Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:18:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008718.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_SRR6008718 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008718.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:18:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008718.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,947,853
Mapped reads	1,487,538 / 76.37%
Unmapped reads	460,315 / 23.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,493 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	32,492 / 1.67%
Duplication rate	1.74%
Clipped reads	547,924 / 28.13%

2.2. ACGT Content

Number/percentage of A's	31,171,511 / 30.61%
Number/percentage of C's	18,092,479 / 17.77%
Number/percentage of T's	30,480,151 / 29.93%
Number/percentage of G's	22,062,265 / 21.67%
Number/percentage of N's	26,512 / 0.03%
GC Percentage	39.43%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.2558

2.4. Mapping Quality

Mean Mapping Quality	48.49

2.5. Mismatches and indels

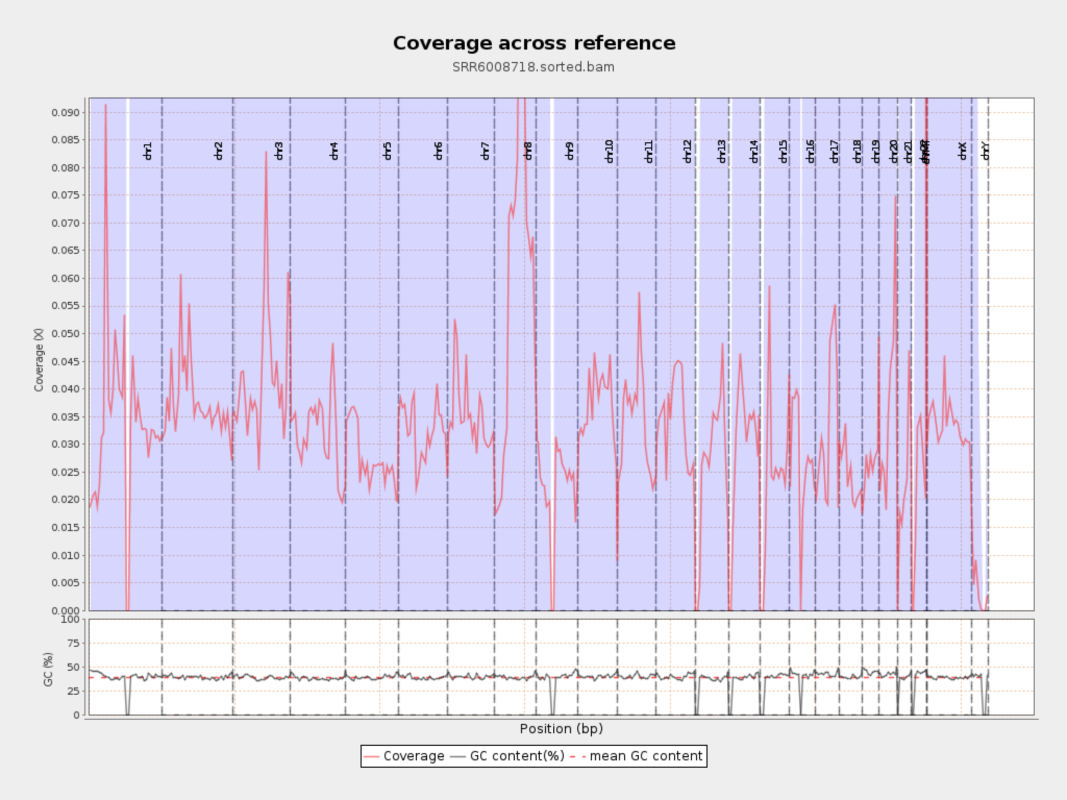
General error rate	0.89%
Mismatches	898,503
Insertions	7,002
Mapped reads with at least one insertion	0.47%
Deletions	27,587
Mapped reads with at least one deletion	1.83%
Homopolymer indels	46.87%

2.6. Chromosome stats

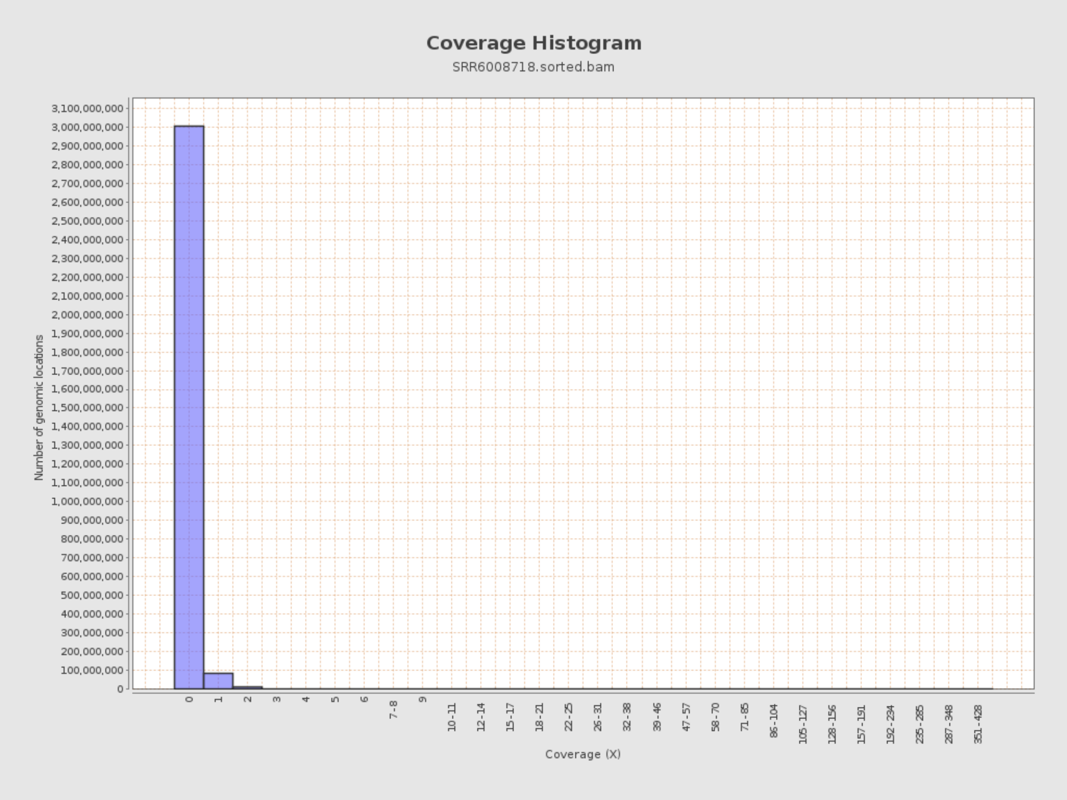
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8349365	0.0335	0.3962
chr2	243199373	9225543	0.0379	0.2999
chr3	198022430	8367588	0.0423	0.2259
chr4	191154276	6075697	0.0318	0.1964
chr5	180915260	4983456	0.0275	0.1803
chr6	171115067	5561459	0.0325	0.2116
chr7	159138663	5678940	0.0357	0.3058

chr8	146364022	8818193	0.0602	0.3824
chr9	141213431	3085430	0.0218	0.2048
chr10	135534747	5108982	0.0377	0.2505
chr11	135006516	4601645	0.0341	0.2573
chr12	133851895	4636807	0.0346	0.203
chr13	115169878	3049008	0.0265	0.1765
chr14	107349540	3193877	0.0298	0.1948
chr15	102531392	2470448	0.0241	0.1694
chr16	90354753	2462724	0.0273	0.1925
chr17	81195210	2715034	0.0334	0.2196
chr18	78077248	1915223	0.0245	0.3705
chr19	59128983	1575333	0.0266	0.234
chr20	63025520	2363533	0.0375	0.2137
chr21	48129895	1120653	0.0233	0.1711
chr22	51304566	1063132	0.0207	0.1562
chrMT	16571	28231	1.7036	2.0729
chrX	155270560	5225882	0.0337	0.2166
chrY	59373566	202549	0.0034	0.0811

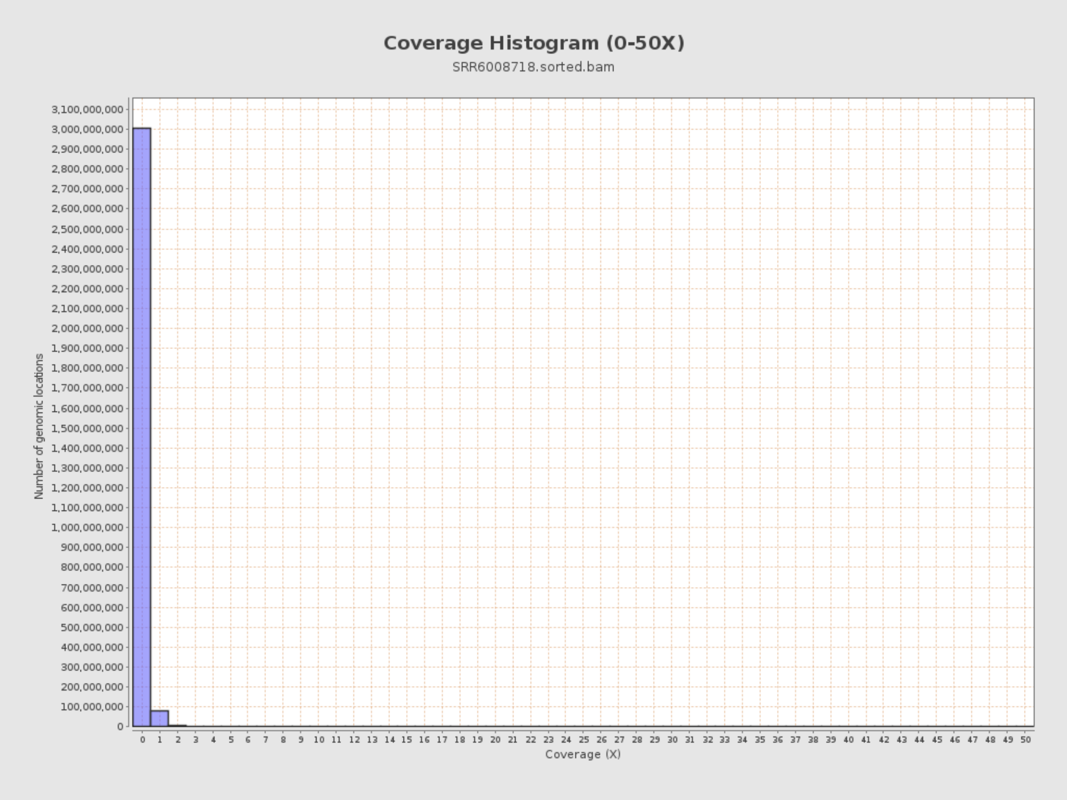
3. Results : Coverage across reference



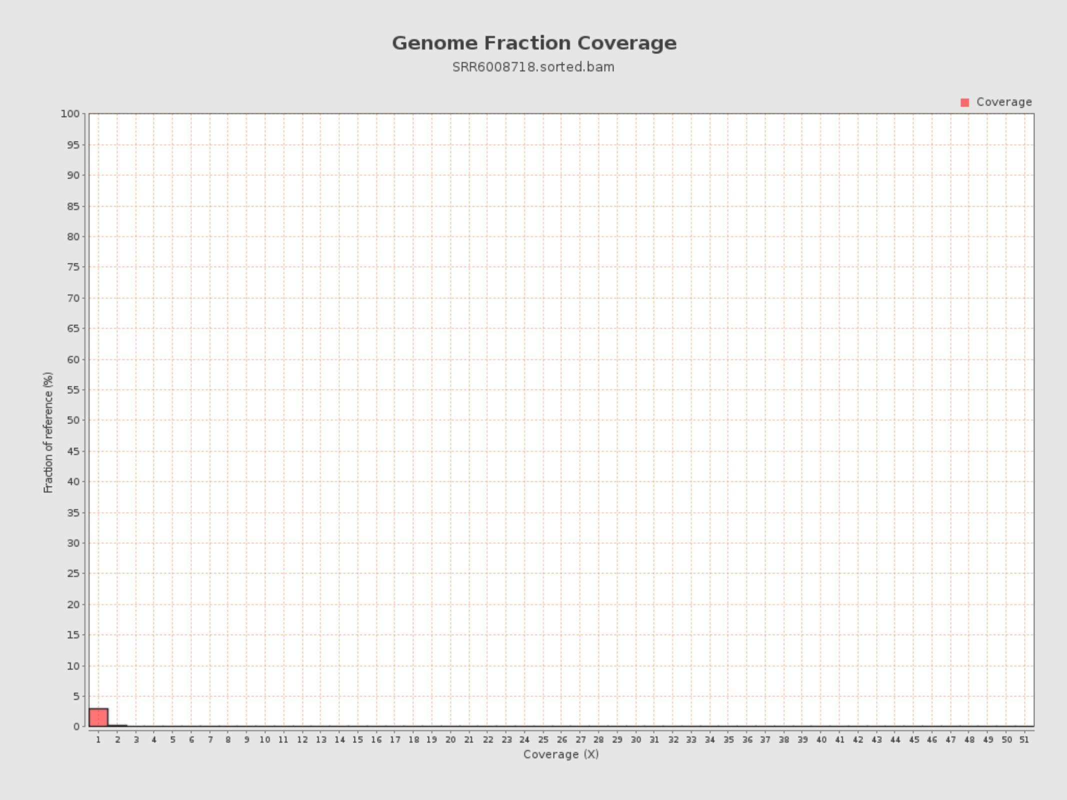
4. Results : Coverage Histogram



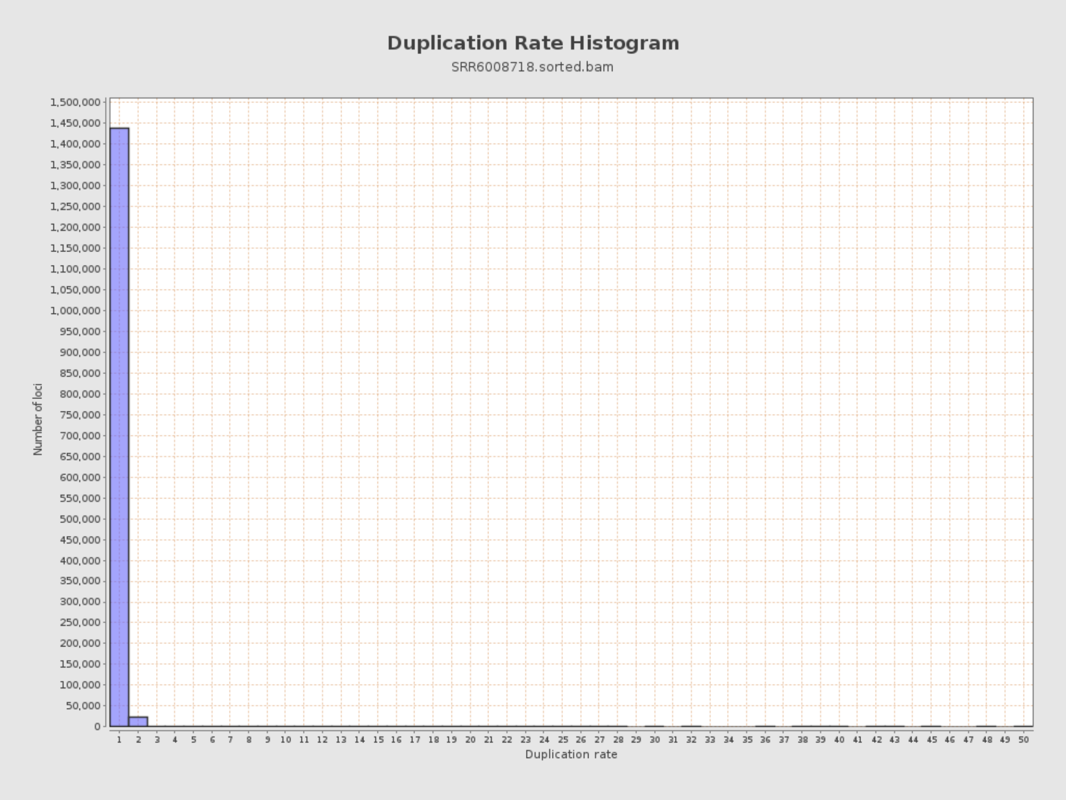
5. Results : Coverage Histogram (0-50X)



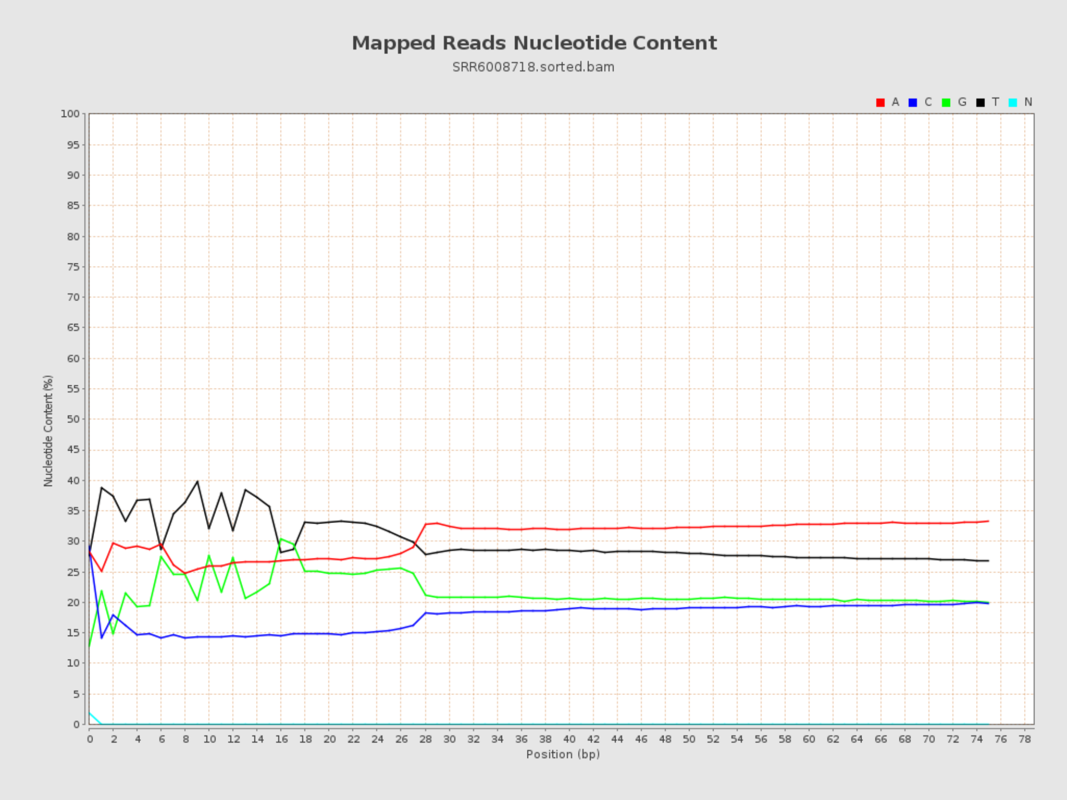
6. Results : Genome Fraction Coverage



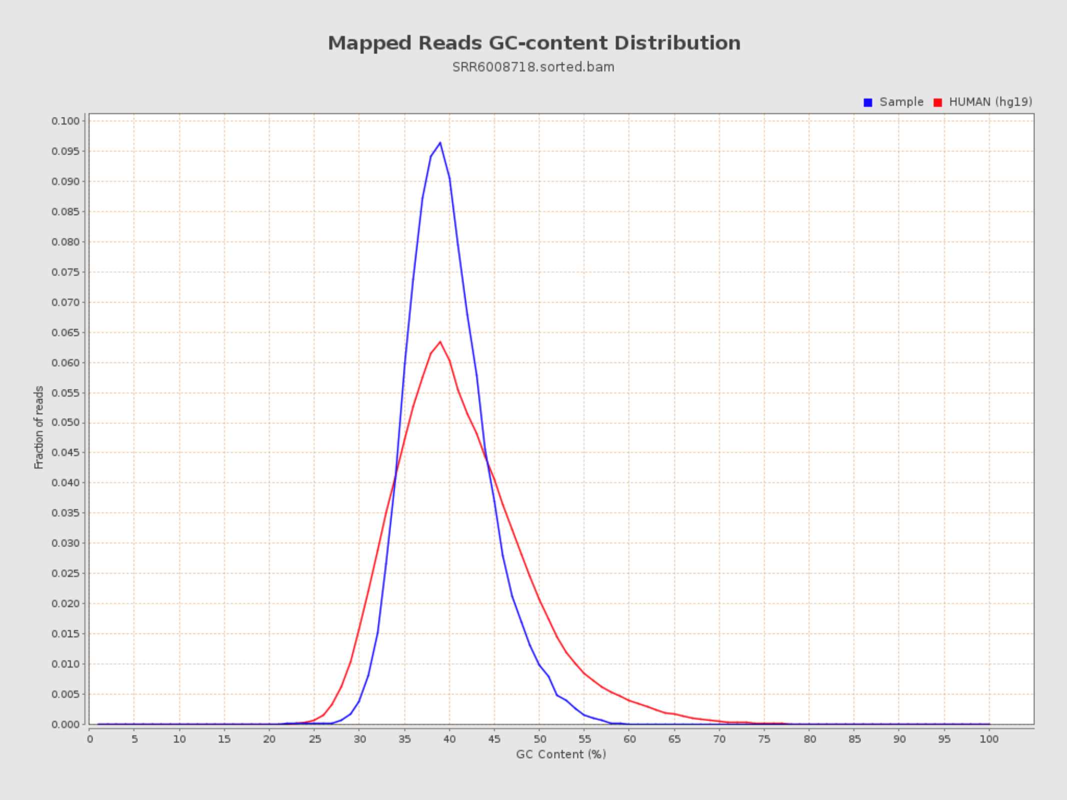
7. Results : Duplication Rate Histogram



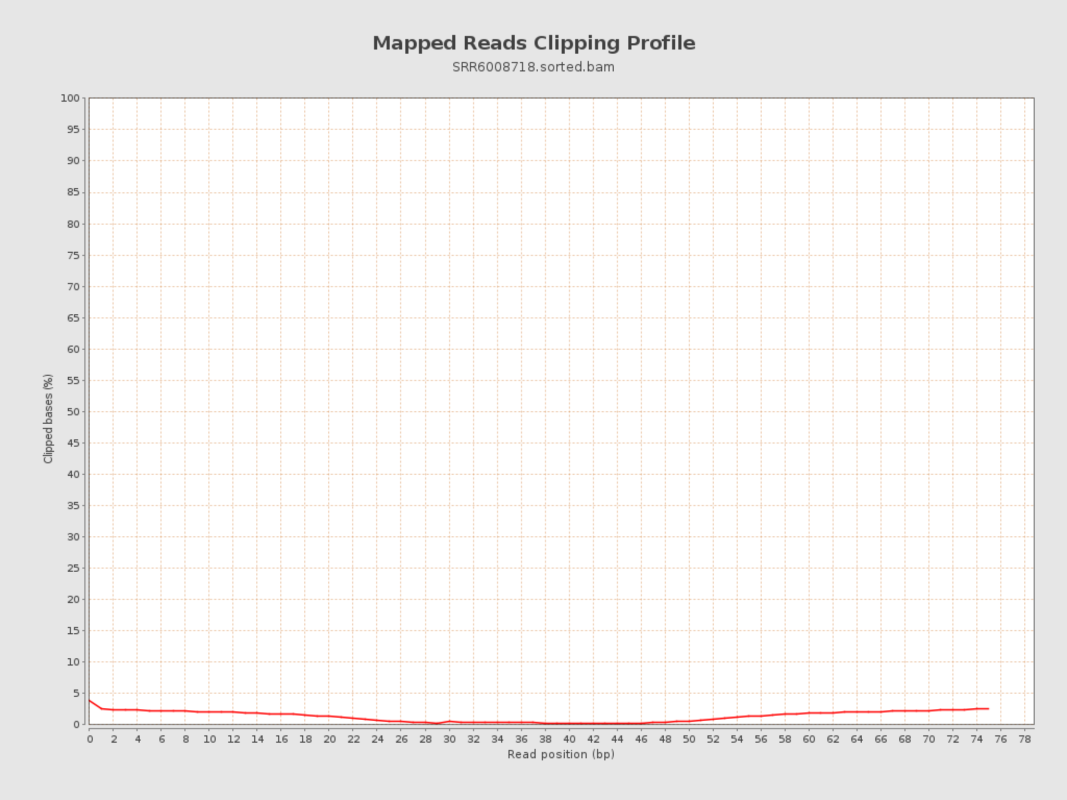
8. Results : Mapped Reads Nucleotide Content



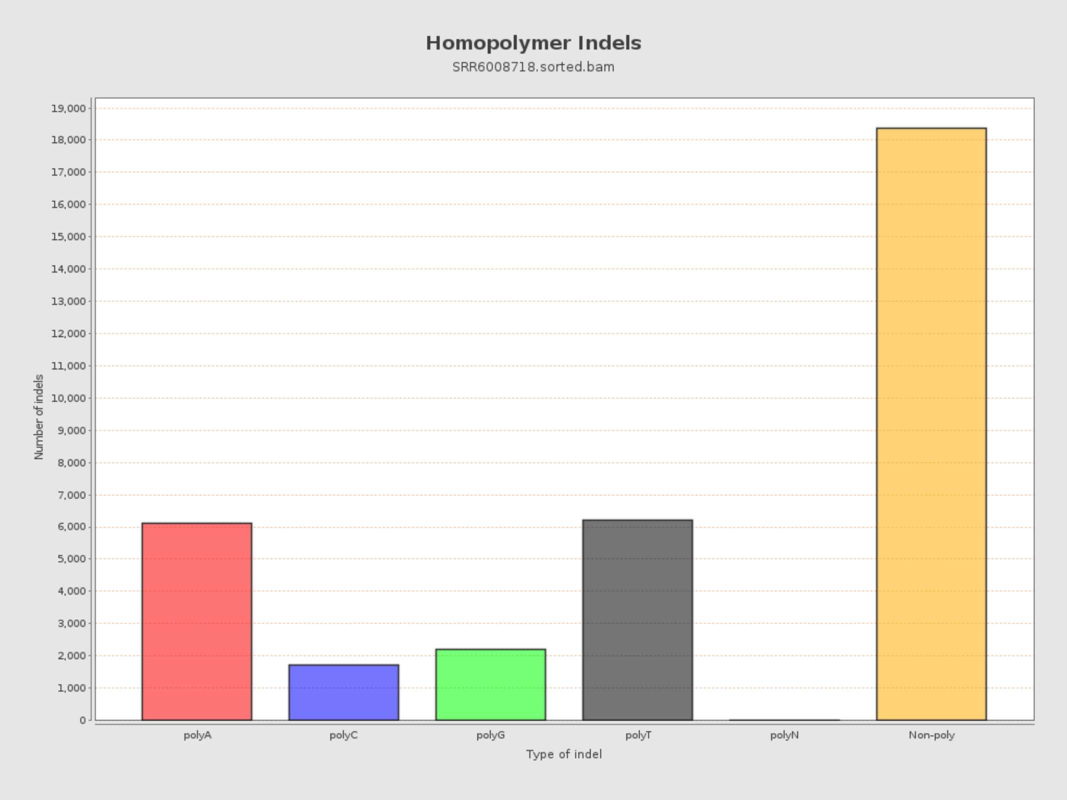
9. Results : Mapped Reads GC-content Distribution



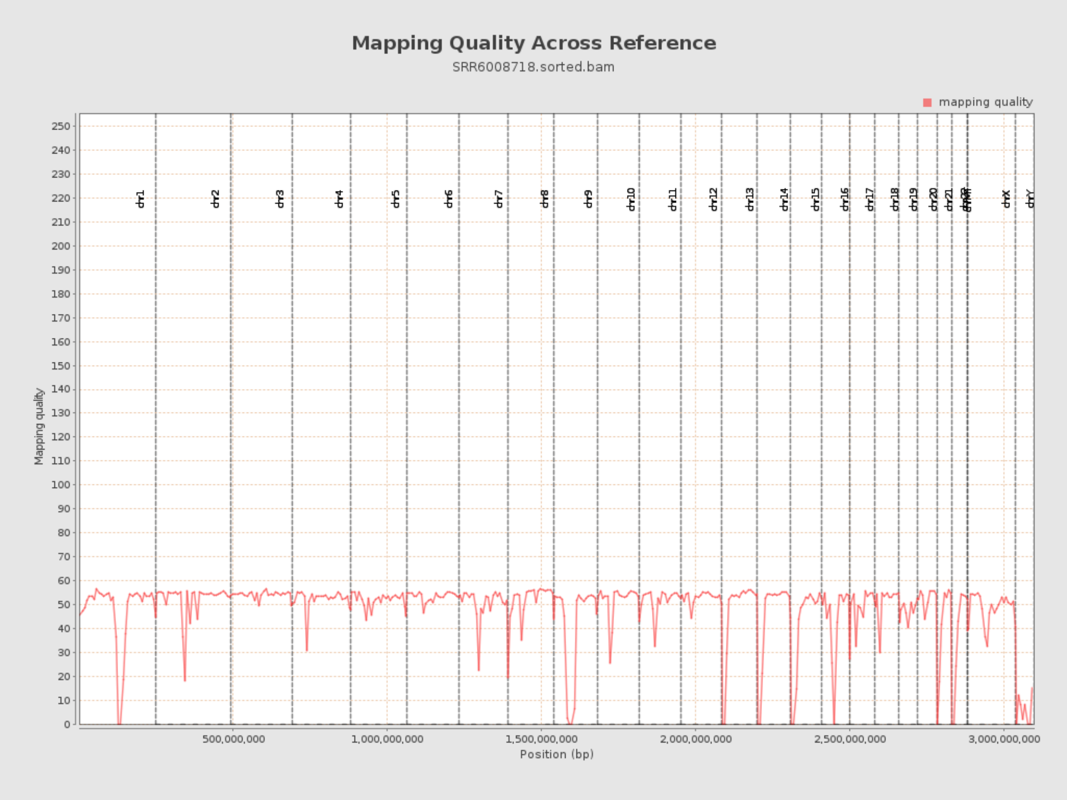
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram