

Position: 971 (Consensus: c Ancestral: a)

year	a	t	c	g	-	n_samples
2015	0.5	0	0.5	0	0	6
2016	0.666667	0	0.333333	0	0	15
2017	0.266667	0	0.733333	0	0	15
2018	0.5	0	0.5	0	0	2
2019	0.333333	0	0.666667	0	0	3
2020	0	0	1	0	0	1
2021	0	0	1	0	0	1

Position: 2597 (Consensus: t Ancestral: a)

year	a	t	c	g	-	n_samples
2015	0.5	0.5	0	0	0	6
2016	0.666667	0.333333	0	0	0	15
2017	0.266667	0.733333	0	0	0	15
2018	0.5	0.5	0	0	0	2
2019	0.333333	0.666667	0	0	0	3
2020	0	1	0	0	0	1
2021	0	1	0	0	0	1

Position: 972 (Consensus: a Ancestral: c)

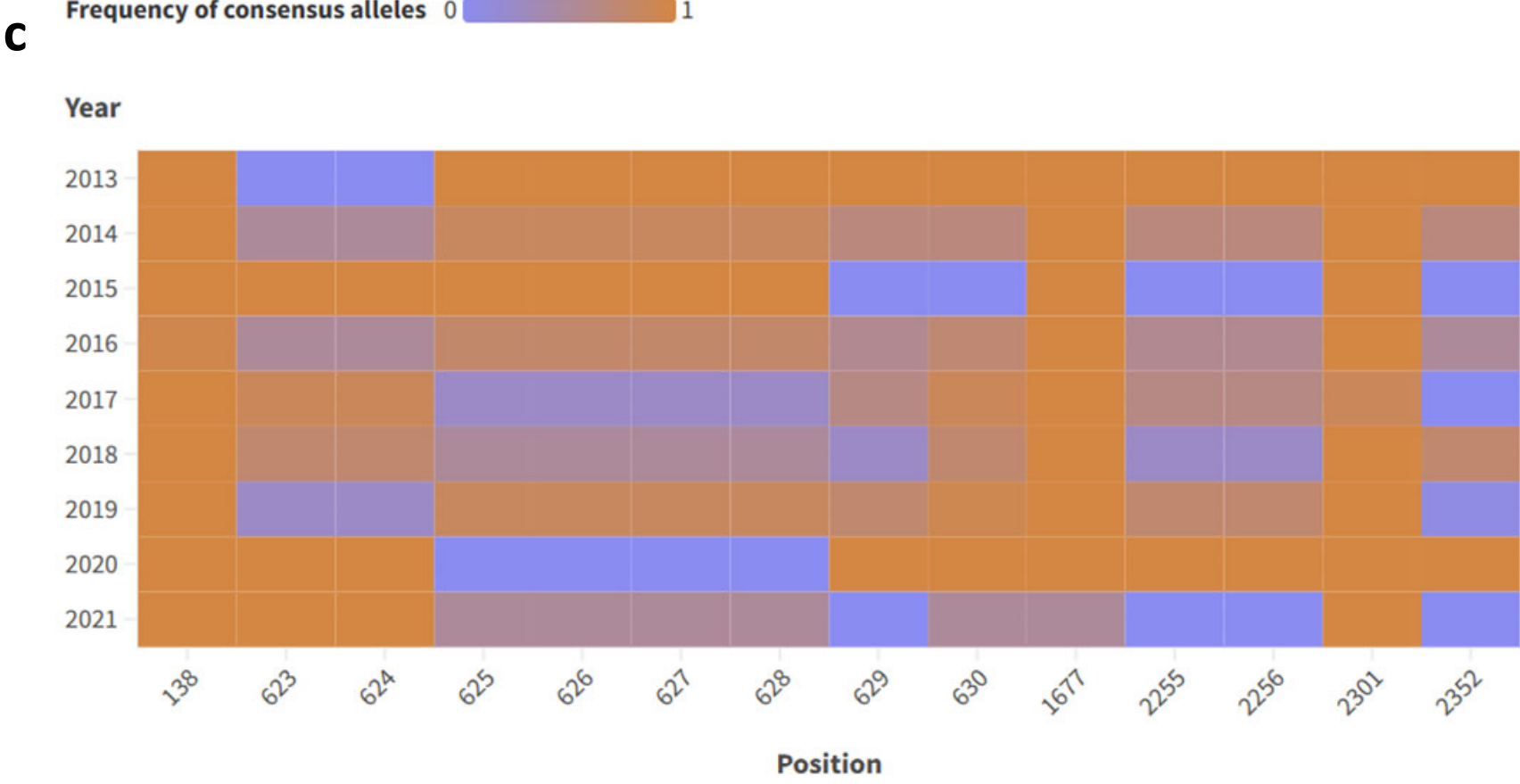
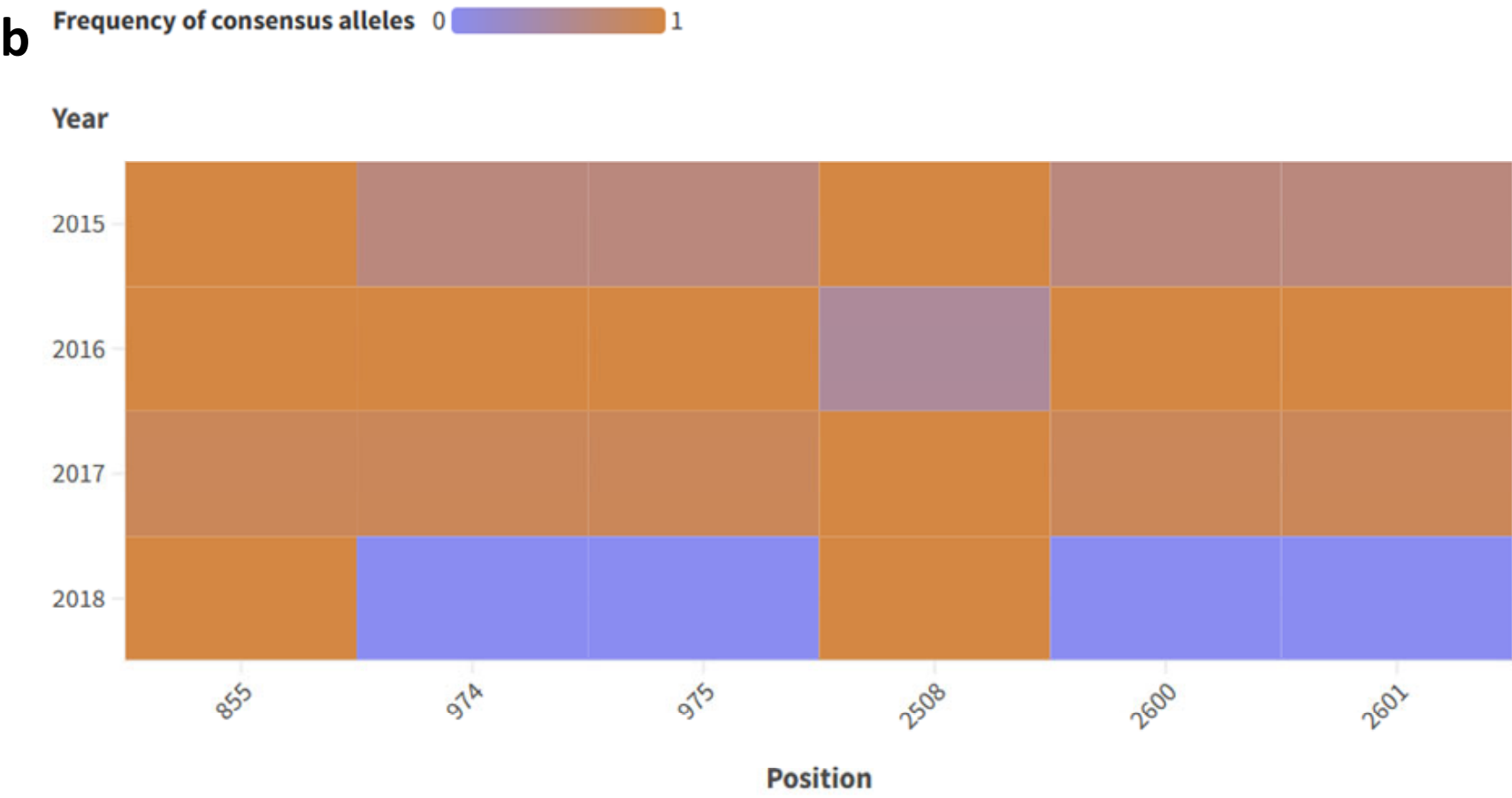
year	a	t	c	g	-	n_samples
2015	0.5	0	0.5	0	0	6
2016	0.333333	0	0.666667	0	0	15
2017	0.733333	0	0.266667	0	0	15
2018	0.5	0	0.5	0	0	2
2019	0.666667	0	0.333333	0	0	3
2020	1	0	0	0	0	1
2021	1	0	0	0	0	1

Position: 2598 (Consensus: a Ancestral: t)

year	a	t	c	g	-	n_samples
2015	0.5	0.5	0	0	0	6
2016	0.333333	0.666667	0	0	0	15
2017	0.733333	0.266667	0	0	0	15
2018	0.5	0.5	0	0	0	2
2019	0.666667	0.333333	0	0	0	3
2020	1	0	0	0	0	1
2021	1	0	0	0	0	1

Position: 1523 (Consensus: c Ancestral: t)

year	a	t	c	g	-	n_samples
2015	0	0.666667	0.333333	0	0	6
2016	0	0.2	0.8	0	0	15
2017	0	0.466667	0.533333	0	0	15
2018	0	0	1	0	0	2
2019	0	0	1	0	0	3
2020	0	0	1	0	0	1
2021	0	0	1	0	0	1

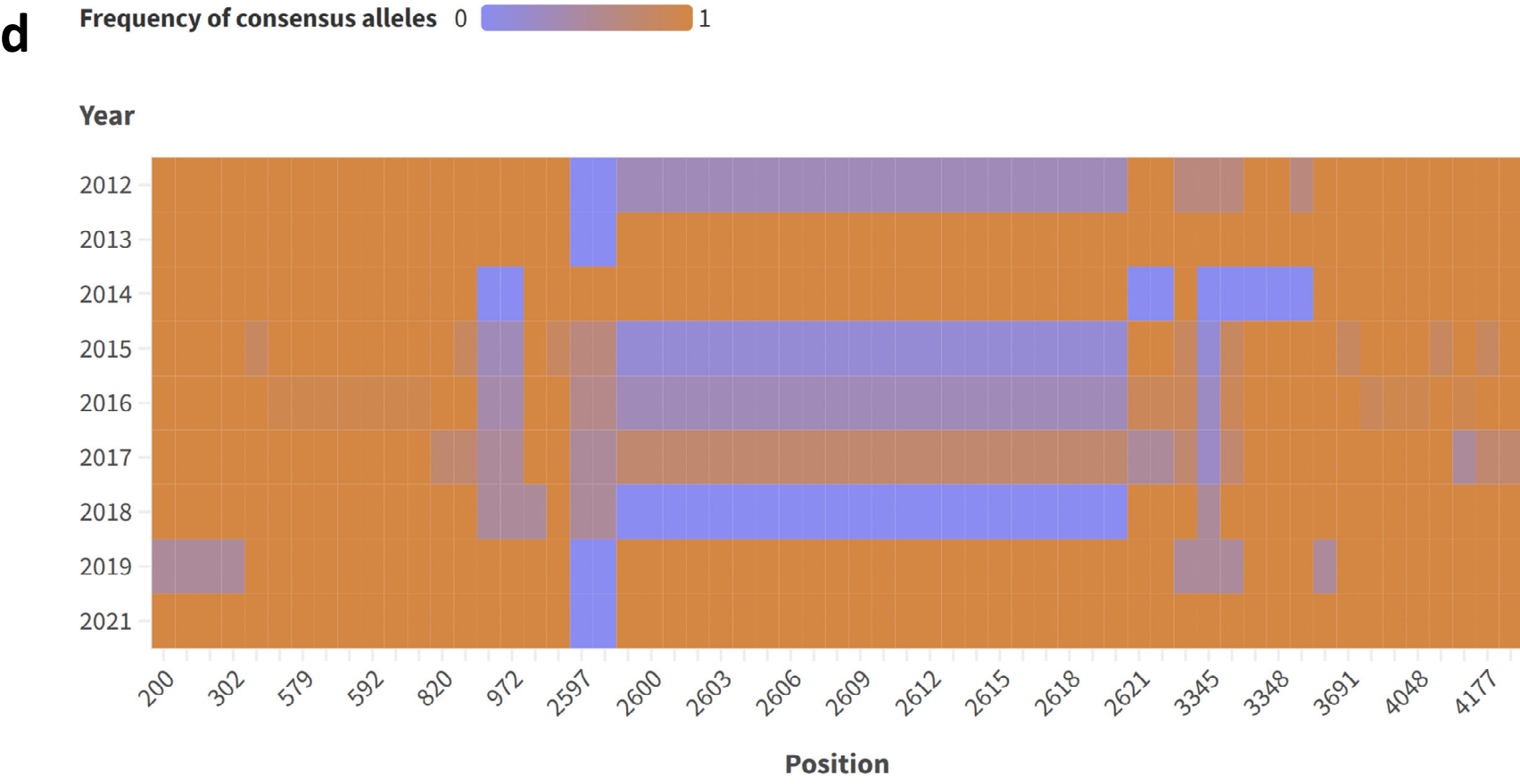


Position: 623 (Consensus: a Ancestral: a)

year	a	t	c	g	-	n_samples
2013	0	0	0	0	1	1
2014	0.5	0	0	0	0.5	6
2015	1	0	0	0	0	1
2016	0.5	0	0	0	0.5	18
2017	0.875	0	0	0	0.125	8
2018	0.75	0	0	0	0.25	4
2019	0.25	0	0	0	0.75	12
2020	1	0	0	0	0	1
2021	1	0	0	0	0	2

Position: 624 (Consensus: t Ancestral: t)

year	a	t	c	g	-	n_samples
2013	0	0	0	0	1	1
2014	0	0.5	0	0	0.5	6
2015	0	1	0	0	0	1
2016	0	0.5	0	0	0.5	18
2017	0	0.875	0	0	0.125	8
2018	0	0.75	0	0	0.25	4
2019	0	0.25	0	0	0.75	12
2020	0	1	0	0	0	1
2021	0	1	0	0	0	2



Position: 2597~2622 (Ancestral: tatgggcggtgggggtggggtttgta)

gene positions (2597~2622)	2012	2013	2014	2015	2016	2017	2018	2019	2021
ta tg..gt ta	2	0	0	1	3	1	1	0	0
-- ---- ta	1	1	0	1	3	1	0	2	2
at tg..gt ta	0	0	0	4	7	0	1	0	0
at ---- --	0	0	1	0	2	2	0	0	0

Supplementary Figure 3. Temporal Patterns of Variable Positions in Alignment. The heat map shows the frequency of consistent sequence alleles in the four structures and the right side of the heat map gives a table of allele frequencies with more variable positions. **a) *DUF_mcr-1_PAP2_DUF***; **b) *IS_mcr-1_PAP2_IS***; **c) *IS_mcr-1_PAP2_TerF***; **d) *IS_mcr-1_PAP2_VWA***.