Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:14:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240243.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_SRR6240243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240243.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:14:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,195,963
Mapped reads	2,605,499 / 81.52%
Unmapped reads	590,464 / 18.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,364 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	473,241 / 14.81%
Duplication rate	12.12%
Clipped reads	1,256,402 / 39.31%

2.2. ACGT Content

Number/percentage of A's	48,310,798 / 28.1%
Number/percentage of C's	31,369,739 / 18.25%
Number/percentage of T's	55,086,839 / 32.04%
Number/percentage of G's	37,133,774 / 21.6%
Number/percentage of N's	17,122 / 0.01%
GC Percentage	39.85%

2.3. Coverage

Mean	0.0556

Standard Deviation	0.6528

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

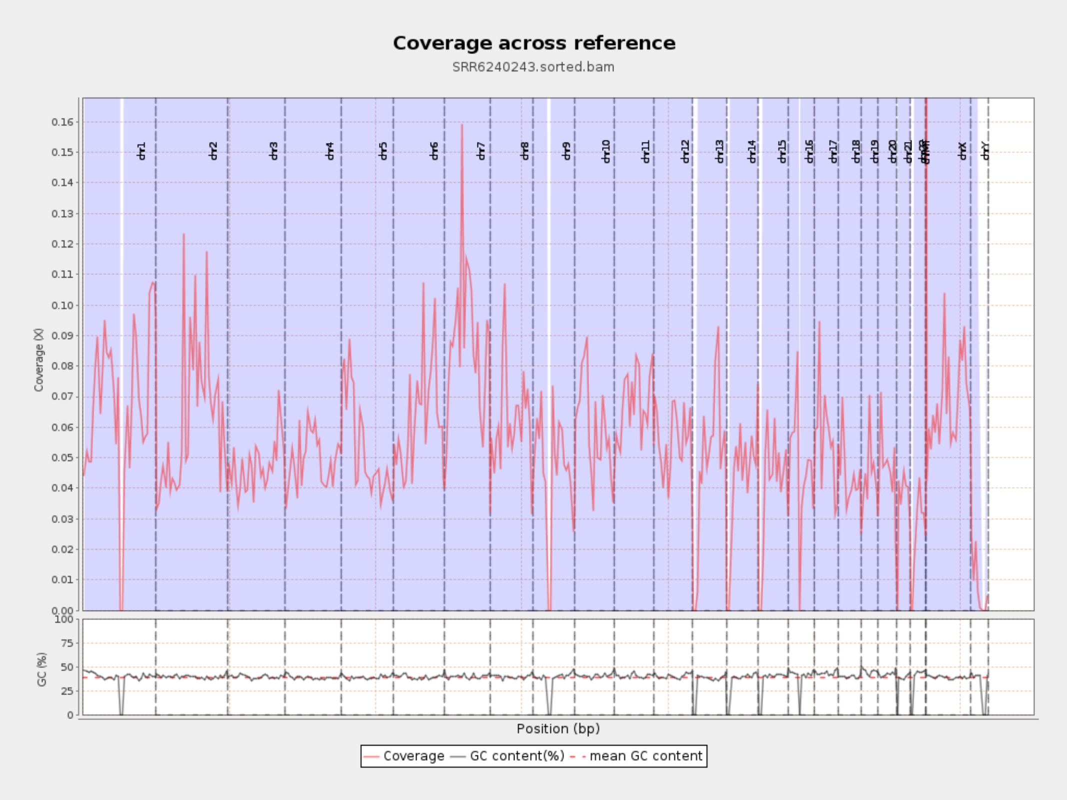
General error rate	0.8%
Mismatches	1,352,838
Insertions	12,244
Mapped reads with at least one insertion	0.47%
Deletions	39,123
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.01%

