

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap 2013/07/03 12:58:11

1. Summary

1.1. Globals

Reference size	4,578,159
Number of reads	775,216
Mapped reads	753,619 / 97.21%
Unmapped reads	21,597 / 2.79%
Paired reads	753,619 / 97.21%
Mapped reads, only first in pair	377,837 / 48.74%
Mapped reads, only second in pair	375,782 / 48.47%
Mapped reads, both in pair	741,597 / 95.66%
Mapped reads, singletons	12,022 / 1.55%
Read min/max/mean length	32 / 251 / 229.56
Clipped reads	173,605 / 22.39%
Duplication rate	29.66%

1.2. ACGT Content

Number/percentage of A's	42,038,970 / 24.73%
Number/percentage of C's	43,057,119 / 25.33%
Number/percentage of T's	41,932,323 / 24.67%
Number/percentage of G's	42,970,647 / 25.28%
Number/percentage of N's	0 / 0%
GC Percentage	50.6%

1.3. Coverage

Mean	37.14
Standard Deviation	12.98

1.4. Mapping Quality

Mean Mapping Quality	50.75
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1.5. Indels

Total reads with indels	17,101
Insertions	8,093
Deletions	9,008
Homopolymer indels	39.21%

1.6. Insert size

Mean	399.19
Median	307

1.7. Chromosome stats

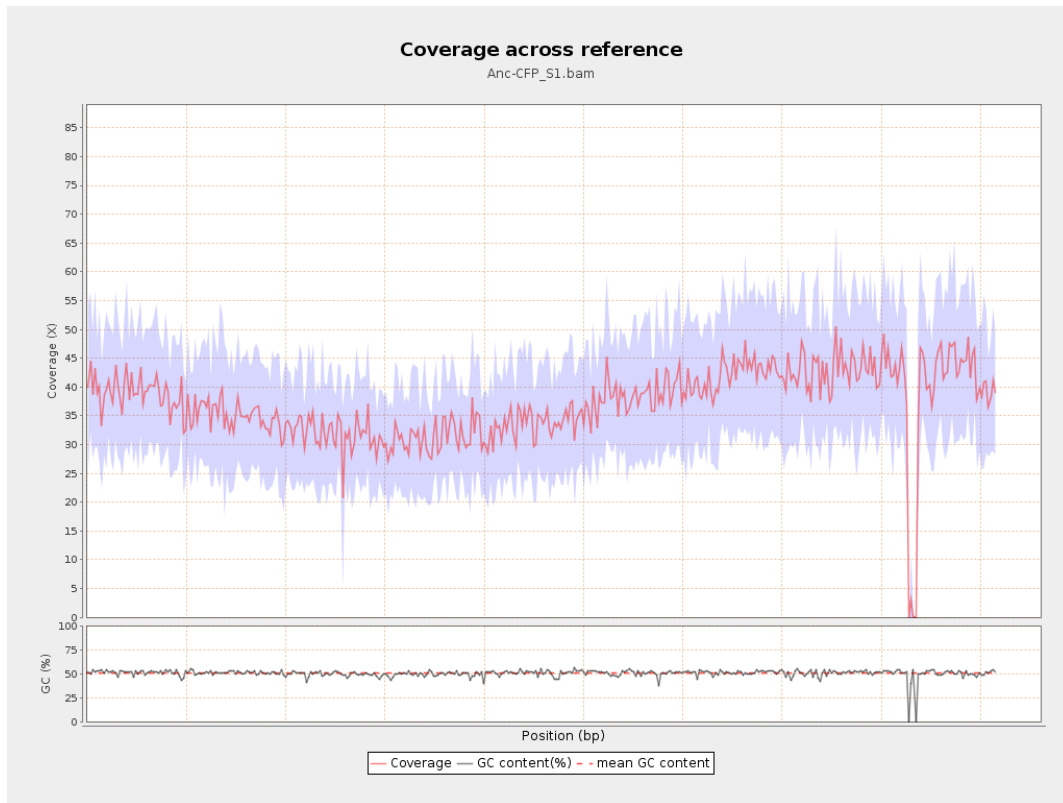
Name	Length	Mapped bases	Mean coverage	Standard deviation
gi_238899406_NC_012759_1	4578159	170014830	37.14	12.96

