Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:34:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080959.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_SRR3080959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080959.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:34:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,582,035
Mapped reads	4,893,865 / 87.67%
Unmapped reads	688,170 / 12.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	53,458 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	383,749 / 6.87%
Duplication rate	6.24%
Clipped reads	2,140,864 / 38.35%

2.2. ACGT Content

Number/percentage of A's	92,088,083 / 28.09%
Number/percentage of C's	57,315,072 / 17.48%
Number/percentage of T's	107,315,331 / 32.73%
Number/percentage of G's	70,488,838 / 21.5%
Number/percentage of N's	648,252 / 0.2%
GC Percentage	38.98%

2.3. Coverage

Mean	0.1059

Standard Deviation	0.7493

2.4. Mapping Quality

Mean Mapping Quality	46.98

2.5. Mismatches and indels

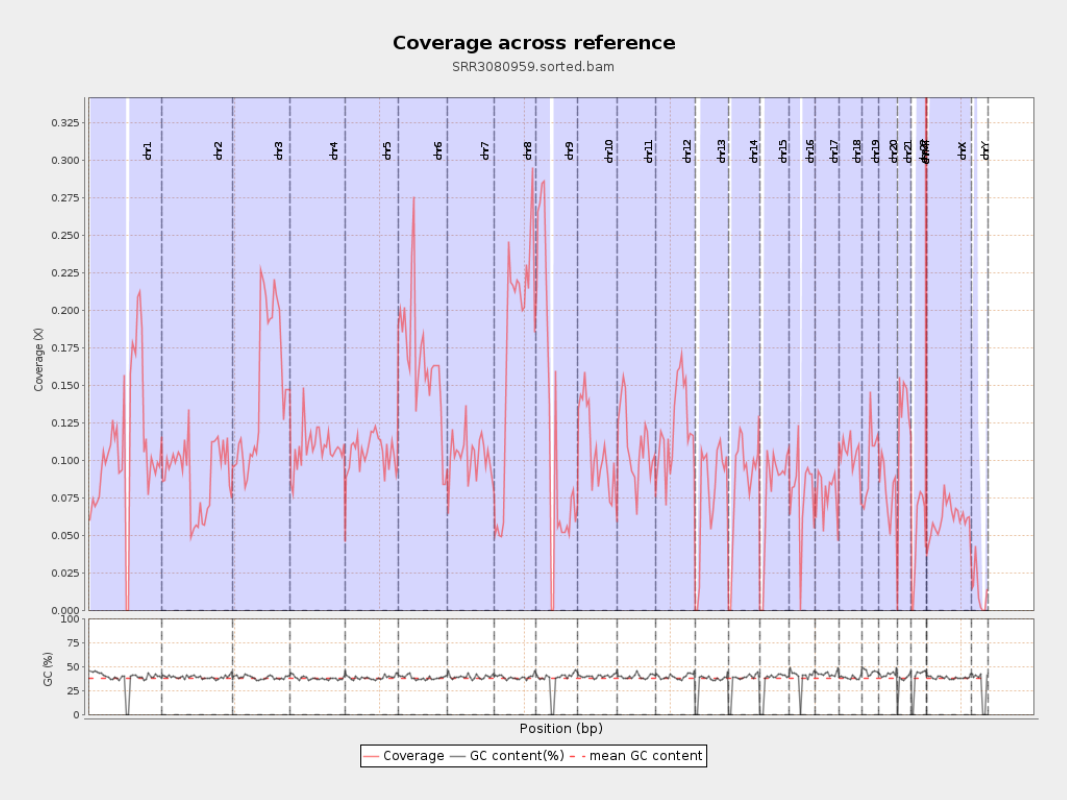
General error rate	1.02%
Mismatches	3,286,486
Insertions	26,376
Mapped reads with at least one insertion	0.53%
Deletions	74,504
Mapped reads with at least one deletion	1.51%
Homopolymer indels	49.36%

