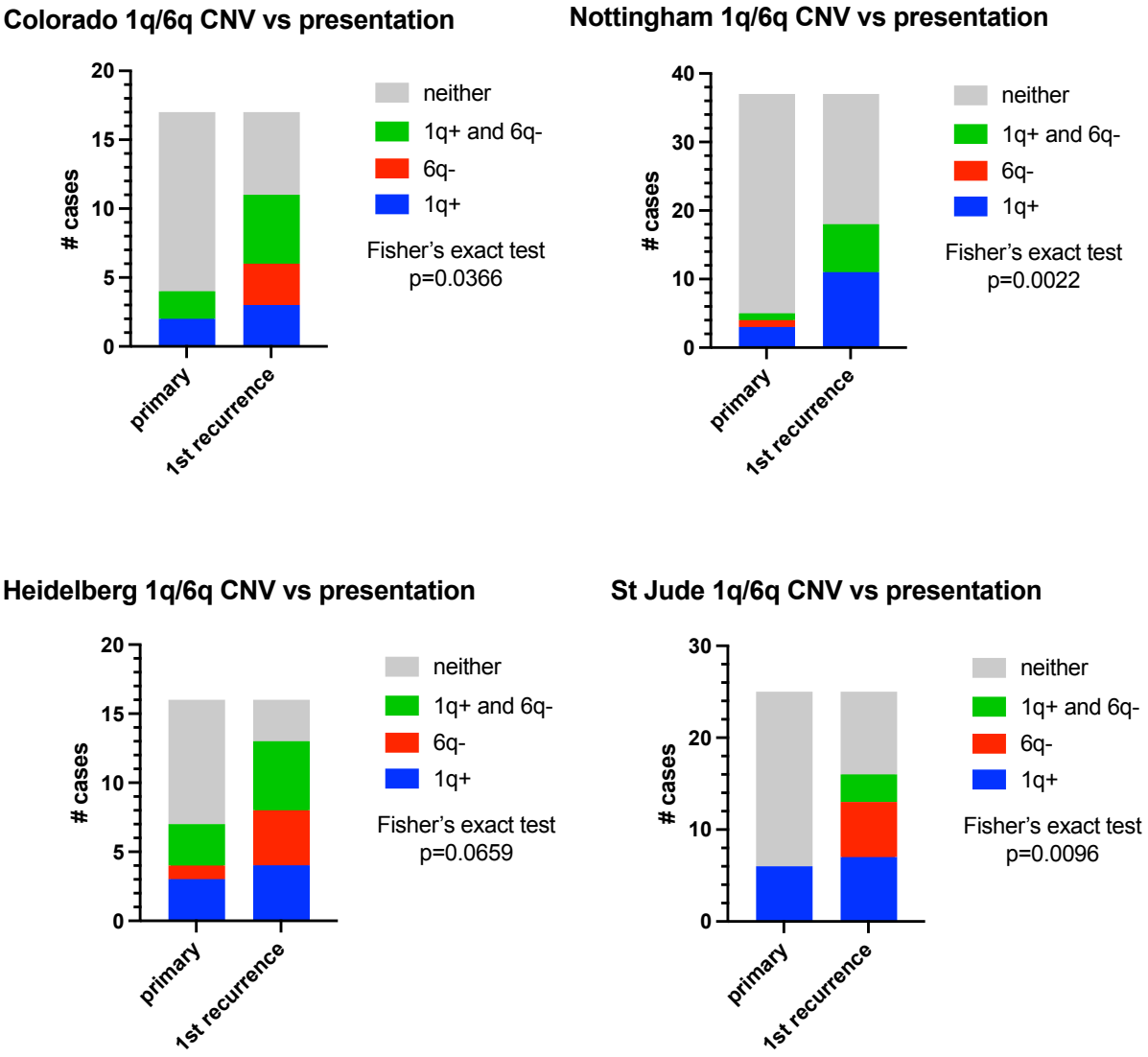
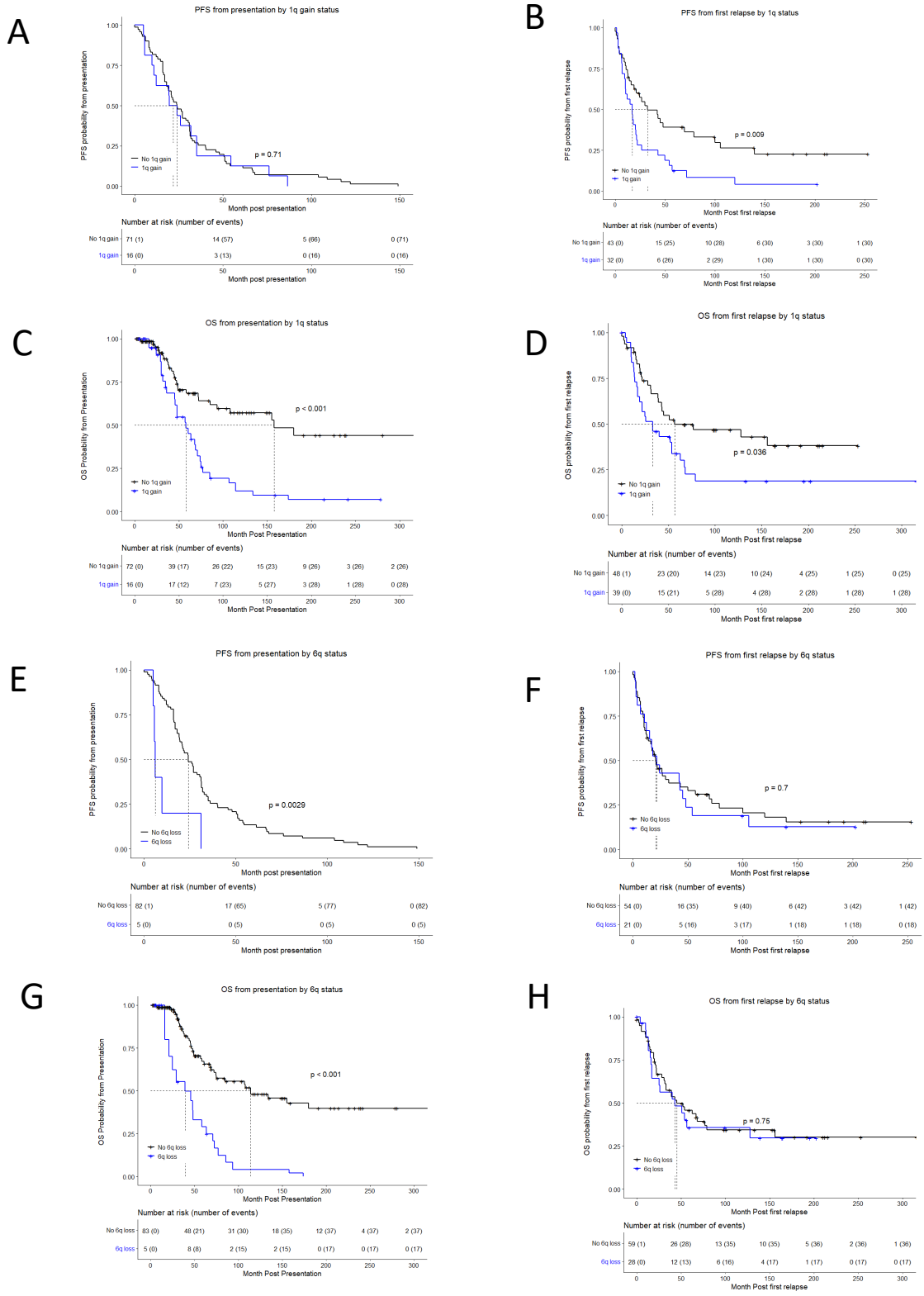
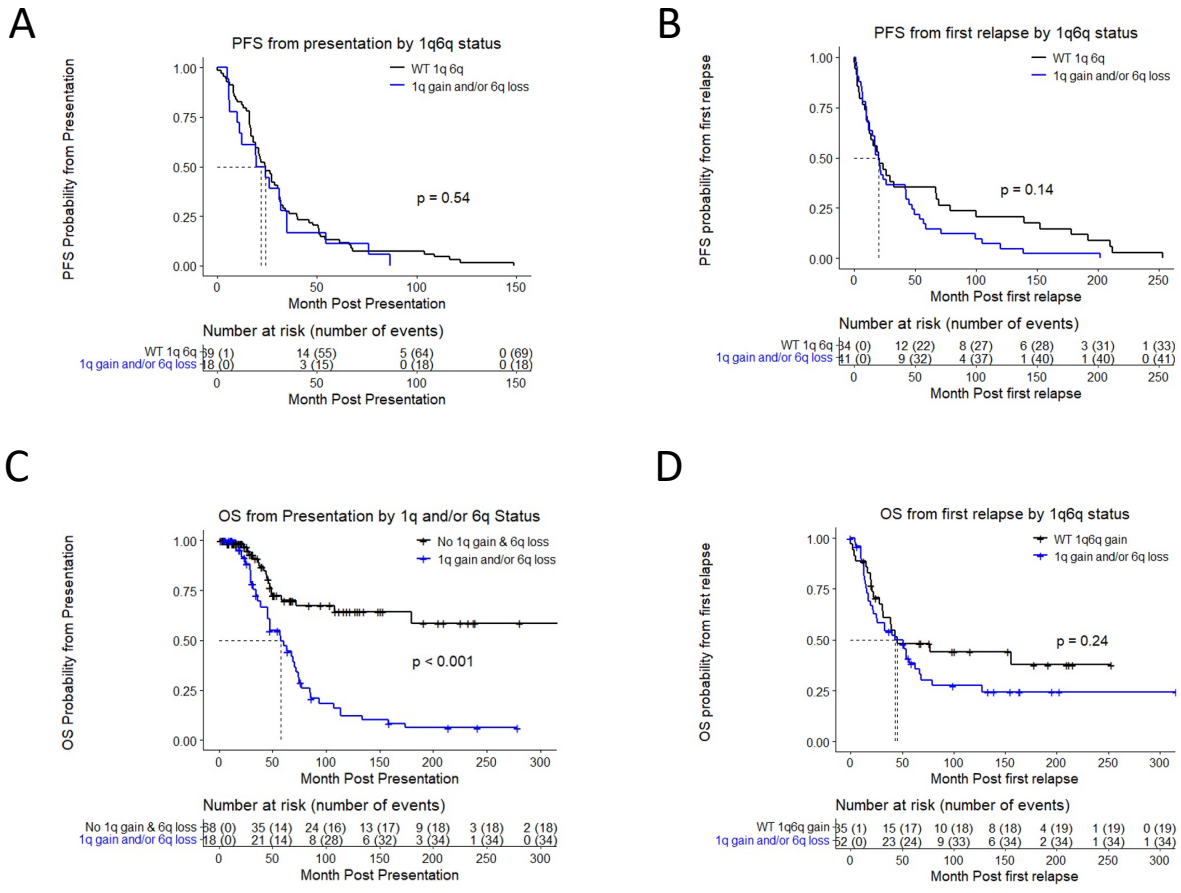


Supplementary figure 1. Increased incidence of chromosome 1q gain and/or 6q loss in PFA at recurrence in all institutional cohorts. Proportions of (i) 1q+ and 6q- co-occurrence (1q+ and 6q-), (ii) 1q+ with wildtype 6q (1q+), (iii) 6q- with wildtype 1q (6q-) and (iv) wildtype 1q and 6q (neither) at presentation and 1st recurrence from the four institutions that contributed to the study.



Supplementary figure 2. Kaplan-Meier plots showing association of 1q+ and 6q- with outcome in PFA. The effect of 1q+ status on PFS from (**A**) presentation and (**B**) 1st recurrence and on OS from (**C**) presentation and (**D**) 1st recurrence. The effect of 6q- status on PFS from (**E**) presentation and (**F**) 1st recurrence and on OS from (**G**) presentation and (**H**) 1st recurrence.

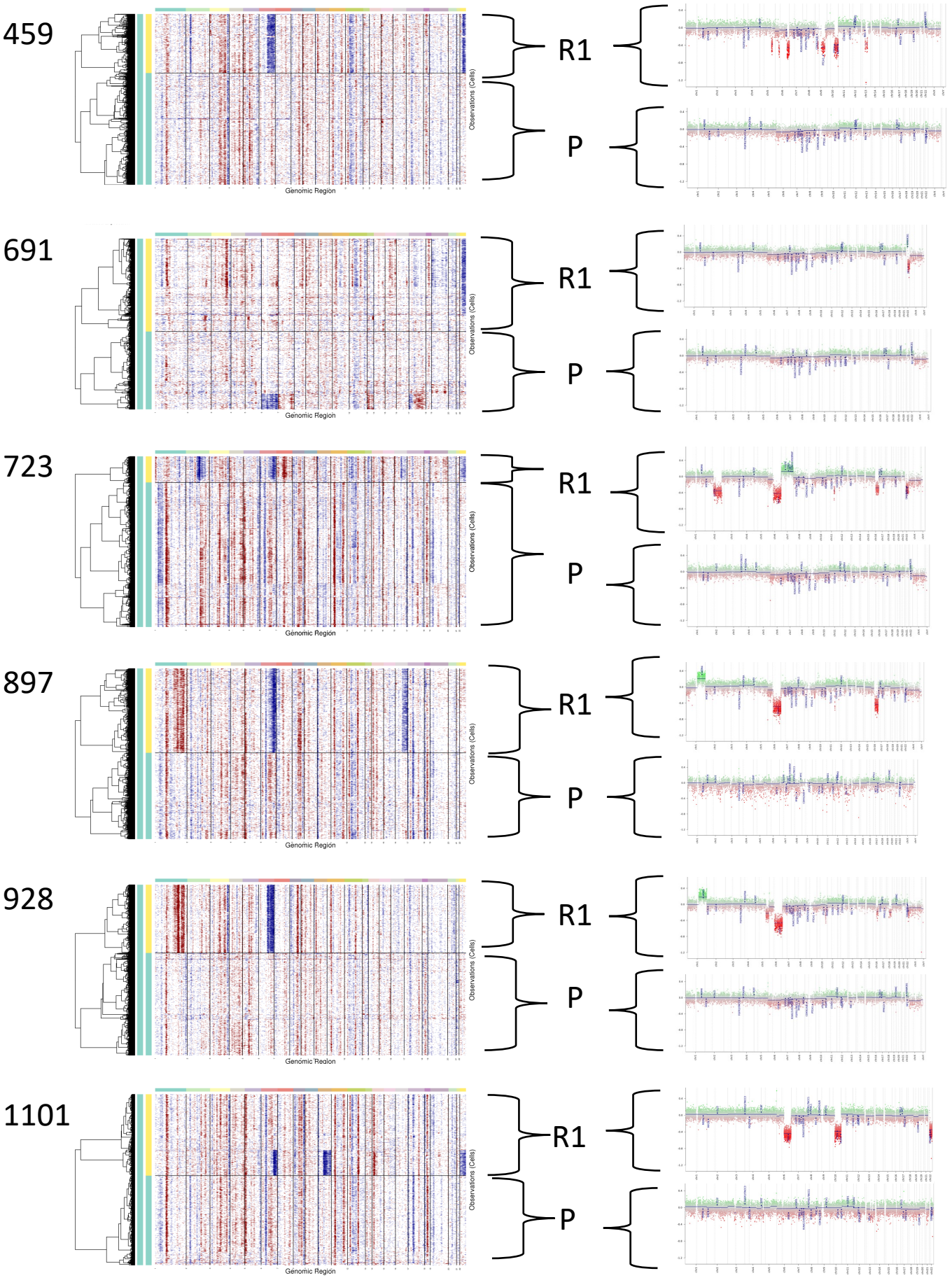


Supplementary figure 3. Kaplan-Meier plots showing association of 1q+ and/or 6q- with outcome in PFA. The effect of 1q+ and/or 6q- status on PFS from (**A**) presentation and (**B**) 1st recurrence and on OS from (**C**) presentation and (**D**) 1st recurrence.

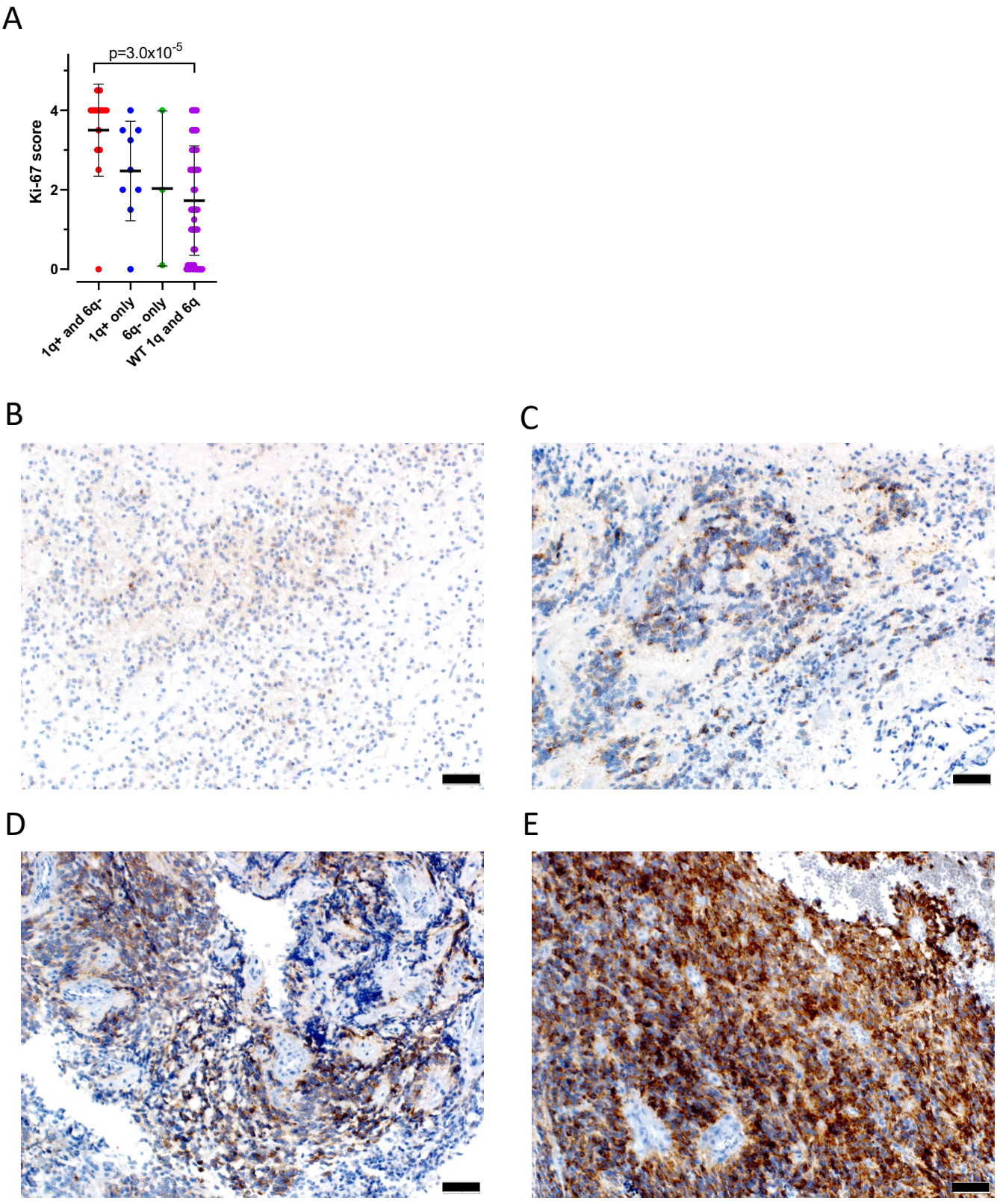
	neuroepithelial						mesenchymal				
	UEC-A	TEC-A	TEC-B	TEC-C	TEC-D	CEC	UEC-B	MEC-A	MEC-B	MEC-C	MEC-D
UEC-A	27.8	7.9	4.4	1.4	1.4	1.0	1.0	0.6	1.0	0.6	0.6
UEC-A/prolif	5.2	0.6	0.6	0.7	0.6	1.0	1.0	1.0	1.0	1.0	0.6
TEC-A/CEC	6.0	31.0	3.7	16.7	4.4	20.6	0.6	1.0	1.0	0.6	0.7
TECD low	1.0	4.4	1.0	1.0	6.0	1.0	1.0	1.0	1.0	0.6	0.7
TECD high	1.8	19.3	3.0	7.9	37.7	0.6	1.8	1.8	0.6	0.6	1.0
CEC	0.6	0.7	0.6	4.4	1.0	47.1	1.0	0.6	1.0	1.0	1.0
MEC	1.0	1.0	0.6	2.4	1.0	0.6	23.4	34.2	35.9	35.9	23.4

Supplementary figure 4. Single nuclei RNAseq neoplastic clusters were annotated using hypergeometric enrichment analysis, which calculates marker gene overlap (displayed as heatmap of $-\log^{10}$ p-values) with previously published neoplastic subpopulation markers[5]

Supplementary Figure 5



Supplementary figure 5. Inference of CNVs (inferCNV) in neoplastic single nuclei in 6 representative PFA presentation (P)/1st recurrence (R1) pairs aligned with CNVs inferred from bulk methylation analysis (CNV plots obtained from molecularneuropathology.org).



Supplementary Figure 6. (**A**) Ki-67 overall score in individual patient samples grouped according to (i) 1q+ and 6q- co-occurrence (1q+ and 6q-; n=14), (ii) 1q+ with wildtype 6q (1q+ only; n=9), (iii) 6q- with wildtype 1q (6q- only; n=3) and (iv) wildtype 1q and 6q (WT 1q and 6q; n=27). COL9A2 staining patterns representative of scoring criteria (**B**) 1, (**C**) 2, (**D**) 3 and (**E**) 4 (size bars = 50μm).