

1 **The multi-speed genome of *Fusarium oxysporum* reveals association of**
2 **histone modifications with sequence divergence and footprints of past**
3 **horizontal chromosome transfer events.**

4

5 Short title: Complex genome organization and adaptivity in *Fusarium oxysporum*

6

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19

20 **Abstract**

21 *Fusarium oxysporum* is an economically important pathogen causing wilting or rotting
22 disease symptoms in a large number of crops. It is proposed to have a structured,
23 “two-speed” genome: i.e. regions containing genes involved in pathogenicity cluster
24 with transposons on separate accessory chromosomes. This is hypothesized to
25 enhance evolvability. Given the continuum of adaptation of all the genes encoded in
26 a genome, however, one would expect a more complex genome structure. By
27 comparing the genome of reference strain Fol4287 to those of 58 other *Fusarium*
28 *oxysporum* strains, we found that some Fol4287 accessory chromosomes are
29 lineage-specific, while others occur in multiple lineages with very high sequence
30 similarity - but only in strains that infect the same host as Fol4287. This indicates that
31 horizontal chromosome transfer has been instrumental in past host-switches.
32 Unexpectedly, we found that the sequence of the three smallest core chromosomes
33 (Chr. 11, 12 and 13) is more divergent than that of the other core chromosomes.
34 Moreover, these chromosomes are enriched in genes involved in metabolism and
35 transport and genes that are differentially regulated during infection. Interestingly,
36 these chromosomes are –like the accessory chromosomes– marked by histone H3
37 lysine 27 trimethylation (H3K27me3) and depleted in histone H3 lysine 4
38 dimethylation (H3K4me2). Detailed genomic analyses revealed a complex, “multi-
39 speed genome” structure in *Fusarium oxysporum*. We found a strong association of
40 H3K27me3 with elevated levels of sequence divergence that is independent of the
41 presence of repetitive elements. This provides new leads into how clustering of
42 genes evolving at similar rates could increase evolvability.

43

44 **Author summary**

45 Fungi that cause disease on plants are an increasingly important threat to food
46 security. New fungal diseases emerge regularly. The agricultural industry makes

47 large investments to breed crops that are resistant to fungal infections, yet rapid
48 adaptation enables fungal pathogens to overcome this resistance within a few years
49 or decades. It has been proposed that genome ‘compartmentalization’ of plant
50 pathogenic fungi, in which infection-related genes are clustered with transposable
51 elements (or ‘jumping genes’) into separate, fast-evolving regions, enhances their
52 adaptivity. Here, we aimed to shed light on the possible interplay between genome
53 organization and adaptation. We measured differences in sequence divergence and
54 dispensability between and within individual chromosomes of the important plant
55 pathogen *Fusarium oxysporum*. Based on these differences we defined four distinct
56 chromosomal categories. We then mapped histone modifications and gene
57 expression levels under different conditions for these four categories. We found a
58 ‘division of labor’ between chromosomes, where some are ‘pathogenicity
59 chromosomes’ - specialized towards infection of a specific host, while others are
60 enriched in genes involved in more generic infection-related processes. Moreover,
61 we confirmed that horizontal transfer of pathogenicity chromosomes likely plays an
62 important role in gain of pathogenicity. Finally, we found that a specific histone
63 modification is associated with increased sequence divergence.

64

65 **Introduction**

66 Genes encode products that are involved in a myriad of biological processes and are
67 subjected to a wide range of selection pressures that may change over time. In
68 pathogenic micro-organisms, fast-evolving genes are often clustered with
69 transposable elements into separate regions, an observation that has led to the “two-
70 speed genome” hypothesis concept [1-3]. A possible advantage for the separate
71 genome regions with different evolutionary rates is that it might improve a genome’s
72 ability to accommodate conflicting evolutionary demands, thus allowing an organism
73 to adapt more quickly to new environments [1-4]. Pathogens secrete specialized
74 proteins, called effectors, that facilitate colonization of a host. These effectors are,

75 however, sometimes recognized by the host immune system and then trigger an
76 immune response. Effectors that trigger an immune response are called avirulence
77 factors. A pathogen can escape this recognition when the avirulence gene is mutated
78 or no longer expressed during infection. There is accumulating evidence that this is
79 more likely to occur when an avirulence gene is located near transposon sequences.
80 The occurrence of multiple almost identical sequences in a genome increases the
81 likelihood of homologous recombination that can result in genome rearrangements or
82 deletions [5], which can contribute to pathogen adaptation [1-3,6-15]. In addition,
83 transposon insertion into an avirulence gene can result in regain of virulence [16-19].
84 If the avirulence gene is indispensable for infection the only option to escape
85 recognition is to alter the amino acid sequence of the effector [20-22]. Moreover, an
86 effector needs to coevolve with its target in the host (see e.g. [23]). Effector genes
87 and other genes that are located in ‘fast’ regions have been found to be under
88 positive selection [24,25] and in general have more polymorphisms [26]. However,
89 with the notable exception of repeat-induced point mutation (RIP) in *Leptosphaeria*
90 species [27,28], no mechanism explaining the link between the proximity of
91 transposons and elevated levels of sequence evolution has yet been firmly
92 established.

93

94 Core and accessory chromosomes in fungi typically not only differ in terms of
95 dispensability. They also show differences in gene- and repeat density and -in
96 species that undergo a sexual cycle- in recombination frequencies [29,30] (see e.g.
97 [13,31] for review). Recent studies on the chromatin of core and accessory regions
98 showed that accessory regions are marked by histone H3 lysine 27 trimethylation
99 (H3K27me3), sometimes called ‘facultative heterochromatin’ [31-34]. One hypothesis
100 is that this allows for concerted regulation of genes involved in similar processes,
101 such as infection [35].

102

103 As a basis for investigating the underlying mechanisms of genome
104 compartmentalization and differences in evolutionary ‘speeds’, a detailed mapping of
105 evolutionary ‘volatility’ across a genome is required and correlations with transposon
106 proximity, histone modifications and gene expression must be established. In this
107 study, we used 58 *Fusarium oxysporum* genome sequences for a detailed
108 comparison of differences in dispensability and levels of sequence divergence
109 between and within chromosomes. We combined this with functional annotation and
110 gene expression data to study the extent to which evolutionary volatility is linked to
111 involvement in infection. To study whether there are differences in chromatin-
112 mediated regulation between and within chromosomes in Fol4287, and whether
113 these differences correlate with differences in dispensability and sequence
114 divergence and gene expression, we determined the distribution of histone marks
115 associated with euchromatin (H3K4me2) and facultative heterochromatin
116 (H3K27me3) *in vitro* and correlated these to gene annotation categories as well as
117 levels of gene expression *in vitro* and *in planta*.

118

119 The *Fusarium oxysporum* species complex (FOSC) comprises strains that can infect
120 over a 100 economically important crops, though most strains are not known to be
121 pathogenic [36,37]. Individual pathogenic strains are mostly specialized towards a
122 single host and are grouped according to host-preference into *formae speciales*
123 (ff.spp.) [36,38-40]. Strains that belong to the same *forma specialis* (f.sp.) have
124 similar effector repertoires [40]. In 2010, Ma et al. reported the genome sequence of
125 the tomato-infecting strain *Fusarium oxysporum* f. sp. *lycopersici* 4287 (Fol4287). Out
126 of 15 chromosomes in Fol4287, only 11 are largely syntenic with chromosomes of
127 *Fusarium verticillioides*, a sister species that is estimated to have diverged about 11
128 Mya [37,41]. From this comparison, these 11 chromosomes constitute the core
129 genome of Fol4287, whereas 4 chromosomes (3, 6, 14 and 15) and two large,

130 presumable translocated, regions (chromosome 1b and 2b) are absent in *Fusarium*
131 *verticillioides* and thus constitute the accessory genome of FoI4287. These
132 chromosomes also have been reported to be largely absent in the strains *Fom*-5190a,
133 *Foc*-38-1, *Fop*-37622, *Fo*5176, and *Fom*001, infecting *Medicago* spp., chickpea, pea,
134 *Brassica* spp. and melon respectively [42], indicating that they are conditionally
135 dispensable in the FOSC. Remarkably, strains that have lost 'core' chromosome 12
136 showed no reduction in virulence in experimental conditions and reduction of growth
137 on only a few tested carbon sources. This indicates that chromosome 12 is also
138 conditionally dispensable and thus not a core chromosome *sensu strictu* [43].

139

140 Interestingly, host-preference in FOSC is often polyphyletic [44-56]. Several studies
141 revealed putative horizontal transfer events of effector genes between FOSC strains
142 that infect the same host [40,57-59], indicating that horizontal transfer may play an
143 important role in host switches [39,40,56,60,61]. Of the four accessory chromosomes
144 in FoI4287, chromosome 14 is undoubtedly a pathogenicity chromosome: all fourteen
145 SIX (Secreted In Xylem) genes – known effector genes in tomato-infecting *Fusarium*
146 *oxysporum* – are located on chromosome 14 [62] (and our unpublished observations).
147 Loss of chromosome 14 leads to loss of pathogenicity in FoI4287 [43]. Importantly,
148 horizontal transfer experiments have shown that acquisition of chromosome 14 by
149 the non-pathogenic strain Fo47 is sufficient to turn this strain pathogenic on tomato,
150 albeit less virulent than the original donor [41,63]. The first horizontal transfer
151 experiment reported for the FOSC used the tomato-infecting strain FoI007, which
152 belongs to the same clonal lineage as FoI4287 yet has a different karyotype: FoI007
153 has a small chromosome that is not present in FoI4287. Interestingly, when this small
154 chromosome co-transferred with chromosome 14, the recipient strains were much
155 more virulent [41]. Recently, a similar experiment with the pathogenicity chromosome
156 of Forc016, causing root-rot in cucurbits, shows that host-switches by horizontal
157 chromosome transfer are not unique to tomato-infecting strains [64].

158

159 The polyphyletic origins of host-specificity, the fact that strains that infect the same
160 host have similar effector repertoires, the frequent observations of horizontal transfer
161 of effector genes, and the fact that horizontal transfer of a pathogenicity chromosome
162 can render a non-pathogenic strain pathogenic all indicate that horizontal
163 chromosome transfer causes host-switches in FOOSC. Our genome dataset includes
164 tomato-infecting strains that belong to different lineages, hence we also used it to
165 detect putative recent horizontal chromosome transfer events.

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167

168

169

170 **Results**

171 **The accessory genome of Fol4287 consists of pathogenicity-related regions**
172 **and lineage-specific regions.**

173 When compared to *F. verticillioides*, the accessory genome of Fol4287 consists of
174 four chromosomes and two large segments on core chromosomes. We compared
175 the genome of Fol4287 to that of a closely related strain that is pathogenic on melon,
176 Fom001, and found that the core chromosomes are almost 100% identical between
177 these strains, but that some of the accessory chromosomes are specific to Fol4287
178 (Fig S1). Chromosomal regions 1b and 2b and chromosome 15, however, align with
179 the genome of the Fom001 with similar levels of sequence similarity as the core
180 chromosomes (Fig S1). This suggests that host-preference is largely determined by
181 genes that are located on three accessory chromosomes. We predict that genes on
182 these chromosomes that are important for tomato infection are also present in other
183 strains that are pathogenic on tomato.

184

185 To further assess which accessory regions correlate with phylogenetic clades
186 (lineage-specific chromosomes), and which with *forma specialis* (pathogenicity
187 chromosomes), we aligned 58 FOOSC genomes to the genome of Fol4287 (Fig S2,
188 Table S1). We found that the four accessory chromosomes are largely clade-specific.
189 Alignments with genomes of strains outside the lineage of Fol4287 (including
190 Fom001) mostly span less than 5 kilobases (kb) and have less than 92% sequence
191 identity. Notable exceptions are chromosome 14 and a recently duplicated region on
192 chromosome 3 and 6. These regions are present in more distantly related tomato-
193 infecting strains with ~100% sequence identity, compared to ~98% identity between
194 core chromosomes (Fig1A, Fig 2, Fig S2). For these regions synteny is also relatively
195 conserved in tomato-infecting isolates, with aligned segments spanning up to 40 kb,
196 whereas for the rest of the accessory genome this is between 5 and 10 kb (Fig S3).

197 In conclusion, accessory chromosomes of Fol4287 largely correlate with
198 phylogenetic clade, but chromosome 14 and regions on chromosome 3 and 6
199 correlate with host and are more conserved in sequence than core chromosomes.

200

201 We then asked whether these pathogenicity regions on chromosome 3 and 6
202 correspond to the small chromosome that was co-transferred with chromosome 14 in
203 in the experiment described in [41], resulting in strains that were more virulent than
204 the ones that received only one chromosome. We sequenced one strain that
205 received chromosome 14 (from Fol007) and one – more virulent – strain that
206 received chromosome 14 and the additional small chromosome. We mapped the
207 reads thus obtained to the genome of Fol4287 and found that exactly those regions
208 in Fol4287 that show hallmarks of horizontal transfer in our genome comparison (Fig
209 1A) correspond to chromosome 14 and the second, smaller ‘pathogenicity’
210 chromosome in Fol007 (Fig 1B).

211

212 Our results strongly suggest that horizontal transfer of chromosomes has indeed
213 played an important role in the emergence of new pathogenic clonal lines in natural
214 settings. Moreover, not all accessory regions in Fol4287 are alike: only some regions
215 are associated with pathogenicity towards tomato. This suggests a division between
216 accessory regions in Fol4287: chromosome 14 and part of chromosome 3/6 are
217 involved in virulence towards tomato whereas the other accessory regions are not.
218 From here on, we refer to the chromosomal regions associated with pathogenicity (i.e.
219 chromosome 14 and part of chromosome 3 and 6) as ‘pathogenicity regions’, and to
220 the rest of the accessory genome of Fol4287 as ‘lineage-specific regions’, as they
221 only occur in strains that belong to the same lineage (vegetative compatibility group)
222 as Fol4287.

223

224 **The core genome can be divided into regions with low divergence and regions**
225 **with high divergence**

226 To compare differences in dispensability among core chromosomes, we applied the
227 same approach to the core genome of Fol4287. We found that all core chromosomes
228 are present in all strains in our dataset, with the notable exception of chromosome 12
229 that is absent in the cucumber-infecting strain Foc037. This strain was included in
230 several bioassays in a previous study, in which its virulence was confirmed [40].
231 Recently, flow cytometry was used to screen for loss of chromosome 1, 12 and 14 in
232 Fol4287 [43]. In all three reported cases in which chromosome 12 was lost, no
233 differences were observed in terms of virulence. Chromosome 12 is thus dispensable
234 for growth as well as virulence, and should thus no longer be considered a core
235 chromosome *sensu strictu*. In addition to complete loss of chromosome 12 in Foc037,
236 we observed large deletions in core chromosomes in two melon-infecting strains:
237 ~0.5 Mb in a subtelomeric region of chromosome 12 in Fom010, and ~0.5 Mb in a
238 subtelomeric region of chromosome 13 in Fom013 (Fig 2).

239

240 In addition to differences in the propensity for loss or large deletions, there are
241 striking differences in the level of sequence conservation within and among core
242 chromosomes. The three smallest core chromosomes of Fol4287 – Chr. 11, 12 and
243 13 – are clearly more divergent than the other, larger core chromosomes (Fig 2) in
244 terms of sequence similarity as well as synteny (Fig S2, Fig S3). Subtelomeric
245 regions of all chromosomes and a ~1 Mb central region of chromosome 4, associated
246 with a genomic rearrangement when compared to *F. verticillioides* [41], also show
247 elevated levels of sequence divergence and lower synteny levels (Fig S2, Fig S3).
248 Notably, these chromosomes are not enriched in repetitive elements and have a
249 similar gene density as other core chromosomes [41] (Fig S4). From here on, we will
250 refer to chromosomes 11, 12 and 13 as ‘fast-core’ chromosomes.

251

252 **Genes on fast-core and accessory chromosomes have lower expression levels.**

253 We hypothesized that genes in different genome compartments exhibit differences in
254 overall expression levels. To assess this, we queried an RNA-seq dataset that was
255 generated to compare gene expression of Fol4287 grown in liquid culture (*in vitro*) to
256 Fol4287 infecting tomato plants (*in planta*, 9 days post inoculation) [65] (Table S2).
257 On the accessory genome, most genes -64% and 68% of genes on the lineage-
258 specific and pathogenicity chromosomal regions respectively- are not expressed *in*
259 *vitro*, (defined here as RPKM \leq 0.1). On the fast-core and the core chromosomes,
260 this is 46% and 25% respectively. *In planta*, 53% of genes on the accessory are not
261 expressed (lineage-specific 51%, pathogenicity 57%), compared to <33% of genes
262 on the fast-core and <19% of genes on the core chromosomes. Of the fast-core
263 chromosomes, chromosome 12 - that is absent from Foc037 - has most genes that
264 are not expressed in the conditions we tested (53% *in vitro*, 37% *in planta*). Overall,
265 genes on the accessory genome and genes located in fast-core chromosomal
266 regions (including the central region on chromosome 4) have lower expression than
267 genes on the core genome, both *in vitro* and *in planta* (average over three biological
268 replicates, Fig S5).

269

270 **Of the accessory genome, only chromosome 14 is enriched for genes that are**
271 **differentially regulated during infection.**

272 We expected that the pathogenicity regions, required for virulence on tomato (Fig 1),
273 would be enriched for genes that are upregulated during infection. When we
274 compared *in vitro* to *in planta* expression levels, we found that chromosome 14 is
275 indeed significantly enriched for genes that are upregulated during infection (P-value
276 $< 9.19 \times 10^{-10}$ after Bonferroni correction, Fig 3, Fig S6). However, the 'pathogenicity-
277 related' regions on chromosome 3 and 6 – although they correspond to the small
278 chromosome in Fol007 that enhances virulence upon horizontal transfer – are not
279 significantly enriched for upregulated genes. Like the other (lineage-specific)

280 accessory regions, here only 3.1% of the genes were upregulated *in planta*,
281 compared to > 14.7% of genes on chromosome 14. Hence of the pathogenicity
282 regions, only chromosome 14 is enriched in genes that are differentially expressed
283 during infection.

284

285 We then asked whether the upregulated genes on chromosome 14 have similar
286 functions as those encoded on chromosome 3 and 6. Of the 61 genes on
287 chromosome 14 that are upregulated during infection, 16 encode small, secreted
288 proteins, 13 of those are SIX (Secreted In Xylem) genes. About a third (19 out of 61)
289 encodes enzymes, of which four are secreted. The remainder of upregulated genes
290 includes three genes encoding for transcription factors, two of which are homologs of
291 *FTF1*, that induces expression of effector genes [65], three putative transposable
292 elements, a transporter, one encoding a membrane protein and one encoding a
293 putative argonaute-like silencing protein (Table S3). The remaining 19 upregulated
294 genes have no known functional domains and contain no secretion signal peptide.
295 The proteins encoded by the 28 upregulated genes located in the pathogenicity
296 regions on chromosome 3 and 6 include ten transposase-like proteins with a domain
297 of unknown function, five enzymes and two small secreted proteins, one of which is a
298 homolog of *SIX8* (Table S4). The three downregulated genes in the pathogenicity
299 regions on chromosome 3 and 6 encode proteins with no known function and without
300 a secretion signal peptide. In conclusion, more than a quarter of the upregulated
301 genes on chromosome 14 encode small, secreted proteins, compared to less than
302 8 % of the upregulated genes on the pathogenicity regions on chromosome 3 and 6.

303

304 **Fast-core regions are enriched for genes upregulated during infection and are**
305 **involved in metabolism, transport and defence.**

306 Interestingly, while on the 'normal' core chromosomes only 4% of the genes is
307 differentially regulated during infection, on the fast-core chromosomes this is > 10%.

308 Hence not only chromosome 14, but also the fast-core chromosomes are significantly
309 enriched for differentially expressed genes (P-value < 1.17×10^{-31}), both up- (P-value
310 < 6.5×10^{-25}) and downregulated (P-value < 1.67×10^{-06}) (Fig 3). Not just fast-core
311 chromosomes 11, 12 and 13, but also the other regions that showed elevated levels
312 of sequence divergence (Fig 1, Fig 2, Fig S2) such as the subtelomeric regions of
313 core chromosomes and the central region on chromosome 4 have more differentially
314 expressed genes than core regions (Fig S6).

315

316 Compared to chromosome 14, the fast-core chromosomes are relatively conserved
317 within the FOOSC (Fig 1, Fig 2, Fig S2), suggesting that the upregulated genes on the
318 fast-core chromosomes are involved in common infection-related processes while
319 chromosome 14 contains host-specific genes. Of the 277 upregulated fast-core
320 genes, 93 (~34%) encode proteins that contain a putative signal peptide for secretion.
321 This is similar to the proportion of upregulated genes on chromosome 14 that encode
322 proteins with a predicted secretion signal peptide, but on chromosome 14 these are
323 mostly small effector genes (Table S4). When we compared the functional
324 annotations of upregulated fast-core genes to that of the rest of the genome, we find
325 that upregulated fast-core genes are enriched for genes involved in metabolism,
326 cellular transport, transport facilitation and transport routes and cell rescue, defense
327 and virulence. More specifically, upregulated fast-core genes are enriched for genes
328 involved in polysaccharide and other C-compound and carbohydrate metabolism,
329 sugar, glucoside, polyol and carboxylate catabolism and extracellular polysaccharide
330 degradation, in transport facilities, C-compound and carbohydrate transport and
331 cellular import, and in degradation/modification of foreign (exogenous)
332 polysaccharides (Table S5). The fact that these genes are differentially expressed
333 during infection suggests that genes in fast-core regions are involved in digestion of
334 plant material and import of products of digestion.

335

336 Not only fast-core genes that are upregulated during infection, are involved in
337 metabolism, cellular transport, transport facilitation and transport routes and cell
338 rescue, defense and virulence: when we also include fast-core genes that are not
339 differentially regulated during infection, or are downregulated during infection, we find
340 that these are involved in the same three broad functional categories (Fig S7) and in
341 'Interaction with the environment'. Metabolic genes on the fast-core are typically
342 involved in 'metabolism of carbon compounds and carbohydrates' (49.6% of
343 metabolic genes) and 'secondary metabolism' (38.7% of metabolic genes). Transport
344 genes are mostly involved in 'transport of carbon compounds and carbohydrates'
345 (50.9% of transport genes), 'cellular import' (61.7% of transport genes) – in particular
346 'non-vesicular cellular import' (46.1% of transport genes) and 'transport facilities'
347 (85.2% of transport genes). Defence genes are mostly genes involved in
348 'detoxification' (67.8% of defence genes) including 'detoxification involving
349 cytochrome P450' (15.3% of defence genes) and in 'disease, virulence and defence'
350 (32.2% of defence genes). This indicates that the clustering of genes that are
351 involved in metabolism, transport and defence on fast-core chromosomes is not
352 limited to genes that are involved in infection.

353

354 **Like accessory chromosomes, fast-core chromosomes are enriched with**
355 **H3K27me3.**

356 Recent studies have revealed differences in chromatin-mediated regulation of core
357 versus accessory chromosomal regions in pathogenic filamentous fungi: under *in*
358 *vitro* conditions accessory chromosomes or chromosomal regions are enriched in
359 H3K27me3, which is correlated with gene silencing, whereas core chromosomes are
360 enriched in H3K4me2, which is correlated with gene activation [31,32,34]. To test
361 whether the same holds true for *Fusarium oxysporum*, we performed ChIP-seq
362 experiments for these two different histone marks (Table S6). We found that in *F.*
363 *oxysporum*, similar to what was reported for *F. graminearum*, *F. fujikuroi* and *Z. tritici*

364 [31,32,34,66], accessory regions are enriched for H3K27me3 and depleted in
365 H3K4me2 (Fig 3, Fig S8). Interestingly, the same holds true for the fast-core
366 chromosomes and sub-telomeric regions, in sharp contrast to the rest of the core
367 genome that is enriched in H3K4me2 and depleted in H3K27me3 (Fig 4, Fig S8, Fig
368 S9, Table S7).

369

370 H3K4me2 was found in or close to coding regions (Kendall's Tau ≤ 0.39 , $p < 1 \times 10^{-300}$),
371 and is negatively correlated with the presence of transposons (Kendall's Tau \leq
372 -0.33 , $p < 1 \times 10^{-300}$). On the core genome, most genes and promoter regions overlap
373 with an H3K4me2-enriched domain, while most transposons overlap with an
374 H3K27me3-enriched domain (Fig S10). H3K4me2-enriched domains on core
375 chromosomes are larger than those on fast-core and accessory chromosomes: they
376 span between 10 and 100 kb on the core genome, compared to between 2.5 and 5
377 kb on the fast-core and accessory chromosomes (Fig 4, Fig S9, Table S7). More
378 than 49% of the core genome is covered in H3K4me2-enriched domains, while only
379 2.5%-13% of the non-core genome is part of an H3K4me2-enriched domain.

380

381 In contrast, more than 72% of the accessory genome, ~93% of the fast-core genome
382 and <27% of the core genome is part of an H3K27me3-enriched domain. H3K27me3
383 is negatively correlated with the presence of coding sequences (Kendall's Tau $\leq -$
384 0.25 , $P < 3 \times 10^{-180}$) and is enriched near or in transposons (Kendall's Tau ≥ 0.35 , P
385 $< 5,9 \times 10^{-283}$). In general, H3K27me3 occurs in larger blocks than H3K4me2, on all
386 chromosomes (Fig 4, Fig S9, Table S7). The average size of an enriched domain
387 ranges between 15 to 60 kb on core chromosomes, where on the fast-core
388 chromosomes domains vary between 57 and 146 kb (domain size averaged per
389 chromosome). Especially on chromosome 12, H3K27me3-enriched domains are
390 large: averaging ~146 kb in one experiment and ~83 kb in the other (Fig 4, Fig S9,
391 Table S7).

392

393 H3K27me3 is associated with facultative heterochromatin, hence we expect low
394 expression of genes that reside in a region that is enriched in this histone
395 modification. In contrast, H3K4me2 is associated with euchromatin, hence we expect
396 high expression levels for genes that are located in regions enriched in this histone
397 mark compared to genes that reside in H3K37me3 domains of enrichment. As
398 mentioned above, the fast-core and accessory chromosomes -enriched in
399 H3K27me3- have more genes with low expression *in vitro* and -to a lesser extent- *in*
400 *planta* than core chromosomes. Genes that are located in regions that are
401 associated with H3K27me3 have lower transcript levels, both in *in vitro* and in *in*
402 *planta* conditions (P value ~ 0, Welch's t-test on ranked data), while genes that are
403 located in regions associated with H3K4me2 have higher transcript levels than the
404 rest of the genome (P value ~ 0, Welch's t-test on ranked data), consistent with the
405 assumed role of these histone marks in gene silencing and activation in other fungi
406 [31-34,66]. When we compared gene expression *in vitro* to *in planta* conditions, we
407 found that most transcriptional changes involve *up-regulation* of genes: 896 out of
408 1036 differentially expressed genes are upregulated *in planta* compared to *in vitro*
409 (>86%) (Table S4, Fig S6). Of these upregulated genes, more than 66% is located in
410 an H3K27me3-enriched domain (P-value < 1.6×10^{-41} , hypergeometric test). The
411 differences in histone codes of core, fast-core and accessory genomes may allow for
412 large-scale coordinated expression of genes that are involved in life-style switches,
413 such as infection.

414

415 **Fast-core chromosomes are not enriched for genes under positive selection.**

416 The differences in functional gene classes enriched in core, fast-core, accessory and
417 pathogenicity chromosomes raises the question to what extent the observed
418 hierarchy in sequence divergence levels (Fig 1, Fig 2) of these four categories of
419 chromosomes can be explained by positive selection. A previous study identified

420 genes under positive selection based on multiple sequence alignments of genes that
421 belong to nine *Fusarium* species, including *F. oxysporum*, comparing synonymous
422 and non-synonymous substitution rates and testing for the occurrence of site-specific
423 balancing selection. This study revealed that all Fol4287 accessory chromosomes
424 (pathogenicity and lineage-specific regions) are enriched for genes that are under
425 positive selection [24]. The core and fast-core chromosomes contain relatively few
426 genes that are inferred to be under positive selection: 308 (< 2.7% of tested core
427 genes) and 66 (< 2.8% of tested fast-core genes) respectively (Table S8), compared
428 to 192 genes located in accessory regions (> 9.8% of tested accessory genes; 8.4%
429 lineage-specific and 12.5% pathogenicity). Differentially expressed genes are not
430 significantly enriched for genes under positive selection (P-value > 0.5). Hence
431 positive or diversifying selection on genes that are located on the fast-core
432 chromosomes does not explain the high levels of sequence divergence we observed.

433

434 We then hypothesized that genes on these chromosomes are under relaxed negative
435 selection, which could also explain differences in sequence divergence: many genes
436 have low expression levels. Moreover, fast-core chromosome 12 can be lost in both
437 Fol4287 and Foq037 without losing virulence [40,43] (Fig 2). Per gene, we inferred
438 the number of synonymous substitutions per synonymous site (d_S), non-synonymous
439 substitutions per non-synonymous site (d_N), as well as their ratio (d_N/d_S) based on
440 alignment with their bidirectional best BLAST hit in *F. verticillioides*. We found that
441 higher substitution rates in genes located on fast-core chromosomes compared to
442 those located on other core chromosomes (P-value < 2.8e-39, P-value < 8e-307, P-
443 value < 0.0015, for d_S , d_N and d_N/d_S respectively, Welch's t-test on ranked data, Fig
444 5A, Fig S11). Synonymous substitutions should be little influenced by relaxed or
445 positive selection, yet we observed also a significantly higher *synonymous*
446 substitution rate on fast-core chromosomes. We therefore conclude that relaxed
447 selection on dispensable genes and genes with low expression levels alone, does

448 not explain differences in sequence divergence between fast-core chromosomes and
449 other core chromosomes.

450

451 **Rate of sequence divergence is elevated in H3K27me3-enriched regions on**
452 **core chromosomes.**

453 Interestingly, both genes on fast-core chromosomes and genes on core
454 chromosomes that are located close to a telomere also have higher d_S and d_N values
455 (Fig 5A, Table S8, Fig S11). When we compare substitution levels for genes that are
456 located in a region enriched in H3K27me3 on core chromosomes, the distribution of
457 d_N and d_S of these genes is similar to those located on the fast-core chromosomes
458 (Fig 5A, Fig S12). If we view the synonymous substitution rate as an approximation
459 of the molecular clock, these results suggest that this “clock is ticking faster” in
460 regions that are enriched in H3K27me3.

461

462 To study differences in rates of sequence evolution in more detail we inferred Single
463 Nucleotide Polymorphisms (SNPs) on two timescales. The cumulative SNP density
464 of the ten tomato-infecting strains that belong to the same VCG as Fol4287 (the
465 bottom tomato-infecting lineage in Figs 1 and 2, see Materials and Methods)
466 approximates the accumulation of mutations on a short timescale. Assuming no
467 horizontal transfers have occurred within this lineage, we can compare accessory
468 chromosomes with core and fast-core chromosomes, as all strains possess
469 Fol4287’s accessory chromosomes, albeit not all complete chromosomes. We found
470 that the accessory chromosomes accumulated more SNPs than the fast-core and
471 core chromosomes, but that the SNPs density of core and fast-core chromosomes is
472 similar (P -value > 0.35 , hypergeometric test, Fig 5, Fig S13, Fig S14). We found that
473 on fast-core chromosomes SNP density was higher in H3K27me3-enriched regions
474 (comprising more than 90% of the fast-core chromosomes), compared to regions that
475 are not enriched in H3K27me3, but that this difference was not significant. However,

476 on core chromosomes H3K27me3-enriched regions have a significantly higher
477 density of SNPs (P-value $< 1.5 \times 10^{-7}$). When we included SNPs in less closely
478 related strains (i.e. all strains in the Clade III, the clade depicted in Fig 1), we found
479 that fast-core chromosomes, the central region on chromosome 4 and sub-telomeric
480 core regions have more SNPs than (other) core regions (Fig S13). Hence, on a
481 longer timescale, as observed when comparing genome sequences, we find that
482 regions that are enriched in H3K27me3, have higher sequence divergence (P-value
483 ~ 0 , hypergeometric test, for both core and fast-core chromosomes). Due to the fact
484 that the accessory chromosomes are absent from a number of strains in Clade III,
485 and the fact that the pathogenicity chromosomes were obtained through horizontal
486 transfer, we cannot directly compare accessory chromosomes to core and fast-core
487 chromosomes. We conclude that, especially on core chromosomes and/or on longer
488 timescales, H3K27me3-enriched regions accumulated more SNPs compared to
489 regions that are not enriched in H3K27me3.

490

491 We calculated correlations between change in gene expression, sequence
492 divergence and histone modifications on core or fast-core chromosomes, and found
493 two clusters -each corresponding to a different 'speed'- where repeat density and
494 SNP density cluster with H3K27me3, while gene density and gene expression levels
495 cluster with H3K4me2 (Fig 6A and B). Interestingly, H3K27me3 correlated most
496 strongly with synonymous substitution rates and SNP densities in Clade III, and
497 much less with repeat density. For accessory chromosomes this distinction was not
498 so clear; we observed mostly very low correlation coefficients between different
499 properties (Fig 6C). In conclusion, fast-core and core chromosomes harbour similar
500 "speeds", but in different quantities. The evolutionary processes underlying the
501 different "speeds" on core and fast-core chromosomes probably have had less
502 influence in shaping the organization of accessory chromosomes.

503

504 Discussion

505 In this study, we found that *F. oxysporum* has a more complex genome organization
506 than previously proposed [41]. While it has been known for several years that *F.*
507 *oxysporum* has core and accessory chromosomes, our more detailed comparisons
508 revealed distinct subcategories. Core chromosomes can be divided into ‘core’ (*sensu*
509 *strictu*) that are indispensable, conserved, enriched in H3K4me2 and not enriched in
510 genes that are differentially expressed during infection and ‘fast-core’ that are
511 conditionally dispensable, less conserved, enriched in H3K27me3 and enriched in
512 genes that are differentially expressed during infection. Similarly, we suggest to
513 classify the accessory genome, which is enriched in H3K27me3, into lineage-specific
514 chromosomes that are specific to a clonal line and pathogenicity chromosomes that
515 are present in all strains that infect a certain host. Apart from distinct chromosomes,
516 we also observed regions -parts of chromosomes- that could be assigned to a
517 different category as the rest of the chromosome, such as sub-telomeres, or
518 translocated segments on *bona fide* core chromosomes that can be classified as
519 fast-core, i.e., segments of core chromosomes 1 and 2 that are lineage-specific, and
520 segments of chromosome 3 and 6 that are considered pathogenicity regions.

521

522 The genome alignments and the analyses of SNP densities along the genome
523 showed that the different subcategories can be ordered into a hierarchy with respect
524 to their rate of sequence divergence: compared to core regions, fast-core regions
525 accumulated more SNPs and alignments of fast-core regions with genome
526 sequences of other FOOSC isolates have lower percent identity. Fol4287’s accessory
527 regions are absent from most strains and accumulated many SNPs on a timescale,
528 on which we found no significant difference between core and fast-core
529 chromosomes. Similarly, synteny is most conserved in core regions, less in fast-core
530 regions, and even less in pathogenicity regions and in lineage-specific regions.

531 Interestingly, we find that -to some extent- different levels in this hierarchy
532 correspond to levels in host-interactions: both fast-core chromosomes and
533 chromosome 14 are enriched for differentially expressed genes, but genes on the
534 less volatile fast-core chromosomes are typically involved in metabolism, transport
535 and defence, whereas chromosome 14 contains many effector genes that are
536 hypothesized to interact with host proteins [67]. The fast-core chromosomes are in
537 general enriched in genes involved in metabolism, transport and defence, importantly,
538 including genes that are not differentially regulated during infection. *F. oxysporum* is
539 not an obligate pathogen and we predict that levels in the observed sequence
540 divergence hierarchy also correspond to different levels on other functional 'axes',
541 including interactions with other soil organisms, where for example lineage-specific
542 regions may play a more important role.

543

544 Although we were able to associate different levels of sequence divergence with
545 different levels of host interaction, this correspondence is not perfect. While
546 pathogenicity chromosome 14 of Fol4287 is enriched in genes with induced
547 expression during infection, the regions on chromosome 3 and 6 are not, neither do
548 these regions encode any known effectors. Yet these regions are important for
549 virulence, as combined horizontal transfer of this region with chromosome 14
550 increases the aggressiveness of the recipient strain compared to strains that receive
551 only chromosome 14 [41]. Moreover, our results show that these regions are present
552 in all tomato-infecting strains, although possibly as a single copy. A remaining
553 question is thus whether these regions on chromosome 3 and 6 contains one or
554 several genes that are important for infection and whether the rest of these regions is
555 'hitchhiking'. In comparison, Fol strains that have lost large segments of chromosome
556 14, including *SIX6*, *SIX9* and *SIX11*, whose products have been found in the xylem
557 sap of infected tomato plants [68], are not significantly less virulent than strains with a
558 complete chromosome 14 in laboratory conditions [43]. This suggests that segments

559 of chromosome 14 may be hitchhiking with genes that are important for infection and
560 that reside on separate regions of chromosome 14, such as *SIX1*, *SIX3* and *SIX5*
561 [69,70]. On the other hand, the genes that may seem redundant for virulence in
562 conditions tested in bioassays may perform a role in other conditions. For example,
563 *SIX6*, found in multiple FOSC strains as well as in *Fusarium hostae* and
564 *Colletotrichum* species, is required for virulence of *F. oxysporum* f. sp. *radicis-*
565 *cucumerinum* towards cucumber only at relatively high temperatures [64]. Despite
566 the fact that genetic hitchhiking and incomplete functional characterizations obscure
567 relations between function and sequence divergence, we were still able to associate
568 physical - with functional clustering, as observed on fast-core regions on core
569 chromosomes, on fast-core chromosomes and on chromosome 14.

570

571 We not only found that pathogenicity chromosomes are specific to tomato-infecting
572 strains, we also found that horizontal chromosome transfer (HCT) most likely played
573 an important role in distributing the pathogenicity regions among different FOSC
574 strains. Population genetic studies in FOSC revealed that pathogenic strains group
575 with non-pathogenic ones [45,48,49,52-54,71-73], consistent with a scenario in which
576 a non-pathogenic strains receives at least part of a pathogenicity chromosome and
577 becomes pathogenic on a specific host. This is more likely to occur than switching
578 from one host to another because first of all, non-pathogens are more abundant and
579 secondly, pathogens may secrete effectors that enhance infection in one host but are
580 recognized in another. The importance of HCT in the emergence of new disease
581 depends, among other factors, on how long a pathogenicity chromosome can remain
582 intact in a population. The small pathogenicity chromosome in Fol007 is part of
583 chromosome 3 and chromosome 6 in Fol4287. Interestingly, no horizontal transfer of
584 chromosome 3 and 6 has been observed in the lab [63]. Although we found that
585 chromosome 14 and part of chromosomes 3 and 6 are present in all tomato-infecting
586 strains included in our dataset, whether these segments are present as a single

587 chromosome, multiple chromosomes or regions attached to other chromosomes,
588 remains to be investigated. The presence of transposons impedes genome assembly
589 from short reads, making it difficult to resolve this question with currently available
590 genome sequences. However, we can conclude that the tomato-infecting strains in
591 our dataset probably arose from a non-pathogenic strain after obtaining one or
592 multiple pathogenicity chromosomes. We found no evidence for horizontal transfer of
593 fast-core chromosomes in this comparison. Nevertheless, given the fact that genes
594 on fast-core chromosomes are involved in infection and that we have observed
595 transfer of core chromosomes in high-throughput experiments [63], we predict that
596 horizontal transfer of core and fast-core chromosomes can also occur in natural
597 settings. Co-transfer of fast-core chromosomes with accessory chromosomes may in
598 some cases even enhance pathogenicity of the recipient strain.

599

600 HCT, or -an extreme case- hybridization, can have an enormous evolutionary impact.
601 As we discussed above, it allows for fast spreading of fitness-enhancing
602 pathogenicity chromosomes. Moreover, it provides a means to escape “Muller’s
603 ratchet” in mainly asexual species by exchanging at least parts of core chromosomes.
604 The transposons that reside on pathogenicity chromosomes can play a role in fast
605 adaptation to host-resistance, [19,74] probably mostly by mediating rearrangements
606 [5,8,75], thus potentially disrupting modular genomic organizations and creating
607 novel chromosome segments. Moreover, transposons may disperse into core
608 chromosomes [76] where the chance of harmful effects of transposon insertion is
609 larger than on dispensable chromosomes. This interplay between beneficial and
610 detrimental effects of transposons and mobile and/or accessory chromosomes on
611 their host genomes has not yet been systematically investigated, even though it may
612 strongly influence evolutionary outcomes, including the emergence of novel
613 pathogens by host jumping. Population genetic studies and experimental evolution,
614 combined with long read sequencing, may shed light on these important issues. We

615 demonstrated here how HCT events can be detected and visualized using whole
616 genome sequencing.

617

618 We found that none of the core chromosomes of *Fol4287* are rich in transposons (Fig
619 S4), but the three smallest core chromosomes, termed 'fast-core', are distinct from
620 the other core chromosomes in terms of sequence divergence, synteny,
621 dispensability, and selected histone modifications. In that respect they are similar to
622 for example accessory regions in *Fusarium graminearum*, that have a higher SNP
623 density, are enriched in H3K27me3, yet are neither depleted in coding sequences
624 nor enriched for repeats [30]. There has been much debate on the influence of
625 chromatin states on *de novo* mutation rates. Constitutive heterochromatin may be
626 less accessible to the DNA repair machinery. Research in cancer cell lines and
627 mammalian germ line cells yielded conflicting results [77]. A recent study in
628 *Schizosaccharomyces pombe* revealed that in this fungus the DNA mismatch repair
629 machinery favours euchromatin. Similar to what we found here (Fig 5, Fig 6), the
630 authors observed a higher mutation rate in (in their case H3K9me2-enriched)
631 heterochromatin [78]. The fact that on core and fast-core chromosomes, H3K27me3
632 strongly associates with higher synonymous substitution rates (Fig 6A, B) and with
633 density of SNPs accumulated on an intermediate timescale, suggests that
634 H3K27me3 is correlated with or actively enhances mutation rates. However, this
635 effect appears insufficient to generate noticeable differences in density of SNPs
636 accumulated on very short timescales. Moreover, we do not find a strong correlation
637 between H3K27me3 and SNP density on accessory chromosomes, which
638 accumulated many more SNPs than fast-core chromosomes with comparable levels
639 of H3K27me3. Accessory chromosomes, particularly pathogenicity chromosomes of
640 strains that infect crops, may experience different selection pressures than core and
641 fast-core chromosomes, which could affect sequence evolution. Additional histone

642 modifications, possibly associated with a high density of repeats, may also further
643 influence mutation rates.

644

645 Genome organization is shaped by a combination of intrinsic molecular mechanisms
646 and natural selection. It is still not completely clear to what extent physical clustering
647 of genes in the same functional category has a selective advantage, such as robust
648 and stable co-regulation, efficient transferability of co-functional genes or increased
649 evolvability due to locally increased mutation rates (including rearrangements), e.g.
650 due to the presence of transposons or due to histone modifications that influence
651 DNA repair efficiency. We here defined two subcategories of the core and the
652 accessory genome and more fine-grained classifications are possible and probably
653 valuable. Our subclassifications reveal a hierarchical modular genome organization -
654 as is found with proteins and protein networks and is associated with evolvability [79-
655 81]. A more detailed classification of genome ‘modules’, identifying more than two or
656 four speeds, may help to disentangle the different molecular mechanisms, selection
657 on the organism level -fitness- and long-term selection on genome structure -
658 evolvability.

659

660 **Materials and methods**

661 **Whole genome alignments.**

662 We used nucmer from the MUMmer package (version 3.23) to align the genome of
663 Fol4287 to the 58 FOSC genomes [40] in our dataset (Table S1,
664 https://github.com/LikeFokkens/whole_genome_alignments). We flagged -
665 maxmatch to allow for more than one alignment per region to be able to identify
666 duplicate regions, other than that we used default settings. We used show-coords
667 with default settings (no filtering) to obtain tab-separated files with aligned regions
668 and custom Python scripts to plot the percent identity (Figs 1, 2, and S2) or length

669 (Fig S3) of these aligned regions ([https://github.com/LikeFokkens/genome-](https://github.com/LikeFokkens/genome-wide_plots)
670 [wide_plots](#)).

671

672 **Illumina sequencing of horizontal chromosome transfer strains.**

673 Two strains, Fo47-1A that obtained one chromosome and Fo47-2A that obtained two
674 chromosomes in the horizontal transfer experiment [41] were stored at -80 °C and
675 revitalized on potato dextrose agar (PDA) plates at 25 °C. An overgrown agar piece
676 was used to inoculate 100 ml NO₃-medium (0.17% yeast nitrogen base, 3% sucrose,
677 100 nM KNO₃). After 5 days at 25 °C shaking at 250 rpm, mycelium was harvested in
678 miracloth (Merck, pore size of 22-27 μM) and dried overnight in the freeze dryer.
679 Genomic DNA was isolated from freeze-dried mycelium as described in [36] and [40]
680 and sequenced on a Illumina Hiseq2000 sequencer at the Beijing Genomics Institute.

681

682 **Read densities of DNA sequencing reads**

683 We removed adapter sequences and low quality reads from reads obtained from
684 Illumina sequencing as described above with fastq-mcf with '-q 20' and a fasta file
685 with all Illumina adapter sequences. We then first mapped these reads to the
686 genome of Fo47 (the acceptor strain in the experiment), extracted the unmapped
687 reads and mapped these unmapped reads to the genome of Fol4287 to identify the
688 regions in Fol4287 that correspond to the chromosomes that were transferred from
689 Fol007 (the donor strain in the experiment). For each strain (Fo47-1A and Fo47-2A),
690 we mapped two libraries, one with insert size 170 bp, and one with insert size 500 bp.
691 We used Bowtie 2 (version 2.2.6) [82], to map reads to the Fo47 genome, applying
692 the following options: '--end-to-end --fr -reorder', for library with insert size 170 we
693 added the options '-I 140 -X 200' and for the library with insert size 500, we added
694 the options '-I 400 -X 600'. We extracted the unmapped reads using samtools view
695 (version 1.3.1), once with options '-Sbf 4 -F264' to extract unmapped reads for which
696 the mate was mapped to a samfile, once with options '-Sbf 8 -F260' to extract

697 mapped reads for which the mate was unmapped to a samfile, and once with options
698 '-Sbf 12 -F256' to extract unmapped reads for which the mate was also unmapped to
699 a samfile. We sorted the samfiles using 'samtools sort' and merged them into a
700 single using 'samtools merge'. We used bedtools (version v2.24.0) 'bam2fastq' to
701 convert the merged bamfile to fastq files. These fastq files were then mapped to the
702 genome of Fo4287 using Bowtie2 with the same options as were used for mapping
703 to the genome of Fo47. We removed putative PCR duplicates from the resulting
704 bamfiles using Picard tools version 1.134 (<http://broadinstitute.github.io/picard>,
705 MarkDuplicates) and used a custom Python script to calculate read densities for 10
706 kb windows and plot these on the genome (Fig 1B)
707 (https://github.com/LikeFokkens/genome-wide_plots). Reads have been uploaded to
708 ENA (accession PRJEB29294).

709

710 **Repeats**

711 Repeats were identified using RepeatMasker (Rebase Libraries 20140131) with '-
712 species ascomycota' and otherwise default options. Repeats labeled as
713 'Low_complexity', 'Simple_repeat', 'rRNA' or 'Satellite/5S' were filtered out. Repeat
714 densities were calculated for 10 kb non-overlapping sliding windows using 'bedtools
715 coverage'.

716

717 **Functional enrichment analyses**

718 We generated lists of (upregulated) genes located on fast-core chromosomes and in
719 pathogenicity regions. We used the FungiFun tool [83] to predict functional
720 enrichment and depletion (<https://elbe.hki-jena.de/fungifun/fungifun.php>), we chose
721 'Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 /
722 NRRL34936)' as species, and set adjusted (~ after FDR correction) P-value < 0.001
723 as significance level (both under Advanced options). Accessory chromosomes
724 typically contain genes with unknown function and less than 14% of genes in

725 pathogenicity regions are annotated in FungiFun (Table S5C). Therefore we relied on
726 the annotation published in [62] for chromosome 14. In addition we used HmmerWeb
727 version 2.24.1 to predict Pfam domains (hmmscan, default settings) and the
728 presence of secretion signal peptides. For the upregulated genes on the fast-core
729 chromosomes we predicted secretion signal peptides via the SignalP 4.1 server,
730 using default settings.

731

732 **Gene expression analyses**

733 To compare *in vitro* and *in planta* gene expression levels, we used a dataset that has
734 been described previously, hence we refer to [65] for an extensive description of
735 methods. We used hypergeometric tests as implemented in scipy with Bonferroni
736 correction to determine whether chromosomal regions are enriched for differentially
737 expressed genes.

738

739 **ChIP-seq experiments and data analyses.**

740 *Fusarium oxysporum* f. sp. *lycopersici* 4287 (FGSC9935) was stored as a
741 monoconidial culture at -80 °C and revitalized on potato dextrose agar (PDA) plates
742 at 25 °C. An overgrown agar piece was used to inoculate 100 ml NO₃-medium
743 (0.17% yeast nitrogen base, 3% sucrose, 100 nM KNO₃). After 3-5 days at 25 °C
744 shaking at 250 rpm, spores were harvested by filtering through miracloth (Merck,
745 pore size of 22-27 μM). Spores were centrifuged for 10 minutes at 2000 rpm,
746 resuspended in sterile MilliQ water and counted [40]. We inoculated 100 ml of fresh
747 NO₃-medium with 10⁷ spores and cultured for 2 days at 25 °C and shaking at 250
748 rpm.

749

750 The ChIP-seq protocol [84] was similar to those used for *S. pombe* [85] and
751 *Neurospora crassa* [86,87]. Here we only refer to important changes made for *F.*
752 *oxysporum* strains. To the 2-day old cultures 20% formaldehyde (final concentration

753 ~0.8%) was added directly to the flask and incubated for 15 min at room temperature
754 while shaking at 100 rpm. After formaldehyde quenching [84], 100-200 mg of the cell
755 pellets were ground in liquid nitrogen. Too much cell mass will decrease ChIP
756 efficiency. Digestion with micrococcal nuclease to release mostly mono- or
757 dinucleosomes was as described [84] but should be optimized for different strains.
758 ChIP-seq libraries were generated as described [84], with Illumina TruSeq adapters,
759 libraries were size-selected between 200-400 bp, amplified with standard Illumina
760 TruSeq PCR primers. Libraries were sequenced on the OSU CGRB Illumina
761 HiSeq2500 machine.

762

763 Adapter sequences were removed from ChIP-seq reads and quality scores converted
764 to Sanger format as described in [32]. Reads were aligned to the genome of Fol4287
765 using 'bwa aln' [88]. Duplicate reads were removed with Picard tools version 1.134
766 (<http://broadinstitute.github.io/picard>, MarkDuplicates) (Table S2). We used RSEG
767 [89] to predict domains of enrichment using default settings and providing a bedfile
768 with gaps in the assembly (N's in the DNA sequence) as 'deadzones'. We obtained
769 two biological replicates for each experiment, one with relatively low and one with
770 relatively high sequencing depth (Table S2). We estimate the reproducibility of our
771 data by calculating the correlation of average read densities in 10 kb non-overlapping
772 sliding windows. We obtained moderate correlation coefficients, ranging from 0,59 to
773 0,66 (Kendall's Tau, Bonferroni-corrected P-value < 0.001) for H3K27me3 and
774 H3K4me2 respectively. Reads have been uploaded to GEO (accession GSE121283).

775

776 **Synonymous and nonsynonymous substitutions**

777 For Fol4287 genes based on alignments and trees with homologs in eight different
778 *Fusarium* species, others [24] calculated omega values (d_N/d_S ratios) and P-values
779 indicating whether a model including site-specific selection fits the data better than a
780 neutral model, for two different assumed distributions of d_N/d_S ratios: one in which

781 omega is either 0 or 1 (M1M2 in Fig 6), and one in which omega follows a beta
782 distribution between 0 and 1 (M7M8 in Fig 6), where models with sites under positive
783 selection (M2 and M8 respectively) have an additional category $\omega > 1$. We
784 downloaded these data from their Supplemental Online Material. In addition, we
785 aligned Fol4287 protein sequences with their bidirectional best blast hits in the *F.*
786 *verticillioides* proteome with Clustal Omega, used PAL2NAL to infer codon
787 alignments and codeml to calculate d_N and d_S values based on these. We filtered out
788 all genes with d_N or $d_S > 1$ (i.e. genes with multiple substitutions).

789

790 **SNP calling**

791 Strains that belong to VCG030 are Fol002, Fol004, Fol007, Fol014, Fol018, Fol026,
792 Fol029, Fol038, Fol073 and Fol074. The 'clade III'- set consists of all strains in
793 VCG030 and Fol016, Fol096, Fol072, Fol075, FolMN25, FoMN14, Fom001, Forc016,
794 Forc024 and Forc031. Fol-CL25 also belongs to this clade, but no raw sequencing
795 reads were publicly available for this strain. Raw sequencing reads were filtered and
796 trimmed using fastq-mcf with '-q 20' and a fasta file with Illumina adapter sequences.
797 Trimmed reads were mapped to the genome sequence of Fol4287 using bowtie2
798 with '--end-to-end --fr -reorder' and '-l 100 -X 300' for strains with an estimated
799 fragment length of 200 (all strains in VCG030 except Fol007) and '-l 400 -X 600' for
800 other strains in clade III ((based on an estimated fragment length of 500). Bam files
801 were processed individually for each sample. The files were sorted and duplicate
802 reads were removed using Picard tools version 1.134
803 (<http://broadinstitute.github.io/picard>, MarkDuplicates). Variant calling was done with
804 the Genome Analysis ToolKit [90] using Haplotypecaller with '-ploidy 1'. Indels were
805 masked and SNP were sorted and filtered using VariantFilter with 'maskExtension 5',
806 'clusterSize 3', 'clusterWindowSize 10', 'MQRankSum < -17.5', 'QD < 1',
807 'ReadPosRankSum < -8.0', 'FS > 60.0', 'MQ < 30.0', 'SOR > 7', 'MQ0 > 3', 'QUAL <
808 30.0', 'DP > 400', 'DP < 10'.

809

810 **Availability of data and scripts.**

811 To facilitate reproducibility of this work and allow others to perform similar analyses,
812 the Python code and Ipython notebooks used to generate the Figures and to
813 calculate statistics in this manuscript and its supplemental online material are
814 available under GNU public license and can be downloaded from
815 https://github.com/LikeFokkens/FOSC_multi-speed-genome . Reads from ChIP-seq
816 experiments and the DNA sequencing of the two horizontal chromosome transfer
817 strains (Fo47-1A and Fo47-2A, Fig 1B) have been submitted to the GEO (accession
818 GSE121283) and the ENA (accession PRJEB29294) respectively.

819

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- 1082

1083 **Figure captions**

1084 **Fig 1. Lineage-specific and pathogenicity regions in the Fol4287 accessory**
1085 **genome.**

1086 **A.** Horizontal bars -colored according to the percent identity in the alignment- indicate
1087 presence of Fol4287 accessory regions 1b and 2b and accessory chromosomes 3, 6,
1088 14 and 15 in 23 other *Fusarium oxysporum* isolates. Leaf nodes in the phylogenetic
1089 tree are colored according to *forma specialis*, isolates causing wilting symptoms are
1090 represented with a circle, those that cause root rot are represented with squares and
1091 those that are non-pathogenic do not have a shape or color. Only alignments that
1092 span more than 1 kb and are more than 90% identical are included. Chromosomal
1093 regions 1b (Supercontig 2.27) and 2b (Supercontig 2.31), part of chromosome 3, part
1094 of chromosome 6 and chromosome 15 are mostly absent or present with relatively
1095 low sequence similarity outside the clonal line of Fol4287. In contrast, chromosome
1096 14, part of chromosome 3 and part of chromosome 6 are present with ~100%
1097 sequence identity in all tomato-infecting isolates that we queried. **B.** Two strains that
1098 respectively received one and two chromosomes in a horizontal transfer experiment
1099 involving Fol007 as chromosome donor and Fo47 as recipient, had been sequenced
1100 previously [62]. We mapped sequencing reads obtained from these strains on the
1101 genome of Fol4287. The density of mapped reads from the strain that received
1102 chromosome 14 is depicted in blue. The density of mapped reads from the strain that
1103 received a small chromosome in addition to chromosome 14 and is more virulent, is
1104 depicted in red. These read densities reveal that that the pathogenicity regions on
1105 chromosome 3 and 6 correspond to a small pathogenicity chromosome in Fol007.
1106 Read densities in regions that have duplicated or triplicated in Fol4287 are $\frac{1}{2}$ and $\frac{1}{3}$
1107 lower respectively than in non-duplicated Fol4287 regions (indicated with green lines).

1108

1109 **Fig 2. Core and fast-core chromosomes in the Fol4287 genome.**

1110 Horizontal bars -colored according to the % identity in the alignment- indicate
1111 presence of Fol4287 core chromosomes 4,5,7,8,11,12, and 13 in 23 other *Fusarium*
1112 *oxysporum* isolates. Leaf nodes in the phylogenetic tree are colored according to
1113 *forma specialis*, isolates causing wilting symptoms are represented with a circle,
1114 those that cause root rot are represented with squares and those that are non-
1115 pathogenic do not have a shape or color. Only alignments that span more than 1 kb
1116 and are more than 90% similar are included. Within the Fol4287 clonal line, all
1117 chromosomes are mostly 100% identical, while when compared to other, more
1118 distant FOSC isolates, the three smallest core chromosomes, 11, 12 and 13, are
1119 more divergent than other core chromosomes (see also Figure S1). We denote these
1120 three chromosomes as fast-core chromosomes.

1121

1122 **Fig 3. Fraction of up- and downregulated genes per chromosome.**

1123 The bars represent the fraction of genes that is upregulated (green) or
1124 downregulated (red) *in planta* compared to *in vitro* per chromosome and per
1125 chromosome category (boxes with black lines). Significant enrichment (P-value <
1126 0.001) of up- or downregulated genes with respect to the rest of the genome is
1127 indicated with asterisk signs. Lineage-specific parts of core (Chr. 1 and 2) or
1128 accessory (Chr. 3 and 6) chromosomes that are lineage-specific are denoted with a #
1129 on the x-axis.

1130

1131 **Fig 4. Core chromosomes are enriched for H3K4me2 and fast-core and**
1132 **accessory chromosomes for H3K27me3.**

1133 We mapped ChIP-seq reads to the genome of Fol4287 and identified domains of
1134 enrichment (DOE). For each chromosome or chromosomal region (x-axis) we plot
1135 how much is covered in a DOE (top panels) and the size-distribution of DOEs
1136 (bottom panels, violin plots). Lineage-specific parts of core (Chr. 1 and 2) or
1137 accessory (Chr. 3 and 6) chromosomes that are lineage-specific are denoted with a #

1138 on the x-axis. The regions on chromosome 3 and on chromosome 6 that are
1139 associated with pathogenicity on tomato are denoted with a ^P. Bars with thick lines
1140 represent the coverage per chromosome category (core, fast-core, lineage specific or
1141 pathogenicity) rather than per chromosome. A. Coverage and size distribution of
1142 DOE of H3K4me2. For most core chromosomes more than 50% is enriched for
1143 H3K4me3, while for the fast-core and accessory chromosomes, this is less than 20%.
1144 The DOE of H3K2me2 are larger on the core chromosomes than in the other regions.
1145 B. Coverage and size distribution of DOE of H3K27me3. For most core
1146 chromosomes less than 50% is enriched for H3K37me3, while for the fast-core
1147 chromosomes more than 80% is covered in H3K27me3 and the lineage-specific and
1148 accessory chromosomes are more enriched in H3K27me3 than the core
1149 chromosomes. In general, the size of the H3K27me3 DOEs is larger than that of
1150 H3K4me2 DOEs (note that y-axis is in log-scale).

1151

1152 **Fig 5. H3K27me3-enriched regions have higher levels of sequence divergence,**
1153 **independent of repeat density.**

1154 These three examples, one core, one fast-core and one accessory chromosome,
1155 demonstrate how presence of H3k27me3 (panel 2) coincides with differential
1156 expression (panel 1), elevated levels of sequence divergence (panel 3-5), but not
1157 necessarily with differences in either gene- or repeat density. The genes on core
1158 chromosome 4 that are differentially expressed during infection (panel 1, blue
1159 squares) are located mostly in the sub-telomeric regions and one central region.
1160 These regions are enriched in H3K27me3 (panel two, orange) and depleted in
1161 H3K4me3 (panel two, green). The fast-core chromosome has many differentially
1162 expressed genes, most of which are upregulated during infection. There are no large
1163 regions that are either enriched or depleted in differentially expressed genes. The
1164 same holds true for H3K27me3, which is relatively equally distributed along the
1165 chromosome. More or less the same holds true for chromosome 14, the

1166 pathogenicity chromosome and the only accessory chromosome that is enriched for
1167 genes that are upregulated during infection. Here also H3K27me3 is relatively
1168 uniformly distributed along the chromosome: unlike core chromosomes, H3K27me3-
1169 ated regions are not interrupted by regions with high levels of H3K4me2. When
1170 looking at sequence divergence on a very short timescale (panel 3, density of SNPs
1171 called in strains that belong to VCG030) there are no distinct differences within and
1172 between the core and fast-core chromosomes, while chromosome 14 clearly has a
1173 higher SNP density (see Figure S14 for more detail). In contrast, on longer
1174 timescales (panel 4, density of SNPs called in strains that belong to clade III, panel 5,
1175 d_N (black) and d_S (blue) based on bidirectional best hits with sister species *F.*
1176 *verticillioides*), we can clearly see that regions that are enriched in H3K27me3 on the
1177 core chromosome correspond with regions with higher d_N and d_S (see also Figure
1178 S14 and Figure S15) and a higher SNP density. Fast-core chromosomes resemble

1180 Sub-telomeric core regions. Note that gene- and repeat density are relatively uniform
1181 on the core and fast-core chromosomes (see also Figure S4). The SNP density of
1182 accessory chromosomes cannot directly be compared to the core and fast-core
1183 chromosomes because they are lost in many strains in Clade III and in *F.*
1184 *verticillioides*. The accessory chromosomes are depleted in genes and enriched in
1185 repeats.

1186

1187 **Figure 6. Clustering of genome characteristics.**

1188 We calculated the following genome characteristics for 6186 10 kb non-overlapping
1189 windows across the entire Fol4287 genome: **Genes (ORFs)**: the number of bp that
1190 are part of a coding region divided by the window size, **Repeats**: the number of bp
1191 that are part of a repeat region divided by the window size, **RPKM *in planta***: mean
1192 (over 3 replicates) RNA-seq read counts for the *in planta* experiment, **RPKM *in***
1193 ***vitro***: mean (over 3 replicates) RNA-seq read counts for the *in vitro* experiment,
1194 **Change in GE**: log₂ fold change in gene expression *in planta* / *in vitro*, **H3K4me2 (a)**
1195 **and (b)**: average read density for the two replicates of the H3K4me2 ChIP-seq
1196 experiment, **H3K27me3 (a) and (b)**: average read density for the two replicates of
1197 the H3K27me3 ChIP-seq experiment, **dN**: average number of nonsynonymous
1198 substitutions per nonsynonymous site dN, **dS**: the average number of synonymous
1199 substitutions per synonymous site dS, **dN/dS**: average ratio between synonymous
1200 and nonsynonymous substitutions, **SNPs VCG030**: density of SNPs in VCG030 with
1201 respect to Fol4287, **SNPs Clade III**: density of SNPs in clade III with respect to
1202 Fol4287. Spearman correlation coefficients (R) are depicted in a heatmap, genome
1203 characteristics were clustered with average linkage using 1-R as a distance measure.
1204 A. Clustering based on core chromosomes. The clustering shows two regimes: one
1205 gene-rich, highly expressed, H3K4me2-ated and one repeat-rich, H3K27me3-ated
1206 with high levels of sequence divergence. B. Clustering based on fast-core
1207 chromosomes (11, 12, 13). As with core chromosomes, the clustering shows two

1208 regimes: one gene-rich, highly expressed, H3K4me2-ated and one repeat-rich,
1209 H3K27me3-ated with high levels of sequence divergence, albeit less pronounced as
1210 correlation coefficient tend to be lower. C. Clustering based on accessory
1211 chromosomes. Unlike the core and fast-core chromosomes, levels of sequence
1212 divergence correlate with gene density and expression level. However, this may be
1213 an artefact from the SNP calling process, in which reads that map to multiple
1214 locations -e.g. reads that map to transposons- are excluded. Due to lack of data
1215 points, dN, dS and dN/dS were excluded.

1216

1217

1218 **Supporting information captions**

1219 **Figure S1. Whole genome alignment of Fol4287 with Fom001.**

1220 The whole genome alignment of tomato-infecting strain Fol4287 with melon-infecting
1221 strain Fom001 is represented here in a dotplot. Lines are coloured according to
1222 percent identity of the aligned segments, only alignments that are more than 90%
1223 identical and span more than 1 kb are included. Thin black vertical lines indicate
1224 Fol4287 chromosomes, grey, semi-transparent lines indicate scaffolds. Unpositioned
1225 scaffolds in Fol4287 are not included. The Fol4287 core chromosomes
1226 (1,2,4,5,7,8,9-13) are almost 99-100% identical in Fom001. With the exception of one
1227 translocation between chromosome 2 and chromosome 10, synteny is conserved in
1228 core chromosomes. In contrast, the accessory chromosomes are mostly absent. We
1229 expect that differences in host preference are largely determined by these accessory
1230 chromosomes. Chromosomal regions 1b, part of chromosome 15 and especially 2b
1231 are absent in sister species *F. verticillioides*, but largely present in Fom001 with high
1232 levels of sequence similarity. In contrast, chromosome 3, 6 and 14 are absent in
1233 Fom001.

1234

1235 **Figure S2. Presence/absence -coloured by % identity- of Fol4287 chromosome** 1236 **sequences in the genomes of 58 other *Fo* strains.**

1237 The phylogenetic tree on the left was inferred using maximum likelihood from a
1238 concatenated alignment of 1194 core genes as described in van Dam et al. (Env.
1239 Microb. 2016). Leaf nodes are colored according to forma specialis; red: tomato,
1240 light-green: melon, green: cucumber, grey: cotton, petrol: watermelon, yellow:
1241 banana, purple: brassicaceae, brown: pea. Leaf nodes are shaped according to
1242 disease symptoms; round: wilting, square: root rot. Forc strains (green squares) are
1243 colored green but are pathogenic on cucumber, melon and watermelon. Strains that
1244 are not pathogenic on plants (to our best knowledge) have no shape, Fo47 and

1245 FoMN14 are non-pathogenic, FOSC-3a is pathogenic on immunocompromised
1246 humans. This plot indicates only presence of sequences and are not informative on
1247 synteny (see Figure S3 for plots colored according to alignment length): this plot only
1248 shows which segments are present, not whether they also occur on the same
1249 configuration/on the same chromosome. In Figure S2A and S2B, only alignments
1250 that span at least 1000 bp in the query genome and are at least 90% identical are
1251 included.

1252 A. Comparison of core chromosomes, i.e. chromosomes that are largely present with
1253 high sequence similarity (>97% identity) in all strains. Part of chromosome 1 and
1254 chromosome 2 are considered accessory regions. Levels of sequence similarity
1255 correspond to the phylogeny. The level of sequence similarity drops in the
1256 subtelomeric regions. Chromosome 4 has a region in the middle with lower levels of
1257 sequence similarity, this region corresponds to the breakpoint of a chromosomal
1258 rearrangement when compared to *F. verticillioides*.

1259 B. Comparison of fast-core and accessory chromosomes. The three smallest core
1260 chromosomes differ markedly from the other 8 core chromosomes depicted in Figure
1261 S2A. The percent identity in the alignments is lower, the difference is small but very
1262 consistent. Moreover, we observed more large-scale deletions in these
1263 chromosomes. The accessory chromosomes are present in only in a small subset of
1264 genomes. Some sequences are present with low sequence similarity (~90%,
1265 depicted in blue), these could correspond to transposons. Alignments of
1266 chromosomal regions 1b and 2b and chromosome 15 with the Fom001 genome have
1267 higher sequence identity and synteny than of chromosome 3 and 6 (Figure 1, Figure
1268 S1). Moreover, chromosome 3 and 6 both contain a region that has been lost in
1269 strains Fol029, Fol018, Fol074 and Fol038. Chromosome 15 and chromosomal
1270 region 1b are absent Fol014, Fol029 and Fol018 and part of chromosome 14 has
1271 been lost in Fol018. Chromosome 1b, 2b, 3, 6, 15 and many of the unpositioned
1272 scaffolds hardly occur outside the clonal lineage of Fol4287. Some of the

1273 unpositioned scaffolds have a similar color pattern as core chromosomes, suggesting
1274 they are part of core chromosomes but could not be placed there due to lack of
1275 resolution in the optical map that was constructed for the reference assembly of
1276 FoI4287. Chromosome 14 and part of chromosome 3 and 6 clearly show hallmarks of
1277 large-scale horizontal transfer but there are also indications of smaller scale putative
1278 transfer events, e.g. part of chromosome 1b that is present in brassicaceae-infecting
1279 strains (indicated with purple circles in the phylogenetic tree). Part of chromosome 15
1280 is also present in other strains, but with normal sequence similarity, suggesting that
1281 this region is lost in many strains rather than horizontally transferred. Comparisons to
1282 outgroup species are needed to confirm this.

1283 C. Presence-absence of core, fast-core and accessory chromosomes with more
1284 lenient cutoffs: all alignments that are more than 80% identical in sequence and span
1285 more than 100 basepairs are included. The patterns we observed above are not
1286 dependent on specific cut-offs, as we observe them with more lenient cut-offs as well.

1287

1288 **Figure S3. Presence/absence -coloured by synteny- of FoI4287 genome**
1289 **sequences in the genomes of 58 other *Fo* isolates.**

1290 The phylogenetic tree on the left was inferred using maximum likelihood from a
1291 concatenated alignment of 1194 core genes as described in van Dam et al. (Env.
1292 Microb. 2016). Leaf nodes are colored according to forma specialis; red: tomato,
1293 light-green: melon, green: cucumber, grey: cotton, petrol: watermelon, yellow:
1294 banana, purple: brassicaceae, brown: pea. Leaf nodes are shaped according to
1295 disease symptoms; round: wilting, square: root rot. Forc isolates (green squares) are
1296 colored green but are pathogenic on cucumbebr, melon and watermelon. Isolates that
1297 are not pathogenic on plants (to our best knowledge) have no shape, Fo47 and
1298 FoMN14 are non-pathogenic, FOsc-3a is pathogenic on immunocompromised
1299 humansIn Figure S3A and S3B, only alignments that span at least 1000 bp in the
1300 query genome and are at least 90% identical are included.

1301 A. Comparison of core chromosomes. Part of chromosome 1 and chromosome 2 are
1302 considered accessory regions. Within the clonal line of Fol4287 and with Fom001,
1303 alignments can span as long as and longer than 50 Mb (plotted in yellow). As with
1304 sequence similarity, synteny levels drop at the subtelomeric regions and in the
1305 middle region of chromosome 4 that corresponds to the breakpoint of a chromosomal
1306 rearrangement when compared to *F. verticillioides*. Fol4287 self-alignment does not
1307 produce only alignments of > 50 Mb in length because the assembly contains gaps.
1308 Chromosomal region 2B is relatively fragmented (contains > 2 times the number of
1309 gaps as e.g. chromosomal region 1B, or Supercontig_2.25 that is of comparable size
1310 and is located on chromosome 3) which is reflected in the low level of synteny in the
1311 Fol4287 self-alignment.

1312 B. Comparison of fast-core and accessory chromosomal regions. The three smallest
1313 core chromosomes differ from the other 8 core chromosomes depicted in Figure S3A,
1314 synteny conservation is less conserved in more distant isolates. Part of chromosome
1315 13 is not syntenic to Fom001, it aligns to a number of relatively small contigs. Notably,
1316 this region is lost in Fom013. The accessory chromosomes are present in only in a
1317 small subset of chromosomes. While for chromosome 14 sequences are conserved
1318 in tomato-infecting isolate, synteny is not, in contrast to the region on chromosome 3
1319 and 6 that is shared between tomato-infecting isolates, where we do observe
1320 conserved synteny.

1321 C. Presence-absence of core, fast-core and accessory chromosomes with more
1322 lenient cutoffs: all alignments that are more than 80% identical in sequence and span
1323 more than 100 basepairs are included. The patterns we observed above are not
1324 dependent on specific cut-offs, as we observe them with more lenient cut-offs as well.

1325

1326 **Figure S4. Gene and repeat density.**

1327 For 10 kb non-overlapping windows, we here plot the fraction of base pairs that is
1328 part of a gene (blue) or a predicted transposable element (grey). The accessory

1329 chromosomes and chromosomal regions are rich in repeats compared to the core
1330 chromosomes, including the fast-core chromosomes. Chromosomes are scaled
1331 according to size.

1332

1333 **Figure S5. Fast-core and accessory chromosomes have lower gene expression**
1334 **levels.**

1335 The expression level in reads per kb per million mapped reads (RPKM), averaged
1336 over three biological replicates. Per chromosome, there are two panels: the top panel
1337 shows *in vitro* gene expression in black dots and the bottom panel *in planta* gene
1338 expression in blue dots. The x-axis show the position of the gene on the genome, the
1339 y-axis the RPKM. Note that the y-axis is log-scaled. We drew a red solid line at $y = 5$
1340 for reference. On core chromosomes, gene expression levels are mostly above this
1341 line, where on fast-core and accessory chromosomes, most gene expression levels
1342 are under 5 RPKM.

1343

1344 **Figure S6. Fast-core and accessory chromosomes have relatively more**
1345 **differentially expressed genes than core chromosomes.**

1346 The x-axis show the position of the gene on the genome, the y-axis the log₂fold
1347 change in gene expression (*in planta/in vitro*) per chromosome. Zero average read
1348 counts have been replaced by 0.1 to avoid infinite ratio's (as in Van der Does et al.
1349 PloS Genetics 2016). Differentially expressed genes are highlighted in blue squares.
1350 Not only fast-core chromosomes and chromosome 14 but also the central fast-core
1351 region on chromosome 4 and the subtelomeric regions have many differentially
1352 expressed genes.

1353

1354 **Figure S7. Functional categories that are overrepresented on the fast-core**
1355 **chromosomes.**

1356 Fraction of annotated genes that are assigned to a FunCat category that is
1357 significantly overrepresented on the fast-core chromosome, compared to all genes
1358 on the genome (P-value < 0.001 after FDR correction). Categories that are also
1359 overrepresented when comparing up-regulated genes to the background of all fast-
1360 core genes are in bold. Percentages are defined with respect to the total number of
1361 annotated genes.

1362

1363 **Figure S8. Read density from ChIP-seq experiments targeted at H3K27me3-**
1364 **ated or H3K4me2-ated regions.**

1365 Average read densities in 10.000 bp non-overlapping sliding windows are depicted in
1366 green (H3K4me2) and orange (H3K27me3). Read densities are normalized with
1367 respect to RPKM to allow for comparisons across experiments. Chromosomes are
1368 scaled to the length of their sequence in the assembly. The core chromosomes -
1369 except chromosome 11, 12 and 13- are largely enriched for H3K4me2, except at the
1370 subtelomeric regions. These small core chromosomes, designated fast-core
1371 chromosomes, are enriched in H3K27me3, similar to accessory chromosomes. Also
1372 the middle region in chromosome 4, which is also more divergent in terms of
1373 sequence similarity and synteny (Figure S2A, Figure S3A) is enriched in H3K27me3
1374 as well. The two histone marks appear to be mutually exclusive.

1375 A. Experiments with high sequencing depth: H3K4me2, experiment id 1358:
1376 19735885 reads, of which 18129305 mapped (91,86 %); H3K27me3, experiment id
1377 1360: 21467536 of which 16243857 mapped (75,76 %), see Table S2.

1378 B. Replicate experiments, with lower sequencing depth: H3K4me2, experiment id
1379 806: 9078423 reads, of which 6699238 mapped (73,79 %); H3K27me3, experiment
1380 id 808: 7891973 of which 5519933 mapped (69,94 %), see Table S2.

1381

1382 **Figure S9. Core chromosomes are enriched for H3K4me2 and fast-core and**
1383 **accessory chromosomes for H3K27me3.**

1384 For each chromosome or chromosomal region (x-axis) we plot how much is covered
1385 in a DOE (top panels) and the size-distribution of DOEs (bottom panels, violinplots).
1386 Lineage-specific regions are denoted with a # on the x-axis. The regions on
1387 chromosome 3 and on chromosome 6 that are associated with pathogenicity on
1388 tomato are denoted with a ^P. Bars with thick lines represent the coverage per
1389 chromosome category (core, fast-core, lineage specific or pathogenicity) rather than
1390 per chromosome.

1391 A. Coverage and size distribution of DOE inferred based on two H3K4me2
1392 experiments (1358 'H3K4me2 (a)' and 806 'H3K4me2 (b)'). B. Coverage and size
1393 distribution of DOE inferred based on two H3K27me3 experiments (1360 'H3K27me3
1394 (a)' and 808 'H3K27me3 (b)'). The coverage of DOEs is lower for 806 'H3K4me2 (b)'
1395 and 808 'H3K27me3 (b)', than for 1358 'H3K4me2 (a)' and 1360 'H3K27me3 (a)', but
1396 the distribution are not qualitatively different.

1397

1398 **Figure S10. Overlap of domains of enrichment with genes, promoters and**
1399 **repeats.**

1400 We used RSEG to identify domains enriched in histone marks H3K4me2 (A) or
1401 H3K27me3 (B), based on mapped reads generated in two independent ChIP-seq
1402 experiments for each mark (left and right panels, 1358 and 806 for H3K4me2, 1360
1403 and 808 for H3K27me3) (see Materials and Methods for more detail). For each
1404 chromosome or chromosomal region, we determine the percentage of genes (top
1405 panel, light blue), promoter regions (defined as up to 1000 base pairs upstream of
1406 first exon, second panel, dark blue), and repeats (as predicted by RepeatMasker,
1407 excluding low-complexity regions and simple repeats, third panel, grey) that overlap
1408 (for more than 90%) with a domain of enrichment. To compare whether certain
1409 elements (e.g. genes) overlap more than expected with a domain of enrichment, we
1410 also plot how much of a chromosome or chromosomal region is part of a domain of
1411 enrichment (bottom panels, dark grey on light grey background). Average values per

1412 chromosome category are also included in the histogram, and designated with black
1413 boxes.

1414 A. H3K4me2 domains occur mainly on the core chromosomes, and very little on the
1415 fast-core and accessory chromosomes. Domains of H3K2me2 are relatively
1416 underrepresented in repeat regions.

1417 B. H3K27me3 domains occur mainly on the fast-core and accessory chromosomes,
1418 and very little on the core chromosomes. Domains of H3K27me3 are
1419 overrepresented in repeat regions on the core chromosomes.

1420

1421 **Figure S11. d_N , d_S and d_N/d_S values along the genome.**

1422 The number of synonymous substitutions per synonymous site d_S , the number of
1423 non-synonymous substitutions per nonsynonymous site d_N (top panels, d_S in blue,
1424 d_N , in black triangles) and their ratio (bottom panel, grey dots) of genes are plotted on
1425 the genome. Genes with $d_N/d_S > 1$ are highlighted with red squares. On the x-axis are
1426 chromosomes, dotted vertical lines denote supercontigs that comprise these
1427 chromosomes. Y-axes are in log scale. Subtelomeric regions have higher d_N and d_S
1428 values, while their ratio is consistent along the genome. The same holds true for the
1429 fast-core chromosomes and the middle region on chromosome 4 that is also
1430 enriched in H3K27me3 and depleted in H3K4me2. The accessory chromosomes
1431 have very little data points, as values are calculated with respect to bidirectional best
1432 blast hits in *F. verticillioides* and these chromosomes do not occur in this species.

1433

1434 **Figure S12. Frequency distribution of d_N and d_S of core and fast-core genes.**

1435 We compare the distributions of all core (light-blue) or all fast-core (light-red) genes
1436 to two subsets of genes (dark-blue and dark-red). One subset consists of genes that
1437 are differentially expressed during infection (DEGs, left panels) and one of genes that
1438 are in an H3K27me3-enriched domain (H3K27me3, right panels).

1439 A. Kernel density estimation of the frequency distribution of d_N . Fast-core genes have
1440 higher d_N values than core genes. Fast-core DEGs have low values d_N compared to
1441 all fast-core genes, while for core genes there is no difference (left panel). Core
1442 genes that are in an H3K27me3-enriched domain have the same distribution as fast-
1443 core genes.

1444 B. Kernel density estimation of the frequency distribution of d_S . Fast-core genes have
1445 higher d_S values than core genes. Core DEGs have higher d_S values than other core
1446 genes, for the fast-core the distribution of d_S of DEGs does not differ much from that
1447 of all fast-core genes. Again, core genes that are in an H3K27me3-enriched domain
1448 have the same distribution as fast-core genes.

1449

1450 **Figure S13. SNP density per 10 kb sliding window, per chromosome.**

1451 We here plot the cumulative SNP density in 10000 bp, non-overlapping sliding
1452 windows. Per chromosome there are two panels: the top panel shows the cumulative
1453 SNP density for all strains in Clade III (see tree in the legend) in purple, whereas the
1454 bottom panel shows shows the cumulative SNP density for all strains in Vegetative
1455 Compatibility Group 030 (VCG030, dark-grey).

1456

1457 **Figure S14. SNP density per 10 kb sliding window, per chromosome.**

1458 We here plot the cumulative SNP density in 10000 bp, non-overlapping sliding
1459 windows. Per chromosome there are two panels: the top panel shows the cumulative
1460 SNP density for all strains in Vegetative Compatibility Group 030 (VCG030, dark-
1461 grey), using a different y-axis scale than in Figure S13 to show that the distribution of
1462 SNPs on fast-core chromosomes is not different from that on core chromosomes.

1463

1464 **Table S1. Strains used in this study.**

1465 **Table S2. Gene expression levels and fold change in gene expression per gene**

1466 **Table S3. Functional analysis of differentially regulated genes on pathogenicity**
1467 **region on chromosome 3 and 6.**

1468 **Table S4. Functional analysis of differentially regulated genes on chromosome**
1469 **14.**

1470 **Table S5A. Functional enrichment of genes that reside on chromosome 11, 12**
1471 **and 13.**

1472 **Table S5B. Functional enrichment of up-regulated genes that reside on**
1473 **chromosome 11, 12 and 13.**

1474 **Table S6. Sequencing depth, mapping and putative PCR duplicates in the ChIP-**
1475 **seq experiments.**

1476 **Table S7A. Domains of enrichment of H3K4me2.**

1477 **Table S7B. Domains of enrichment of H3K27me3.**

1478 **Table S8. Statistics of selection per gene.**

1479

1480

1481

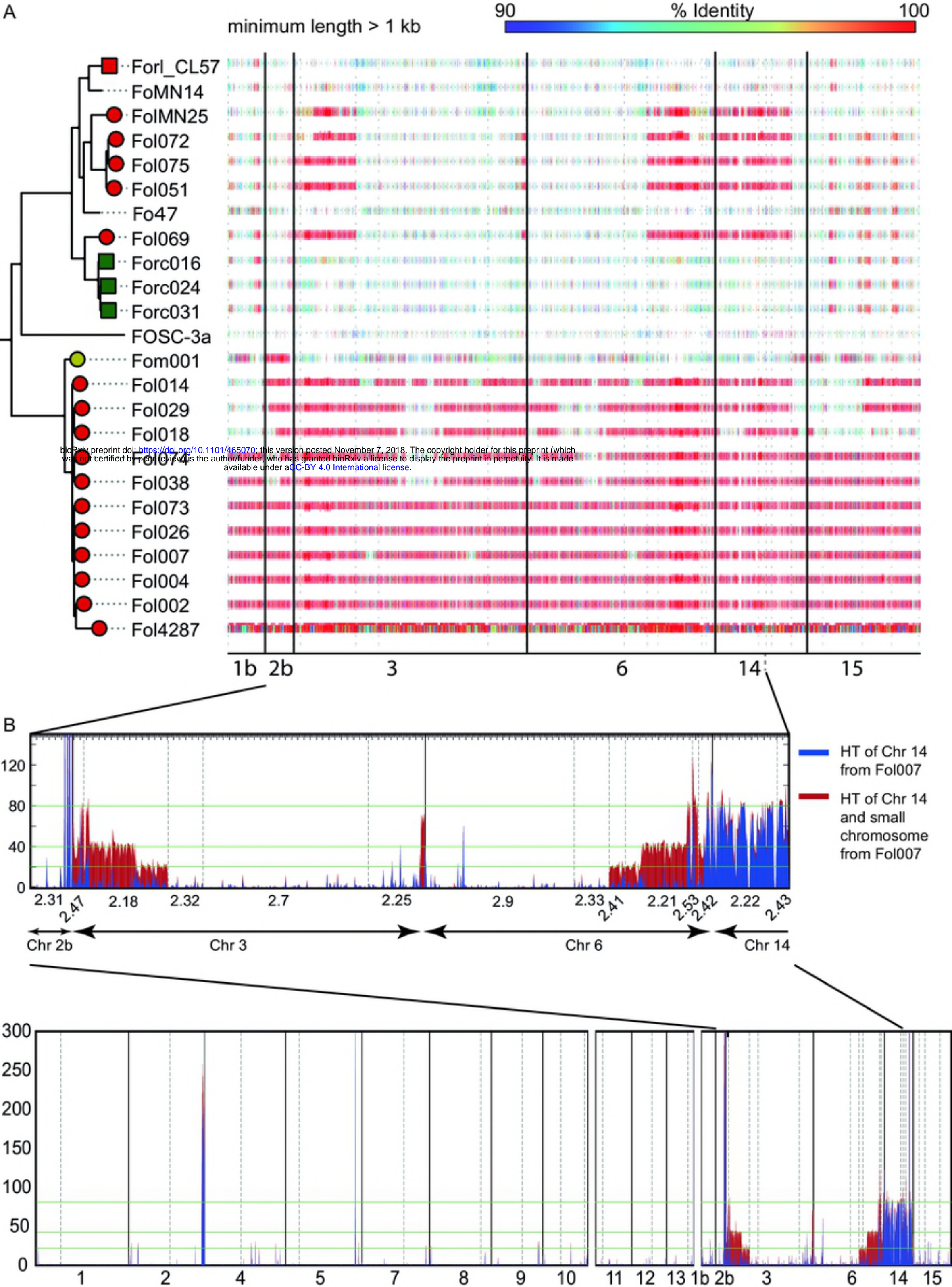


Figure 1

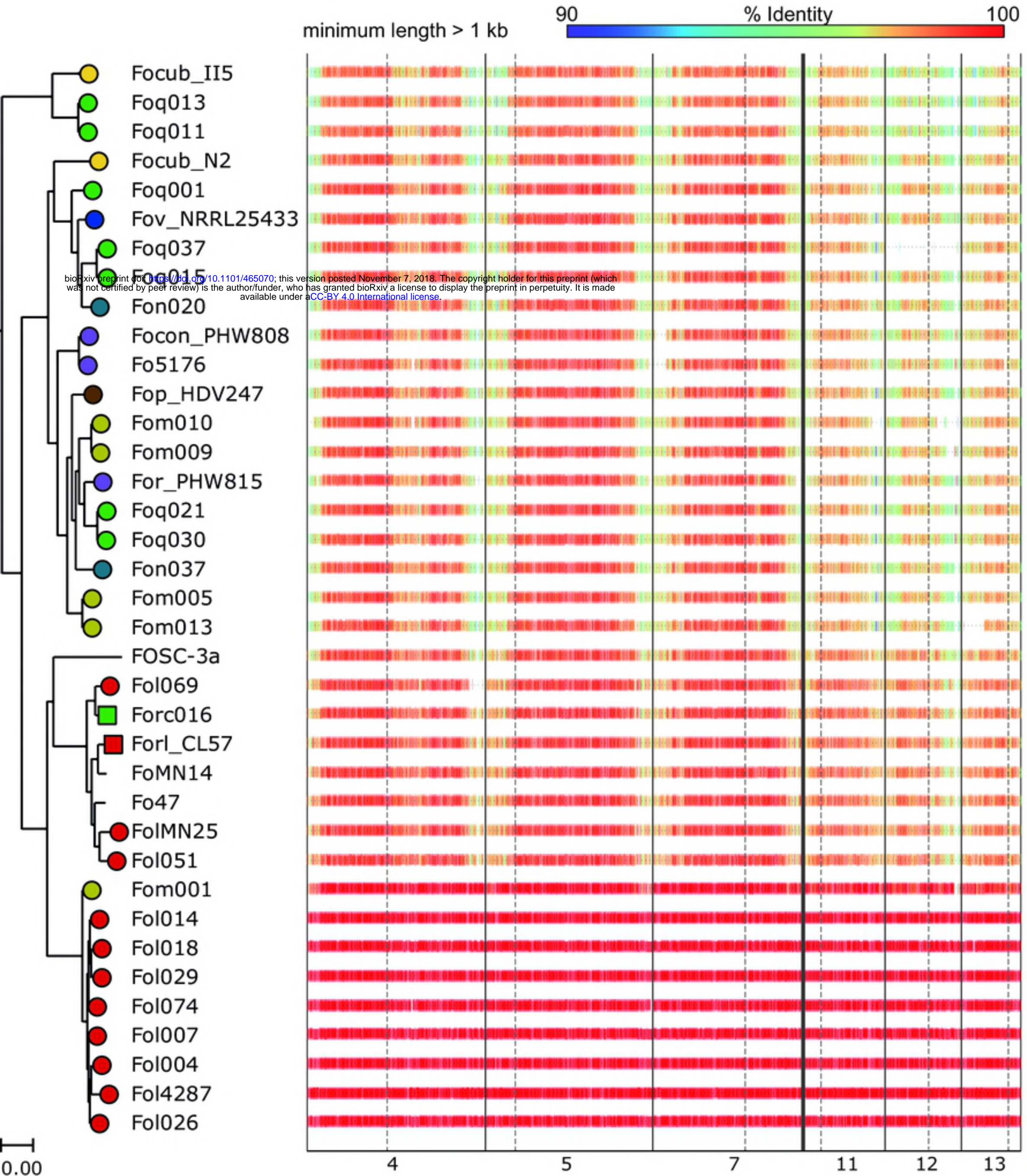


Figure 2

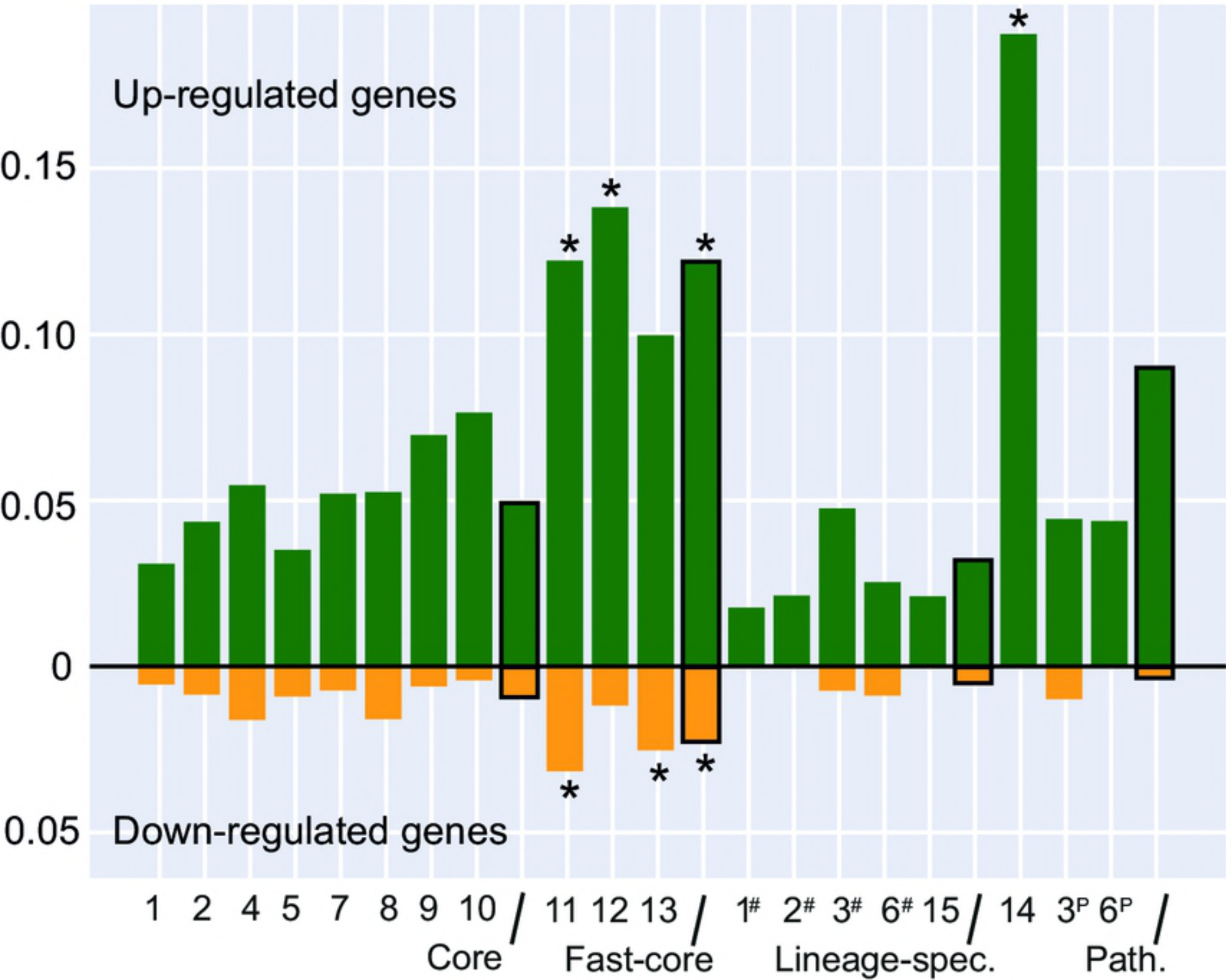


Figure 3

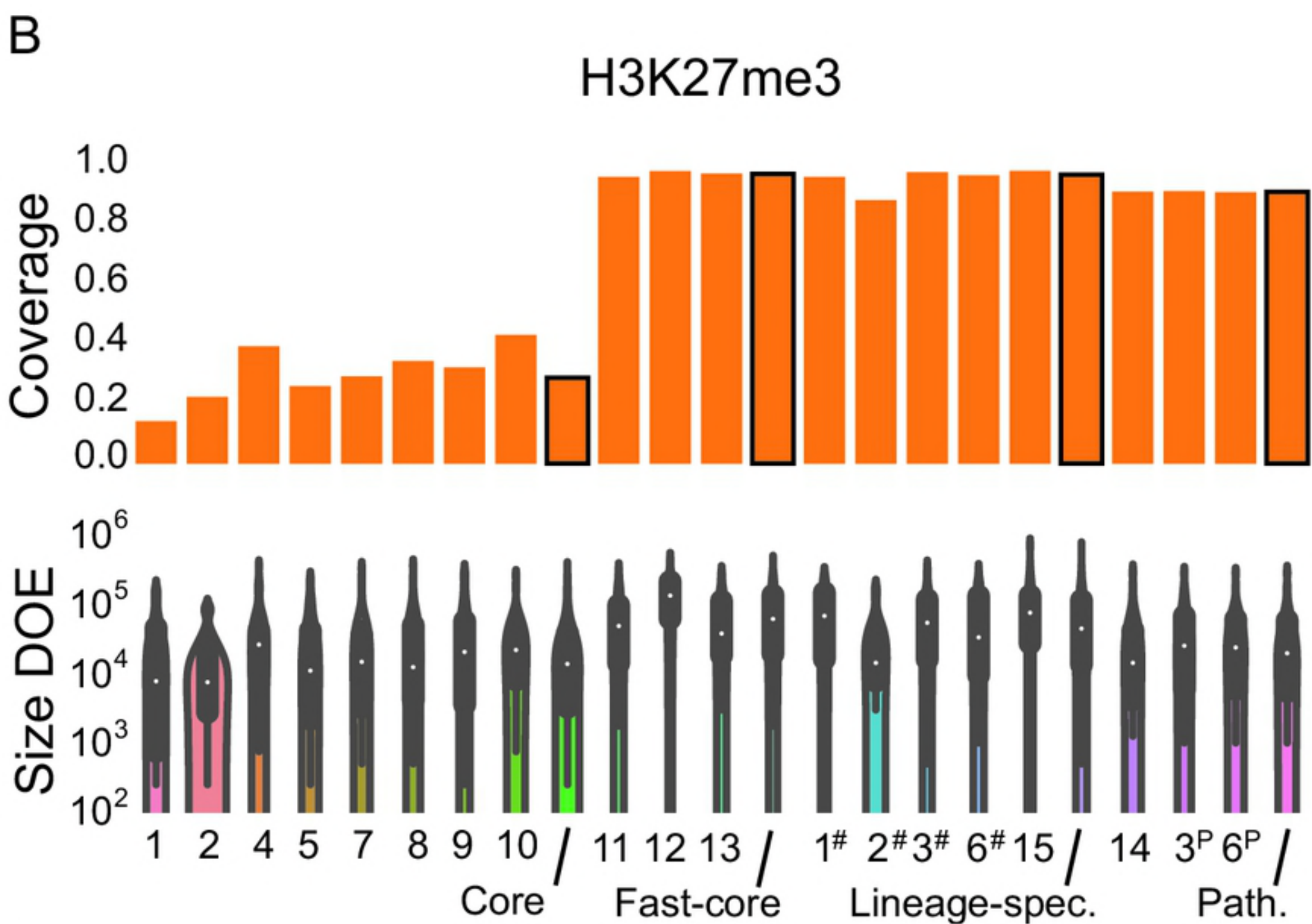
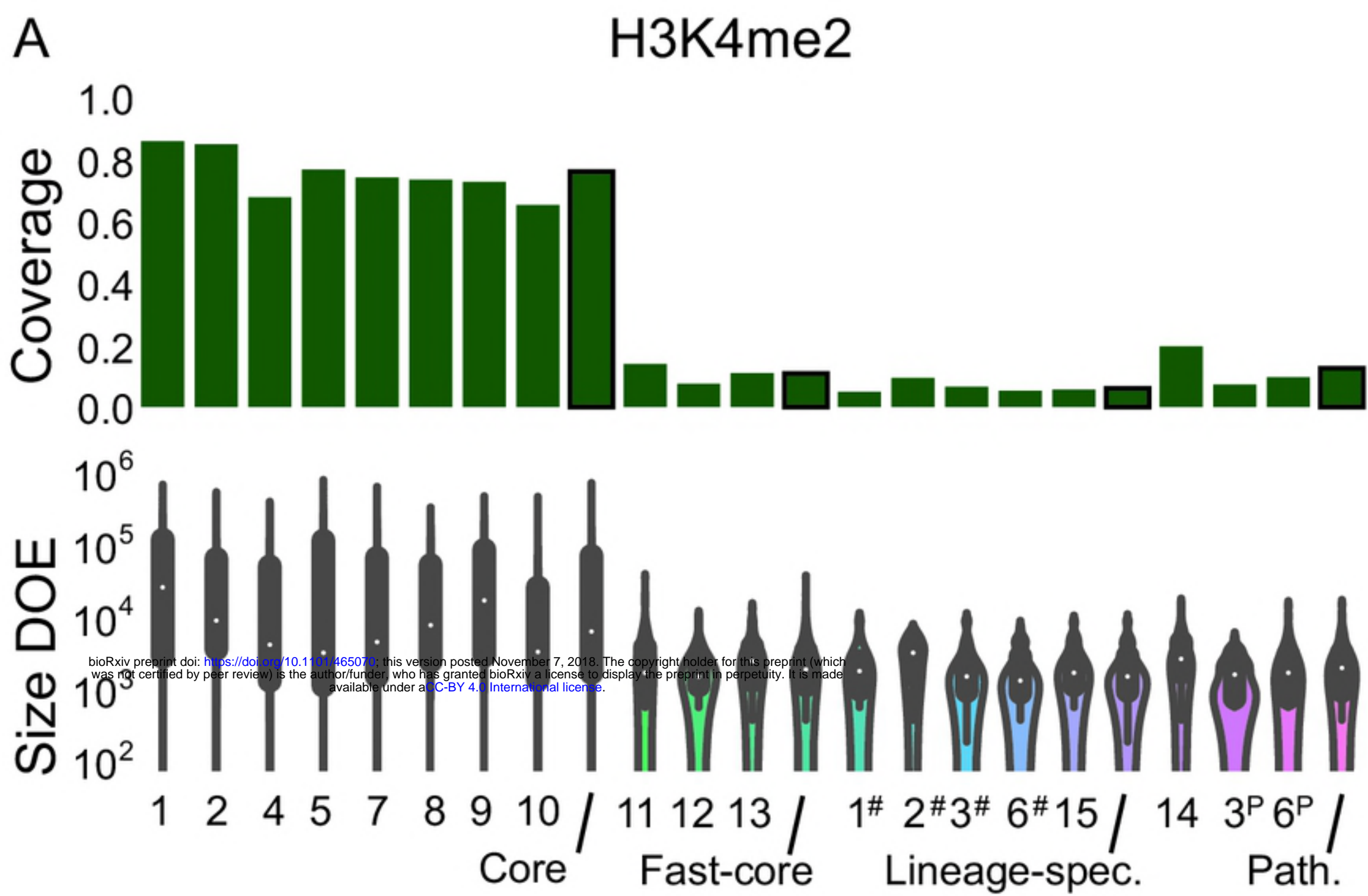
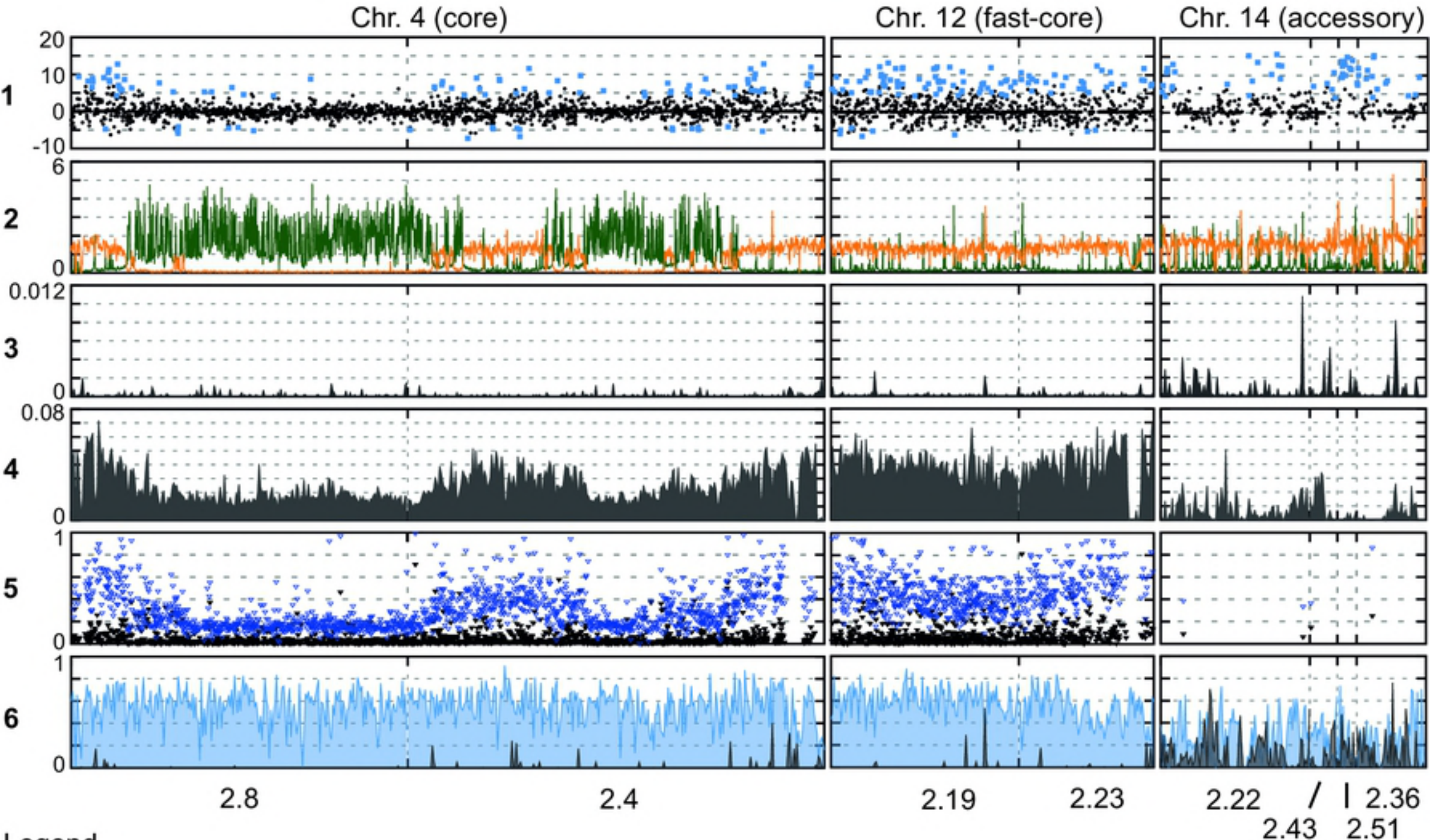


Figure 4



Legend

1 Log2 fold change in gene expression

- differentially expressed
- not differentially expressed

2 Normalized read densities ChIP-seq

- H3K4me2
- H3K27me3

3 SNPs short timescale

- number of SNPs in VCG030 / window size

4 SNPs intermediate timescale

- number of SNPs in Clade III / window size

5 Sequence divergence coding sequences

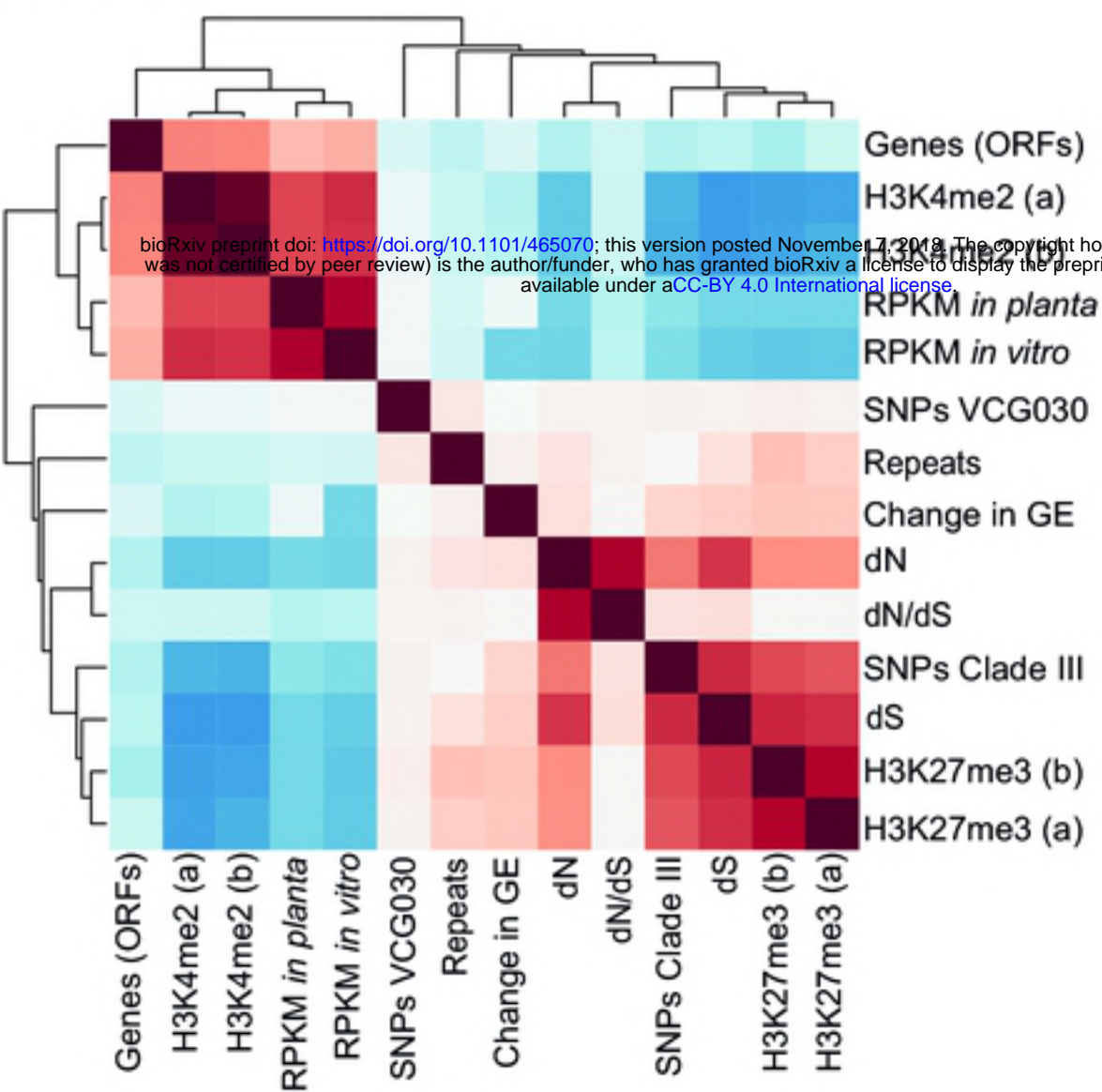
- ▽ synonymous substitutions: dS
- ▽ nonsynonymous substitutions: dN

6 Gene and repeat density

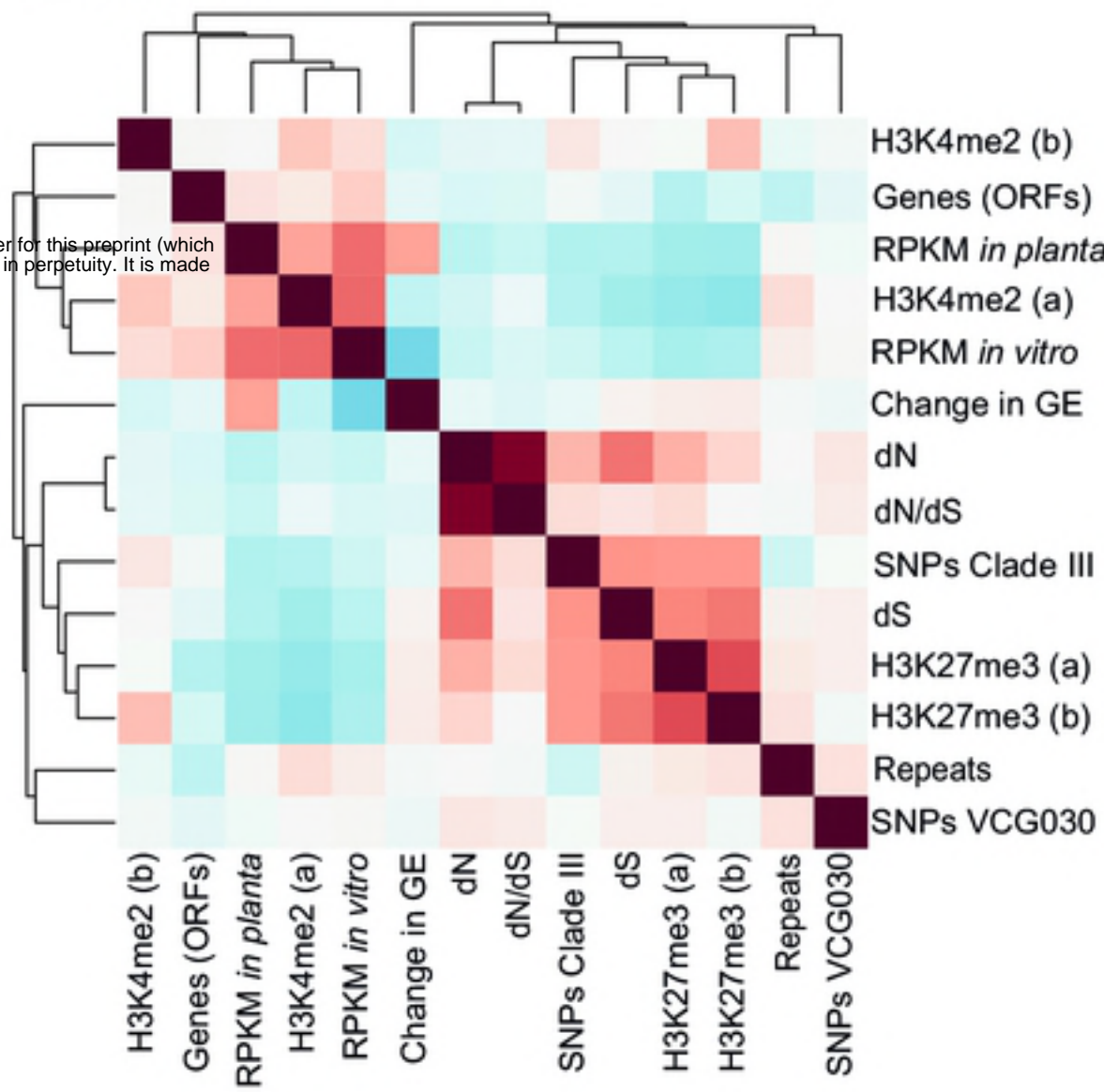
- Gene density
- Repeat density

Figure 5

A. Core



B. Fast-core



C. Accessory

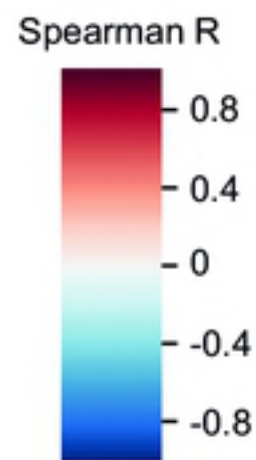
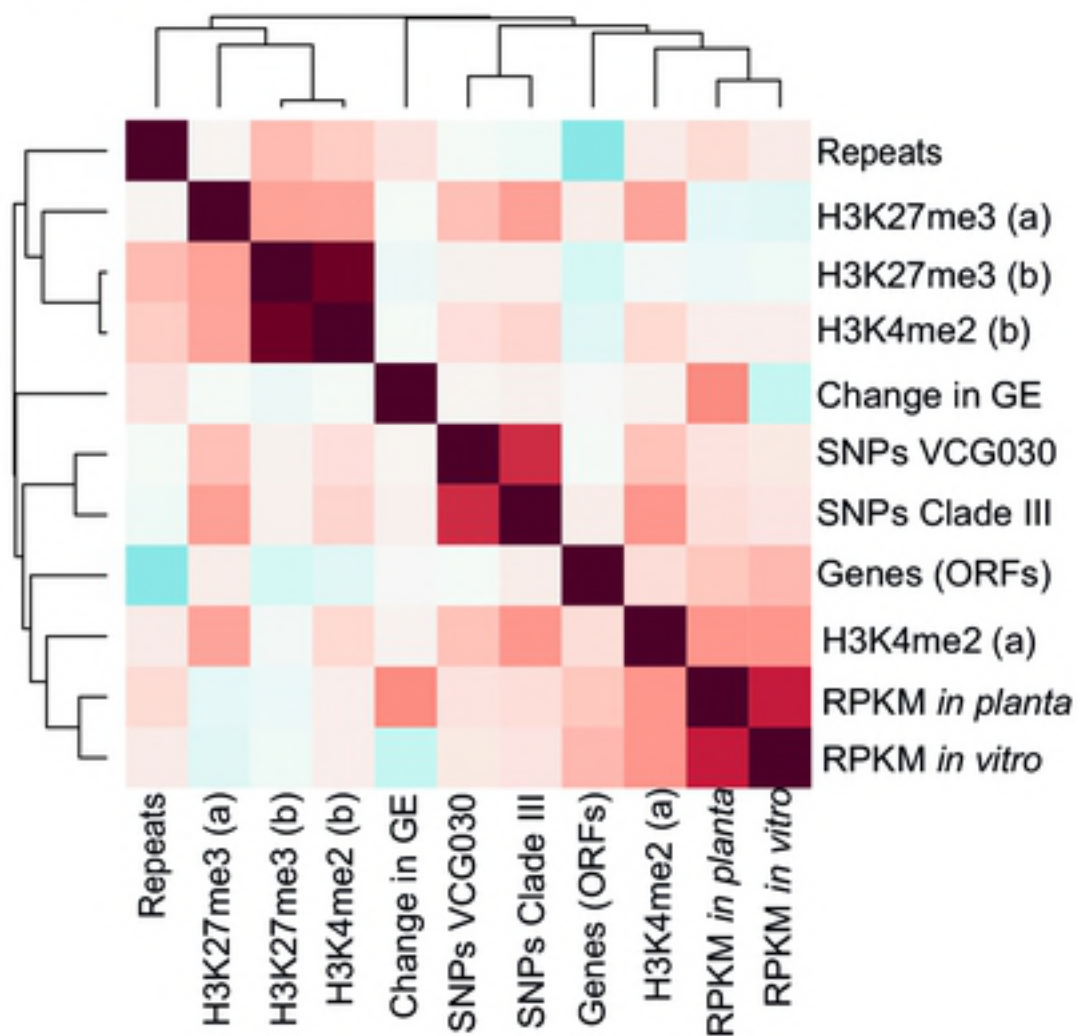


Figure 6