

Go to imaging tab in SAV. From drop down list for cycle, lane, surface, swath and section choose 1 of single options . That will display one row of data. Select it and look at tombnail pictures while toggling through base checkboxes. Observe the cluster density in images and compare it with corrected % for A, C, G and T nucleotides. In this example observe lack of correlation of clusters on image for corrected call for A and C nucleotides and also C and G.

Cycle 4
▼

Lane 1
▼

Surface Bottom
▼

Swath Left
▼

Section 1
▼

A
 C
 G
 T

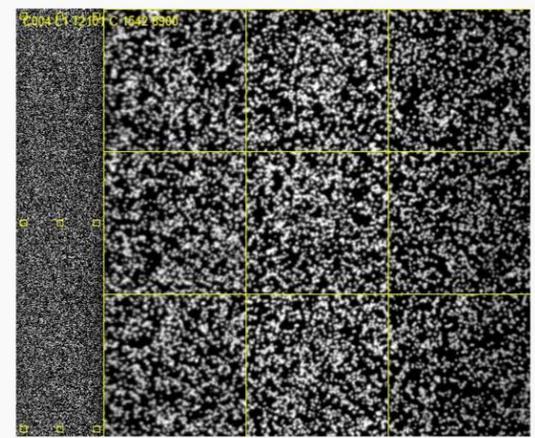
Index	Lane	Tile	Section	Cycle	Surface	Swath	Time	P90 A	P90 C	P90 G	P90 T	Error Rate	Corrected %A	Corrected %C	Corrected %G	Corrected %T	Col
30724	1	2101	1	4	Bottom	Left	05/30/201...	6947	9007	3156	5657	0.081	31.3	18.7	24.2	25.8	0

A%=31.3

Cycle 4 Lane 1 Surface Bottom Swath Left Section 1

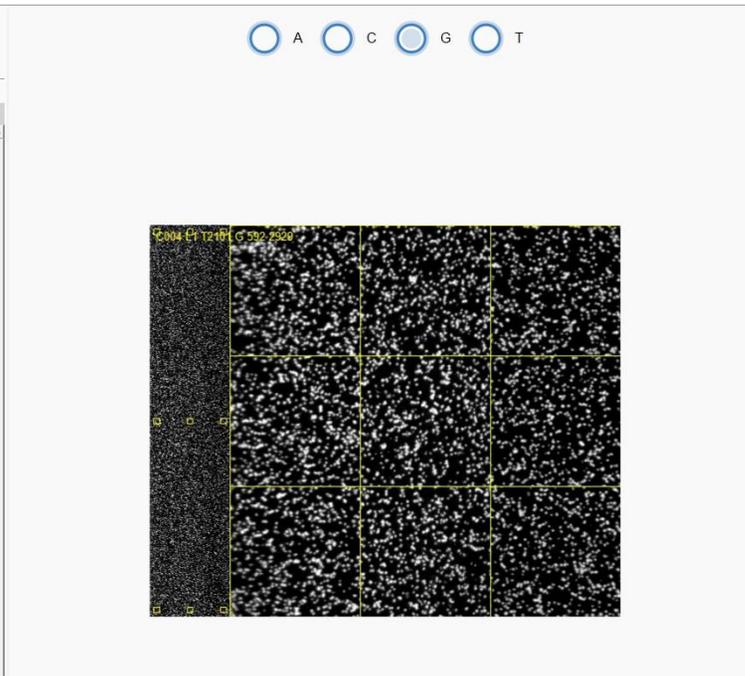
Index	Lane	Tile	Section	Cycle	Surface	Swath	Time	P90 A	P90 C	P90 G	P90 T	Error Rate	Corrected %A	Corrected %C	Corrected %G	Corrected %T	Col
30724	1	2101	1	4	Bottom	Left	05/30/201...	6947	9007	3156	5657	0.081	31.3	18.7	24.2	25.8	0

A C G T



C%= 18.7

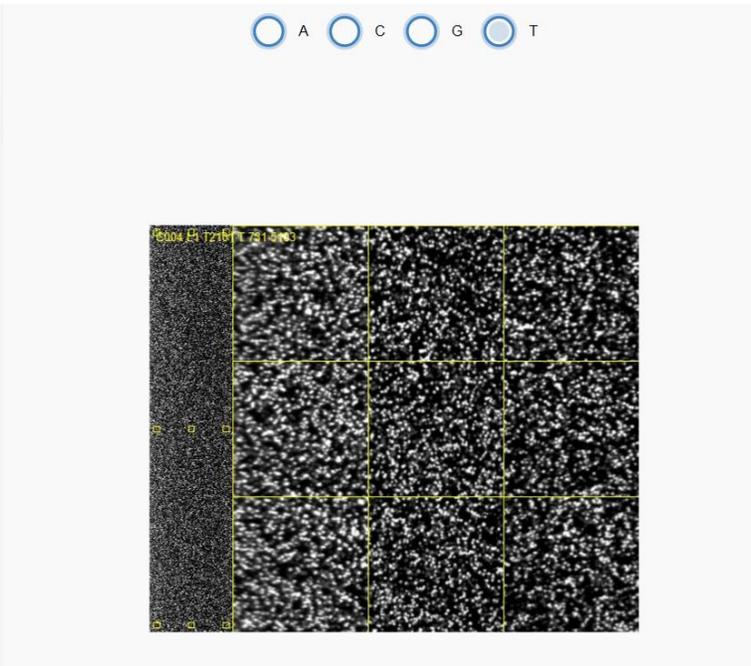
Index	Lane	Tile	Section	Cycle	Surface	Swath	Time	P90 A	P90 C	P90 G	P90 T	Error Rate	Corrected %A	Corrected %C	Corrected %G	Corrected %T	Col
30724	1	2101	1	4	Bottom	Left	05/30/201...	6947	9007	3156	5657	0.081	31.3	18.7	24.2	25.8	0



G%= 24

Cycle 4 Lane 1 Surface Bottom Swath Left Section 1

Index	Lane	Tile	Section	Cycle	Surface	Swath	Time	P90 A	P90 C	P90 G	P90 T	Error Rate	Corrected %A	Corrected %C	Corrected %G	Corrected %T	Col
30724	1	2101	1	4	Bottom	Left	05/30/201...	6947	9007	3156	5657	0.081	31.3	18.7	24.2	25.8	0



T%=25.8