2.6. Chromosome stats

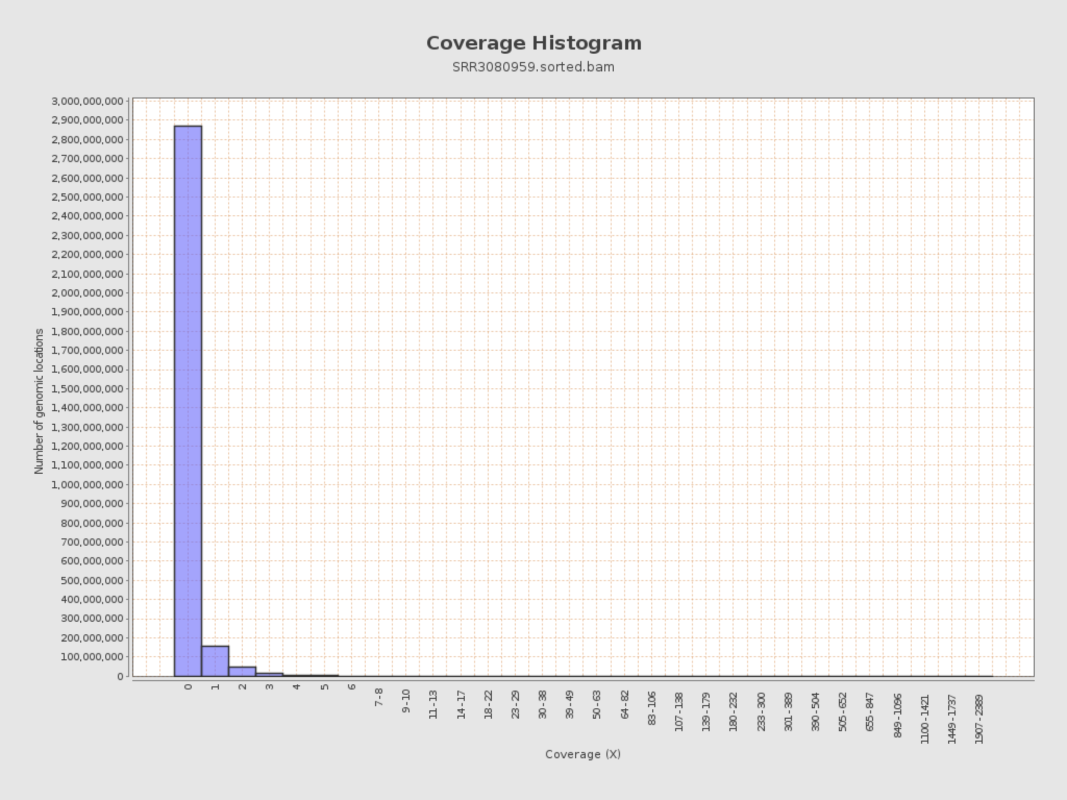
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27000981	0.1083	1.2232
chr2	243199373	21999262	0.0905	0.6472
chr3	198022430	29016448	0.1465	0.5207
chr4	191154276	20652366	0.108	0.4762
chr5	180915260	19119727	0.1057	0.4411
chr6	171115067	28307486	0.1654	0.7954
chr7	159138663	16449321	0.1034	0.712

chr8	146364022	25751905	0.1759	1.5498
chr9	141213431	17015114	0.1205	0.8567
chr10	135534747	14609034	0.1078	0.6311
chr11	135006516	14778617	0.1095	0.5693
chr12	133851895	16312811	0.1219	0.4973
chr13	115169878	8806509	0.0765	0.3716
chr14	107349540	9018604	0.084	0.5049
chr15	102531392	8049573	0.0785	0.3765
chr16	90354753	7010150	0.0776	0.4712
chr17	81195210	6169526	0.076	0.3921
chr18	78077248	8149442	0.1044	1.4149
chr19	59128983	5907884	0.0999	0.9094
chr20	63025520	5052110	0.0802	0.4093
chr21	48129895	6077571	0.1263	0.5778
chr22	51304566	2594148	0.0506	0.2973
chrMT	16571	34887	2.1053	2.0039
chrX	155270560	9373228	0.0604	0.3803
chrY	59373566	721916	0.0122	0.2385

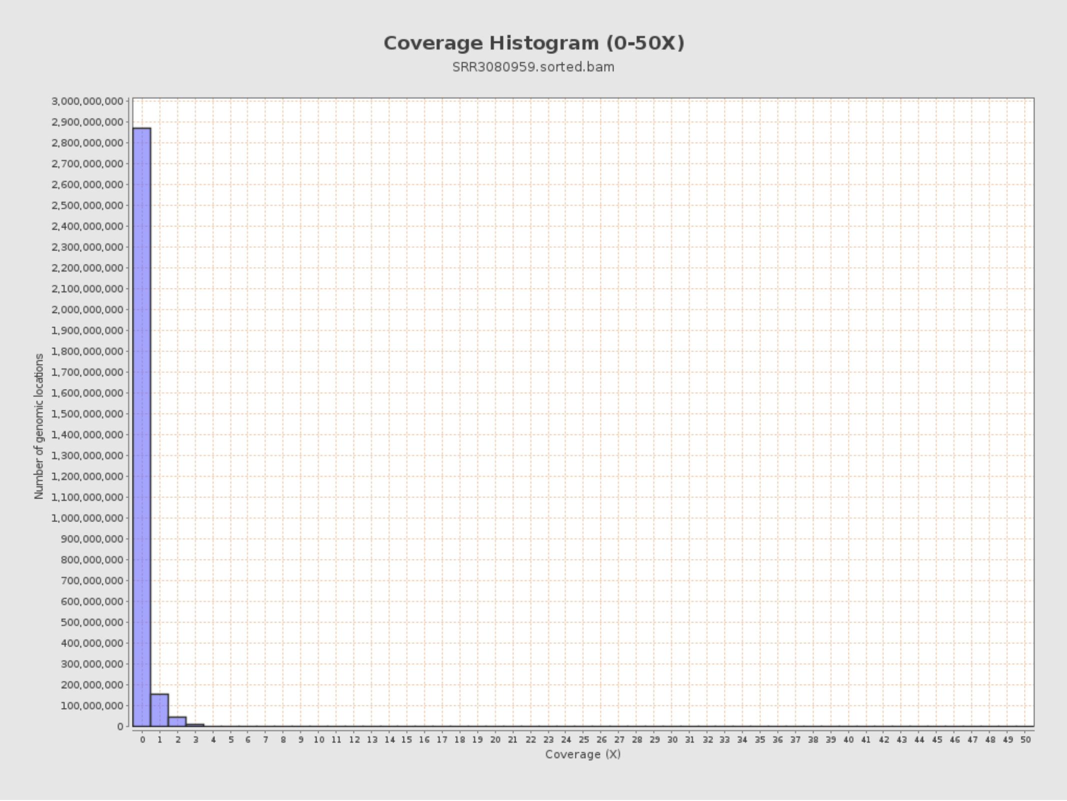
3. Results : Coverage across reference



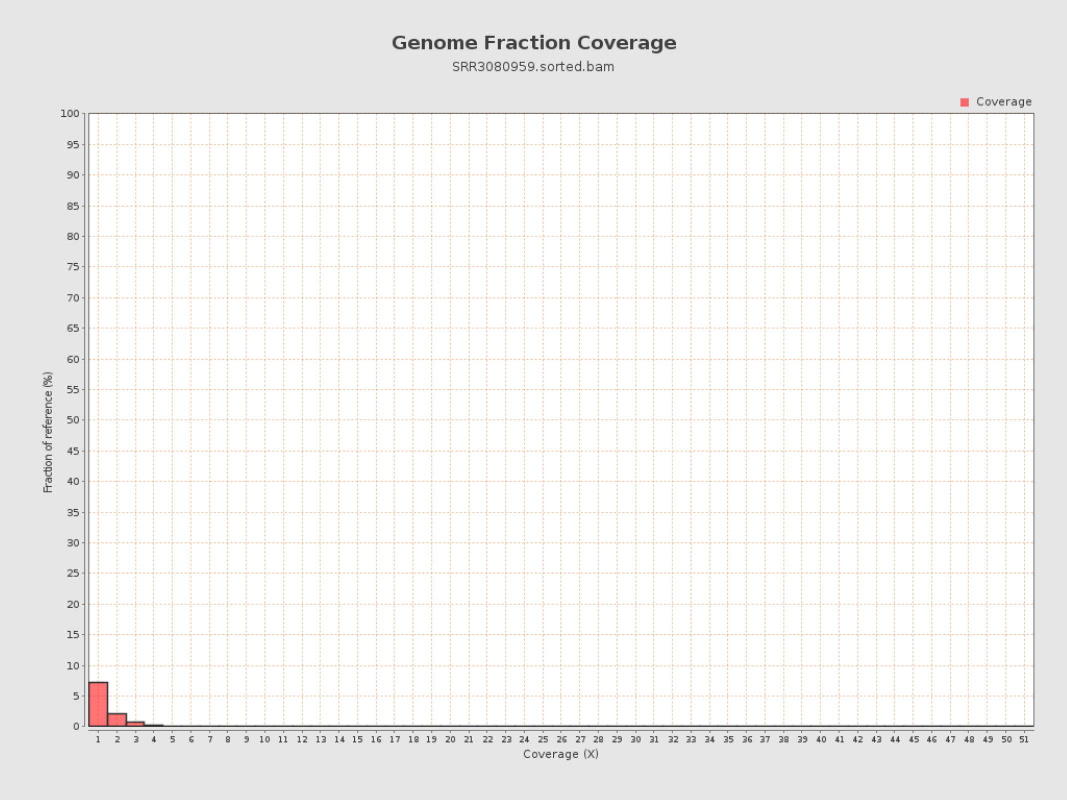
4. Results : Coverage Histogram



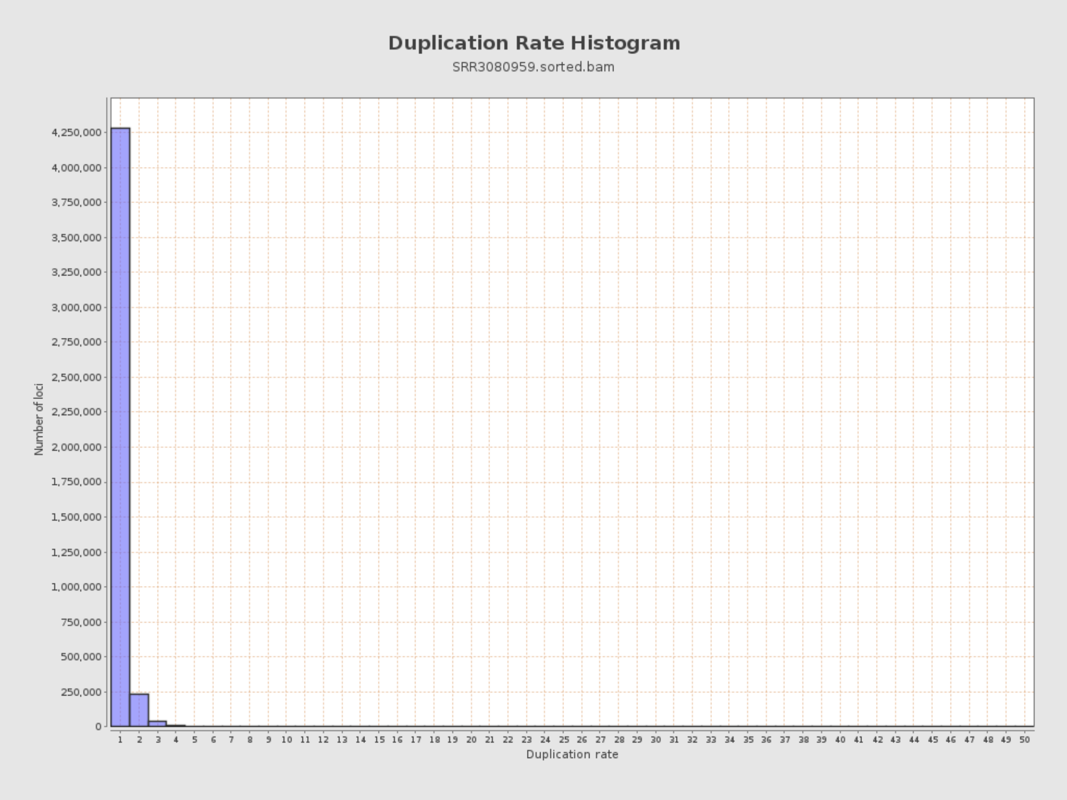
5. Results : Coverage Histogram (0-50X)



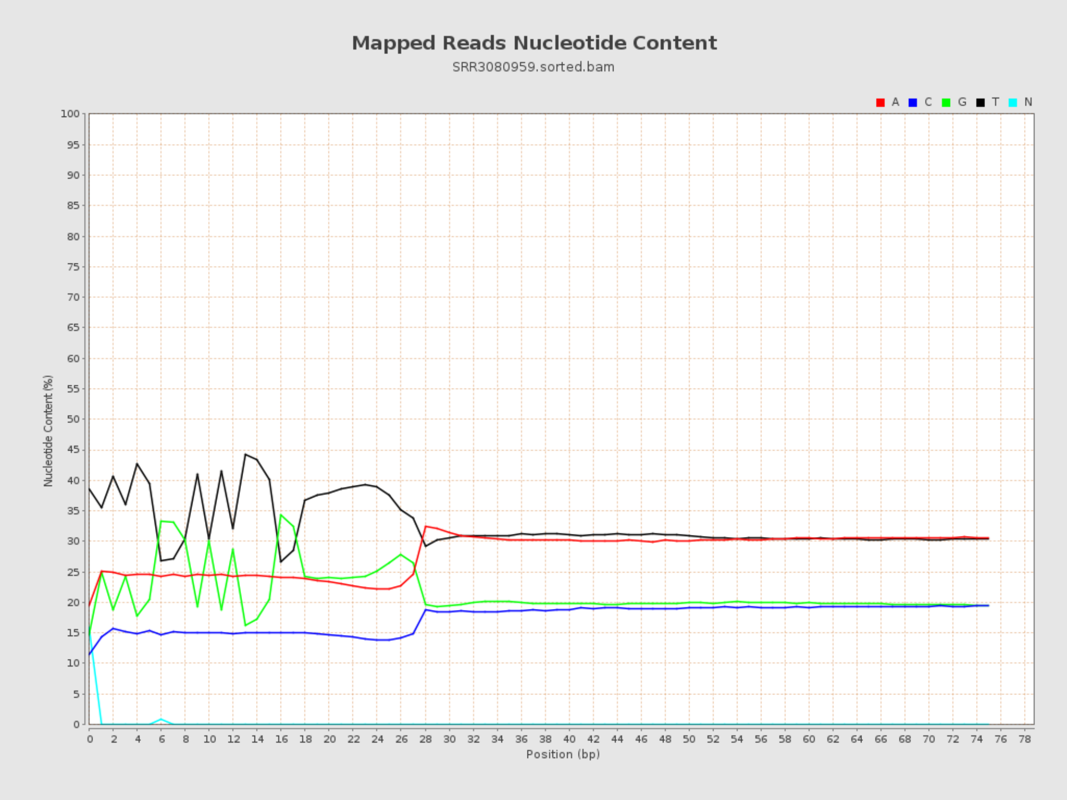
6. Results : Genome Fraction Coverage



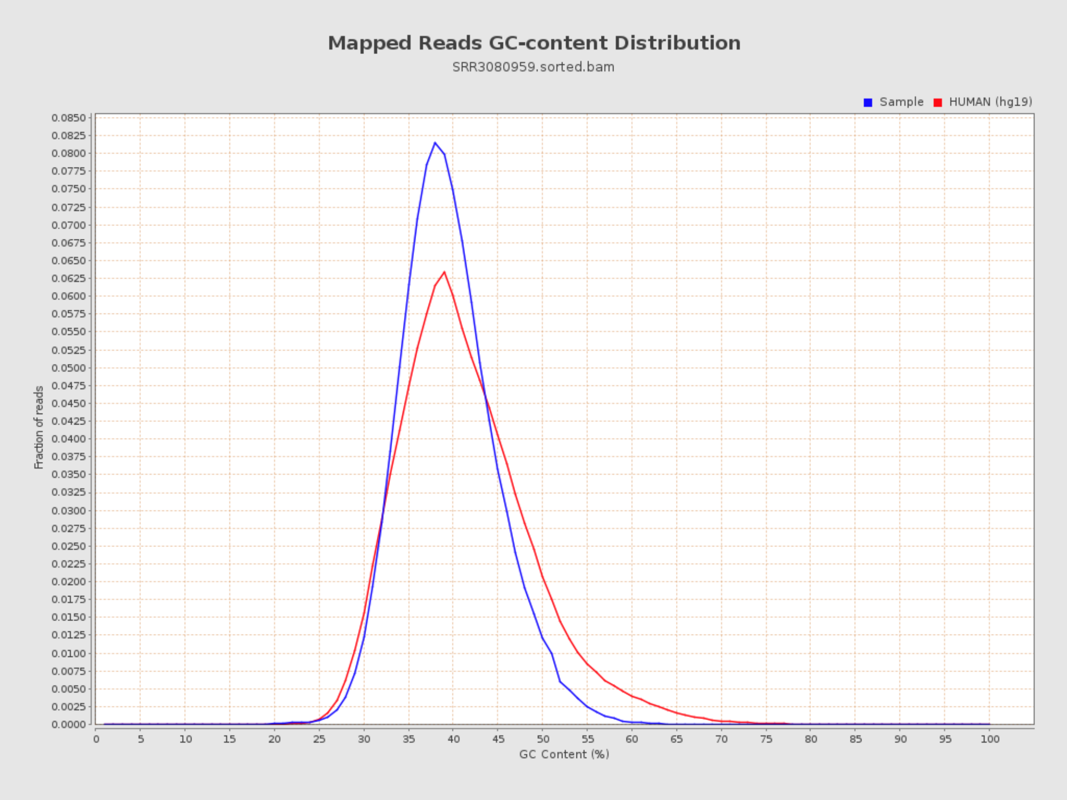
7. Results : Duplication Rate Histogram



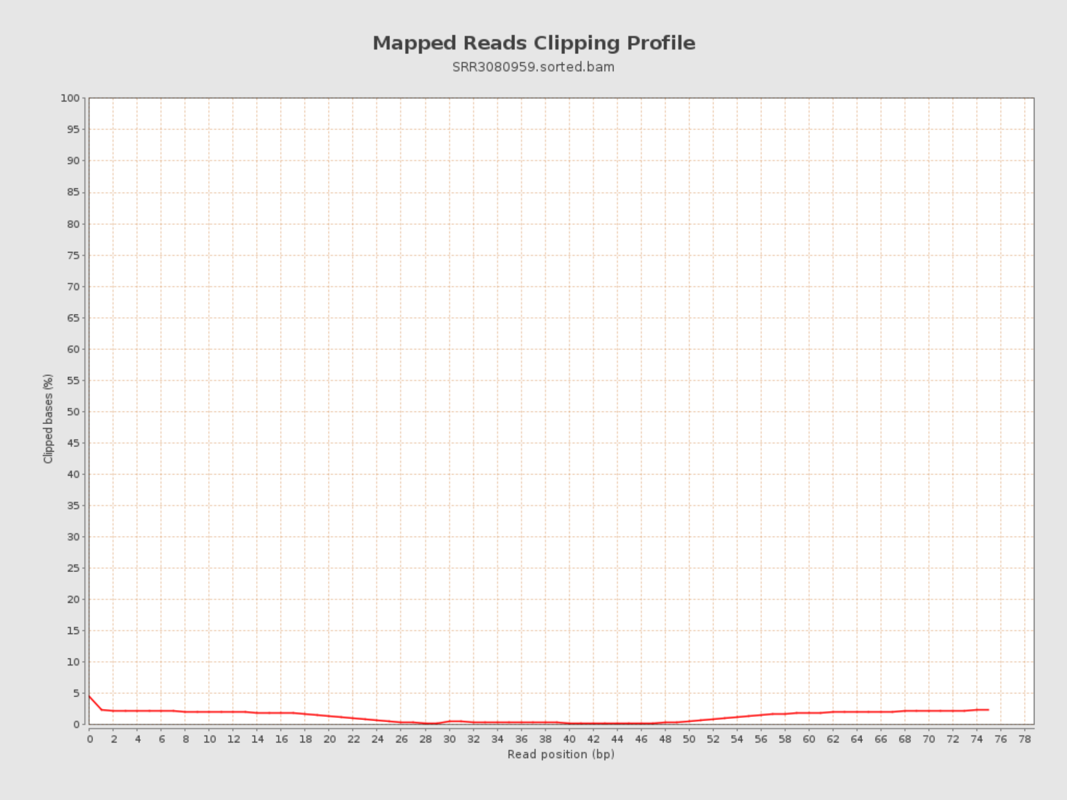
8. Results : Mapped Reads Nucleotide Content



