

# Pawel Rosikiewicz

lead researcher & Project Manager for 5 years

I created entire end-to-end system for production  
& identification of polyploid microorganisms

LABORATORY

MOLECULAR BIOLOGY  
& BIOINFORMATICS

VARIANT CALLING  
DATA ANALYSIS

MY ROLE



EXPERIMENT DESIGN



NGS SEQUENCING



MANAGED LAB TEAM



VARIANT CALLING

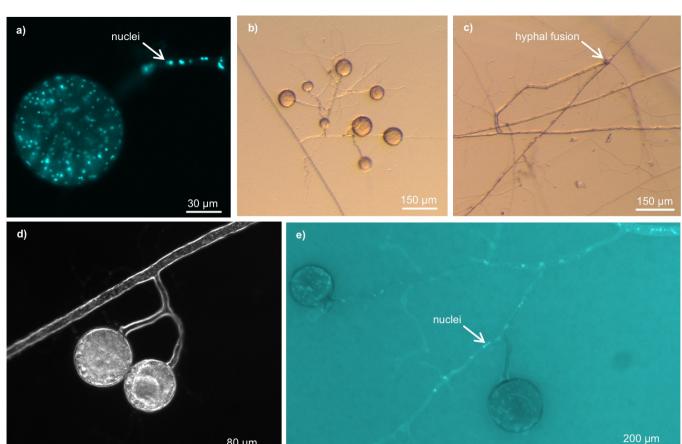


SNP DATA ANALYSIS



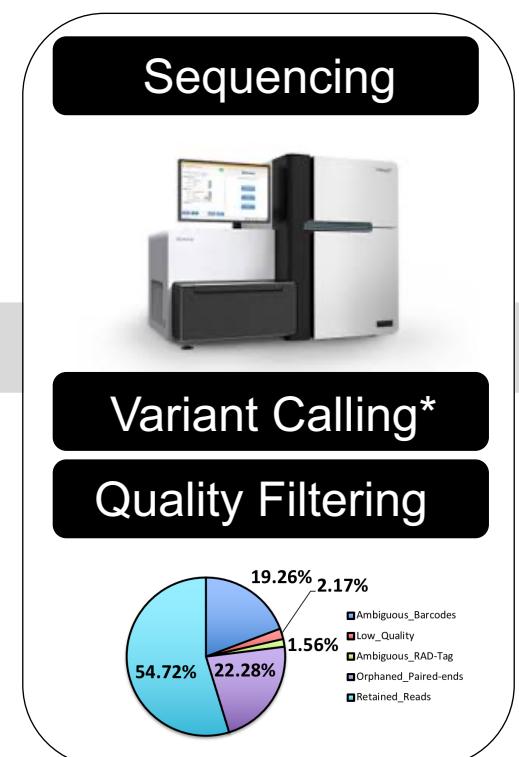
CUSTOM PIPELINES

MY PROJECT



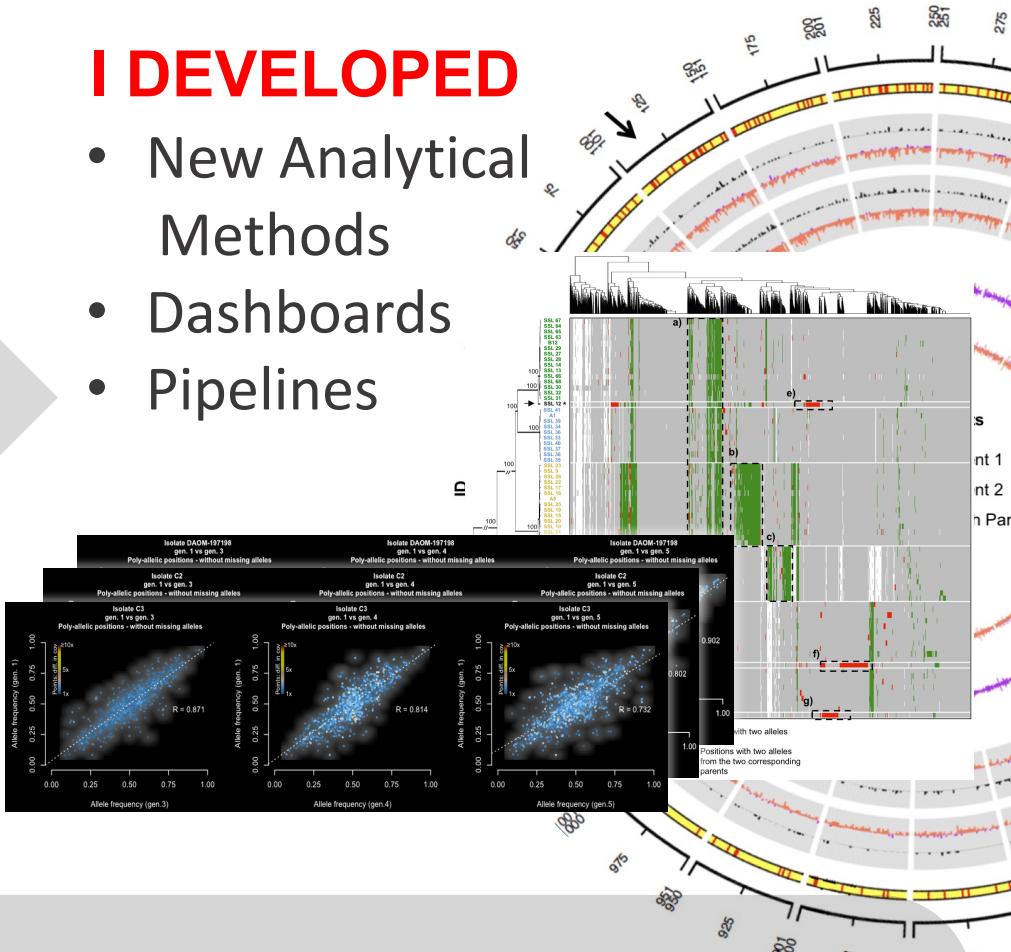
## MY MAIN EXPERIMENT

- Took 5 years
- >25.000 bio-samples
- 3TB of raw data



## I DEVELOPED

- New Analytical Methods
- Dashboards
- Pipelines



## PRODUCTS GENERATED WITH MY PROJECT

IMPACT

*IN VITRO*  
CULTURE SYSTEM

IMPLEMENTED IN  
INDUSTRY



<https://doi.org/10.1007/s00572-017-0763-2>

MY NGS PROTOCOL

USED OVER 6000x

60 NEW STRAINS  
OF MICROORGANISMS

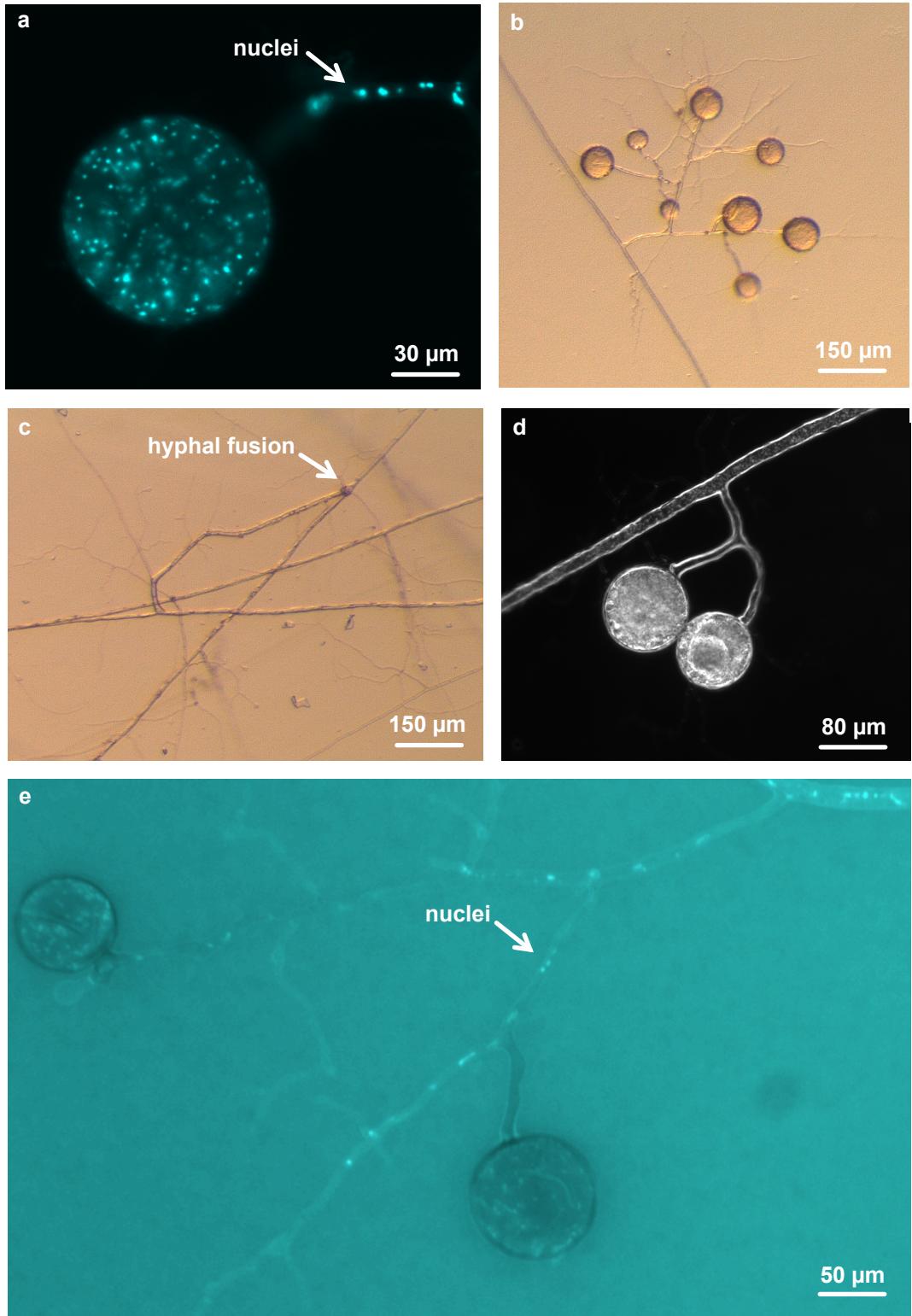
TESTED FOR USE IN  
AGRONOMY



<https://doi.org/10.1371/journal.pone.0226497>



<https://www.biorxiv.org/content/10.1101/830547v1>



**Figure 1**

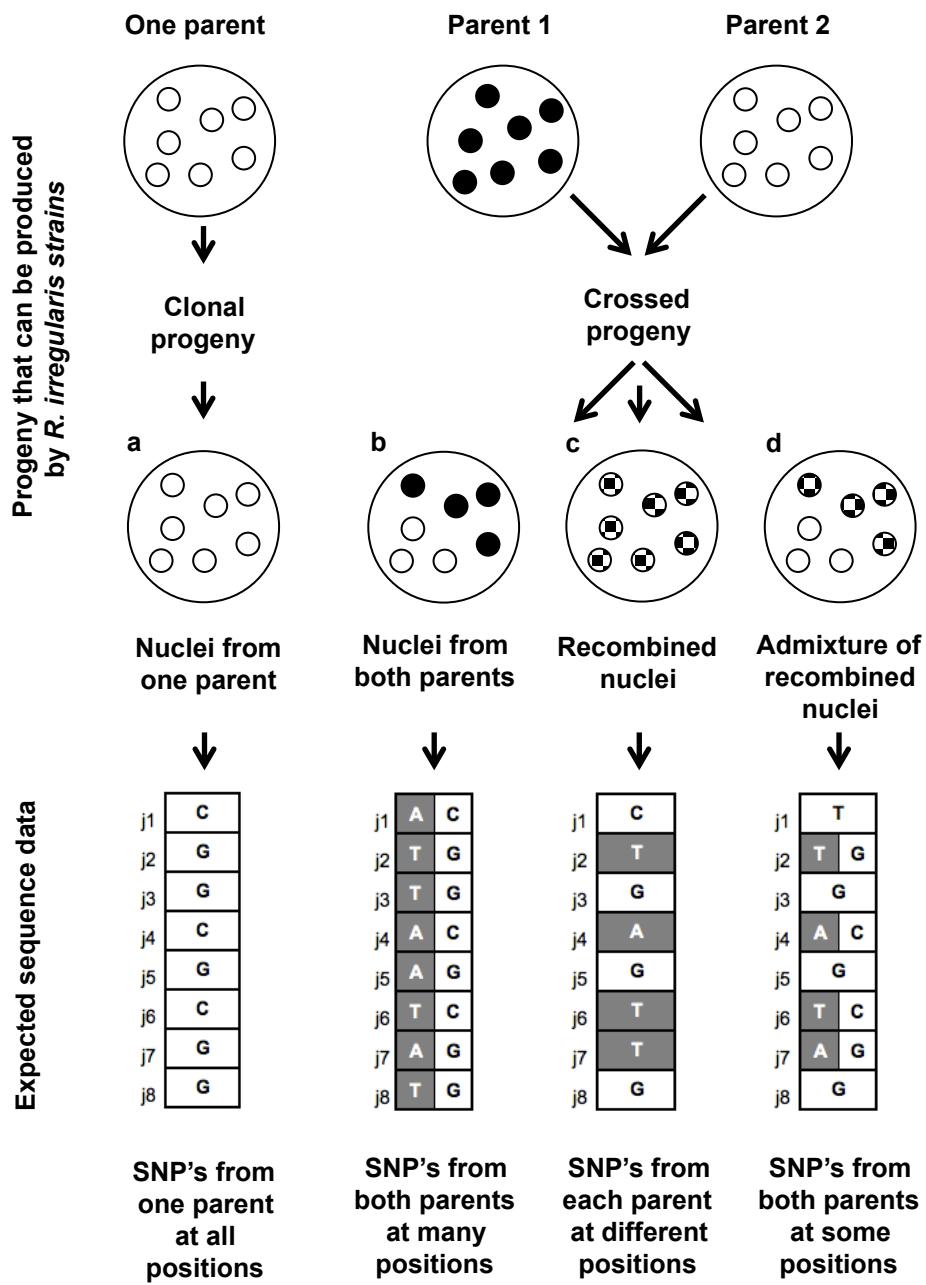


Figure 2

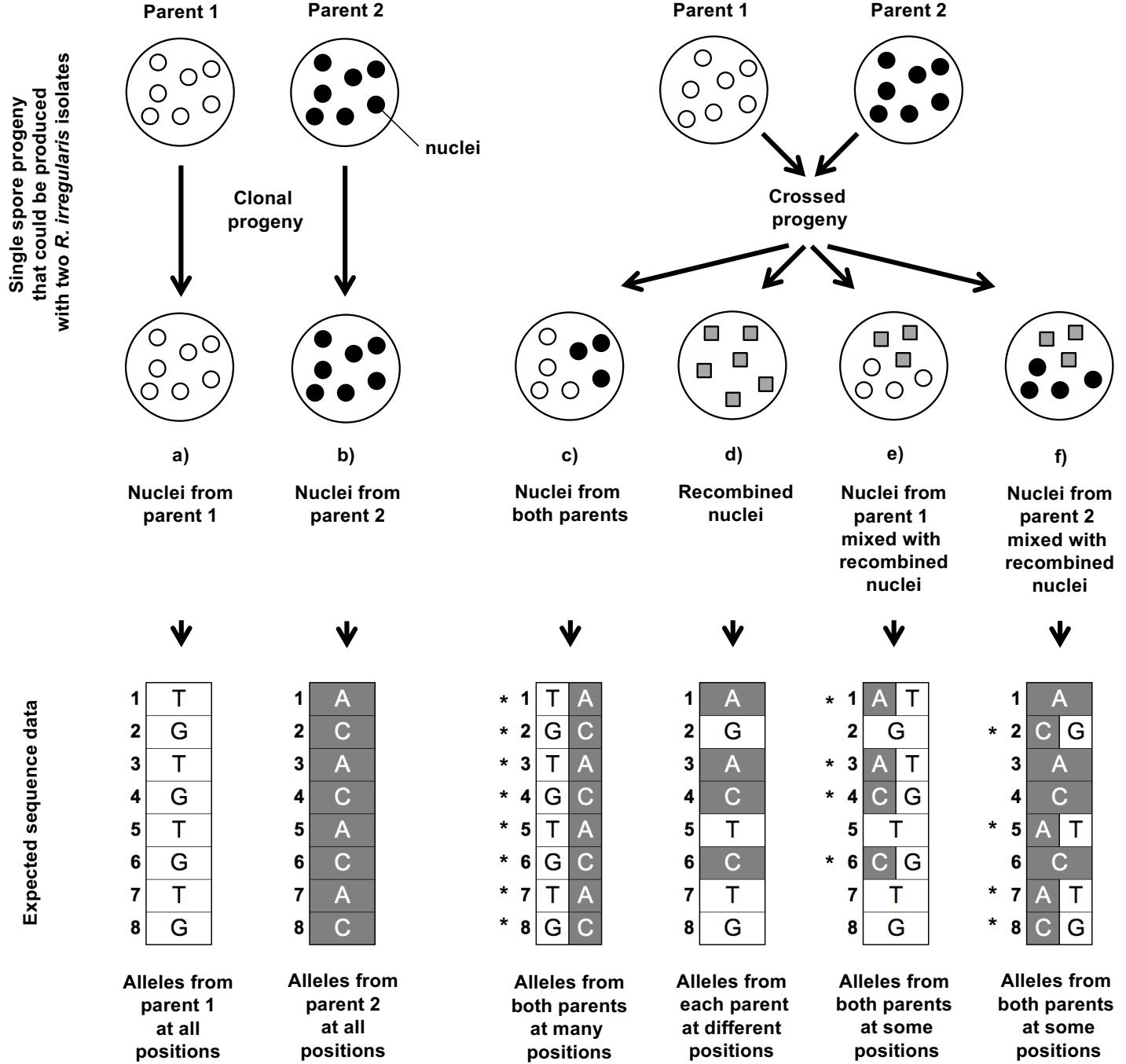


Fig.2

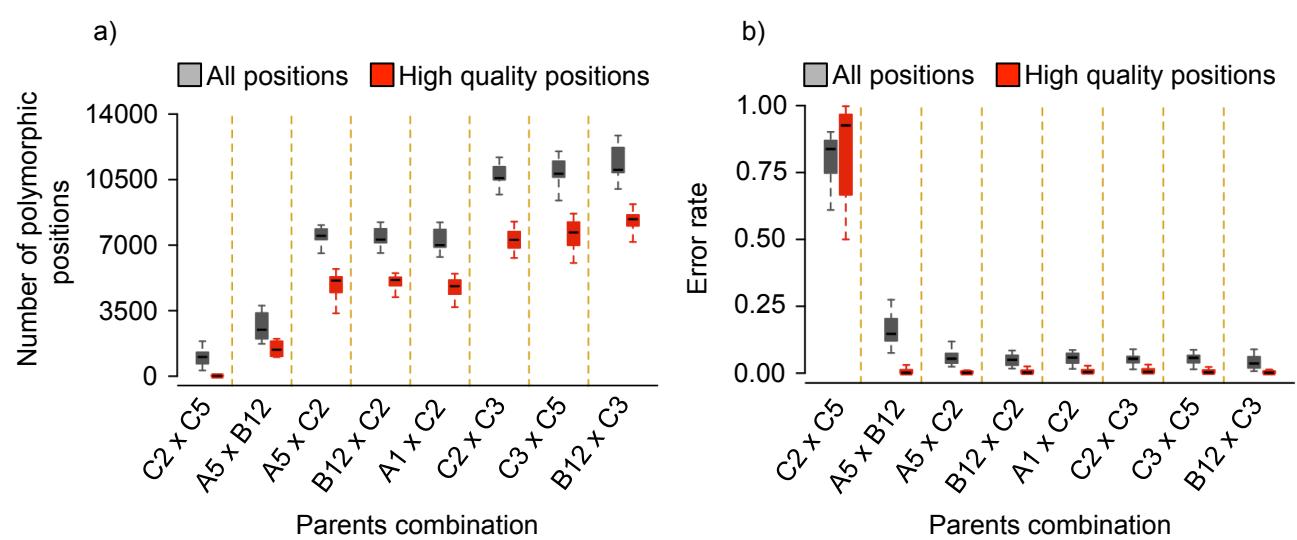
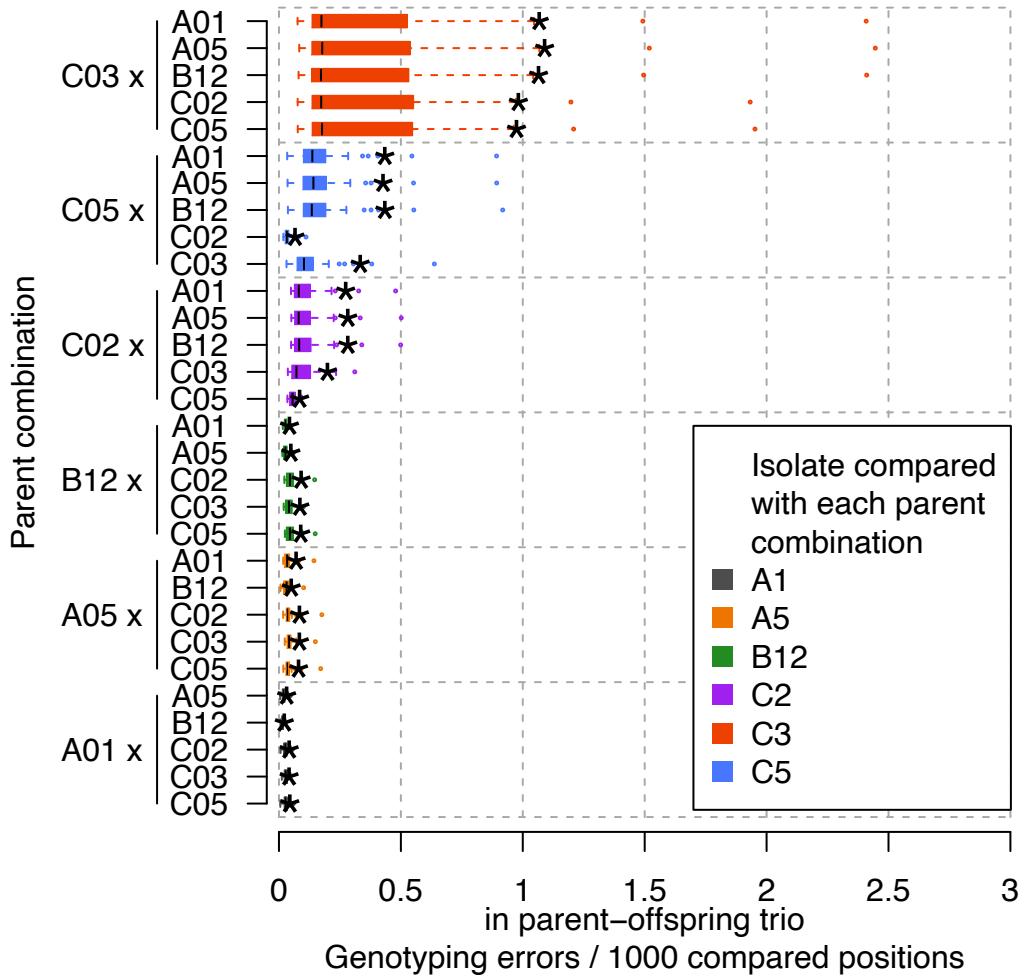
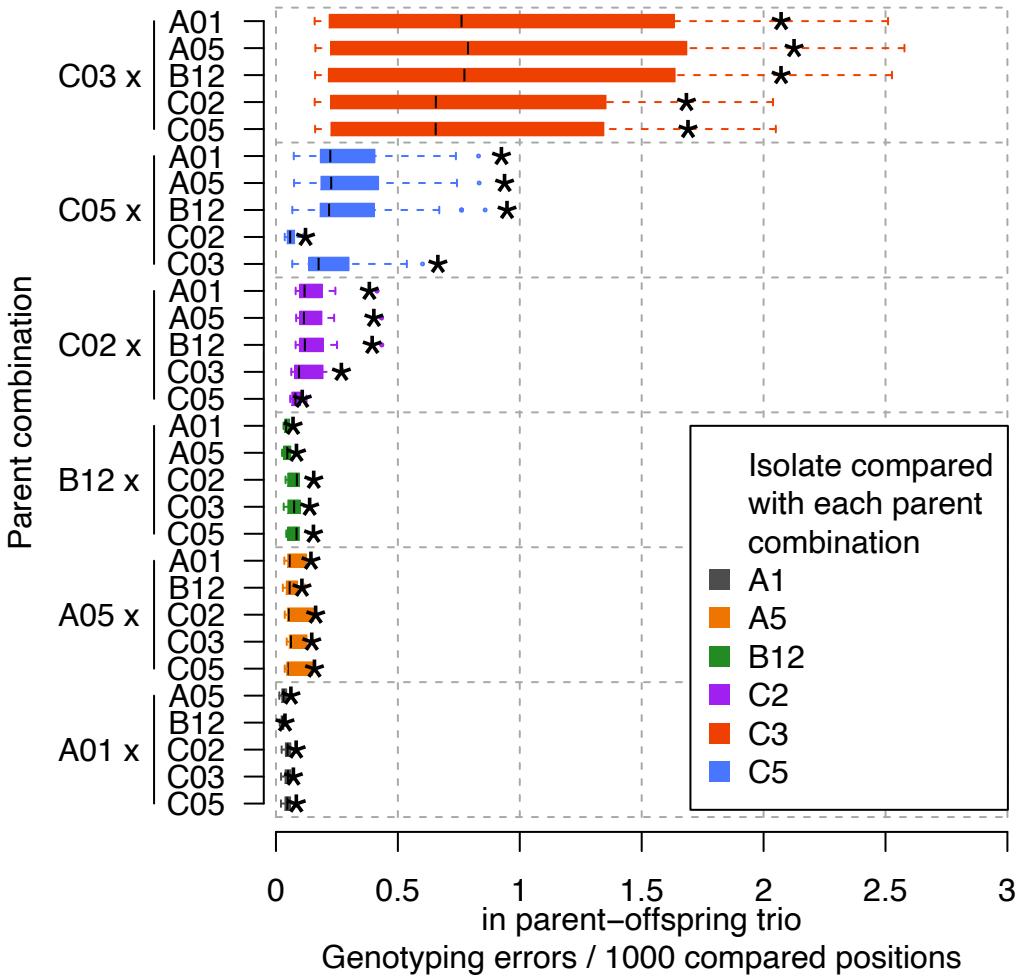


Figure 3





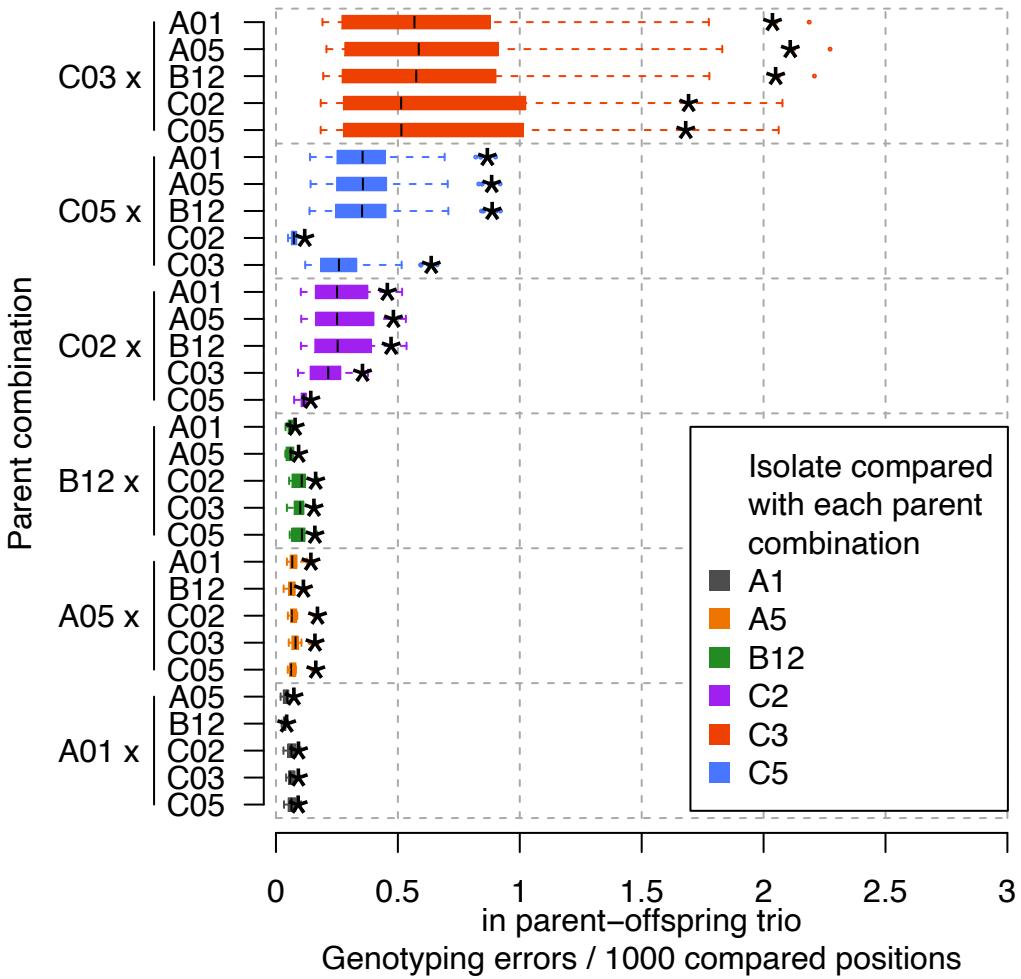
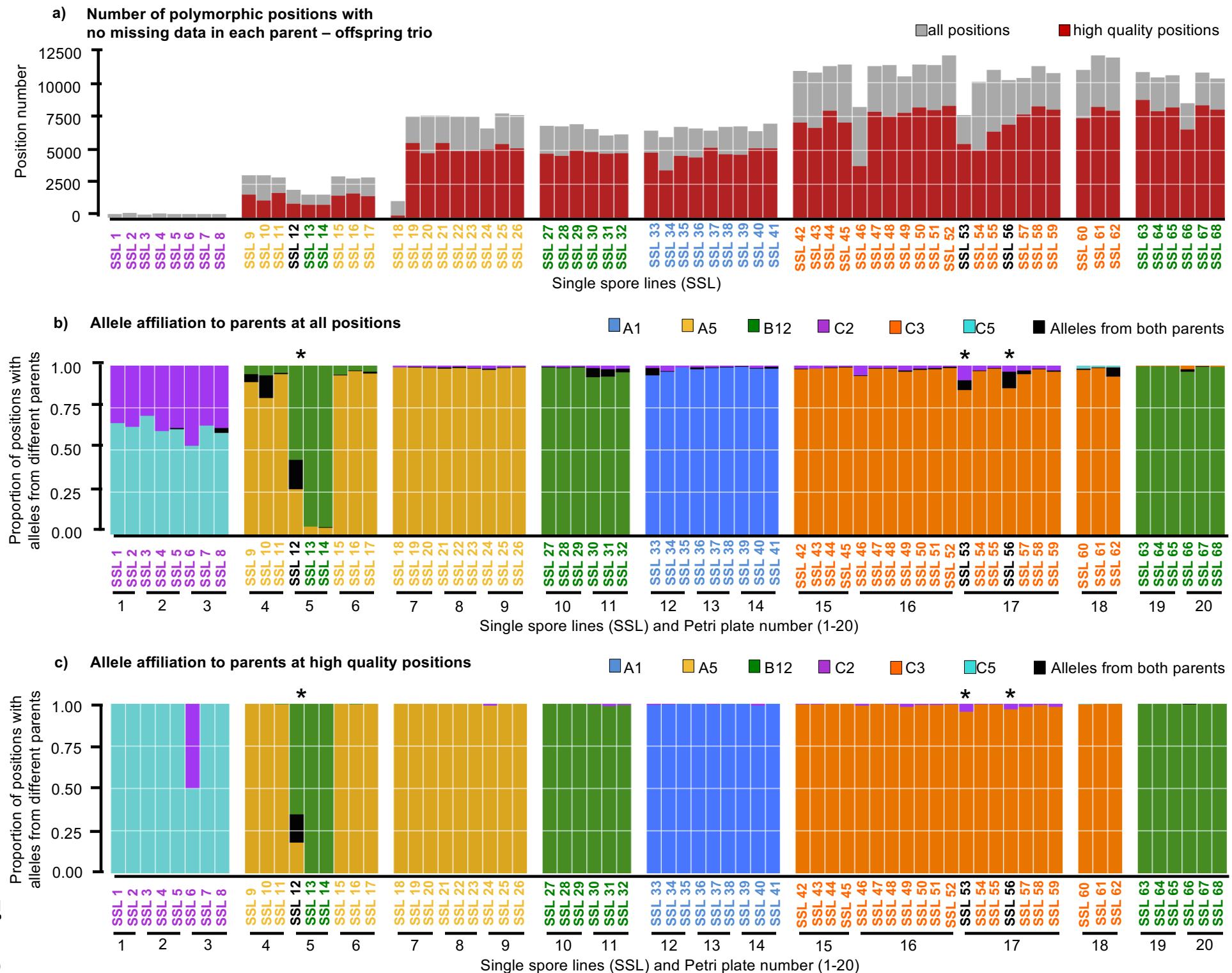
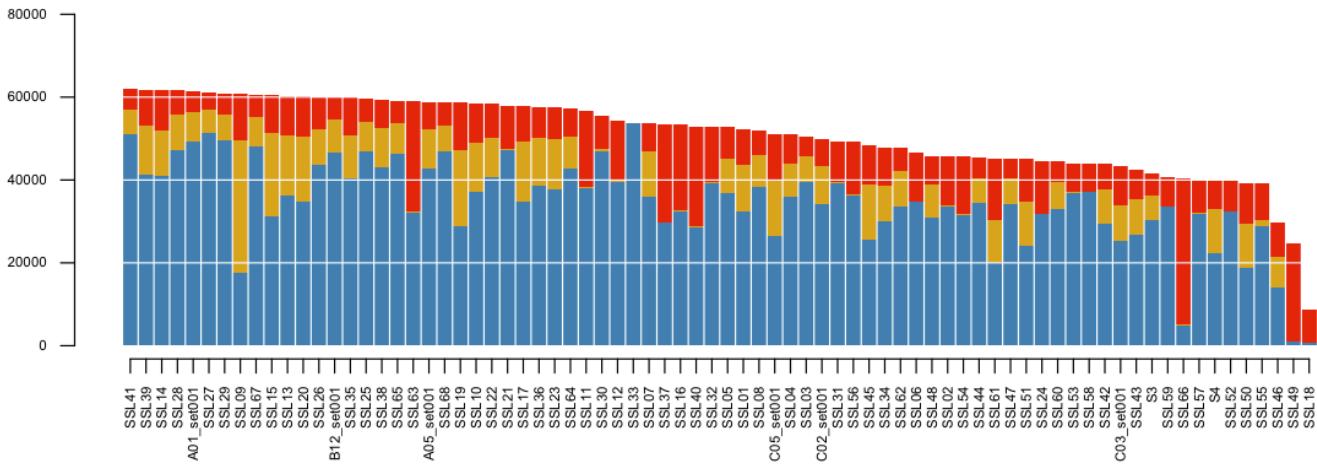


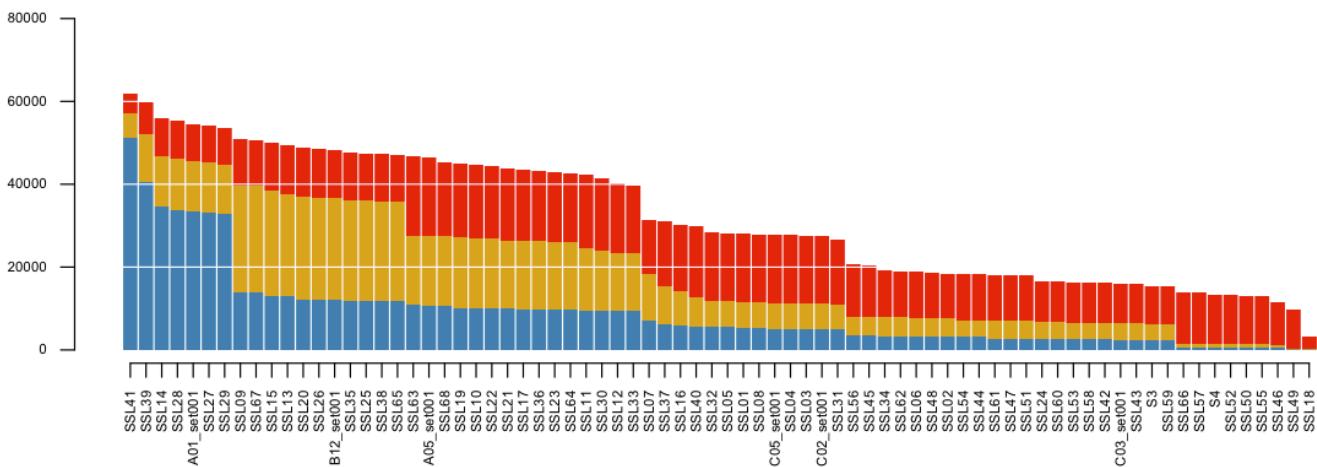
Fig. 4



**Par\_and\_CRL**



**Par\_and\_CRL**



Pentral Combination	Single spore Line	Single spore line classification	Number of positions with nucleotides from			Expected number of errors	P value		Pentral Combination	Single spore Line	Single spore line classification	Number of positions with nucleotides from			Expected number of errors	P value	
			p1	p1/p2	p2		p1	p2				p1	p1/p2	p2	p1	p2	
C2 x C5	SSL01	C2 / C5 cl	203	0	105	255 (=19)	-	-	C2 x C5	SSL01	C2 / C5 cl	1	0	0	1 (=0)	-	-
	SSL02	C2 / C5 cl	248	0	142	324 (=24)	-	-		SSL02	C2 / C5 cl	2	0	0	2 (=1)	-	-
	SSL03	C2 / C5 cl	195	0	82	230 (=17)	-	-		SSL03	C2 / C5 cl	2	0	0	2 (=1)	-	-
	SSL04	C2 / C5 cl	214	0	135	289 (=21)	-	-		SSL04	C2 / C5 cl	1	0	0	1 (=0)	-	-
	SSL05	C2 / C5 cl	186	2	110	247 (=18)	-	-		SSL05	C2 / C5 cl	2	0	0	2 (=1)	-	-
	SSL06	C2 / C5 cl	169	0	154	268 (=20)	-	-		SSL06	C2 / C5 cl	1	0	1	2 (=1)	-	-
	SSL07	C2 / C5 cl	188	0	103	241 (=18)	-	-		SSL07	C2 / C5 cl	2	0	0	2 (=1)	-	-
	SSL08	C2 / C5 cl	194	9	119	267 (=19)	-	-		SSL08	C2 / C5 cl	2	0	0	2 (=1)	-	-
A5 x B12	SSL09	A5 cl	2850	153	157	447 (=139)	-	***	A5 x B12	SSL09	A5 cl	1754	0	0	20 (=31)	-	***
	SSL10	A5 cl	2543	427	178	446 (=138)	-	***		SSL10	A5 cl	1317	0	1	15 (=23)	-	***
	SSL11	A5 cl	2862	20	127	426 (=132)	-	***		SSL11	A5 cl	1839	3	5	21 (=32)	-	***
	SSL12	Crossed line	555	363	1164	364 (=119)	***	***		SSL12	Crossed line	193	177	698	12 (=19)	***	***
	SSL13	B12 cl	79	1	1660	304 (=100)	***	-		SSL13	B12 cl	0	0	995	11 (=17)	***	-
	SSL14	B12 cl	68	5	1670	305 (=100)	***	-		SSL14	B12 cl	0	0	965	11 (=17)	***	-
	SSL15	A5 cl	2910	17	163	437 (=136)	-	***		SSL15	A5 cl	1659	0	1	19 (=29)	-	***
	SSL16	A5 cl	2839	12	82	415 (=129)	-	***		SSL16	A5 cl	1818	0	6	20 (=32)	-	***
	SSL17	A5 cl	2858	31	110	424 (=132)	-	***		SSL17	A5 cl	1617	0	0	18 (=28)	-	***
A5 x C2	SSL18	A5 cl	1251	0	13	59 (=18)	-	***	A5 x C2	SSL18	A5 cl	177	0	0	2 (=3)	-	***
	SSL19	A5 cl	7438	20	65	354 (=106)	-	***		SSL19	A5 cl	5529	0	2	19 (=30)	-	***
	SSL20	A5 cl	7472	27	79	356 (=106)	-	***		SSL20	A5 cl	4775	0	2	17 (=26)	-	***
	SSL21	A5 cl	7444	71	70	357 (=106)	-	***		SSL21	A5 cl	5535	0	3	19 (=30)	-	***
	SSL22	A5 cl	7447	34	64	355 (=106)	-	***		SSL22	A5 cl	4946	0	0	17 (=27)	-	***
	SSL23	A5 cl	7332	43	95	351 (=105)	-	***		SSL23	A5 cl	4958	0	0	17 (=27)	-	***
	SSL24	A5 cl	6448	61	112	311 (=93)	-	***		SSL24	A5 cl	5017	1	55	18 (=28)	-	***
	SSL25	A5 cl	7635	26	73	364 (=109)	-	***		SSL25	A5 cl	5450	0	0	19 (=30)	-	***
B12 x C2	SSL26	A5 cl	7529	24	57	358 (=107)	-	***	B12 x C2	SSL26	A5 cl	5139	0	0	18 (=28)	-	***
	SSL27	B12 cl	6734	26	54	268 (=98)	-	***		SSL27	B12 cl	4763	0	3	10 (=17)	-	***
	SSL28	B12 cl	6693	24	64	266 (=97)	-	***		SSL28	B12 cl	4609	0	2	10 (=16)	-	***
	SSL29	B12 cl	6858	21	41	272 (=99)	-	***		SSL29	B12 cl	4985	0	0	11 (=17)	-	***
	SSL30	B12 cl	6130	365	99	259 (=95)	-	***		SSL30	B12 cl	4867	1	20	11 (=17)	-	***
	SSL31	B12 cl	5697	254	134	239 (=87)	-	***		SSL31	B12 cl	4678	0	67	10 (=17)	-	***
	SSL32	B12 cl	5945	151	101	243 (=89)	-	***		SSL32	B12 cl	4776	2	30	10 (=17)	-	***
A1 x C2	SSL33	A1 cl	6098	281	85	339 (=120)	-	***	A1 x C2	SSL33	A1 cl	4806	0	33	37 (=60)	-	***
	SSL34	A1 cl	5781	20	187	314 (=112)	-	***		SSL34	A1 cl	3530	0	7	27 (=44)	-	***
	SSL35	A1 cl	6659	11	67	354 (=125)	-	***		SSL35	A1 cl	4584	0	5	35 (=57)	-	***
	SSL36	A1 cl	6482	63	79	348 (=123)	-	***		SSL36	A1 cl	4456	0	5	34 (=55)	-	***
	SSL37	A1 cl	6375	18	70	339 (=120)	-	***		SSL37	A1 cl	5170	0	24	39 (=64)	-	***
	SSL38	A1 cl	6676	24	36	354 (=125)	-	***		SSL38	A1 cl	4721	0	6	36 (=58)	-	***
	SSL39	A1 cl	6746	9	35	357 (=126)	-	***		SSL39	A1 cl	4665	0	0	35 (=58)	-	***
	SSL40	A1 cl	6318	10	103	338 (=120)	-	***		SSL40	A1 cl	5094	0	55	39 (=64)	-	***
C2 x C3	SSL41	A1 cl	6841	66	53	365 (=130)	-	***	C2 x C3	SSL41	A1 cl	5156	0	0	39 (=64)	-	***
	SSL42	C3 cl	196	58	10620	708 (=190)	***	-		SSL42	C3 cl	25	0	0	100 (=128)	***	***
	SSL43	C3 cl	182	27	10531	700 (=187)	***	-		SSL43	C3 cl	16	0	6633	94 (=120)	***	-
	SSL44	C3 cl	132	44	11041	731 (=196)	***	-		SSL44	C3 cl	11	0	7905	112 (=143)	***	-
	SSL45	C3 cl	97	35	11211	739 (=198)	***	-		SSL45	C3 cl	10	0	7027	100 (=127)	***	-
	SSL46	C3 cl	470	19	7707	534 (=143)	***	-		SSL46	C3 cl	47	0	3807	55 (=70)	***	-
	SSL47	C3 cl	167	43	10992	730 (=195)	***	-		SSL47	C3 cl	12	0	7838	111 (=142)	***	-
	SSL48	C3 cl	155	45	11091	736 (=197)	***	-		SSL48	C3 cl	18	0	7509	107 (=136)	***	-
C2 x C3	SSL49	Crossed line	654	460	6485	495 (=133)	***	***	C2 x C3	SSL49	Crossed line	493	9	5221	81 (=104)	***	***
	SSL50	C3 cl	308	35	9722	656 (=176)	***	-		SSL50	C3 cl	20	0	4973	71 (=90)	***	-
	SSL51	C3 cl	167	32	10743	713 (=191)	***	-		SSL51	C3 cl	22	0	6356	90 (=115)	***	-
	SSL52	C3 cl	309	53	10086	681 (=182)	***	-		SSL52	C3 cl	146	0	7633	110 (=141)	***	-
	SSL53	C3 cl	188	108	11045	739 (=198)	***	-		SSL53	C3 cl	51	0	8128	116 (=148)	***	-
	SSL54	C3 cl	156	88	11036	735 (=197)	***	-		SSL54	C3 cl	45	0	7936	113 (=144)	***	-
	SSL55	Crossed line	381	974	8849	665 (=178)	***	***		SSL55	Crossed line	213	1	6672	98 (=125)	***	*
	SSL56	C3 cl	103	88	11834	783 (=210)	***	-		SSL56	C3 cl	16	0	8275	118 (=150)	***	-
C3 x C5	SSL57	C3 cl	294	245	9793	673 (=180)	***	-	C3 x C5	SSL57	C3 cl	141	1	7524	109 (=139)	***	-
	SSL58	C3 cl	203	53	10979	732 (=196)	***	-		SSL58	C3 cl	62	0	8166	117 (=149)	***	-
	SSL59	C3 cl	308	87	10292	696 (=186)	***	-		SSL59	C3 cl	142	0	7859	113 (=145)	***	-
	S3	C3 cl	345	107	9174	627 (=168)	***	-		S3	C3 cl	14	0	6060	86 (=110)	***	-
	S4	C2 cl	8094	350	279	633 (=170)	-	***		S4	C2 cl	5120	0	14	35 (=43)	-	***
	SSL60	C3 cl	10677	51	211	697 (=185)	-	***		SSL60	C3 cl	7338	0	18	101 (=129)	-	***
	SSL61	C3 cl	11825	65	113	765 (=202)	-	***		SSL61	C3 cl	8215	0	7	113 (=145)	-	***
	SSL62	C3 cl	11096	632	121	755 (=200)	-	***		SSL62	C3 cl	7906	0	11	108 (=139)	-	***
B12 x C3	SSL63	B12 cl	10737	12	28	226 (=88)	-	***	B12 x C3	SSL63	B12 cl	8703	0	1	9 (=16)	-	***
	SSL64	B12 cl	10341	16	38	218 (=85)	-	***		SSL64	B12 cl	7902	0	1	8 (=15)	-	***
	SSL65	B12 cl	10514	8	32	222 (=87)	-	***		SSL65	B12 cl	8171	0	1	9 (=15)	-	***
	SSL66	B12 cl	8203	105	189	179 (=70)	-	***		SSL66	Crossed line	6945	4	125	9 (=15)	***	***
	SSL67	B12 cl	10655	42	38	226 (=88)	-	***		SSL67	B12 cl	8314	0	0	9 (=16)	-	***
	SSL68	B12 cl	10222	12	68	216 (=85)	-	***		SSL68	B12 cl	7986	0	2	8 (=15)	-	***

### Legend

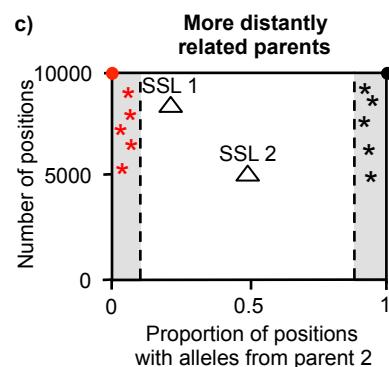
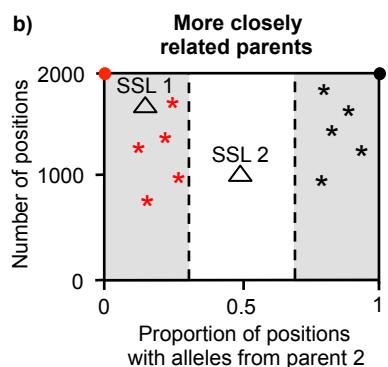
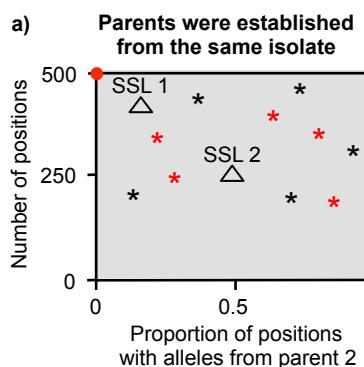
- Parent 1 - reference consensus
- \* Parent 1 – consensus built from test replicates of parent 1

- Parent 2 - reference consensus
- \* Parent 2 - consensus built from test replicates of parent 2

△ Single spore line (SSL)

--- Sensitivity limit:  
the proportion of alleles from the other parent that is sufficient in order to classify SSL as crossed line

### All positions in each consensus (a-c)



### High quality positions in each consensus (d-f)

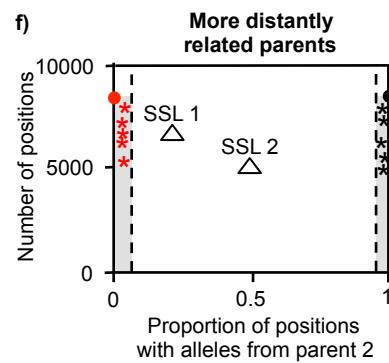
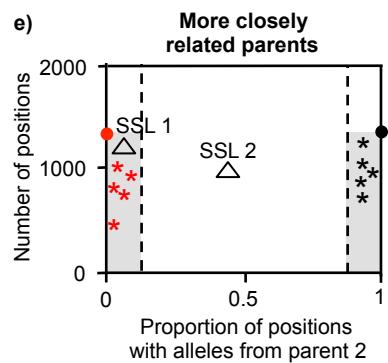
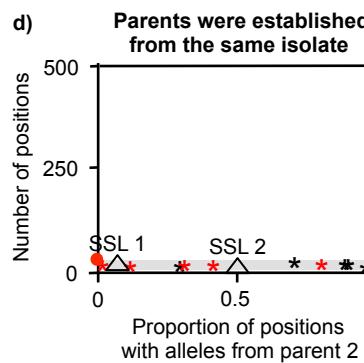


Fig. S3

```

> var.mat[which(var.mat[,2]=="p.11g"),]  gen 1    gen 2    gen 3    gen 4    gen 5
   m      m      com m      var      m
738  ." "p.11g" ." "-" ." "A/G" ." "z; -; -; A" ";- A; A; A; A; A" ";-; -; -; -; A; -" ";- G; -; -; -; -" ";- A; -; -; -; -
16521 ." "p.11g" ." "-" ." "G/T" ." "-; G; -; -" "G; -; -; -; -; -" "-; G; -; G; -; G" "-; T; -; T; -" "-; -; G; -; -;
25040 ." "p.11g" ." "-" ." "A/G" ." "-; -; -; G" "-; G; -; -; G; G" "-; -; -; G; G; -" "-; -; -; A; -" "-; -; -; A; -;
26071 ." "p.11g" ." "-" ." "A/G" ." "-; -; -; G" "-; G; -; G; -" "-; -; -; G; -" "G; -; -; -; -" "-; -; A; -" "-; -; A; -;
39010 ." "p.11g" ." "-" ." "C/T" ." "-; T; -; T" "-; T; T; T; T; T" "-; T; -; T; T; -" "T; -; -; -; -" "-; -; -; C; -;
55111 ." "p.11g" ." "-" ." "A/G" ." "z; A; A; -" "-; G; -; -; -; -" "-; -; A; -; -; -" "-; A; -; -; A; -" "A; -; -; -; -
55112 ." "p.11g" ." "-" ." "C/T" ." "z; C; C; -" "-; T; -; -; -; -" "-; -; C; -; -; -" "-; C; -; -; C; -" "C; -; -; -; -
55114 ." "p.11g" ." "-" ." "A/G" ." "z; G; G; -" "-; A; -; -; -; -" "-; -; G; -; -; -" "-; G; -; -; G; -" "G; -; -; -; -
68895 ." "p.11g" ." "-" ." "A/G" ." "-; -; G; -" "-; A; -; -; -; -" "G; -; G; -; G; -" "-; G; -; G; -; G" "-; G; G; G; -; G
96668 ." "p.11g" ." "-" ." "A/G" ." "-; G; -; -" "-; A; -; -; -; A" "A; -; -; A; -; A" "-; A; A; A; A; A" "A; A; A; A; A; A"
96672 ." "p.11g" ." "-" ." "A/G" ." "-; G; -; -" "-; A; -; -; -; A" "A; -; A; A; -; A" "-; A; A; A; A; A" "A; A; A; A; A; A"
96675 ." "p.11g" ." "-" ." "C/T" ." "-; C; -; -" "-; T; -; T; -; T" "T; -; T; T; -; T" "-; T; T; T; T; T" "T; T; T; T; T; T"
96676 ." "p.11g" ." "-" ." "C/T" ." "-; T; -; -" "-; C; -; C; -; C" "C; C; C; C; -; C" "-; C; C; C; C; C" "C; C; C; C; C; C"
103772 ." "p.11g" ." "-" ." "C/T" ." "C; C; C; C" "C; C; C; C; C; C" "C; C; C; -; C; C" "T; T; -; T; T; T" "T; T; -; T; T; T"
103776 ." "p.11g" ." "-" ." "A/C" ." "C; C; -; -" "-; C; -; C; -; -" "-; C; C; -; C; C" "A; A; -; A; A; A" "A; A; -; A; A; A"
> var.mat[which(var.mat[,2]=="p.21a"),]

```

## Coding

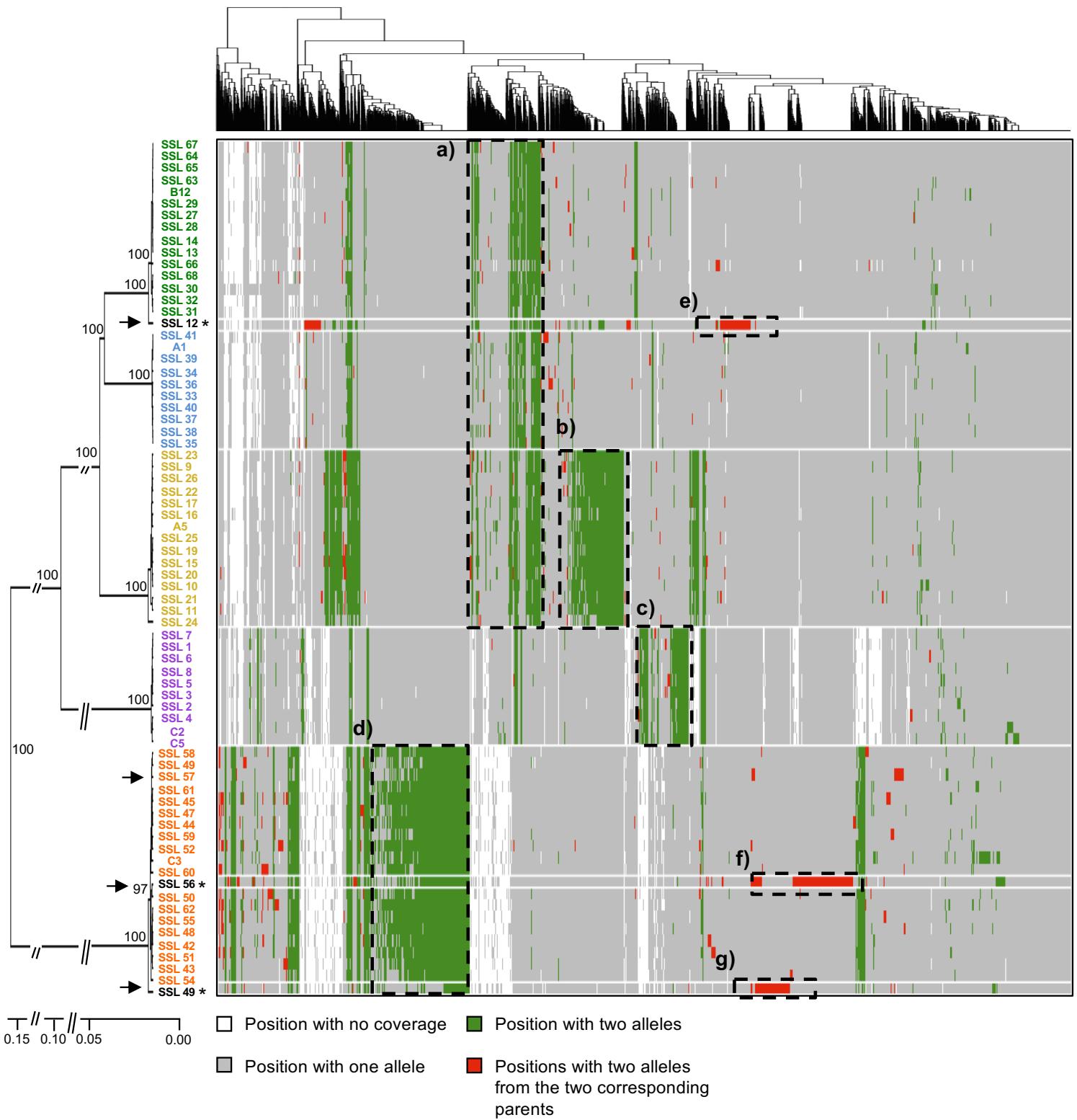
```

> var.mat[which(var.mat[,2]=="p.21g"),]
   m     m    com m    var   m
9853  ." "p.21g" ." "-" ." "A/G" ." "G; G; -; -" "G; -; G; -; -; -" "G; G; G; G; G; G" "A; A; A; A; A; A" "A; A; -; A; -; A"
13077  ." "p.21g" ." "-" ." "A/T" ." "-; -; A; -" "A; A; A; A; A; -" "A; -; -; -; -; -" "T; T; -; T; -; T" "T; T; -; T; T; T"
14664  ." "p.21g" ." "-" ." "C/T" ." "-; -; z; T" "-; T; T; T; T; T" "-; T; -; T; -; T" "-; C; -; -; -; -" "-; -; -; C; -; -
15340  ." "p.21g" ." "-" ." "A/G" ." "-; -; -; G" "-; G; G; G; G; G" "-; G; -; G; G; G" "-; -; G; -; -; -" "-; -; A; -; -
23285  ." "p.21g" ." "-" ." "A/T" ." "-; A; A; A;" "A; -; A; -; A; -" "-; -; A; A; -; -" "-; T; -; -; -; -" "A; -; -; -; A; -"
42562  ." "p.21g" ." "-" ." "C/T" ." "-; -; -; T" "-; T; T; T; T; T" "-; T; -; T; -; T" "-; -; -; -; -; T" "C; -; -; -; -
42563  ." "p.21g" ." "-" ." "C/T" ." "-; -; -; T" "-; T; T; T; T; T" "-; T; -; T; -; T" "-; -; -; -; -; T" "C; -; -; -; -
52827  ." "p.21g" ." "-" ." "A/C" ." "z; -; -; C" "-; C; -; -; -; -" "-; -; -; C; -; -" "-; -; -; -; -; C" "-; -; -; A; -; -
52828  ." "p.21g" ." "-" ." "C/T" ." "z; -; -; C" "-; C; -; -; -; -" "-; -; -; C; -; -" "-; -; -; -; -; C" "-; -; -; T; -; -
63714  ." "p.21g" ." "-" ." "G/T" ." "-; G; G; G" "G; G; G; G; G; G" "-; -; -; G; G; G" "-; -; -; G; -; G" "-; -; -; -; T;
69110  ." "p.21g" ." "-" ." "A/T" ." "z; -; -; T" "-; T; T; -; -; T" "-; T; -; T; -; -" "T; -; -; T; -; -" "A; -; A; -; -
69113  ." "p.21g" ." "-" ." "C/T" ." "z; -; -; T" "-; T; T; -; -; T" "-; T; -; T; -; -" "T; -; -; T; -; -" "-; -; C; -; -
73451  ." "p.21g" ." "-" ." "A/G" ." "-; A; -; A;" "-; A; A; A; A; A" "-; A; -; A; -; -" "A; -; -; -; -; -" "-; -; -; -; G;
86008  ." "p.21g" ." "-" ." "C/T" ." "-; -; -; C" "-; C; C; C; C; C" "C; C; -; C; C; C" "C; -; C; -; C; C" "-; -; T; -; -
86009  ." "p.21g" ." "-" ." "A/G" ." "-; -; -; A" "-; A; A; A; A; A" "A; A; -; A; A; A" "A; -; A; -; A; A" "-; -; G; -; -
93810  ." "p.21g" ." "-" ." "C/T" ." "-; -; -; C" "T; T; -; -; -; T" "-; -; T; T; -; -" "-; -; -; T; -; T" "T; -; T; -; -
93811  ." "p.21g" ." "-" ." "G/T" ." "-; -; -; T" "G; G; -; -; -; G" "-; -; G; G; -; -" "-; -; -; G; -; G" "G; -; G; -; -
94164  ." "p.21g" ." "-" ." "A/G" ." "A; A; A; A;" "-; -; -; A; -; -" "A; -; A; -; -; -" "G; -; -; G; G; G" "-; -; A; A; -;
94165  ." "p.21g" ." "-" ." "C/T" ." "T; T; T; T" "T; -; -; T; -; -" "T; -; T; -; -; -" "C; -; -; C; C; C" "-; -; T; T; -;
94166  ." "p.21g" ." "-" ." "C/T" ." "-; T; T; T" "T; -; -; T; -; -" "T; -; T; -; -; -" "C; -; -; C; C; C" "-; -; T; T; -;
94167  ." "p.21g" ." "-" ." "C/T" ." "-; T; T; T" "T; -; -; T; -; -" "T; -; T; -; -; -" "C; -; -; C; C; C" "-; -; T; T; -;
95769  ." "p.21g" ." "-" ." "C/T" ." "-; -; C; C" "-; C; C; -; C; -" "C; -; C; -; C; -" "-; -; -; -; -; T" "-; -; -; C; C; -
104613  ." "p.21g" ." "-" ." "G/T" ." "-; -; -; G" "-; G; G; G; G; G" "-; G; -; G; G; G" "-; T; -; -; -; -" "-; -; -; -; G;

```

# Not Coding

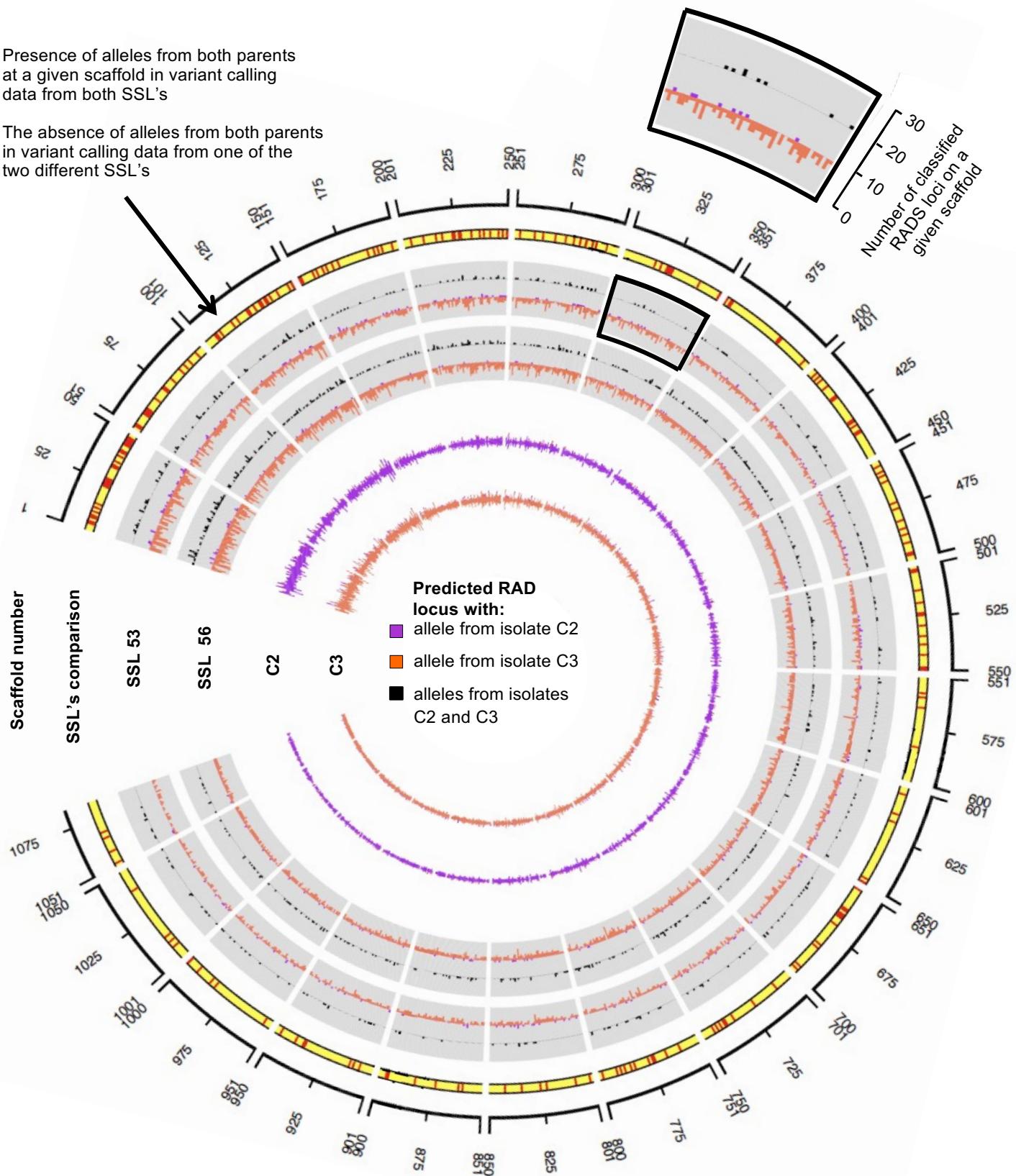
Position ID	Position category	Common alleles	Variable alleles
-------------	-------------------	----------------	------------------

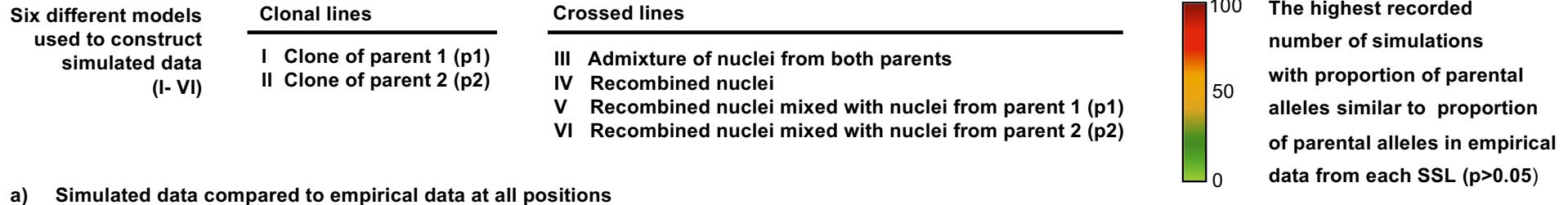


**Fig. 6**

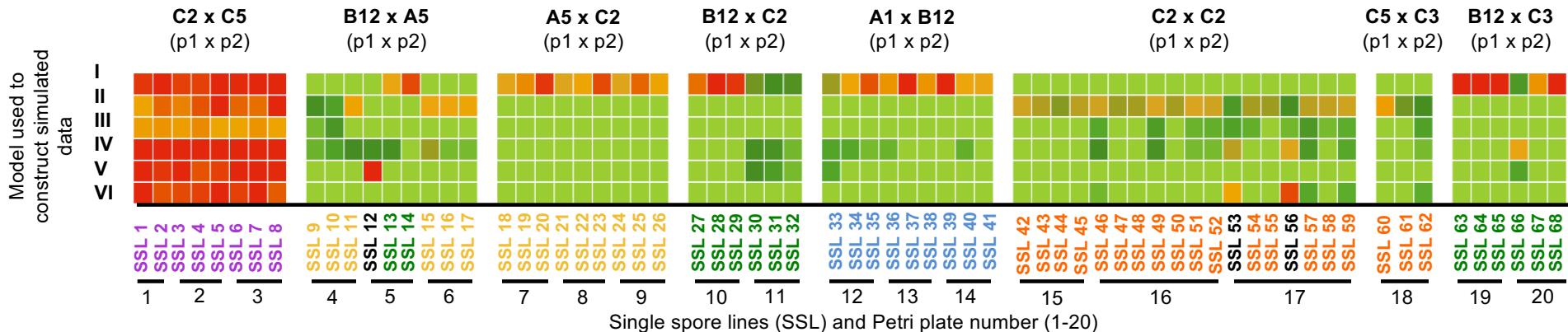
■ Presence of alleles from both parents at a given scaffold in variant calling data from both SSL's

■ The absence of alleles from both parents in variant calling data from one of the two different SSL's

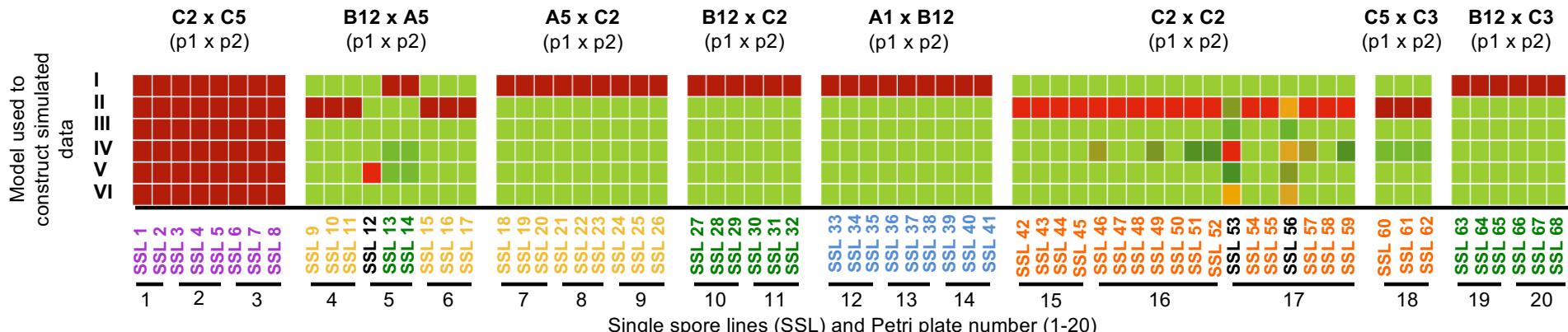




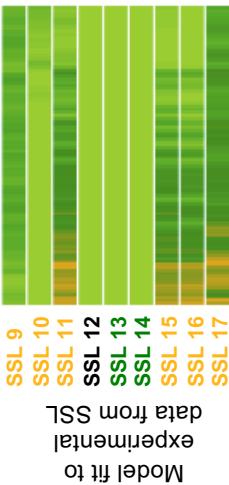
a) Simulated data compared to empirical data at all positions



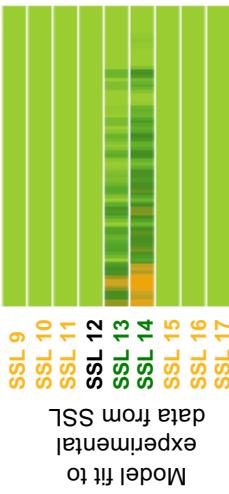
b) Simulated data compared to empirical data at high quality positions



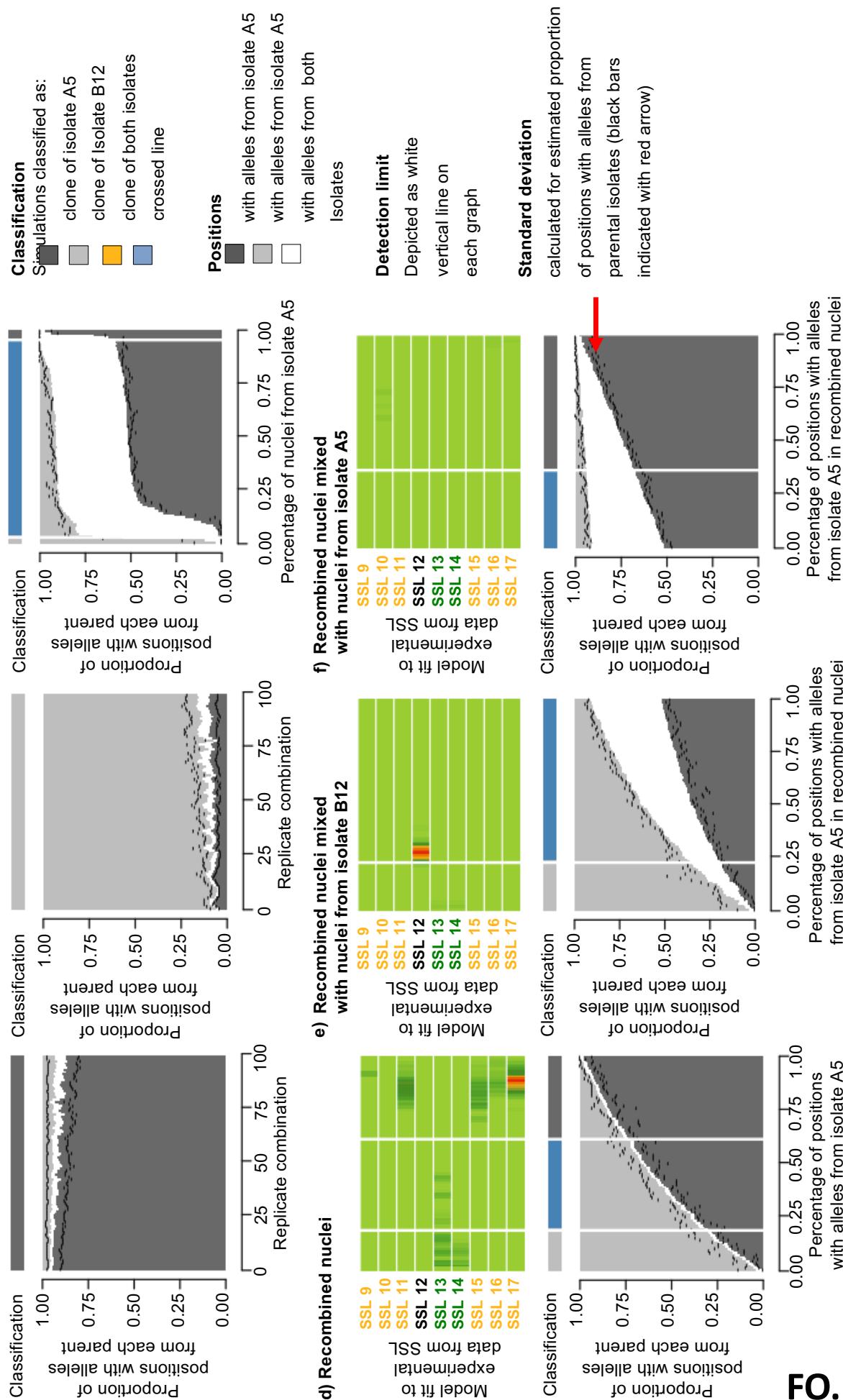
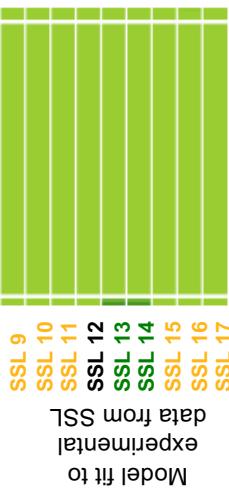
### a) Clones of isolate A5

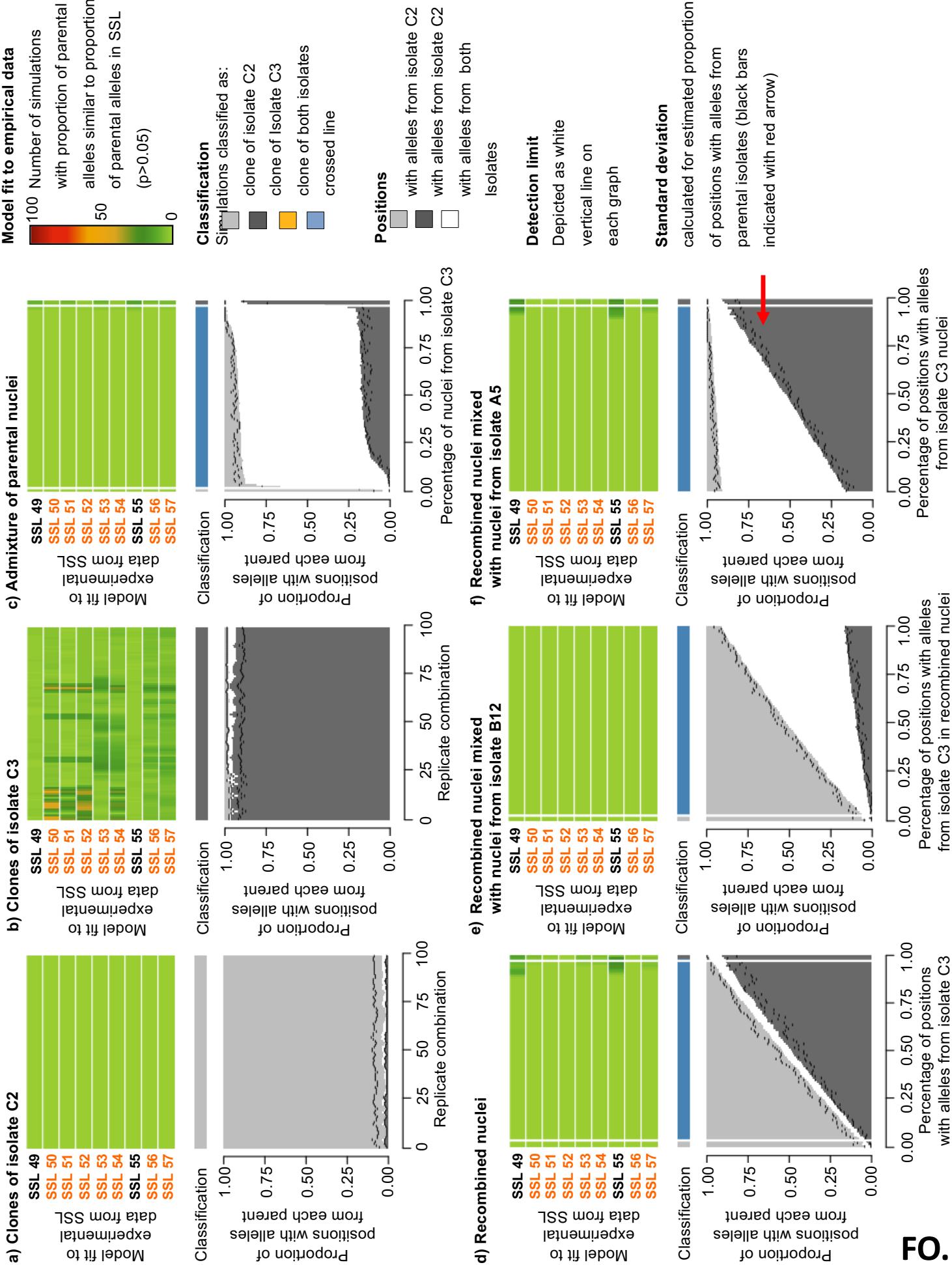


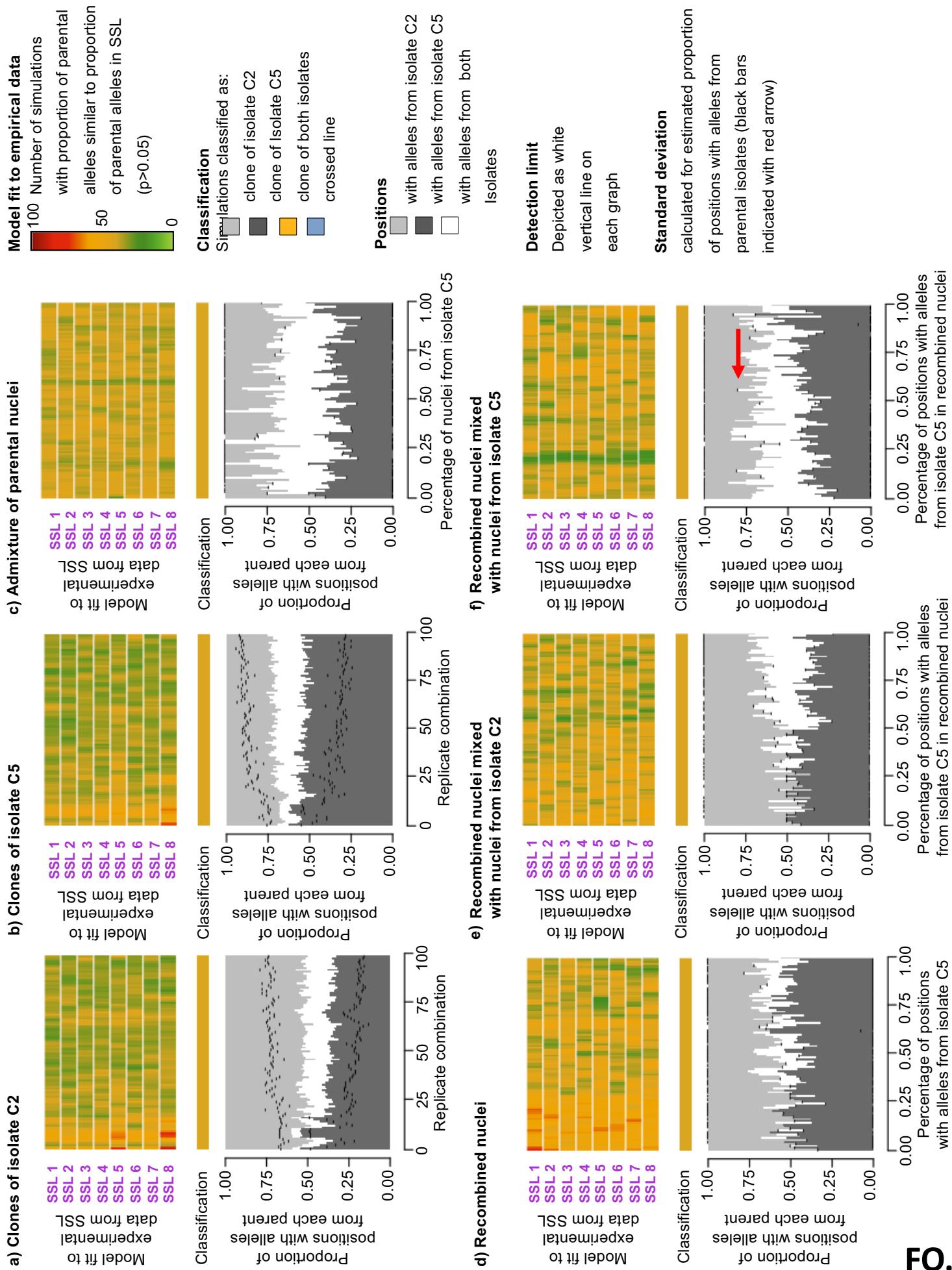
### b) Clones of isolate B12

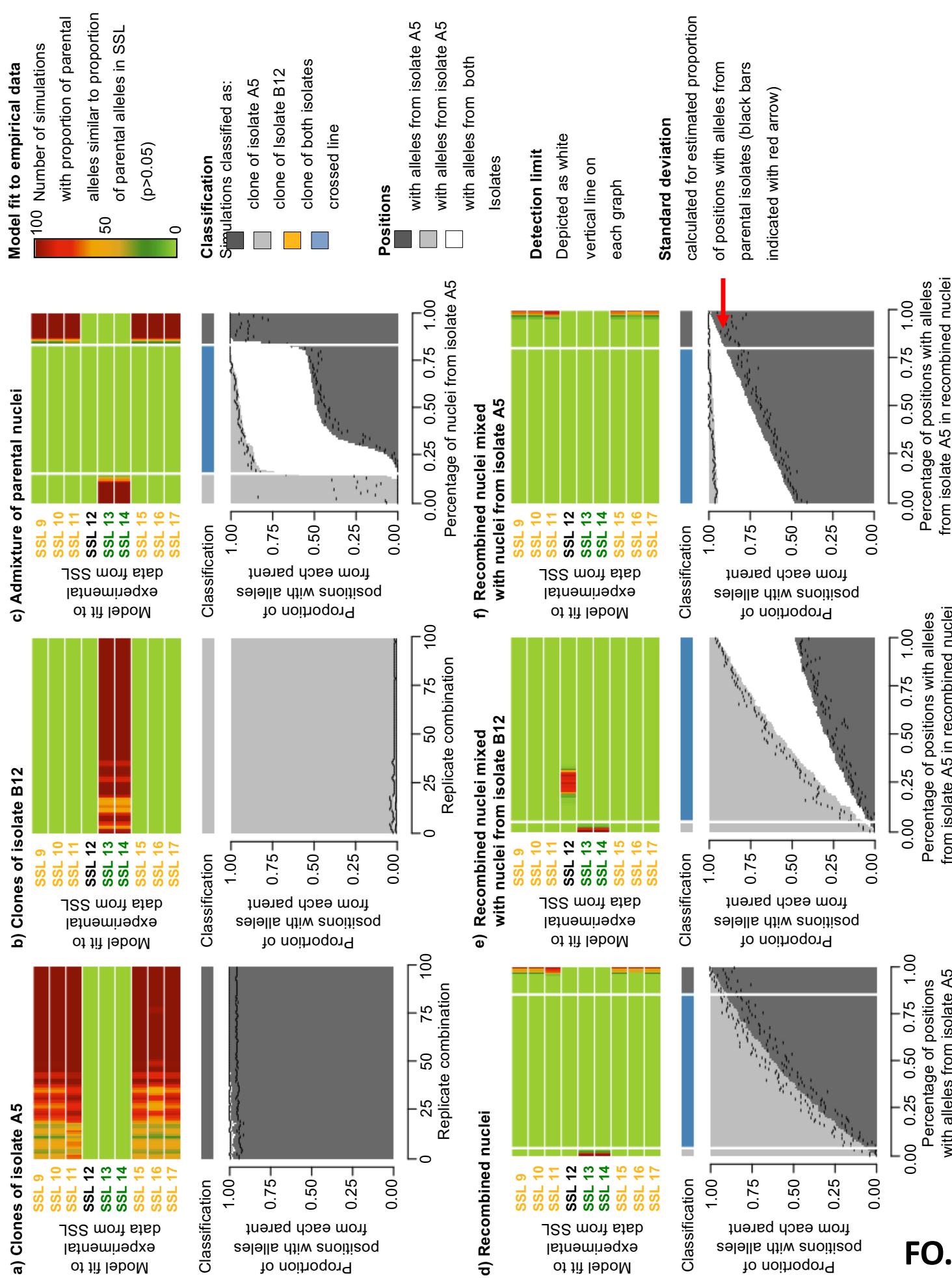


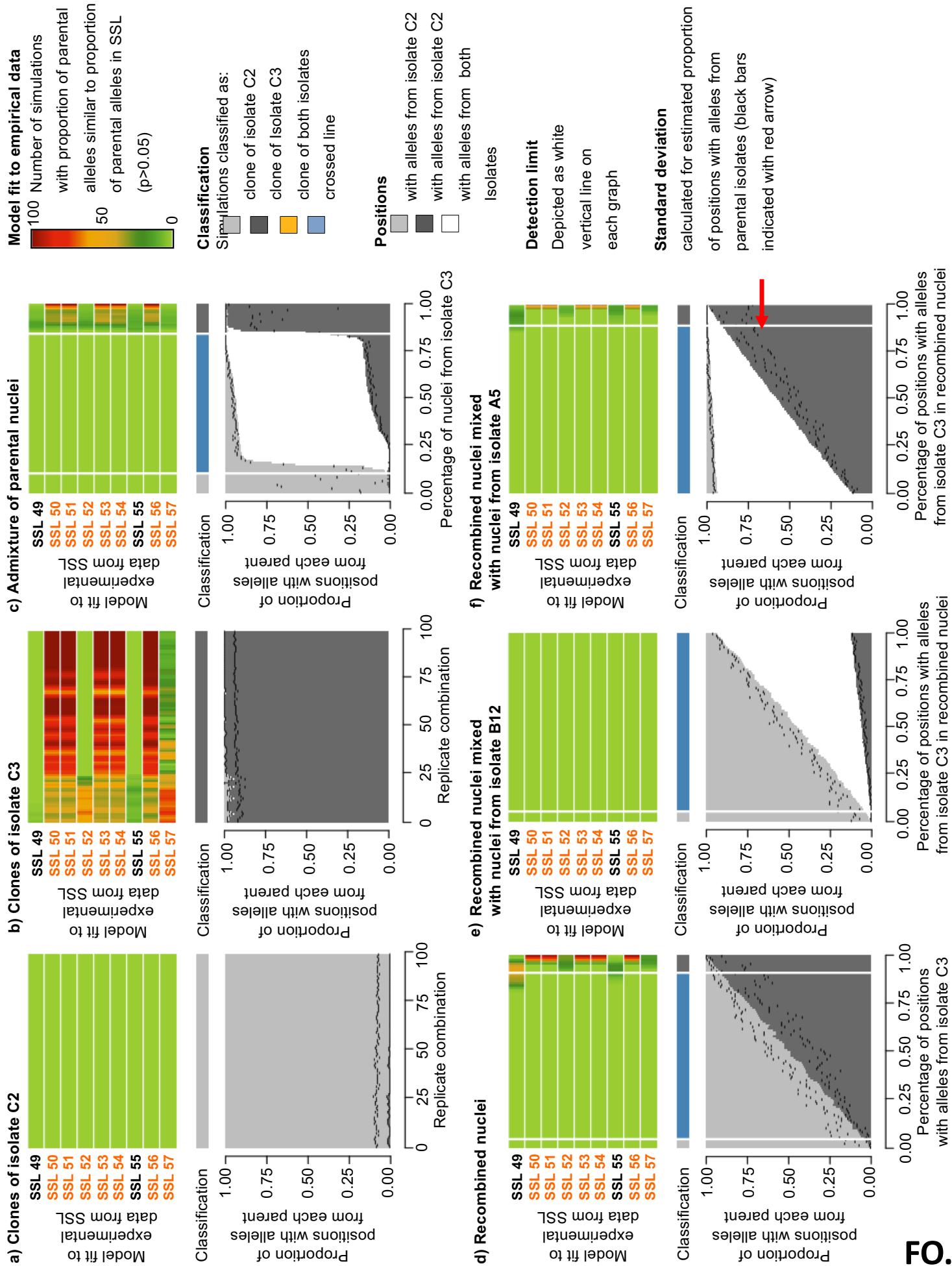
### c) Admixture of parental nuclei

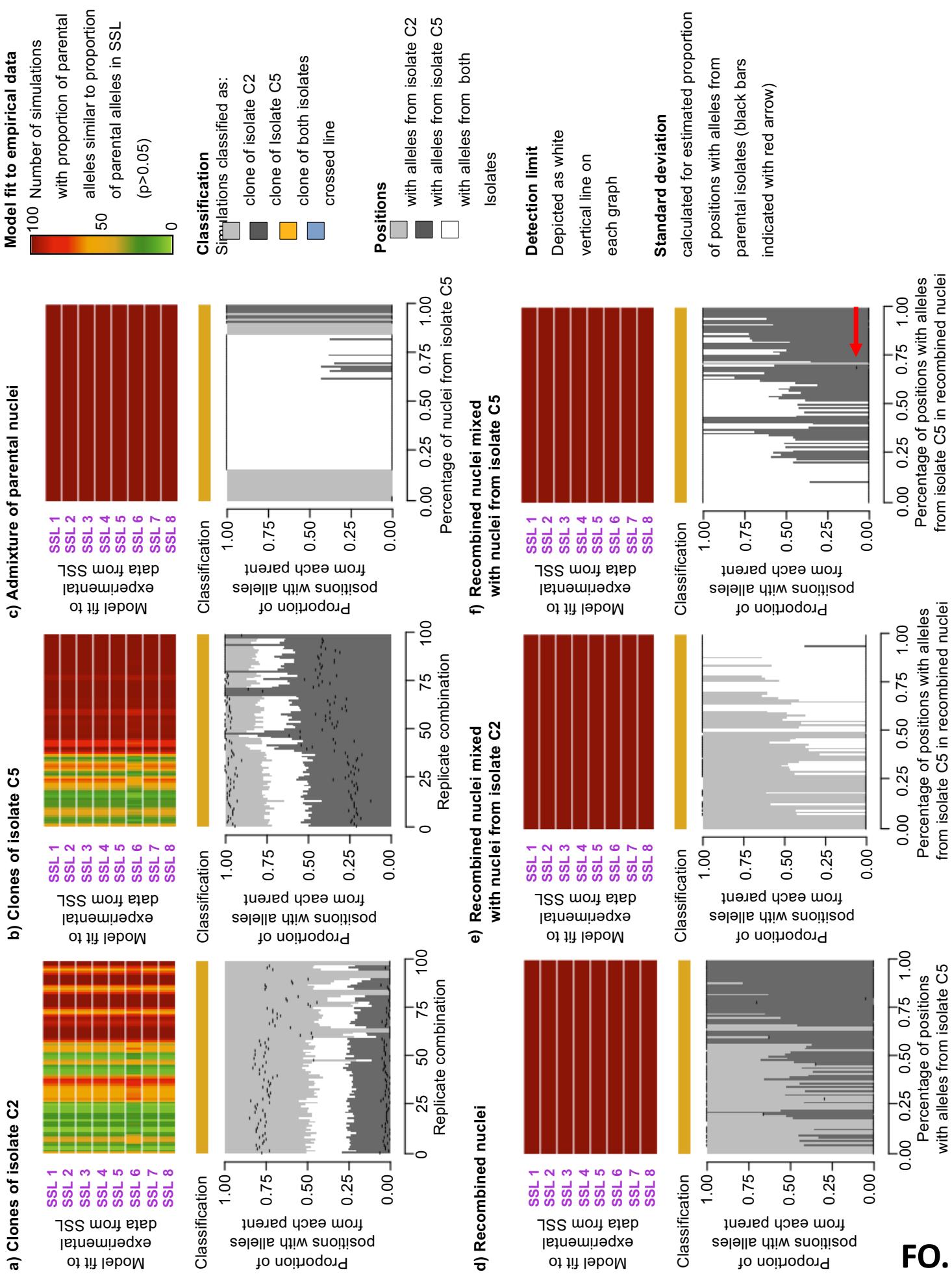






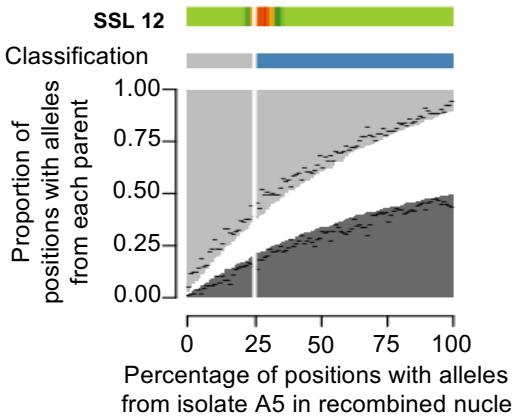




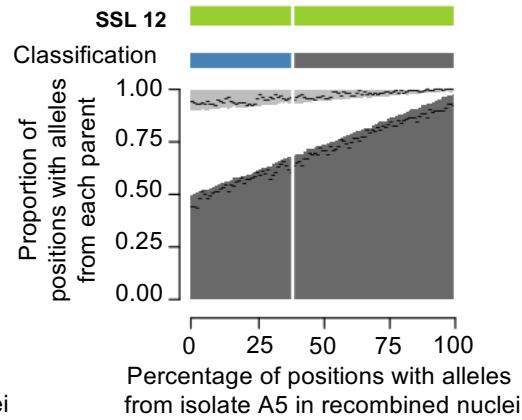


## All positions

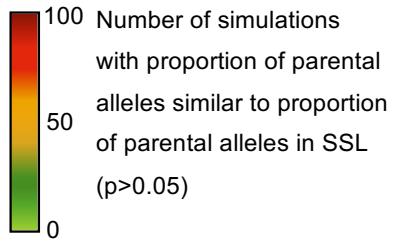
a) 10% of recombined nuclei mixed with nuclei from isolate B12



b) 10% of recombined nuclei mixed with nuclei from isolate A5



## Model fit to empirical data



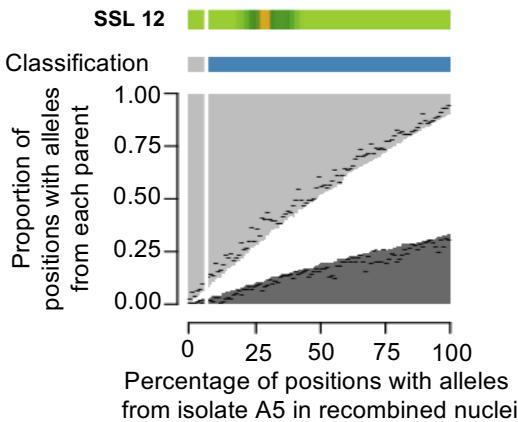
## Classification

Simulations classified as:

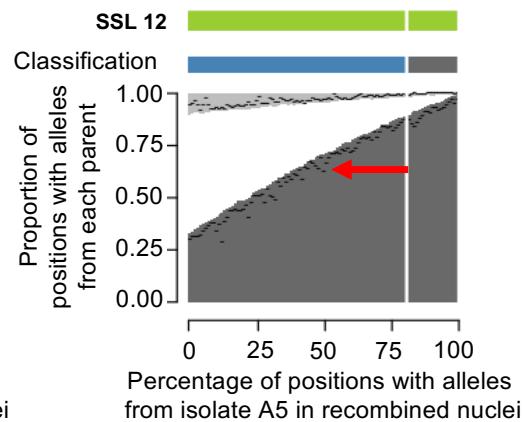
- clone of isolate A5
- clone of Isolate B12
- clone of both isolates
- crossed line

## High quality positions

a) 10% of recombined nuclei mixed with nuclei from isolate B12



b) 10% of recombined nuclei mixed with nuclei from isolate A5



## Detection limit

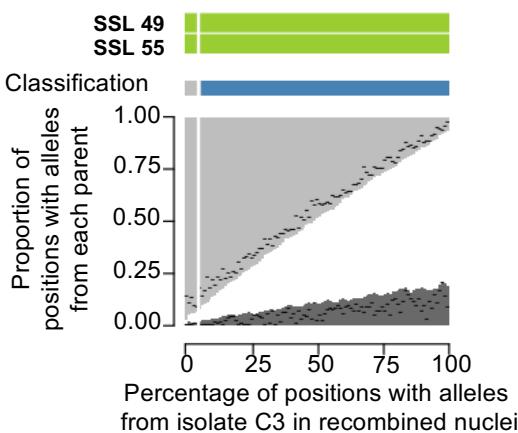
Depicted as white vertical line on each graph

## Standard deviation

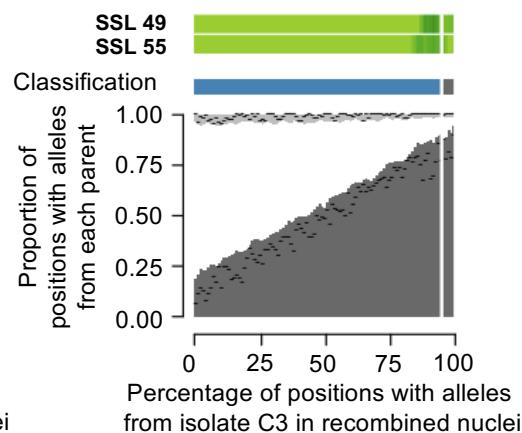
calculated for estimated proportion of positions with alleles from parental isolates (black bars indicated with red arrow)

## All positions

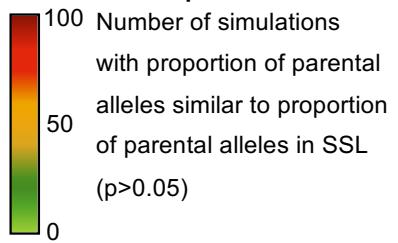
a) 10% of recombined nuclei mixed with nuclei from isolate C2



b) 10% of recombined nuclei mixed with nuclei from isolate C3

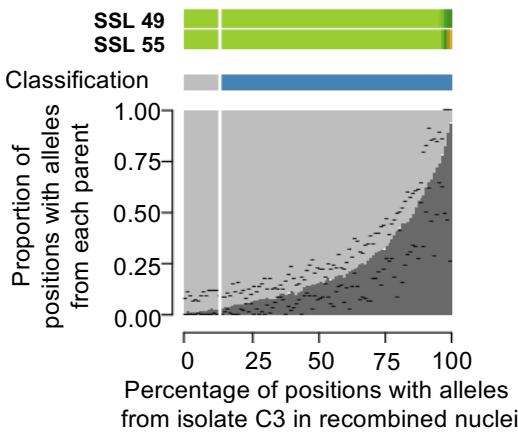


## Model fit to empirical data

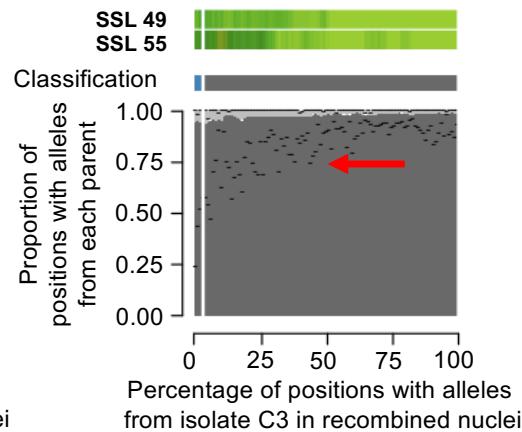


## High quality positions

a) 10% of recombined nuclei mixed with nuclei from isolate C2



b) 10% of recombined nuclei mixed with nuclei from isolate C3



## Classification

Simulations classified as:

- clone of isolate C2
- clone of Isolate C3
- clone of both isolates
- crossed line

## Positions

- with alleles from isolate C2
- with alleles from isolate C3
- with alleles from both Isolates

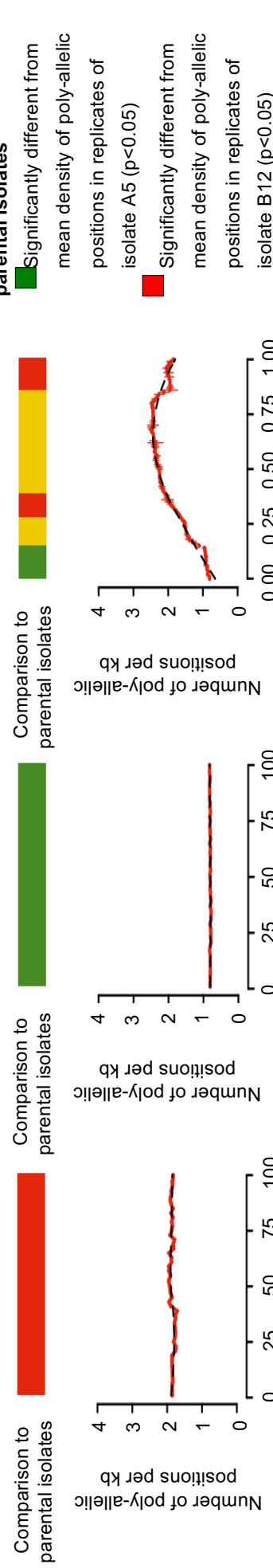
## Detection limit

Depicted as white vertical line on each graph

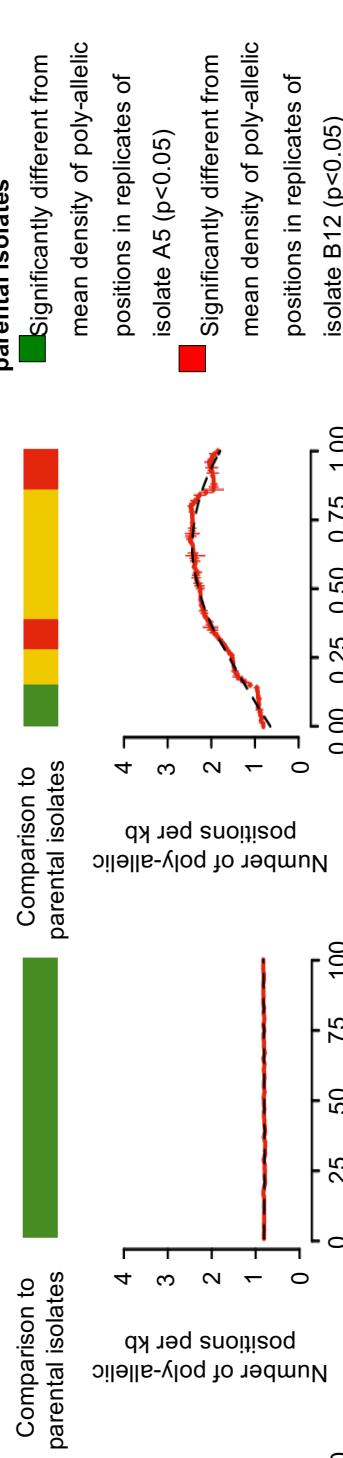
## Standard deviation

calculated for estimated proportion of positions with alleles from parental isolates (black bars indicated with red arrow)

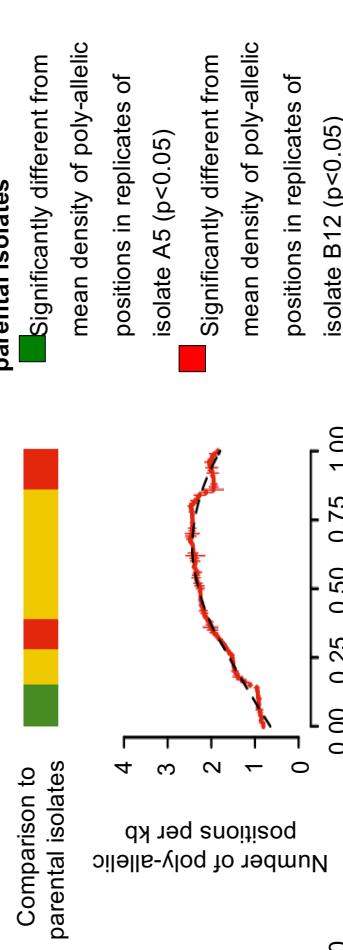
### a) Clones of isolate A5



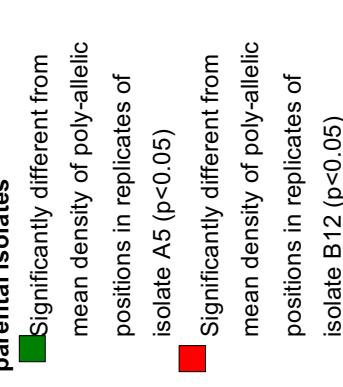
### b) Clones of isolate B12



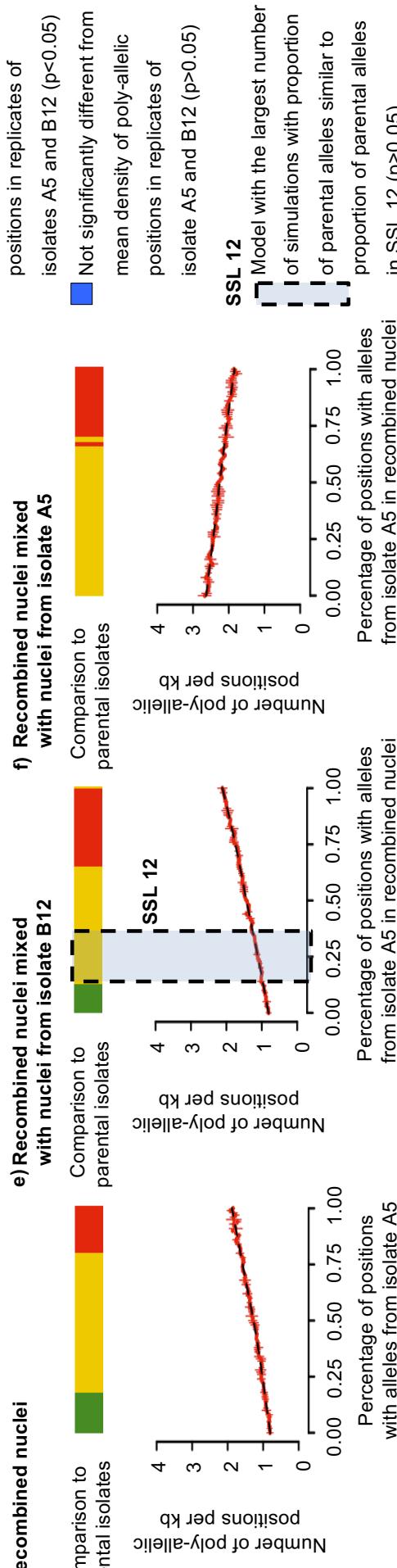
### c) Admixture of parental nuclei



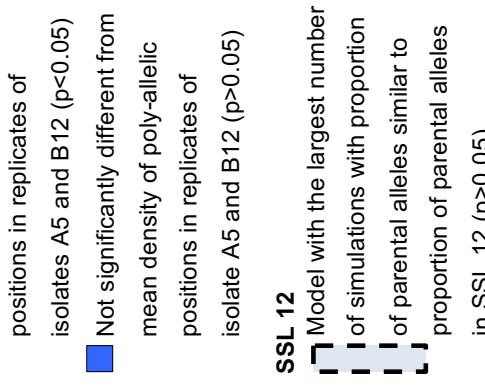
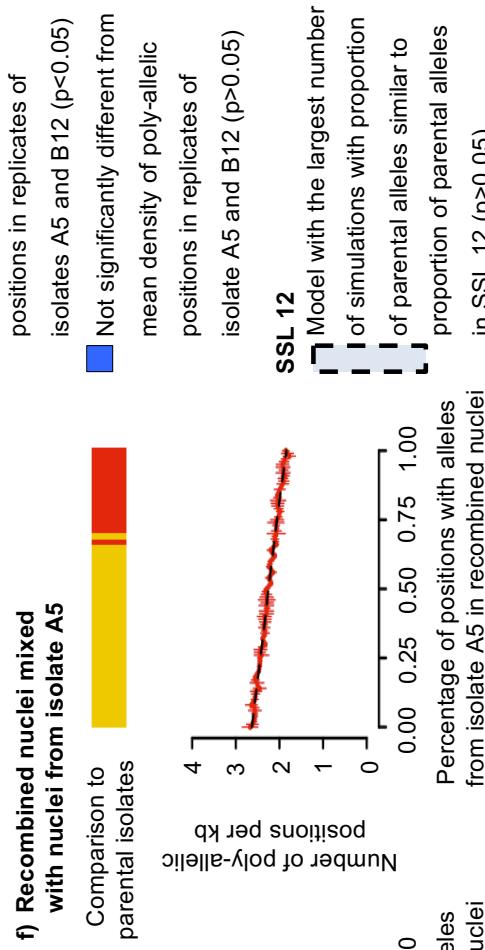
### Comparison to parental isolates



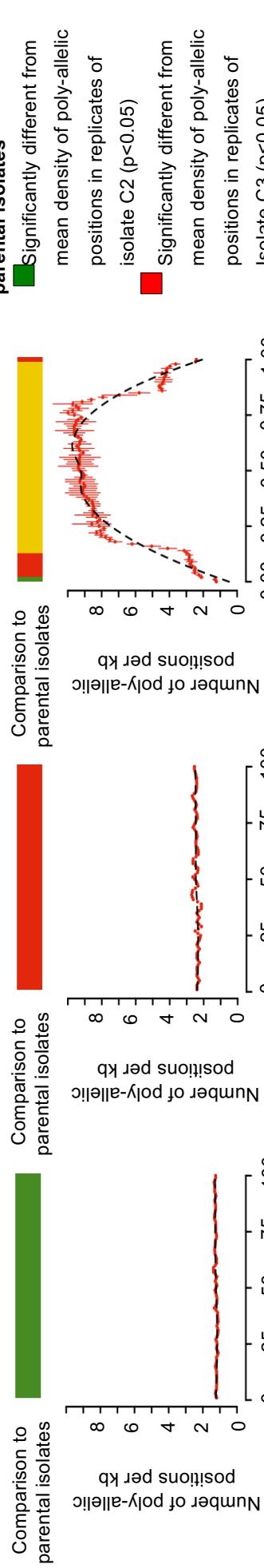
### d) Recombined nuclei



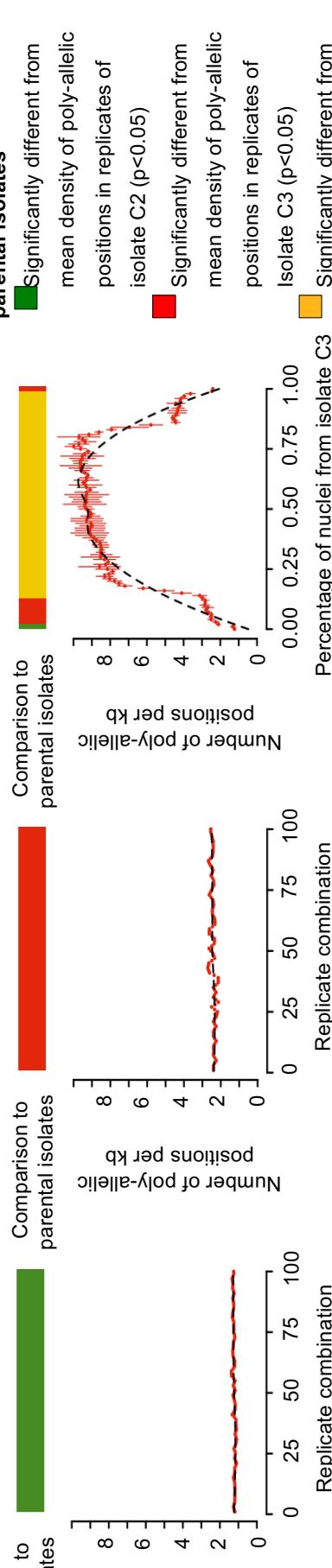
### f) Recombined nuclei mixed with nuclei from isolate A5



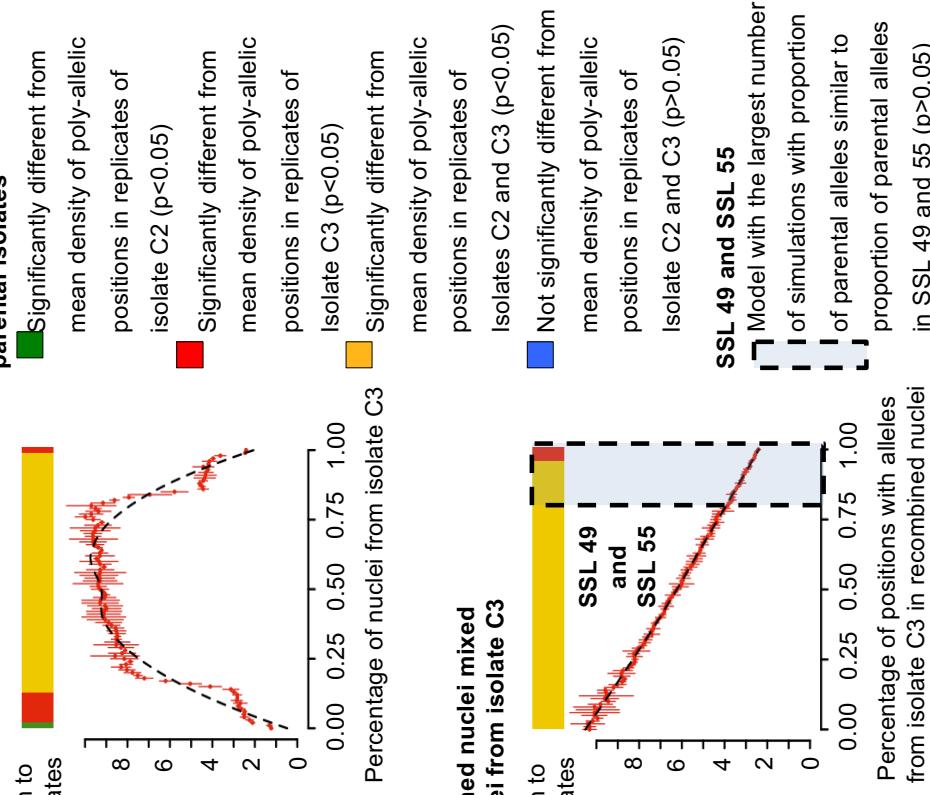
### a) Clones of isolate C2



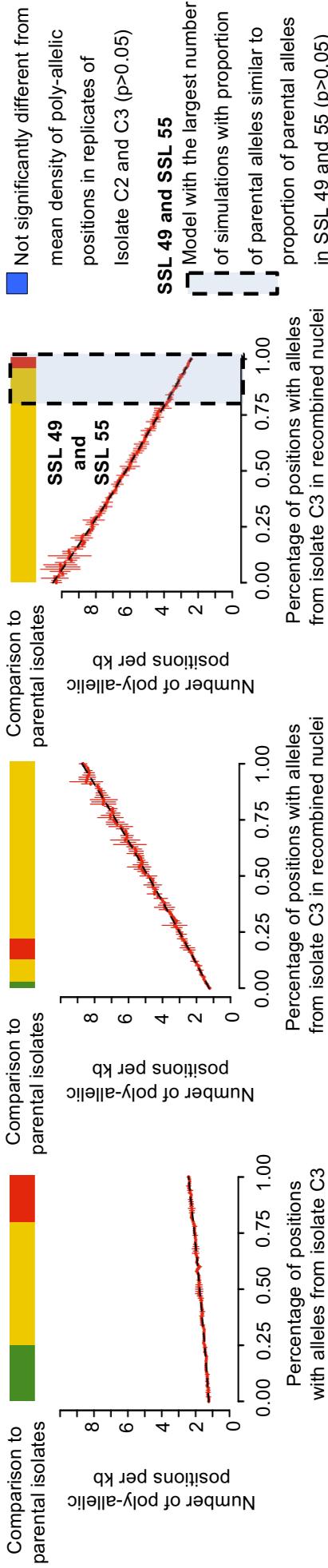
### b) Clones of isolate C3



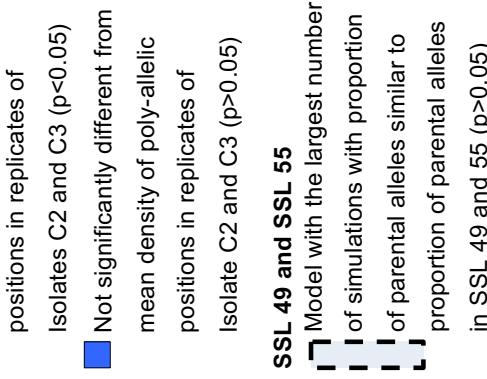
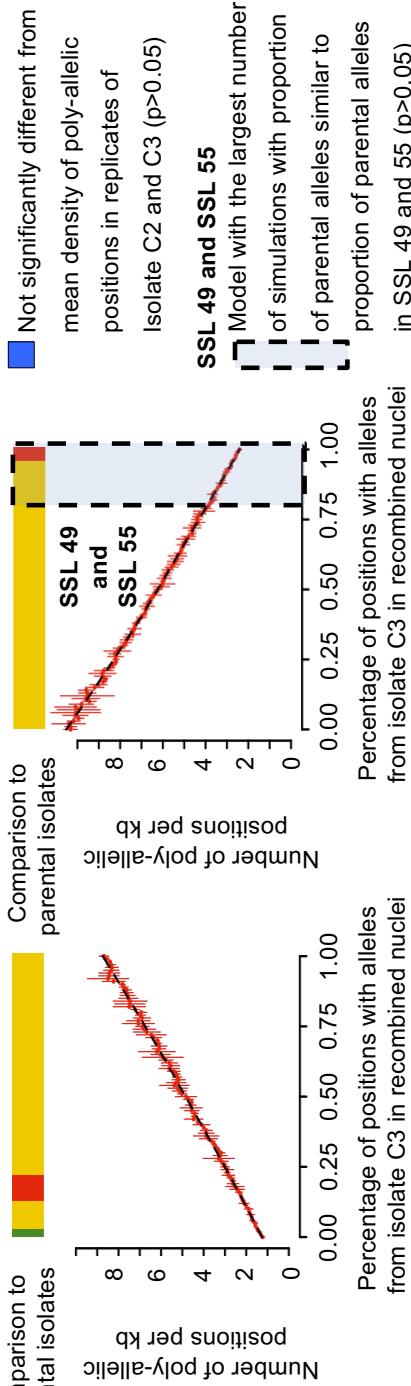
### c) Admixture of parental nuclei



### d) Recombined nuclei



### e) Recombined nuclei mixed with nuclei from isolate C2



Significantly different from mean density of poly-allelic positions in replicates of isolate C2 ( $p<0.05$ )

Significantly different from mean density of poly-allelic positions in replicates of isolate C3 ( $p<0.05$ )

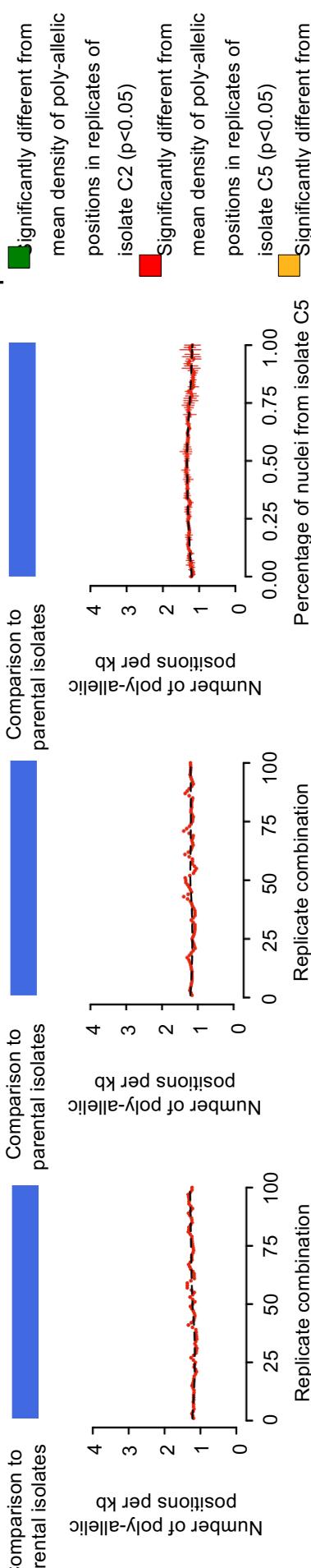
Significantly different from mean density of poly-allelic positions in replicates of isolate C3 ( $p<0.05$ )

Significantly different from mean density of poly-allelic positions in replicates of Isolates C2 and C3 ( $p<0.05$ )

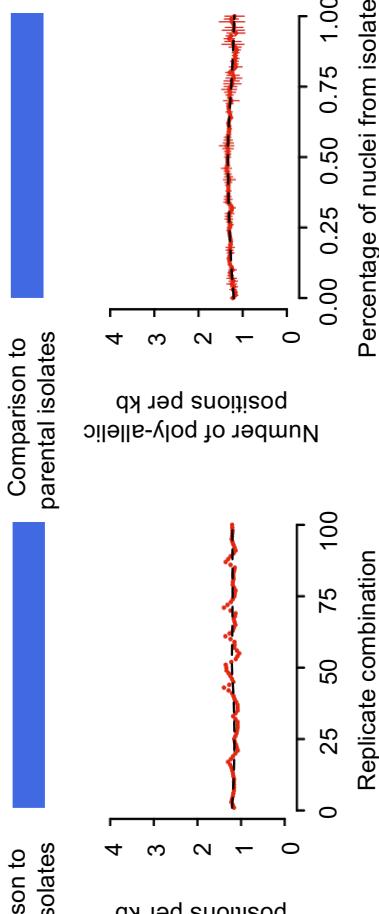
Not significantly different from mean density of poly-allelic positions in replicates of Isolate C2 and C3 ( $p>0.05$ )

Model with the largest number of simulations with proportion of parental alleles similar to proportion of parental alleles in SSL 49 and 55 ( $p>0.05$ )

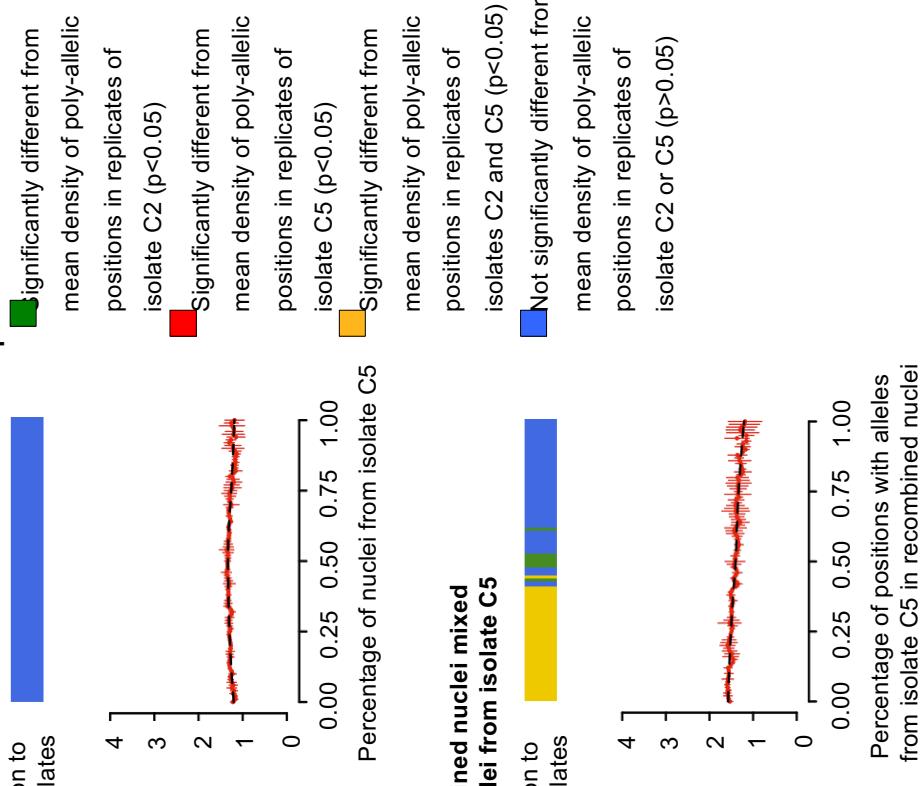
a) Clones of isolate C2



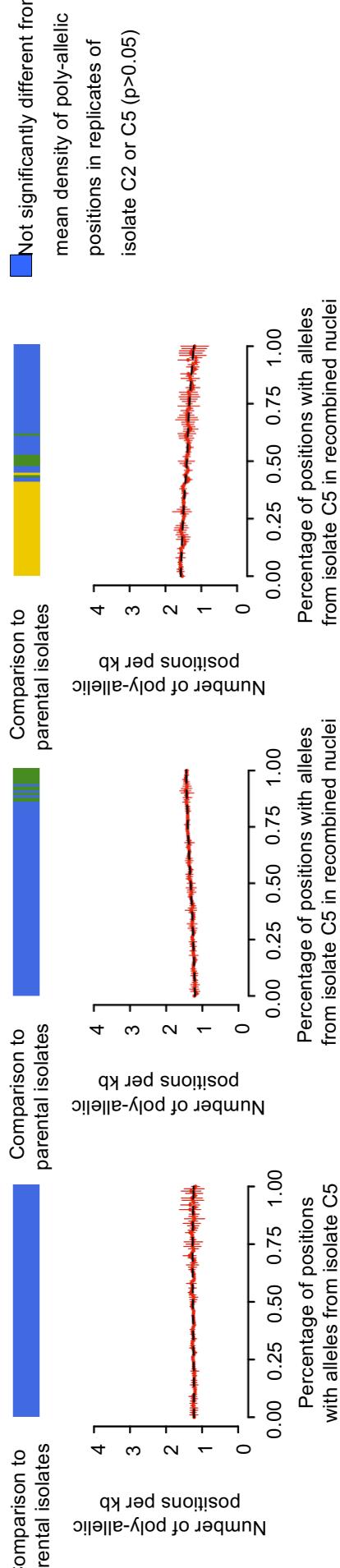
b) Clones of isolate C5



c) Admixture of parental nuclei



d) Recombined nuclei



e) Recombined nuclei mixed with nuclei from isolate C2