2. Input data & parameters

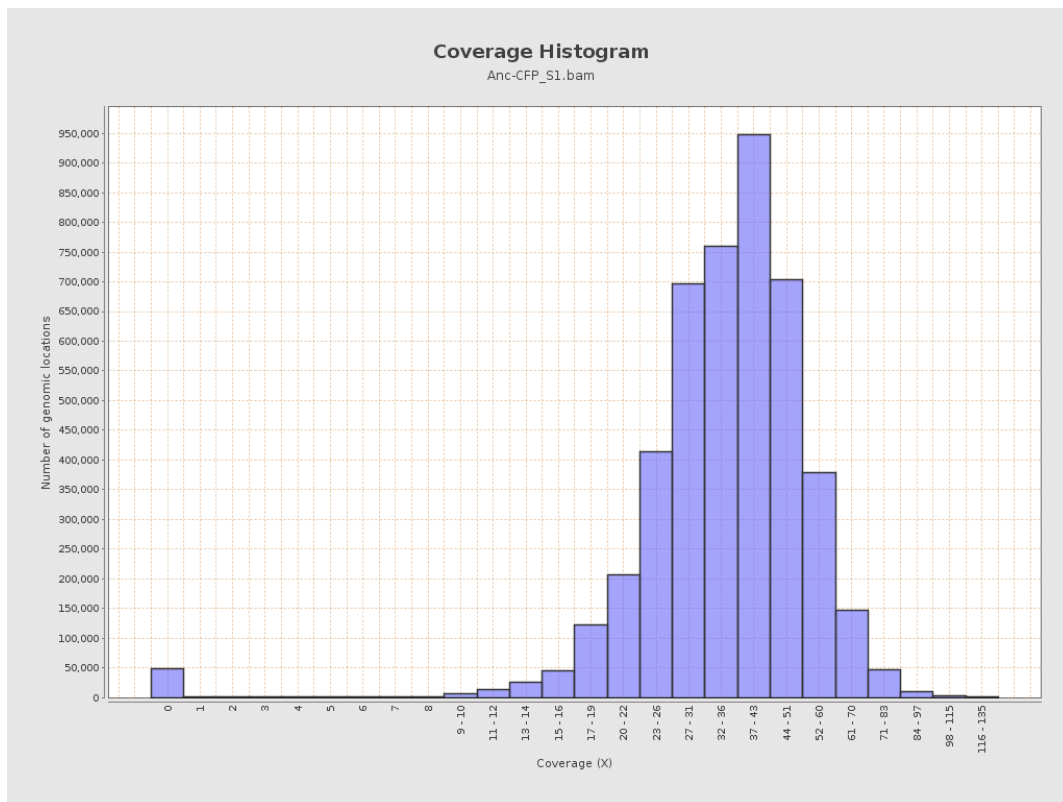
2.1. Alignment

BAM file:	Anc-CFP_S1.bam
Program:	bwa (0.6.1-r104-tpx)
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Wed Jul 03 12:58:10 WEST 2013
Draw chromosome limits:	no

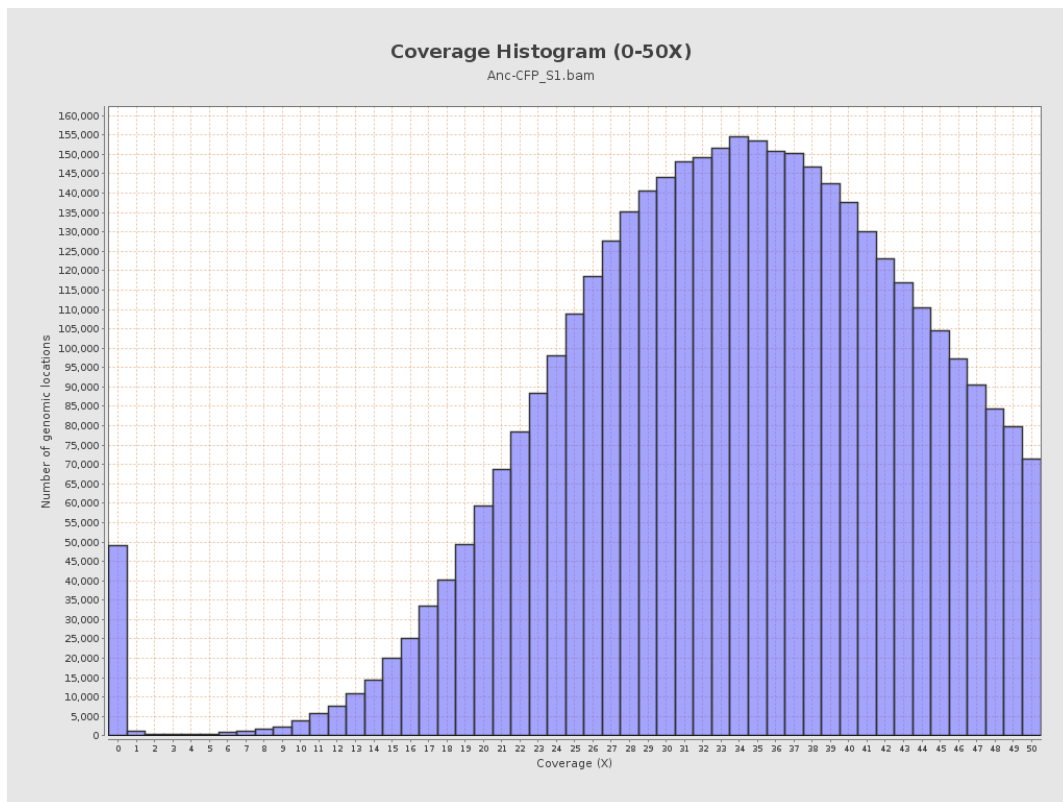
3. Coverage across reference



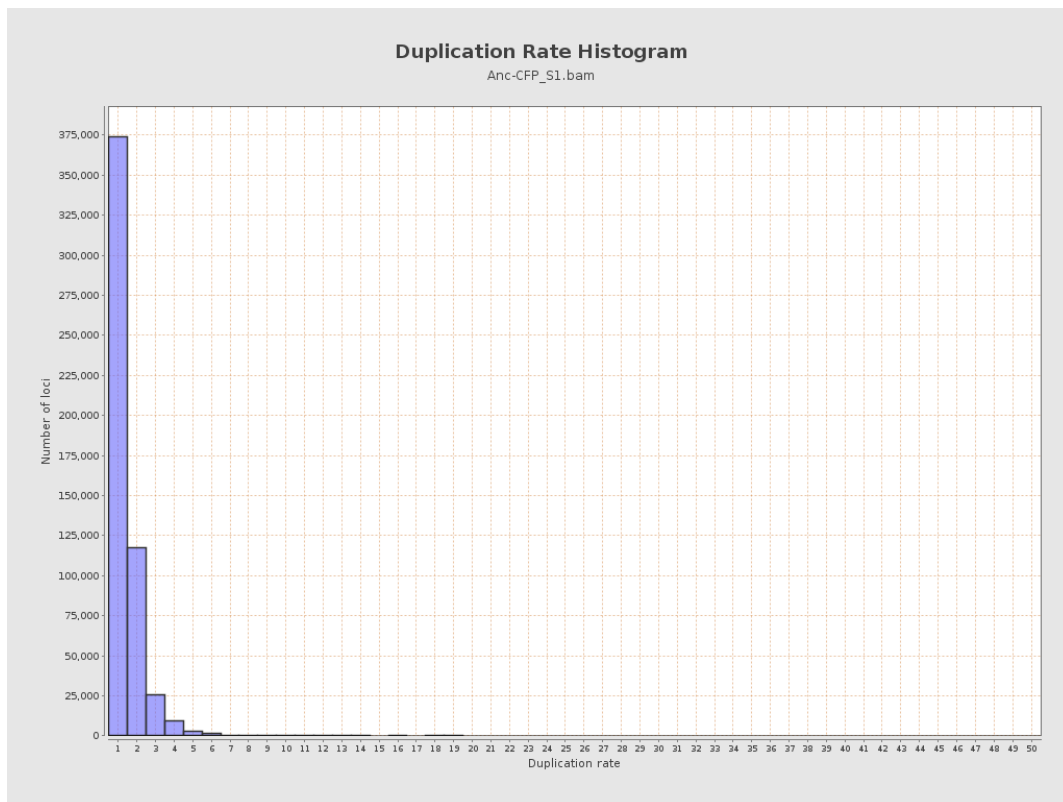
4. Coverage Histogram



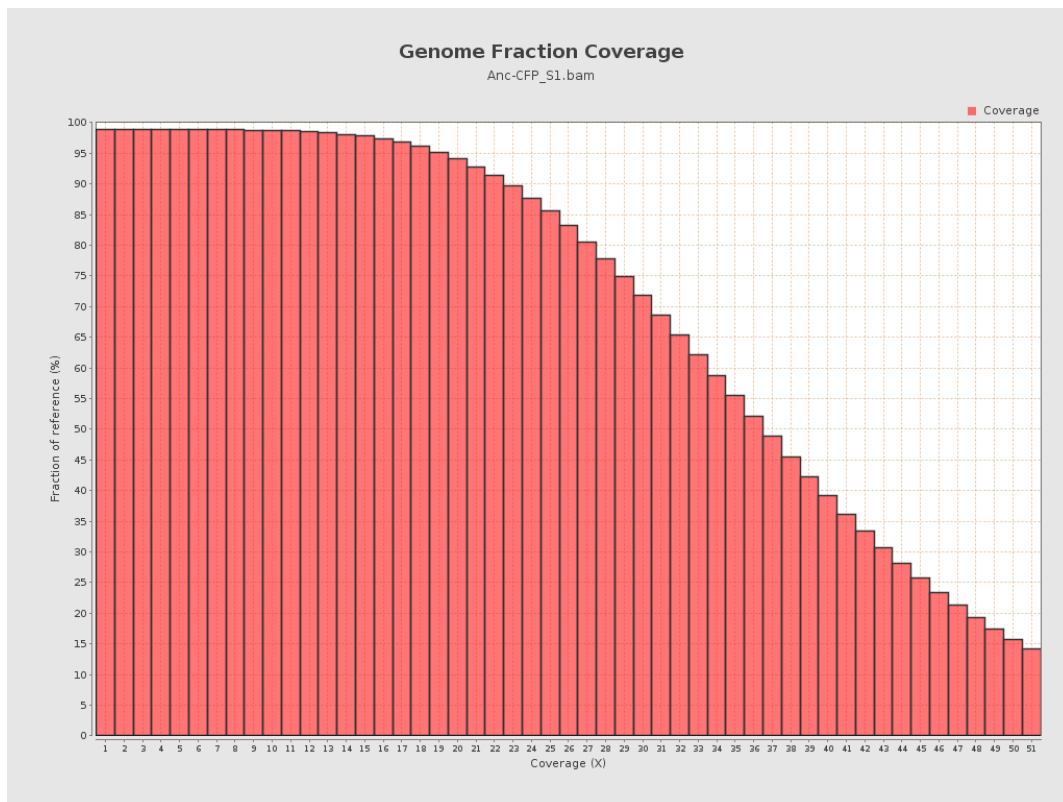
5. Coverage Histogram (0-50X)



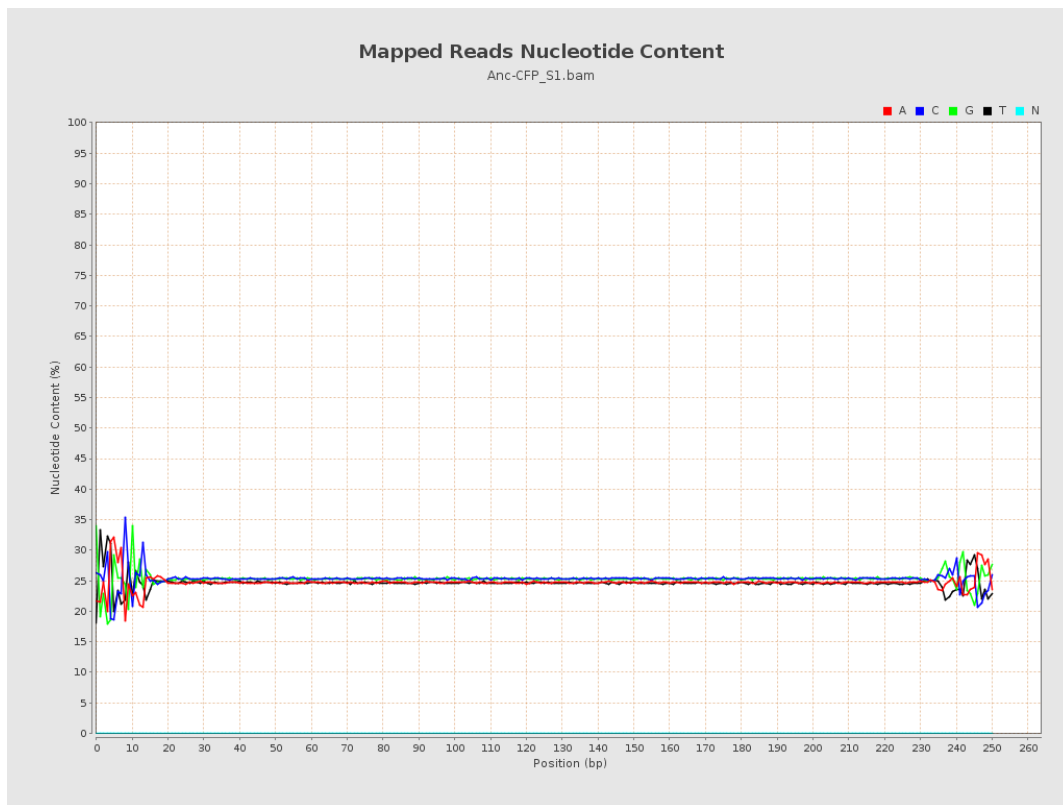
6. Duplication Rate Histogram



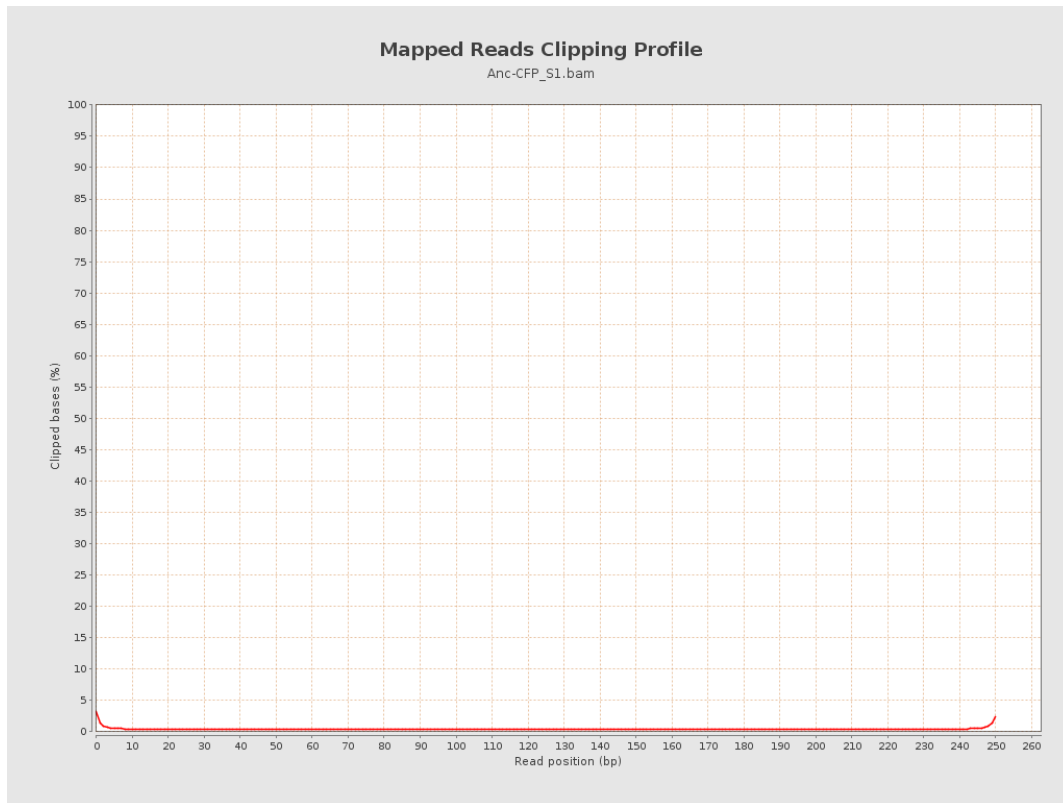
7. Genome Fraction Coverage



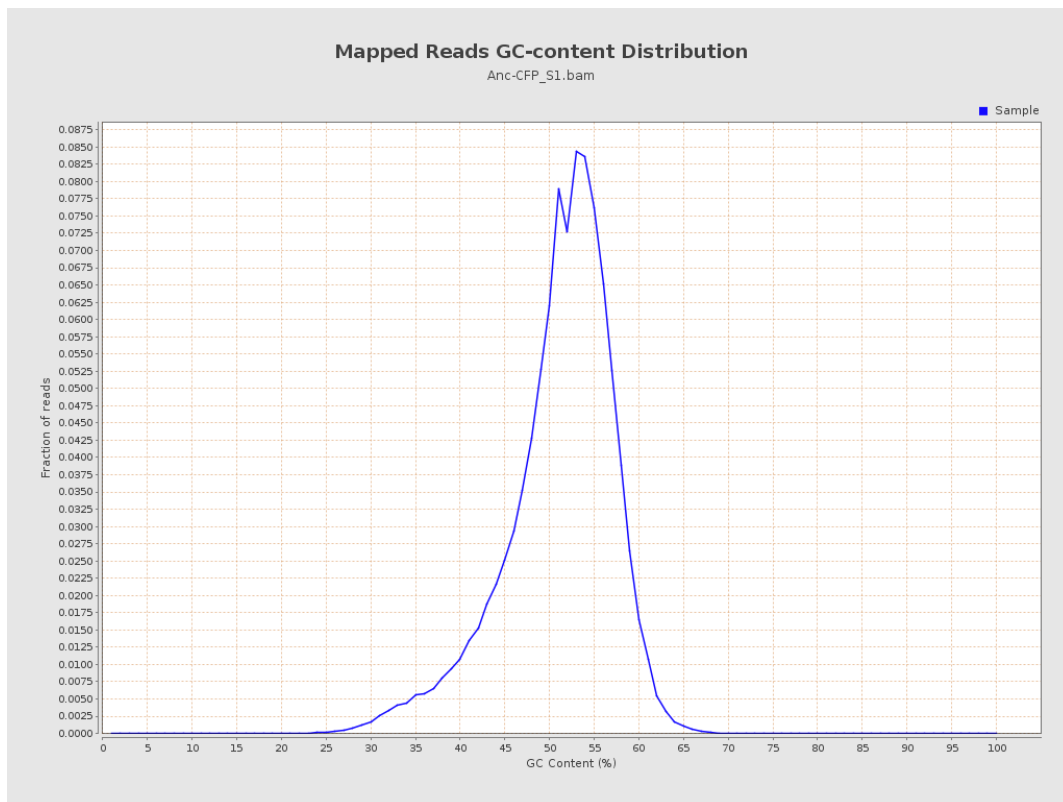
8. Mapped Reads Nucleotide Content



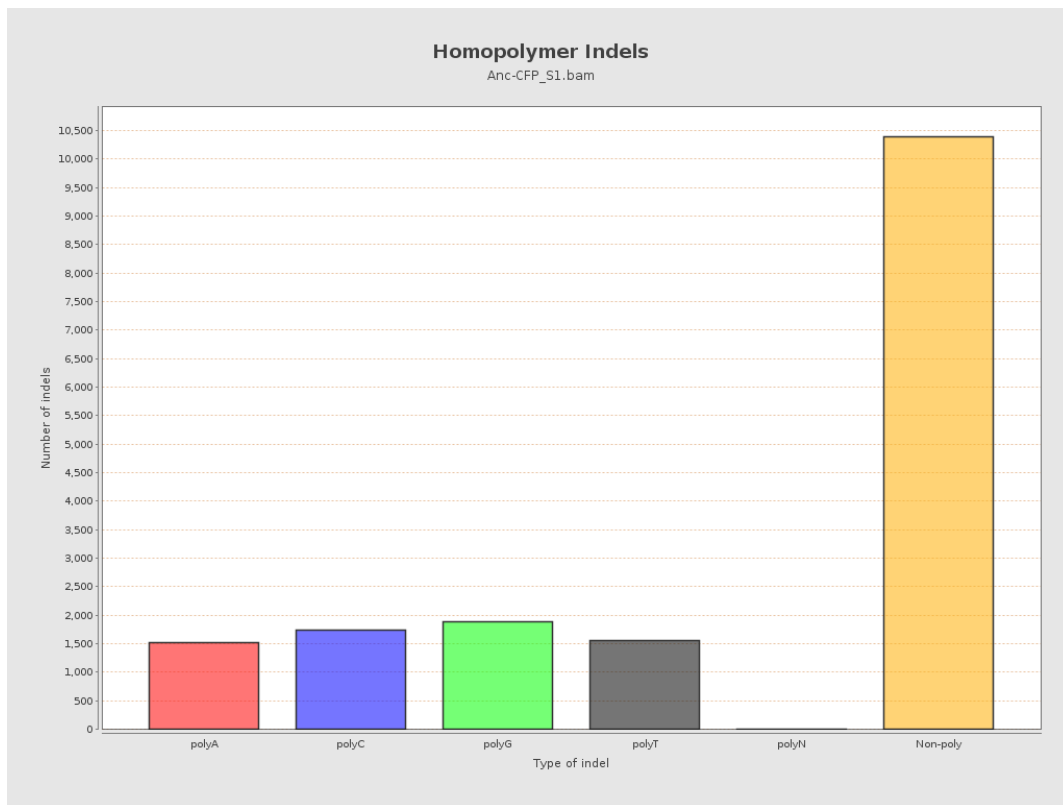
9. Mapped Reads Clipping Profile



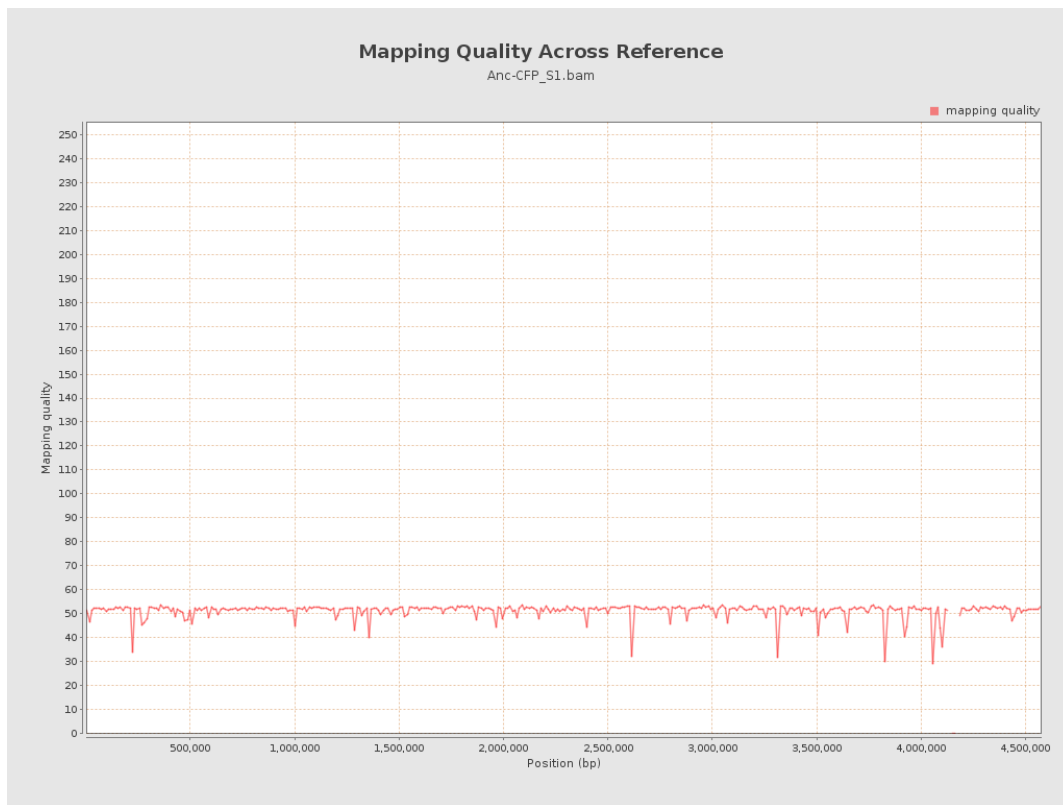
10. Mapped Reads GC-content Distribution



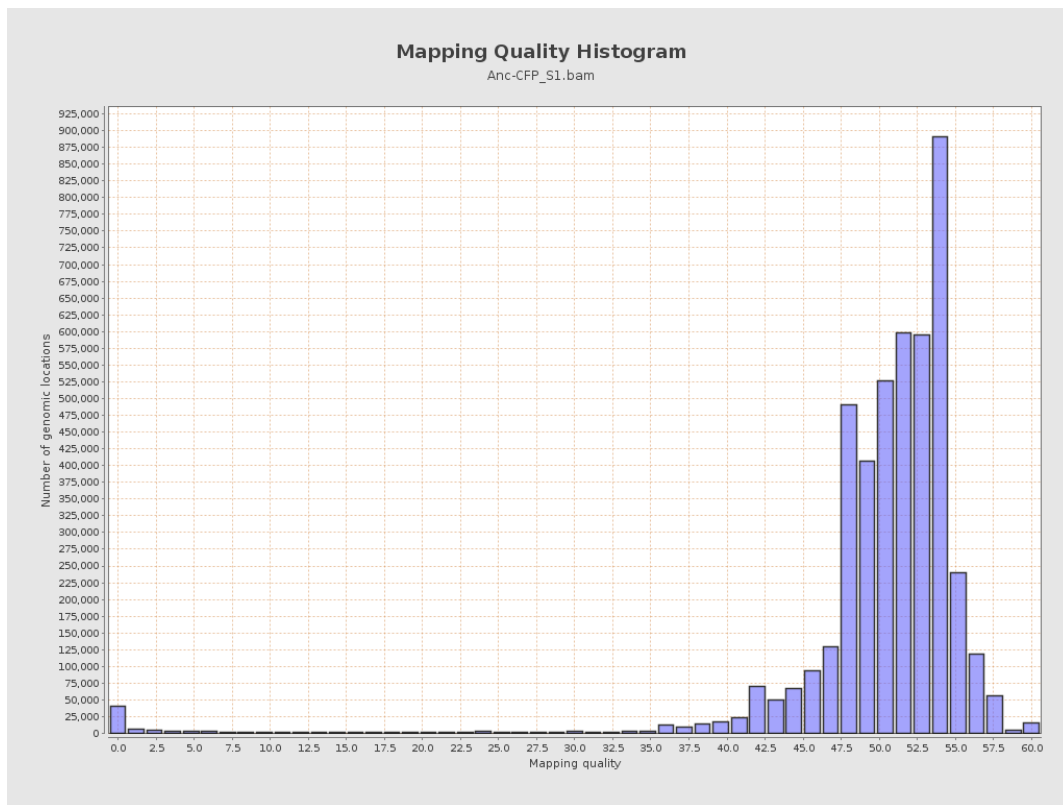
11. Homopolymer Indels



12. Mapping Quality Across Reference



13. Mapping Quality Histogram



14. Insert Size Across Reference



15. Insert Size Histogram

