

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:31:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR23117307.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_SRR23117307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR23117307.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:31:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR23117307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,953,048
Mapped reads	6,426,043 / 92.42%
Unmapped reads	527,005 / 7.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	75,765 / 1.09%
Read min/max/mean length	25 / 386 / 261.74
Duplicated reads (estimated)	3,610,370 / 51.92%
Duplication rate	34.78%
Clipped reads	6,501,748 / 93.51%

2.2. ACGT Content

Number/percentage of A's	457,664,451 / 28.3%
Number/percentage of C's	343,472,290 / 21.24%
Number/percentage of T's	462,082,680 / 28.57%
Number/percentage of G's	354,157,325 / 21.9%
Number/percentage of N's	0 / 0%
GC Percentage	43.13%

2.3. Coverage

Mean	0.5236

Standard Deviation	8.2671
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2.4. Mapping Quality

Mean Mapping Quality	52.03
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2.5. Mismatches and indels

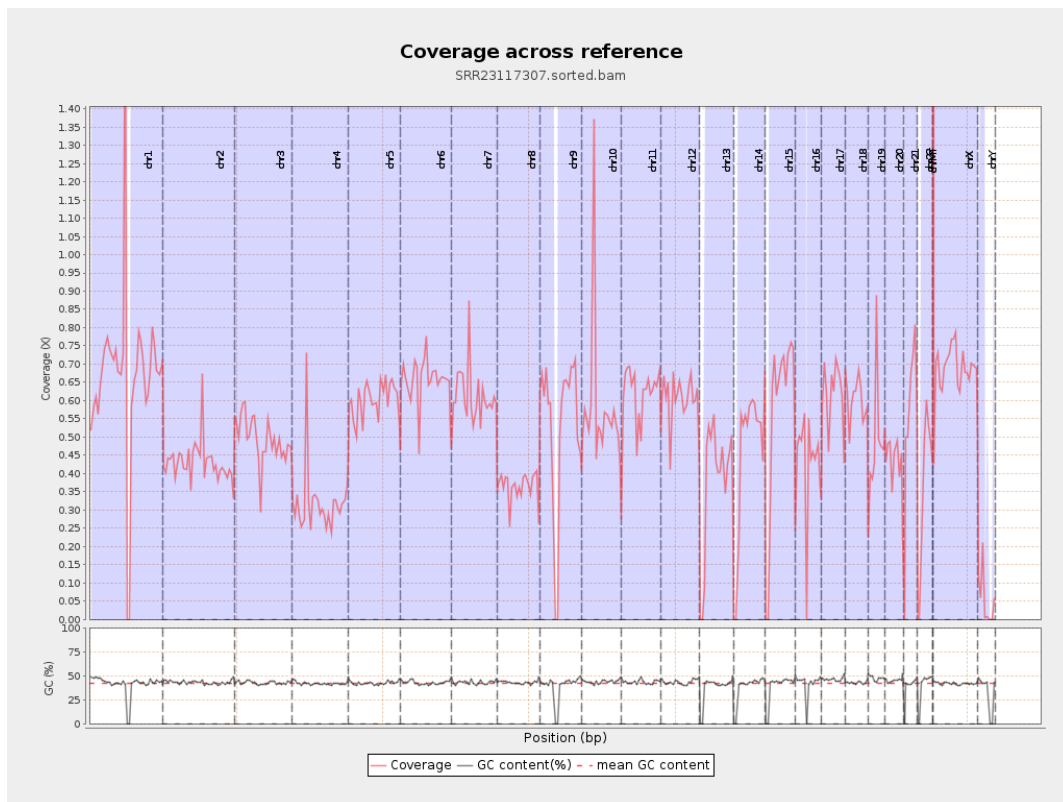
General error rate	1.2%
Mismatches	11,384,181
Insertions	6,936,273
Mapped reads with at least one insertion	48.32%
Deletions	2,813,977
Mapped reads with at least one deletion	28.5%
Homopolymer indels	30.92%

2.6. Chromosome stats

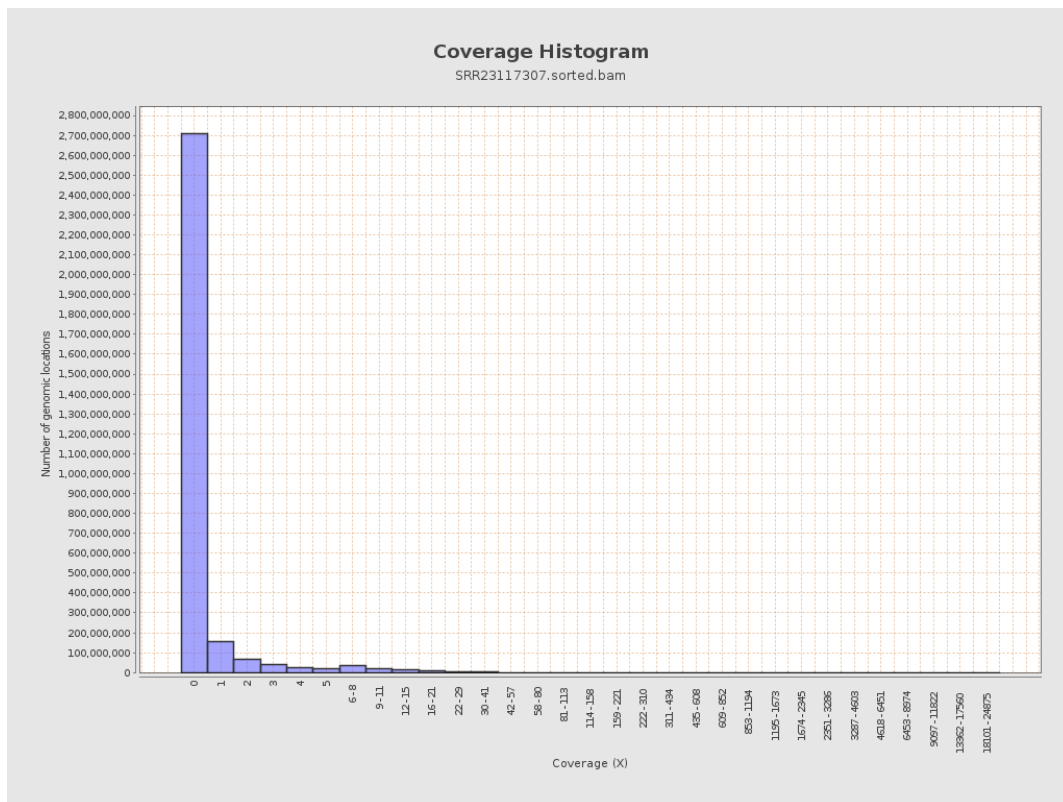
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	168061545	0.6743	24.6791
chr2	243199373	104723888	0.4306	4.1288
chr3	198022430	97779612	0.4938	2.1433
chr4	191154276	60951860	0.3189	3.409
chr5	180915260	108571869	0.6001	2.475
chr6	171115067	112641000	0.6583	2.672
chr7	159138663	97222437	0.6109	8.4184

chr8	146364022	53215508	0.3636	1.7635
chr9	141213431	75613358	0.5355	2.7851
chr10	135534747	78058803	0.5759	11.1079
chr11	135006516	83334288	0.6173	2.5744
chr12	133851895	81436764	0.6084	2.5607
chr13	115169878	44014063	0.3822	1.899
chr14	107349540	49098726	0.4574	2.128
chr15	102531392	57956610	0.5653	2.512
chr16	90354753	38181409	0.4226	3.9421
chr17	81195210	50771195	0.6253	2.7395
chr18	78077248	46801788	0.5994	3.9204
chr19	59128983	29122707	0.4925	13.5317
chr20	63025520	27302571	0.4332	3.0589
chr21	48129895	27534899	0.5721	3.69
chr22	51304566	18760632	0.3657	1.9921
chrMT	16571	215666	13.0147	39.2341
chrX	155270560	106357249	0.685	2.8841
chrY	59373566	3212587	0.0541	2.6867

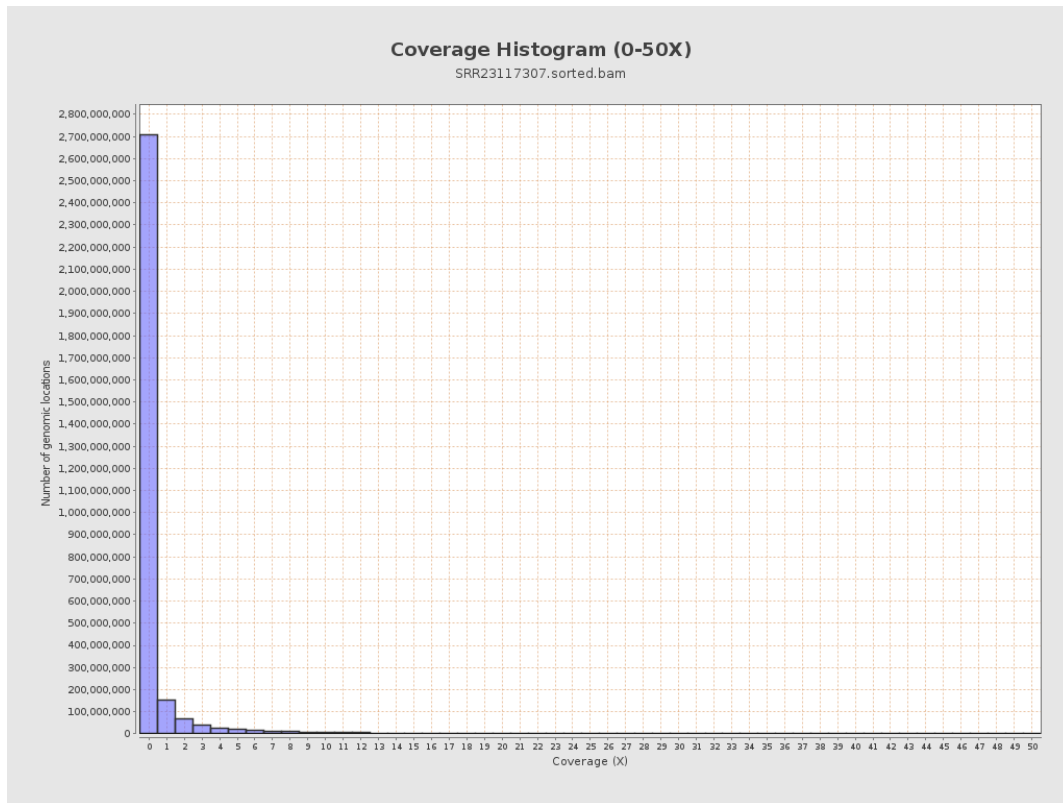
3. Results : Coverage across reference



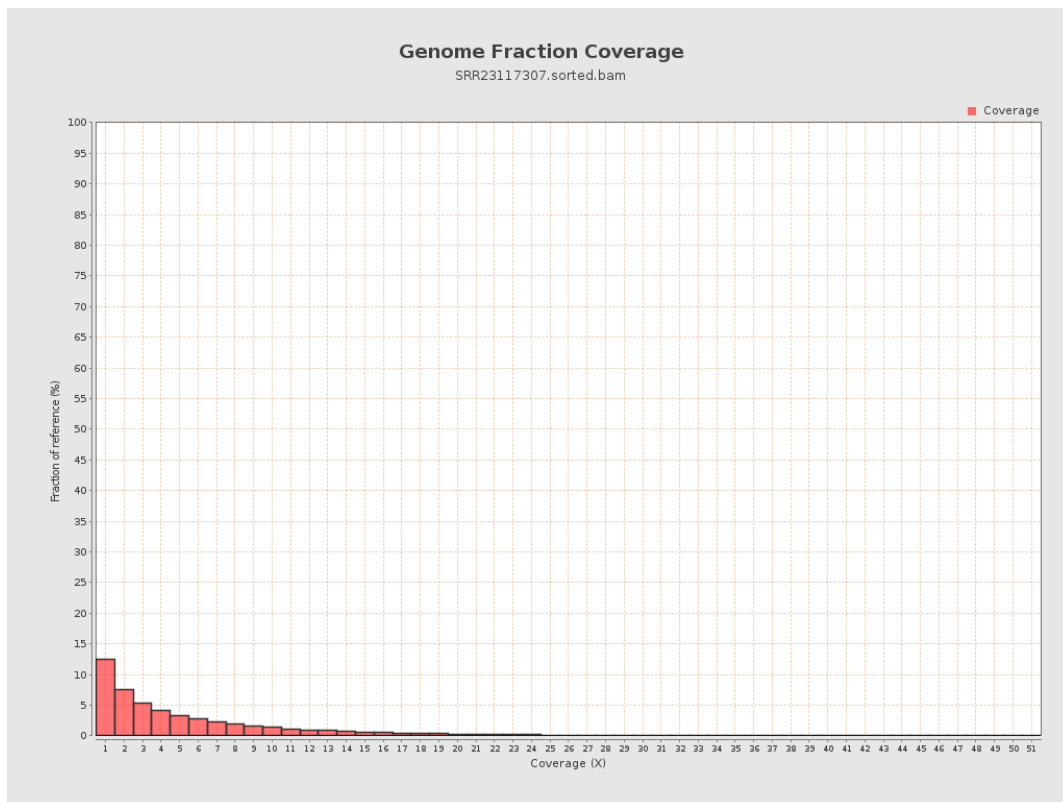
4. Results : Coverage Histogram



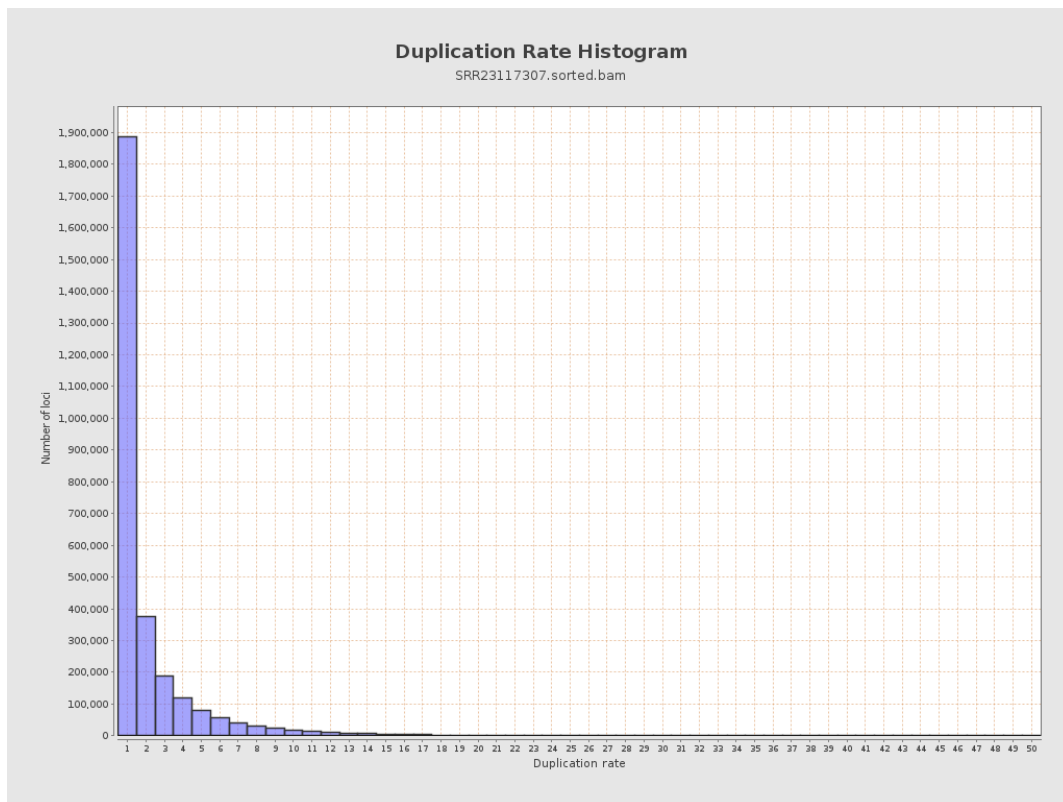
5. Results : Coverage Histogram (0-50X)



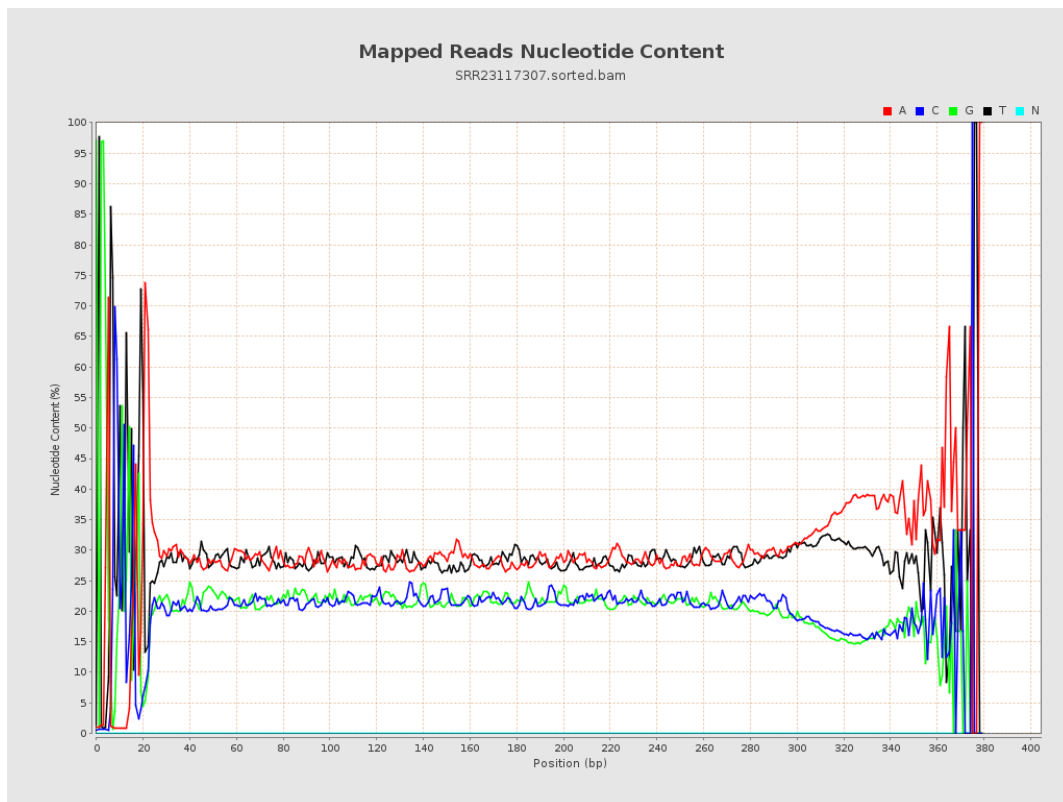
6. Results : Genome Fraction Coverage



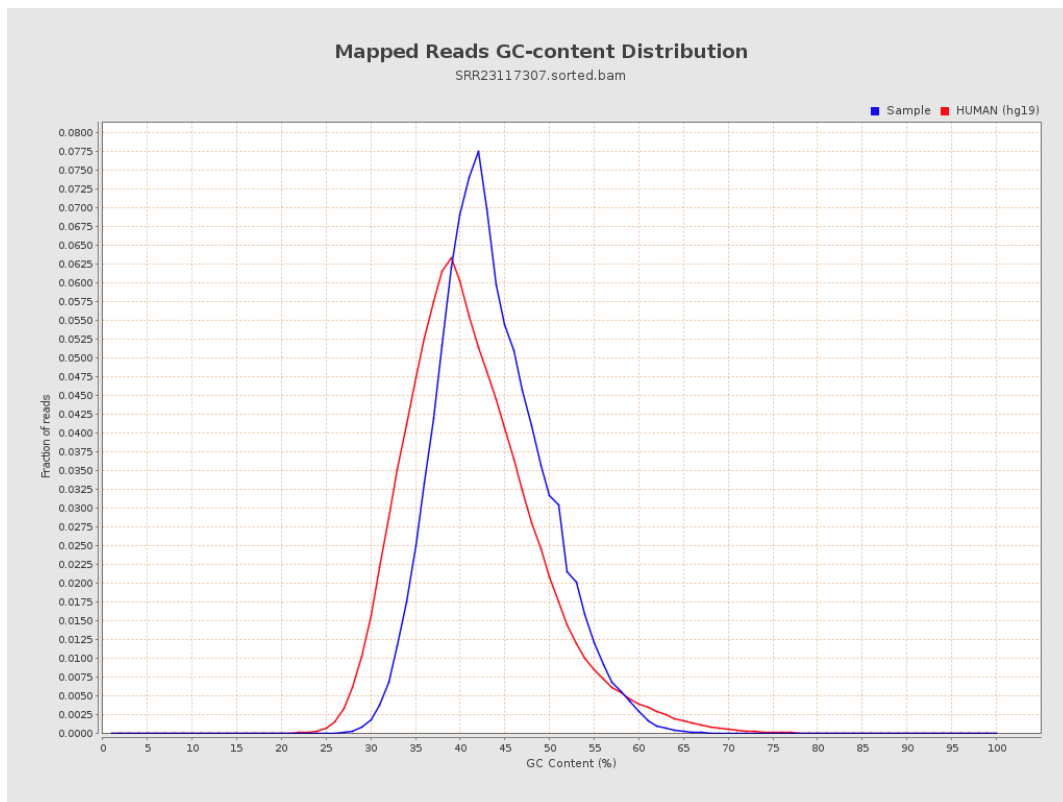
7. Results : Duplication Rate Histogram



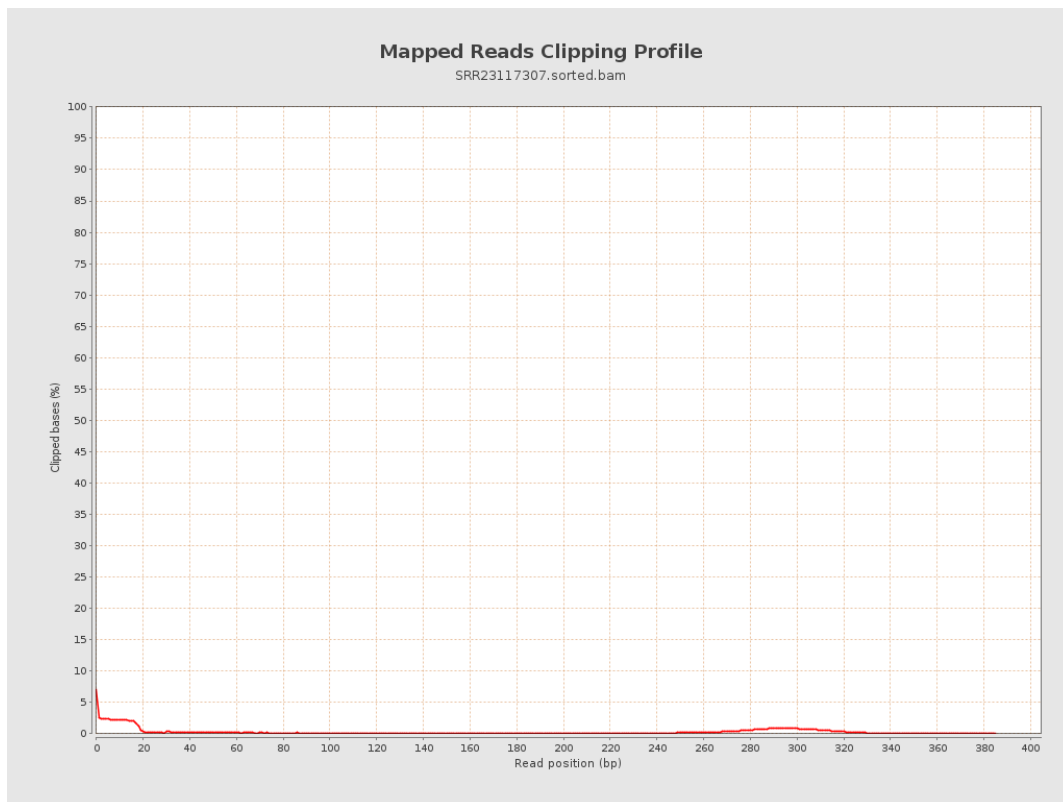
8. Results : Mapped Reads Nucleotide Content



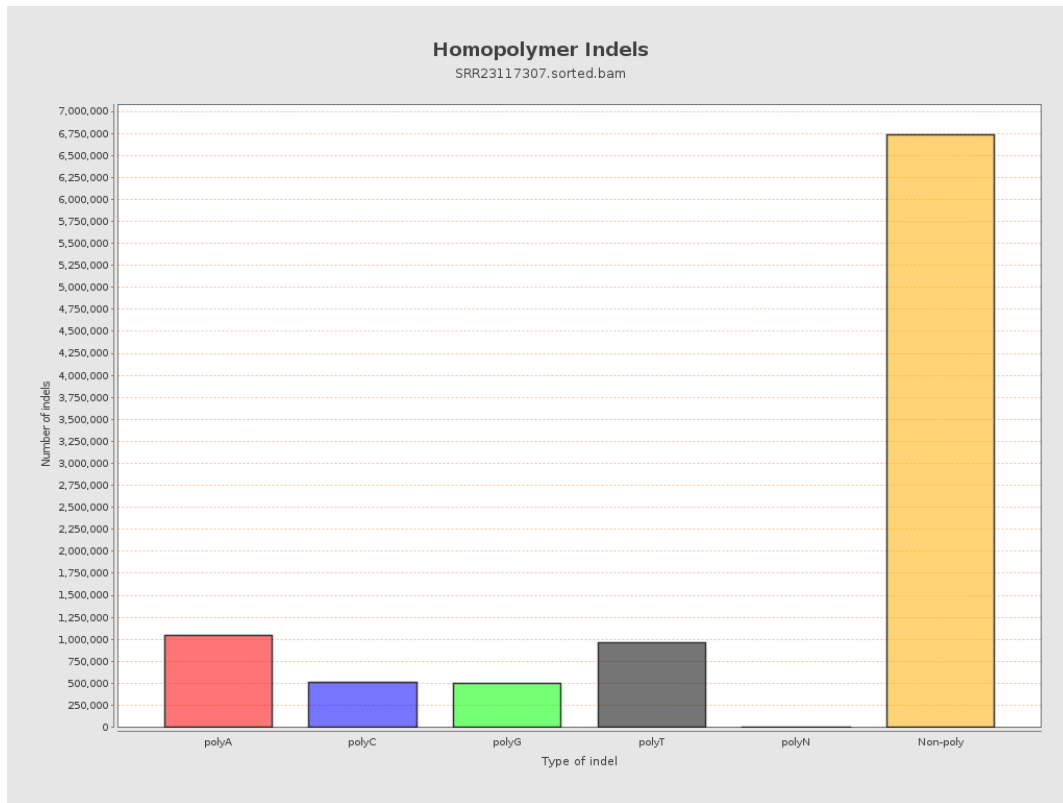
9. Results : Mapped Reads GC-content Distribution



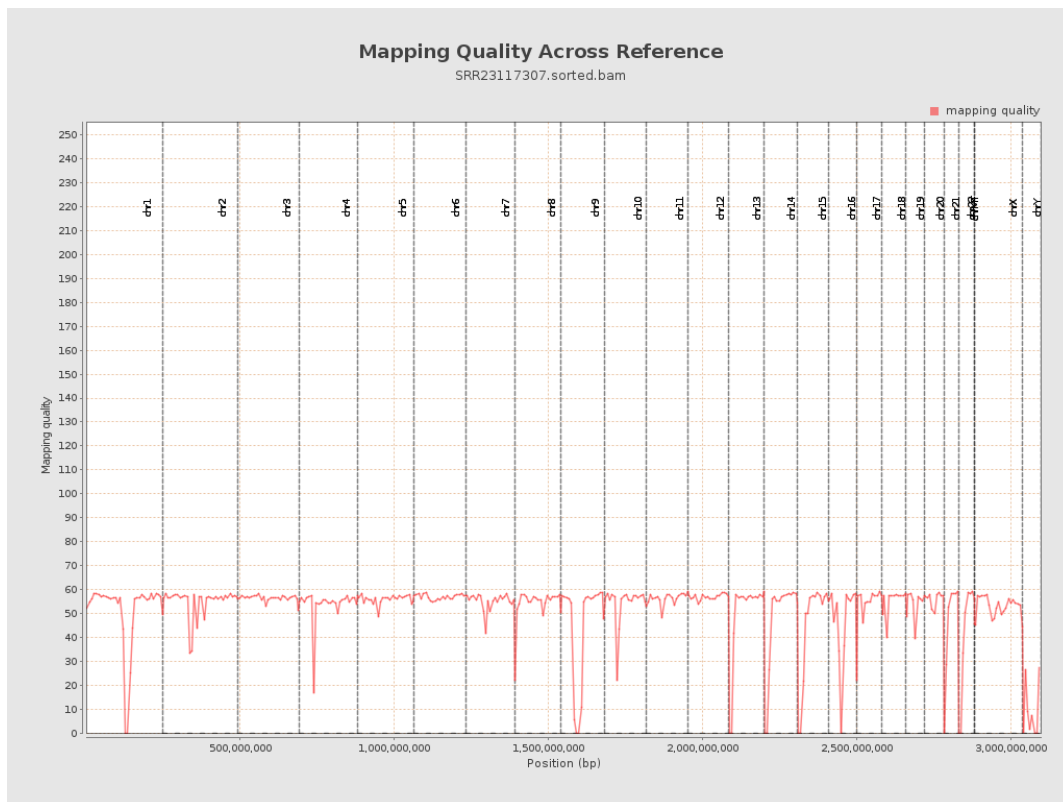
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

