Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:43:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240063.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_SRR6240063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:43:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,818,179
Mapped reads	2,512,425 / 89.15%
Unmapped reads	305,754 / 10.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,116 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	119,421 / 4.24%
Duplication rate	3.38%
Clipped reads	937,161 / 33.25%

2.2. ACGT Content

Number/percentage of A's	49,712,336 / 28.89%
Number/percentage of C's	31,932,448 / 18.56%
Number/percentage of T's	54,738,379 / 31.81%
Number/percentage of G's	35,682,142 / 20.74%
Number/percentage of N's	16,947 / 0.01%
GC Percentage	39.29%

2.3. Coverage

Mean	0.0556

Standard Deviation	0.6344

2.4. Mapping Quality

Mean Mapping Quality	47.57

2.5. Mismatches and indels

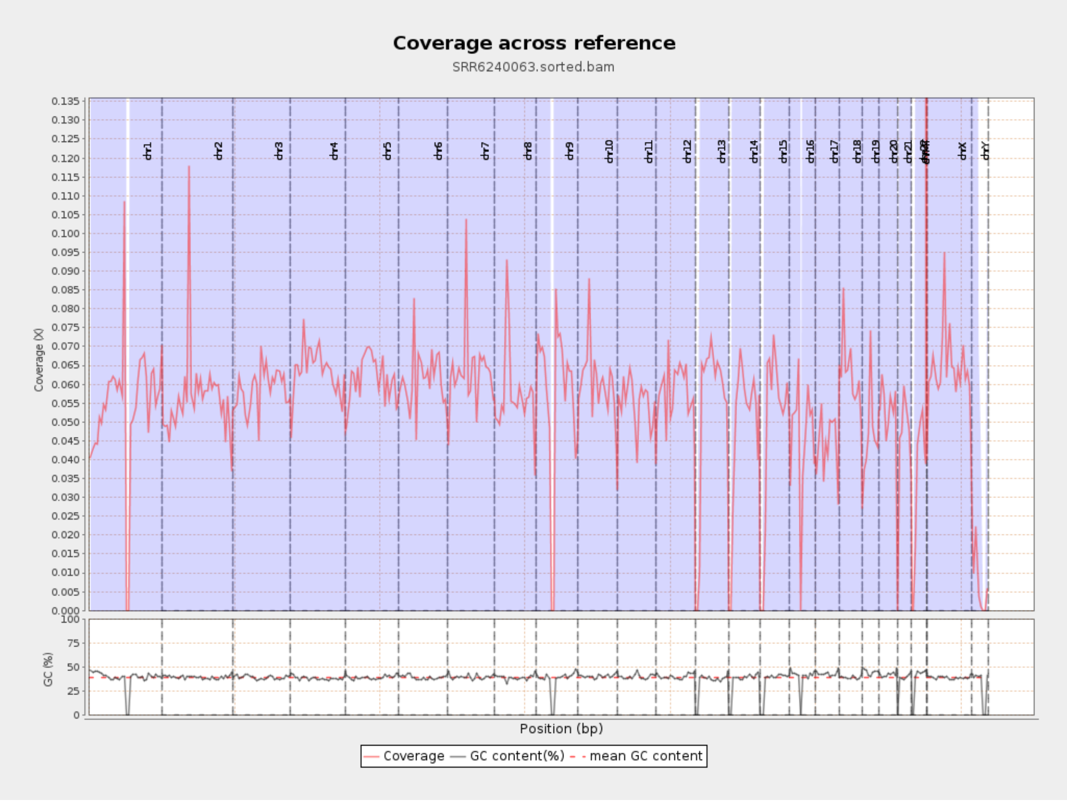
General error rate	0.79%
Mismatches	1,335,806
Insertions	12,687
Mapped reads with at least one insertion	0.5%
Deletions	37,692
Mapped reads with at least one deletion	1.48%
Homopolymer indels	48.05%

2.6. Chromosome stats

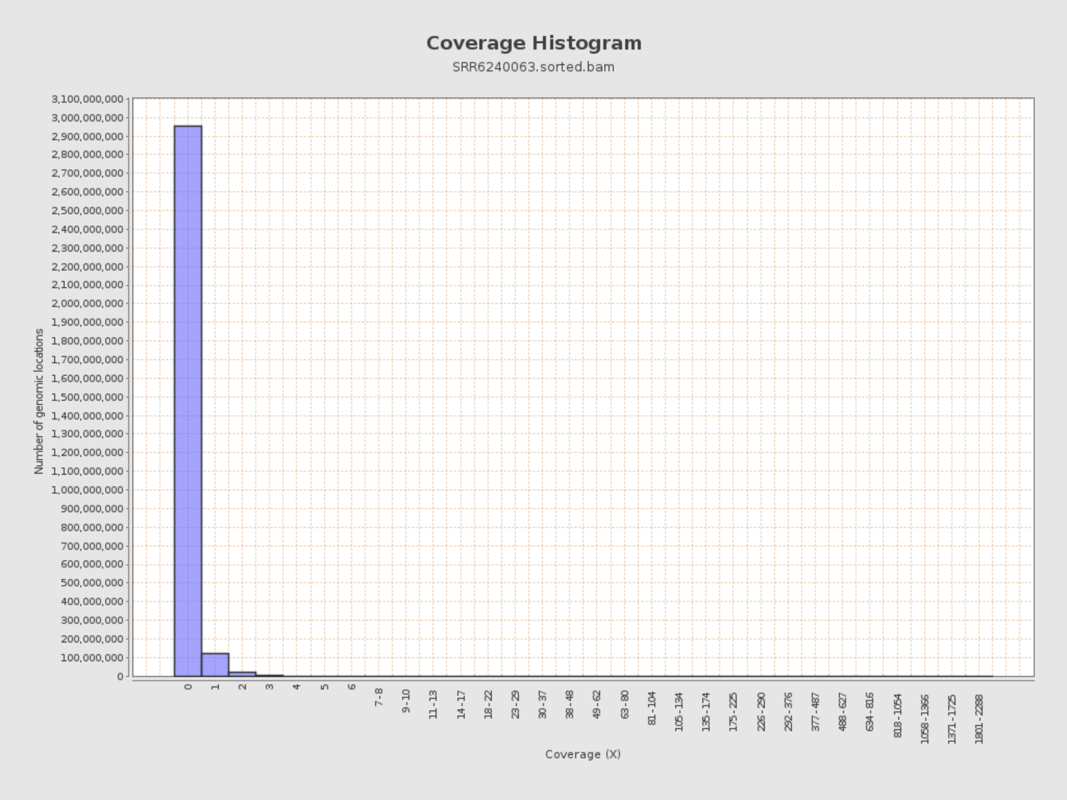
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13530983	0.0543	1.2896
chr2	243199373	13784775	0.0567	0.5709
chr3	198022430	11634103	0.0588	0.282
chr4	191154276	12130940	0.0635	0.3212
chr5	180915260	11188371	0.0618	0.2934
chr6	171115067	10470364	0.0612	0.3839
chr7	159138663	10172479	0.0639	0.6689

chr8	146364022	8356950	0.0571	1.4196
chr9	141213431	8067893	0.0571	0.5685
chr10	135534747	8283707	0.0611	0.44
chr11	135006516	7388725	0.0547	0.4251
chr12	133851895	7805213	0.0583	0.2996
chr13	115169878	6084340	0.0528	0.2673
chr14	107349540	5165582	0.0481	0.296
chr15	102531392	5023176	0.049	0.263
chr16	90354753	4145858	0.0459	0.3021
chr17	81195210	3528000	0.0435	0.2889
chr18	78077248	4925022	0.0631	1.096
chr19	59128983	2787196	0.0471	0.7527
chr20	63025520	3346870	0.0531	0.2871
chr21	48129895	2133150	0.0443	0.28
chr22	51304566	1675441	0.0327	0.2059
chrMT	16571	128190	7.7358	4.8695
chrX	155270560	9973200	0.0642	0.357
chrY	59373566	418077	0.007	0.1634

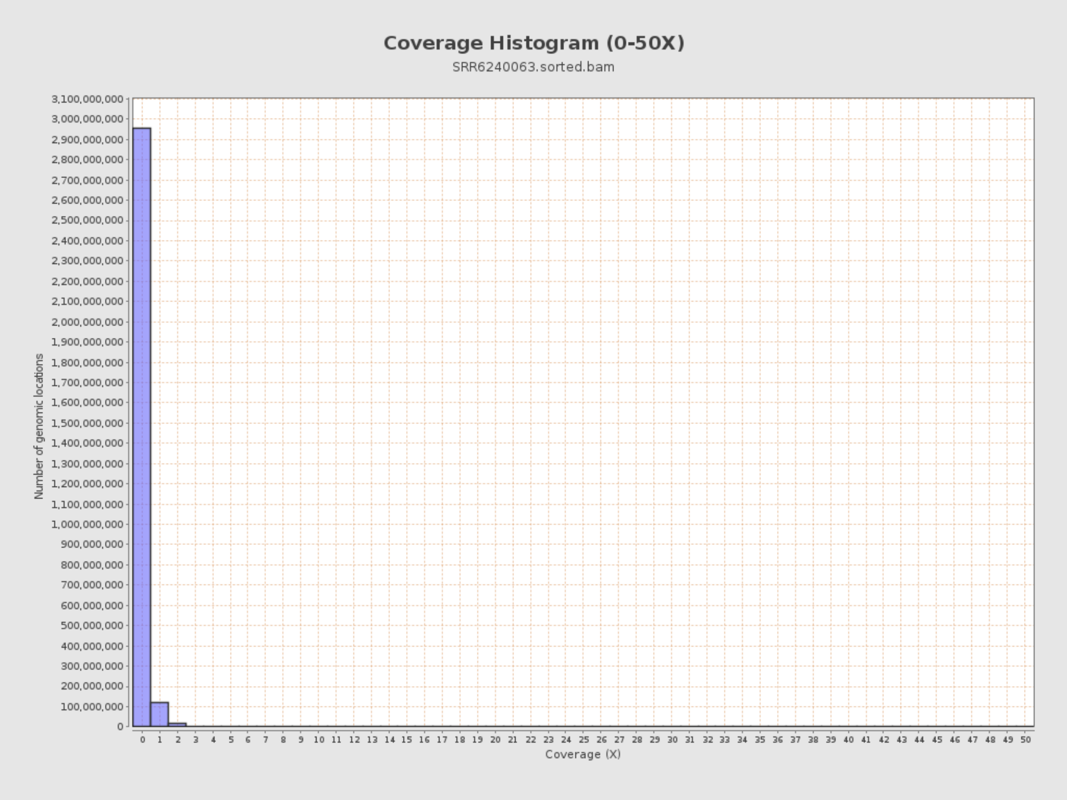
3. Results : Coverage across reference



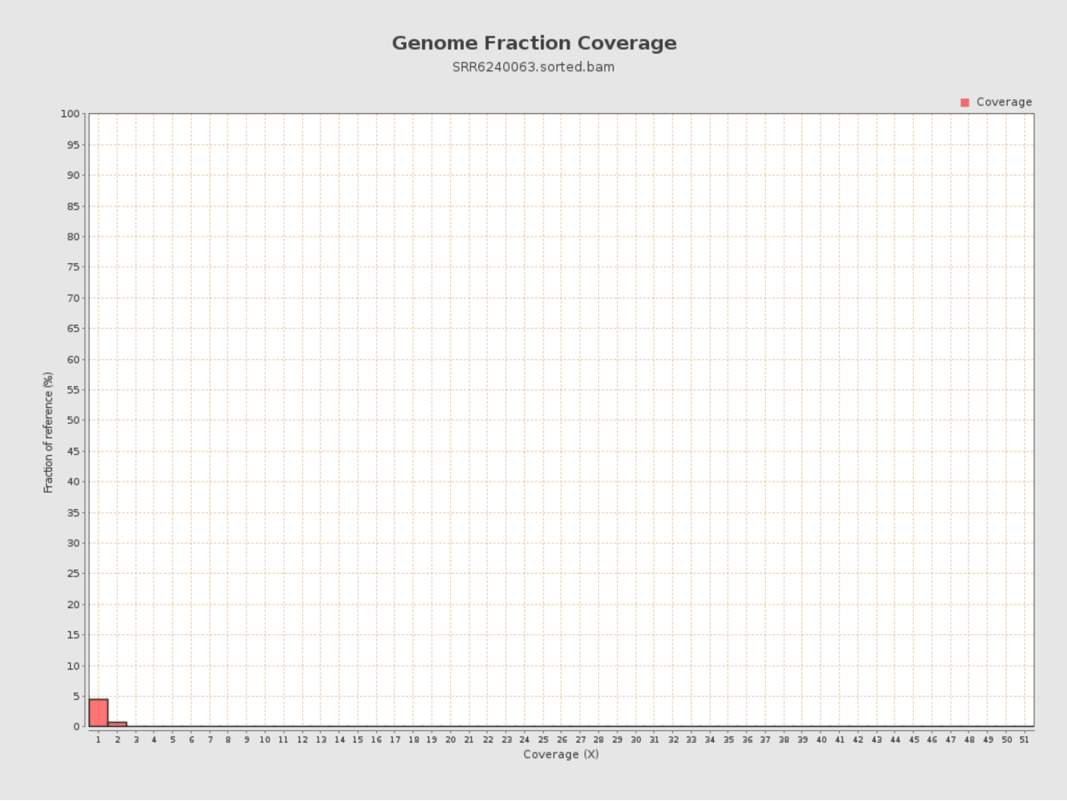
4. Results : Coverage Histogram



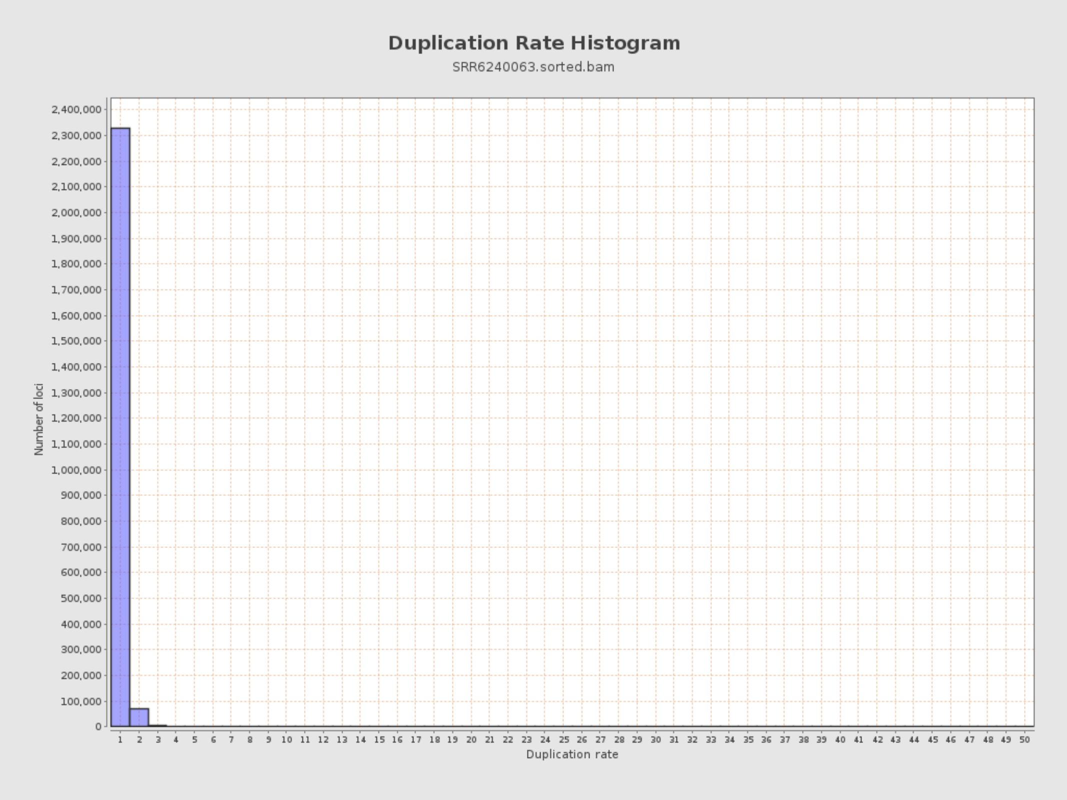
5. Results : Coverage Histogram (0-50X)



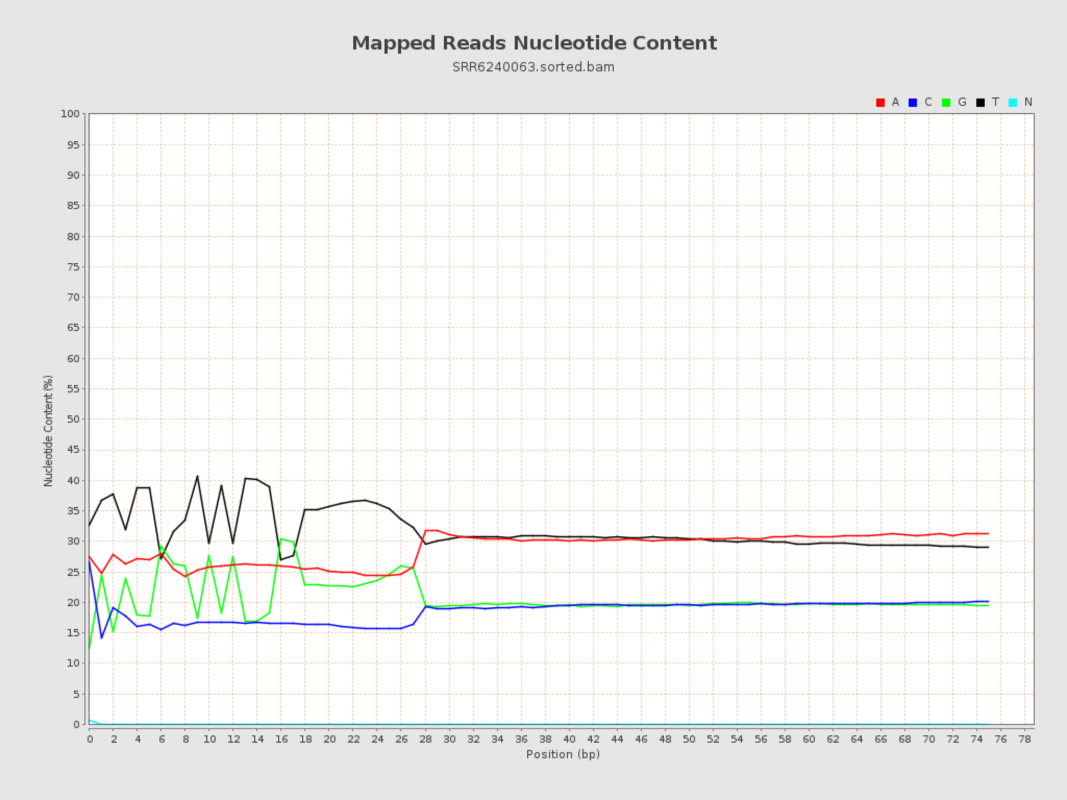
6. Results : Genome Fraction Coverage



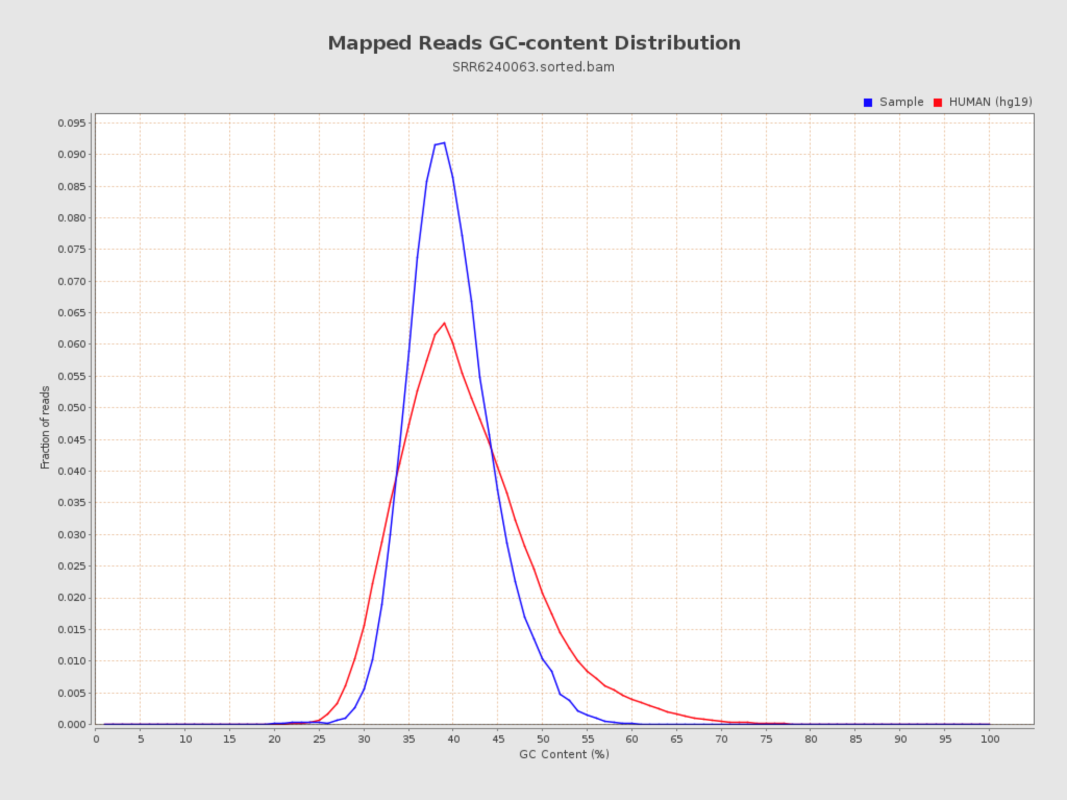
7. Results : Duplication Rate Histogram



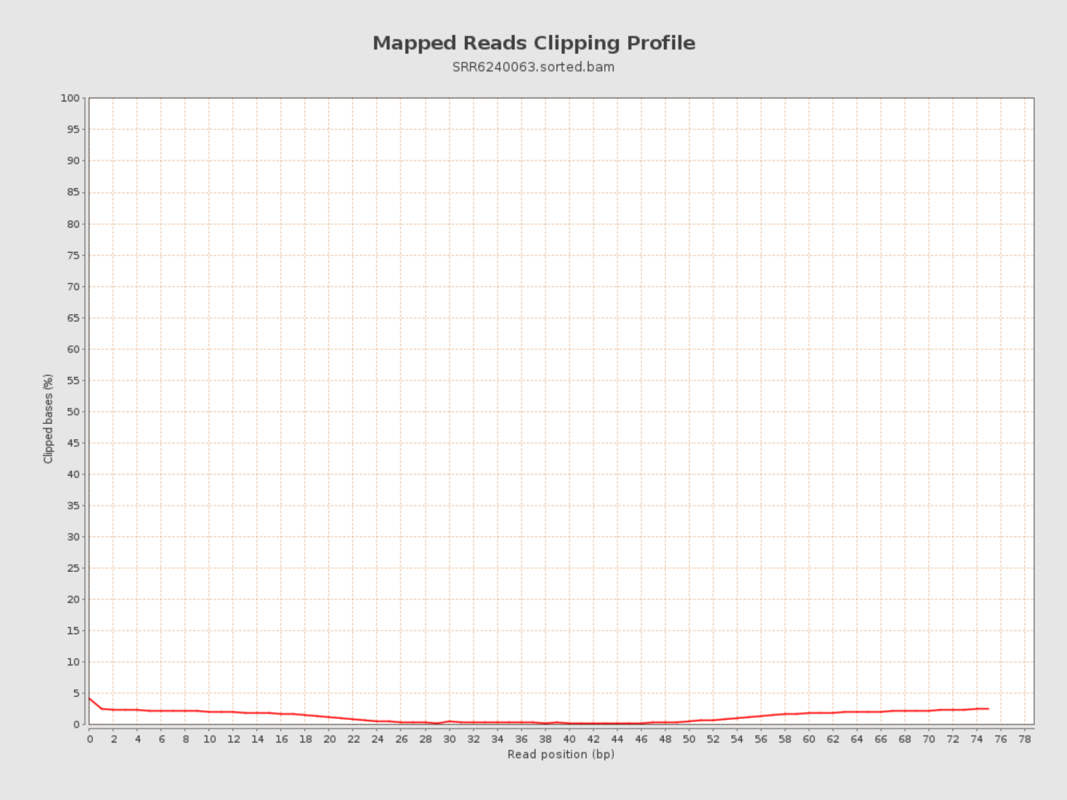
8. Results : Mapped Reads Nucleotide Content



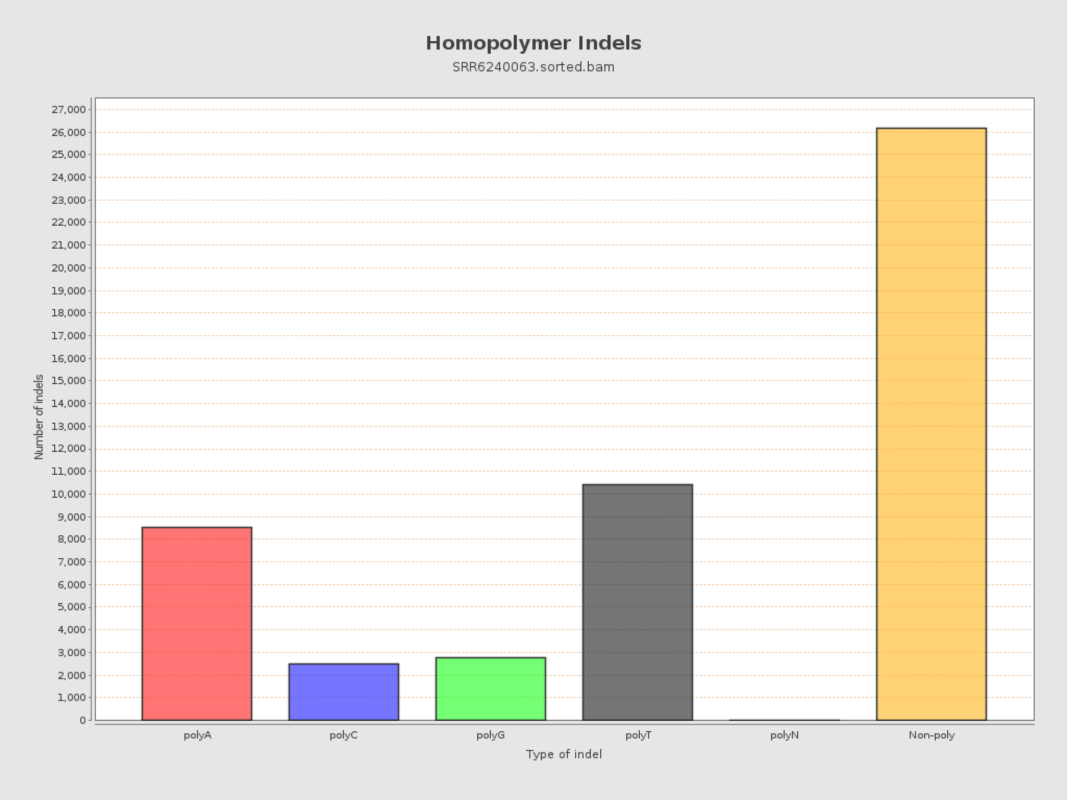
9. Results : Mapped Reads GC-content Distribution



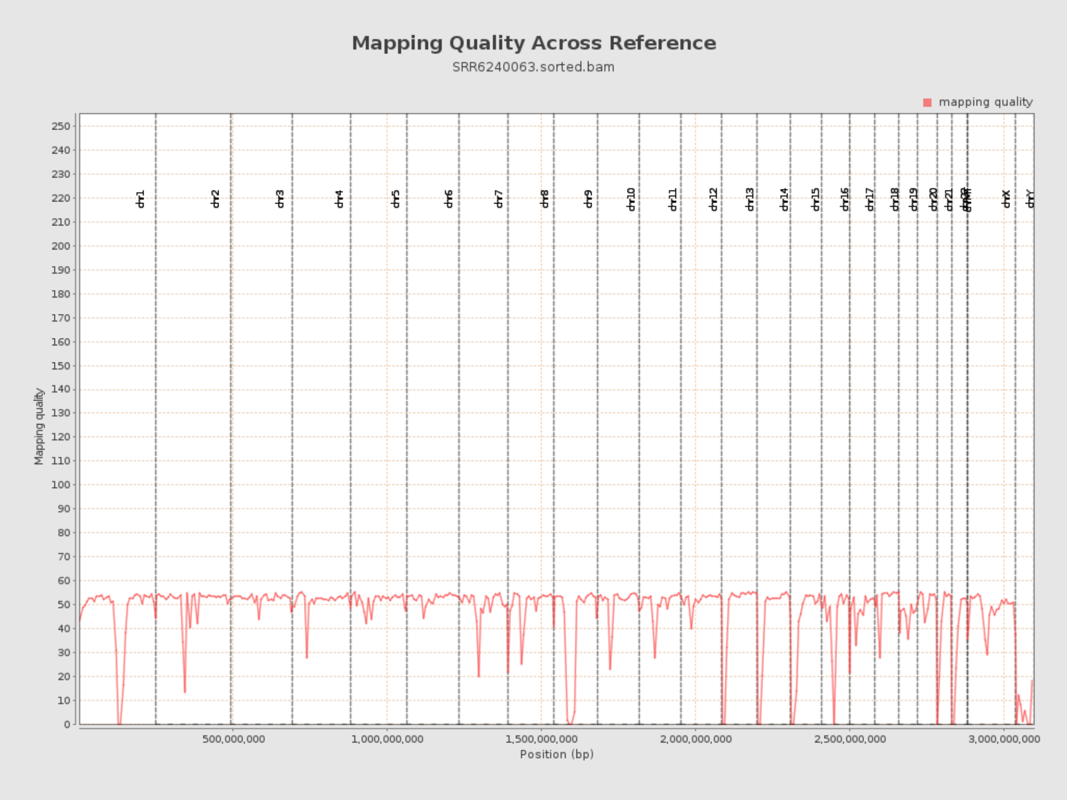
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram