

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:05:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716710.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR9716710 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716710.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:05:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716710.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,745,169
Mapped reads	8,178,770 / 93.52%
Unmapped reads	566,399 / 6.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	164,441 / 1.88%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	1,165,118 / 13.32%
Duplication rate	10.11%
Clipped reads	8,323,815 / 95.18%

2.2. ACGT Content

Number/percentage of A's	155,206,704 / 24.66%
Number/percentage of C's	134,538,946 / 21.38%
Number/percentage of T's	189,129,746 / 30.05%
Number/percentage of G's	150,502,955 / 23.91%
Number/percentage of N's	24,147 / 0%
GC Percentage	45.29%

2.3. Coverage

Mean	0.2034

Standard Deviation	1.4004
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2.4. Mapping Quality

Mean Mapping Quality	46.44
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2.5. Mismatches and indels

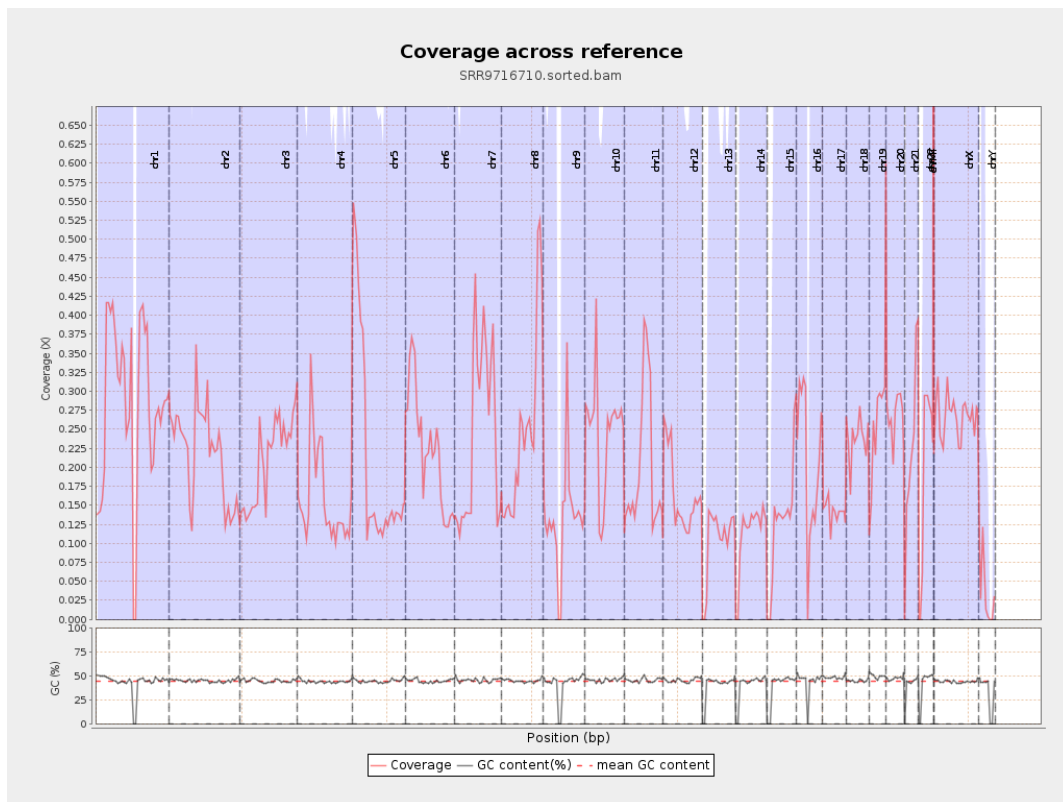
General error rate	0.68%
Mismatches	4,128,277
Insertions	56,659
Mapped reads with at least one insertion	0.68%
Deletions	115,808
Mapped reads with at least one deletion	1.39%
Homopolymer indels	38%

2.6. Chromosome stats

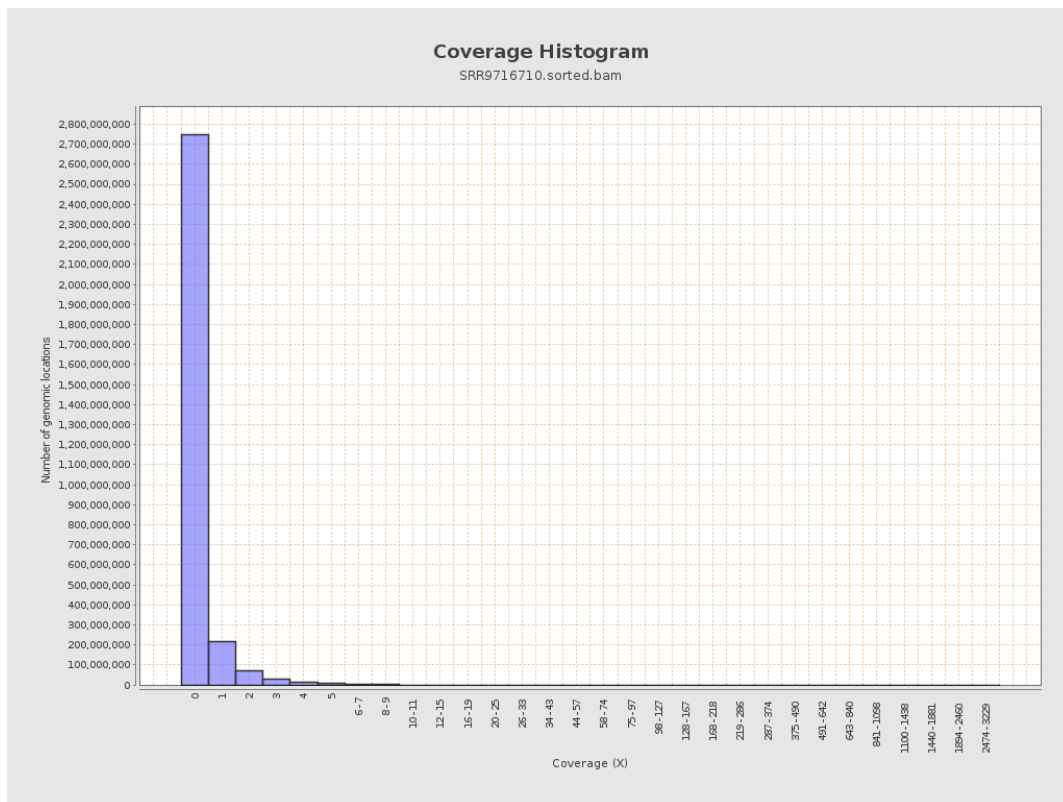
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	70415877	0.2825	2.8941
chr2	243199373	52969579	0.2178	1.5093
chr3	198022430	41336362	0.2087	0.781
chr4	191154276	29909695	0.1565	1.1549
chr5	180915260	37648685	0.2081	0.8124
chr6	171115067	38134684	0.2229	0.9086
chr7	159138663	39438034	0.2478	2.002

chr8	146364022	36324852	0.2482	1.3247
chr9	141213431	18659841	0.1321	0.9425
chr10	135534747	33203724	0.245	1.864
chr11	135006516	27321706	0.2024	1.1779
chr12	133851895	21975732	0.1642	0.6773
chr13	115169878	11864895	0.103	0.5156
chr14	107349540	12070845	0.1124	0.6538
chr15	102531392	13117453	0.1279	0.5966
chr16	90354753	18785780	0.2079	0.8698
chr17	81195210	11436854	0.1409	0.7857
chr18	78077248	18504926	0.237	1.5641
chr19	59128983	15646590	0.2646	2.0931
chr20	63025520	16766343	0.266	0.973
chr21	48129895	10884639	0.2262	1.0895
chr22	51304566	9743488	0.1899	0.7684
chrMT	16571	25273	1.5251	2.0523
chrX	155270560	41446066	0.2669	0.978
chrY	59373566	2005807	0.0338	1.0549

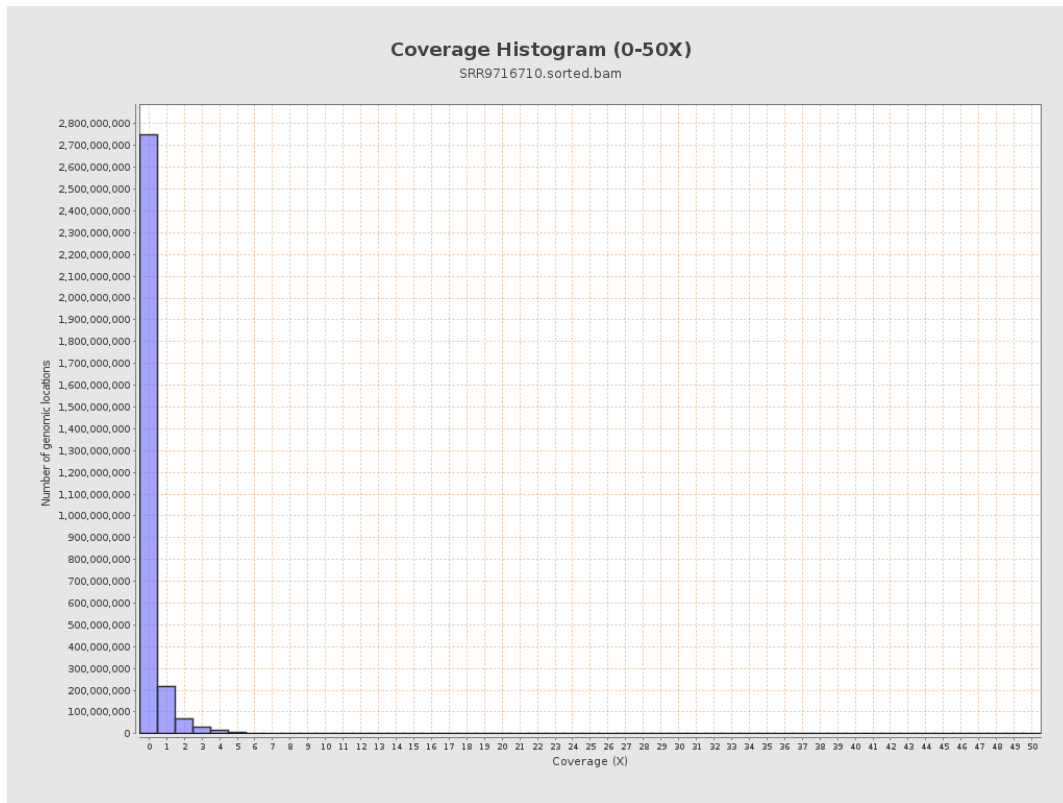
3. Results : Coverage across reference



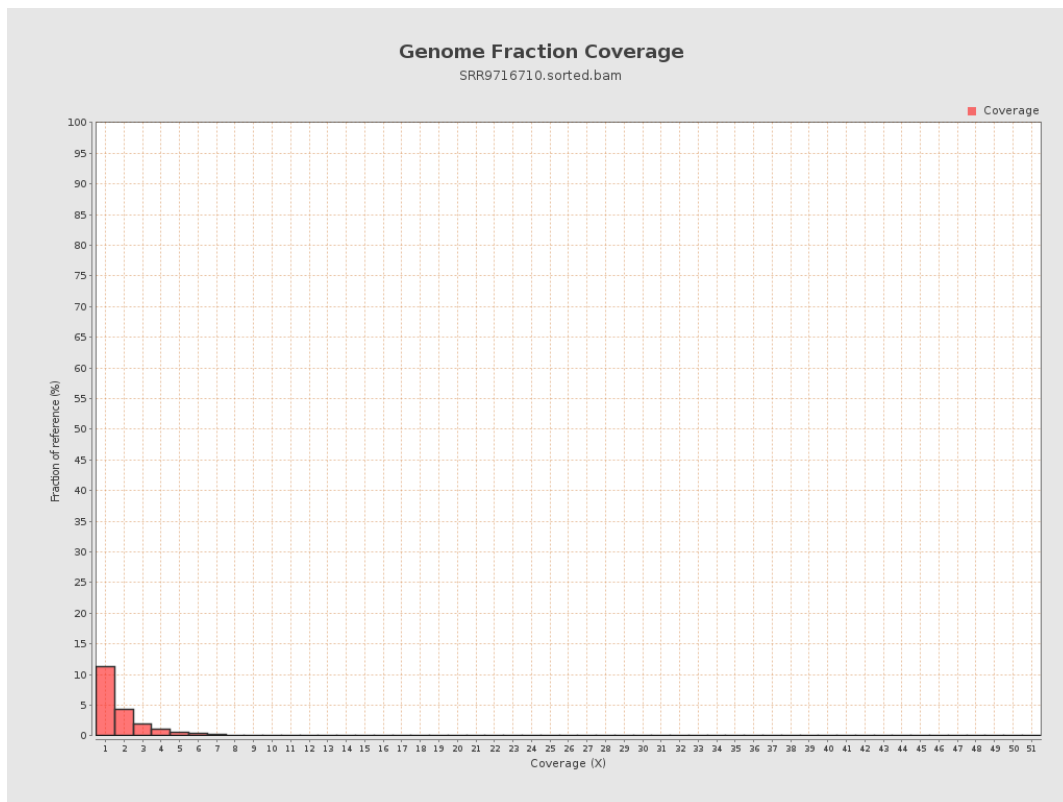
4. Results : Coverage Histogram



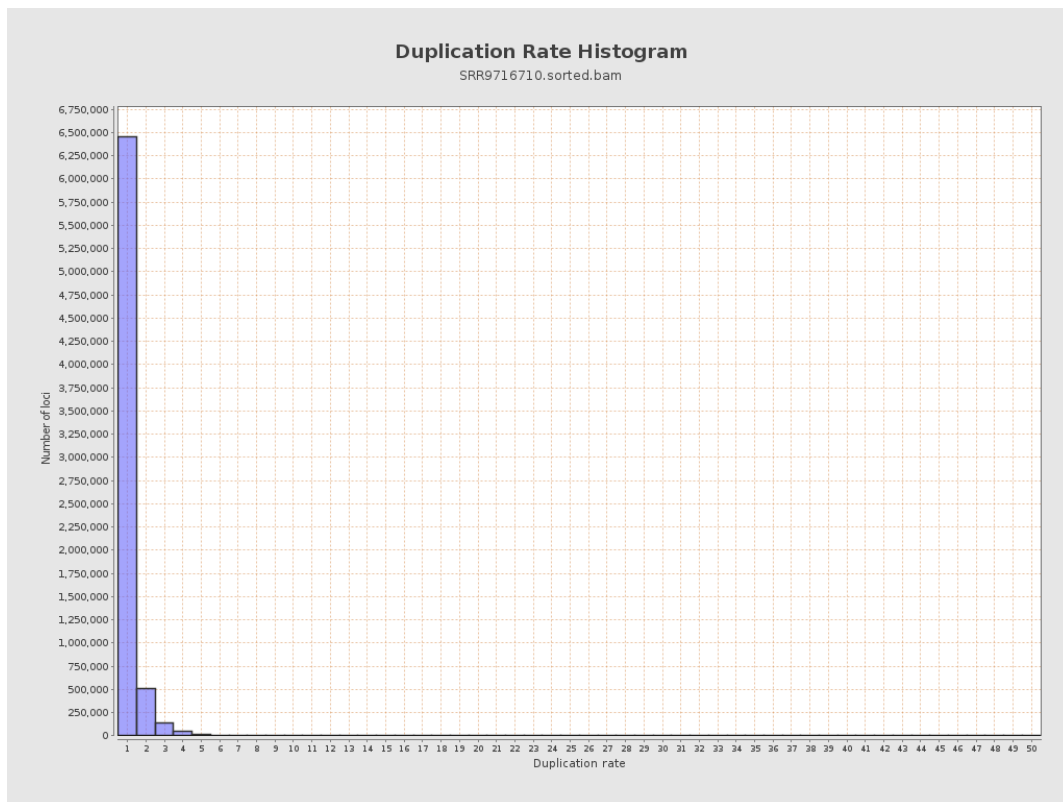
5. Results : Coverage Histogram (0-50X)



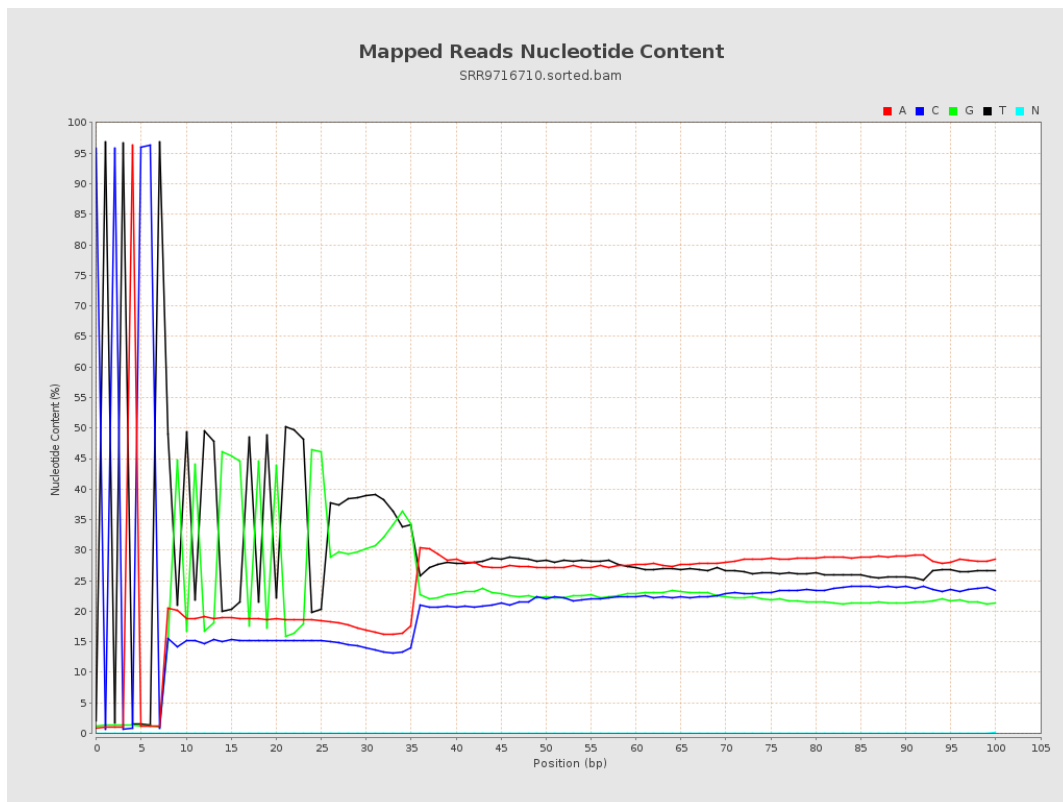
6. Results : Genome Fraction Coverage



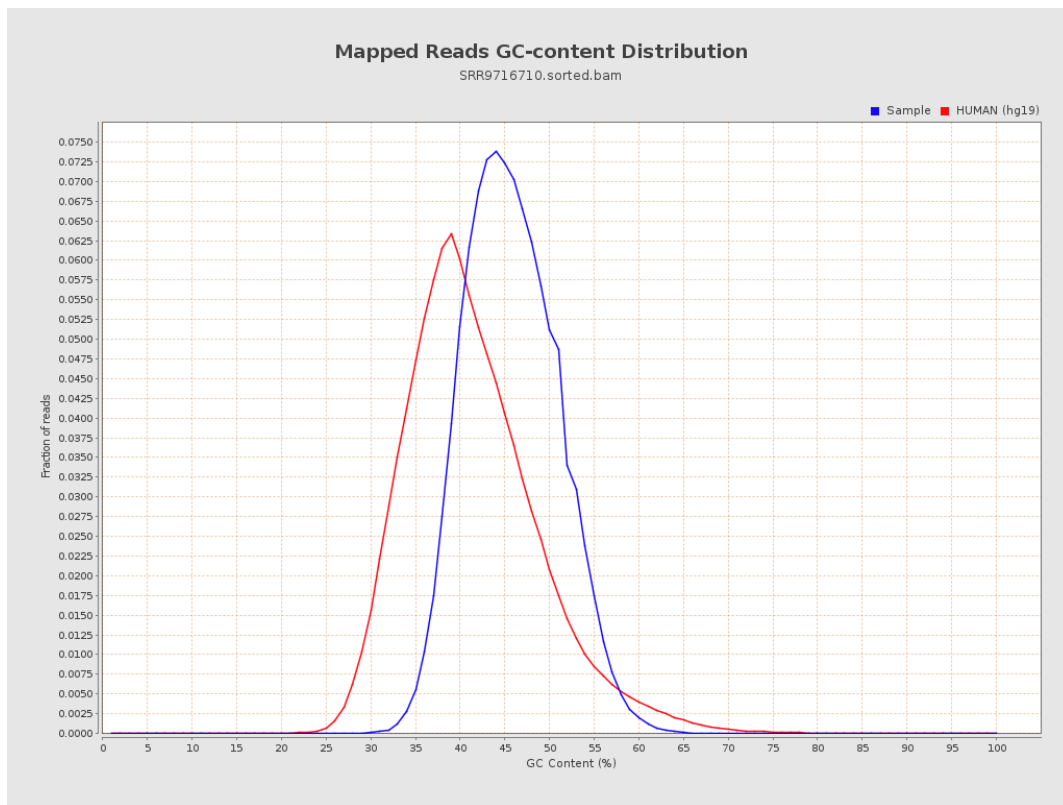
7. Results : Duplication Rate Histogram



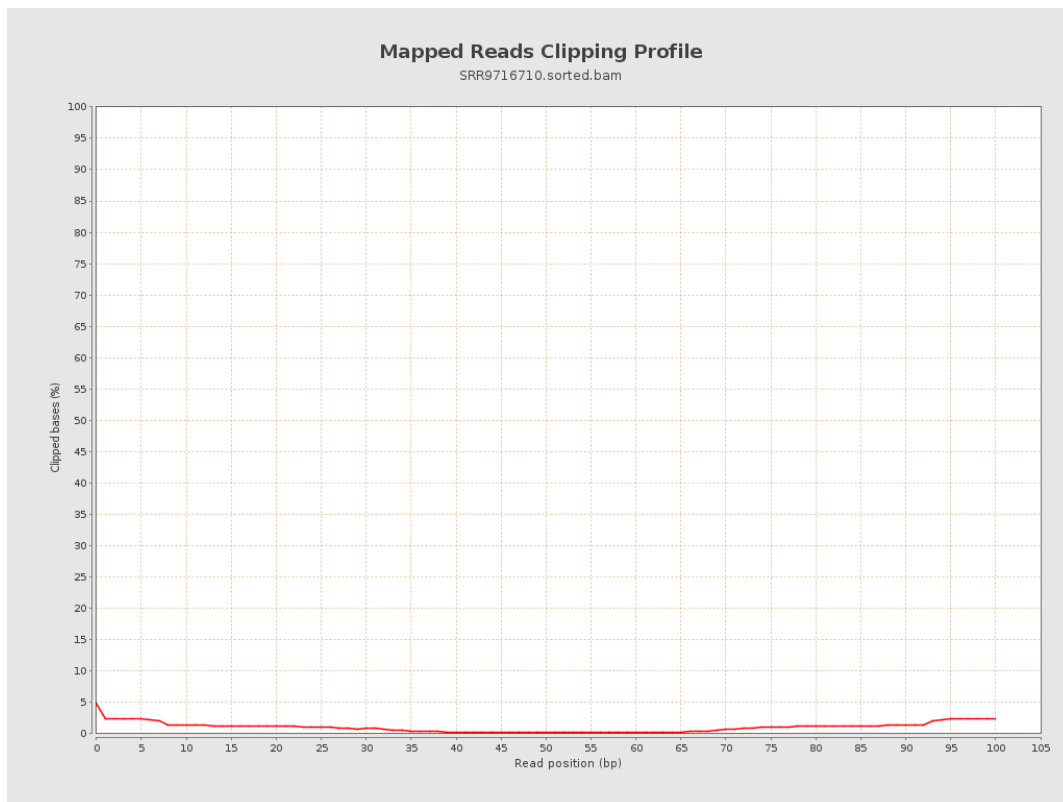
8. Results : Mapped Reads Nucleotide Content



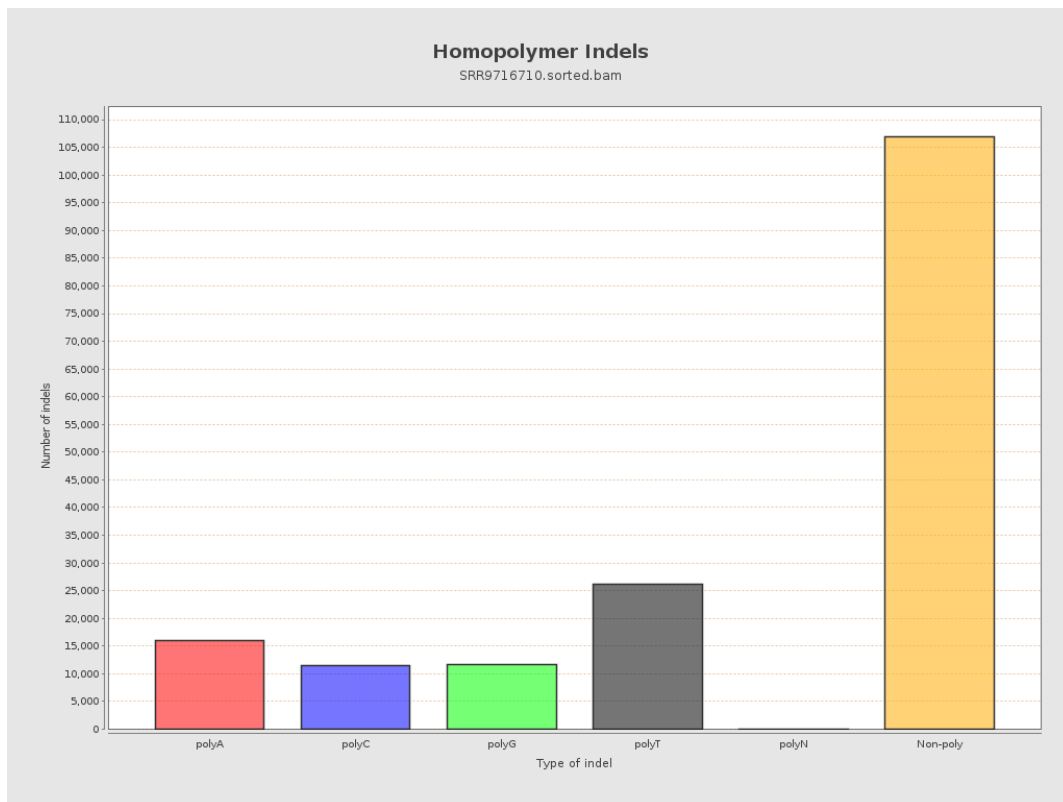
9. Results : Mapped Reads GC-content Distribution



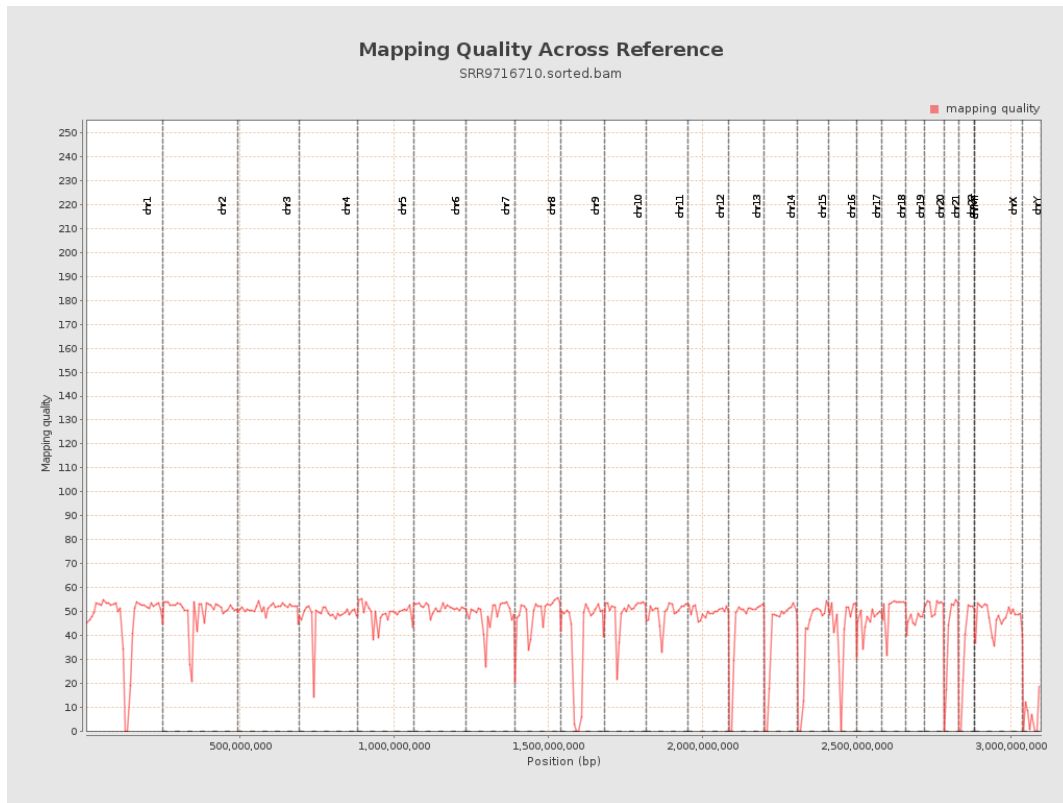
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

