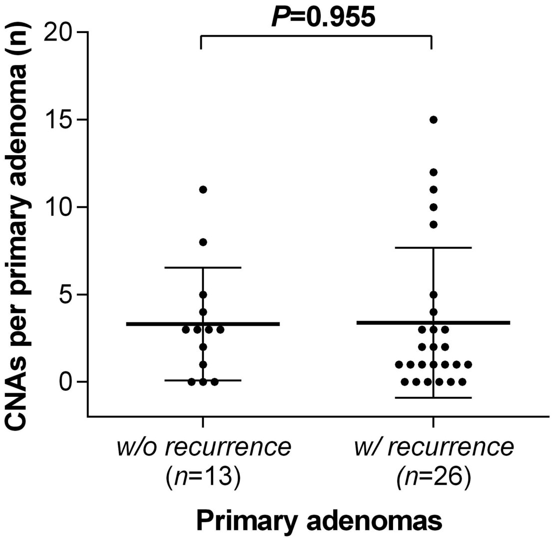
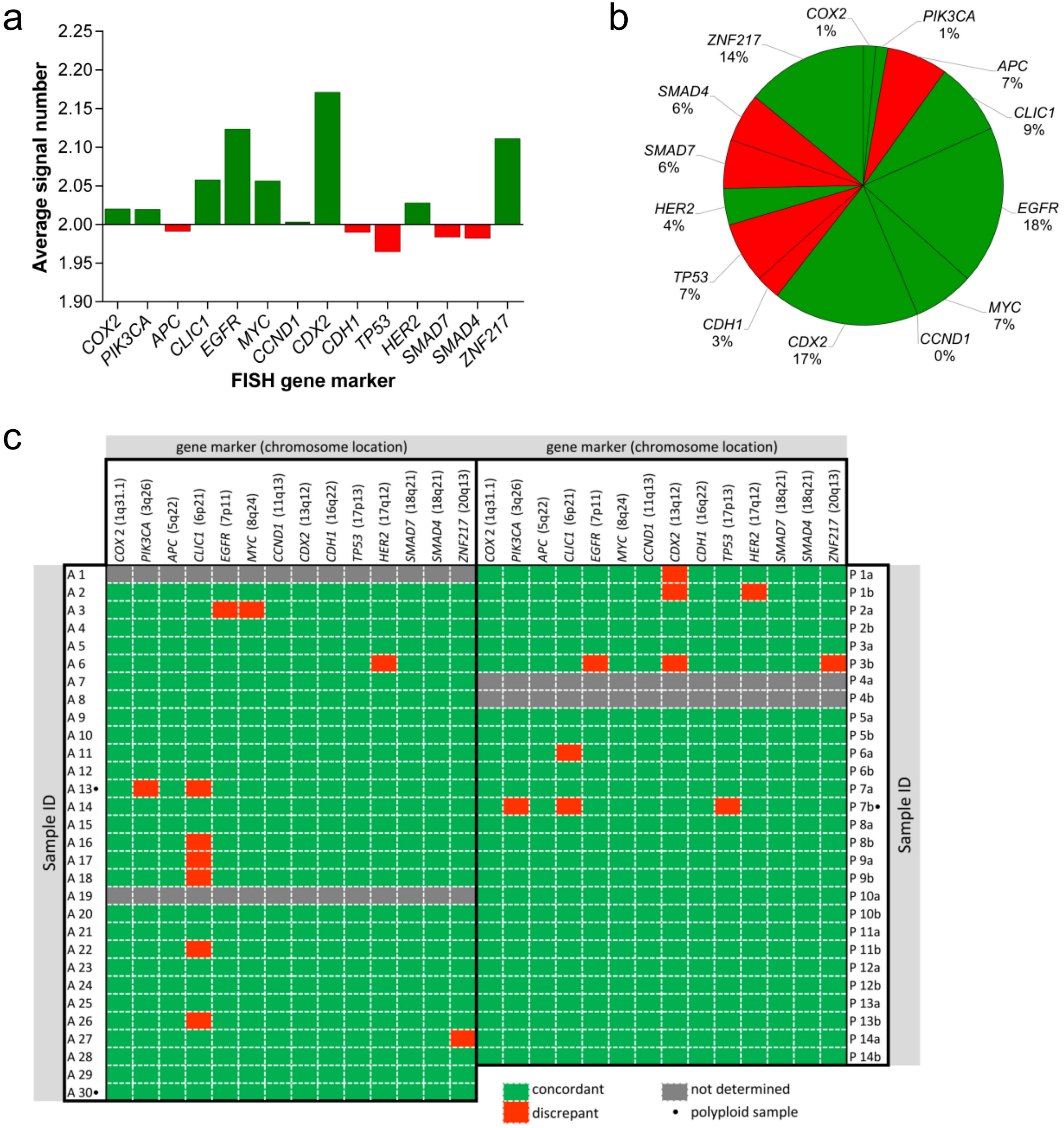


Supporting Information Figure 1



gene marker (chromosome location)

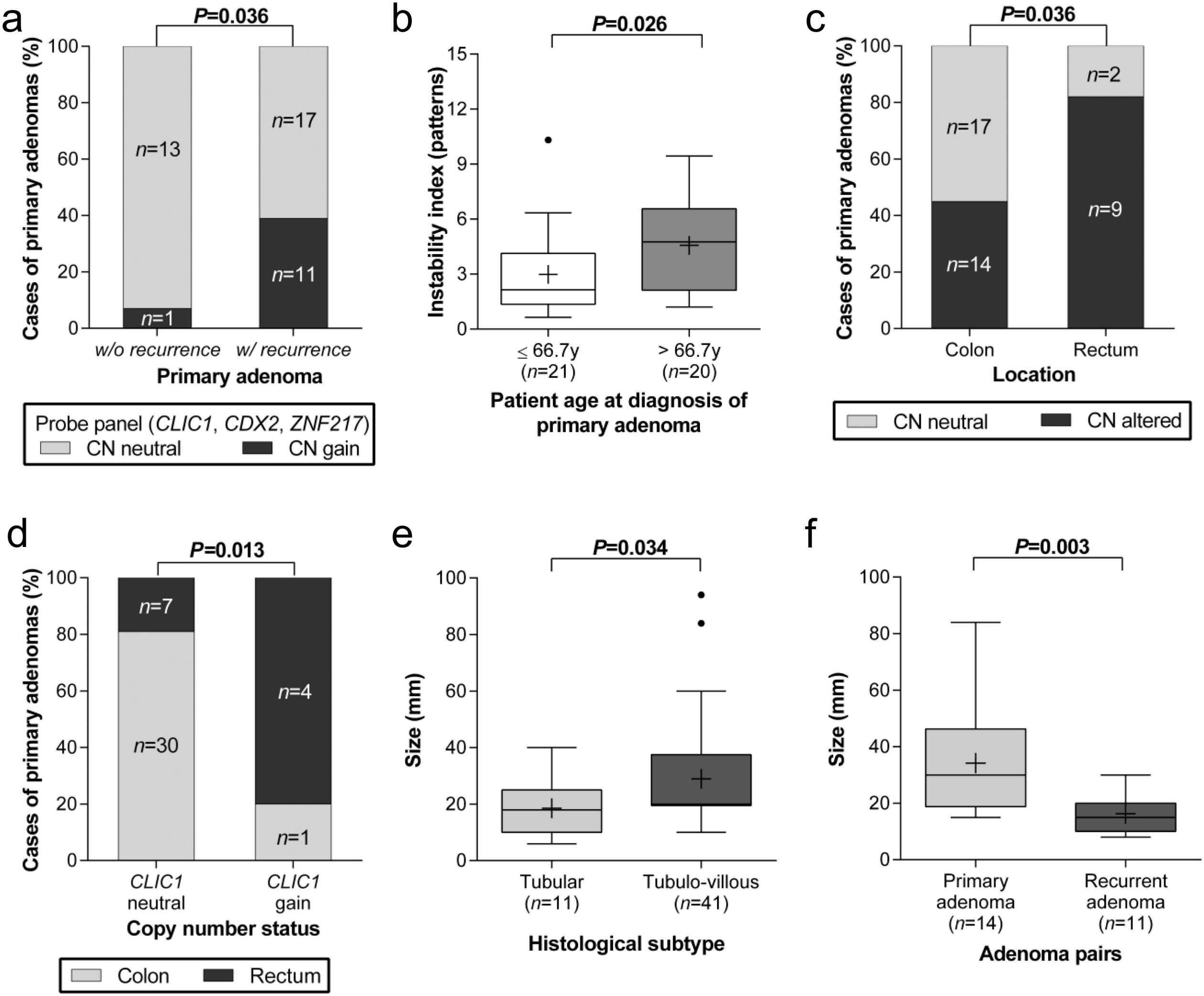
Sample ID	*COX2* (1q31.1)	*PIK3CA* (3q26)	*APC* (5q22)	*CLIC1* (6p21)	*EGFR* (7p11)	*MYC* (8q24)	*CCND1* (11q13)	*CDX2* (13q12)	*CDH1* (16q22)	*TP53* (17p13)	*HER2* (17q12)	*SMAD7* (18q21)	*SMAD4* (18q21)	*ZNF217* (20q13)
A 1	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
A 2	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 3	🟩	🟩	🟩	🟩	🟥	🟥	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 4	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 5	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 6	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟥	🟩	🟩	🟩
A 7	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 8	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 9	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 10	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 11	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 12	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 13•	🟩	🟥	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 14	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 15	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 16	🟩	🟩	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 17	🟩	🟩	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 18	🟩	🟩	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 19	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
A 20	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 21	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 22	🟩	🟩	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 23	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 24	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 25	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 26	🟩	🟩	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 27	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟥
A 28	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 29	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
A 30•	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩

gene marker (chromosome location)

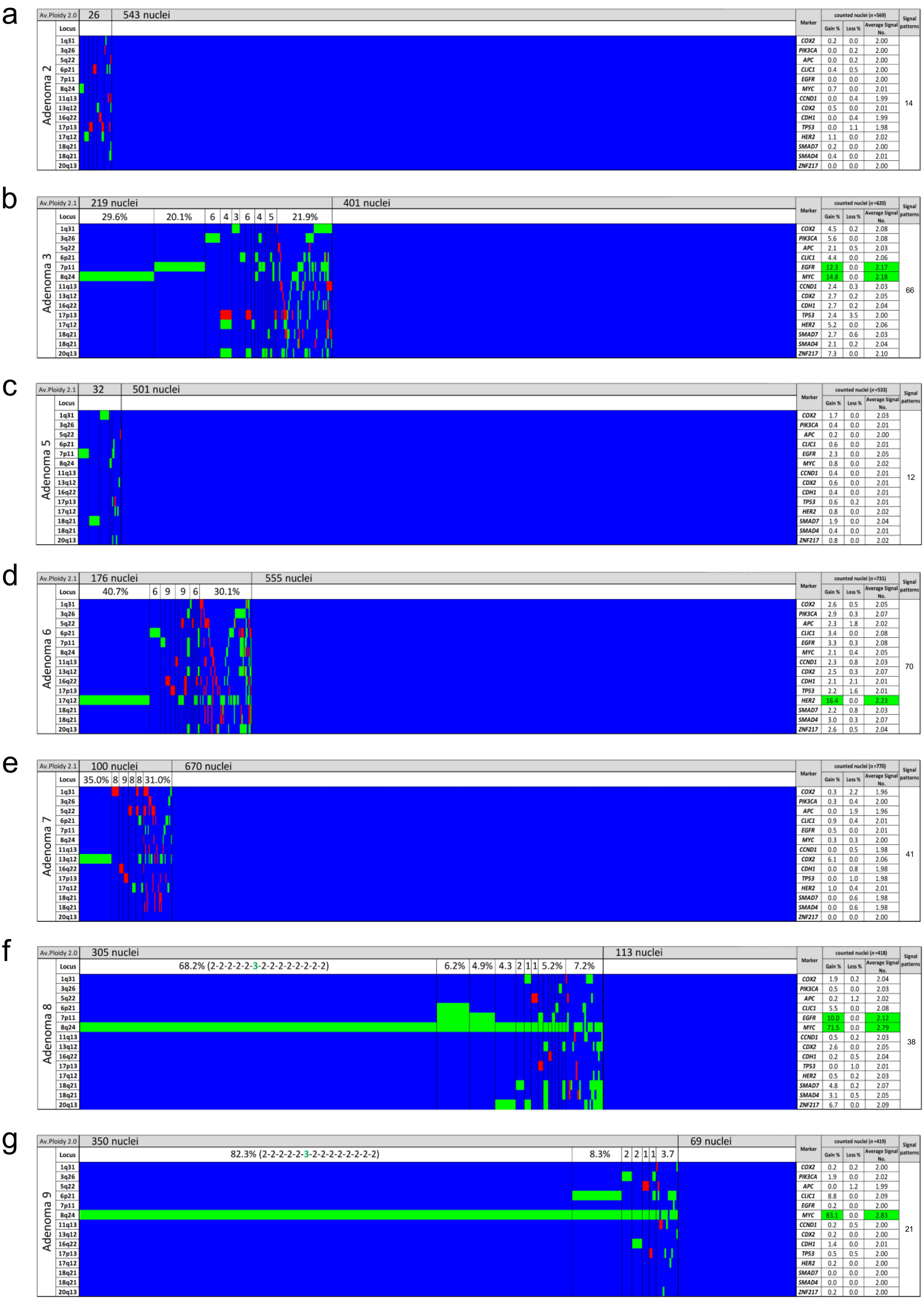
Sample ID	*COX2* (1q31.1)	*PIK3CA* (3q26)	*APC* (5q22)	*CLIC1* (6p21)	*EGFR* (7p11)	*MYC* (8q24)	*CCND1* (11q13)	*CDX2* (13q12)	*CDH1* (16q22)	*TP53* (17p13)	*HER2* (17q12)	*SMAD7* (18q21)	*SMAD4* (18q21)	*ZNF217* (20q13)
P 1a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟩
P 1b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟥	🟩	🟩	🟥	🟩	🟩	🟩
P 2a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 2b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 3a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 3b	🟩	🟩	🟩	🟩	🟥	🟩	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟥
P 4a	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
P 4b	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
P 5a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 5b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 6a	🟩	🟩	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 6b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 7a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 7b•	🟩	🟥	🟩	🟥	🟩	🟩	🟩	🟩	🟩	🟥	🟩	🟩	🟩	🟩
P 8a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 8b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 9a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 9b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 10a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 10b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 11a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 11b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 12a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 12b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 13a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 13b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 14a	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
P 14b	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩

🟩 concordant
🟥 discrepant
▨ not determined
• polyploid sample

Supporting Information Figure 2



Supporting Information Figure 3



a – Adenoma 2

Marker	counted nuclei (*n* =569)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.2	0.0	2.00	14
PIK3CA	0.0	0.2	2.00	
APC	0.0	0.2	2.00	
CLIC1	0.4	0.5	2.00	
EGFR	0.0	0.0	2.00	
MYC	0.7	0.0	2.01	
CCND1	0.0	0.4	1.99	
CDX2	0.5	0.0	2.01	
CDH1	0.0	0.4	1.99	
TP53	0.0	1.1	1.98	
HER2	1.1	0.0	2.02	
SMAD7	0.2	0.0	2.00	
SMAD4	0.4	0.0	2.01	
ZNF217	0.0	0.0	2.00	

b – Adenoma 3

Marker	counted nuclei (*n* =620)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	4.5	0.2	2.08	66
PIK3CA	5.6	0.0	2.08	
APC	2.1	0.5	2.03	
CLIC1	4.4	0.0	2.06	
EGFR	12.3	0.0	2.17	
MYC	14.8	0.0	2.18	
CCND1	2.4	0.3	2.03	
CDX2	2.7	0.2	2.05	
CDH1	2.7	0.2	2.04	
TP53	2.4	3.5	2.00	
HER2	5.2	0.0	2.06	
SMAD7	2.7	0.6	2.03	
SMAD4	2.1	0.2	2.04	
ZNF217	7.3	0.0	2.10	

c – Adenoma 5

Marker	counted nuclei (*n* =533)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	1.7	0.0	2.03	12
PIK3CA	0.4	0.0	2.01	
APC	0.2	0.0	2.00	
CLIC1	0.6	0.0	2.01	
EGFR	2.3	0.0	2.05	
MYC	0.8	0.0	2.02	
CCND1	0.4	0.0	2.01	
CDX2	0.6	0.0	2.01	
CDH1	0.4	0.0	2.01	
TP53	0.6	0.2	2.01	
HER2	0.8	0.0	2.02	
SMAD7	1.9	0.0	2.04	
SMAD4	0.4	0.0	2.01	
ZNF217	0.8	0.0	2.02	

d – Adenoma 6

Marker	counted nuclei (*n* =731)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	2.6	0.5	2.05	70
PIK3CA	2.9	0.3	2.07	
APC	2.3	1.8	2.02	
CLIC1	3.4	0.0	2.08	
EGFR	3.3	0.3	2.08	
MYC	2.1	0.4	2.05	
CCND1	2.3	0.8	2.03	
CDX2	2.5	0.3	2.07	
CDH1	2.1	2.1	2.01	
TP53	2.2	1.6	2.01	
HER2	16.4	0.0	2.23	
SMAD7	2.2	0.8	2.03	
SMAD4	3.0	0.3	2.07	
ZNF217	2.6	0.5	2.04	

e – Adenoma 7

Marker	counted nuclei (*n* =770)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.3	2.2	1.96	41
PIK3CA	0.3	0.4	2.00	
APC	0.0	1.9	1.96	
CLIC1	0.9	0.4	2.01	
EGFR	0.5	0.0	2.01	
MYC	0.3	0.3	2.00	
CCND1	0.0	0.5	1.98	
CDX2	6.1	0.0	2.06	
CDH1	0.0	0.8	1.98	
TP53	0.0	1.0	1.98	
HER2	1.0	0.4	2.01	
SMAD7	0.0	0.6	1.98	
SMAD4	0.0	0.6	1.98	
ZNF217	0.0	0.0	2.00	

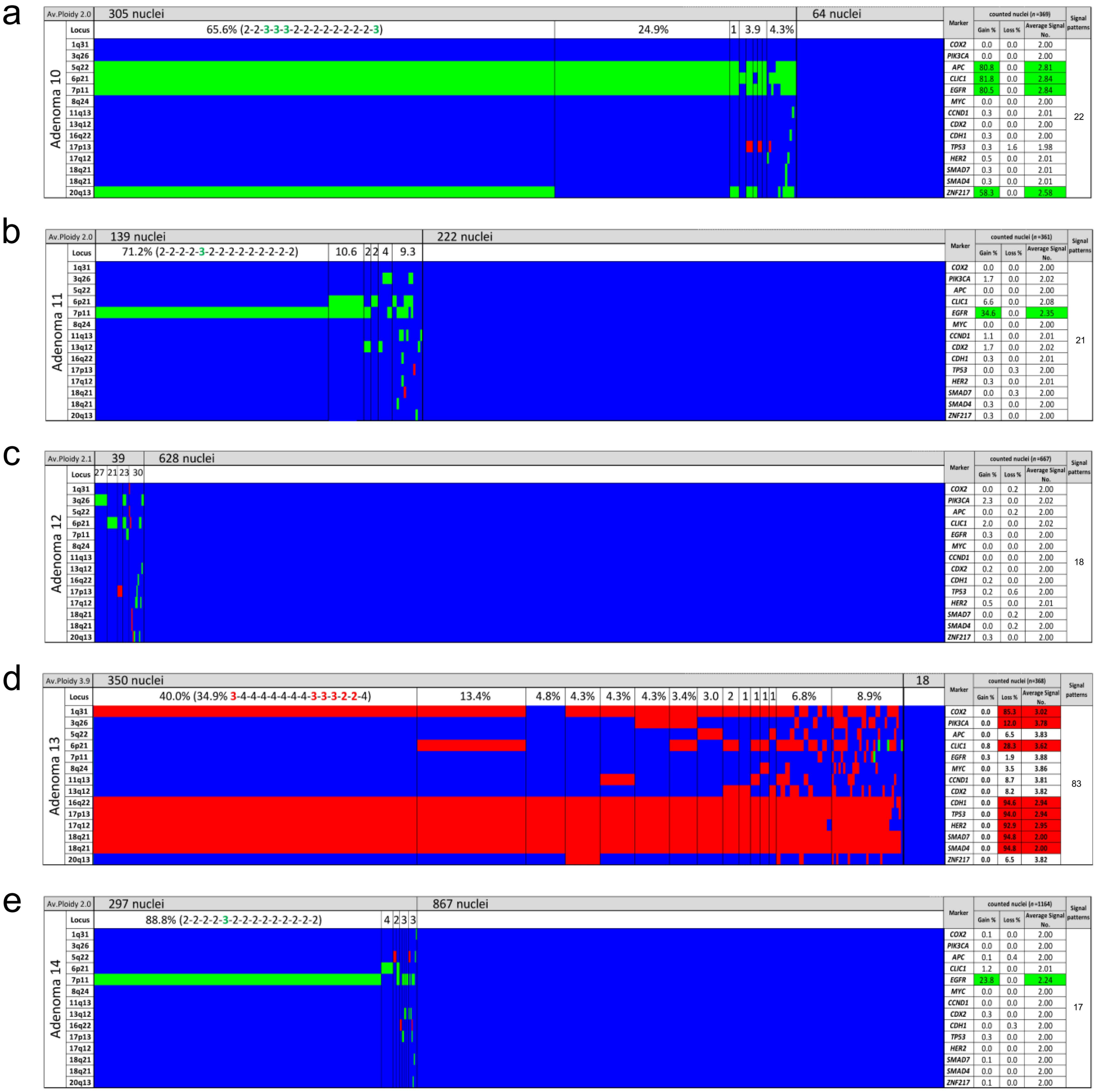
f – Adenoma 8

Marker	counted nuclei (*n* =418)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	1.9	0.2	2.04	38
PIK3CA	0.5	0.0	2.03	
APC	0.2	1.2	2.02	
CLIC1	5.5	0.0	2.08	
EGFR	10.0	0.0	2.12	
MYC	71.5	0.0	2.79	
CCND1	0.5	0.2	2.03	
CDX2	2.6	0.0	2.05	
CDH1	0.2	0.5	2.04	
TP53	0.0	1.0	2.01	
HER2	0.5	0.2	2.03	
SMAD7	4.8	0.2	2.07	
SMAD4	3.1	0.5	2.05	
ZNF217	6.7	0.0	2.09	

g – Adenoma 9

Marker	counted nuclei (*n* =419)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.2	0.2	2.00	21
PIK3CA	1.9	0.0	2.02	
APC	0.0	1.2	1.99	
CLIC1	8.8	0.0	2.09	
EGFR	0.2	0.0	2.00	
MYC	83.1	0.0	2.83	
CCND1	0.2	0.5	2.00	
CDX2	0.2	0.0	2.00	
CDH1	1.4	0.0	2.01	
TP53	0.5	0.5	2.00	
HER2	0.2	0.0	2.00	
SMAD7	0.0	0.0	2.00	
SMAD4	0.0	0.0	2.00	
ZNF217	0.2	0.0	2.00	

Supporting Information Figure 4



a

Marker	counted nuclei (*n* =369)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.00	22
PIK3CA	0.0	0.0	2.00	
APC	80.8	0.0	2.81	
CLIC1	81.8	0.0	2.84	
EGFR	80.5	0.0	2.84	
MYC	0.0	0.0	2.00	
CCND1	0.3	0.0	2.01	
CDX2	0.0	0.0	2.00	
CDH1	0.3	0.0	2.00	
TP53	0.3	1.6	1.98	
HER2	0.5	0.0	2.01	
SMAD7	0.3	0.0	2.01	
SMAD4	0.3	0.0	2.01	
ZNF217	58.3	0.0	2.58	

b

Marker	counted nuclei (*n* =361)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.00	21
PIK3CA	1.7	0.0	2.02	
APC	0.0	0.0	2.00	
CLIC1	6.6	0.0	2.08	
EGFR	34.6	0.0	2.35	
MYC	0.0	0.0	2.00	
CCND1	1.1	0.0	2.01	
CDX2	1.7	0.0	2.02	
CDH1	0.3	0.0	2.01	
TP53	0.0	0.3	2.00	
HER2	0.3	0.0	2.01	
SMAD7	0.0	0.3	2.00	
SMAD4	0.3	0.0	2.00	
ZNF217	0.3	0.0	2.00	

c

Marker	counted nuclei (*n* =667)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.2	2.00	18
PIK3CA	2.3	0.0	2.02	
APC	0.0	0.2	2.00	
CLIC1	2.0	0.0	2.02	
EGFR	0.3	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.2	0.0	2.00	
CDH1	0.2	0.0	2.00	
TP53	0.2	0.6	2.00	
HER2	0.5	0.0	2.01	
SMAD7	0.0	0.2	2.00	
SMAD4	0.0	0.2	2.00	
ZNF217	0.3	0.0	2.00	

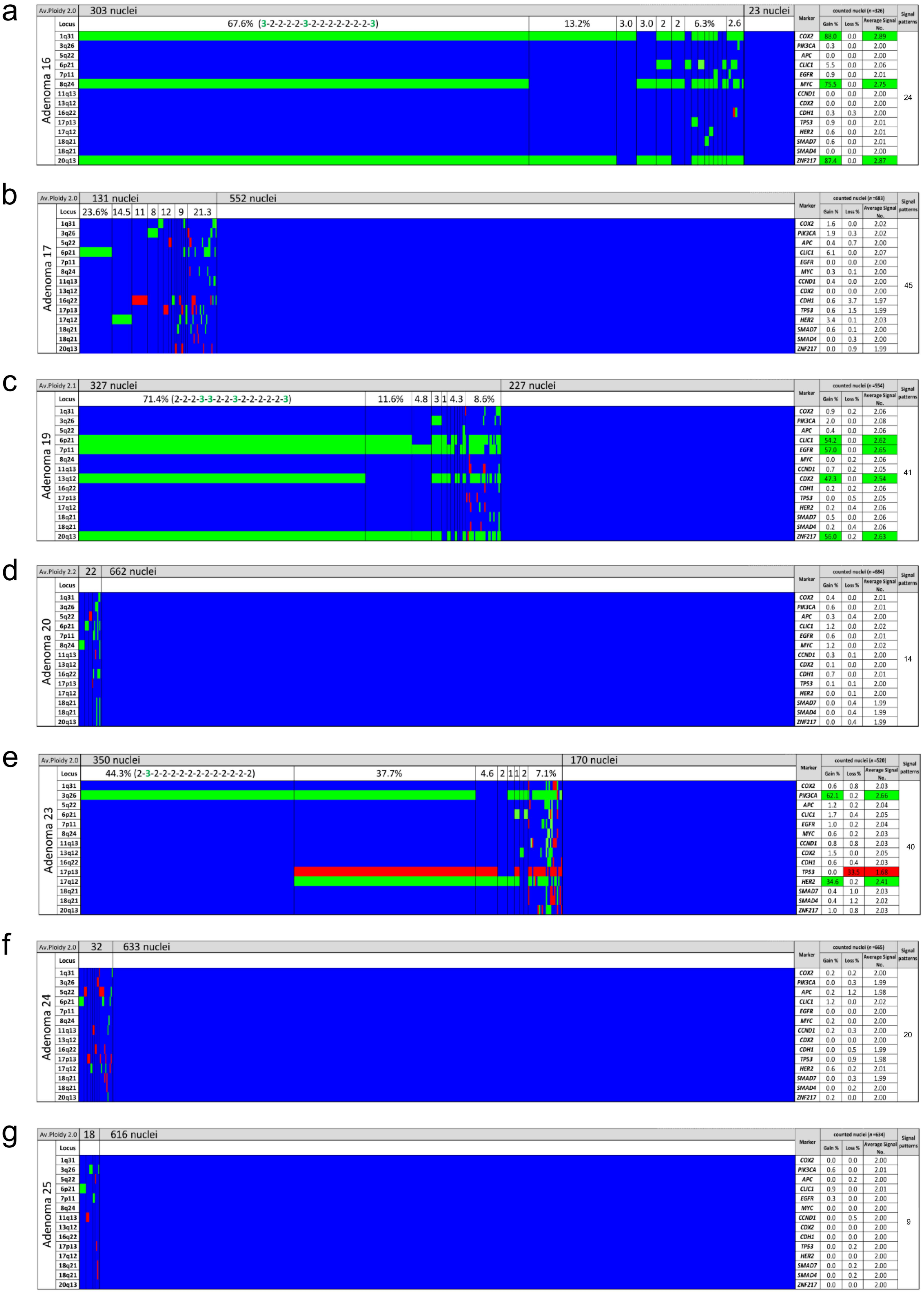
d

Marker	counted nuclei (n=368)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	85.3	3.02	83
PIK3CA	0.0	12.0	3.78	
APC	0.0	6.5	3.83	
CLIC1	0.8	28.3	3.62	
EGFR	0.3	1.9	3.88	
MYC	0.0	3.5	3.86	
CCND1	0.0	8.7	3.81	
CDX2	0.0	8.2	3.82	
CDH1	0.0	94.6	2.94	
TP53	0.0	94.0	2.94	
HER2	0.0	92.9	2.95	
SMAD7	0.0	94.8	2.00	
SMAD4	0.0	94.8	2.00	
ZNF217	0.0	6.5	3.82	

e

Marker	counted nuclei (*n* =1164)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.1	0.0	2.00	17
PIK3CA	0.0	0.0	2.00	
APC	0.1	0.4	2.00	
CLIC1	1.2	0.0	2.01	
EGFR	23.8	0.0	2.24	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.3	0.0	2.00	
CDH1	0.0	0.3	2.00	
TP53	0.3	0.0	2.00	
HER2	0.0	0.0	2.00	
SMAD7	0.1	0.0	2.00	
SMAD4	0.0	0.0	2.00	
ZNF217	0.1	0.0	2.00	

Supporting Information Figure 5



a Adenoma 16

Locus	Marker	counted nuclei (*n* =326)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	88.0	0.0	2.89	24
3q26	*PIK3CA*	0.3	0.0	2.00	
5q22	*APC*	0.0	0.0	2.00	
6p21	*CLIC1*	5.5	0.0	2.06	
7p11	*EGFR*	0.9	0.0	2.01	
8q24	*MYC*	75.5	0.0	2.75	
11q13	*CCND1*	0.0	0.0	2.00	
13q12	*CDX2*	0.0	0.0	2.00	
16q22	*CDH1*	0.3	0.3	2.00	
17p13	*TP53*	0.9	0.0	2.01	
17q12	*HER2*	0.6	0.0	2.01	
18q21	*SMAD7*	0.6	0.0	2.01	
18q21	*SMAD4*	0.0	0.0	2.00	
20q13	*ZNF217*	87.4	0.0	2.87	

b Adenoma 17

Locus	Marker	counted nuclei (*n* =683)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	1.6	0.0	2.02	45
3q26	*PIK3CA*	1.9	0.3	2.02	
5q22	*APC*	0.4	0.7	2.00	
6p21	*CLIC1*	6.1	0.0	2.07	
7p11	*EGFR*	0.0	0.0	2.00	
8q24	*MYC*	0.3	0.1	2.00	
11q13	*CCND1*	0.4	0.0	2.00	
13q12	*CDX2*	0.0	0.0	2.00	
16q22	*CDH1*	0.6	3.7	1.97	
17p13	*TP53*	0.6	1.5	1.99	
17q12	*HER2*	3.4	0.1	2.03	
18q21	*SMAD7*	0.6	0.1	2.00	
18q21	*SMAD4*	0.0	0.3	2.00	
20q13	*ZNF217*	0.0	0.9	1.99	

c Adenoma 19

Locus	Marker	counted nuclei (*n* =554)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	0.9	0.2	2.06	41
3q26	*PIK3CA*	2.0	0.0	2.08	
5q22	*APC*	0.4	0.0	2.06	
6p21	*CLIC1*	54.2	0.0	2.62	
7p11	*EGFR*	57.0	0.0	2.65	
8q24	*MYC*	0.0	0.2	2.06	
11q13	*CCND1*	0.7	0.2	2.05	
13q12	*CDX2*	47.3	0.0	2.54	
16q22	*CDH1*	0.2	0.2	2.06	
17p13	*TP53*	0.0	0.5	2.05	
17q12	*HER2*	0.2	0.4	2.06	
18q21	*SMAD7*	0.5	0.0	2.06	
18q21	*SMAD4*	0.2	0.4	2.06	
20q13	*ZNF217*	56.0	0.2	2.63	

d Adenoma 20

Locus	Marker	counted nuclei (*n* =684)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	0.4	0.0	2.01	14
3q26	*PIK3CA*	0.6	0.0	2.01	
5q22	*APC*	0.3	0.4	2.00	
6p21	*CLIC1*	1.2	0.0	2.02	
7p11	*EGFR*	0.6	0.0	2.01	
8q24	*MYC*	1.2	0.0	2.02	
11q13	*CCND1*	0.3	0.1	2.00	
13q12	*CDX2*	0.1	0.0	2.00	
16q22	*CDH1*	0.7	0.0	2.01	
17p13	*TP53*	0.1	0.1	2.00	
17q12	*HER2*	0.0	0.1	2.00	
18q21	*SMAD7*	0.0	0.4	1.99	
18q21	*SMAD4*	0.0	0.4	1.99	
20q13	*ZNF217*	0.0	0.4	1.99	

e Adenoma 23

Locus	Marker	counted nuclei (*n* =520)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	0.6	0.8	2.03	40
3q26	*PIK3CA*	62.1	0.2	2.66	
5q22	*APC*	1.2	0.2	2.04	
6p21	*CLIC1*	1.7	0.4	2.05	
7p11	*EGFR*	1.0	0.2	2.04	
8q24	*MYC*	0.6	0.2	2.03	
11q13	*CCND1*	0.8	0.8	2.03	
13q12	*CDX2*	1.5	0.0	2.05	
16q22	*CDH1*	0.6	0.4	2.03	
17p13	*TP53*	0.0	33.5	1.68	
17q12	*HER2*	34.6	0.2	2.41	
18q21	*SMAD7*	0.4	1.0	2.03	
18q21	*SMAD4*	0.4	1.2	2.02	
20q13	*ZNF217*	1.0	0.8	2.03	

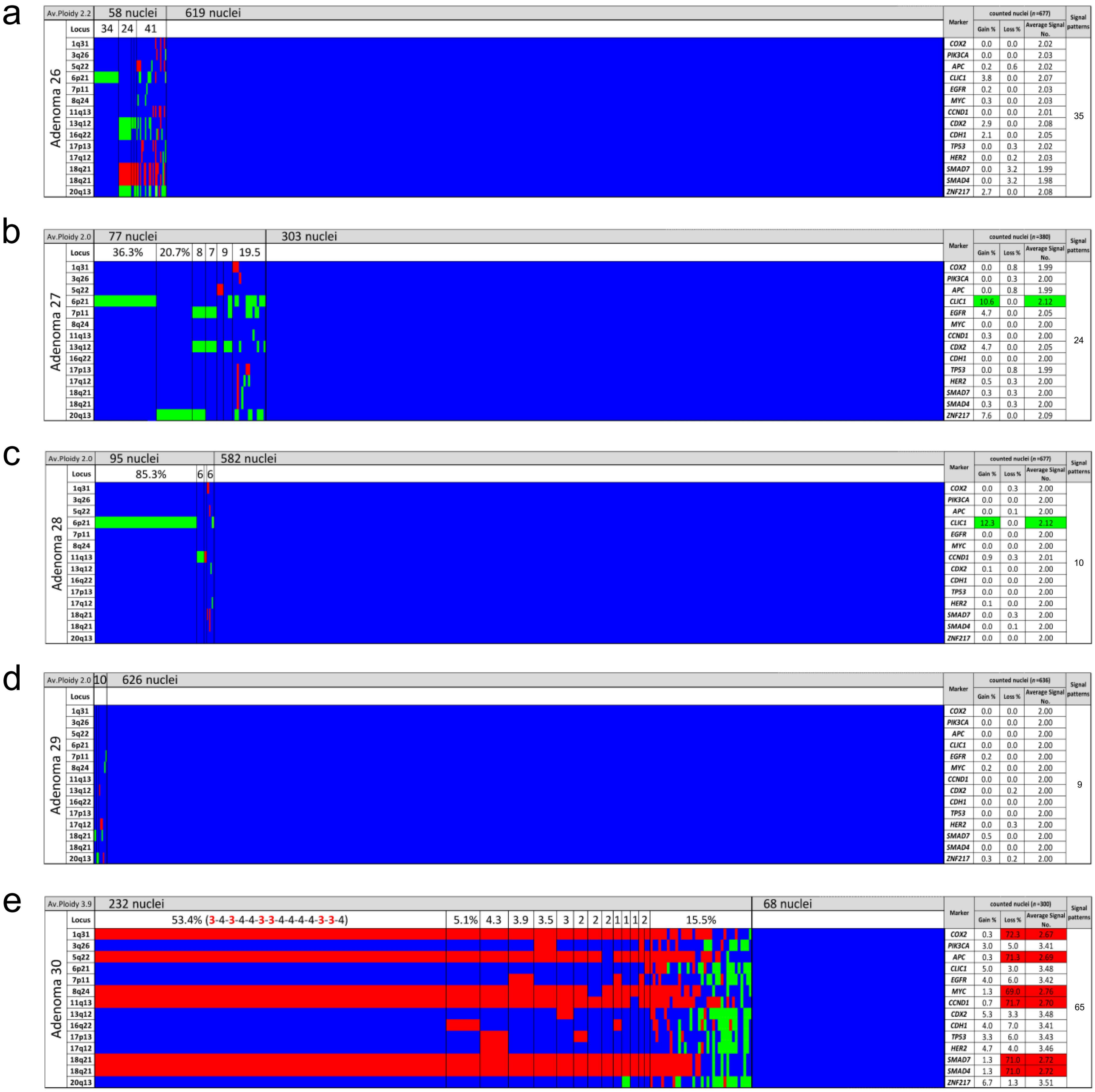
f Adenoma 24

Locus	Marker	counted nuclei (*n* =665)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	0.2	0.2	2.00	20
3q26	*PIK3CA*	0.0	0.3	1.99	
5q22	*APC*	0.2	1.2	1.98	
6p21	*CLIC1*	1.2	0.0	2.02	
7p11	*EGFR*	0.0	0.0	2.00	
8q24	*MYC*	0.2	0.0	2.00	
11q13	*CCND1*	0.2	0.3	2.00	
13q12	*CDX2*	0.0	0.0	2.00	
16q22	*CDH1*	0.0	0.5	1.99	
17p13	*TP53*	0.0	0.9	1.98	
17q12	*HER2*	0.6	0.2	2.01	
18q21	*SMAD7*	0.0	0.3	1.99	
18q21	*SMAD4*	0.0	0.2	2.00	
20q13	*ZNF217*	0.2	0.0	2.00	

g Adenoma 25

Locus	Marker	counted nuclei (*n* =634)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	0.0	0.0	2.00	9
3q26	*PIK3CA*	0.6	0.0	2.01	
5q22	*APC*	0.0	0.2	2.00	
6p21	*CLIC1*	0.9	0.0	2.01	
7p11	*EGFR*	0.3	0.0	2.00	
8q24	*MYC*	0.0	0.0	2.00	
11q13	*CCND1*	0.0	0.5	2.00	
13q12	*CDX2*	0.0	0.0	2.00	
16q22	*CDH1*	0.0	0.0	2.00	
17p13	*TP53*	0.0	0.2	2.00	
17q12	*HER2*	0.0	0.0	2.00	
18q21	*SMAD7*	0.0	0.2	2.00	
18q21	*SMAD4*	0.0	0.2	2.00	
20q13	*ZNF217*	0.0	0.0	2.00	

Supporting Information Figure 6



Marker	counted nuclei (*n*=677)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.02	35
PIK3CA	0.0	0.0	2.03	
APC	0.2	0.6	2.02	
CLIC1	3.8	0.0	2.07	
EGFR	0.2	0.0	2.03	
MYC	0.3	0.0	2.03	
CCND1	0.0	0.0	2.01	
CDX2	2.9	0.0	2.08	
CDH1	2.1	0.0	2.05	
TP53	0.0	0.3	2.02	
HER2	0.0	0.2	2.03	
SMAD7	0.0	3.2	1.99	
SMAD4	0.0	3.2	1.98	
ZNF217	2.7	0.0	2.08	

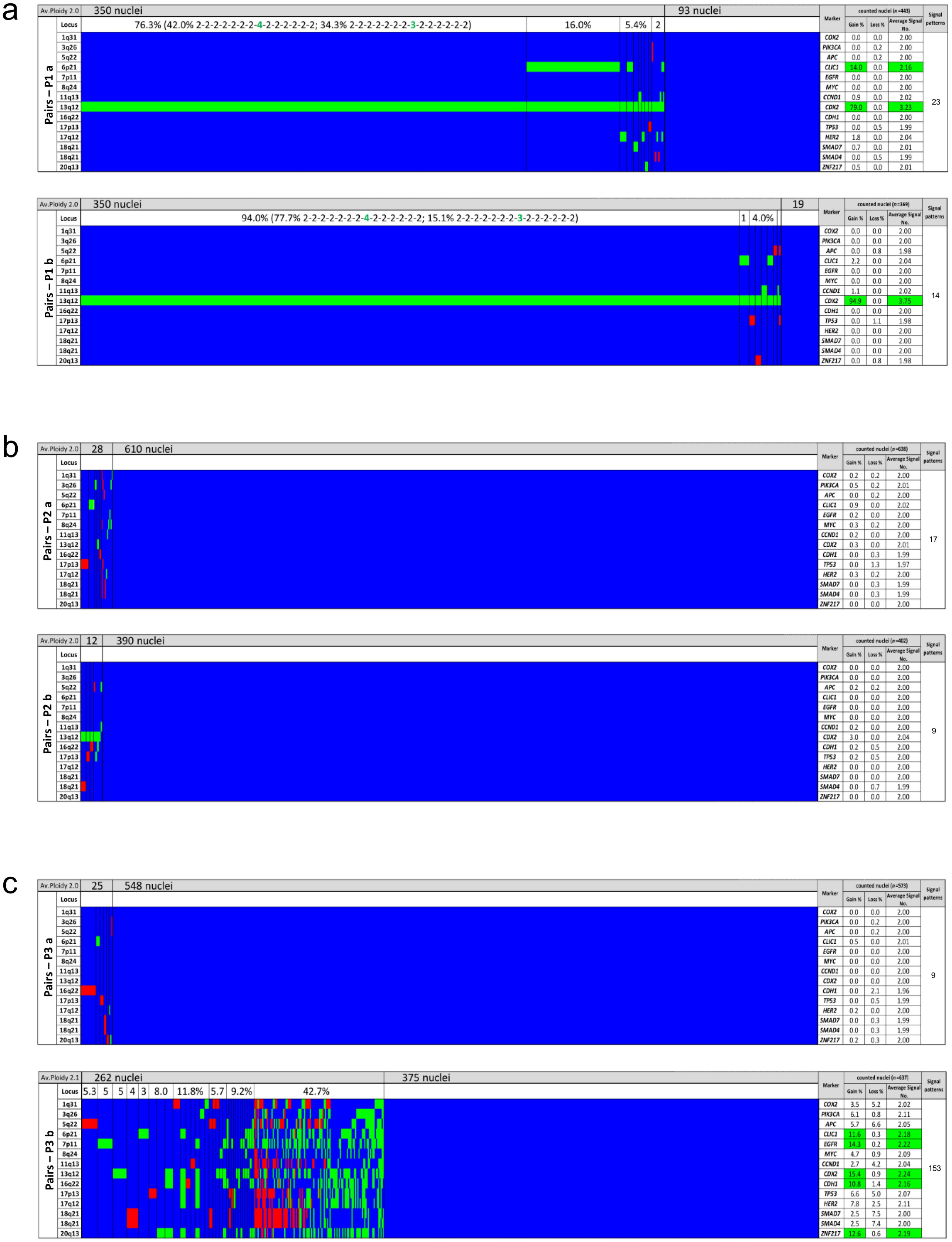
Marker	counted nuclei (*n*=380)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.8	1.99	24
PIK3CA	0.0	0.3	2.00	
APC	0.0	0.8	1.99	
CLIC1	10.6	0.0	2.12	
EGFR	4.7	0.0	2.05	
MYC	0.0	0.0	2.00	
CCND1	0.3	0.0	2.00	
CDX2	4.7	0.0	2.05	
CDH1	0.0	0.0	2.00	
TP53	0.0	0.8	1.99	
HER2	0.5	0.3	2.00	
SMAD7	0.3	0.3	2.00	
SMAD4	0.3	0.3	2.00	
ZNF217	7.6	0.0	2.09	

Marker	counted nuclei (n =677)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.3	2.00	10
PIK3CA	0.0	0.0	2.00	
APC	0.0	0.1	2.00	
CLIC1	12.3	0.0	2.12	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.9	0.3	2.01	
CDX2	0.1	0.0	2.00	
CDH1	0.0	0.0	2.00	
TP53	0.0	0.0	2.00	
HER2	0.1	0.0	2.00	
SMAD7	0.0	0.3	2.00	
SMAD4	0.0	0.1	2.00	
ZNF217	0.0	0.0	2.00	

Marker	counted nuclei (*n*=636)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.00	9
PIK3CA	0.0	0.0	2.00	
APC	0.0	0.0	2.00	
CLIC1	0.0	0.0	2.00	
EGFR	0.2	0.0	2.00	
MYC	0.2	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.0	0.2	2.00	
CDH1	0.0	0.0	2.00	
TP53	0.0	0.0	2.00	
HER2	0.0	0.3	2.00	
SMAD7	0.5	0.0	2.00	
SMAD4	0.0	0.0	2.00	
ZNF217	0.3	0.2	2.00	

Marker	counted nuclei (*n*=300)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.3	72.3	2.67	65
PIK3CA	3.0	5.0	3.41	
APC	0.3	71.3	2.69	
CLIC1	5.0	3.0	3.48	
EGFR	4.0	6.0	3.42	
MYC	1.3	69.0	2.76	
CCND1	0.7	71.7	2.70	
CDX2	5.3	3.3	3.48	
CDH1	4.0	7.0	3.41	
TP53	3.3	6.0	3.43	
HER2	4.7	4.0	3.46	
SMAD7	1.3	71.0	2.72	
SMAD4	1.3	71.0	2.72	
ZNF217	6.7	1.3	3.51	

Supporting Information Figure 7



Pairs – P1 a

Marker	counted nuclei (*n* =443)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.00	23
PIK3CA	0.0	0.2	2.00	
APC	0.0	0.2	2.00	
CLIC1	14.0	0.0	2.16	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.9	0.0	2.02	
CDX2	79.0	0.0	3.23	
CDH1	0.0	0.0	2.00	
TP53	0.0	0.5	1.99	
HER2	1.8	0.0	2.04	
SMAD7	0.7	0.0	2.01	
SMAD4	0.0	0.5	1.99	
ZNF217	0.5	0.0	2.01	

Pairs – P1 b

Marker	counted nuclei (*n* =369)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.00	14
PIK3CA	0.0	0.0	2.00	
APC	0.0	0.8	1.98	
CLIC1	2.2	0.0	2.04	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	1.1	0.0	2.02	
CDX2	94.9	0.0	3.75	
CDH1	0.0	0.0	2.00	
TP53	0.0	1.1	1.98	
HER2	0.0	0.0	2.00	
SMAD7	0.0	0.0	2.00	
SMAD4	0.0	0.0	2.00	
ZNF217	0.0	0.8	1.98	

Pairs – P2 a

Marker	counted nuclei (*n* =638)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.2	0.2	2.00	17
PIK3CA	0.5	0.2	2.01	
APC	0.0	0.2	2.00	
CLIC1	0.9	0.0	2.02	
EGFR	0.2	0.0	2.00	
MYC	0.3	0.2	2.00	
CCND1	0.2	0.0	2.00	
CDX2	0.3	0.0	2.01	
CDH1	0.0	0.3	1.99	
TP53	0.0	1.3	1.97	
HER2	0.3	0.2	2.00	
SMAD7	0.0	0.3	1.99	
SMAD4	0.0	0.3	1.99	
ZNF217	0.0	0.0	2.00	

Pairs – P2 b

Marker	counted nuclei (*n* =402)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.00	9
PIK3CA	0.0	0.0	2.00	
APC	0.2	0.2	2.00	
CLIC1	0.0	0.0	2.00	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.2	0.0	2.00	
CDX2	3.0	0.0	2.04	
CDH1	0.2	0.5	2.00	
TP53	0.2	0.5	2.00	
HER2	0.0	0.0	2.00	
SMAD7	0.0	0.0	2.00	
SMAD4	0.0	0.7	1.99	
ZNF217	0.0	0.0	2.00	

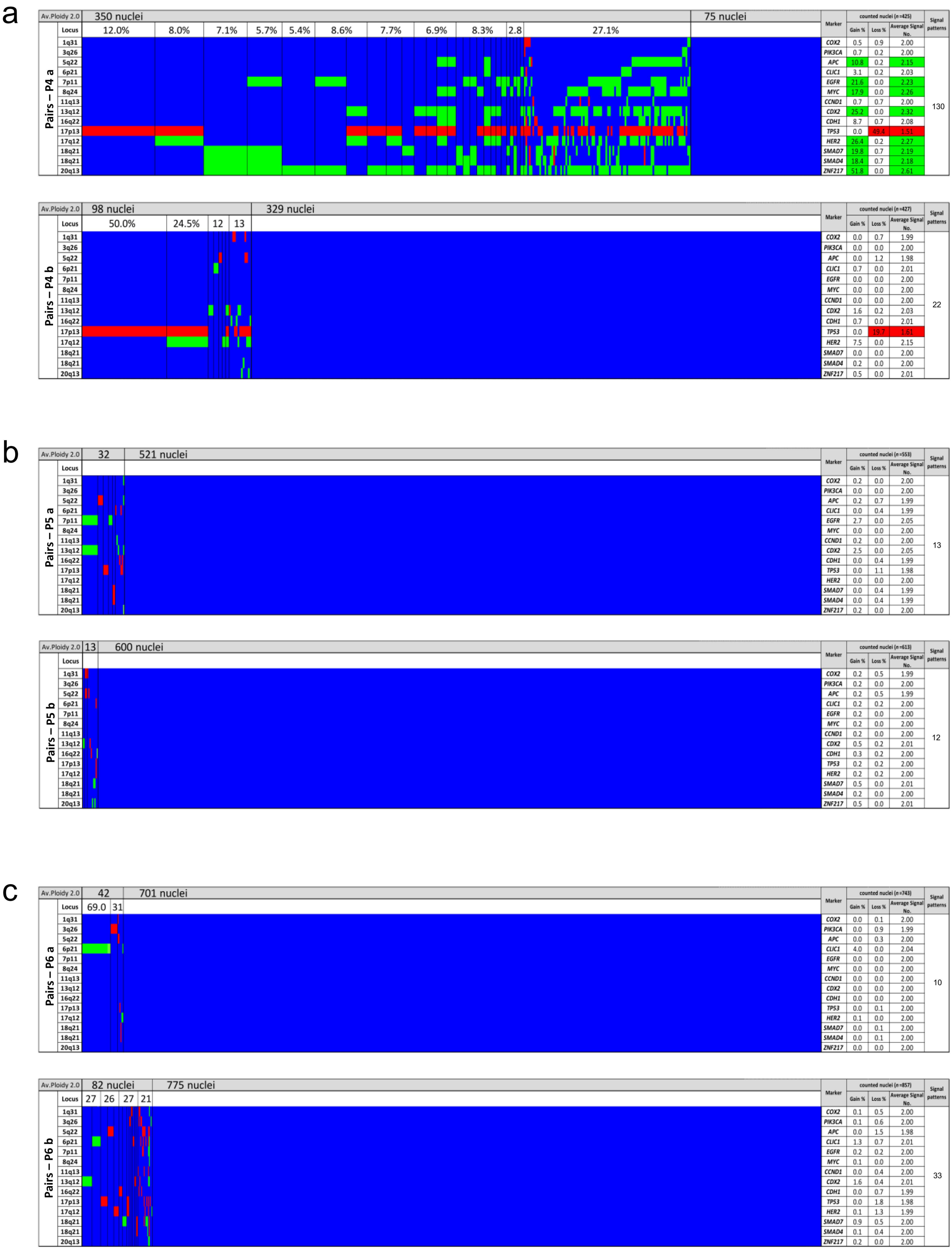
Pairs – P3 a

Marker	counted nuclei (*n* =573)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.00	9
PIK3CA	0.0	0.2	2.00	
APC	0.0	0.2	2.00	
CLIC1	0.5	0.0	2.01	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.0	0.0	2.00	
CDH1	0.0	2.1	1.96	
TP53	0.0	0.5	1.99	
HER2	0.2	0.0	2.00	
SMAD7	0.0	0.3	1.99	
SMAD4	0.0	0.3	1.99	
ZNF217	0.2	0.3	2.00	

Pairs – P3 b

Marker	counted nuclei (*n* =637)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	3.5	5.2	2.02	153
PIK3CA	6.1	0.8	2.11	
APC	5.7	6.6	2.05	
CLIC1	11.6	0.3	2.18	
EGFR	14.3	0.2	2.22	
MYC	4.7	0.9	2.09	
CCND1	2.7	4.2	2.04	
CDX2	15.4	0.9	2.24	
CDH1	10.8	1.4	2.16	
TP53	6.6	5.0	2.07	
HER2	7.8	2.5	2.11	
SMAD7	2.5	7.5	2.00	
SMAD4	2.5	7.4	2.00	
ZNF217	12.6	0.6	2.19	

Supporting Information Figure 8



Marker	counted nuclei (*n* =425)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.5	0.9	2.00	130
PIK3CA	0.7	0.2	2.00	
APC	10.8	0.2	2.15	
CLIC1	3.1	0.2	2.03	
EGFR	21.6	0.0	2.23	
MYC	17.9	0.0	2.26	
CCND1	0.7	0.7	2.00	
CDX2	25.2	0.0	2.32	
CDH1	8.7	0.7	2.08	
TP53	0.0	49.4	1.51	
HER2	26.4	0.2	2.27	
SMAD7	19.8	0.7	2.19	
SMAD4	18.4	0.7	2.18	
ZNF217	51.8	0.0	2.61	

Marker	counted nuclei (*n* =427)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.7	1.99	22
PIK3CA	0.0	0.0	2.00	
APC	0.0	1.2	1.98	
CLIC1	0.7	0.0	2.01	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	1.6	0.2	2.03	
CDH1	0.7	0.0	2.01	
TP53	0.0	19.7	1.61	
HER2	7.5	0.0	2.15	
SMAD7	0.0	0.0	2.00	
SMAD4	0.2	0.0	2.00	
ZNF217	0.5	0.0	2.01	

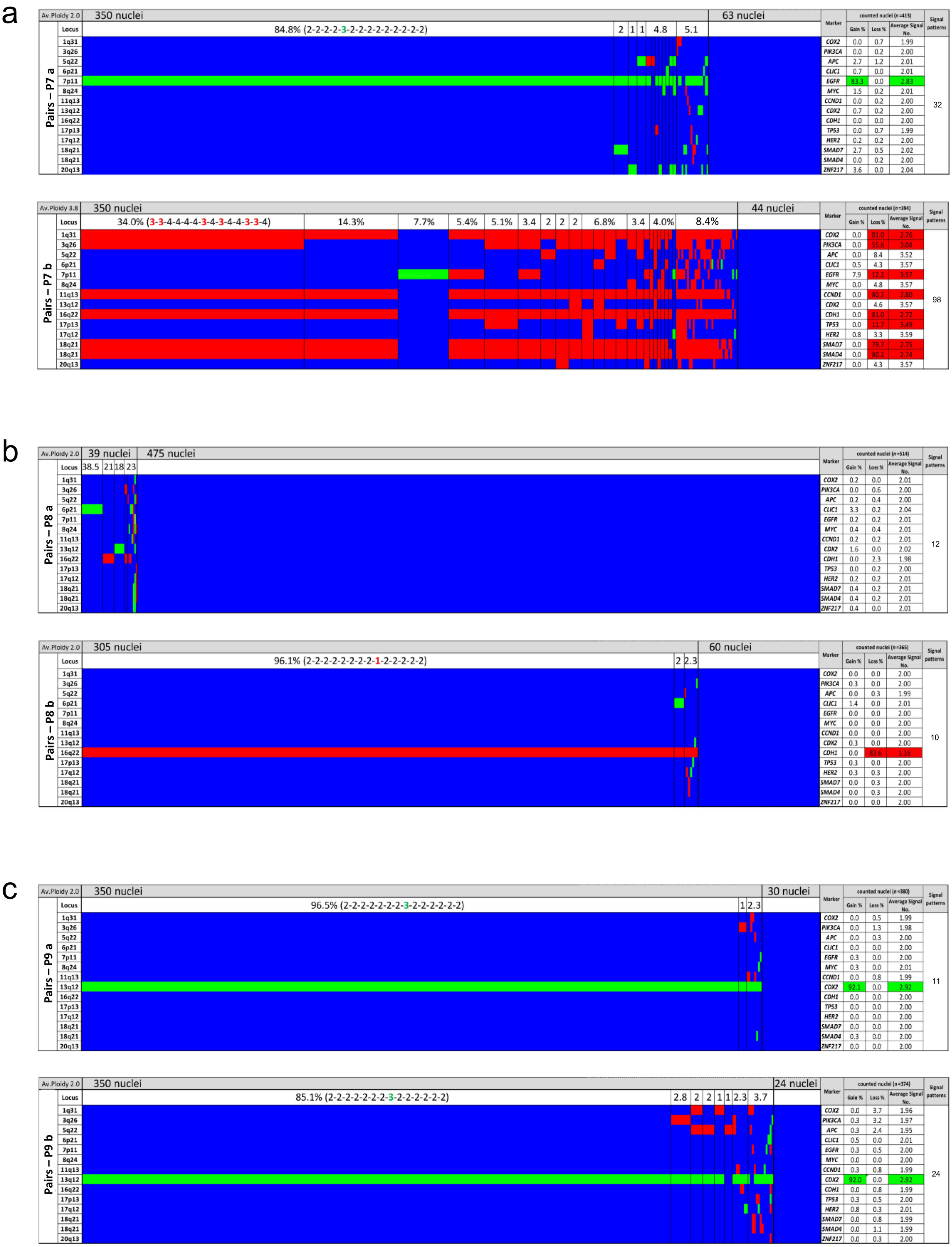
Marker	counted nuclei (*n* =553)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.2	0.0	2.00	13
PIK3CA	0.0	0.0	2.00	
APC	0.2	0.7	1.99	
CLIC1	0.0	0.4	1.99	
EGFR	2.7	0.0	2.05	
MYC	0.0	0.0	2.00	
CCND1	0.2	0.0	2.00	
CDX2	2.5	0.0	2.05	
CDH1	0.0	0.4	1.99	
TP53	0.0	1.1	1.98	
HER2	0.0	0.0	2.00	
SMAD7	0.0	0.4	1.99	
SMAD4	0.0	0.4	1.99	
ZNF217	0.2	0.0	2.00	

Marker	counted nuclei (*n* =613)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.2	0.5	1.99	12
PIK3CA	0.2	0.0	2.00	
APC	0.2	0.5	1.99	
CLIC1	0.2	0.2	2.00	
EGFR	0.2	0.0	2.00	
MYC	0.2	0.0	2.00	
CCND1	0.2	0.0	2.00	
CDX2	0.5	0.2	2.01	
CDH1	0.3	0.2	2.00	
TP53	0.2	0.2	2.00	
HER2	0.2	0.2	2.00	
SMAD7	0.5	0.0	2.01	
SMAD4	0.2	0.0	2.00	
ZNF217	0.5	0.0	2.01	

Marker	counted nuclei (*n* =743)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.1	2.00	10
PIK3CA	0.0	0.9	1.99	
APC	0.0	0.3	2.00	
CLIC1	4.0	0.0	2.04	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.0	0.0	2.00	
CDH1	0.0	0.0	2.00	
TP53	0.0	0.1	2.00	
HER2	0.1	0.0	2.00	
SMAD7	0.0	0.1	2.00	
SMAD4	0.0	0.1	2.00	
ZNF217	0.0	0.0	2.00	

Marker	counted nuclei (*n* =857)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.1	0.5	2.00	33
PIK3CA	0.1	0.6	2.00	
APC	0.0	1.5	1.98	
CLIC1	1.3	0.7	2.01	
EGFR	0.2	0.2	2.00	
MYC	0.1	0.0	2.00	
CCND1	0.0	0.4	2.00	
CDX2	1.6	0.4	2.01	
CDH1	0.0	0.7	1.99	
TP53	0.0	1.8	1.98	
HER2	0.1	1.3	1.99	
SMAD7	0.9	0.5	2.00	
SMAD4	0.1	0.4	2.00	
ZNF217	0.2	0.0	2.00	

Supporting Information Figure 9



Marker	counted nuclei (*n*=413)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.7	1.99	32
PIK3CA	0.0	0.2	2.00	
APC	2.7	1.2	2.01	
CLIC1	0.7	0.0	2.01	
EGFR	83.3	0.0	2.83	
MYC	1.5	0.2	2.01	
CCND1	0.0	0.2	2.00	
CDX2	0.7	0.2	2.00	
CDH1	0.0	0.0	2.00	
TP53	0.0	0.7	1.99	
HER2	0.2	0.2	2.00	
SMAD7	2.7	0.5	2.02	
SMAD4	0.0	0.2	2.00	
ZNF217	3.6	0.0	2.04	

Marker	counted nuclei (*n*=394)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	81.0	2.76	98
PIK3CA	0.0	55.6	3.04	
APC	0.0	8.4	3.52	
CLIC1	0.5	4.3	3.57	
EGFR	7.9	12.2	3.57	
MYC	0.0	4.8	3.57	
CCND1	0.0	80.2	2.80	
CDX2	0.0	4.6	3.57	
CDH1	0.0	81.0	2.72	
TP53	0.0	11.7	3.49	
HER2	0.8	3.3	3.59	
SMAD7	0.0	79.7	2.75	
SMAD4	0.0	80.2	2.74	
ZNF217	0.0	4.3	3.57	

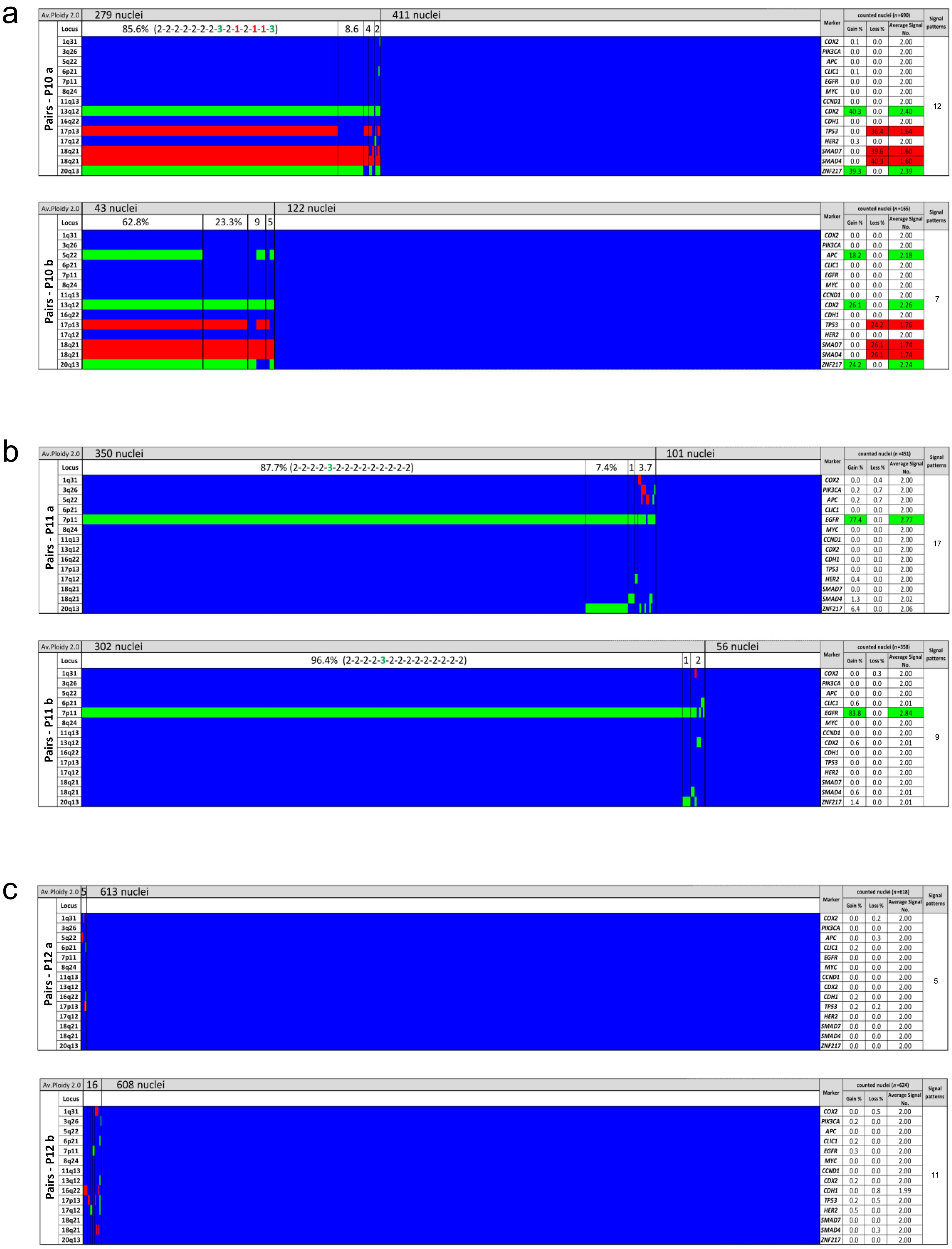
Marker	counted nuclei (*n*=514)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.2	0.0	2.01	12
PIK3CA	0.0	0.6	2.00	
APC	0.2	0.4	2.00	
CLIC1	3.3	0.2	2.04	
EGFR	0.2	0.2	2.01	
MYC	0.4	0.4	2.01	
CCND1	0.2	0.2	2.01	
CDX2	1.6	0.0	2.02	
CDH1	0.0	2.3	1.98	
TP53	0.0	0.2	2.00	
HER2	0.2	0.2	2.01	
SMAD7	0.4	0.2	2.01	
SMAD4	0.4	0.2	2.01	
ZNF217	0.4	0.0	2.01	

Marker	counted nuclei (*n*=365)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.00	10
PIK3CA	0.3	0.0	2.00	
APC	0.0	0.3	1.99	
CLIC1	1.4	0.0	2.01	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.3	0.0	2.00	
CDH1	0.0	83.6	1.16	
TP53	0.3	0.0	2.00	
HER2	0.3	0.3	2.00	
SMAD7	0.0	0.3	2.00	
SMAD4	0.0	0.3	2.00	
ZNF217	0.0	0.0	2.00	

Marker	counted nuclei (n=380)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.5	1.99	11
PIK3CA	0.0	1.3	1.98	
APC	0.0	0.3	2.00	
CLIC1	0.0	0.0	2.00	
EGFR	0.3	0.0	2.00	
MYC	0.3	0.0	2.01	
CCND1	0.0	0.8	1.99	
CDX2	92.1	0.0	2.92	
CDH1	0.0	0.0	2.00	
TP53	0.0	0.0	2.00	
HER2	0.0	0.0	2.00	
SMAD7	0.0	0.0	2.00	
SMAD4	0.3	0.0	2.00	
ZNF217	0.0	0.0	2.00	

Marker	counted nuclei (n=374)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	3.7	1.96	24
PIK3CA	0.3	3.2	1.97	
APC	0.3	2.4	1.95	
CLIC1	0.5	0.0	2.01	
EGFR	0.3	0.5	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.3	0.8	1.99	
CDX2	92.0	0.0	2.92	
CDH1	0.0	0.8	1.99	
TP53	0.3	0.5	2.00	
HER2	0.8	0.3	2.01	
SMAD7	0.0	0.8	1.99	
SMAD4	0.0	1.1	1.99	
ZNF217	0.0	0.3	2.00	

Supporting Information Figure 10



Marker	counted nuclei (*n* =690)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.1	0.0	2.00	12
PIK3CA	0.0	0.0	2.00	
APC	0.0	0.0	2.00	
CLIC1	0.1	0.0	2.00	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	40.3	0.0	2.40	
CDH1	0.0	0.0	2.00	
TP53	0.0	36.4	1.64	
HER2	0.3	0.0	2.00	
SMAD7	0.0	39.6	1.60	
SMAD4	0.0	40.3	1.60	
ZNF217	39.3	0.0	2.39	

Marker	counted nuclei (*n* =165)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.0	2.00	7
PIK3CA	0.0	0.0	2.00	
APC	18.2	0.0	2.18	
CLIC1	0.0	0.0	2.00	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	26.1	0.0	2.26	
CDH1	0.0	0.0	2.00	
TP53	0.0	24.2	1.76	
HER2	0.0	0.0	2.00	
SMAD7	0.0	26.1	1.74	
SMAD4	0.0	26.1	1.74	
ZNF217	24.2	0.0	2.24	

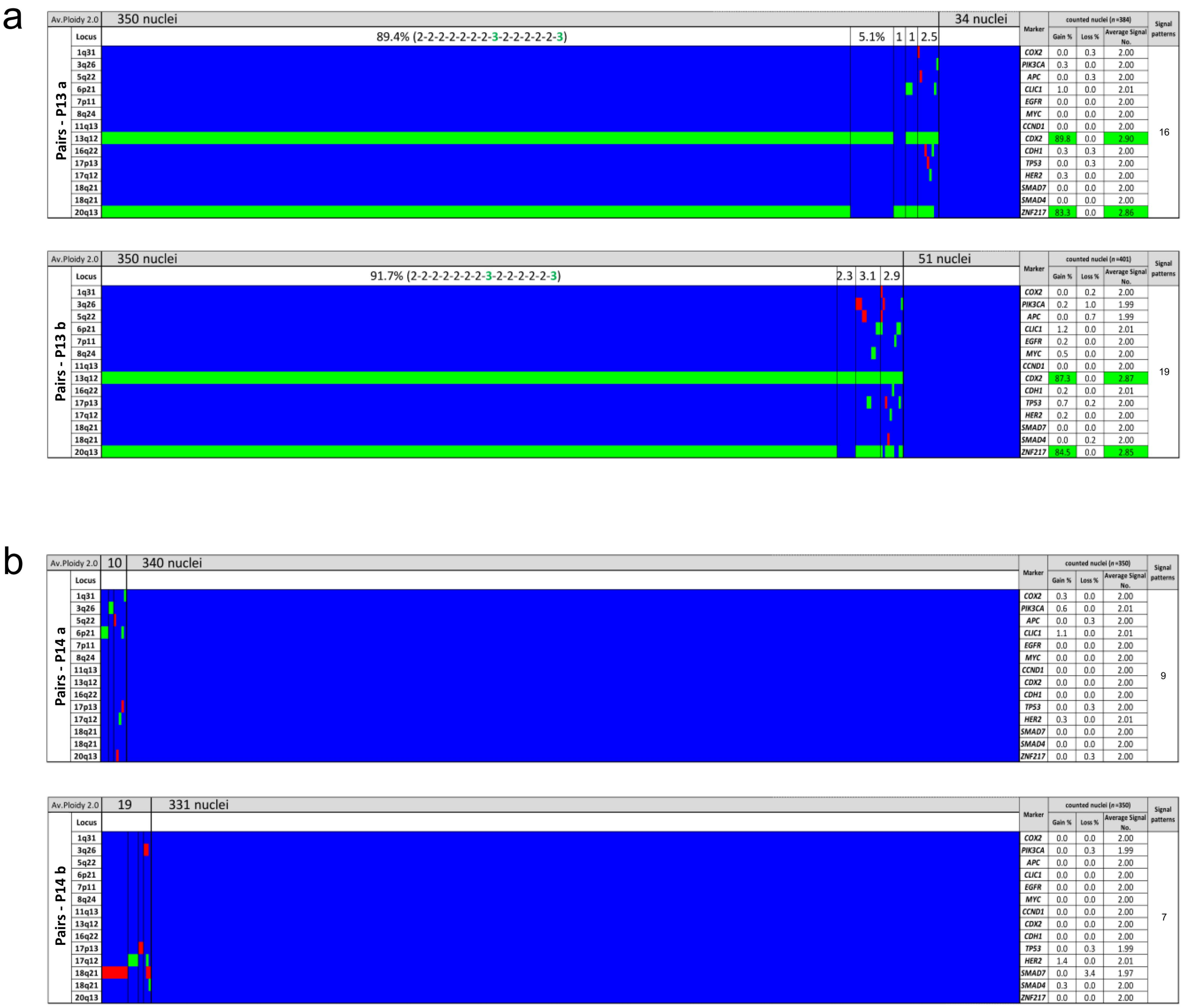
Marker	counted nuclei (n =451)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.4	2.00	17
PIK3CA	0.2	0.7	2.00	
APC	0.2	0.7	2.00	
CLIC1	0.0	0.0	2.00	
EGFR	77.4	0.0	2.77	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.0	0.0	2.00	
CDH1	0.0	0.0	2.00	
TP53	0.0	0.0	2.00	
HER2	0.4	0.0	2.00	
SMAD7	0.0	0.0	2.00	
SMAD4	1.3	0.0	2.02	
ZNF217	6.4	0.0	2.06	

Marker	counted nuclei (n =358)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.3	2.00	9
PIK3CA	0.0	0.0	2.00	
APC	0.0	0.0	2.00	
CLIC1	0.6	0.0	2.01	
EGFR	83.8	0.0	2.84	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.6	0.0	2.01	
CDH1	0.0	0.0	2.00	
TP53	0.0	0.0	2.00	
HER2	0.0	0.0	2.00	
SMAD7	0.0	0.0	2.00	
SMAD4	0.6	0.0	2.01	
ZNF217	1.4	0.0	2.01	

Marker	counted nuclei (n =618)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.2	2.00	5
PIK3CA	0.0	0.0	2.00	
APC	0.0	0.3	2.00	
CLIC1	0.2	0.0	2.00	
EGFR	0.0	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.0	0.0	2.00	
CDH1	0.2	0.0	2.00	
TP53	0.2	0.2	2.00	
HER2	0.0	0.0	2.00	
SMAD7	0.0	0.0	2.00	
SMAD4	0.0	0.0	2.00	
ZNF217	0.0	0.0	2.00	

Marker	counted nuclei (*n* =624)			Signal patterns
	Gain %	Loss %	Average Signal No.	
COX2	0.0	0.5	2.00	11
PIK3CA	0.2	0.0	2.00	
APC	0.0	0.0	2.00	
CLIC1	0.2	0.0	2.00	
EGFR	0.3	0.0	2.00	
MYC	0.0	0.0	2.00	
CCND1	0.0	0.0	2.00	
CDX2	0.2	0.0	2.00	
CDH1	0.0	0.8	1.99	
TP53	0.2	0.5	2.00	
HER2	0.5	0.0	2.00	
SMAD7	0.0	0.0	2.00	
SMAD4	0.0	0.3	2.00	
ZNF217	0.0	0.0	2.00	

Supporting Information Figure 11



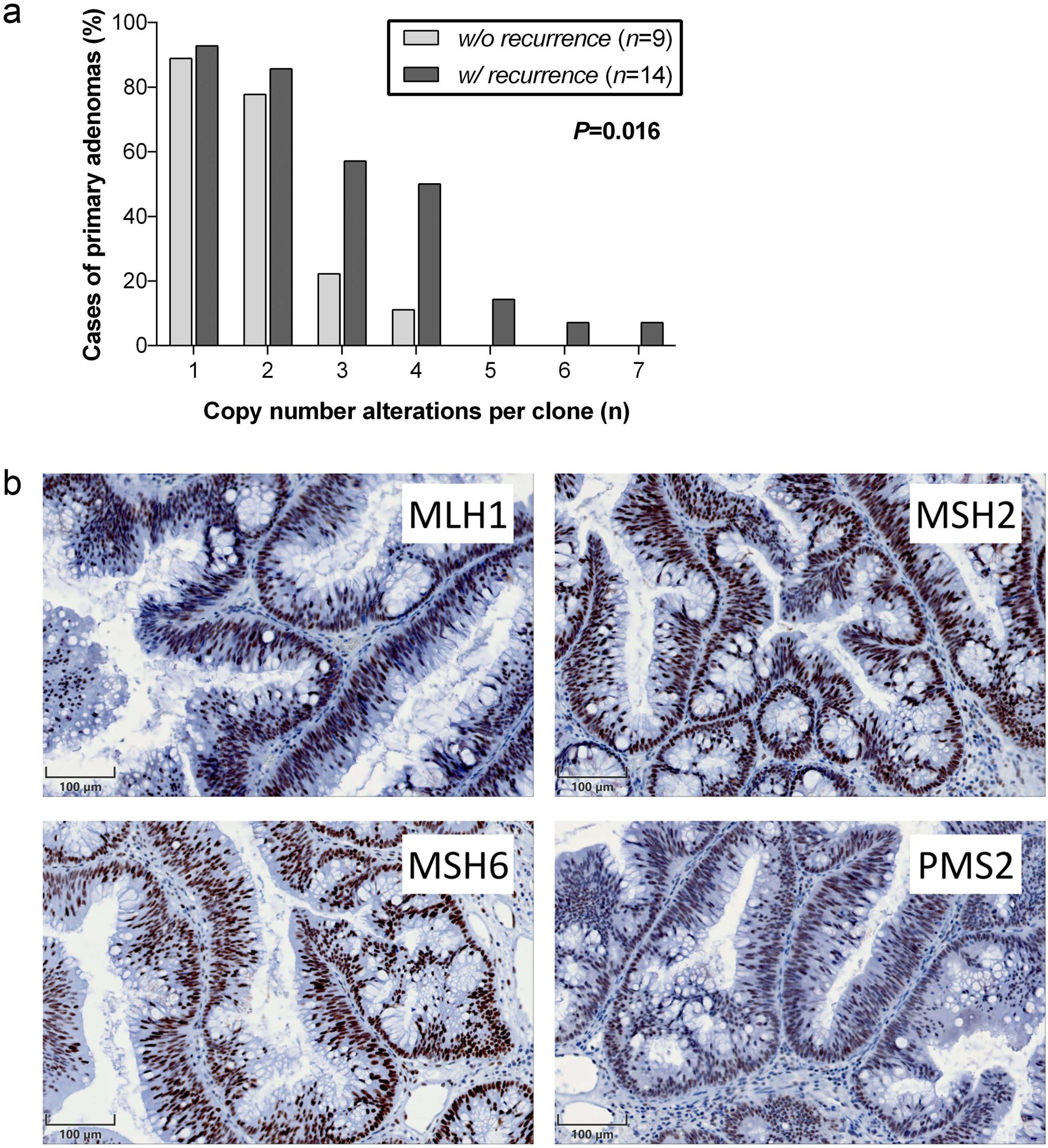
Locus	Marker	counted nuclei (*n* =384)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	0.0	0.3	2.00	16
3q26	*PIK3CA*	0.3	0.0	2.00	
5q22	*APC*	0.0	0.3	2.00	
6p21	*CLIC1*	1.0	0.0	2.01	
7p11	*EGFR*	0.0	0.0	2.00	
8q24	*MYC*	0.0	0.0	2.00	
11q13	*CCND1*	0.0	0.0	2.00	
13q12	*CDX2*	89.8	0.0	2.90	
16q22	*CDH1*	0.3	0.3	2.00	
17p13	*TP53*	0.0	0.3	2.00	
17q12	*HER2*	0.3	0.0	2.00	
18q21	*SMAD7*	0.0	0.0	2.00	
18q21	*SMAD4*	0.0	0.0	2.00	
20q13	*ZNF217*	83.3	0.0	2.86	

Locus	Marker	counted nuclei (*n* =401)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	0.0	0.2	2.00	19
3q26	*PIK3CA*	0.2	1.0	1.99	
5q22	*APC*	0.0	0.7	1.99	
6p21	*CLIC1*	1.2	0.0	2.01	
7p11	*EGFR*	0.2	0.0	2.00	
8q24	*MYC*	0.5	0.0	2.00	
11q13	*CCND1*	0.0	0.0	2.00	
13q12	*CDX2*	87.3	0.0	2.87	
16q22	*CDH1*	0.2	0.0	2.01	
17p13	*TP53*	0.7	0.2	2.00	
17q12	*HER2*	0.2	0.0	2.00	
18q21	*SMAD7*	0.0	0.0	2.00	
18q21	*SMAD4*	0.0	0.2	2.00	
20q13	*ZNF217*	84.5	0.0	2.85	

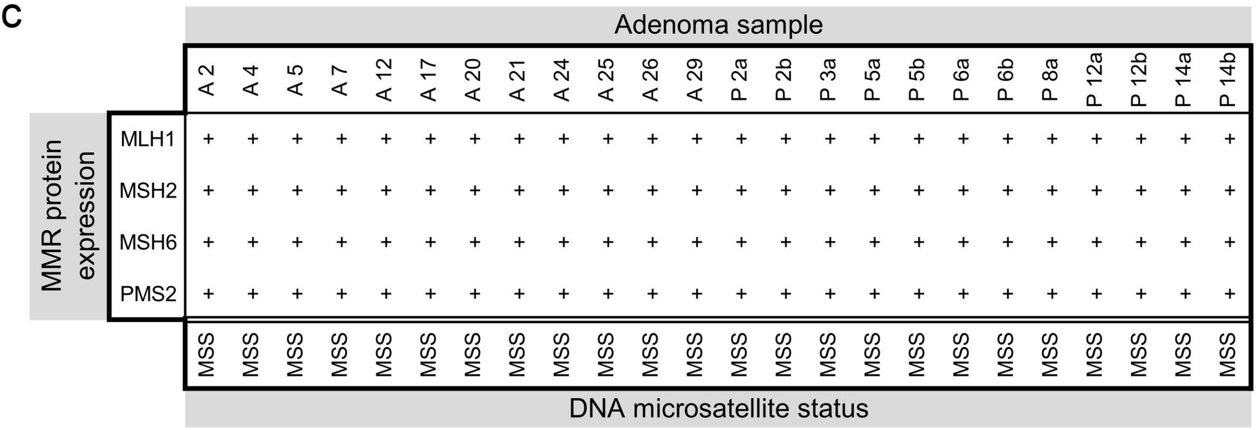
Locus	Marker	counted nuclei (*n* =350)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	0.3	0.0	2.00	9
3q26	*PIK3CA*	0.6	0.0	2.01	
5q22	*APC*	0.0	0.3	2.00	
6p21	*CLIC1*	1.1	0.0	2.01	
7p11	*EGFR*	0.0	0.0	2.00	
8q24	*MYC*	0.0	0.0	2.00	
11q13	*CCND1*	0.0	0.0	2.00	
13q12	*CDX2*	0.0	0.0	2.00	
16q22	*CDH1*	0.0	0.0	2.00	
17p13	*TP53*	0.0	0.3	2.00	
17q12	*HER2*	0.3	0.0	2.01	
18q21	*SMAD7*	0.0	0.0	2.00	
18q21	*SMAD4*	0.0	0.0	2.00	
20q13	*ZNF217*	0.0	0.3	2.00	

Locus	Marker	counted nuclei (*n* =350)			Signal patterns
		Gain %	Loss %	Average Signal No.	
1q31	*COX2*	0.0	0.0	2.00	7
3q26	*PIK3CA*	0.0	0.3	1.99	
5q22	*APC*	0.0	0.0	2.00	
6p21	*CLIC1*	0.0	0.0	2.00	
7p11	*EGFR*	0.0	0.0	2.00	
8q24	*MYC*	0.0	0.0	2.00	
11q13	*CCND1*	0.0	0.0	2.00	
13q12	*CDX2*	0.0	0.0	2.00	
16q22	*CDH1*	0.0	0.0	2.00	
17p13	*TP53*	0.0	0.3	1.99	
17q12	*HER2*	1.4	0.0	2.01	
18q21	*SMAD7*	0.0	3.4	1.97	
18q21	*SMAD4*	0.3	0.0	2.00	
20q13	*ZNF217*	0.0	0.0	2.00	

Supporting Information Figure 12

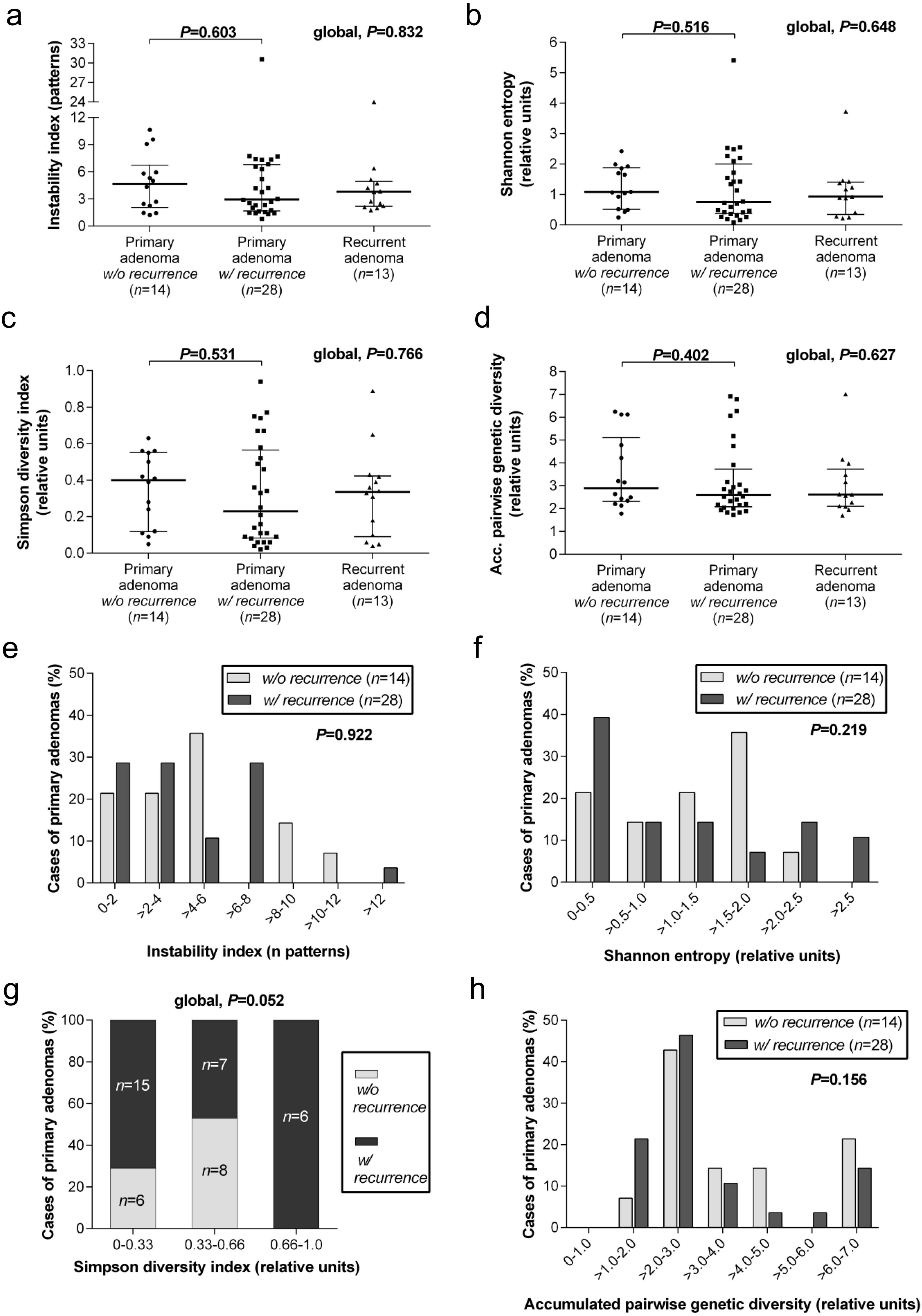


c

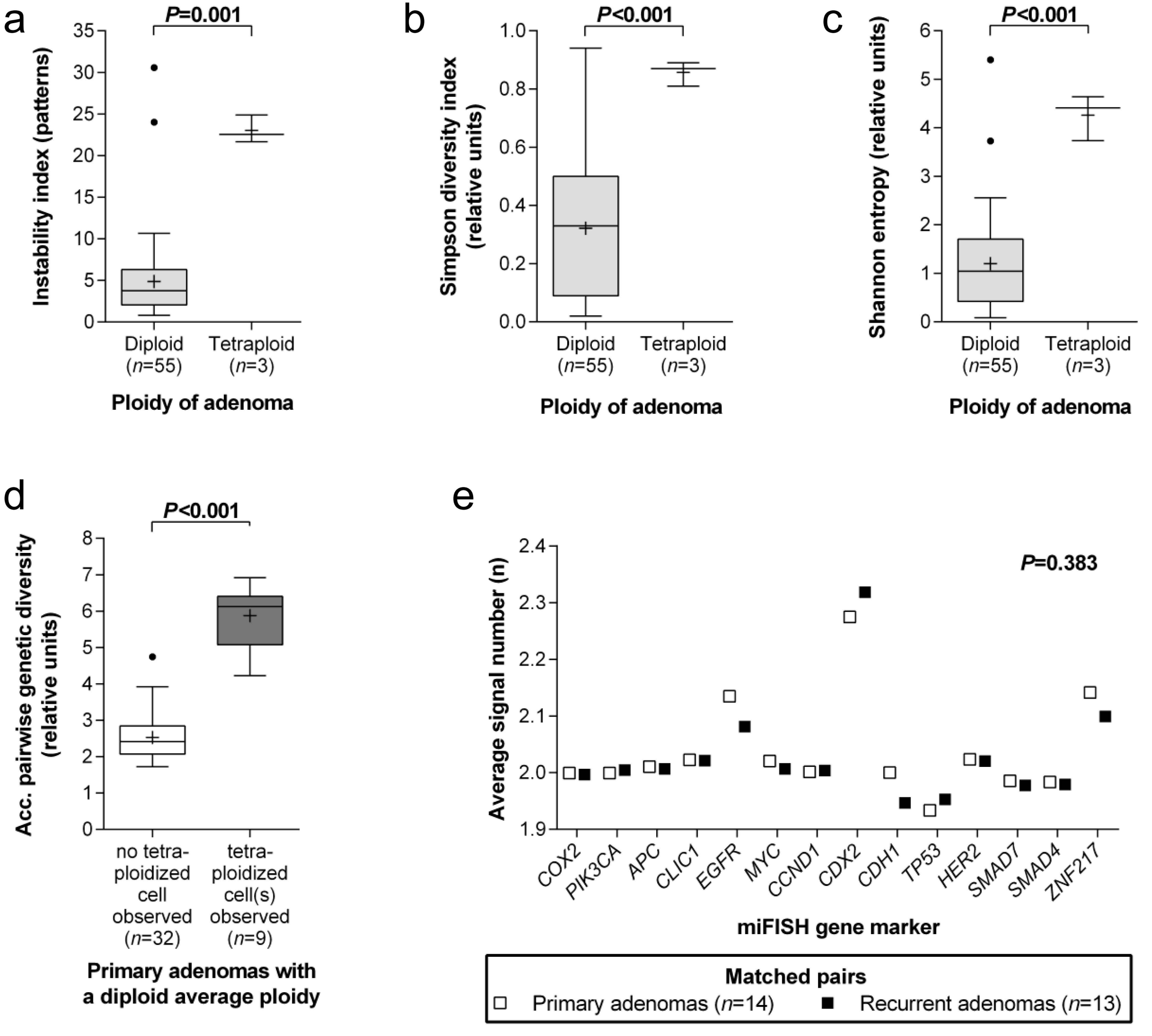


MMR protein expression	A 2	A 4	A 5	A 7	A 12	A 17	A 20	A 21	A 24	A 25	A 26	A 29	P 2a	P 2b	P 3a	P 5a	P 5b	P 6a	P 6b	P 8a	P 12a	P 12b	P 14a	P 14b
MLH1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
MSH2	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
MSH6	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PMS2	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DNA microsatellite status	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS

Supporting Information Figure 13

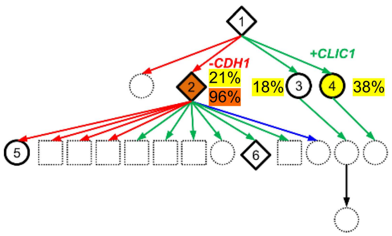


Supporting Information Figure 14



Supporting Information Figure 15

a **Simplification pattern** (pair P8)



Nodes (clone fractions)

○ ◌ Primary adenoma

□ ⬚ Recurrent adenoma

◇ ◇ Shared by both

n≥2 *n*=1

Major clones

Primary adenoma

Recurrent adenoma

Percentages annotated to the clones display the frequency of observation within the aberrant clone population (threshold 5%).

Signal patterns

Signal counts of gene probes are sorted in the following order: *COX2*, *PIK3CA*, *APC*, *CLIC1*, *EGFR*, *MYC*, CEP10, *CCND1*, *CDX2*, *CDH1*, *TP53*, *HER2*, *SMAD7*, *SMAD4*, *ZNF217*

Brackets: number of cells in (●) primary and (■) recurrent adenoma

1: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 475, ■ 60)
2: 2,2,2,2,2,2,2,2,2,1,2,2,2,2,2 (● 8, ■ 293)
3: 2,2,2,2,2,2,2,2,3,2,2,2,2,2,2 (● 7, ■ 0)
4: 2,2,2,3,2,2,2,2,2,2,2,2,2,2,2 (● 15, ■ 0)
5: 2,1,2,2,2,2,2,2,2,1,2,2,2,2,2 (● 2, ■ 0)
6: 2,2,2,3,2,2,2,2,2,1,2,2,2,2,2 (● 1, ■ 5)

Edges (genomic event)

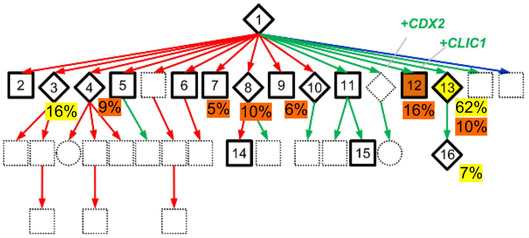
→ Copy number gain

→ Copy number loss

→ Whole genome duplication (WGD)

→ Multiple copy number alterations

b **Complexity pattern** (pair P6)



Nodes (clone fractions)

○ ◌ Primary adenoma

□ ⬚ Recurrent adenoma

◇ ◇ Shared by both

n≥2 *n*=1

Major clones

Primary adenoma

Recurrent adenoma

Percentages annotated to the clones display the frequency of observation within the aberrant clone population (threshold 5%).

Signal patterns

Signal counts of gene probes are sorted in the following order: *COX2*, *PIK3CA*, *APC*, *CLIC1*, *EGFR*, *MYC*, CEP10, *CCND1*, *CDX2*, *CDH1*, *TP53*, *HER2*, *SMAD7*, *SMAD4*, *ZNF217*

Brackets: number of cells in (●) primary and (■) recurrent adenoma

1: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 701, ■ 775)
2: 1,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 2)
3: 2,1,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 7, ■ 2)
4: 2,2,1,2,2,2,2,2,2,2,2,2,2,2,2 (● 1, ■ 7)
5: 2,2,2,1,2,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 2)
6: 2,2,2,2,2,2,2,2,1,2,2,2,2,2,2 (● 0, ■ 2)
7: 2,2,2,2,2,2,2,2,2,1,2,2,2,2,2 (● 0, ■ 4)
8: 2,2,2,2,2,2,2,2,2,2,1,2,2,2,2 (● 1, ■ 8)
9: 2,2,2,2,2,2,2,2,2,2,2,1,2,2,2 (● 0, ■ 5)
10: 2,2,2,2,2,2,2,2,2,2,2,2,1,1,2 (● 1, ■ 2)
11: 2,2,2,2,2,2,2,2,2,2,2,2,3,2,2 (● 0, ■ 2)
12: 2,2,2,2,2,2,2,2,3,2,2,2,2,2,2 (● 0, ■ 13)
13: 2,2,2,3,2,2,2,2,2,2,2,2,2,2,2 (● 26, ■ 8)
14: 2,2,2,2,2,2,2,2,2,2,1,1,2,2,2 (● 0, ■ 3)
15: 2,2,2,2,2,2,2,2,2,2,2,2,4,2,2 (● 0, ■ 3)
16: 2,2,2,4,2,2,2,2,2,2,2,2,2,2,2 (● 3, ■ 2)

Edges (genomic event)

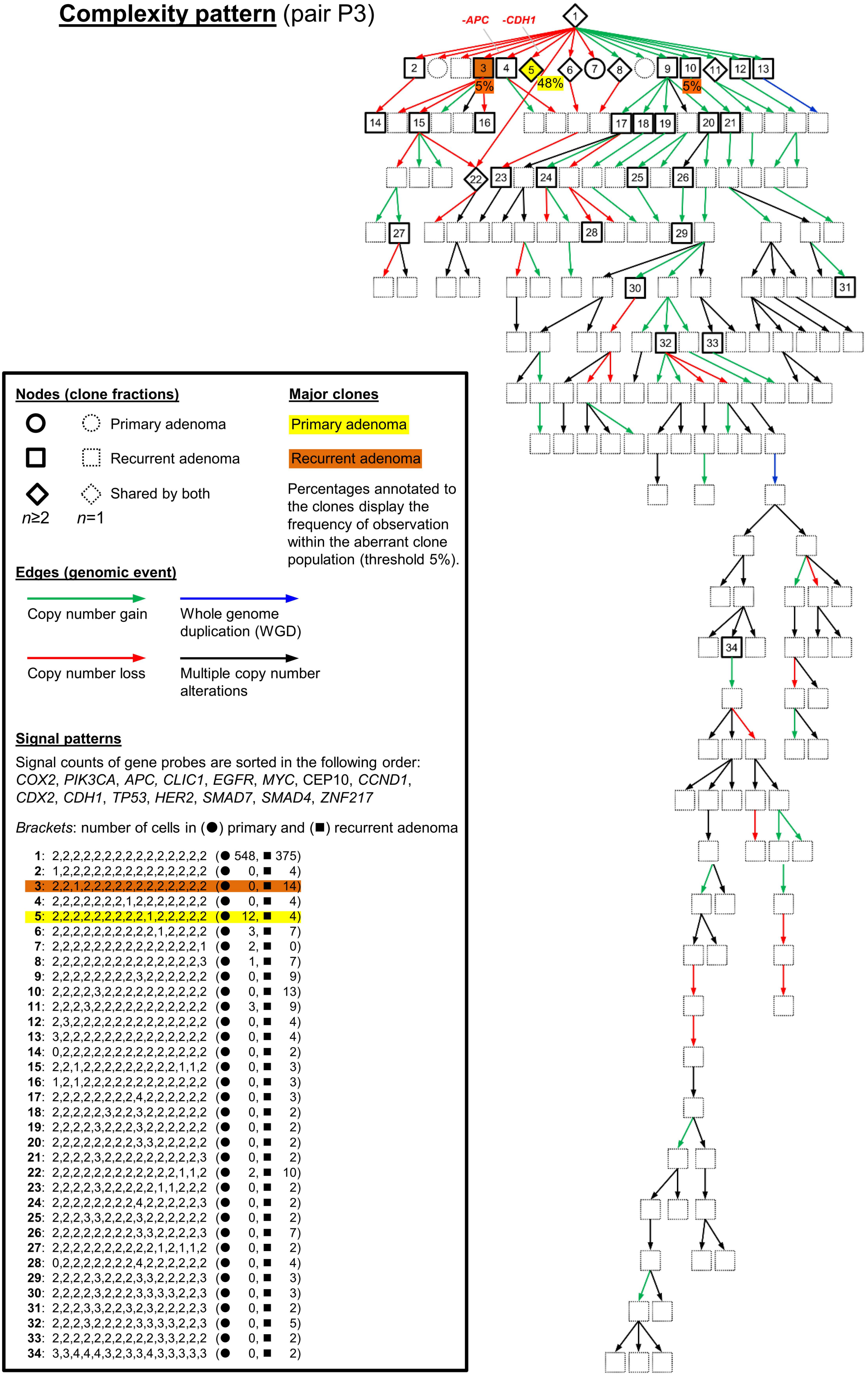
→ Copy number gain

→ Copy number loss

→ Whole genome duplication (WGD)

Supporting Information Figure 16

Complexity pattern (pair P3)



Nodes (clone fractions)

○ ◌ Primary adenoma

□ ⬚ Recurrent adenoma

◇ ◇ Shared by both

$n\geq2$ $n=1$

Major clones

Primary adenoma

Recurrent adenoma

Percentages annotated to the clones display the frequency of observation within the aberrant clone population (threshold 5%).

Edges (genomic event)

Copy number gain

Whole genome duplication (WGD)

Copy number loss

Multiple copy number alterations

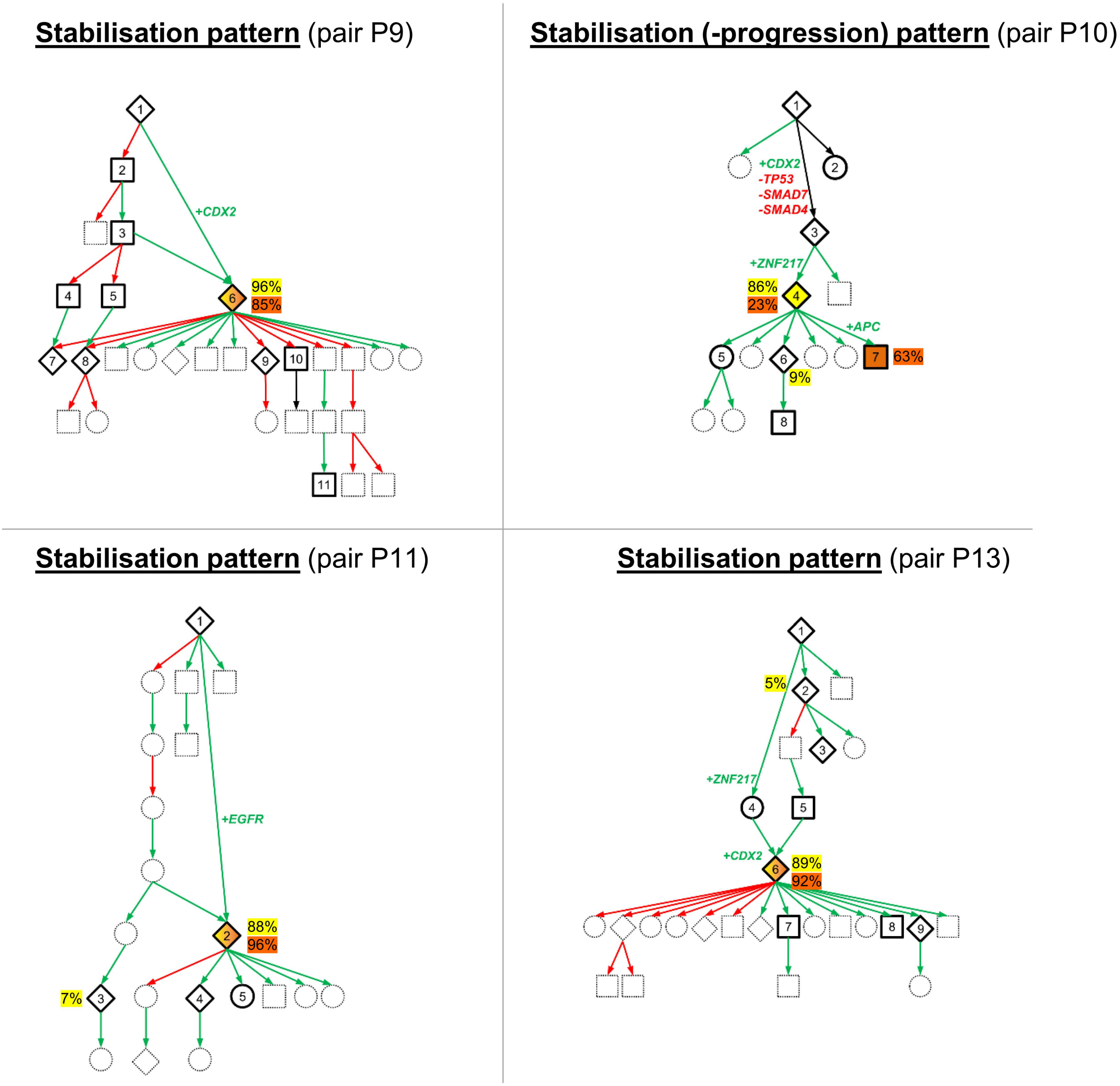
Signal patterns

Signal counts of gene probes are sorted in the following order: *COX2*, *PIK3CA*, *APC, CLIC1*, *EGFR*, *MYC*, CEP10, *CCND1*, *CDX2*, *CDH1*, *TP53*, *HER2*, *SMAD7*, *SMAD4*, *ZNF217*

Brackets: number of cells in (●) primary and (■) recurrent adenoma

1: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 548, ■ 375)
2: 1,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 4)
3: 2,2,1,2,2,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 14)
4: 2,2,2,2,2,2,2,1,2,2,2,2,2,2,2 (● 0, ■ 4)
5: 2,2,2,2,2,2,2,2,2,1,2,2,2,2,2 (● 12, ■ 4)
6: 2,2,2,2,2,2,2,2,2,2,1,2,2,2,2 (● 3, ■ 7)
7: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,1 (● 2, ■ 0)
8: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,3 (● 1, ■ 7)
9: 2,2,2,2,2,2,2,2,3,2,2,2,2,2,2 (● 0, ■ 9)
10: 2,2,2,2,3,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 13)
11: 2,2,2,3,2,2,2,2,2,2,2,2,2,2,2 (● 3, ■ 9)
12: 2,3,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 4)
13: 3,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 4)
14: 0,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 2)
15: 2,2,1,2,2,2,2,2,2,2,2,2,1,1,2 (● 0, ■ 3)
16: 1,2,1,2,2,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 3)
17: 2,2,2,2,2,2,2,2,4,2,2,2,2,2,2 (● 0, ■ 3)
18: 2,2,2,2,2,3,2,2,3,2,2,2,2,2,2 (● 0, ■ 2)
19: 2,2,2,2,3,2,2,2,3,2,2,2,2,2,2 (● 0, ■ 2)
20: 2,2,2,2,2,2,2,2,3,3,2,2,2,2,2 (● 0, ■ 2)
21: 2,2,2,2,3,2,2,2,2,2,2,2,2,2,3 (● 0, ■ 2)
22: 2,2,2,2,2,2,2,2,2,2,2,2,1,1,2 (● 2, ■ 10)
23: 2,2,2,2,3,2,2,2,2,2,1,1,2,2,2 (● 0, ■ 2)
24: 2,2,2,2,2,2,2,2,4,2,2,2,2,2,3 (● 0, ■ 2)
25: 2,2,2,3,3,2,2,2,3,2,2,2,2,2,2 (● 0, ■ 2)
26: 2,2,2,2,2,2,2,2,3,3,2,2,2,2,3 (● 0, ■ 7)
27: 2,2,2,2,2,2,2,2,2,2,1,2,1,1,2 (● 0, ■ 2)
28: 0,2,2,2,2,2,2,2,4,2,2,2,2,2,2 (● 0, ■ 4)
29: 2,2,2,2,3,2,2,2,3,3,2,2,2,2,3 (● 0, ■ 3)
30: 2,2,2,2,3,2,2,2,3,3,3,3,2,2,3 (● 0, ■ 3)
31: 2,2,2,3,3,2,2,3,2,3,2,2,2,2,3 (● 0, ■ 2)
32: 2,2,2,3,2,2,2,2,3,3,3,3,2,2,3 (● 0, ■ 5)
33: 2,2,2,2,2,2,2,2,2,2,3,3,2,2,2 (● 0, ■ 2)
34: 3,3,4,4,4,3,2,3,3,4,3,3,3,3,3 (● 0, ■ 2)

Supporting Information Figure 17



Stabilisation pattern (pair P9)

Stabilisation (-progression) pattern (pair P10)

Stabilisation pattern (pair P11)

Stabilisation pattern (pair P13)

Nodes (clone fractions)

○ ◌ Primary adenoma

□ ⬚ Recurrent adenoma

◇ ◇ Shared by both

n≥2 *n*=1

Edges (genomic event)

→ Copy number gain

→ Copy number loss

→ Whole genome duplication (WGD)

→ Multiple copy number alterations

Major clones

Primary adenoma

Recurrent adenoma

Shared by both

Percentages annotated to the clones display the frequency of observation within the aberrant clone population (threshold 5%).

Signal patterns

Signal counts of gene probes are sorted in the following order: *COX2*, *PIK3CA*, *APC*, *CLIC1*, *EGFR*, *MYC*, CEP10, *CCND1*, *CDX2*, *CDH1*, *TP53*, *HER2*, *SMAD7*, *SMAD4*, *ZNF217*

Brackets: number of cells in (●) primary and (■) recurrent adenoma

(pair P9)

1: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 30, ■ 24)
2: 2,2,1,2,2,2,2,2,2,2,2,2,2,2,2 (● 0, ■ 4)
3: 2,2,1,2,2,2,2,2,3,2,2,2,2,2,2 (● 0, ■ 6)
4: 2,1,1,2,2,2,2,2,3,2,2,2,2,2,2 (● 0, ■ 2)
5: 1,2,1,2,2,2,2,2,3,2,2,2,2,2,2 (● 0, ■ 6)
6: 2,2,2,2,2,2,2,2,3,2,2,2,2,2,2 (● 337, ■ 298)
7: 2,1,2,2,2,2,2,2,3,2,2,2,2,2,2 (● 4, ■ 10)
8: 1,2,2,2,2,2,2,2,3,2,2,2,2,2,2 (● 1, ■ 5)
9: 2,2,2,2,2,2,2,1,3,2,2,2,2,2,2 (● 2, ■ 2)
10: 2,2,2,2,2,2,2,2,3,1,2,2,2,2,2 (● 0, ■ 2)
11: 2,2,2,2,2,2,2,2,3,2,2,3,2,2,2 (● 0, ■ 2)

(pair P10)

1: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 411, ■ 122)
2: 2,2,2,2,2,2,2,2,3,2,2,2,1,1,2 (● 2, ■ 0)
3: 2,2,2,2,2,2,2,2,3,2,1,2,1,1,2 (● 5, ■ 1)
4: 2,2,2,2,2,2,2,2,3,2,1,2,1,1,3 (● 239, ■ 10)
5: 2,2,2,2,2,2,2,2,3,2,1,2,2,1,3 (● 2, ■ 0)
6: 2,2,2,2,2,2,2,2,3,2,2,2,1,1,3 (● 24, ■ 2)
7: 2,2,3,2,2,2,2,2,3,2,1,2,1,1,3 (● 0, ■ 27)
8: 2,2,3,2,2,2,2,2,3,2,2,2,1,1,3 (● 0, ■ 2)

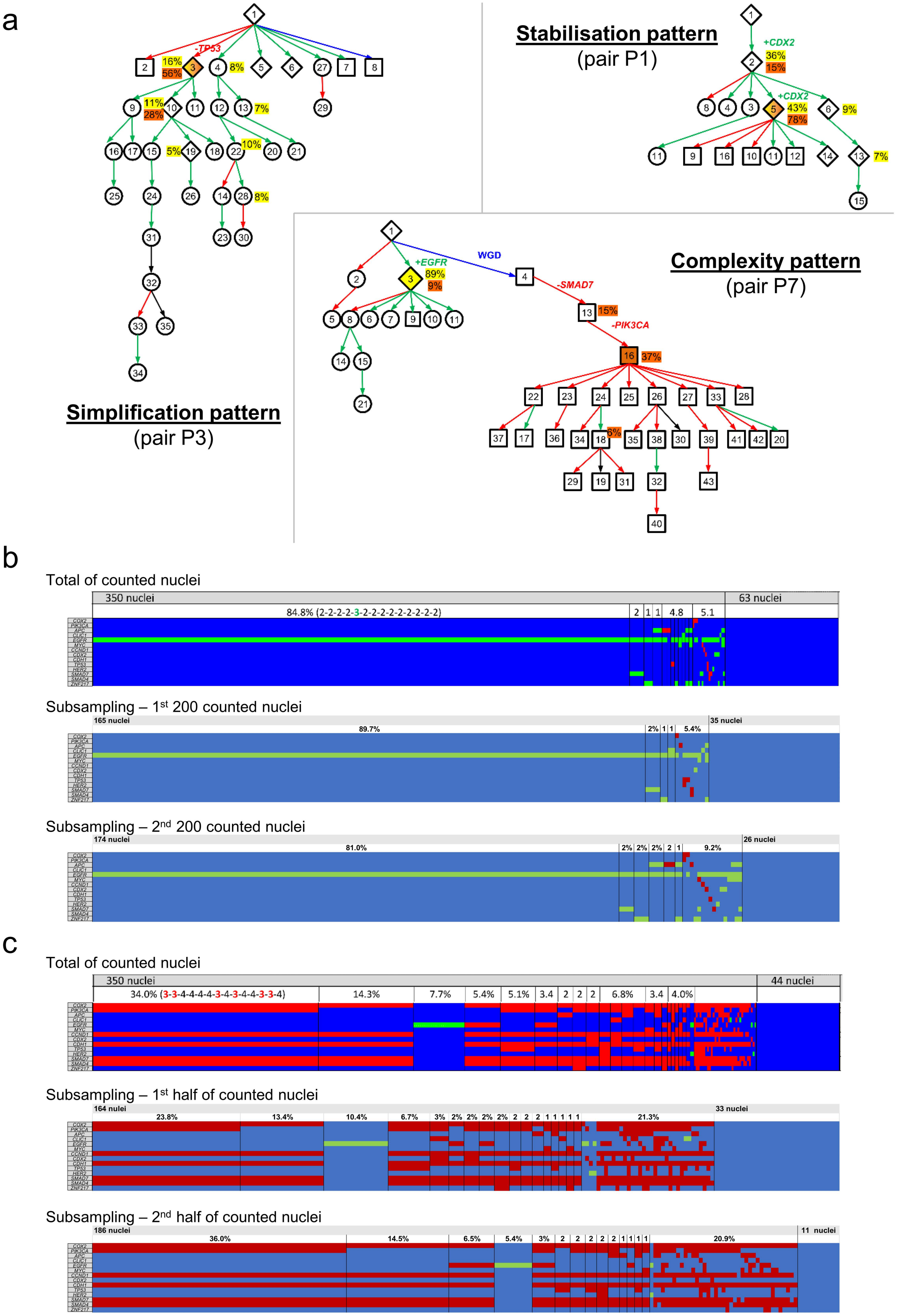
(pair P11)

1: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 101, ■ 56)
2: 2,2,2,2,3,2,2,2,2,2,2,2,2,2,2 (● 307, ■ 291)
3: 2,2,2,2,3,2,2,2,2,2,2,2,2,2,3 (● 26, ■ 4)
4: 2,2,2,2,3,2,2,2,2,2,2,2,2,3,2 (● 4, ■ 1)
5: 2,2,2,2,3,2,2,2,2,2,2,3,2,2,2 (● 2, ■ 0)

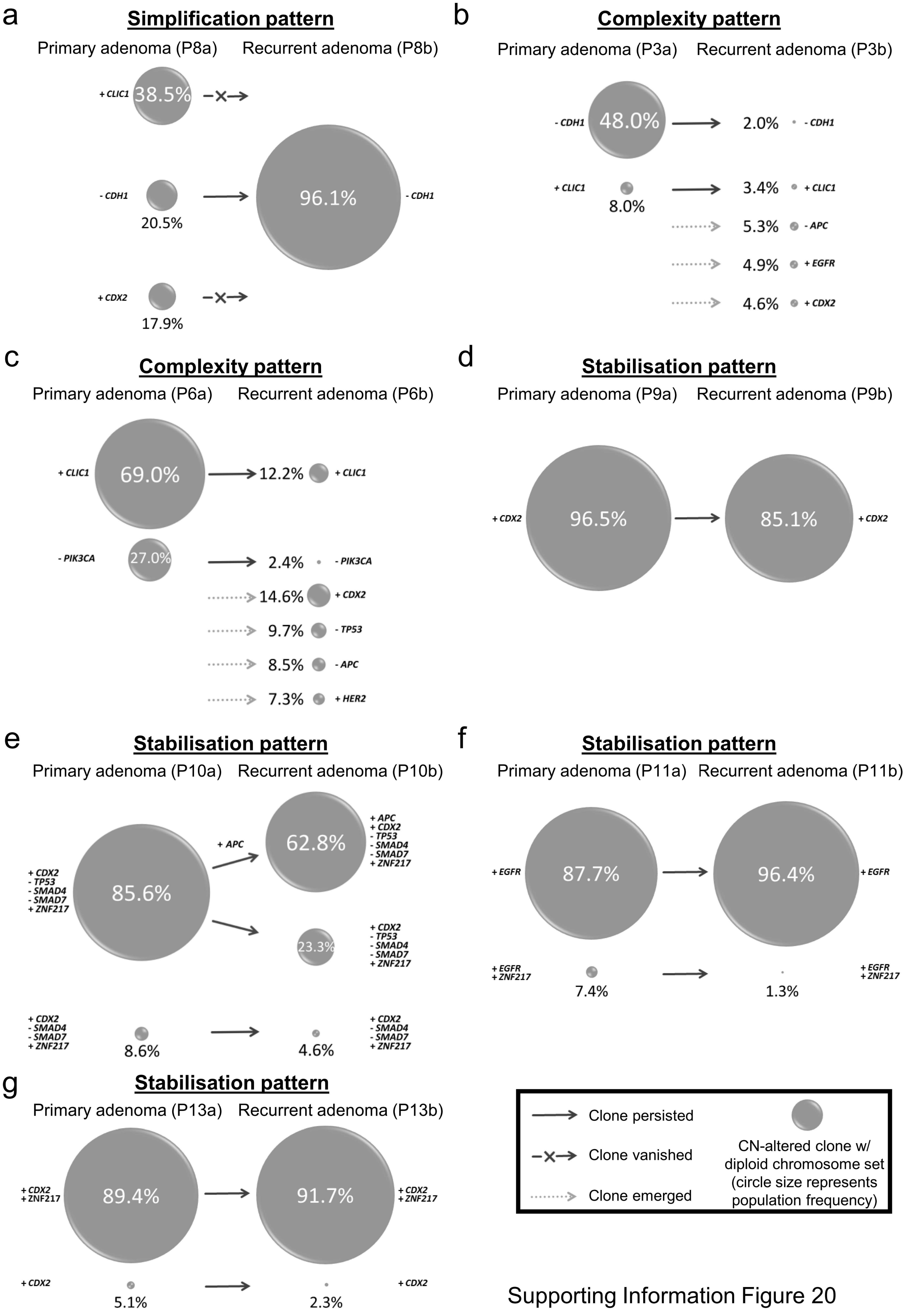
(pair P13)

1: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,2 (● 34, ■ 51)
2: 2,2,2,2,2,2,2,2,3,2,2,2,2,2,2 (● 18, ■ 8)
3: 2,2,2,3,2,2,2,2,3,2,2,2,2,2,2 (● 2, ■ 1)
4: 2,2,2,2,2,2,2,2,2,2,2,2,2,2,3 (● 0, ■ 5)
5: 2,1,2,2,2,2,2,2,3,2,2,2,2,2,3 (● 0, ■ 2)
6: 2,2,2,2,2,2,2,2,3,2,2,2,2,2,3 (● 313, ■ 321)
7: 2,2,2,2,2,2,2,2,3,2,3,2,2,2,3 (● 0, ■ 2)
8: 2,2,2,2,2,3,2,2,3,2,2,2,2,2,3 (● 0, ■ 2)
9: 2,2,2,3,2,2,2,2,3,2,2,2,2,2,3 (● 3, ■ 2)

Supporting Information Figure 18



Supporting Information Figure 19



Supporting Information Figure 20

a

“Zero” pattern

Primary adenoma (P5a) Recurrent adenoma (P5b)

No characteristic clone → No characteristic clone

b

“Zero” pattern

Primary adenoma (P12a) Recurrent adenoma (P12b)

No characteristic clone → No characteristic clone

c

“Zero” pattern

Primary adenoma (P14a) Recurrent adenoma (P14b)

No characteristic clone → No characteristic clone

Supporting Information Figure 21