Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:31:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236120.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_SRR6236120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:31:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,508,939
Mapped reads	3,045,881 / 86.8%
Unmapped reads	463,058 / 13.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,627 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	249,285 / 7.1%
Duplication rate	6.4%
Clipped reads	1,322,308 / 37.68%

2.2. ACGT Content

Number/percentage of A's	57,370,861 / 28.25%
Number/percentage of C's	35,407,194 / 17.43%
Number/percentage of T's	66,833,633 / 32.91%
Number/percentage of G's	43,377,974 / 21.36%
Number/percentage of N's	113,317 / 0.06%
GC Percentage	38.79%

2.3. Coverage

Mean	0.0656

Standard Deviation	0.7668

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

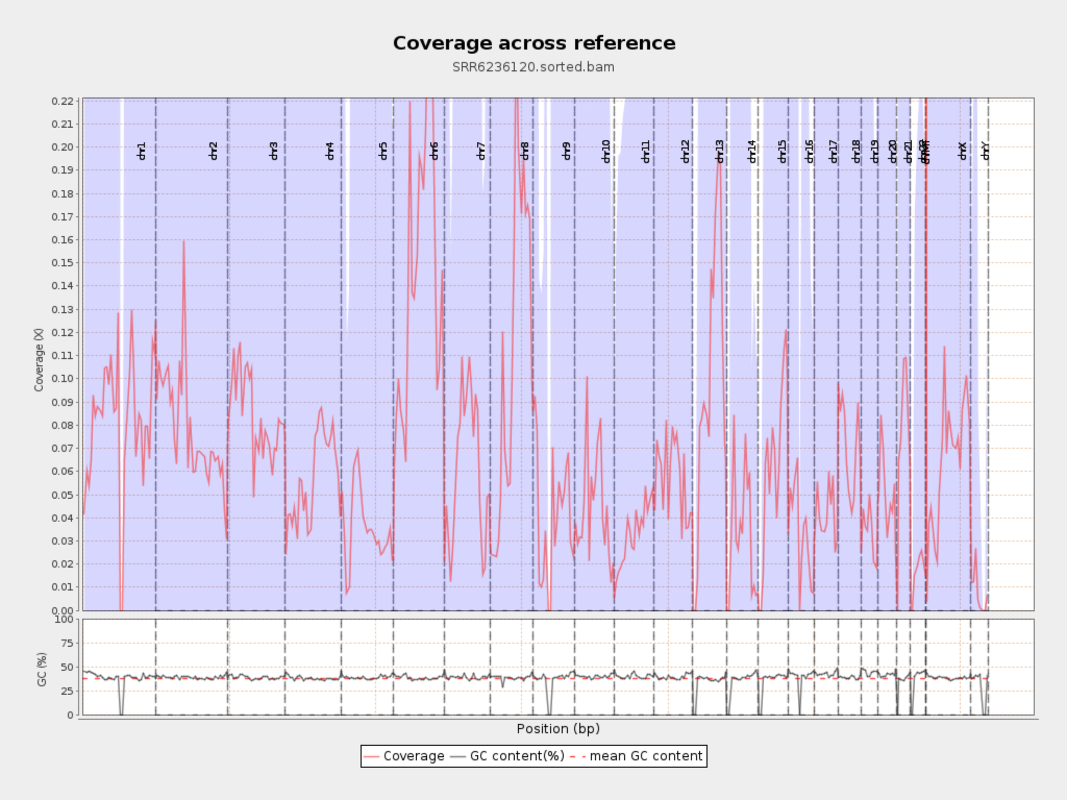
General error rate	0.84%
Mismatches	1,686,036
Insertions	14,805
Mapped reads with at least one insertion	0.48%
Deletions	64,418
Mapped reads with at least one deletion	2.09%
Homopolymer indels	46.21%

2.6. Chromosome stats

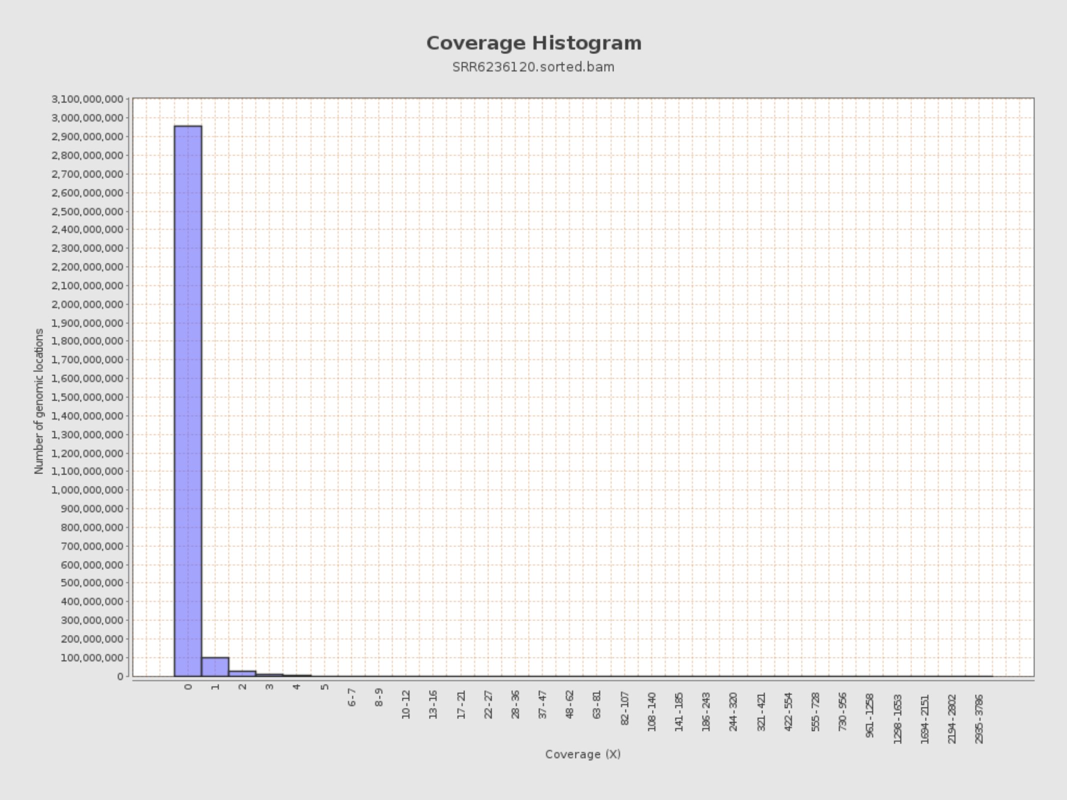
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20337070	0.0816	1.0036
chr2	243199373	19216834	0.079	0.6689
chr3	198022430	16722223	0.0844	0.3972
chr4	191154276	10916411	0.0571	0.3457
chr5	180915260	6546146	0.0362	0.2608
chr6	171115067	25661641	0.15	0.965
chr7	159138663	9768066	0.0614	0.6126

chr8	146364022	16570879	0.1132	2.4767
chr9	141213431	5615508	0.0398	0.4599
chr10	135534747	5978118	0.0441	0.5088
chr11	135006516	4438611	0.0329	0.3126
chr12	133851895	7668630	0.0573	0.3375
chr13	115169878	11419210	0.0992	0.4384
chr14	107349540	3610945	0.0336	0.2743
chr15	102531392	6294040	0.0614	0.3399
chr16	90354753	2966857	0.0328	0.2887
chr17	81195210	3420996	0.0421	0.3008
chr18	78077248	5559807	0.0712	0.8772
chr19	59128983	2051284	0.0347	0.594
chr20	63025520	3315952	0.0526	0.3269
chr21	48129895	3706083	0.077	0.3952
chr22	51304566	837797	0.0163	0.1651
chrMT	16571	138572	8.3623	5.8177
chrX	155270560	9990646	0.0643	0.3873
chrY	59373566	462769	0.0078	0.1836

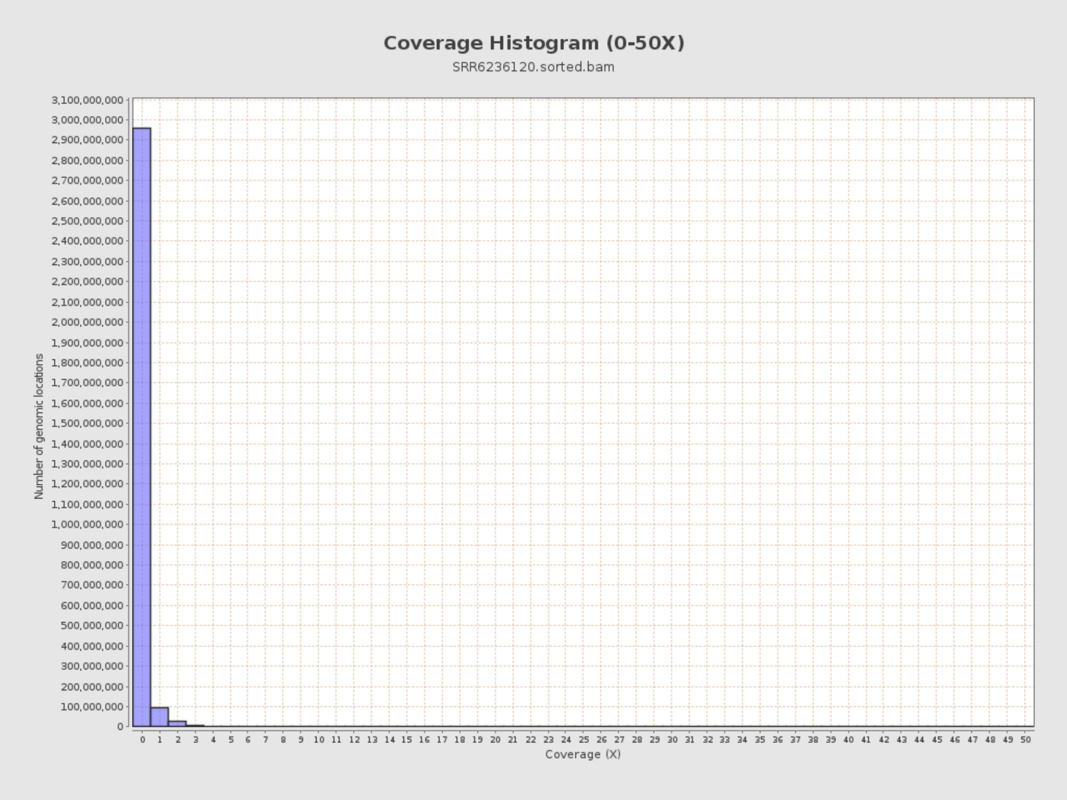
3. Results : Coverage across reference



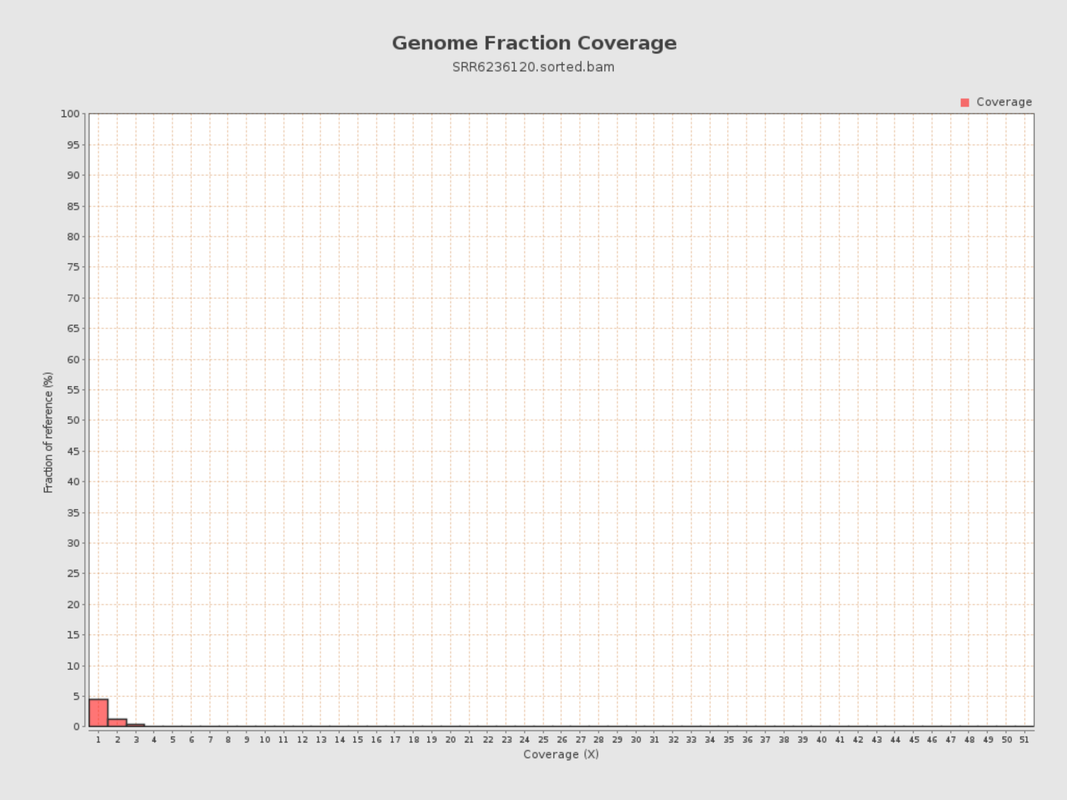
4. Results : Coverage Histogram



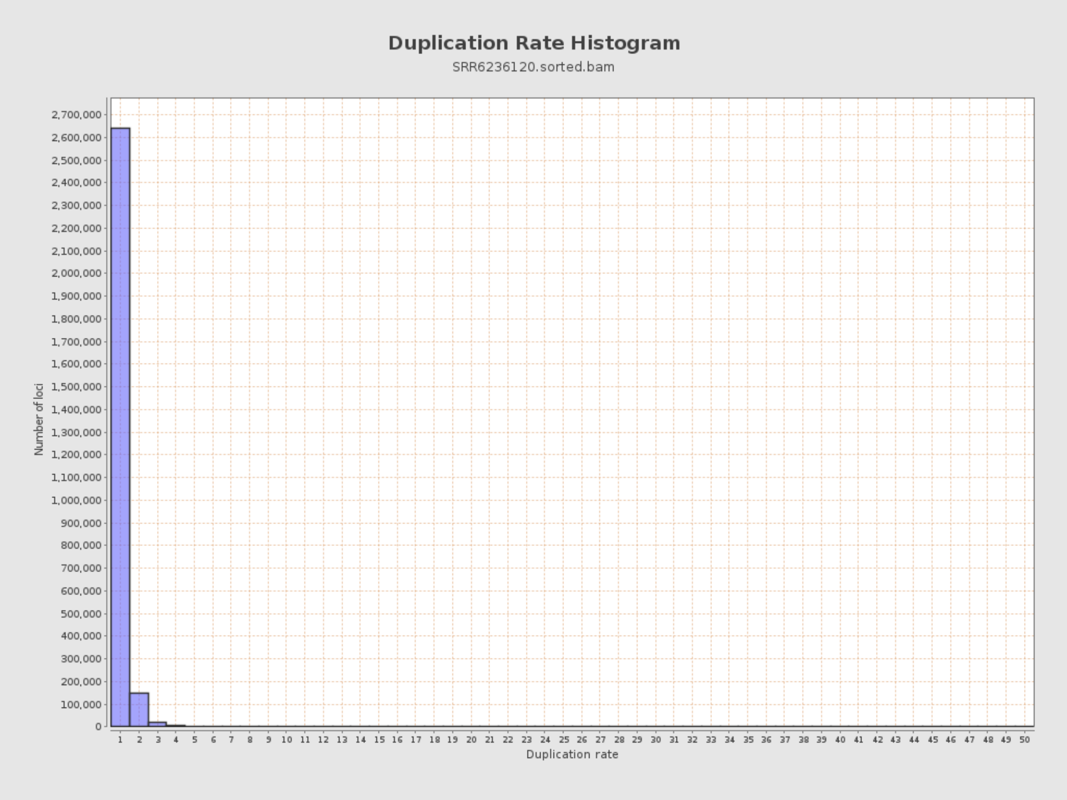
5. Results : Coverage Histogram (0-50X)



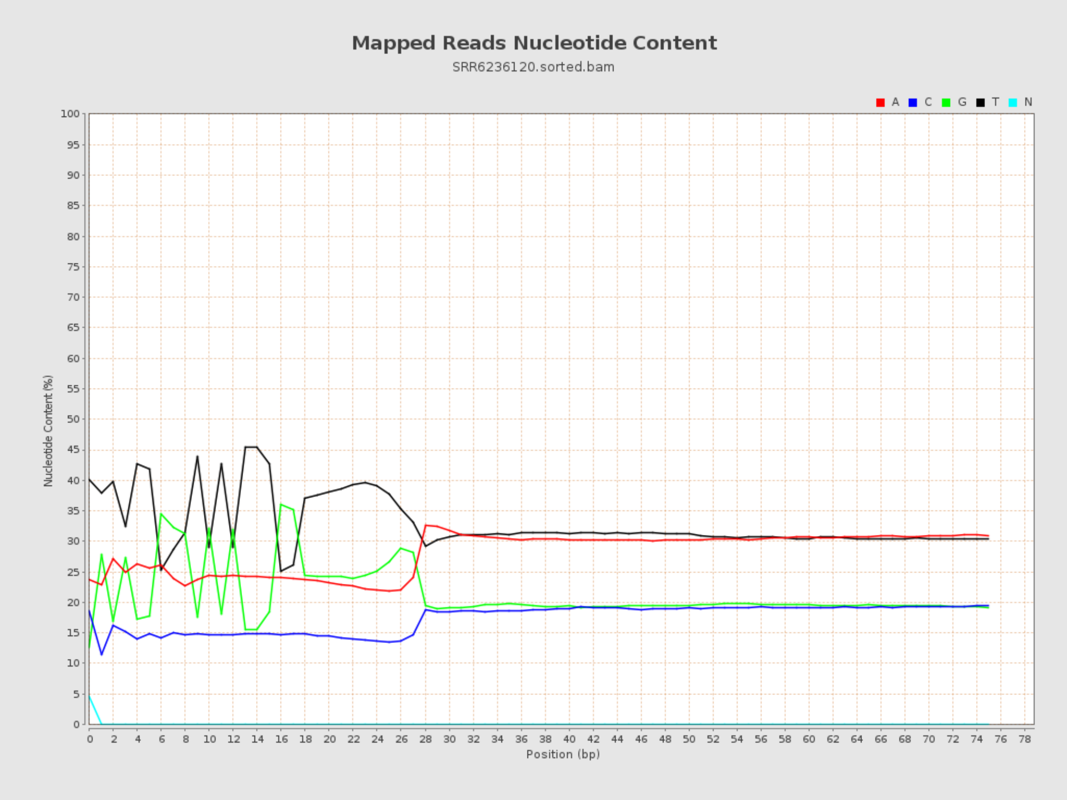
6. Results : Genome Fraction Coverage



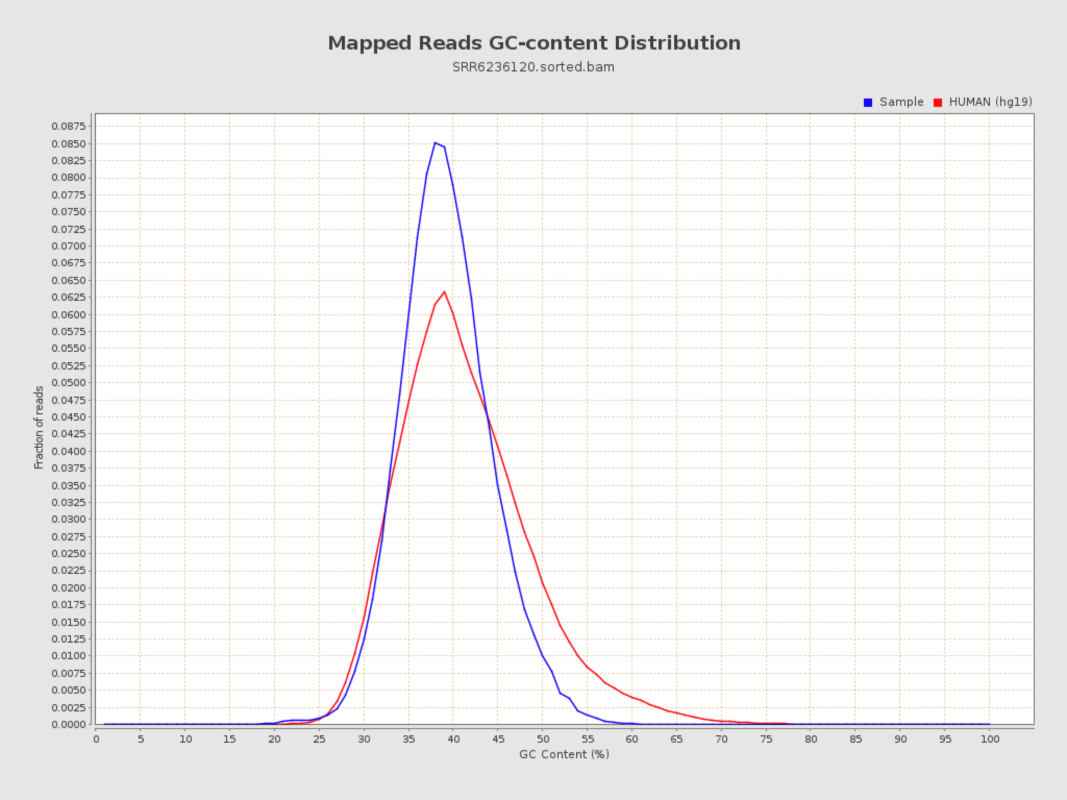
7. Results : Duplication Rate Histogram



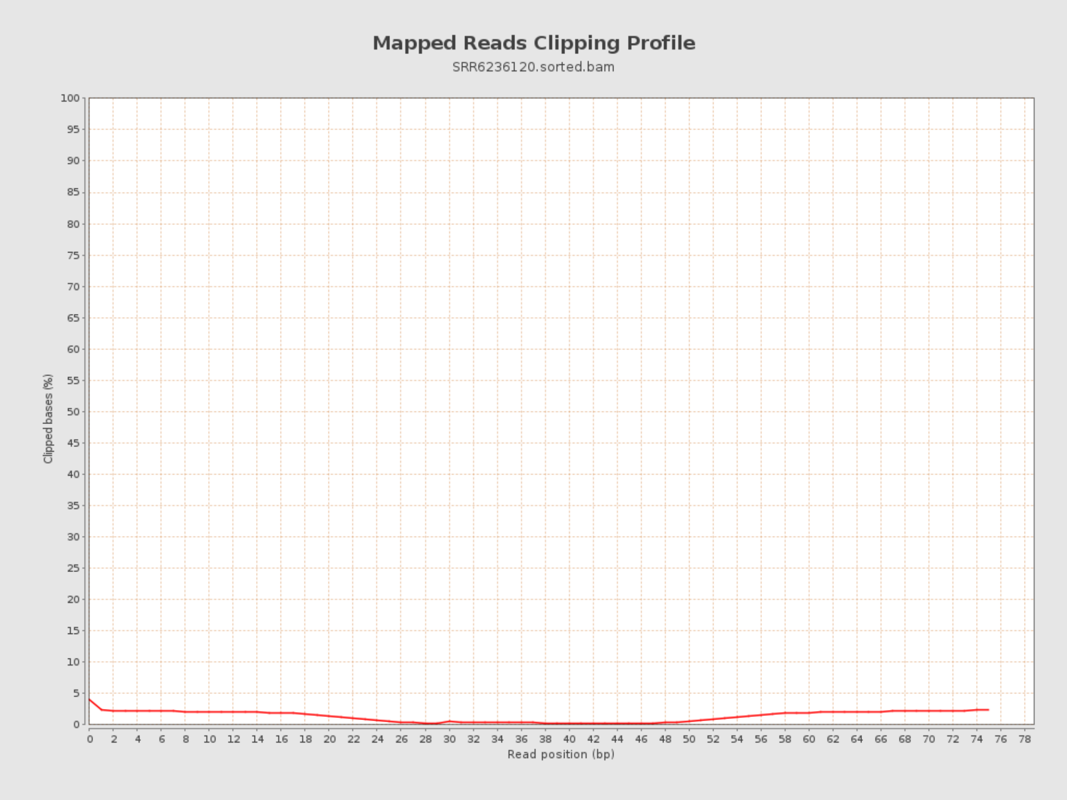
8. Results : Mapped Reads Nucleotide Content



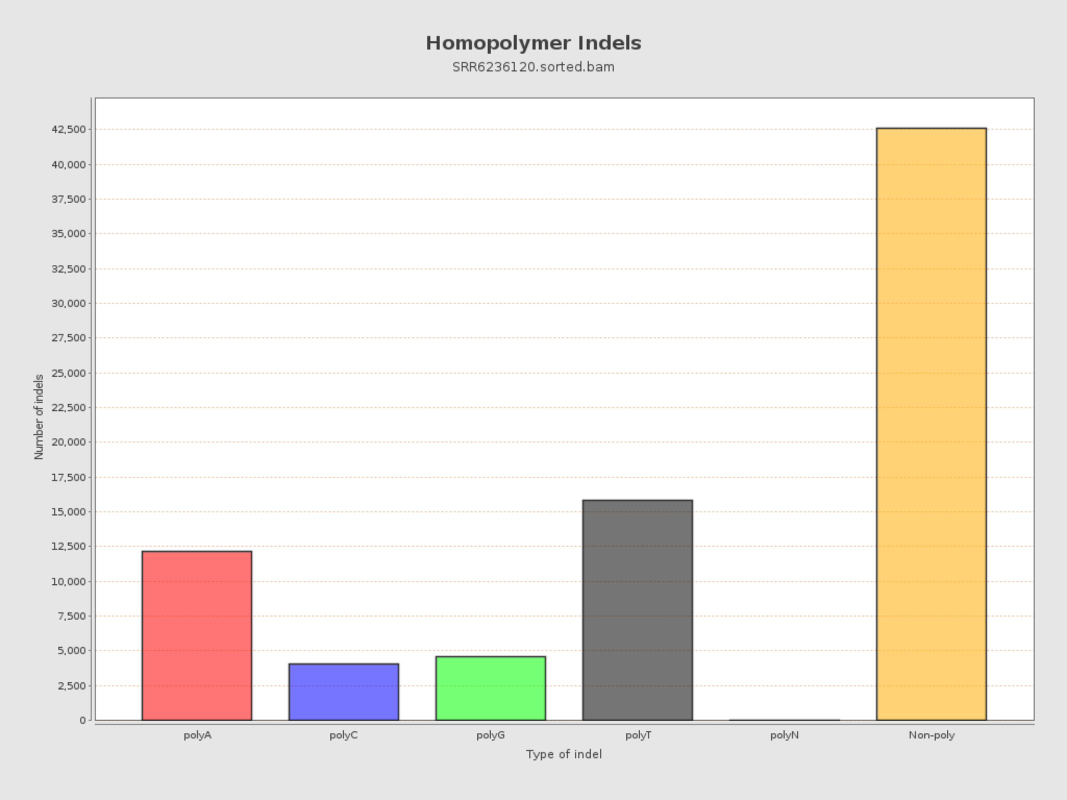
9. Results : Mapped Reads GC-content Distribution



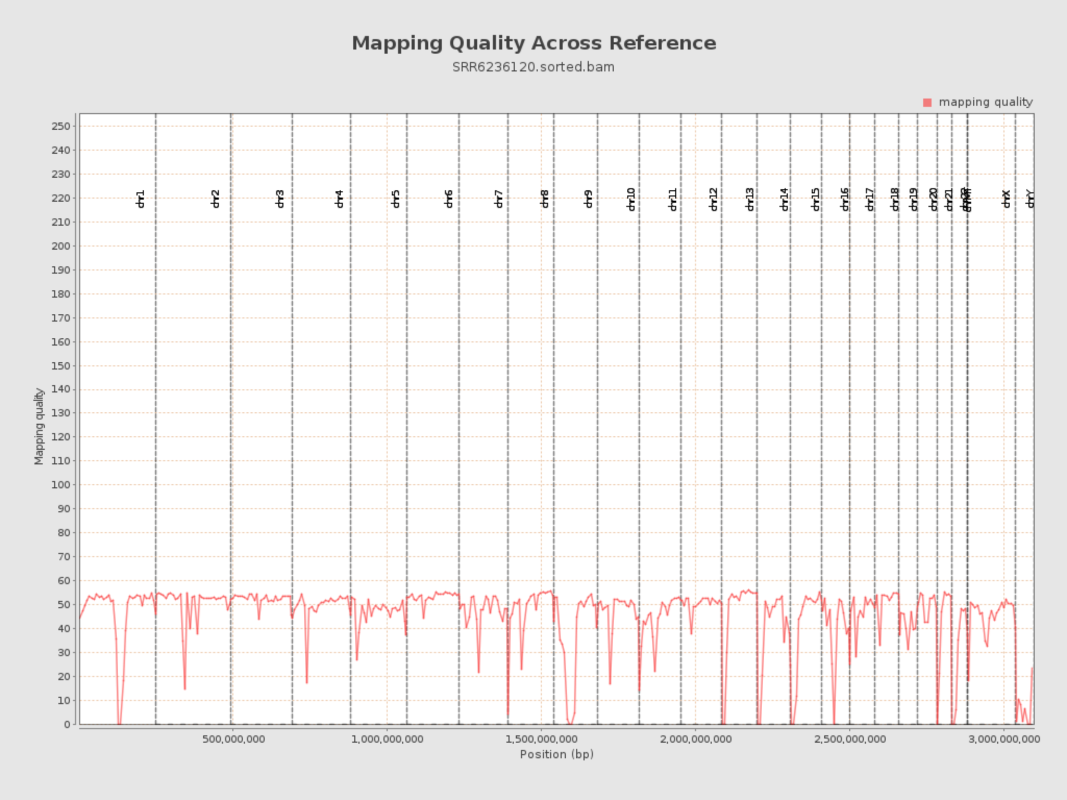
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram