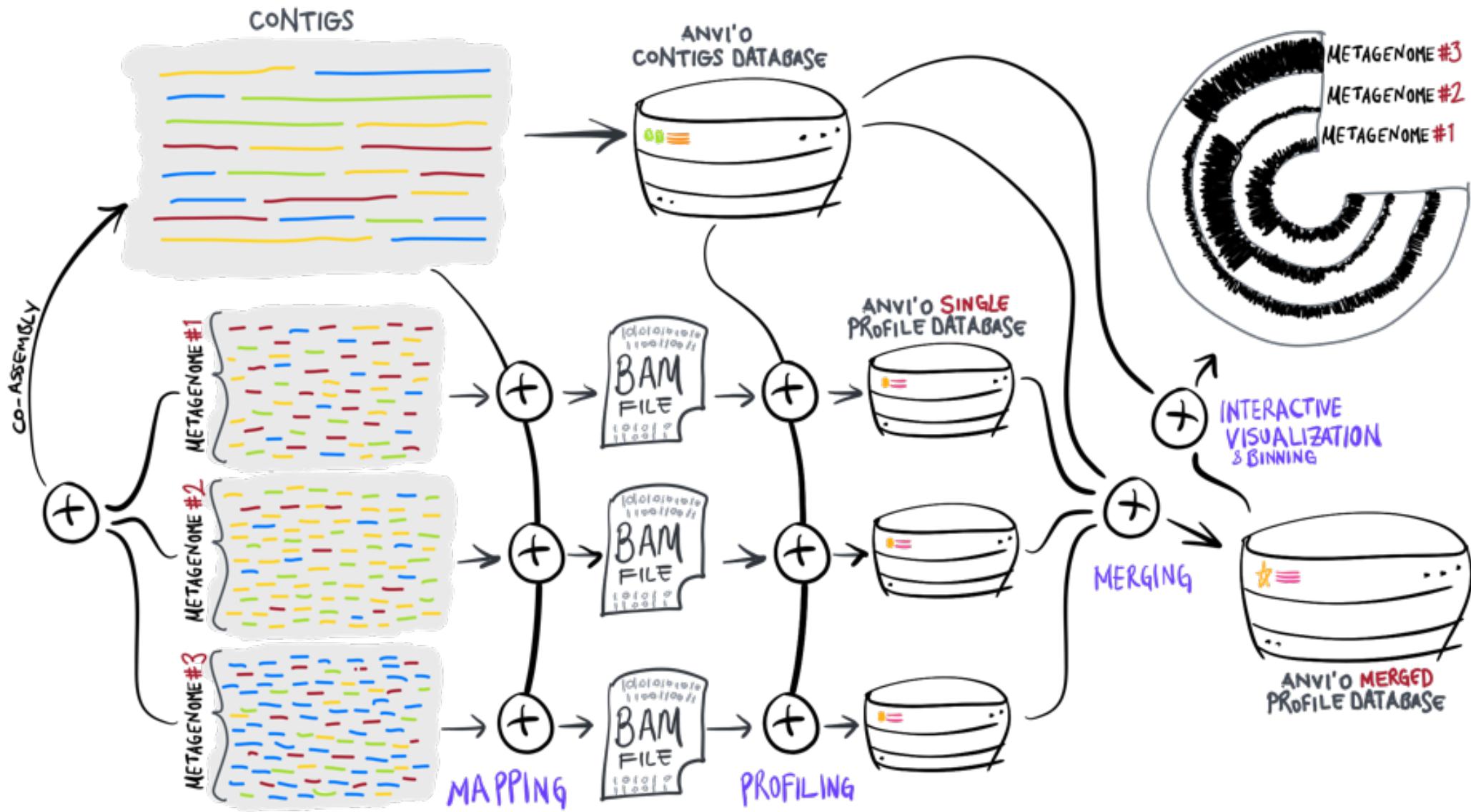


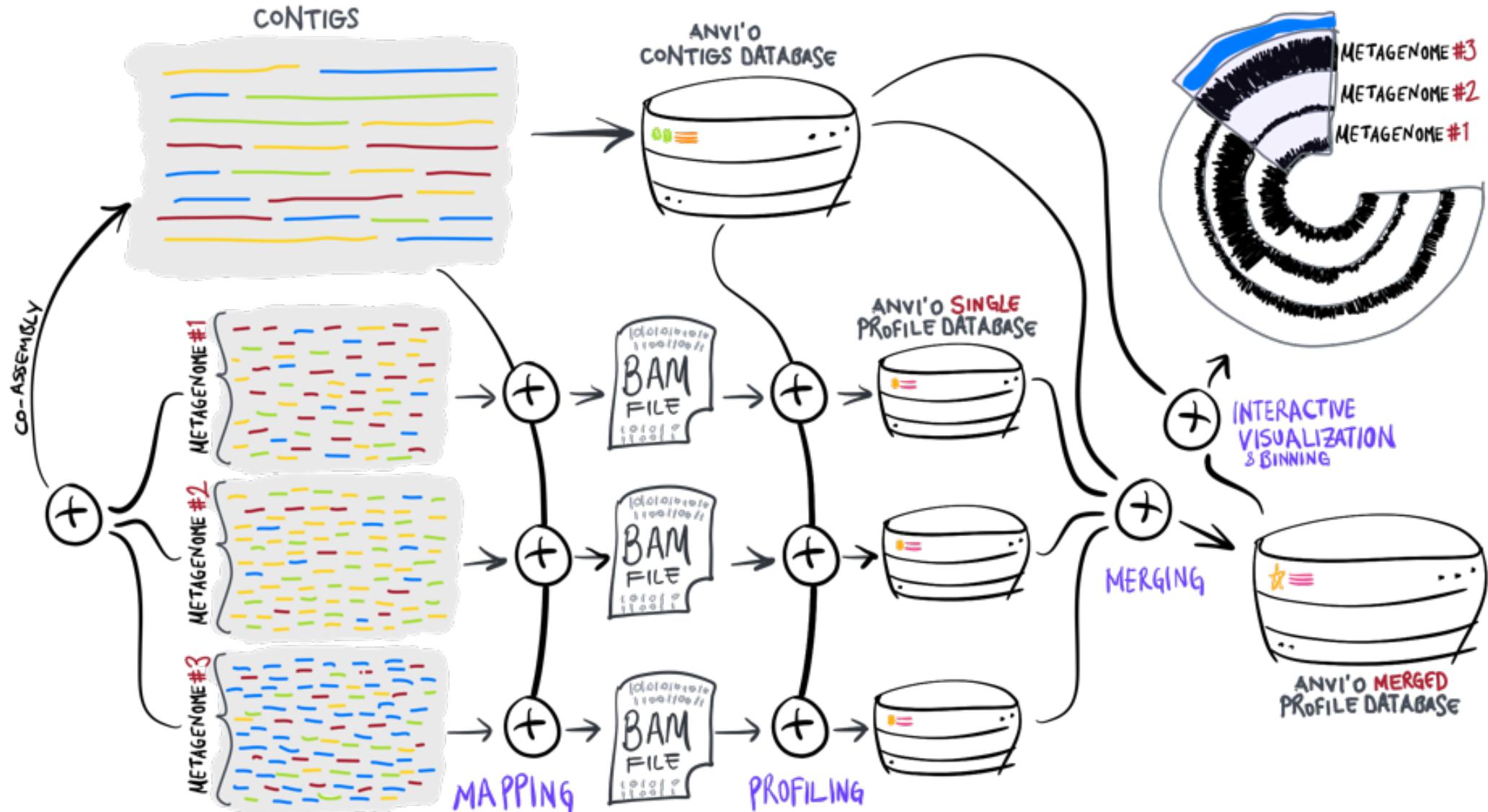


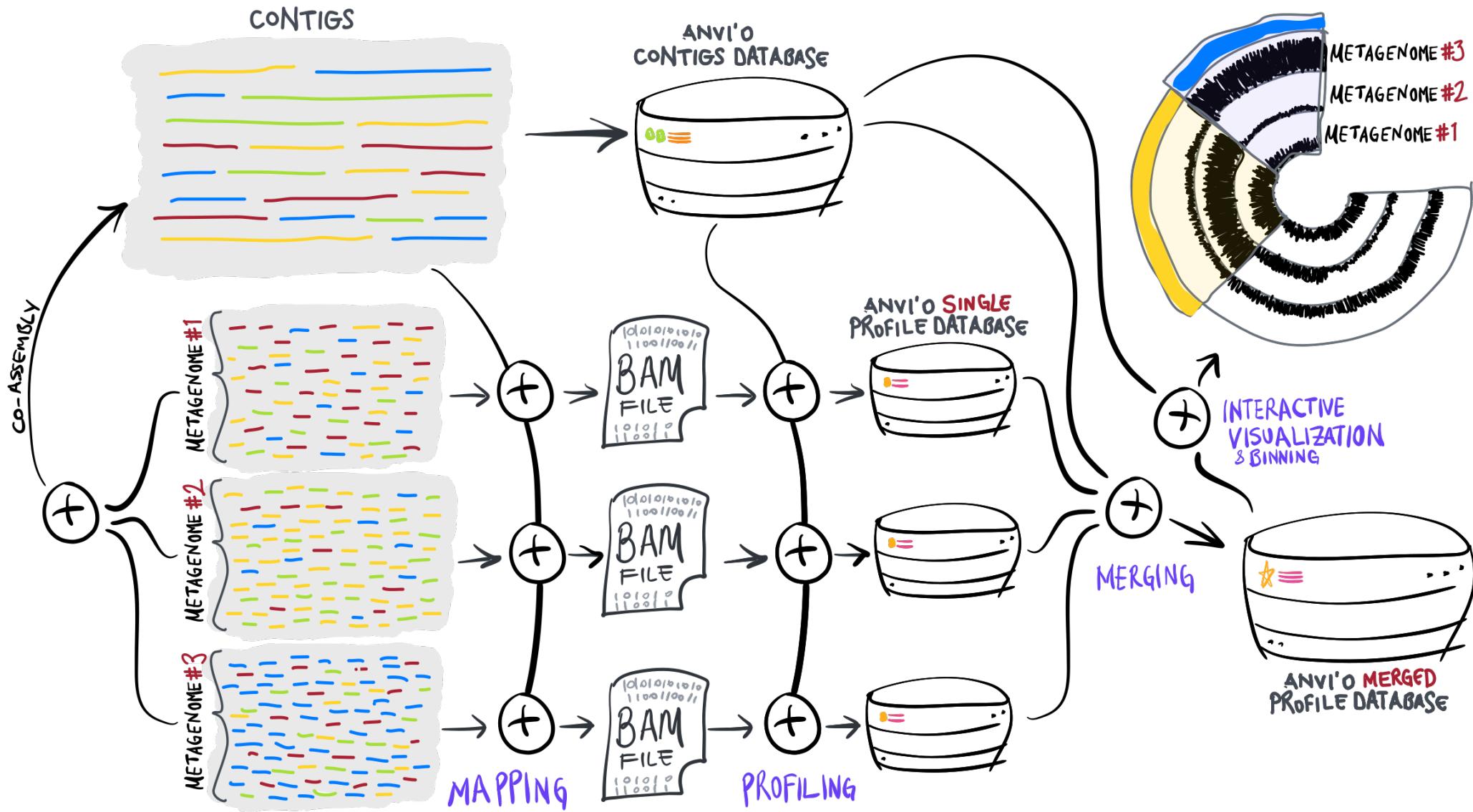


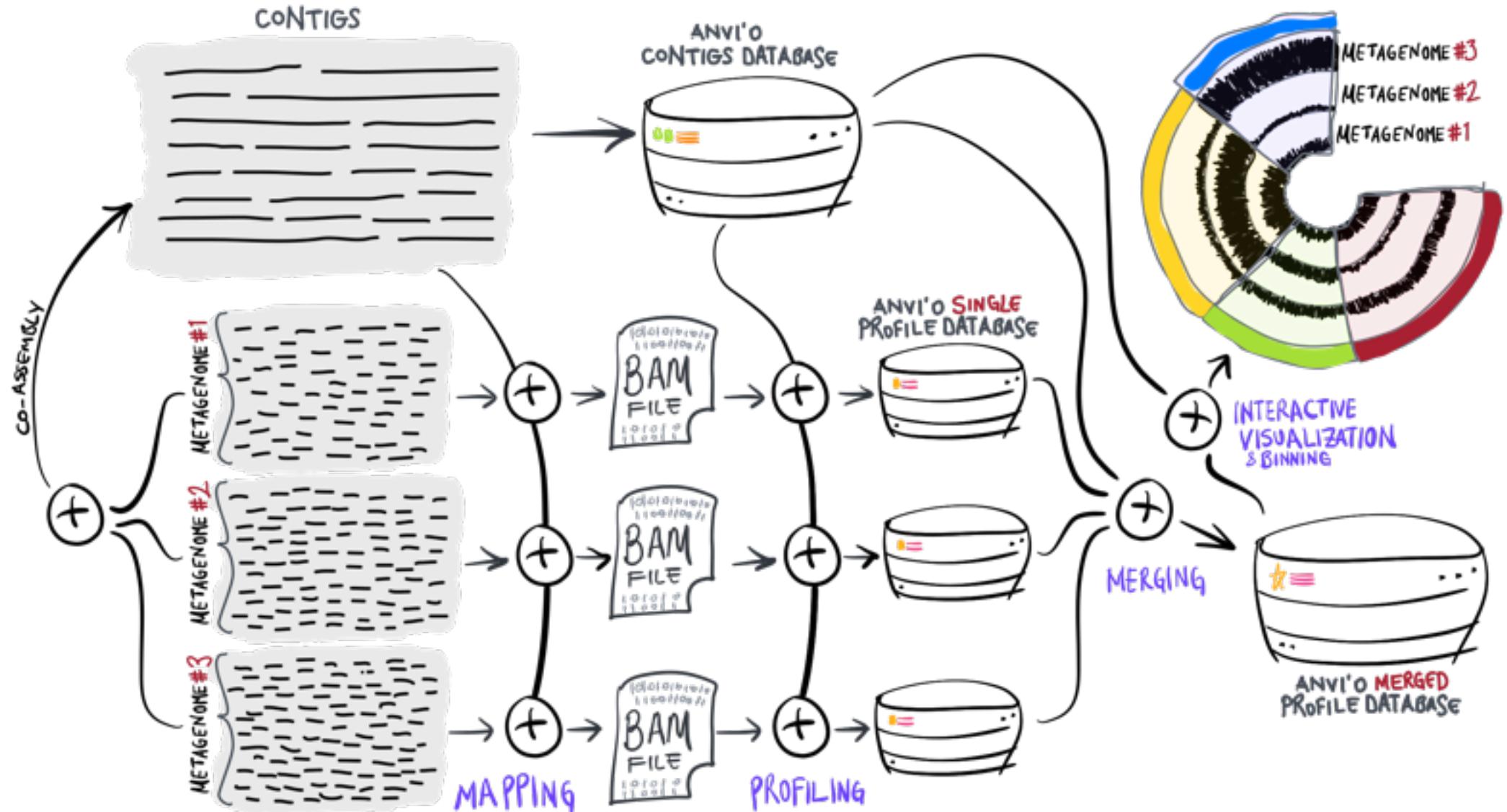






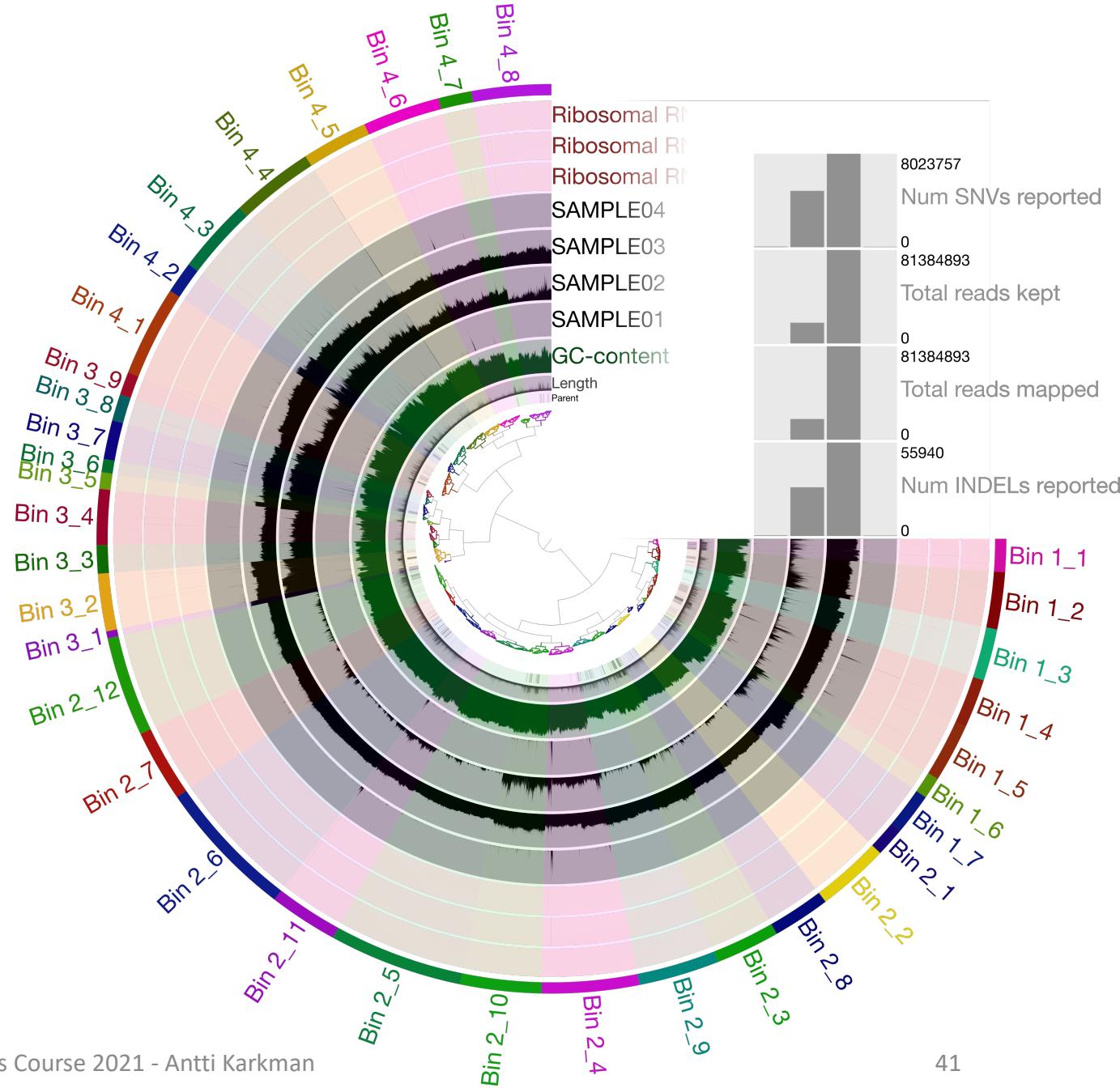




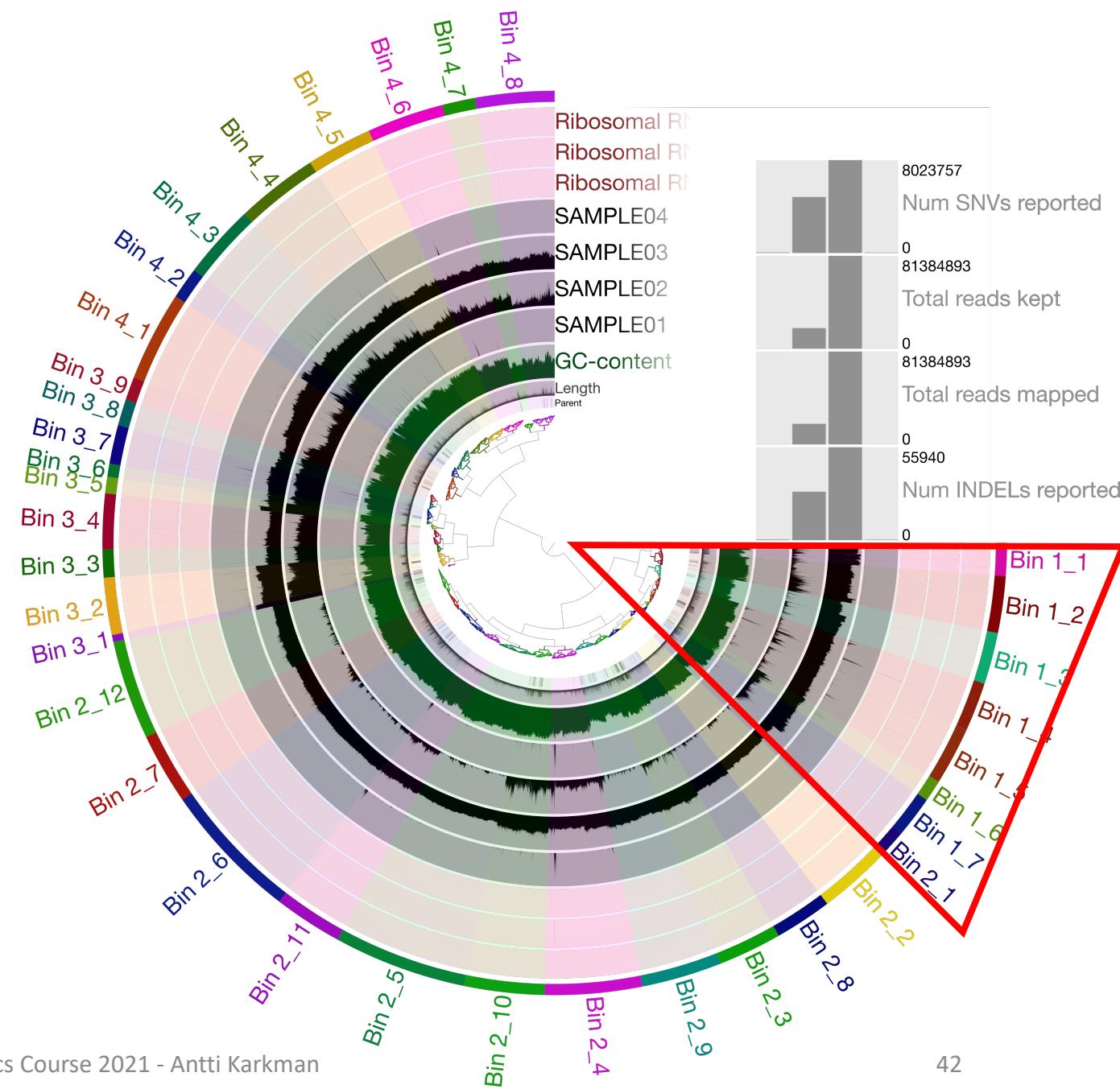


<http://merenlab.org/momics>

Anvi'o interactive view



Anvi'o interactive view



Anvi'o interactive view

