

GENETICS

BEST NGS ALIGNMENT VIEWER

25.11.2009

Features	CGAT	ICV	MapView	Mapview	IGV/IGV2
Native Format	CGAT	IGV	MAP	MAP	IGV
User Interface	X11/Qt	Java	AET	OpenGL	Carbon
Link-like	Yes	Yes	Yes	Yes	Yes
Windows	No	Yes	Yes	3rd-party	Yes
Zoom out	Yes	Yes	Yes	Yes	via terminal
Quick overview	Yes	Yes	Linked	No	No
Display mapQ	Yes	Partial	No	Yes	4 colors
Gradient baseQ	Yes	Yes	No	Yes	4 colors
Paired-end	Yes	No	Yes	No	Original only
Long reads	Yes	Yes	No	No	Yes
Deletion	Yes	Yes	No	No	Yes
Insertion	Yes	Partial	No	No	Yes
Filtering	Yes	No	No	No	No
Editing	Yes	No	No	No	No
Annotation Track	No	Yes	No	No	No
Multiple tracks	No	Yes	No	No	No

[Heng Li](#) has an excellent overview table on next generation sequence alignment viewers (as well as alignment programs) – thanks to TB for pointing me to that site. The Broad Institute has just bought another 30 Illumina Genome Analyzer – they now own 89 so the Broad people might have clearly a need for visualizing data.

The best choice is not easy to make – I am trying now the [IGV](#) in my lung sequence project. Another interesting piece of software not listed by the Heng Li table is [annoj](#) that looks promising too, yea, yea.