Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:06:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240220.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_SRR6240220 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240220.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:06:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240220.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,784,816
Mapped reads	2,344,611 / 84.19%
Unmapped reads	440,205 / 15.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,426 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	139,695 / 5.02%
Duplication rate	4.69%
Clipped reads	1,003,455 / 36.03%

2.2. ACGT Content

Number/percentage of A's	45,491,804 / 28.72%
Number/percentage of C's	29,827,147 / 18.83%
Number/percentage of T's	49,788,932 / 31.44%
Number/percentage of G's	33,249,887 / 20.99%
Number/percentage of N's	14,458 / 0.01%
GC Percentage	39.83%

2.3. Coverage

Mean	0.0512

Standard Deviation	0.5303

2.4. Mapping Quality

Mean Mapping Quality	47.05

2.5. Mismatches and indels

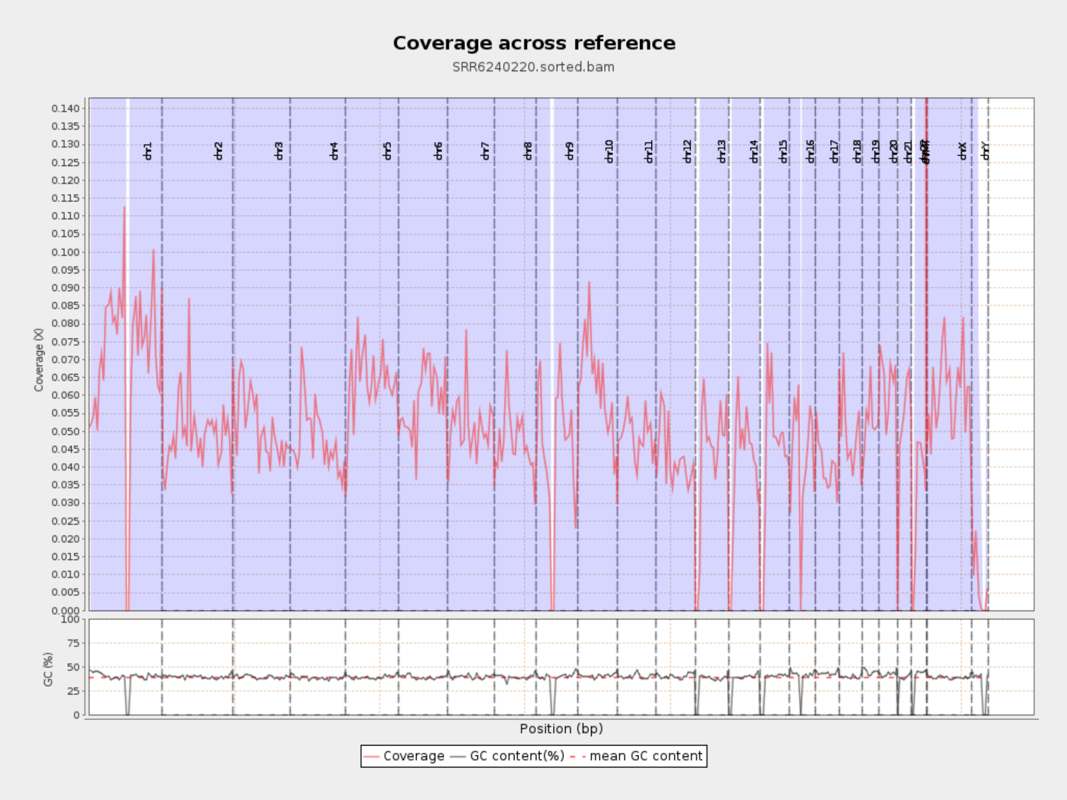
General error rate	0.8%
Mismatches	1,249,619
Insertions	11,913
Mapped reads with at least one insertion	0.5%
Deletions	36,816
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.29%

2.6. Chromosome stats

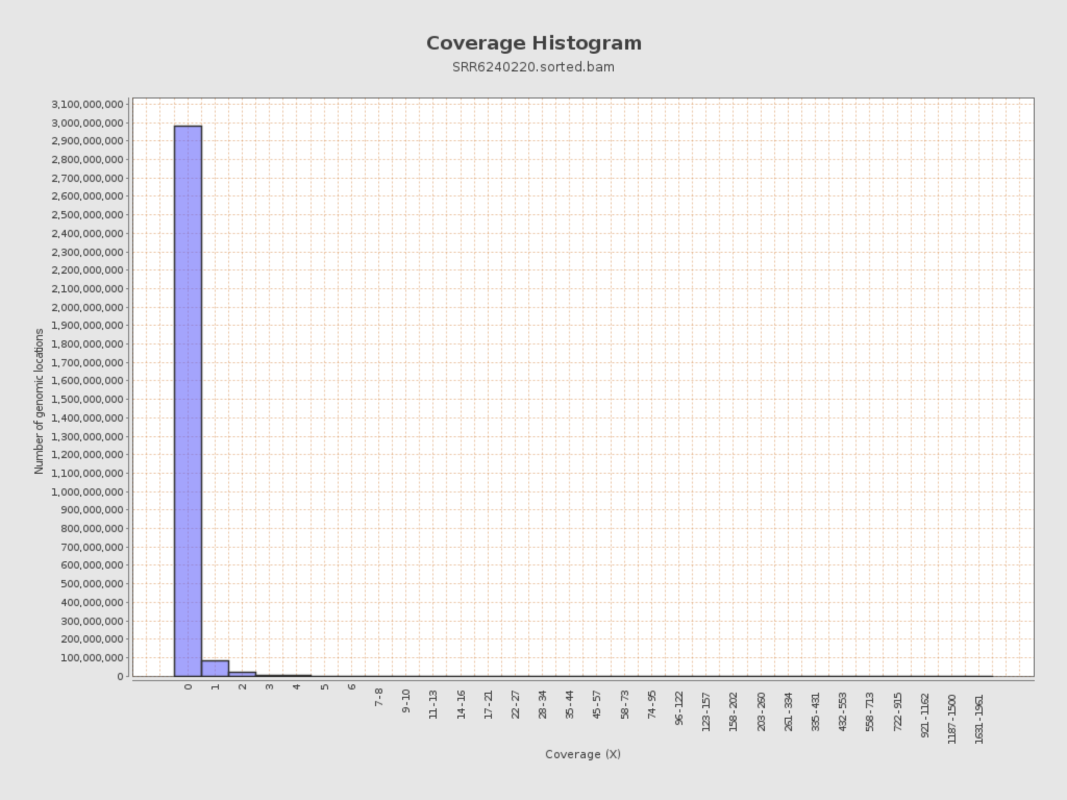
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17673749	0.0709	1.0022
chr2	243199373	11985754	0.0493	0.4681
chr3	198022430	10224112	0.0516	0.304
chr4	191154276	9134615	0.0478	0.3023
chr5	180915260	11618857	0.0642	0.337
chr6	171115067	9982172	0.0583	0.3424
chr7	159138663	8251407	0.0519	0.4762

chr8	146364022	6879186	0.047	1.1816
chr9	141213431	6326499	0.0448	0.4488
chr10	135534747	8596943	0.0634	0.4475
chr11	135006516	6580957	0.0487	0.4452
chr12	133851895	5691695	0.0425	0.2784
chr13	115169878	4829077	0.0419	0.271
chr14	107349540	4237704	0.0395	0.2918
chr15	102531392	4458409	0.0435	0.2788
chr16	90354753	3888059	0.043	0.311
chr17	81195210	3243714	0.0399	0.2914
chr18	78077248	3884093	0.0497	0.8657
chr19	59128983	3120342	0.0528	0.5894
chr20	63025520	3957122	0.0628	0.3419
chr21	48129895	2462056	0.0512	0.3184
chr22	51304566	1535285	0.0299	0.2232
chrMT	16571	25103	1.5149	1.8198
chrX	155270560	9408661	0.0606	0.3605
chrY	59373566	441897	0.0074	0.1642

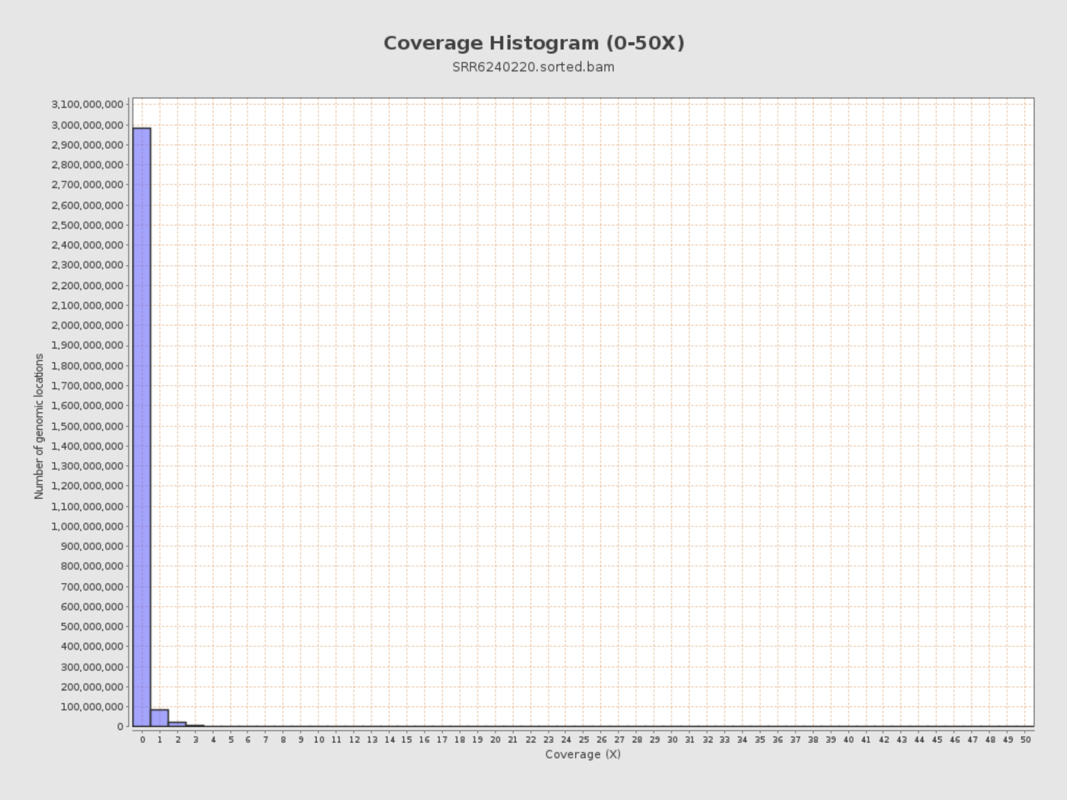
3. Results : Coverage across reference



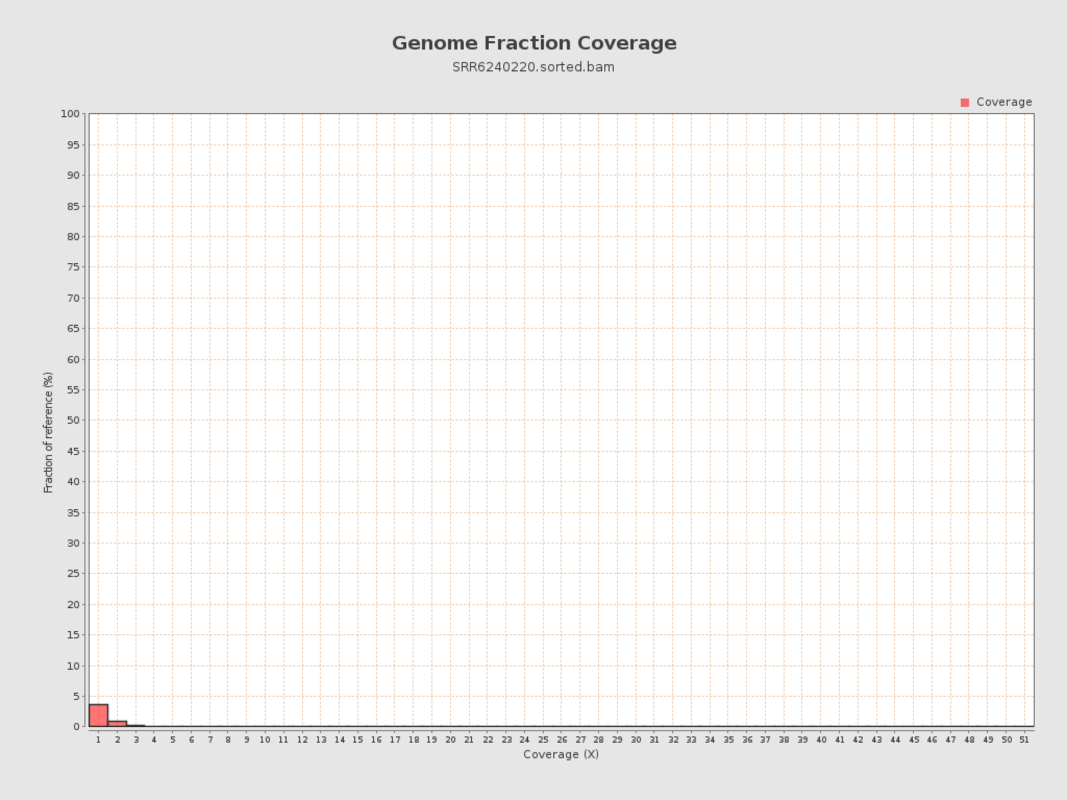
4. Results : Coverage Histogram



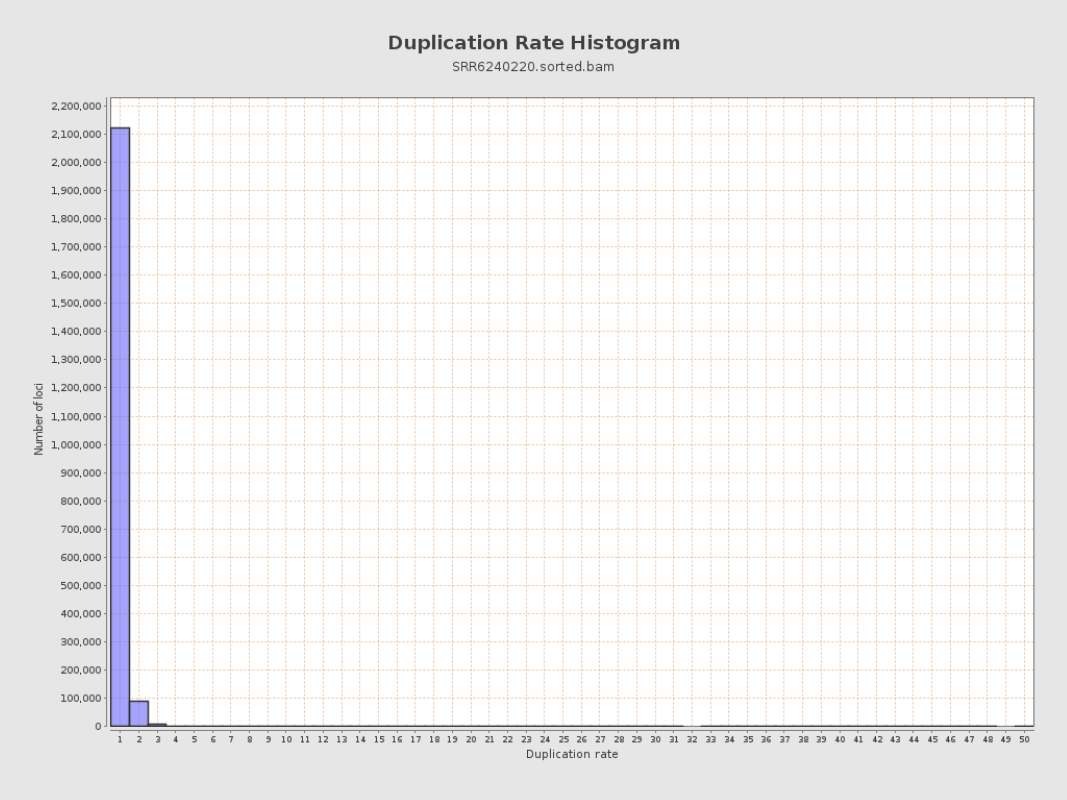
5. Results : Coverage Histogram (0-50X)



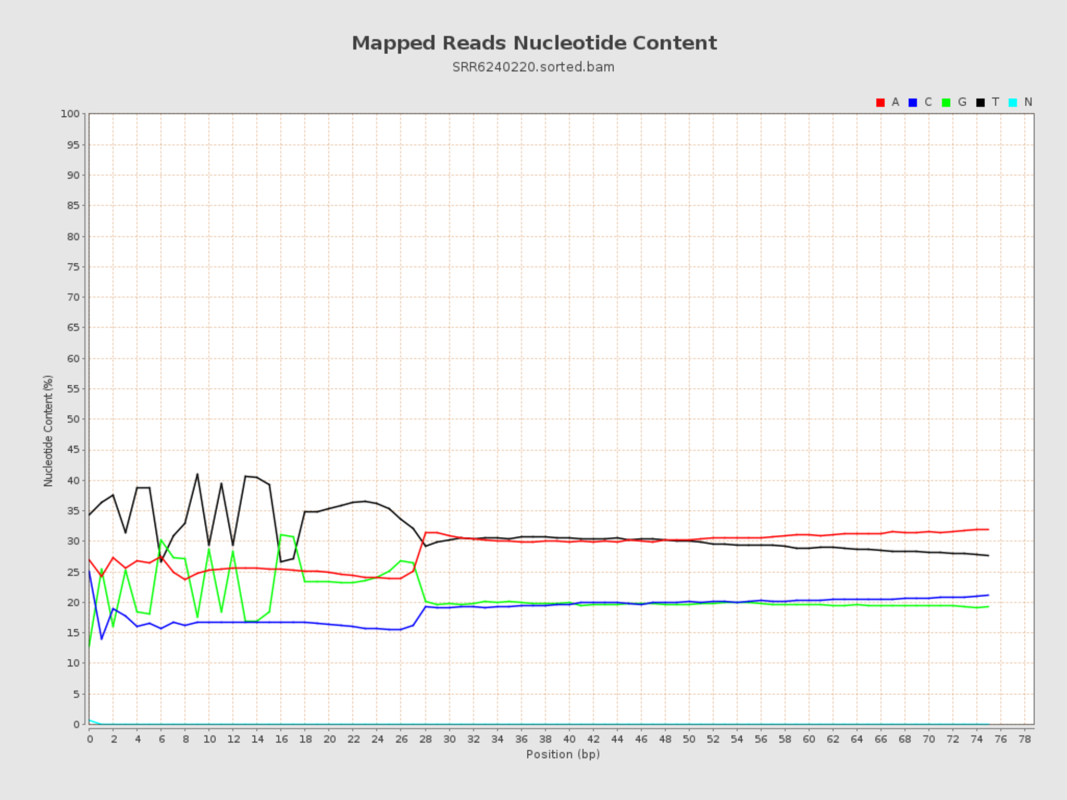
6. Results : Genome Fraction Coverage



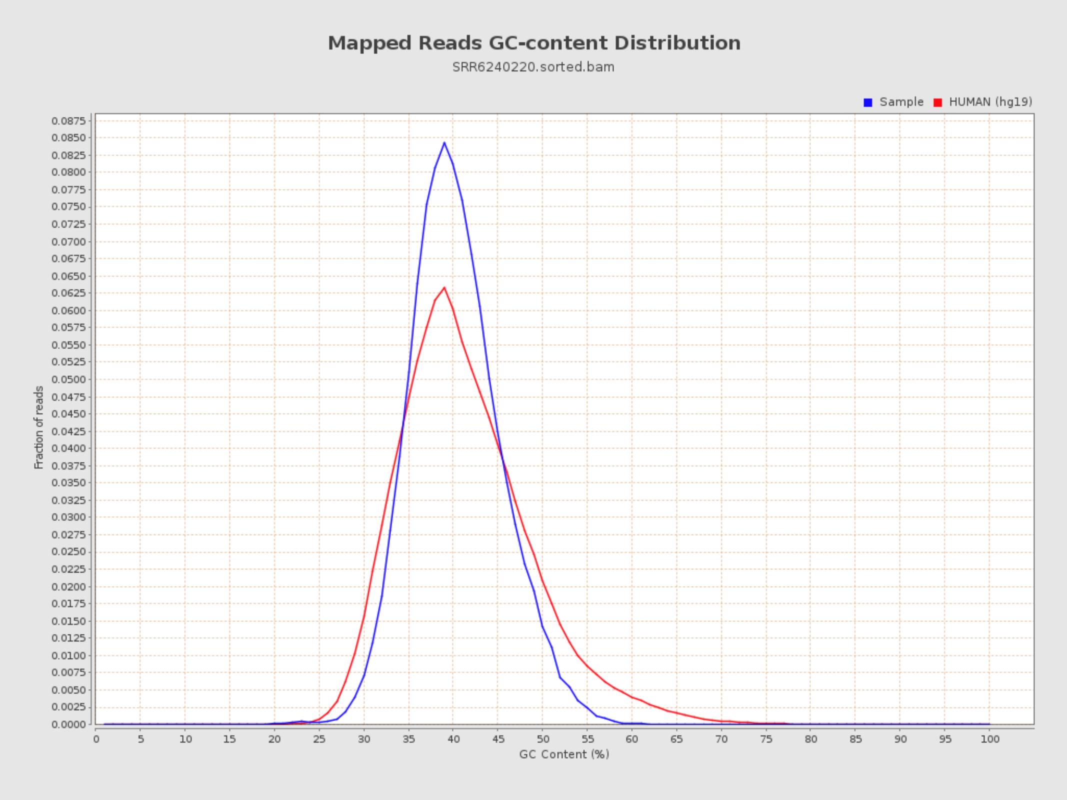
7. Results : Duplication Rate Histogram



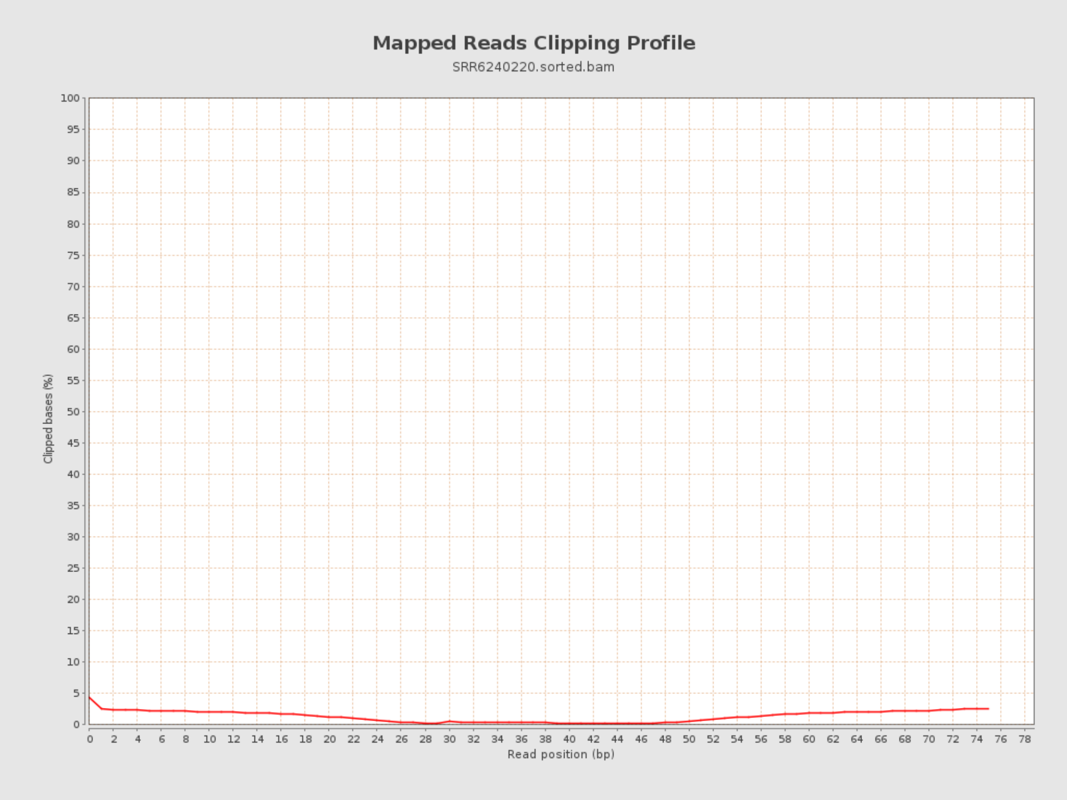
8. Results : Mapped Reads Nucleotide Content



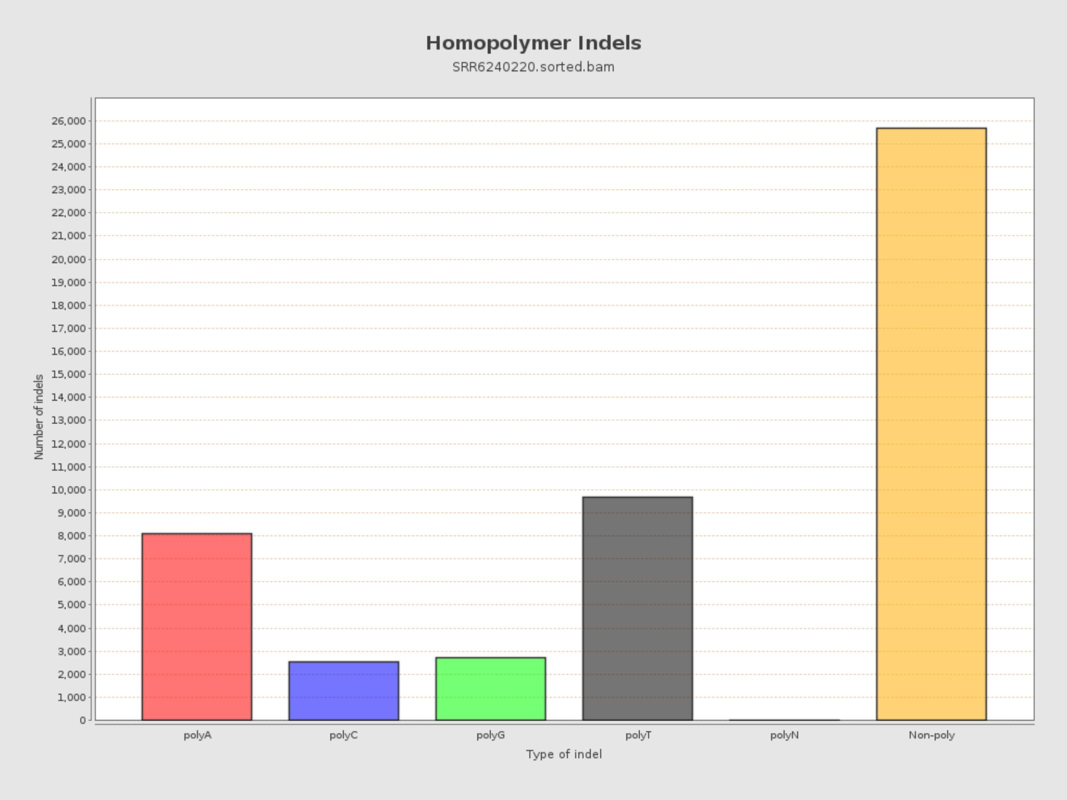
9. Results : Mapped Reads GC-content Distribution



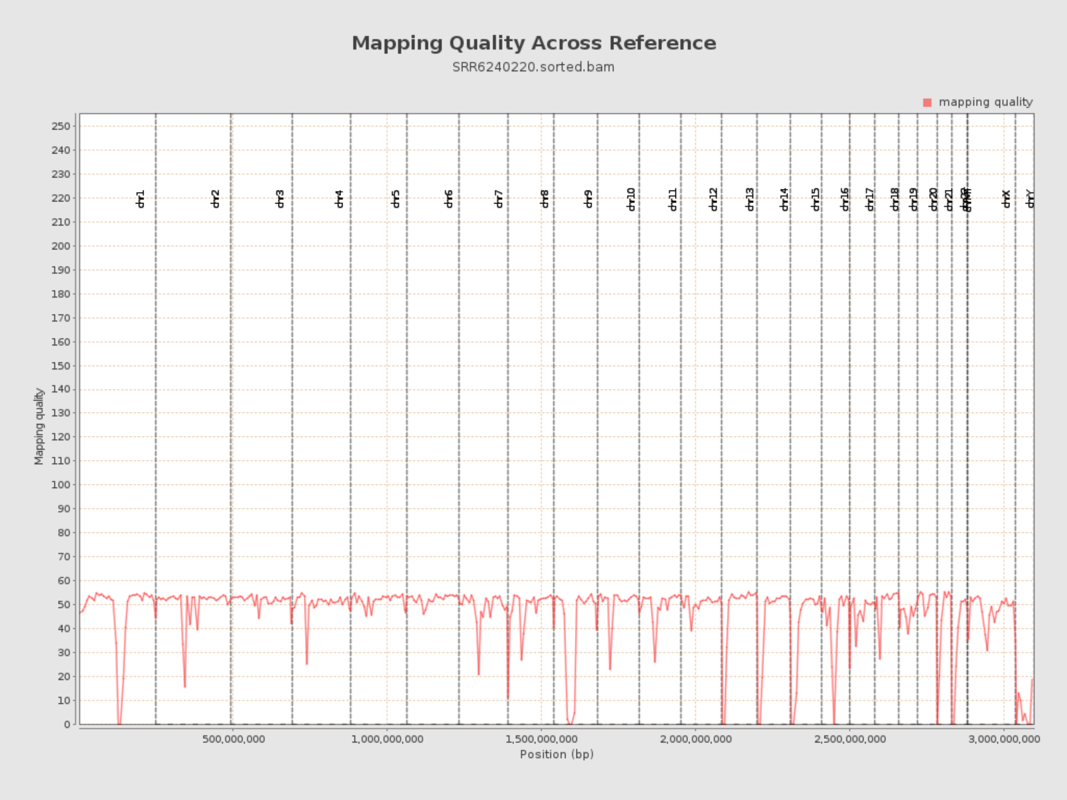
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram