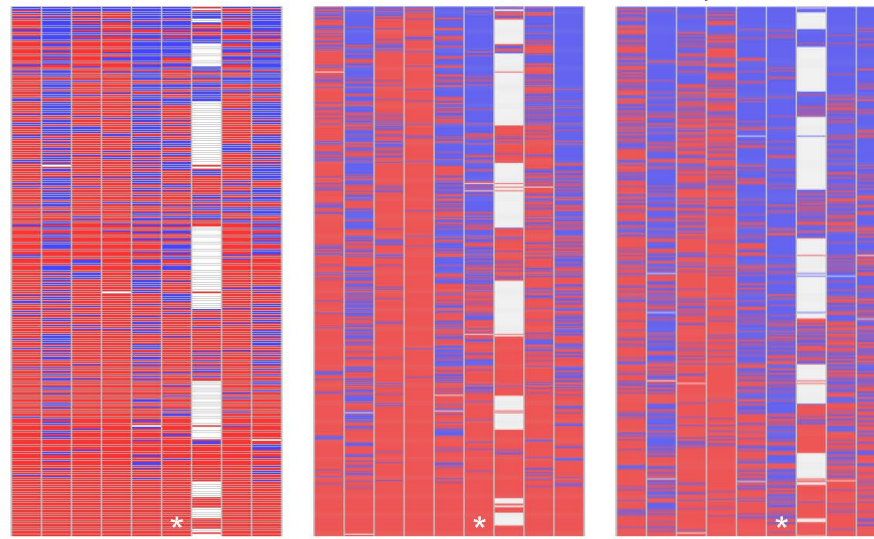


A**Figure S2*****CHP2***

NC 9

NC 13

patient



Methylation [%]
of reads

73.0
301

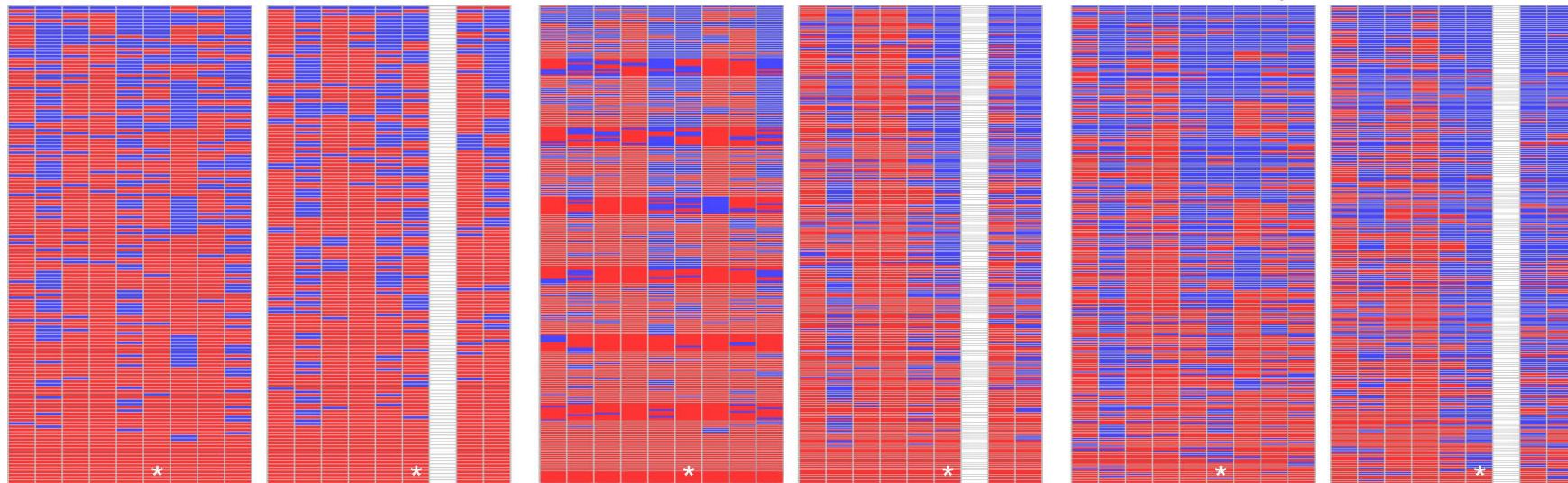
69.4
579

49.9
567

NC 9

NC 13

patient



Allele
Methylation [%]
of reads

G
71.3
148

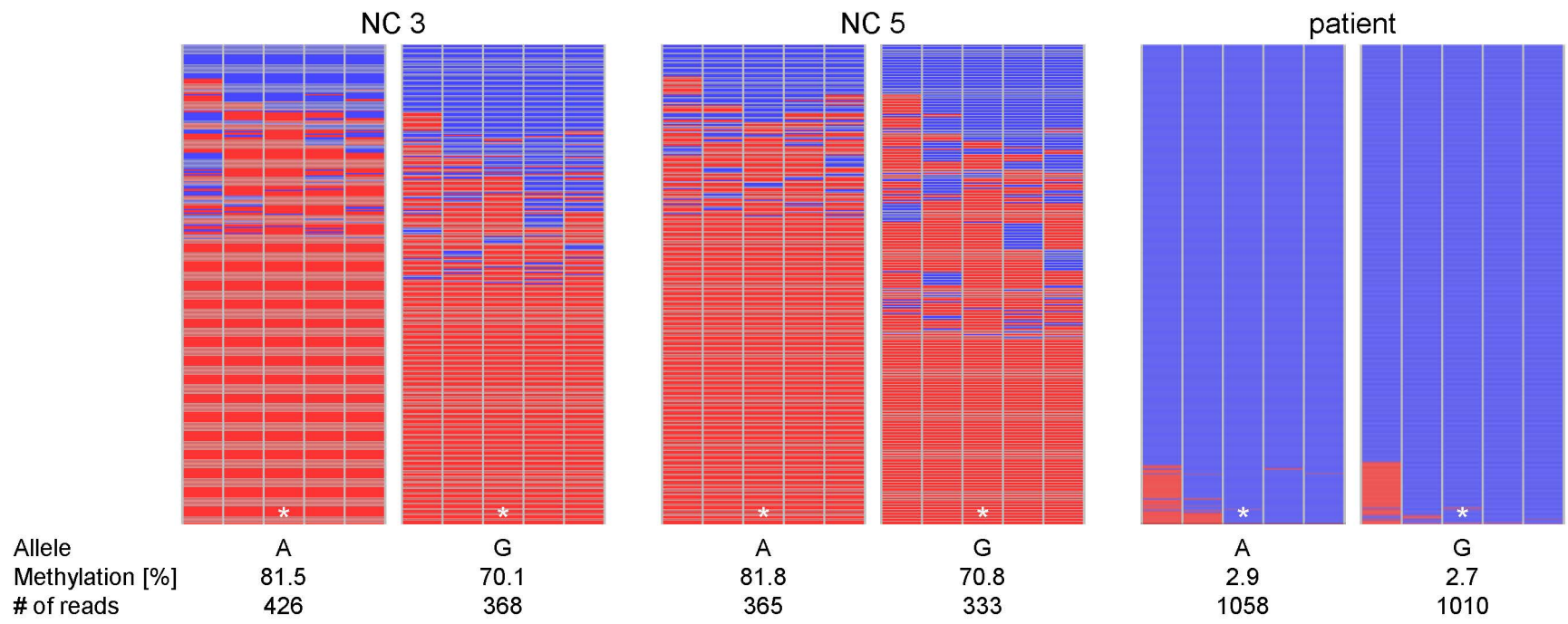
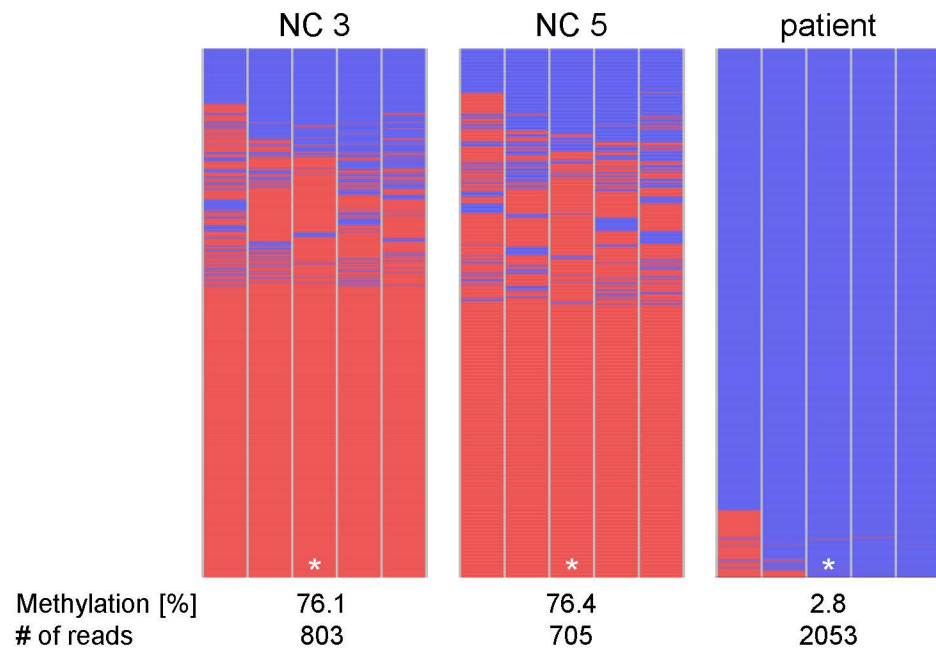
C
74.6
149

G
73.8
278

C
64.9
291

G
54.9
252

C
45.3
302

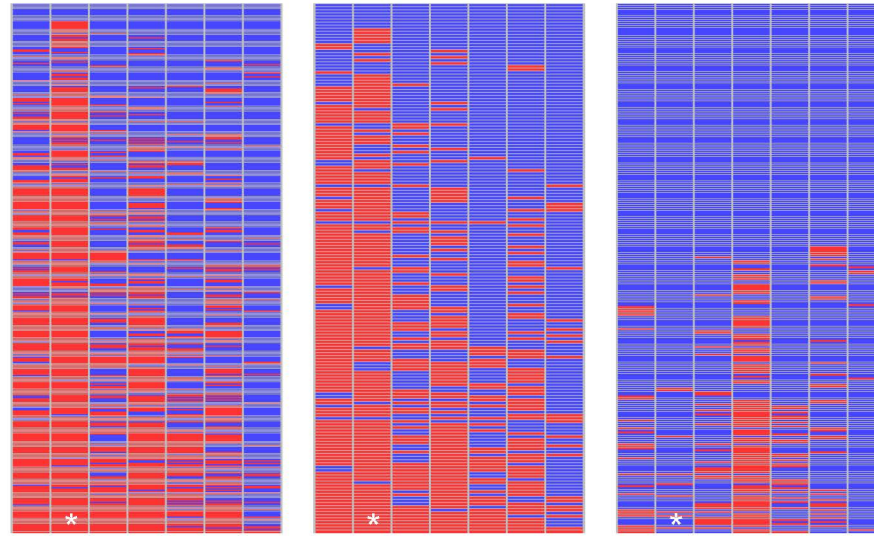
B**Figure S2*****KCNAB3***

C**Figure S2*****MAMDC2***

NC 2

NC 5

patient



Methylation [%]
of reads

44.9
393

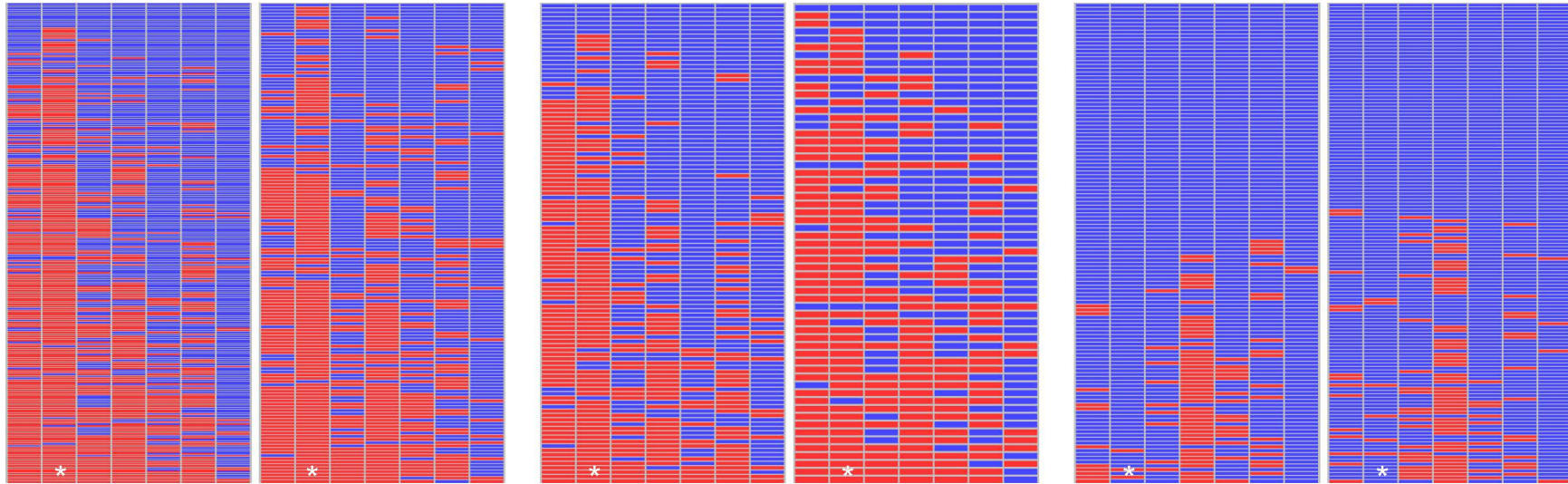
45.6
173

12.1
266

NC 2

NC 5

patient



Allele
Methylation [%]
of reads

C
44.6
241

A
44.3
149

C
40.9
110

A
50.6
61

C
12.3
140

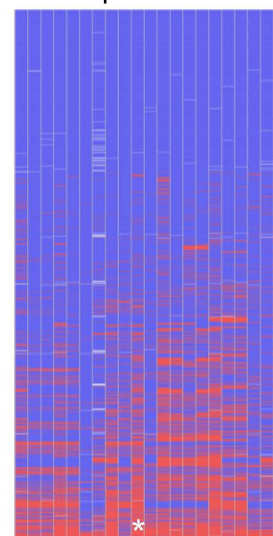
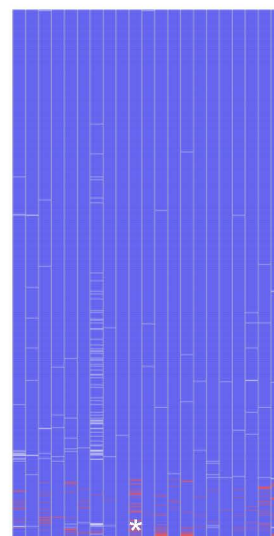
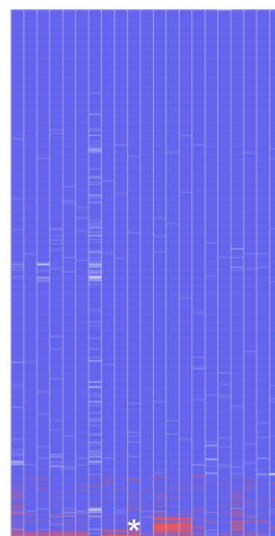
A
11.9
126

D**Figure S2*****TSPO***

NC 18

NC 19

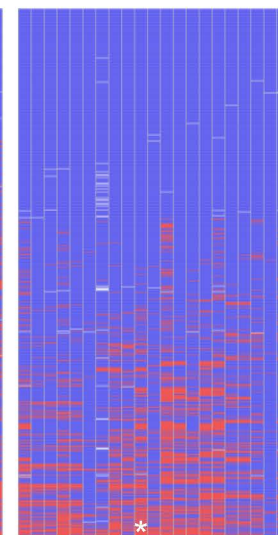
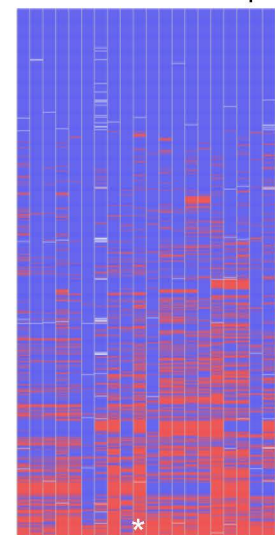
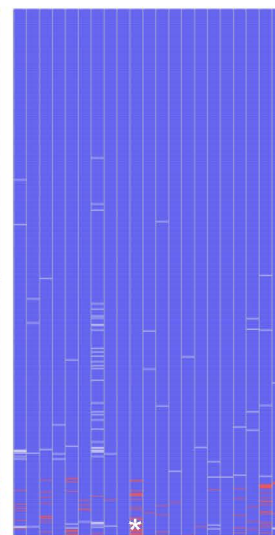
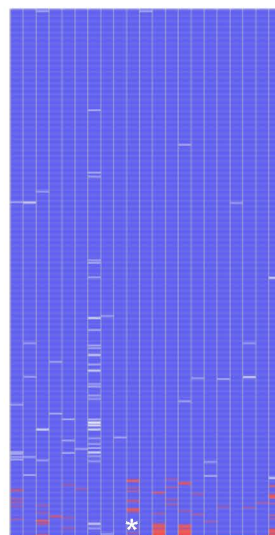
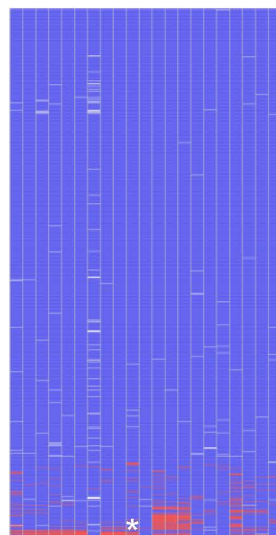
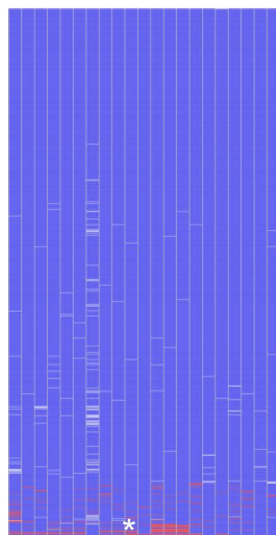
patient

Methylation [%]
of reads1.5
26810.7
141618.3
1993

NC 18

NC 19

patient

Allele
Methylation [%]
of readsG
1.0
1415T
2.0
1252G
0.8
645T
0.6
769G
22.4
1066T
13.5
922