

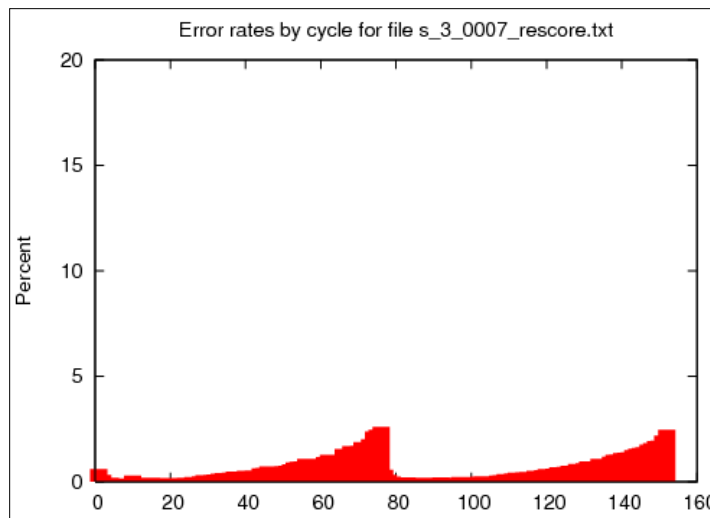
Acceptable Metrics and Plots (Human Genomic samples)

Summary.htm

	76 cycle	101 cycle
% Error Rate	< 2%	< 3%
% PF Clusters	> 50%	> 50%
% Align Rate	> 80%	> 80%
Phasing	< 0.4%	< 0.4%
Prephasing	< 0.3 %	< 0.3%

Check **standard deviations** for each of these as well as **tile specific** metrics.

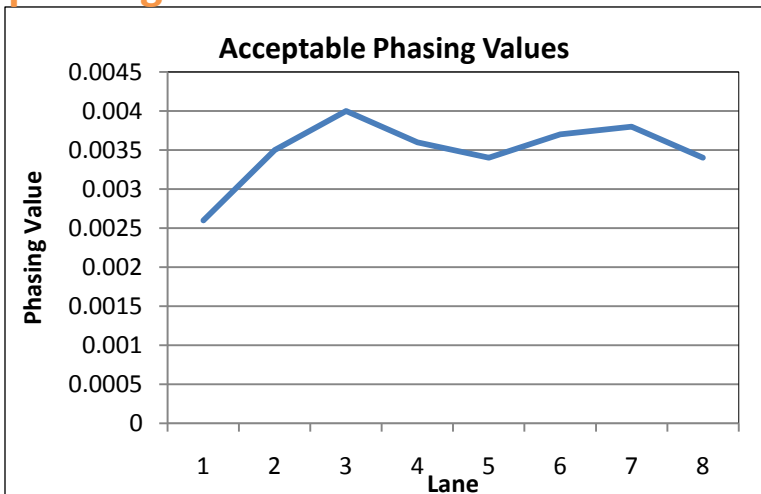
rescore.png



A good example of a 76 cycle error plot.

Error rates don't spike dramatically and stay below 3% for most of the run. This lane average error rate was $1.1\% \pm 0.12\%$

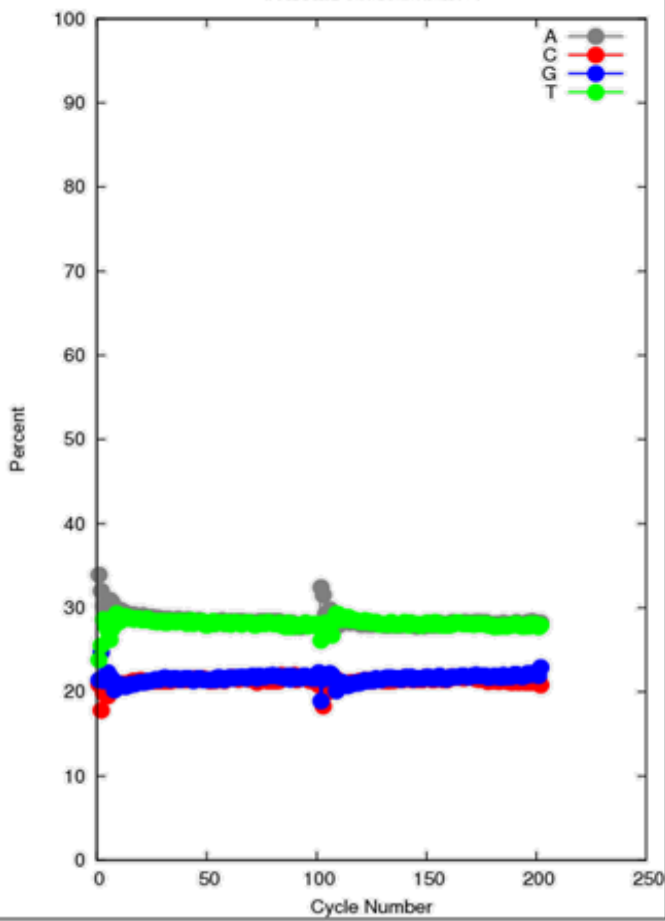
phasing.txt



Manually plotted from text file in Excel– no plot is provided in the pipeline.

Notice there is no extreme gradient and all values stay at or below 4%

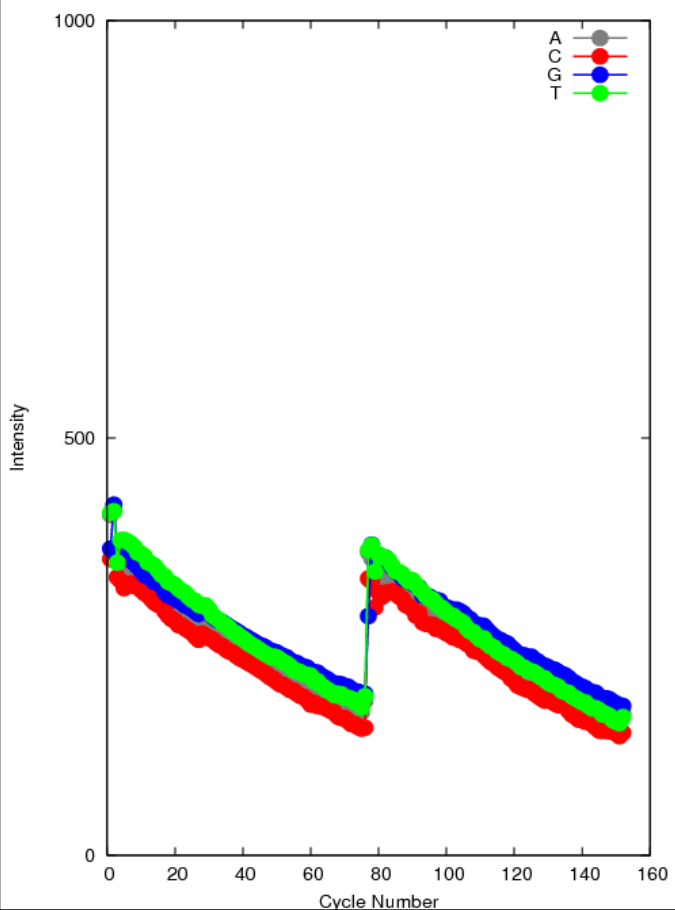
Percent Basecalls lane 2



This [percent_base.png](#) plot is an expected example of a WGS Human sample lane.

This plot can differ depending on your sample GC content.

Called intensities lane 3



This [call.png](#) plot displays an optimal intensity degradation for a 75 cycle paired run.

The large spike at cycle 77 is expected; this is the beginning of Read 2 when cluster intensity is regenerated. (here, about 100% regeneration)