Sequences, activity maps and epigenetic landscapes of Arabidopsis nucleolus organizers

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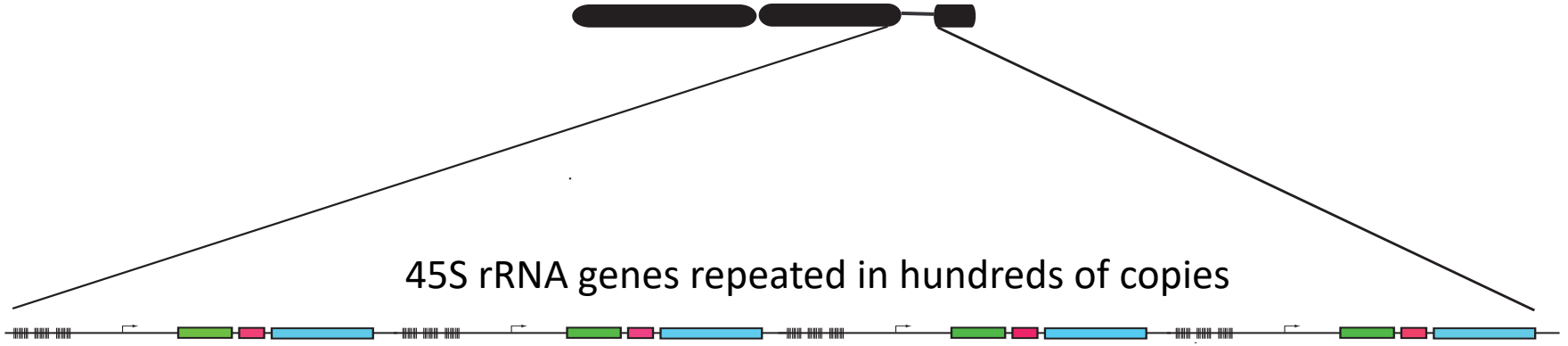
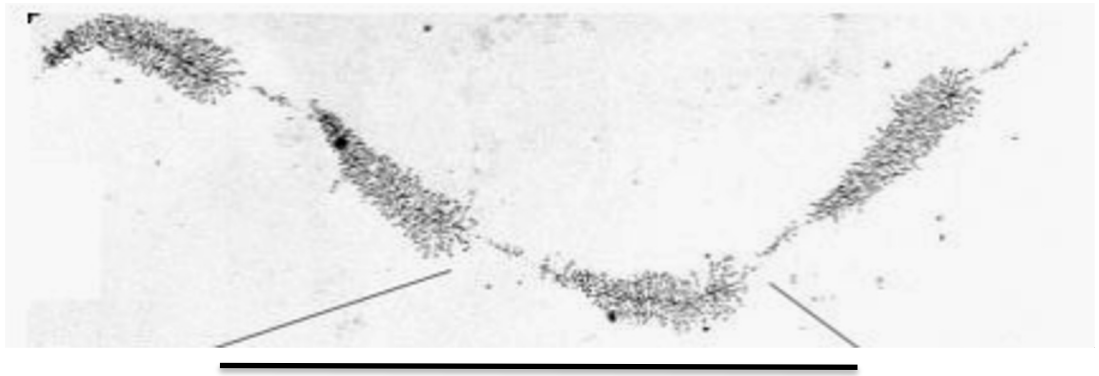
“Sequence and epigenetic landscapes of active and silent nucleolus organizer regions in Arabidopsis”

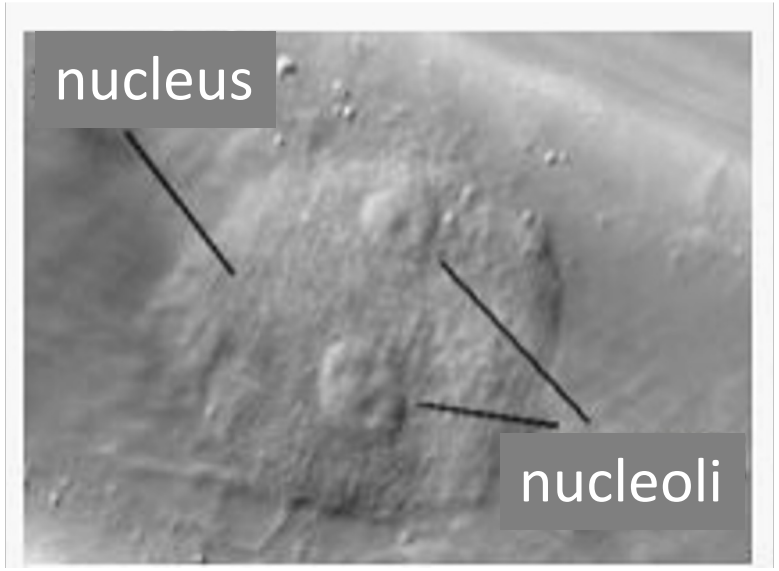
Published, November 2023; PMID: 37910609

rRNA gene clusters, when active, give rise to the nucleolus.
They are thus known as nucleolus organizer regions (NORs)





one 45S rRNA gene



Back in 1995-'96:

Use of RFLPs larger than 100 kbp to map the position and internal organization of the nucleolus organizer region on chromosome 2 in *Arabidopsis thaliana*

Gregory P. Copenhaver, Jed H. Doelling, J. Scott Gens, Craig S. Pikaard

First published: February 1995 | https://doi.org/10.1046/j.1365-313X.1995.7020273.x | Citations

RFLP and physical mapping with an rDNA-specific endonuclease reveals that nucleolus organizer regions of Arabidopsis thaliana adjoin the telomeres on chromosomes 2 and 4

G P Copenhaver [1], C S Pikaard

Affiliations + expand

PMID: 8820610 DOI: 10.1046/j.1365-313x.1996.09020259.x

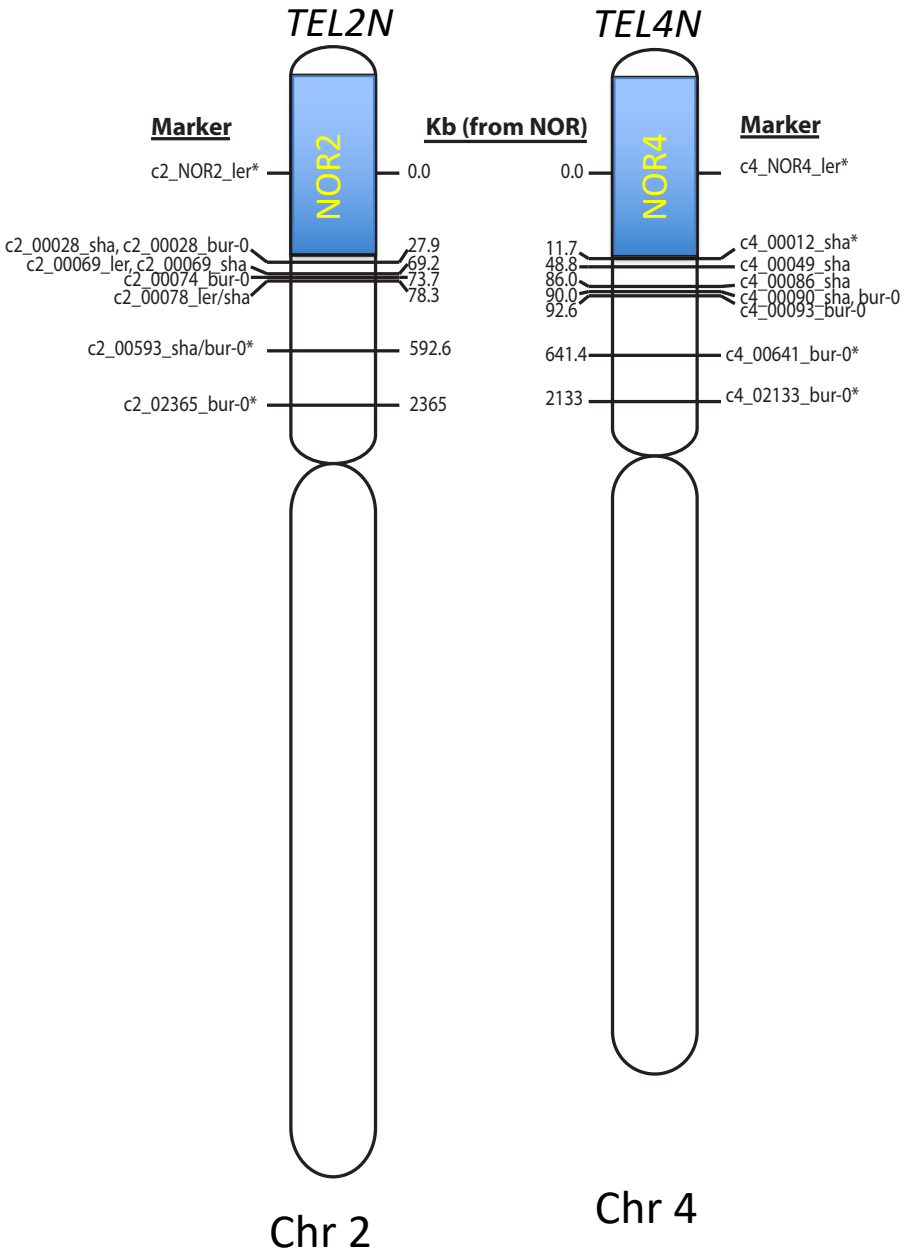
Two-dimensional RFLP analyses reveal megabase-sized clusters of rRNA gene variants in Arabidopsis thaliana, suggesting local spreading of variants as the mode for gene homogenization during concerted evolution

G P Copenhaver [1], C S Pikaard

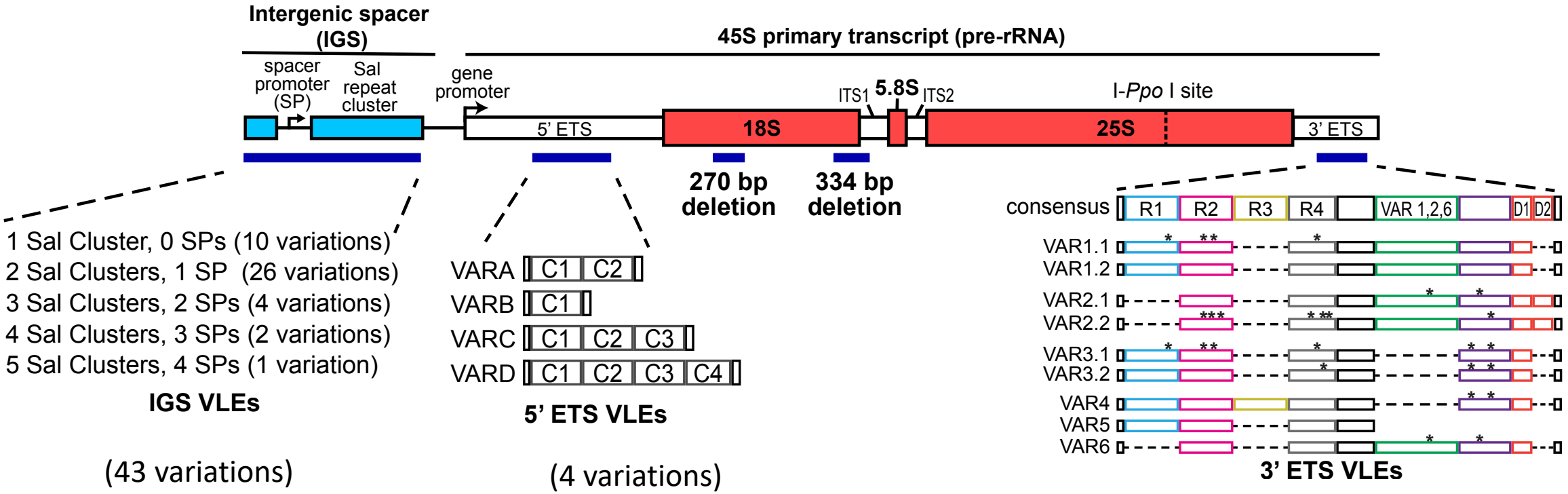
Affiliations + expand

PMID: 8820611 DOI: 10.1046/j.1365-313x.1996.09020273.x

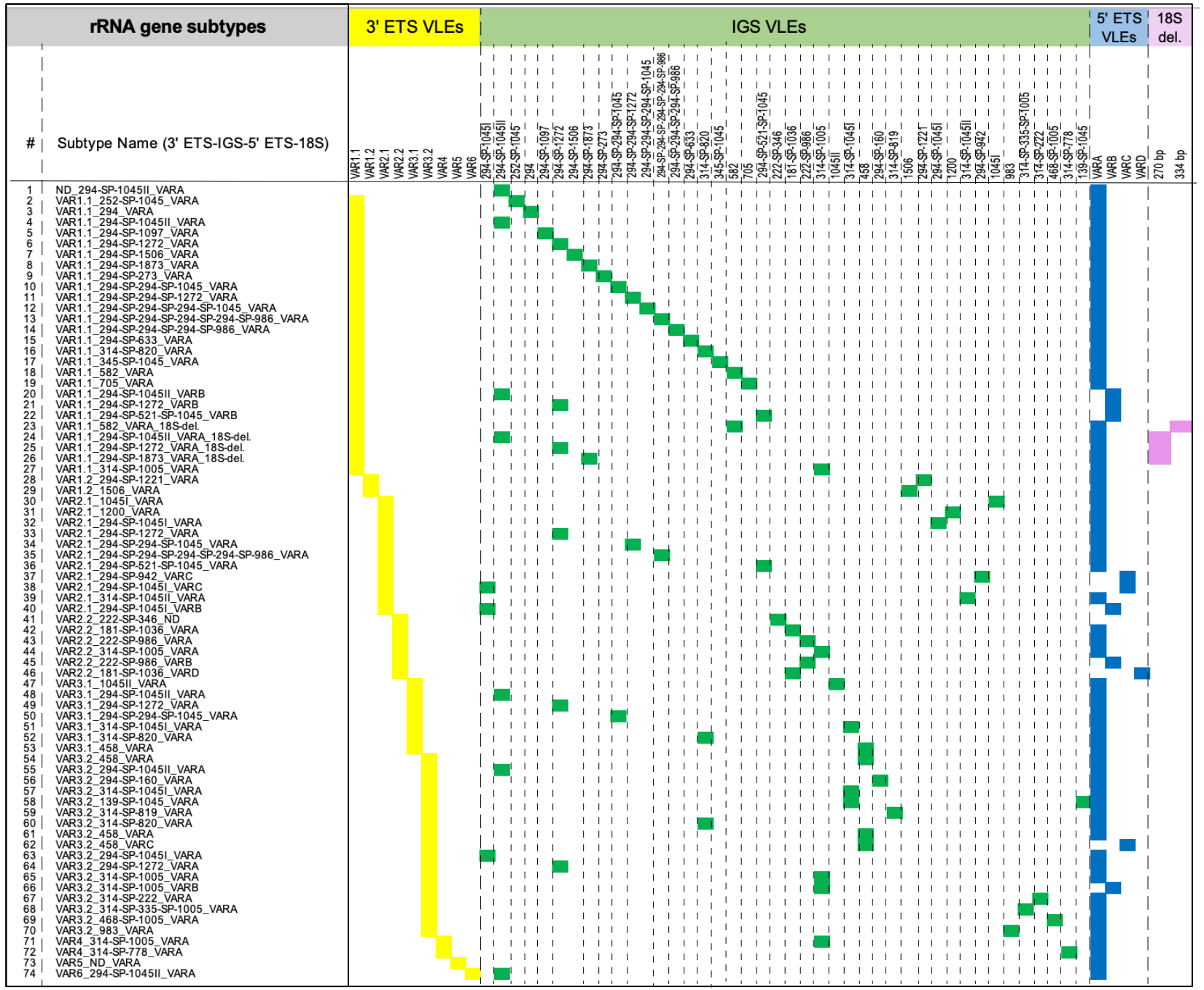
- *A. thaliana* has two NORs
- The NORs mapped to the very tops of chromosomes 2 and 4. We named them *NOR2* and *NOR4.*
- Telomere repeats cap the most distal rRNA genes of both NORs. We named the telomere loci *TEL2N* and *TEL4N*
- We estimated that the NORs consisted of ~375 rRNA genes and were each ~3.7-4 Mbp long (in accessions Ler-0 and Col-0).


TEL2N
TEL4N
Marker
Kb (from NOR)
Marker
NOR2
NOR4
c2_NOR2_ler*
0.0
0.0
c4_NOR4_ler*
c2_00028_sha, c2_00028_bur-0
27.9
11.7
c4_00012_sha*
c2_00069_ler, c2_00069_sha
69.2
48.8
c4_00049_sha
c2_00074_bur-0
73.7
86.0
c4_00086_sha
c2_00078_ler/sha
78.3
90.0
c4_00090_sha, bur-0
92.6
c4_00093_bur-0
c2_00593_sha/bur-0*
592.6
641.4
c4_00641_bur-0*
c2_02365_bur-0*
2365
2133
c4_02133_bur-0*
Chr 2
Chr 4

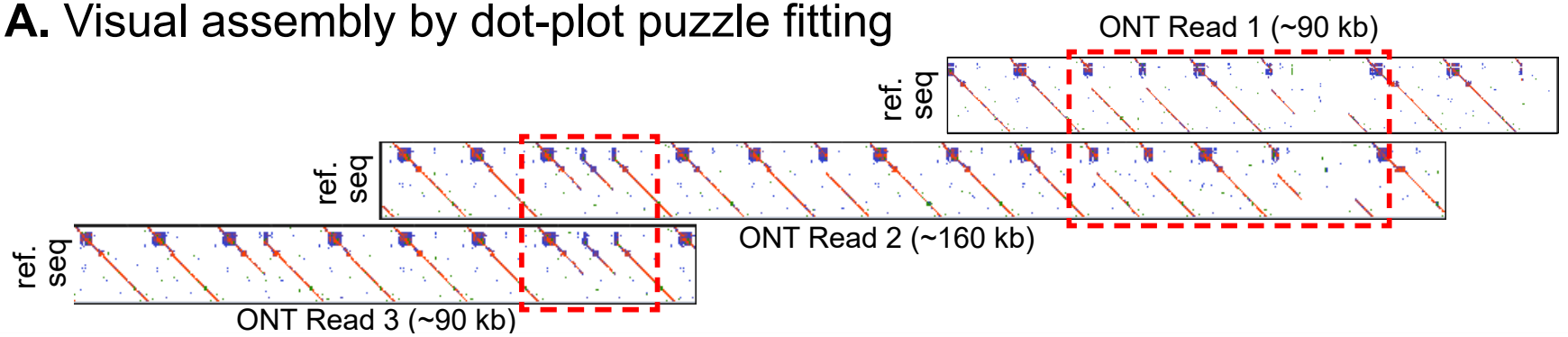
A. thaliana rRNA genes are nearly identical in 'sequence complexity', but there is variation



Variation in the accession (strain) Col-0

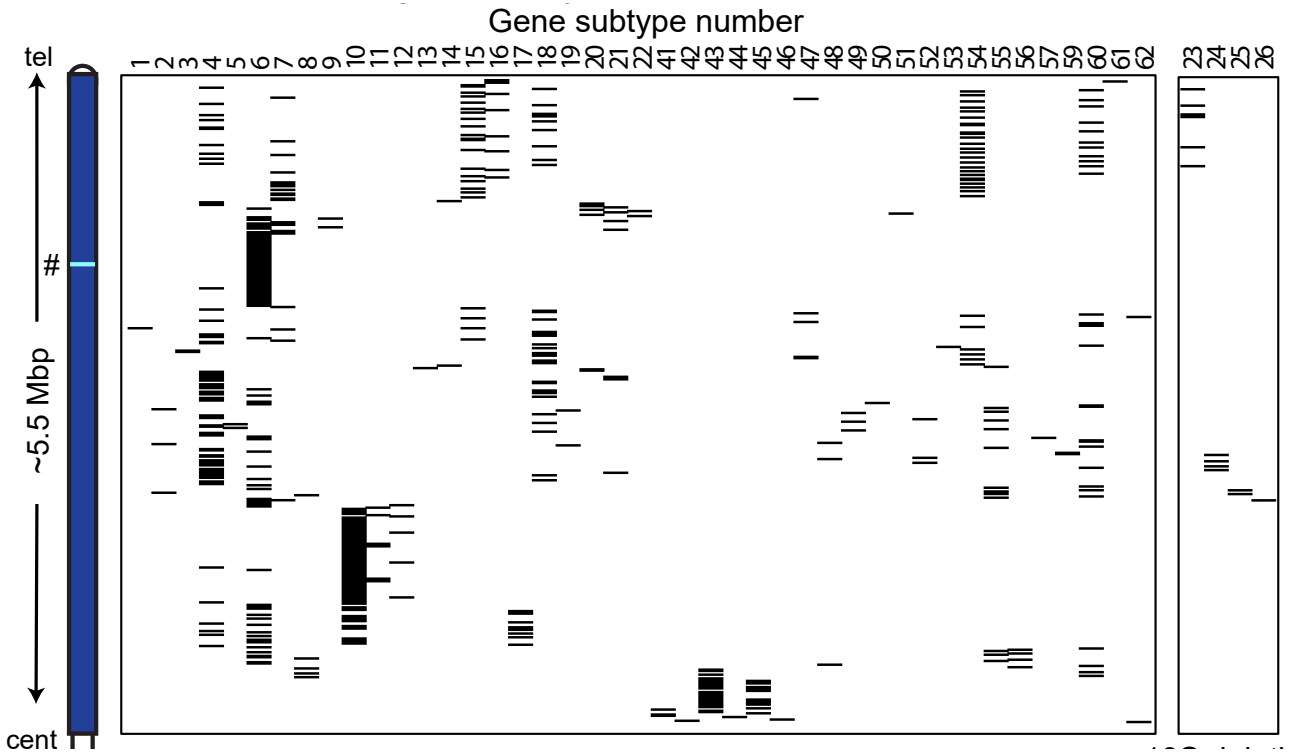

rRNA gene subtypes
3' ETS VLEs
IGS VLEs
5' ETS VLEs
18S del.
Subtype Name (3' ETS-IGS-5' ETS-18S)
1 ND_294-SP-1045II_VARA
2 VAR1.1_252-SP-1045_VARA
3 VAR1.1_294_VARA
4 VAR1.1_294-SP-1045II_VARA
5 VAR1.1_294-SP-1097_VARA
6 VAR1.1_294-SP-1272_VARA
7 VAR1.1_294-SP-1506_VARA
8 VAR1.1_294-SP-1873_VARA
9 VAR1.1_294-SP-273_VARA
10 VAR1.1_294-SP-294-SP-1045_VARA
11 VAR1.1_294-SP-294-SP-1272_VARA
12 VAR1.1_294-SP-294-SP-294-SP-1045_VARA
13 VAR1.1_294-SP-294-SP-294-SP-294-SP-986_VARA
14 VAR1.1_294-SP-294-SP-294-SP-986_VARA
15 VAR1.1_294-SP-633_VARA
16 VAR1.1_314-SP-820_VARA
17 VAR1.1_345-SP-1045_VARA
18 VAR1.1_582_VARA
19 VAR1.1_705_VARA
20 VAR1.1_294-SP-1045II_VARB
21 VAR1.1_294-SP-1272_VARB
22 VAR1.1_294-SP-521-SP-1045_VARB
23 VAR1.1_582_VARA_18S-del.
24 VAR1.1_294-SP-1045II_VARA_18S-del.
25 VAR1.1_294-SP-1272_VARA_18S-del.
26 VAR1.1_294-SP-1873_VARA_18S-del.
27 VAR1.1_314-SP-1005_VARA
28 VAR1.2_294-SP-1221_VARA
29 VAR1.2_1506_VARA
30 VAR2.1_1045I_VARA
31 VAR2.1_1200_VARA
32 VAR2.1_294-SP-1045I_VARA
33 VAR2.1_294-SP-1272_VARA
34 VAR2.1_294-SP-294-SP-1045_VARA
35 VAR2.1_294-SP-294-SP-294-SP-294-SP-986_VARA
36 VAR2.1_294-SP-521-SP-1045_VARA
37 VAR2.1_294-SP-942_VARC
38 VAR2.1_294-SP-1045I_VARC
39 VAR2.1_314-SP-1045II_VARA
40 VAR2.1_294-SP-1045I_VARB
41 VAR2.2_222-SP-346_ND
42 VAR2.2_181-SP-1036_VARA
43 VAR2.2_222-SP-986_VARA
44 VAR2.2_314-SP-1005_VARA
45 VAR2.2_222-SP-986_VARB
46 VAR2.2_181-SP-1036_VARD
47 VAR3.1_1045II_VARA
48 VAR3.1_294-SP-1045II_VARA
49 VAR3.1_294-SP-1272_VARA
50 VAR3.1_294-SP-294-SP-1045_VARA
51 VAR3.1_314-SP-1045I_VARA
52 VAR3.1_314-SP-820_VARA
53 VAR3.1_458_VARA
54 VAR3.2_458_VARA
55 VAR3.2_294-SP-1045II_VARA
56 VAR3.2_294-SP-160_VARA
57 VAR3.2_314-SP-1045I_VARA
58 VAR3.2_139-SP-1045_VARA
59 VAR3.2_314-SP-819_VARA
60 VAR3.2_314-SP-820_VARA
61 VAR3.2_458_VARA
62 VAR3.2_458_VARC
63 VAR3.2_294-SP-1045I_VARA
64 VAR3.2_294-SP-1272_VARA
65 VAR3.2_314-SP-1005_VARA
66 VAR3.2_314-SP-1005_VARB
67 VAR3.2_314-SP-222_VARA
68 VAR3.2_314-SP-335-SP-1005_VARA
69 VAR3.2_468-SP-1005_VARA
70 VAR3.2_983_VARA
71 VAR4_314-SP-1005_VARA
72 VAR4_314-SP-778_VARA
73 VAR5_ND_VARA
74 VAR6_294-SP-1045II_VARA
VAR1.1
VAR1.2
VAR2.1
VAR2.2
VAR3.1
VAR3.2
VAR4
VAR5
VAR6
294-SP-1045I
294-SP-1045II
252-SP-1045
294
294-SP-1097
294-SP-1272
294-SP-1506
294-SP-1873
294-SP-273
294-SP-294-SP-1045
294-SP-294-SP-1272
294-SP-294-SP-294-SP-1045
294-SP-294-SP-294-SP-294-SP-986
294-SP-294-SP-294-SP-986
294-SP-633
314-SP-820
345-SP-1045
582
705
294-SP-521-SP-1045
222-SP-346
181-SP-1036
222-SP-986
314-SP-1005
1045II
314-SP-1045I
458
294-SP-160
314-SP-819
1506
294-SP-1221
294-SP-1045I
1200
314-SP-1045II
294-SP-942
1045I
983
314-SP-335-SP-1005
314-SP-222
468-SP-1005
314-SP-778
139-SP-1045
VARA
VARB
VARC
VARD
270 bp
334 bp

A. Visual assembly by dot-plot puzzle fitting

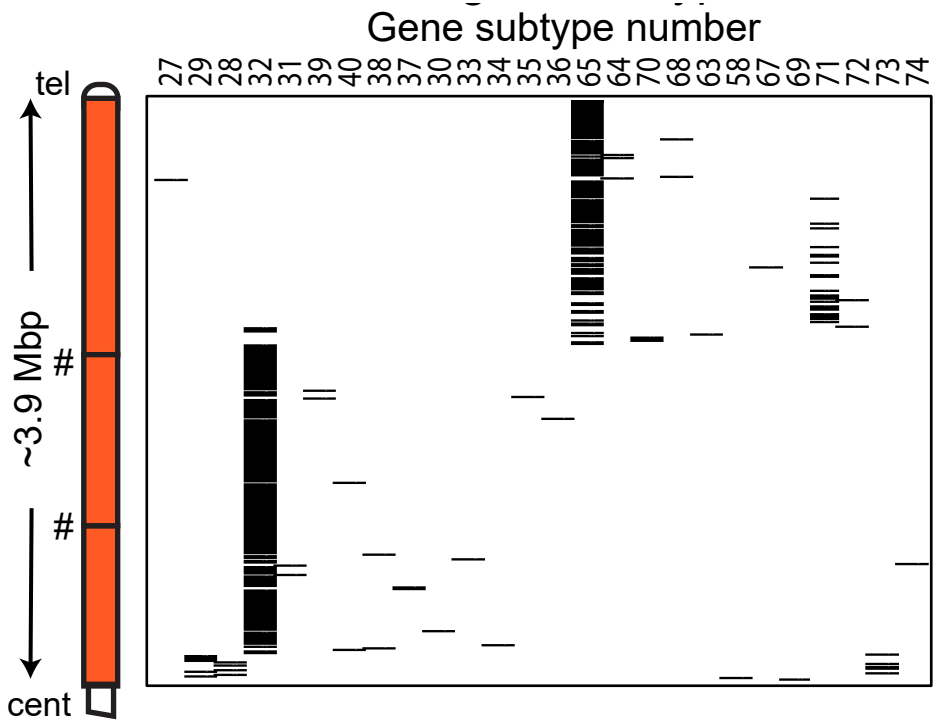


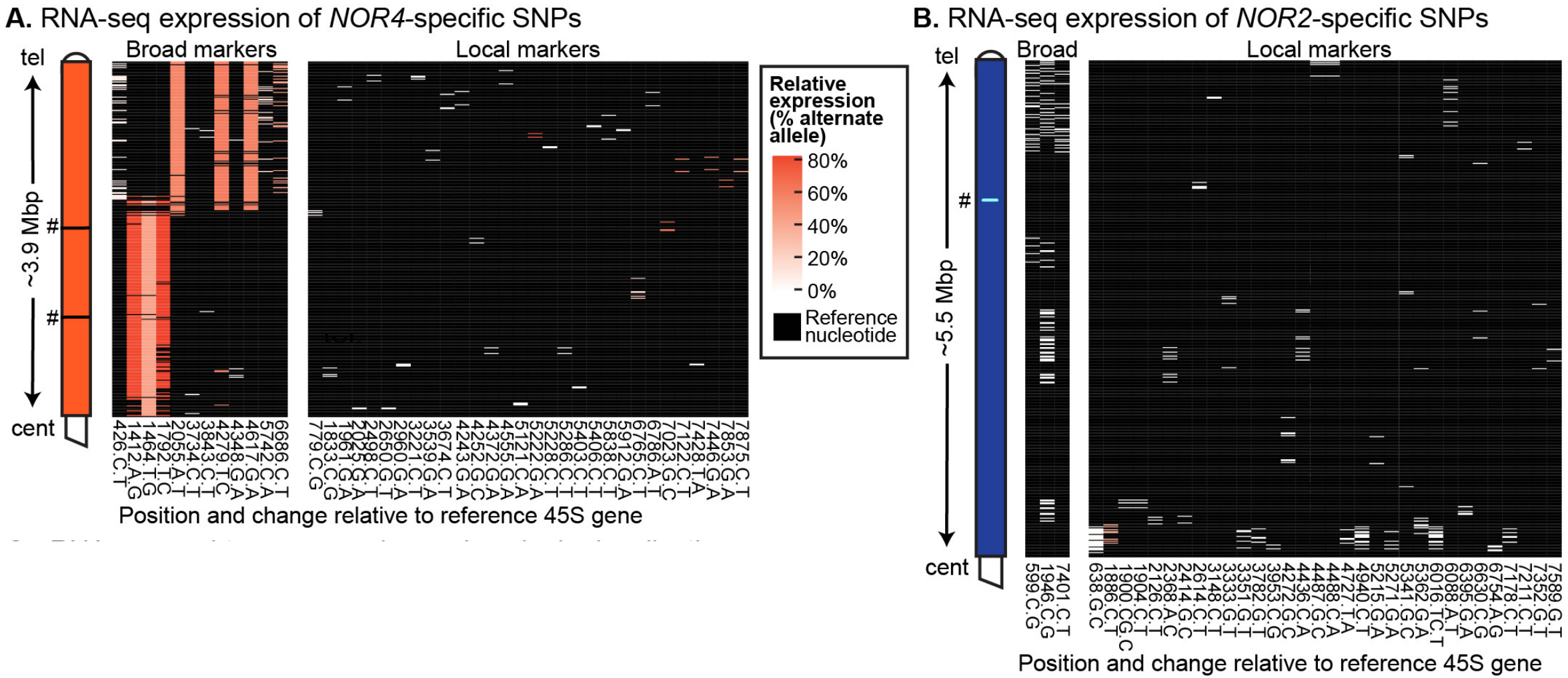
Nastva McKinlay

***NOR2*: ~5.5 Mbp; composed of 47 rRNA gene subtypes**



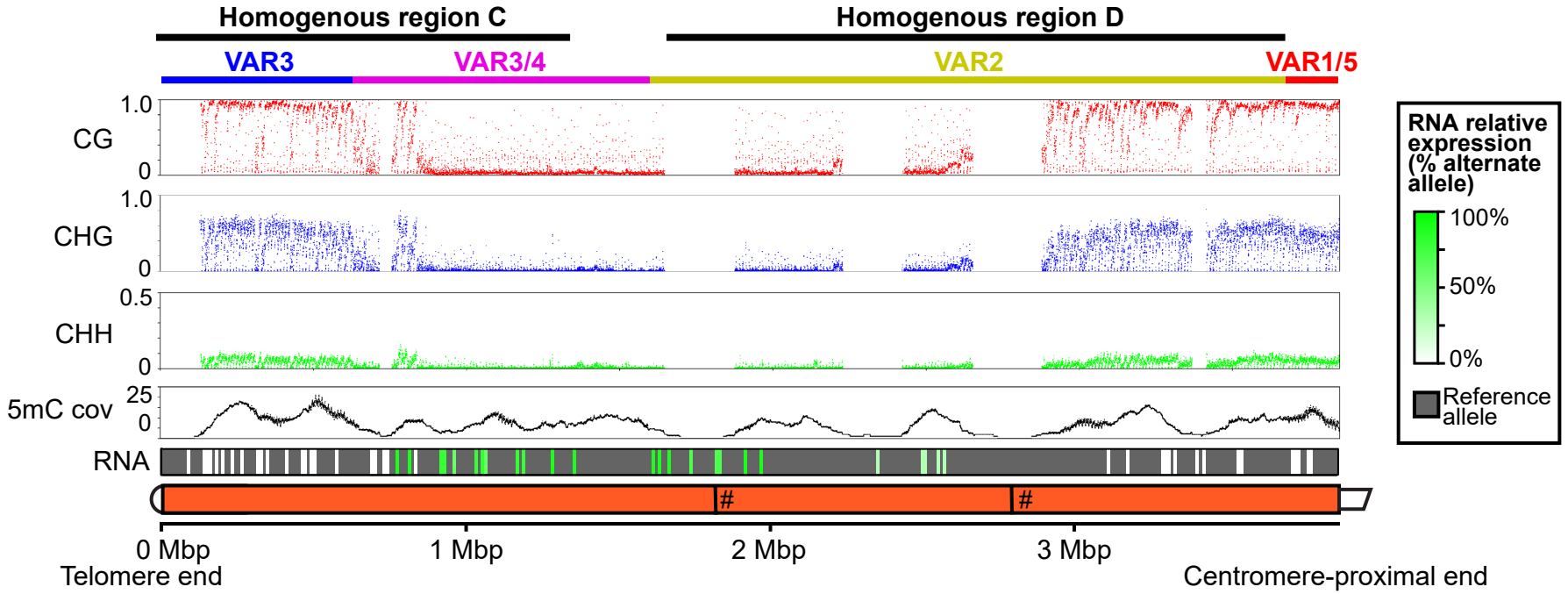
***NOR4*: ~3.9 Mbp; composed of 27 rRNA gene subtypes**



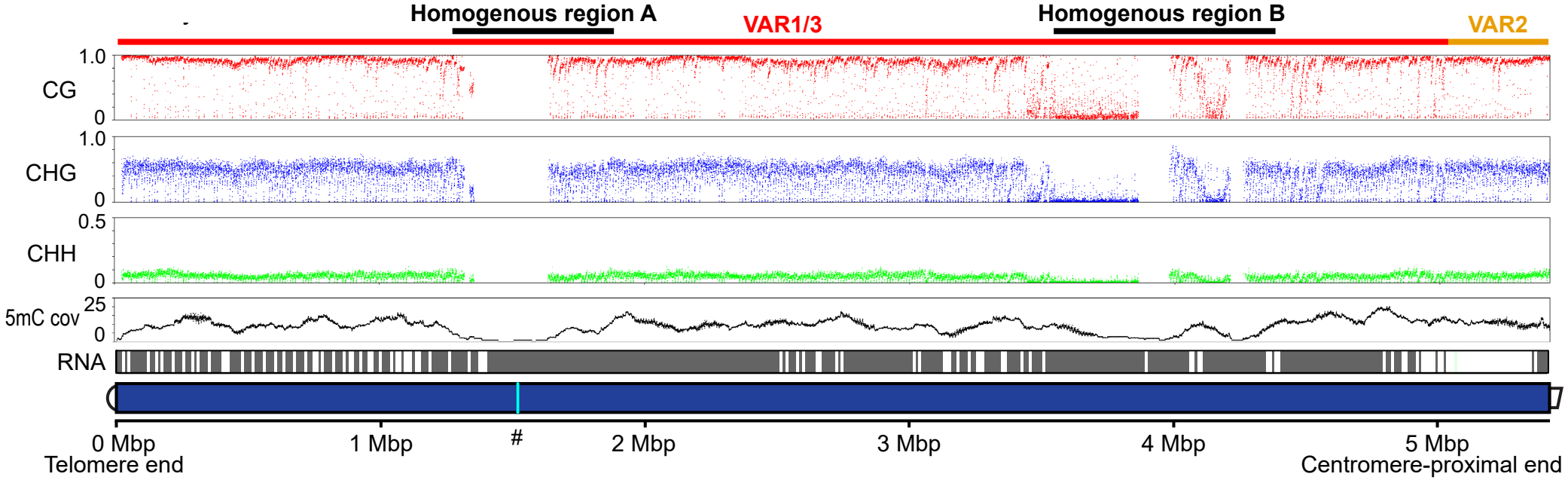

A. RNA-seq expression of NOR4-specific SNPs
tel
~3.9 Mbp
#
#
cent
Broad markers
Local markers
Relative expression (% alternate allele)
80%
60%
40%
20%
0%
Reference nucleotide
Position and change relative to reference 45S gene
B. RNA-seq expression of NOR2-specific SNPs
tel
~5.5 Mbp
#
cent
Broad
Local markers
Position and change relative to reference 45S gene

Cytosine methylation and rRNA gene expression

NOR4



NOR2



- The NOR sequences fill the last remaining gaps in the *A. thaliana Col-0* reference genome, adding ~ 9.4 million basepairs of sequence and positional information for ~900 rRNA genes of 74 subtypes

- The dominant NOR, *NOR4* is not uniformly active: a central, ~2 Mbp region accounts for most rRNA synthesis (during vegetative growth).

- *NOR2* is mostly, but not entirely, silenced. This involves histone deacetylation and cytosine methylation.

- Enables the first whole-NOR analyses of selective rRNA gene activity, the epigenetic phenomenon known as nucleolar dominance

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