

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:34:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240250.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_SRR6240250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240250.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:34:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,602,451
Mapped reads	1,265,509 / 78.97%
Unmapped reads	336,942 / 21.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,709 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	179,758 / 11.22%
Duplication rate	10.93%
Clipped reads	675,129 / 42.13%

2.2. ACGT Content

Number/percentage of A's	22,607,683 / 27.63%
Number/percentage of C's	14,944,476 / 18.27%
Number/percentage of T's	26,229,985 / 32.06%
Number/percentage of G's	18,027,992 / 22.03%
Number/percentage of N's	7,348 / 0.01%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.322
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2.4. Mapping Quality

Mean Mapping Quality	46.31
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2.5. Mismatches and indels

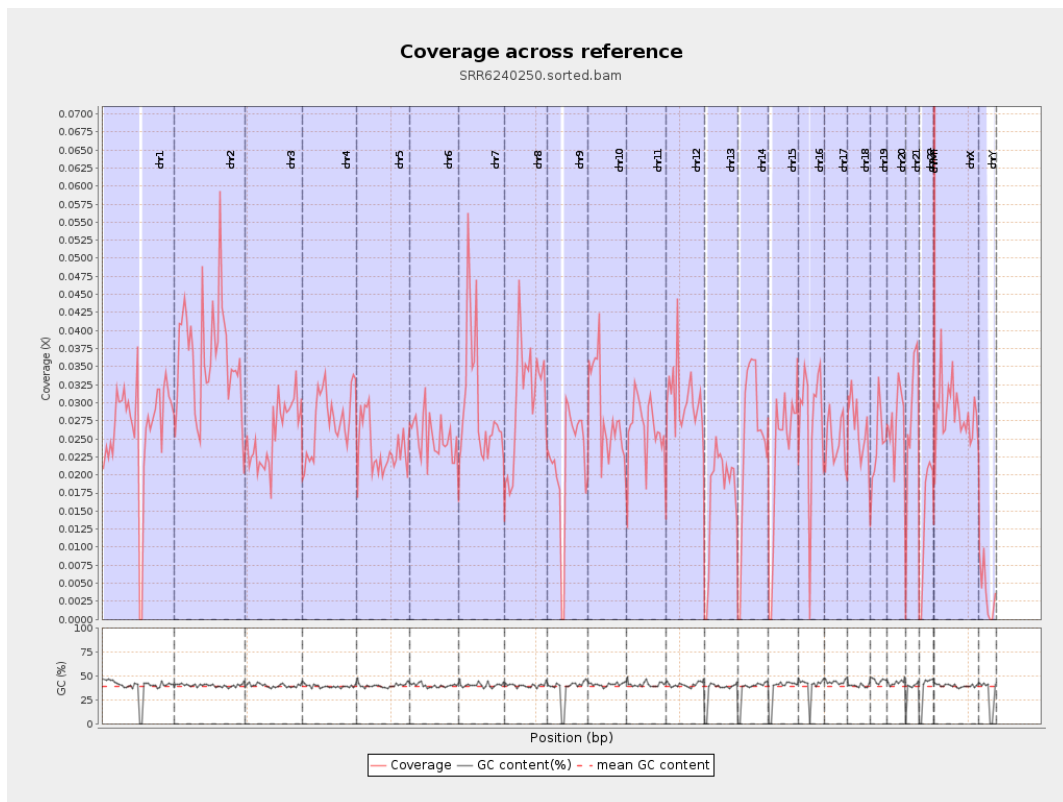
General error rate	0.84%
Mismatches	680,978
Insertions	5,621
Mapped reads with at least one insertion	0.44%
Deletions	21,939
Mapped reads with at least one deletion	1.72%
Homopolymer indels	48.79%

2.6. Chromosome stats

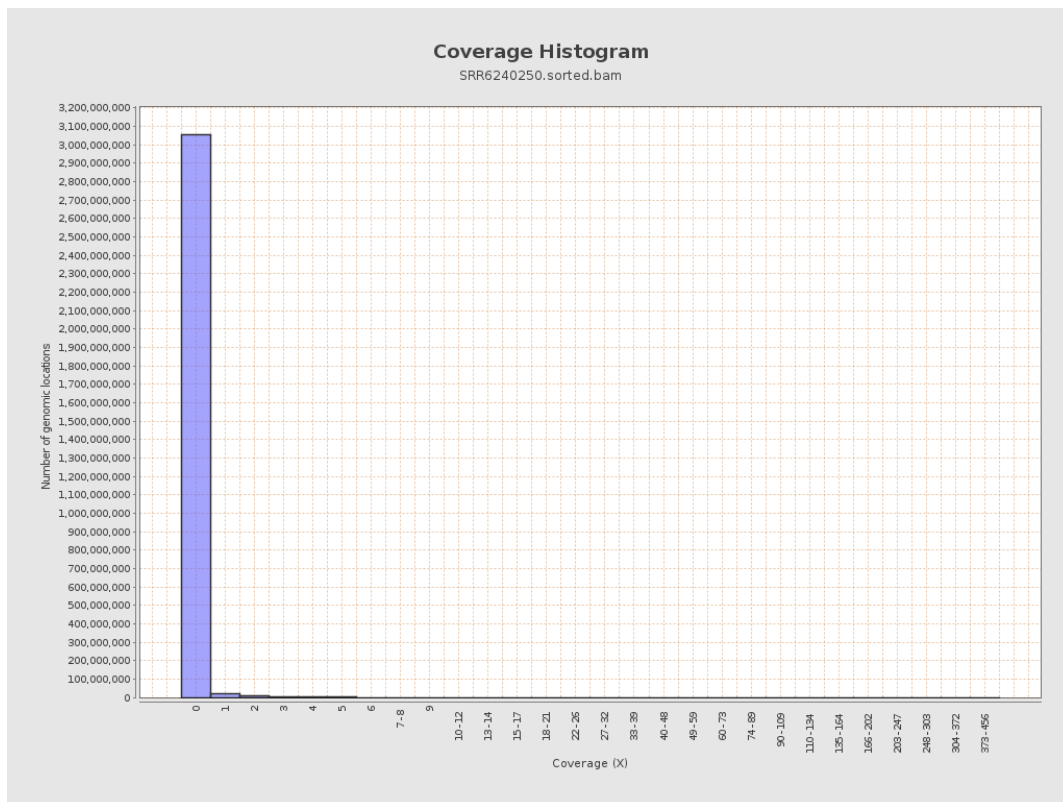
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6585366	0.0264	0.4276
chr2	243199373	8859744	0.0364	0.395
chr3	198022430	5089108	0.0257	0.2705
chr4	191154276	5258372	0.0275	0.2841
chr5	180915260	4289549	0.0237	0.2619
chr6	171115067	4296732	0.0251	0.2882
chr7	159138663	4744902	0.0298	0.4107

chr8	146364022	4504662	0.0308	0.4062
chr9	141213431	3075814	0.0218	0.2876
chr10	135534747	3863125	0.0285	0.3181
chr11	135006516	3608992	0.0267	0.3055
chr12	133851895	4105856	0.0307	0.2999
chr13	115169878	2003986	0.0174	0.2271
chr14	107349540	2722590	0.0254	0.2797
chr15	102531392	2328260	0.0227	0.2696
chr16	90354753	2473763	0.0274	0.2819
chr17	81195210	1995045	0.0246	0.2682
chr18	78077248	2075649	0.0266	0.4087
chr19	59128983	1448786	0.0245	0.3306
chr20	63025520	1726163	0.0274	0.2813
chr21	48129895	1370064	0.0285	0.2935
chr22	51304566	733177	0.0143	0.1934
chrMT	16571	16954	1.0231	1.833
chrX	155270560	4458993	0.0287	0.298
chrY	59373566	220287	0.0037	0.0968

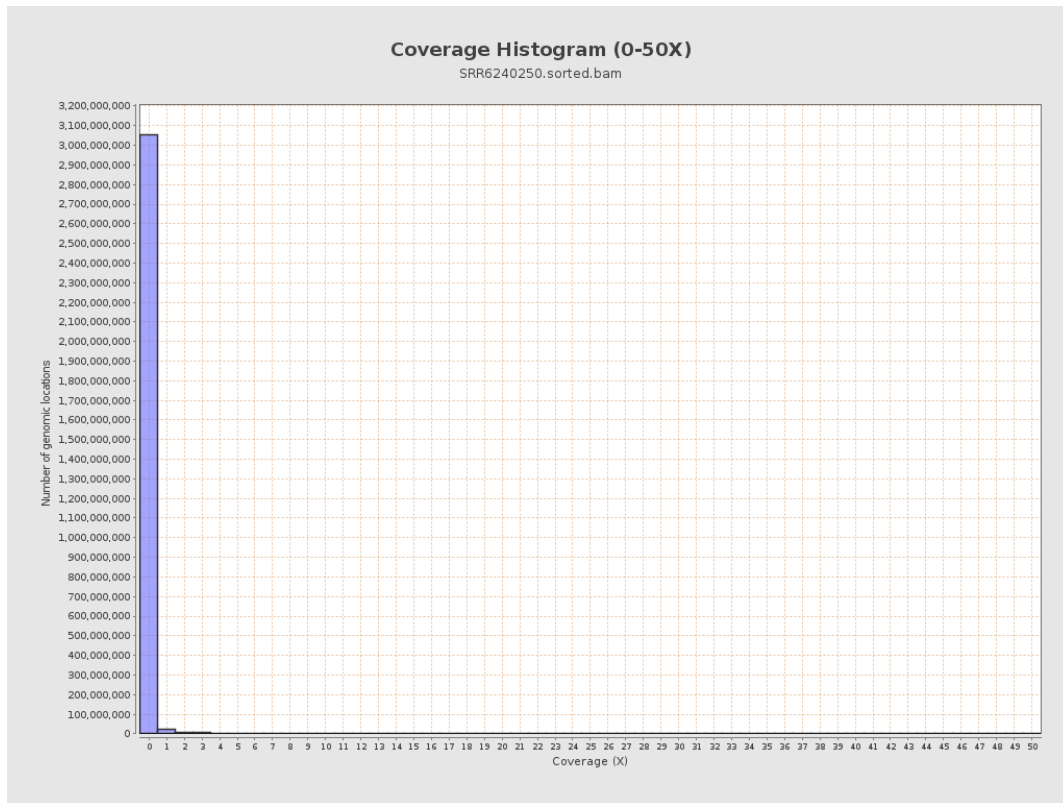
3. Results : Coverage across reference



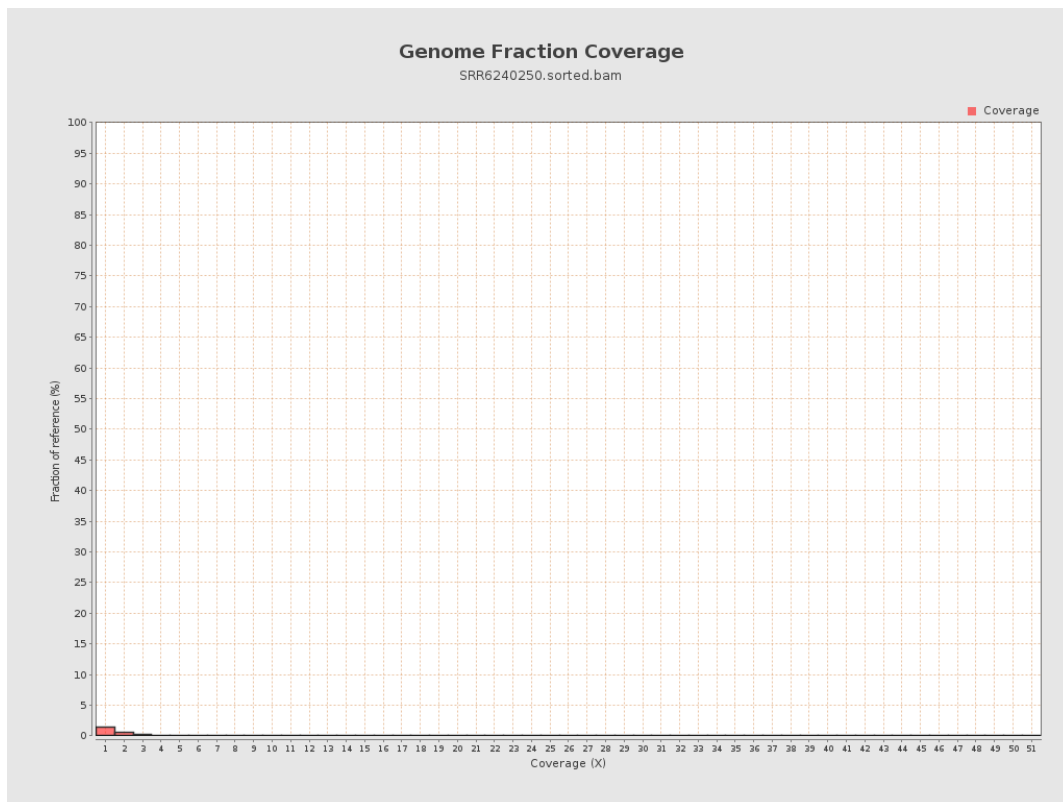
4. Results : Coverage Histogram



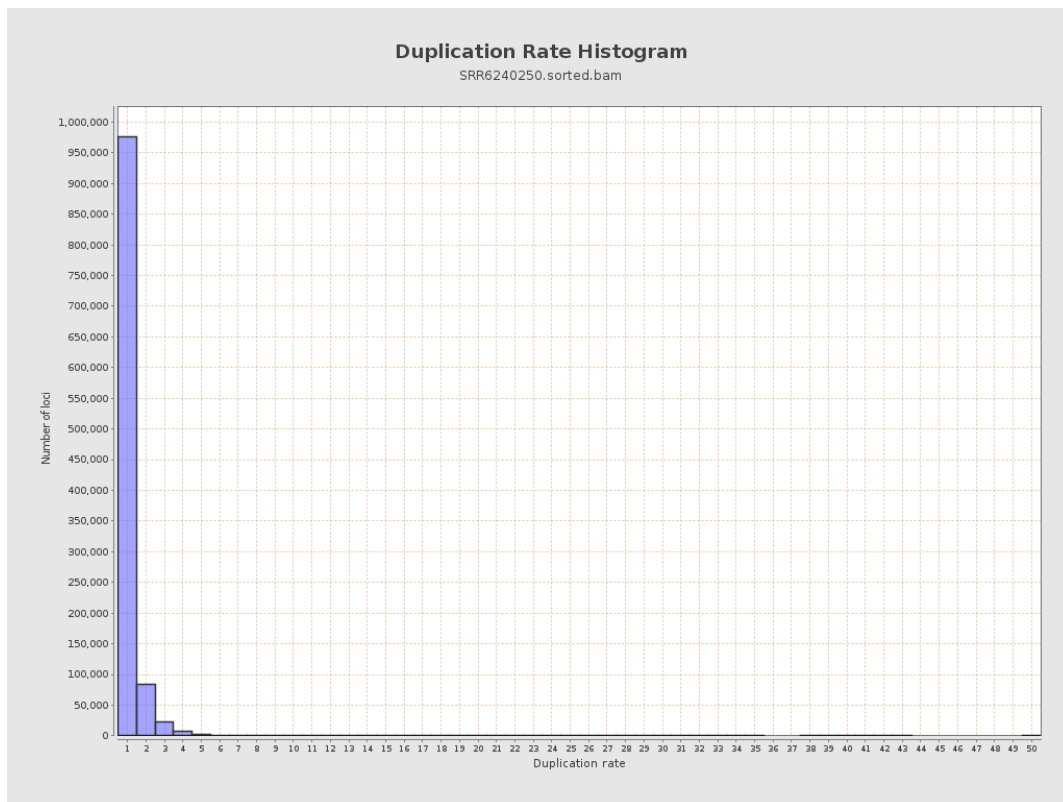
5. Results : Coverage Histogram (0-50X)



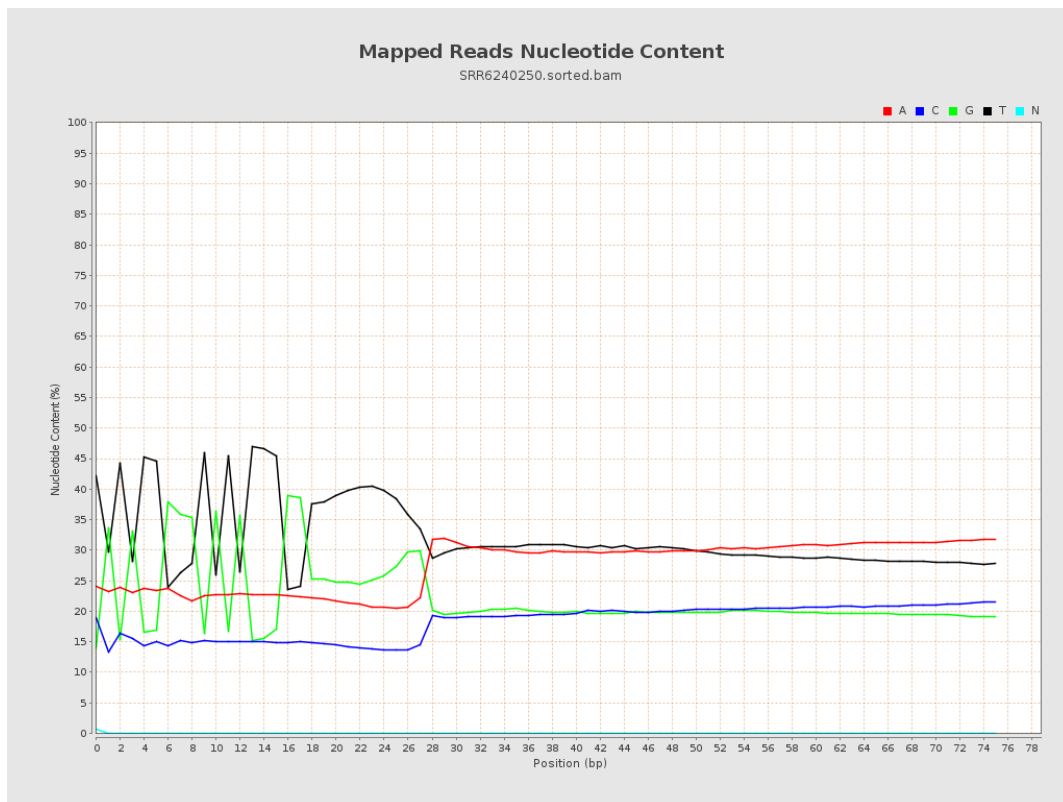
6. Results : Genome Fraction Coverage



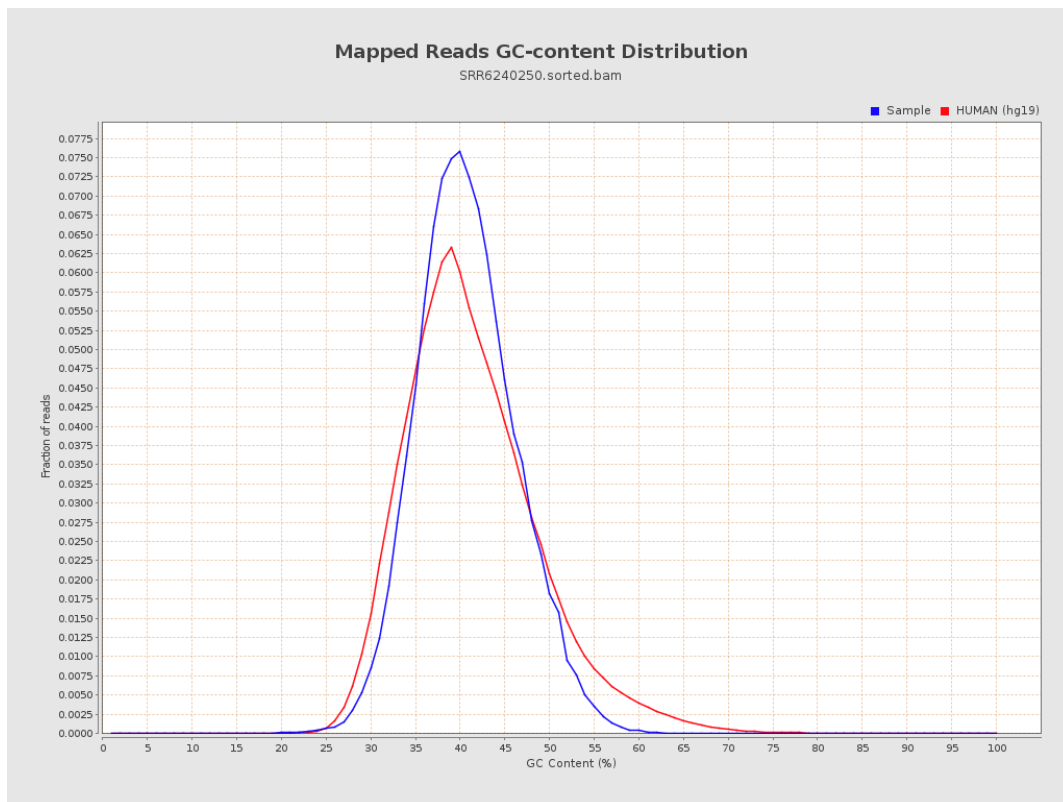
7. Results : Duplication Rate Histogram



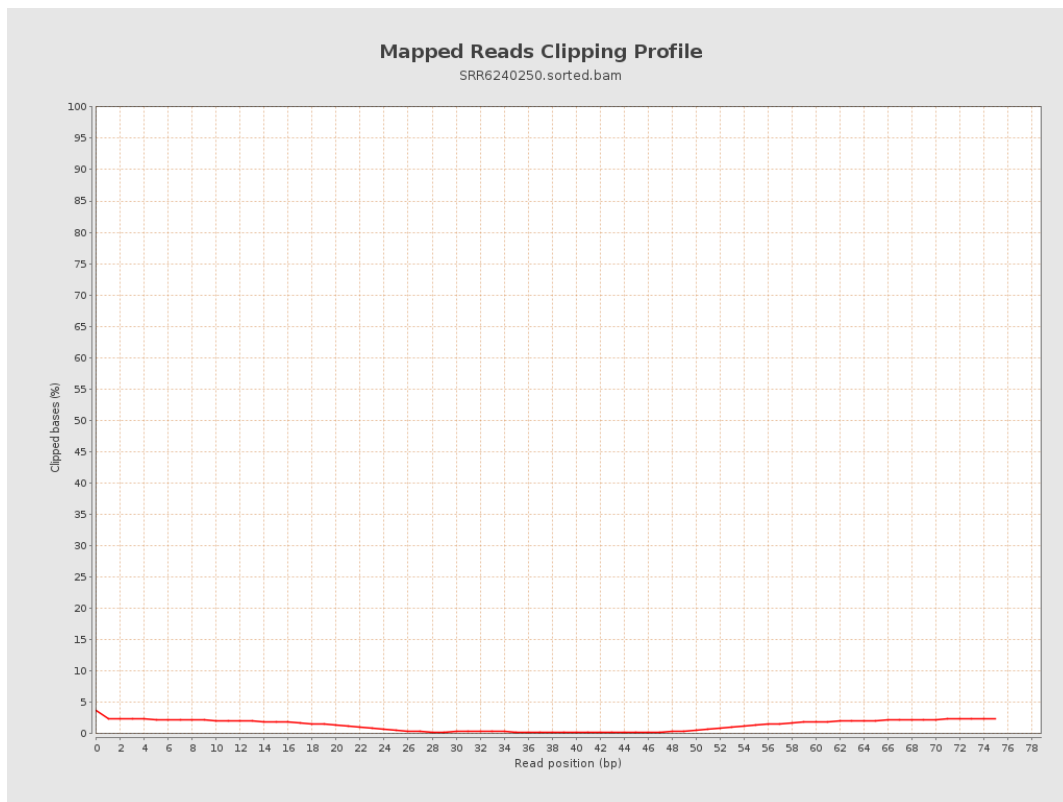
8. Results : Mapped Reads Nucleotide Content



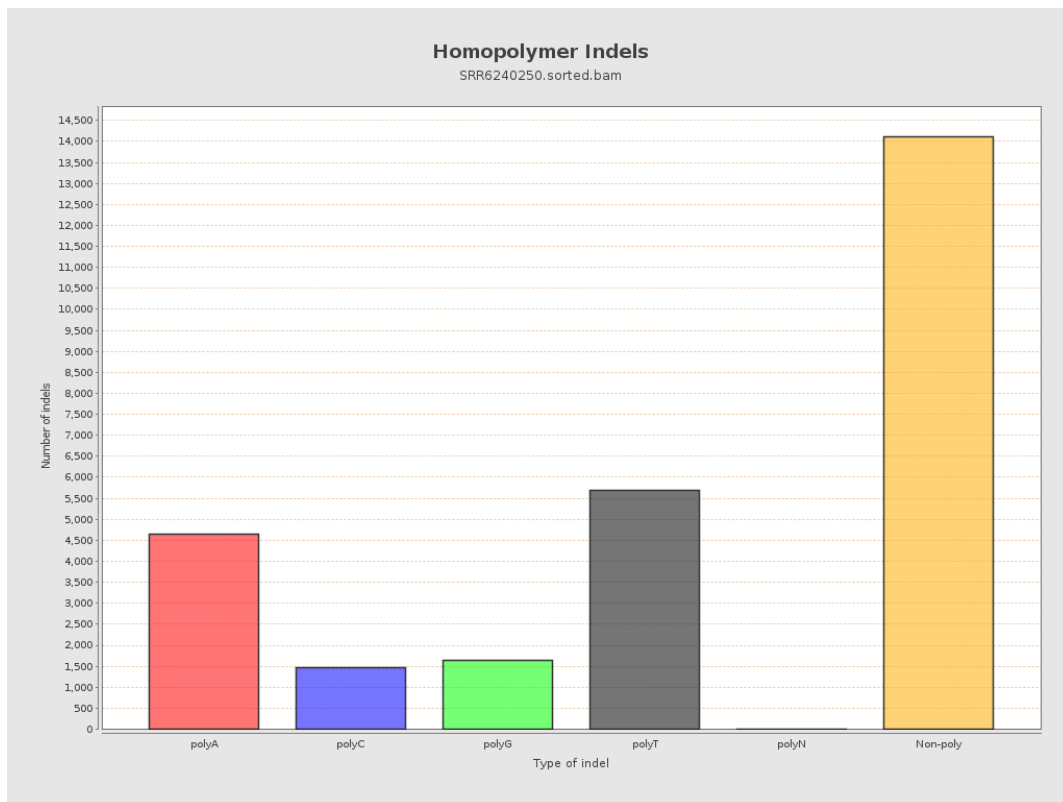
9. Results : Mapped Reads GC-content Distribution



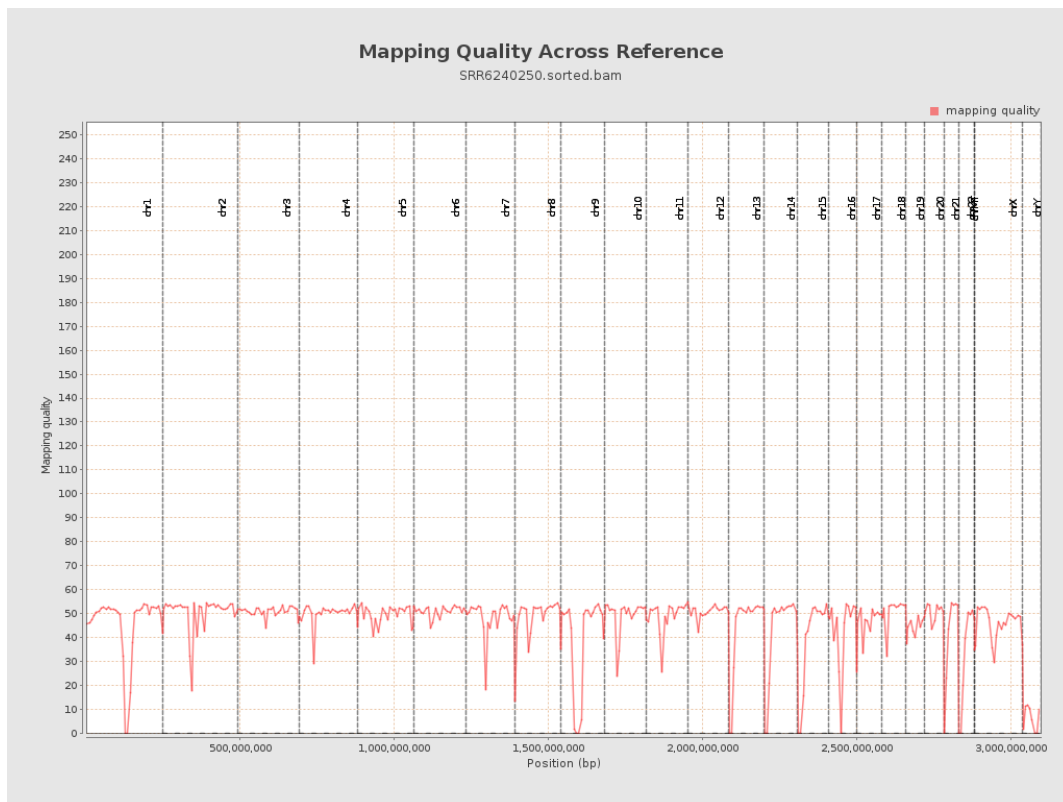
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