2.6. Chromosome stats

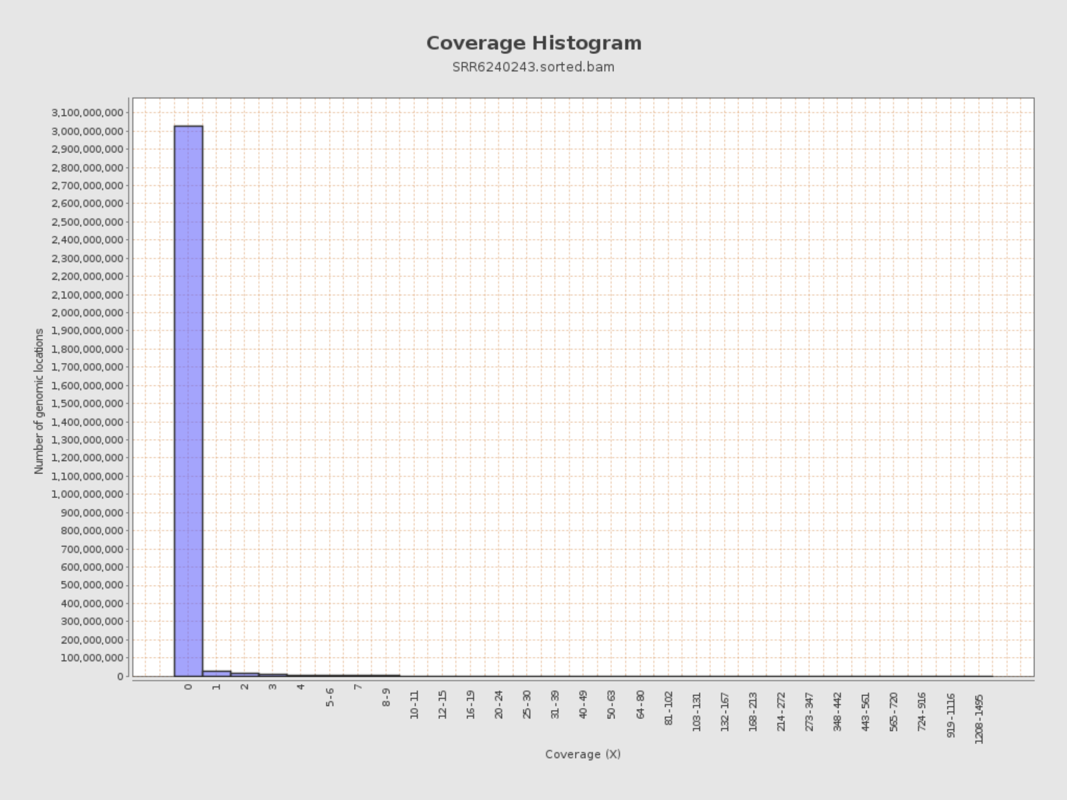
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16852573	0.0676	0.9002
chr2	243199373	15242439	0.0627	0.7241
chr3	198022430	9372444	0.0473	0.4462
chr4	191154276	9428850	0.0493	0.4644
chr5	180915260	9535474	0.0527	0.472
chr6	171115067	11011390	0.0644	0.5847
chr7	159138663	14011104	0.088	1.0578

chr8	146364022	9134276	0.0624	1.0387
chr9	141213431	6499754	0.046	0.6133
chr10	135534747	8140074	0.0601	0.5694
chr11	135006516	9052151	0.067	0.6171
chr12	133851895	7494105	0.056	0.4952
chr13	115169878	5528681	0.048	0.4581
chr14	107349540	4507689	0.042	0.4537
chr15	102531392	4112442	0.0401	0.4229
chr16	90354753	4100479	0.0454	0.4594
chr17	81195210	4671943	0.0575	0.5094
chr18	78077248	3507909	0.0449	1.0651
chr19	59128983	2624781	0.0444	0.6019
chr20	63025520	3031743	0.0481	0.4522
chr21	48129895	1714945	0.0356	0.4078
chr22	51304566	1277433	0.0249	0.3142
chrMT	16571	21754	1.3128	2.4365
chrX	155270560	10641376	0.0685	0.565
chrY	59373566	469948	0.0079	0.1771

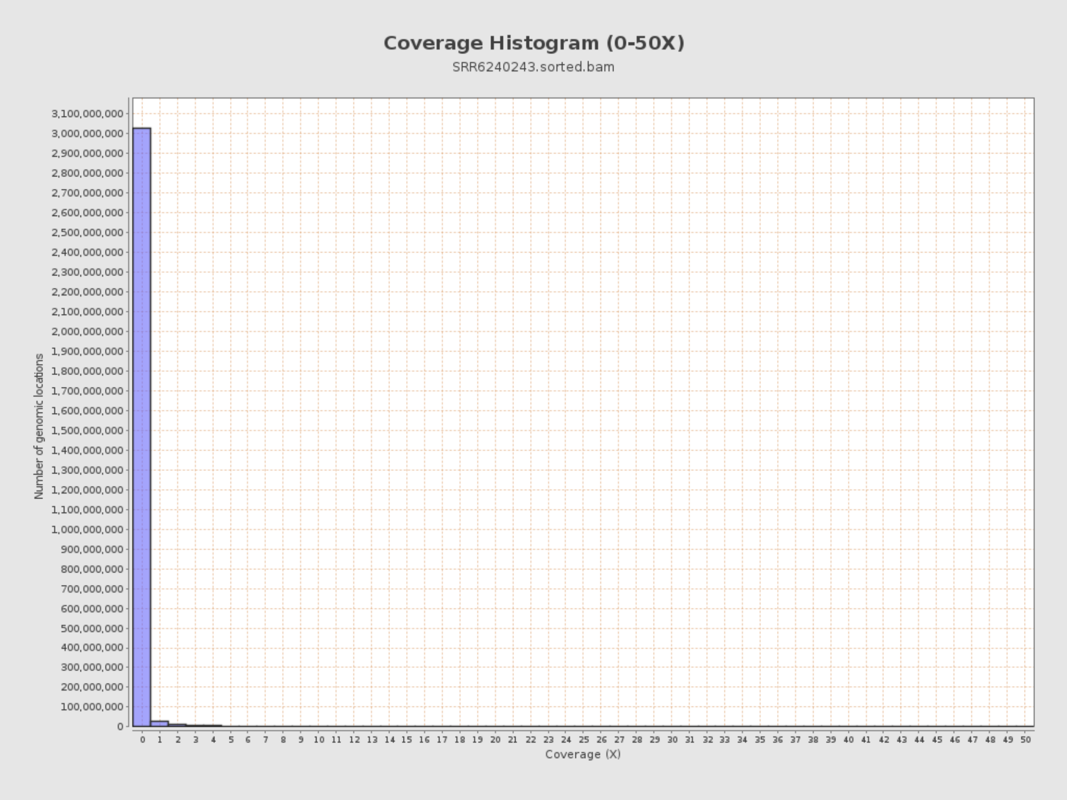
3. Results : Coverage across reference



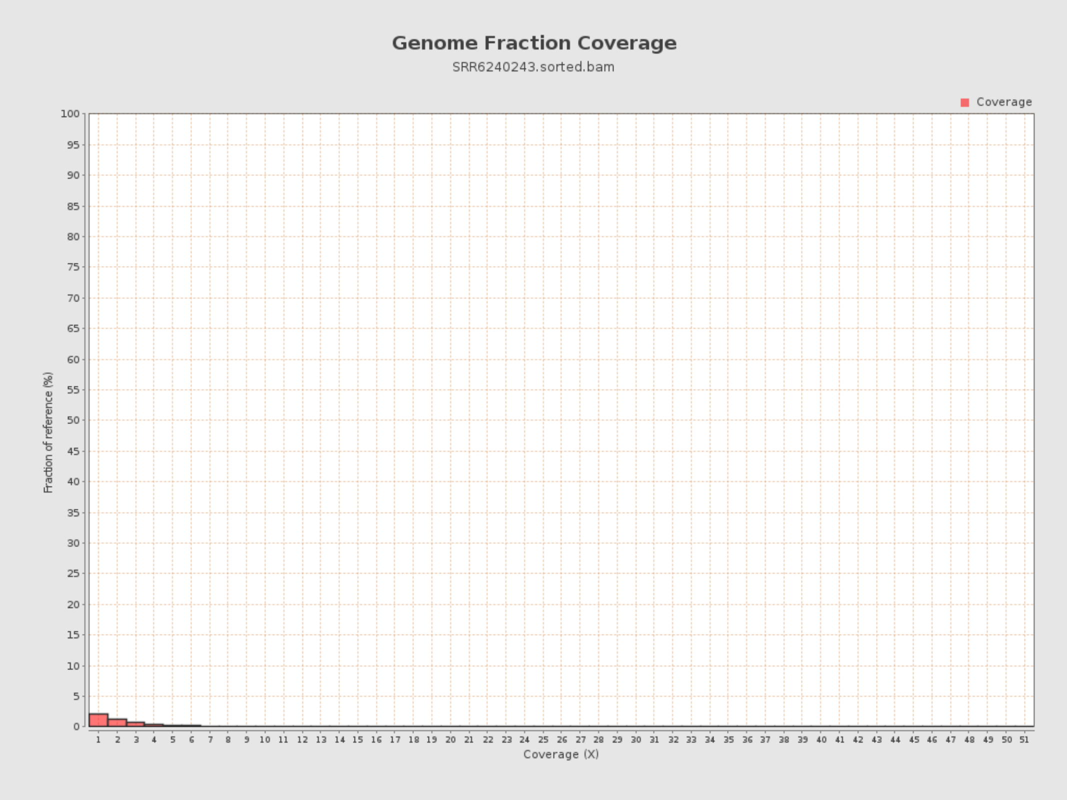
4. Results : Coverage Histogram



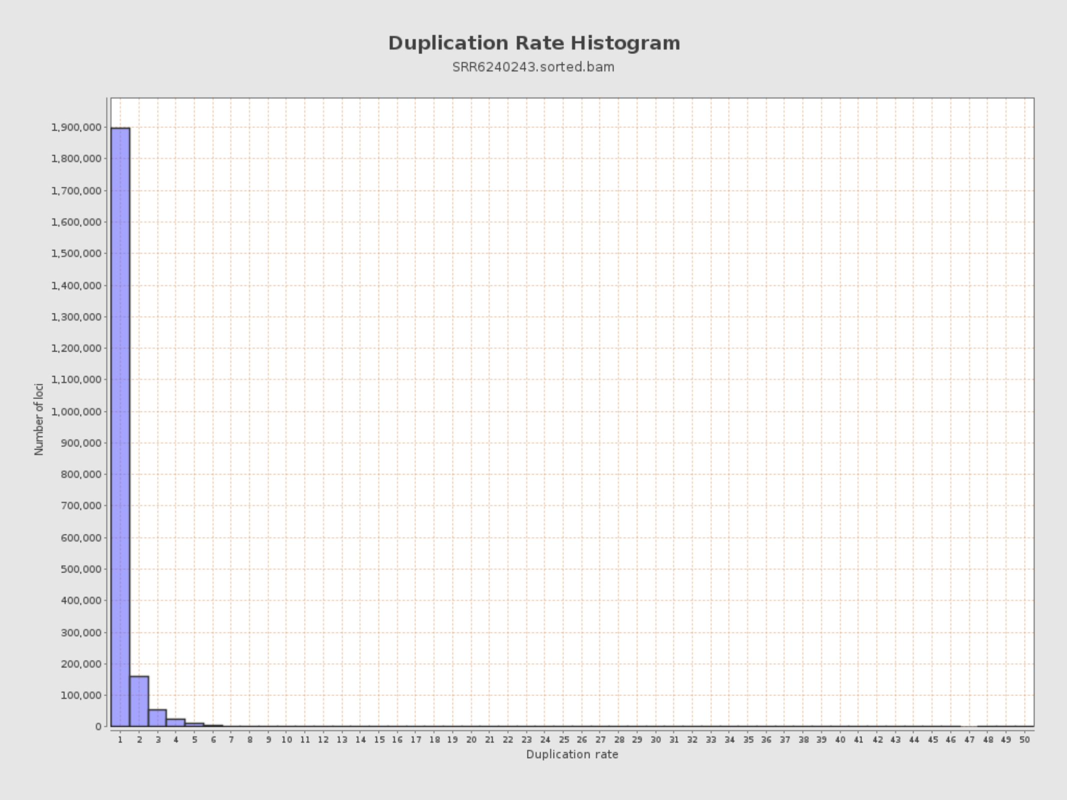
5. Results : Coverage Histogram (0-50X)



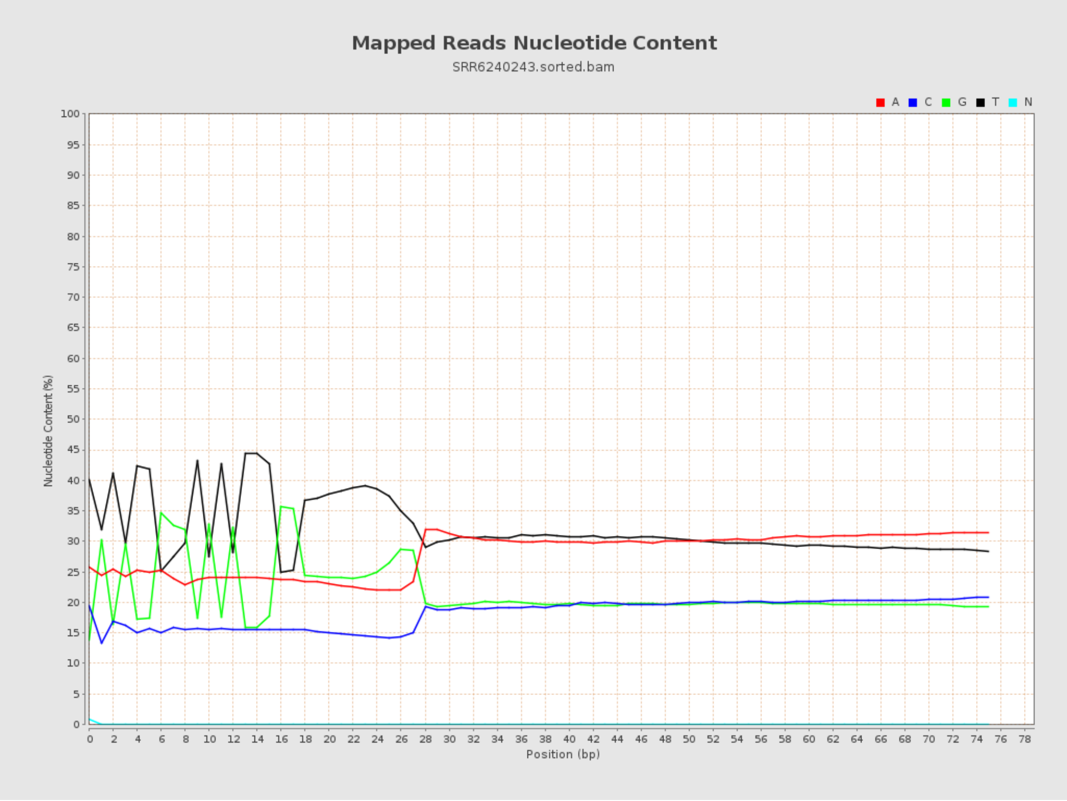
6. Results : Genome Fraction Coverage



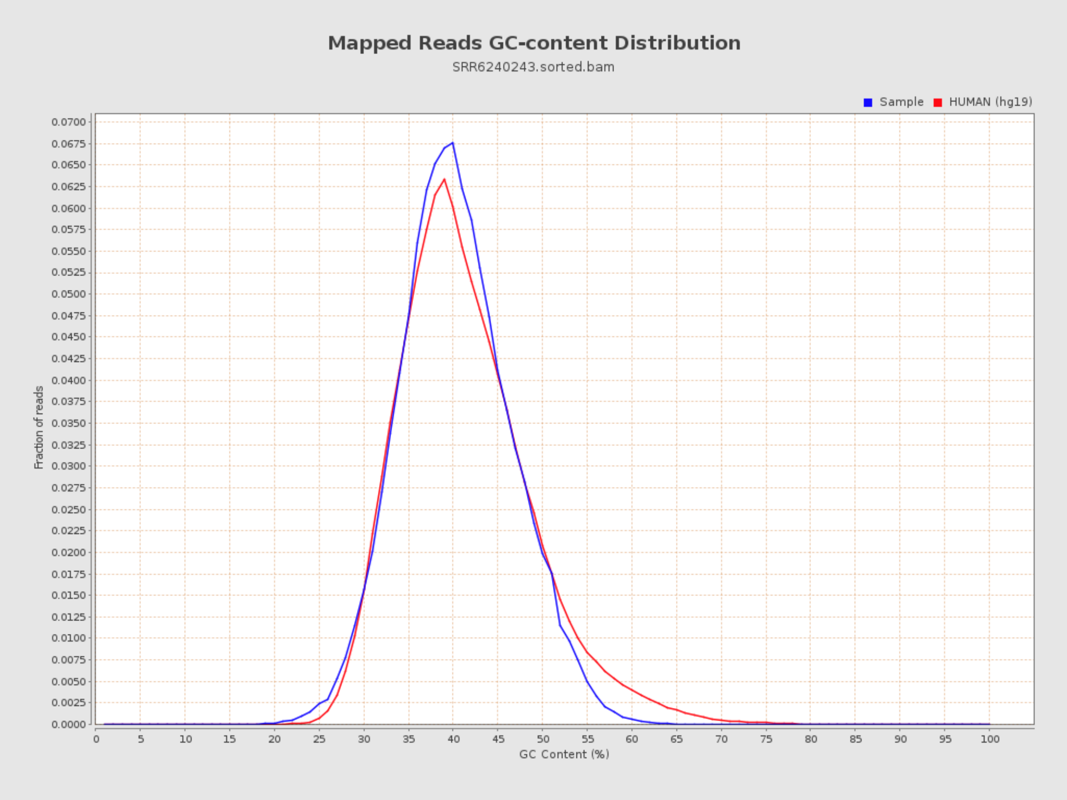
7. Results : Duplication Rate Histogram



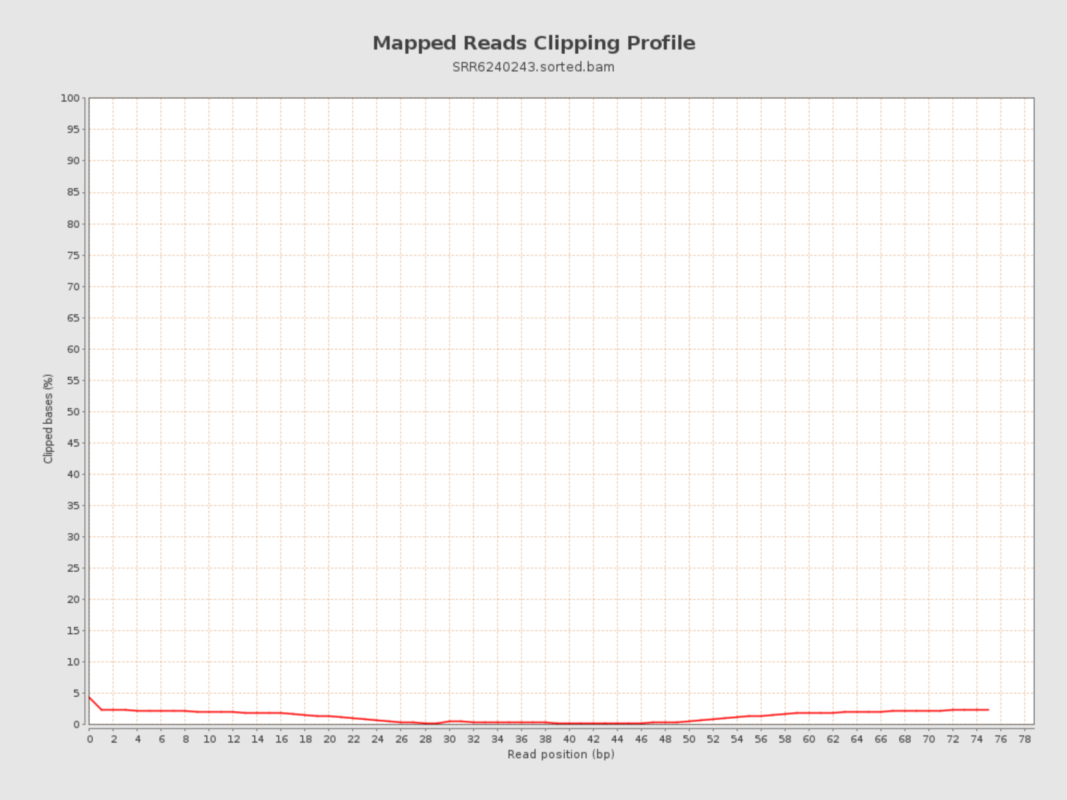
8. Results : Mapped Reads Nucleotide Content



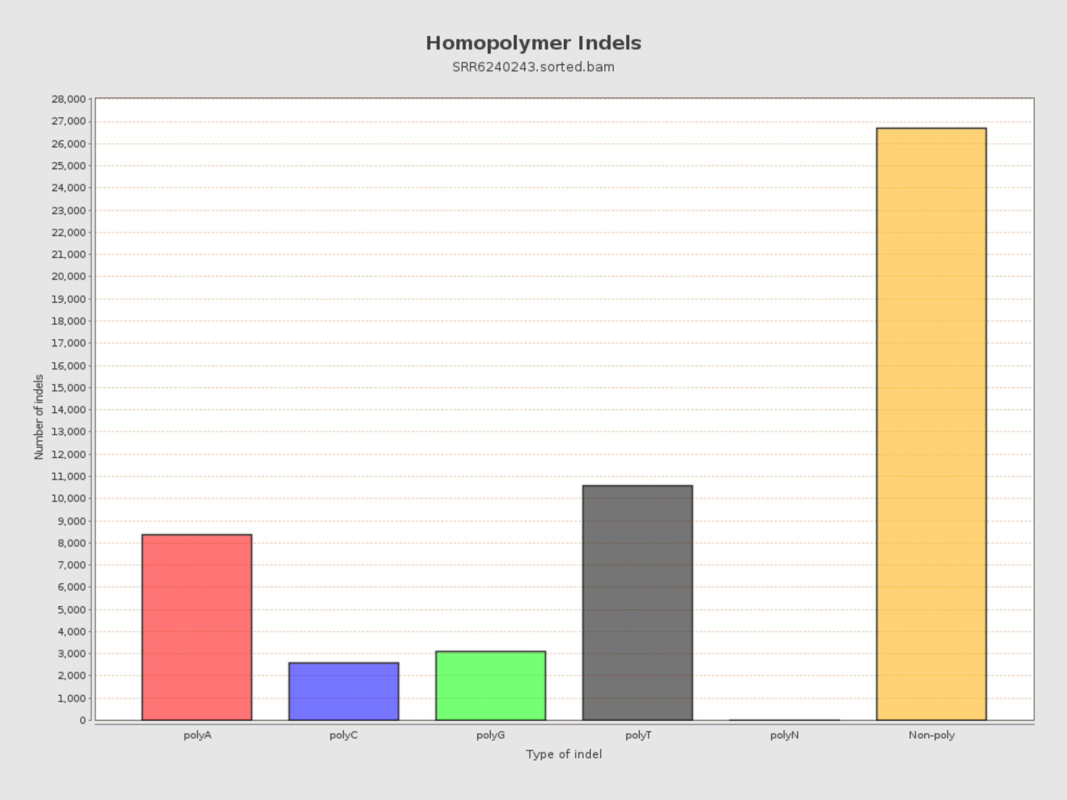
9. Results : Mapped Reads GC-content Distribution



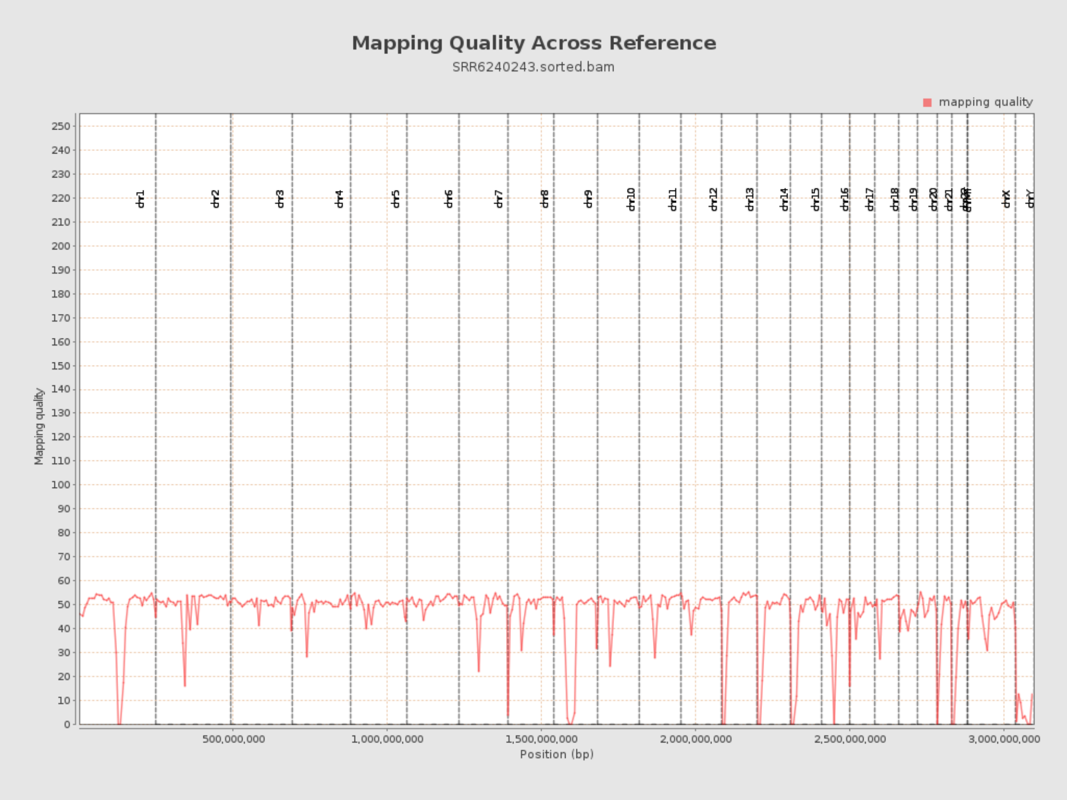
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram