



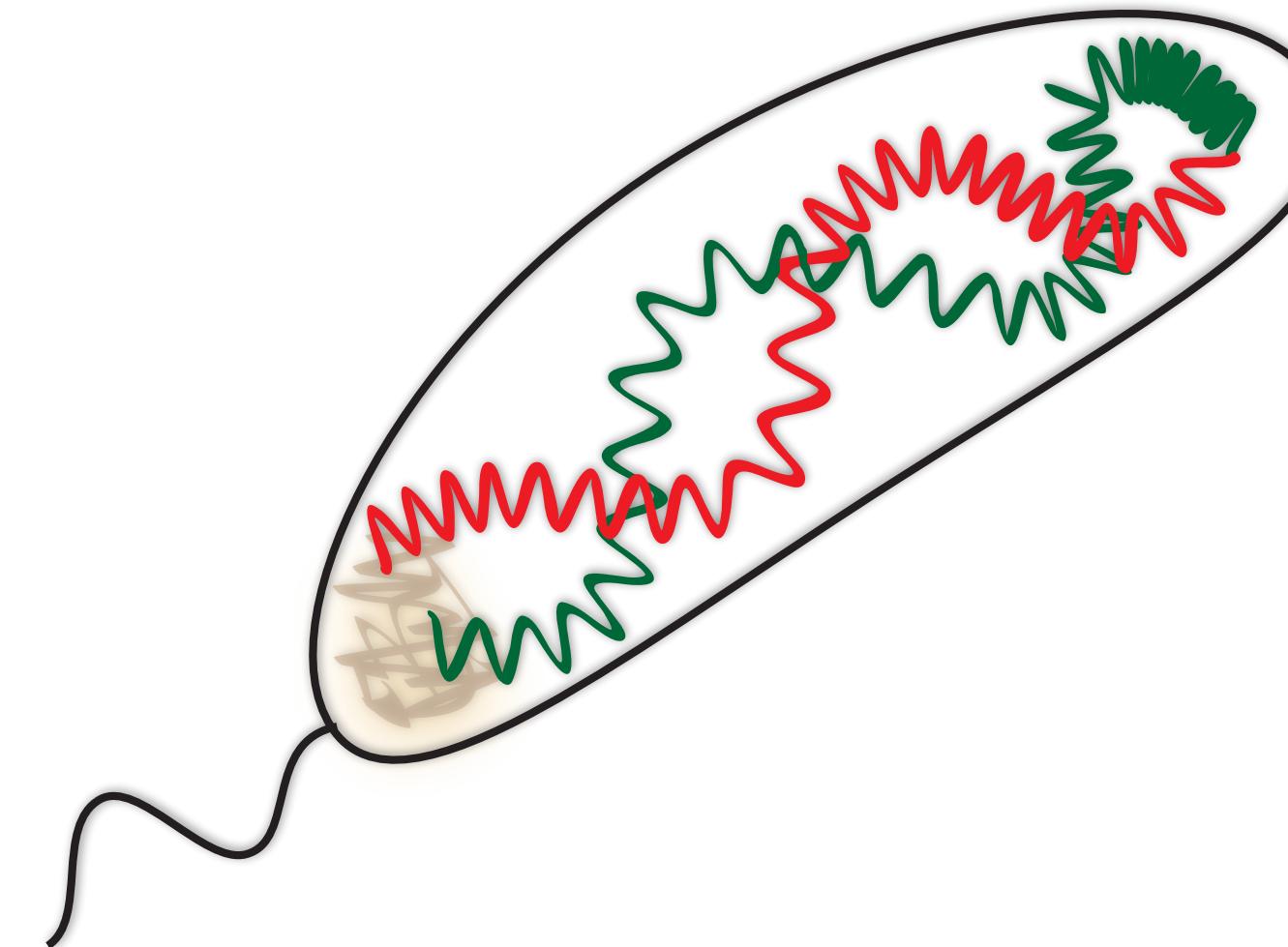
# The Three-Dimensional Architecture of a Bacterial Genome and Its Alteration by Genetic Perturbation

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CNAG-CRG · ICREA

<http://marciuslab.org>  
<http://3DGenomes.org>  
<http://cnag.crg.eu>

**cnag CRG** · ICREA

# Caulobacter crescentus genome



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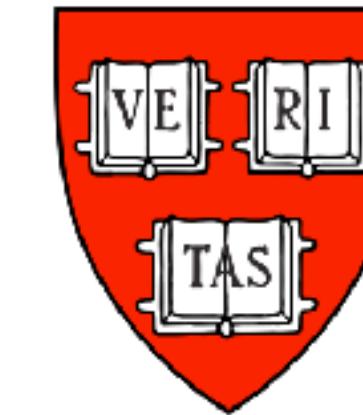


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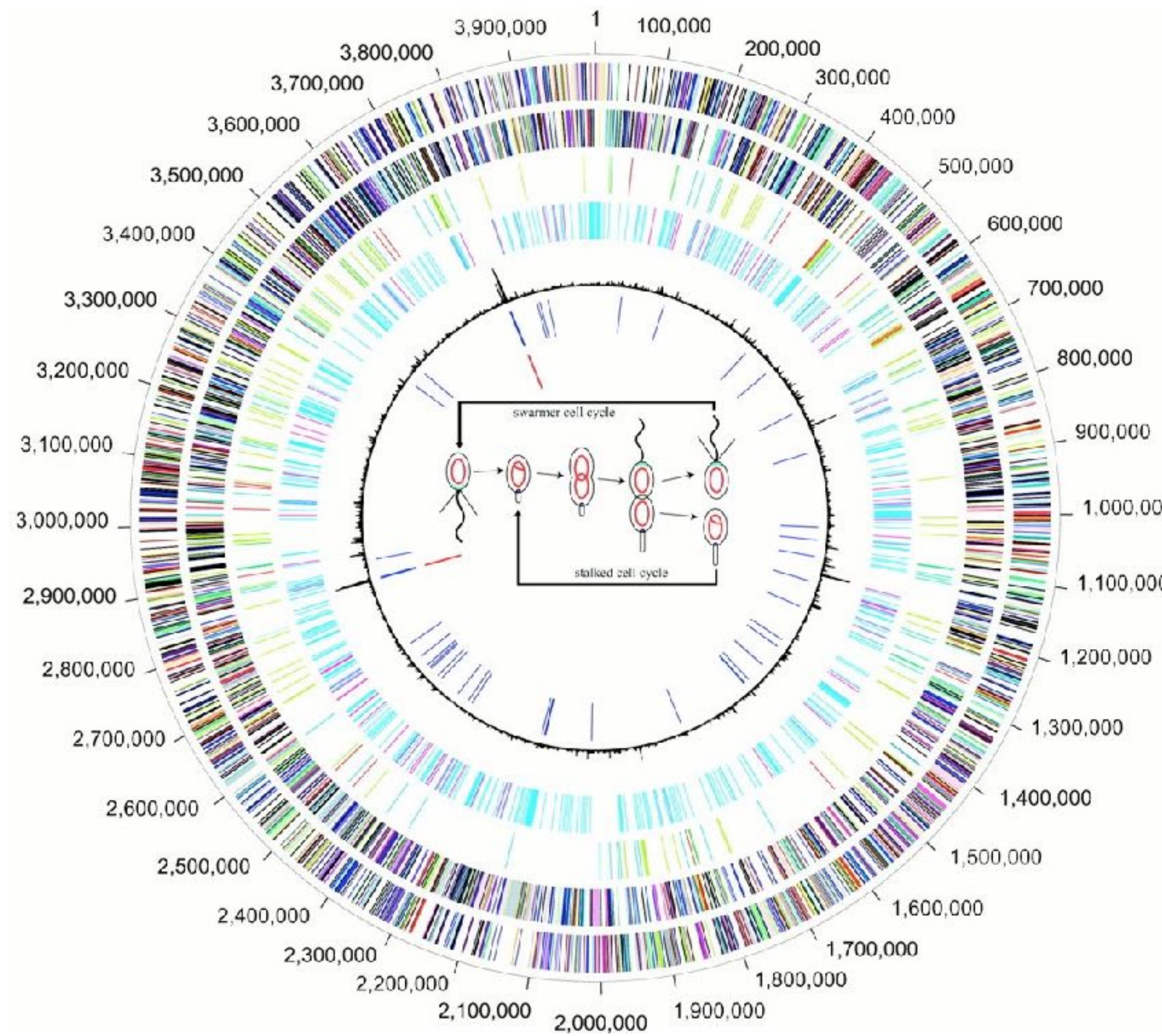


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# The 3D architecture of Caulobacter Crescentus

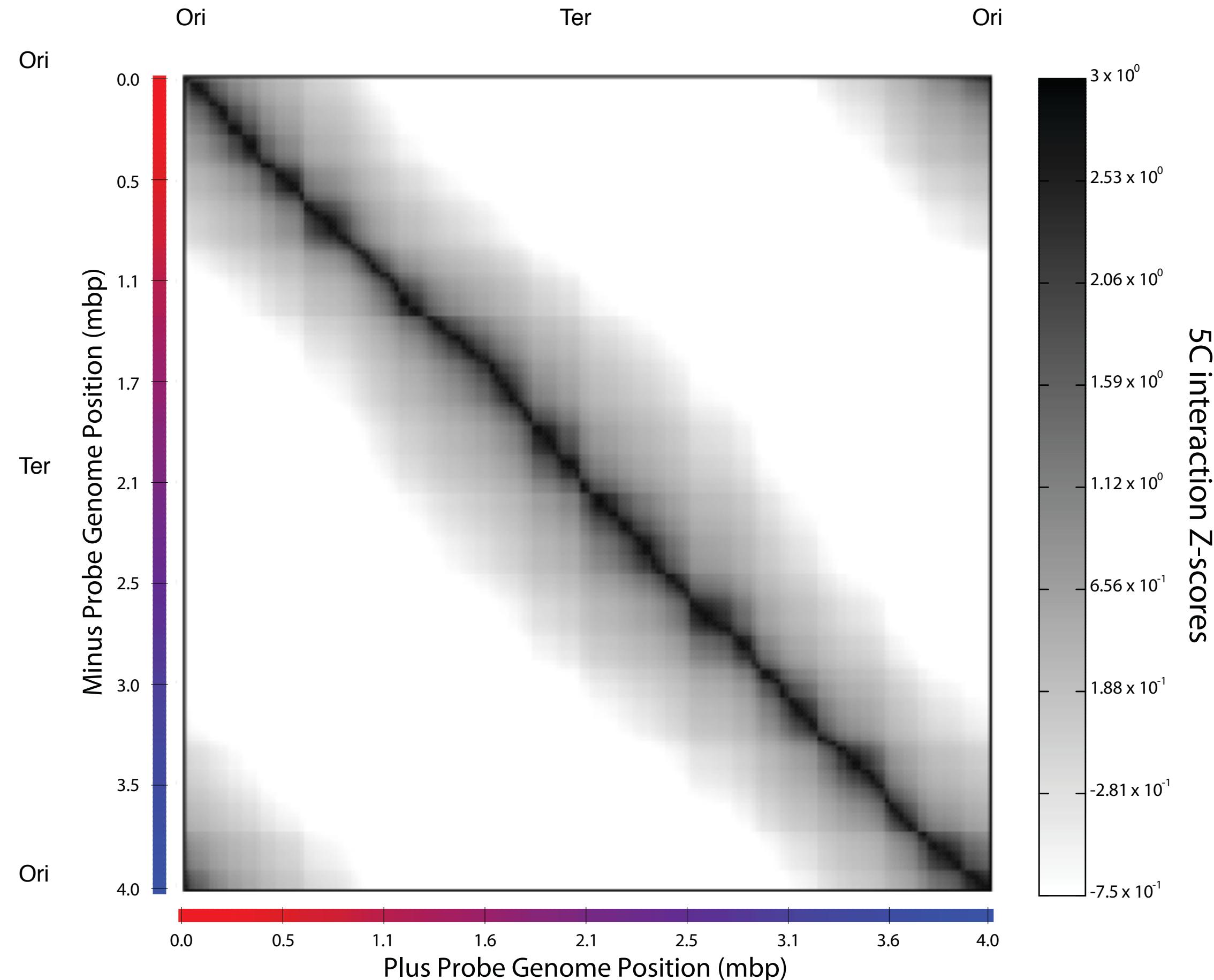
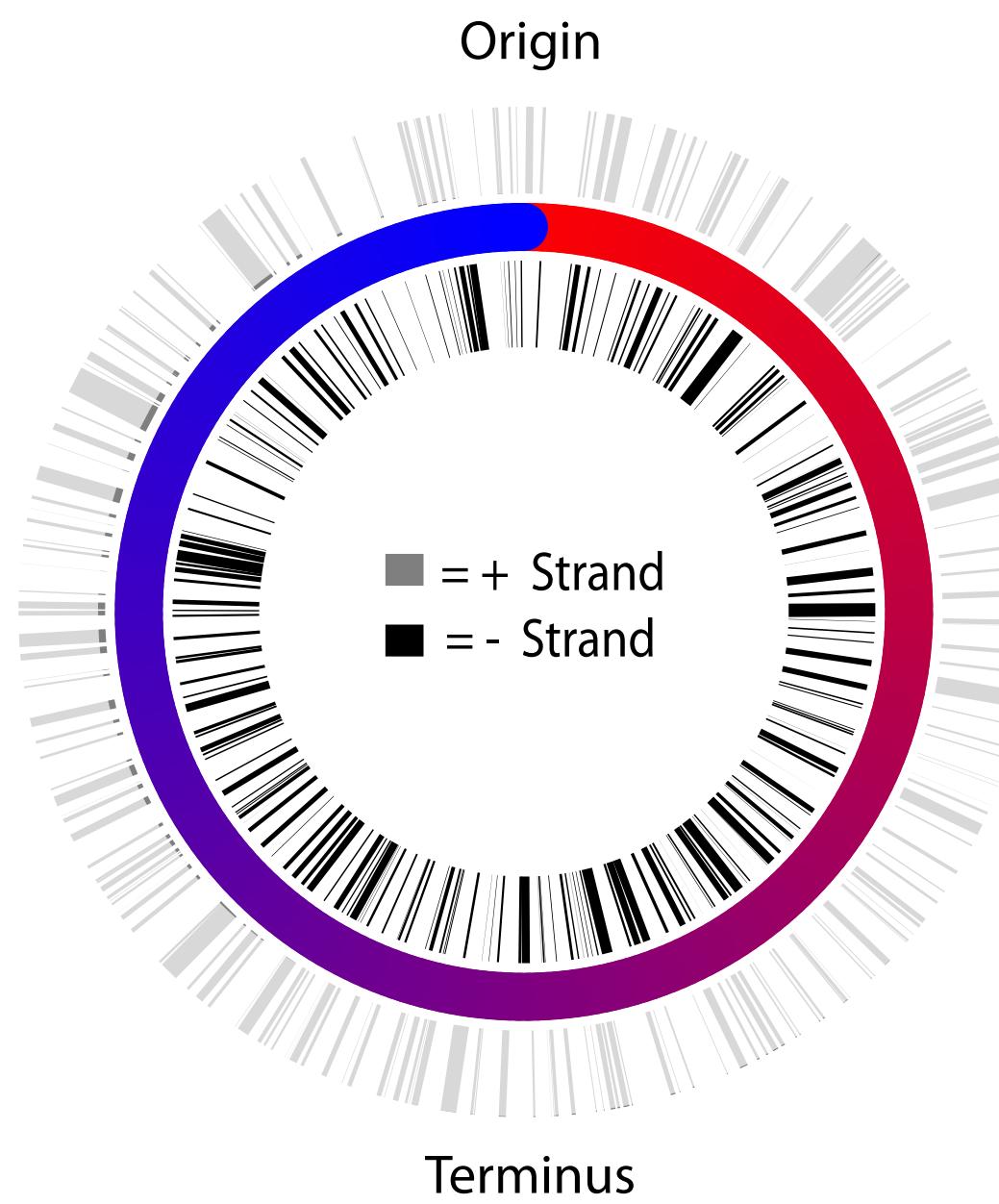
4,016,942 bp & 3,767 genes



Nierman W C et al. PNAS 2001 98:4136-4141

# The 3D architecture of Caulobacter Crescentus

4,016,942 bp & 3,767 genes

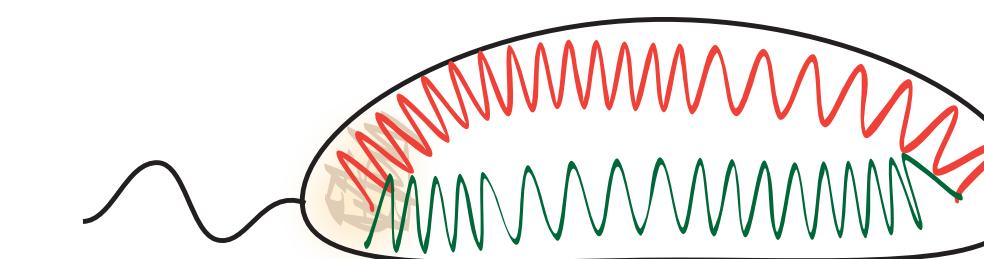
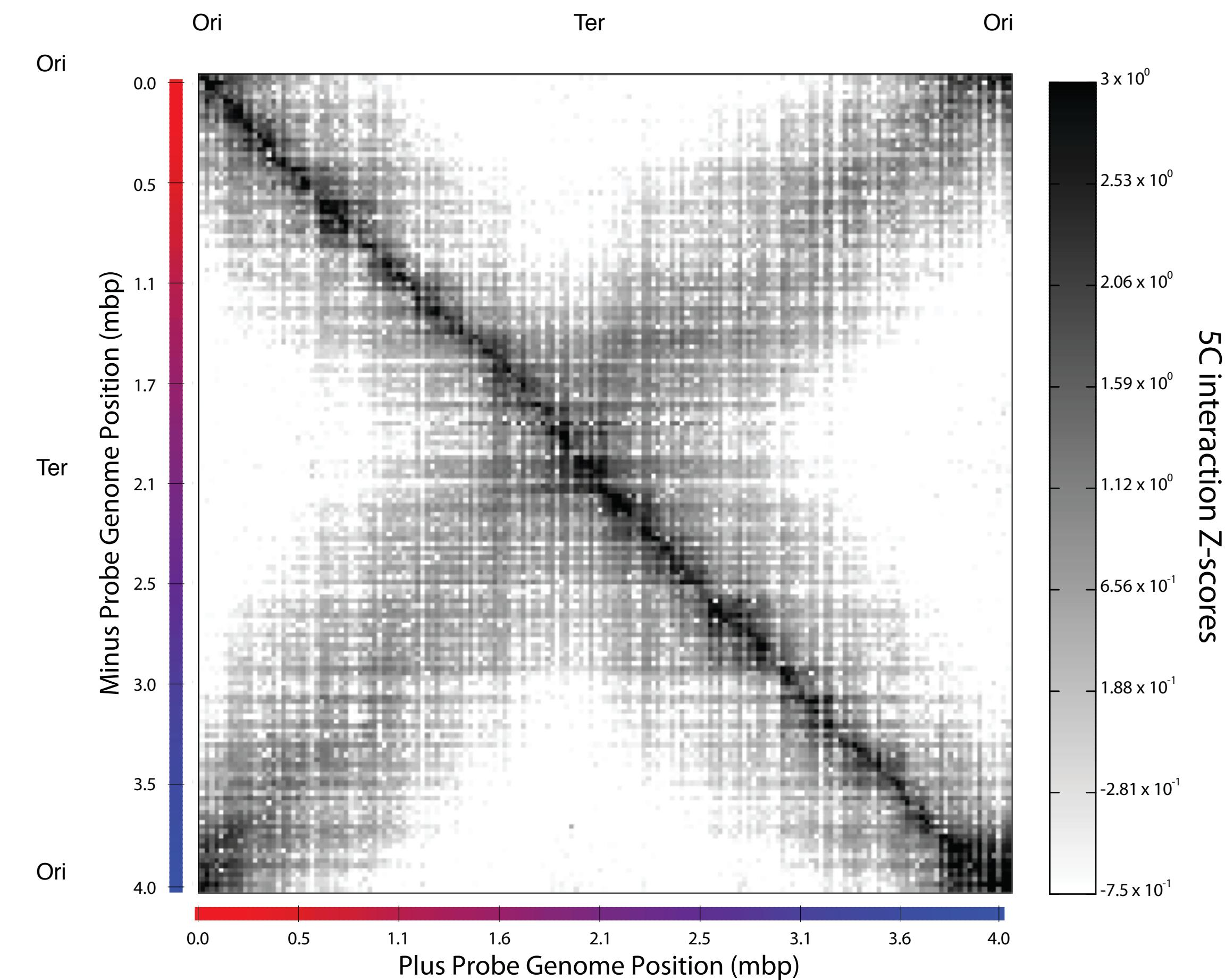
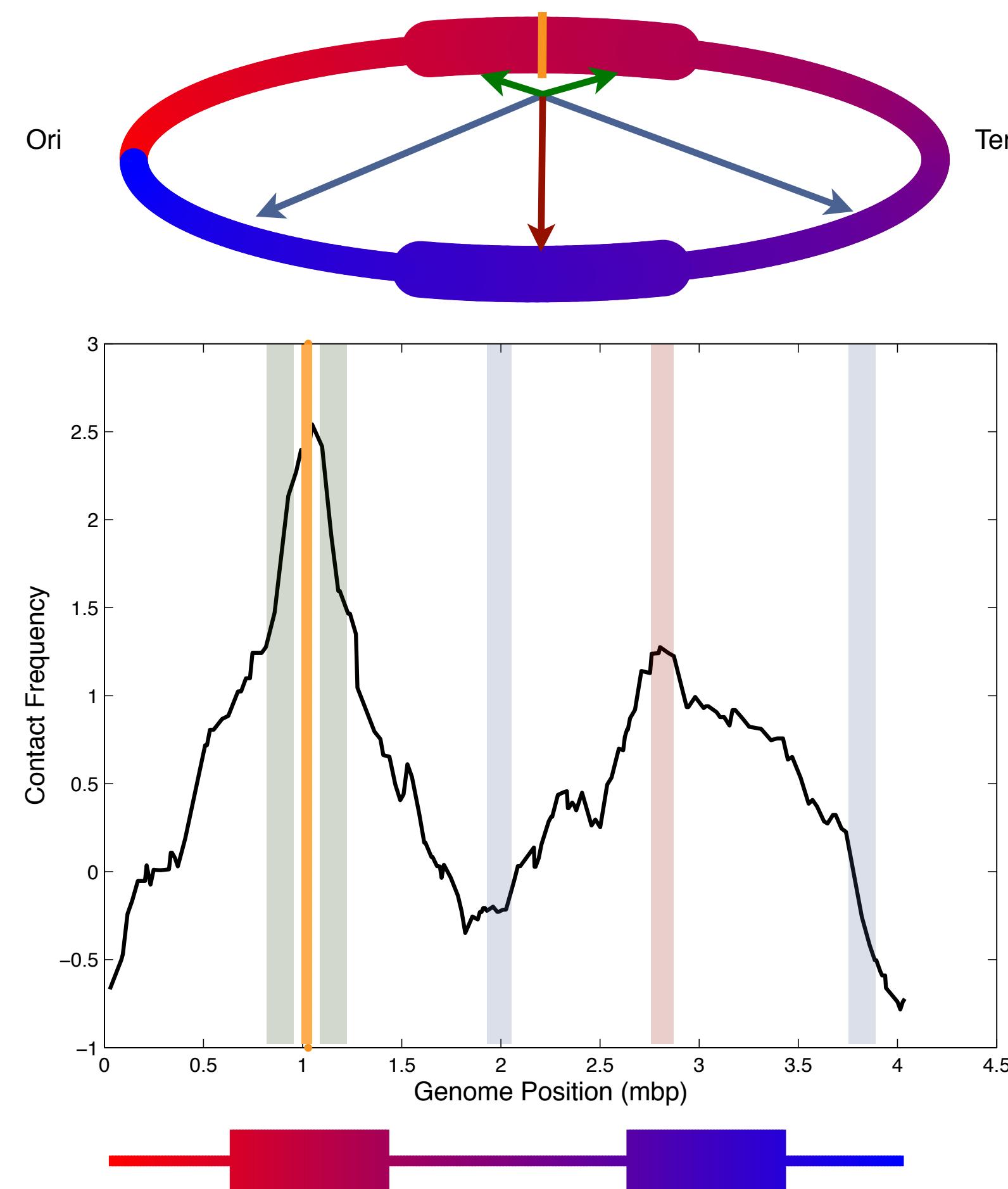


169 5C primers on + strand  
170 5C primers on - strand  
**28,730 chromatin interactions**

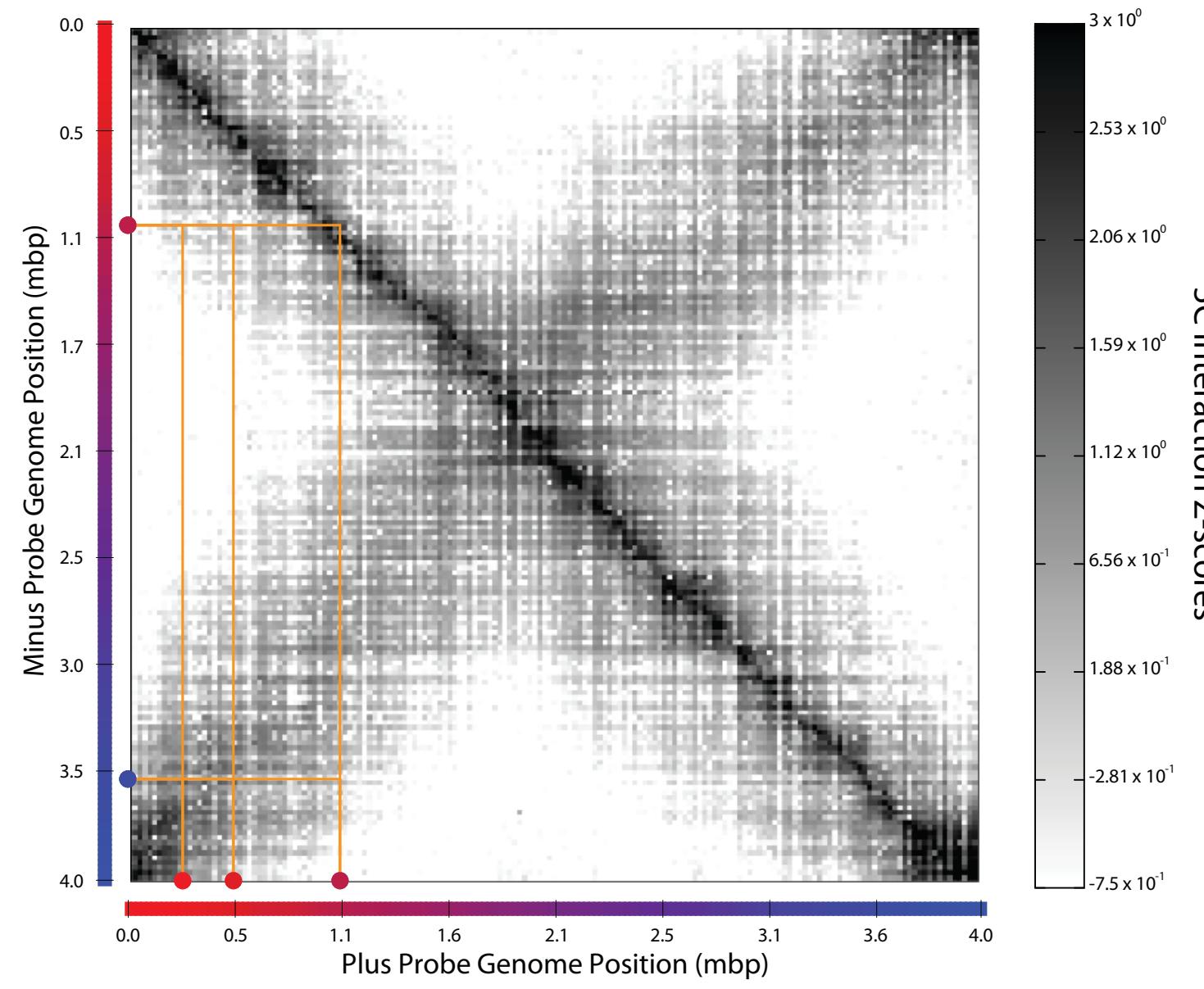
**~13Kb**

# 5C interaction matrix

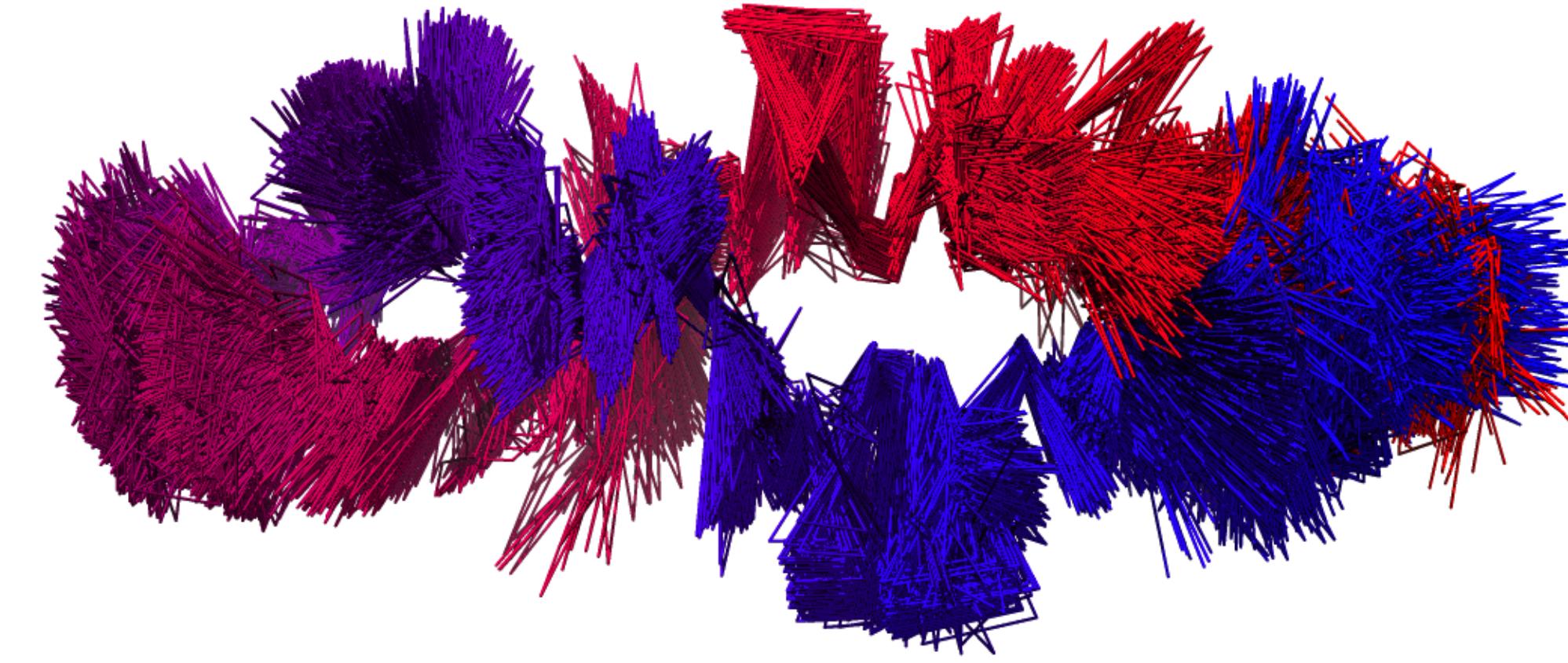
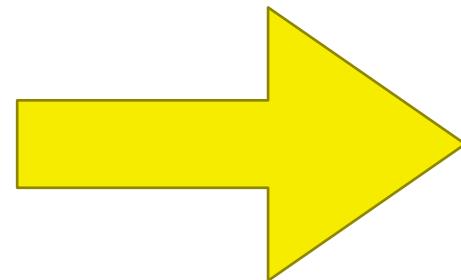
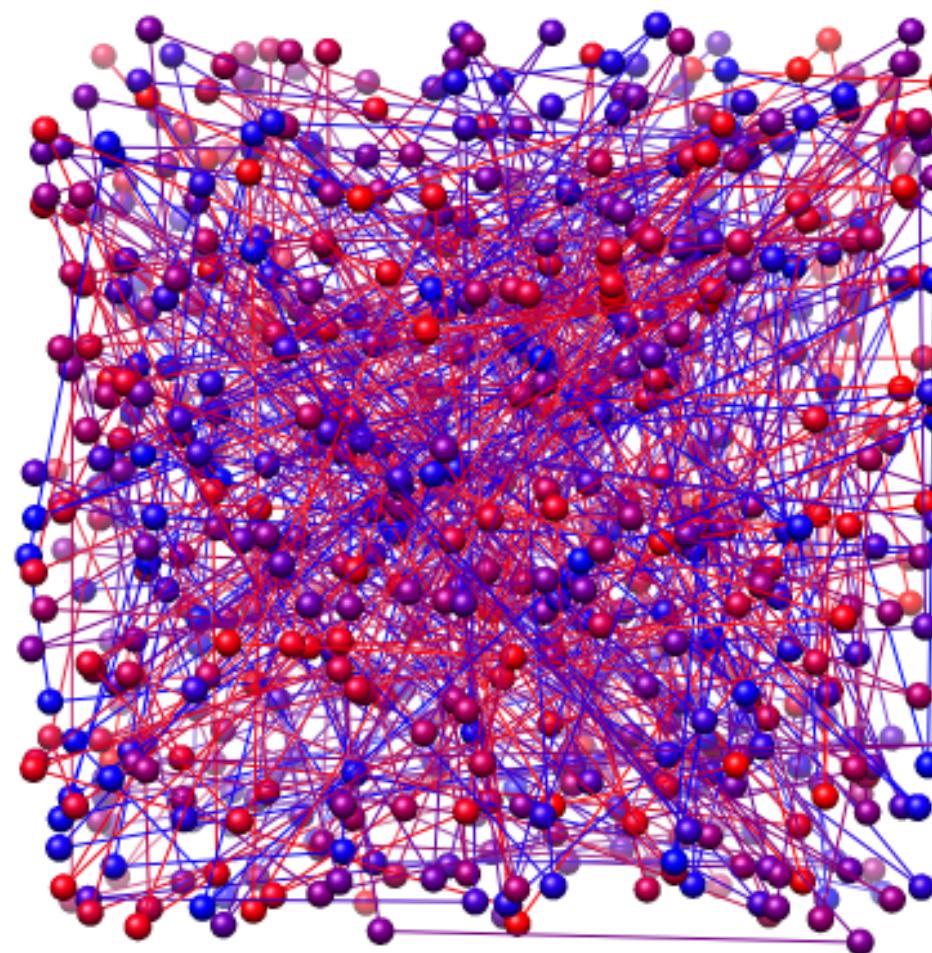
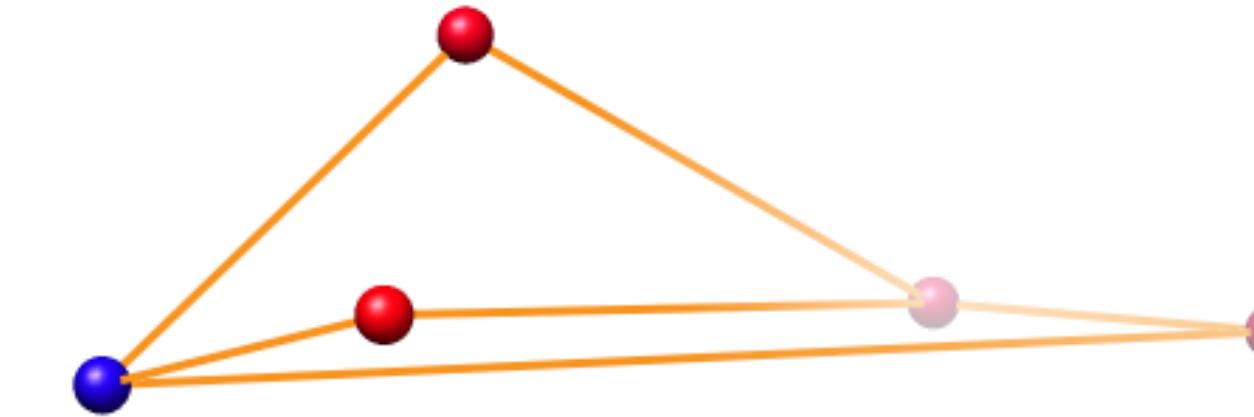
*ELLIPSOID* for *Caulobacter crescentus*



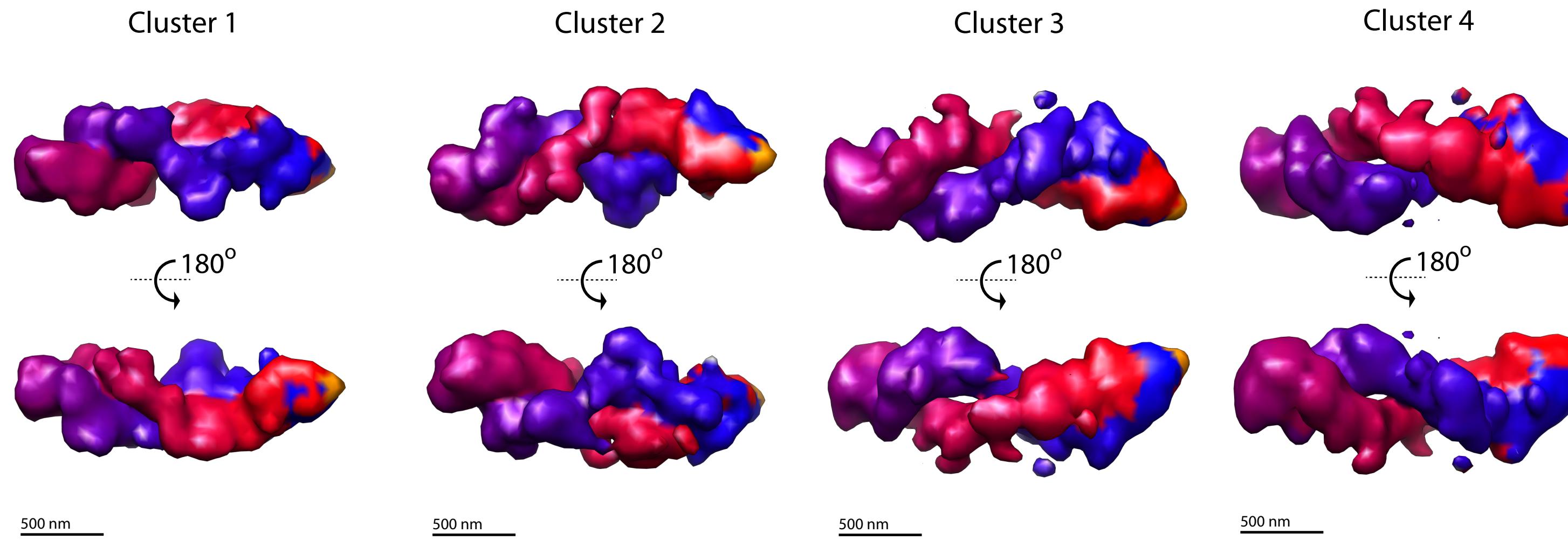
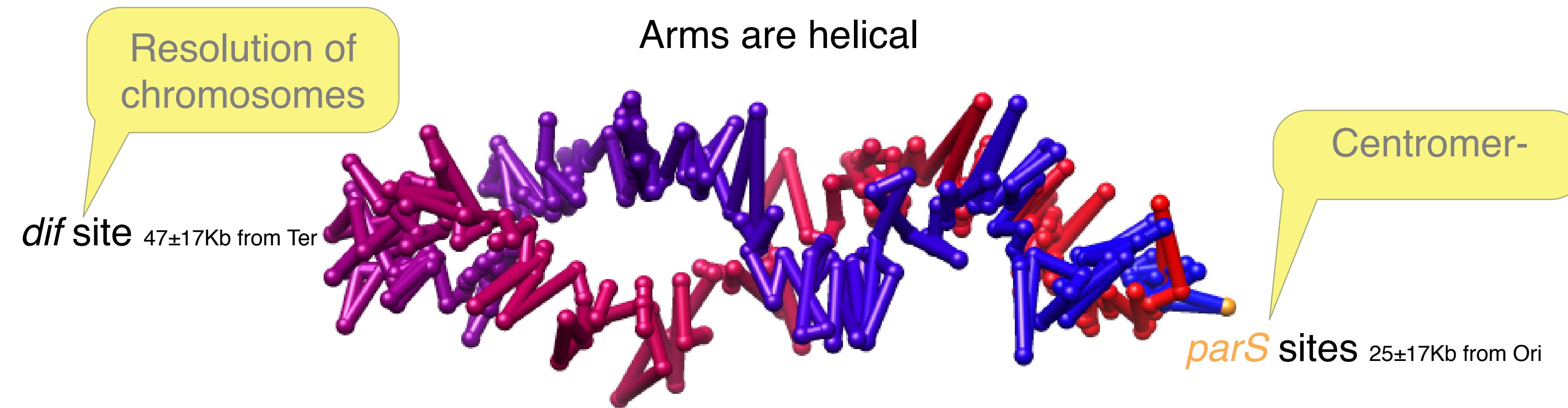
# 3D model building with TADbit



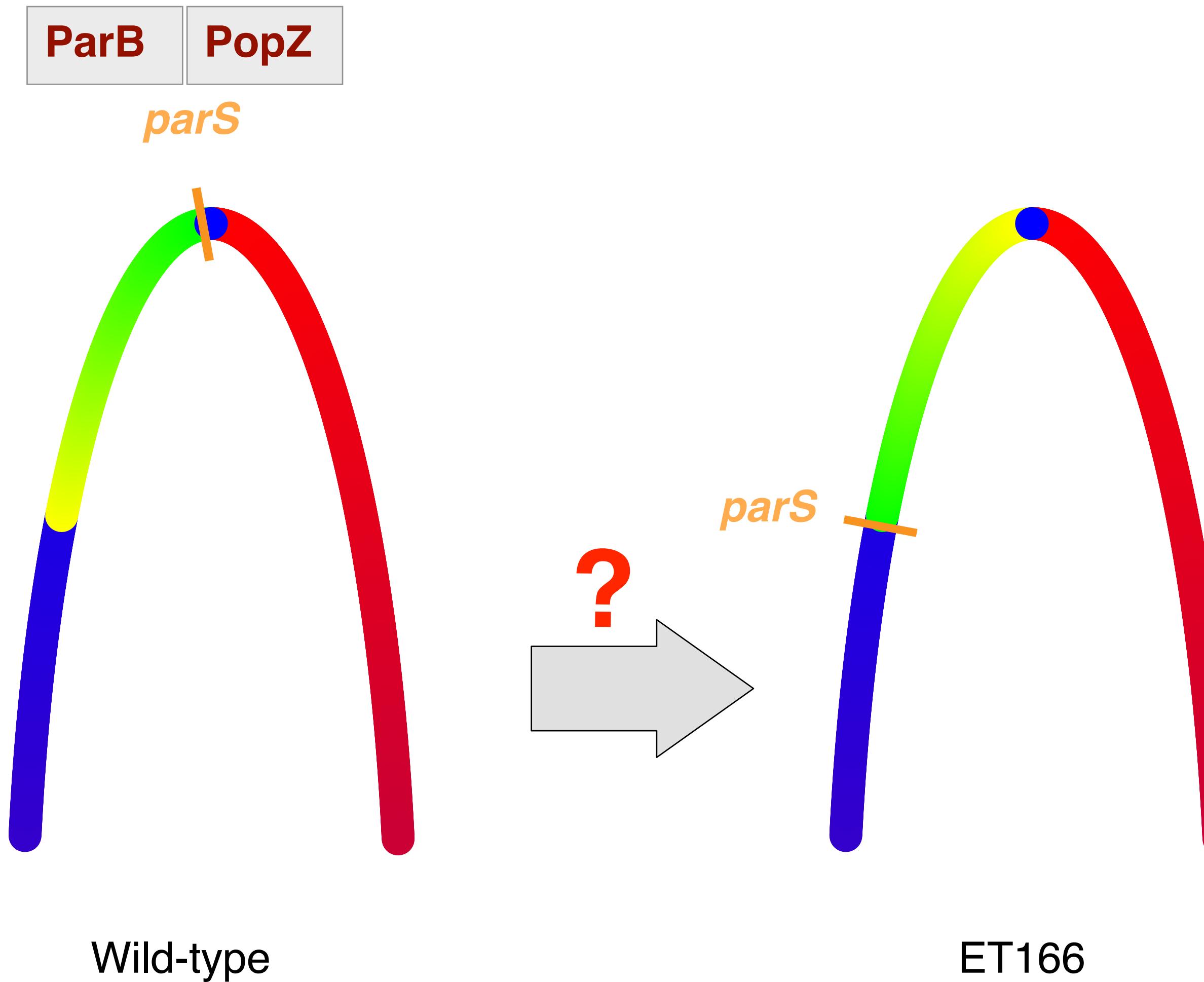
**339 mers**



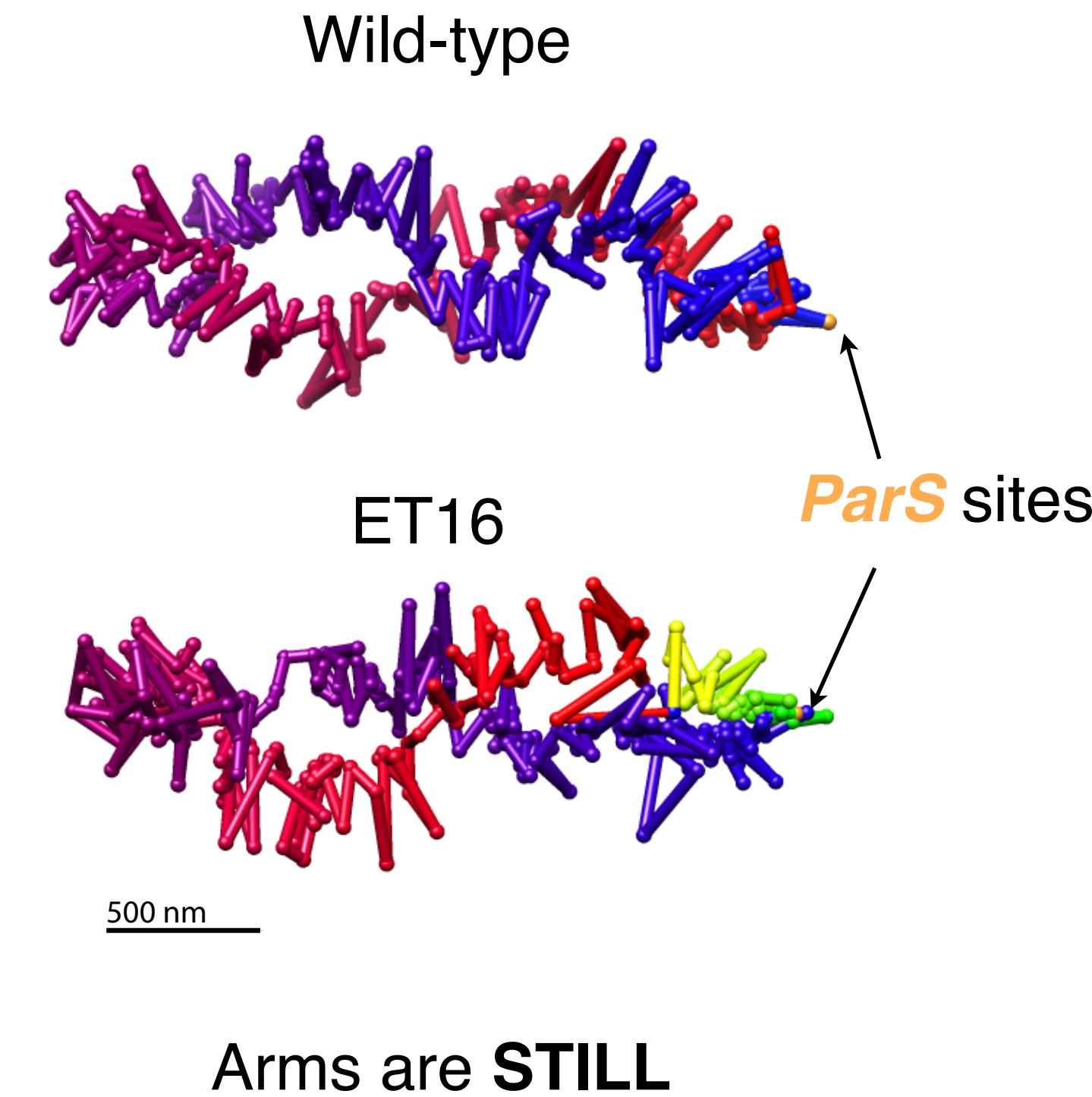
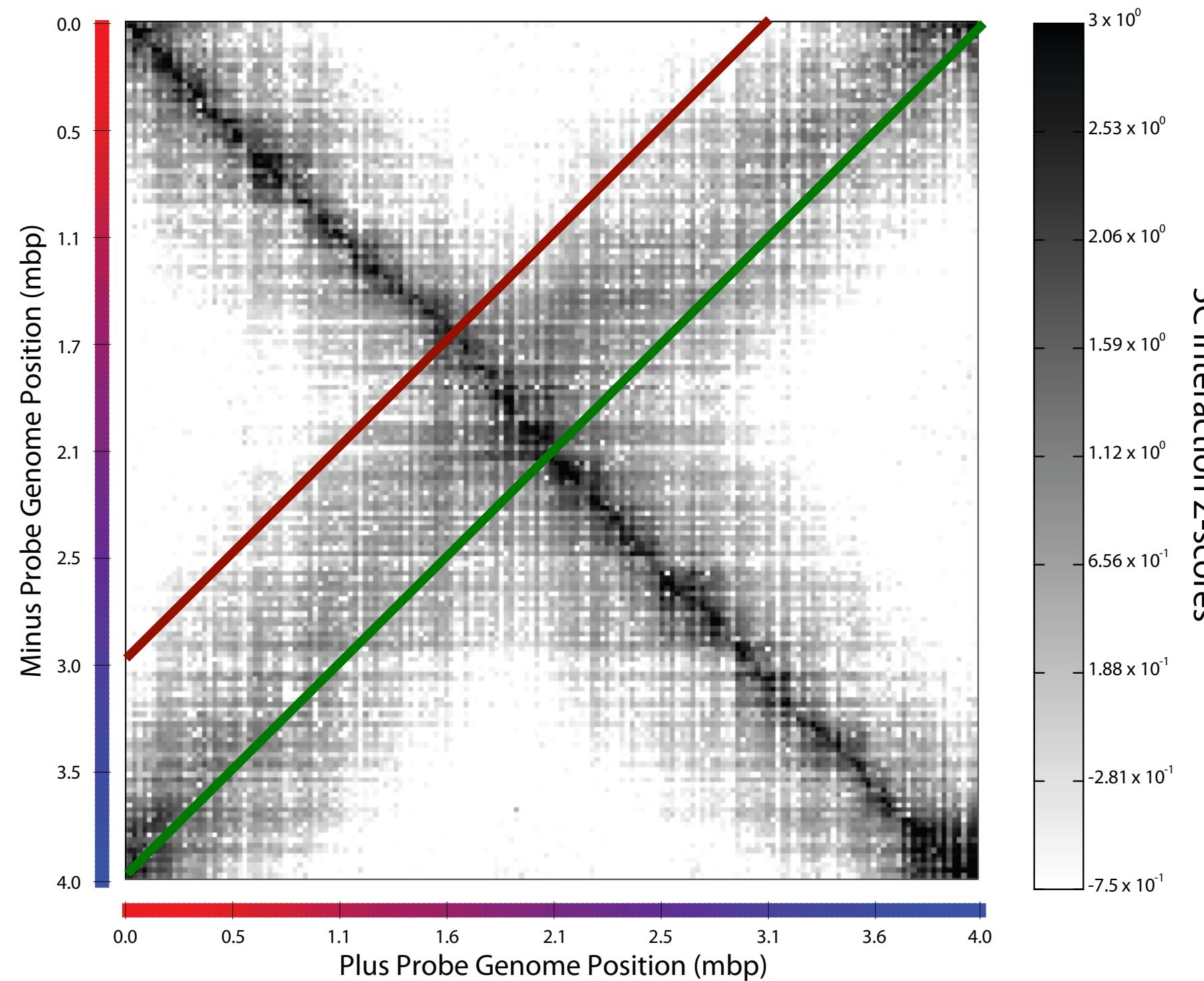
# Genome organization in *Caulobacter crescentus*



# Moving the *parS* sites 400 Kb away from Ori

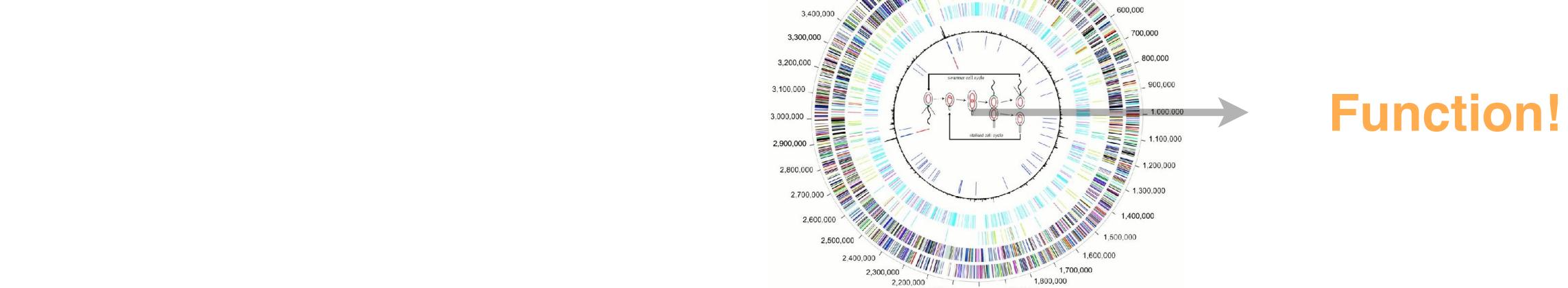
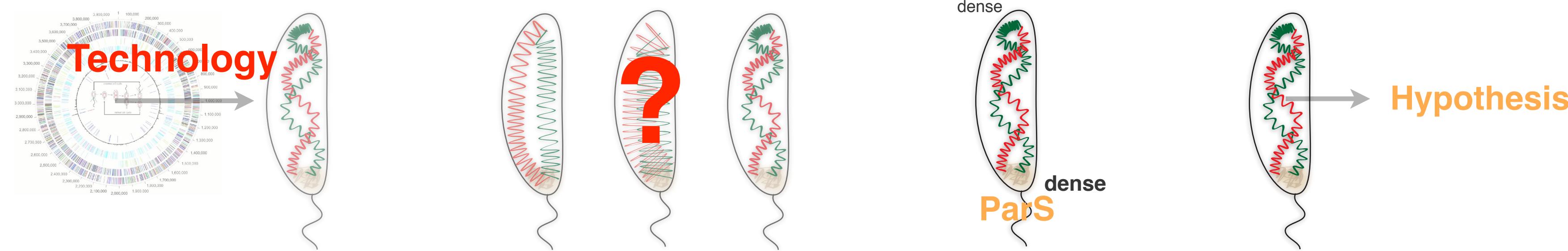
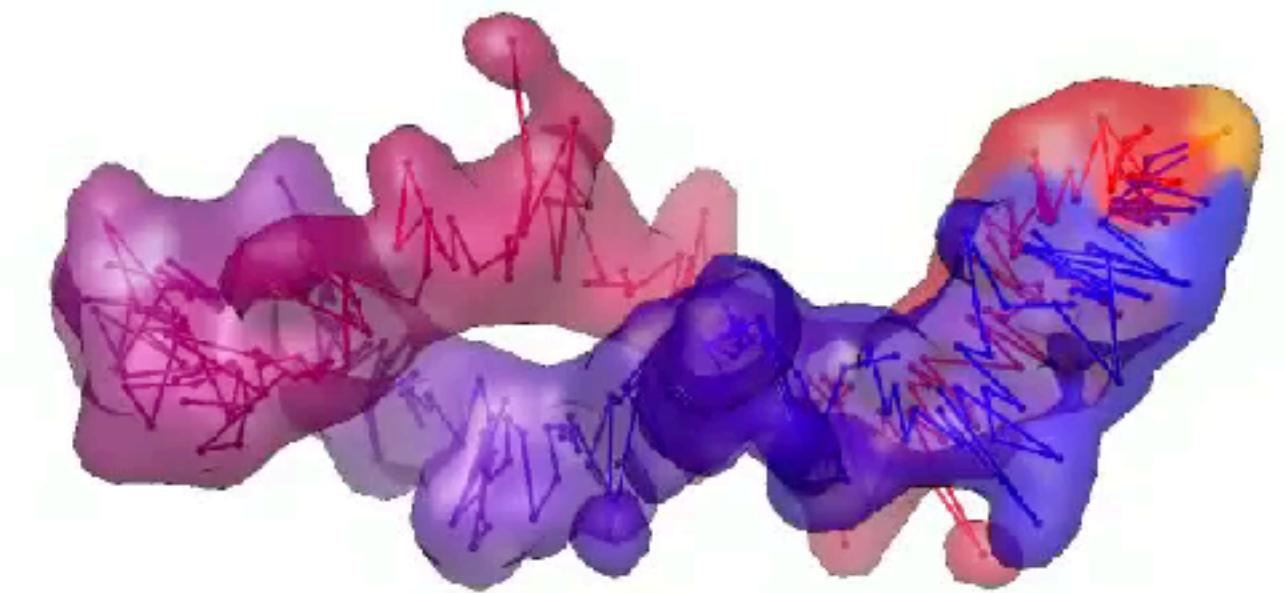


# Moving the *parS* sites results in whole genome rotation!



# From Sequence to Function

## Genome architecture in *Caulobacter*



# Bacteria has also TADs (CIDs)

Le, T. B. K., Imakaev, M. V., Mirny, L. A., & Laub, M. T. (2013). High-Resolution Mapping of the Spatial Organization of a Bacterial Chromosome. *Science* (New York, NY), 1242059