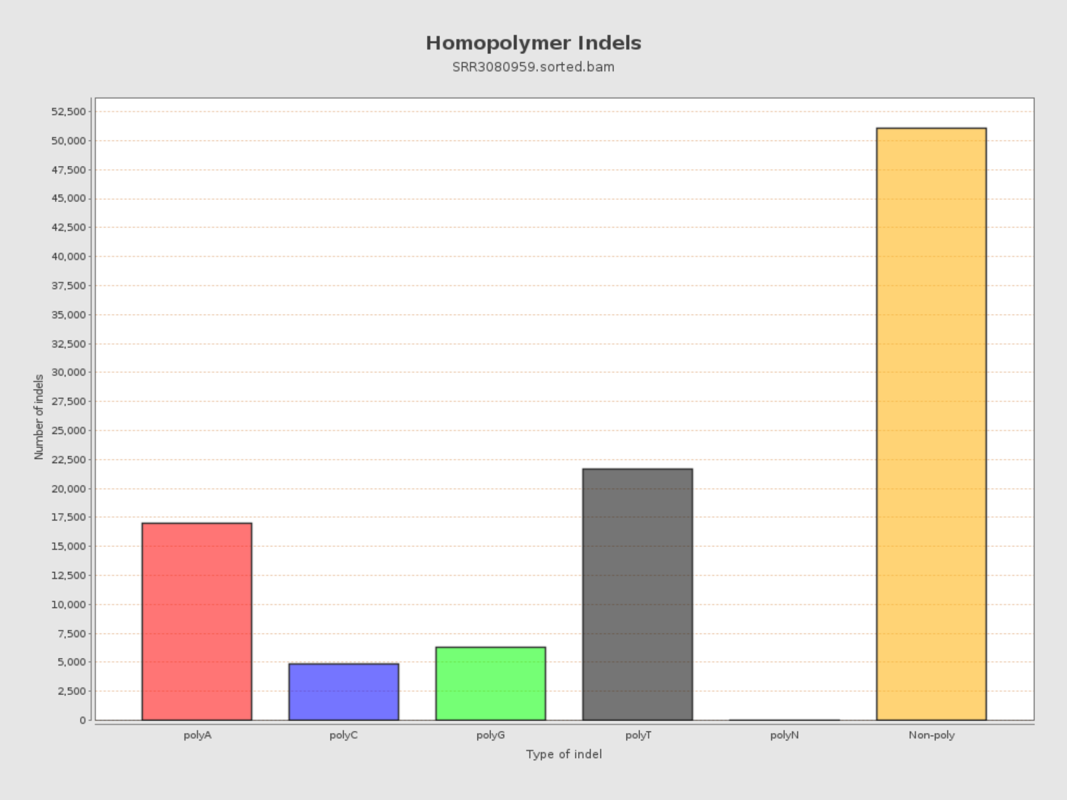
9. Results : Mapped Reads GC-content Distribution



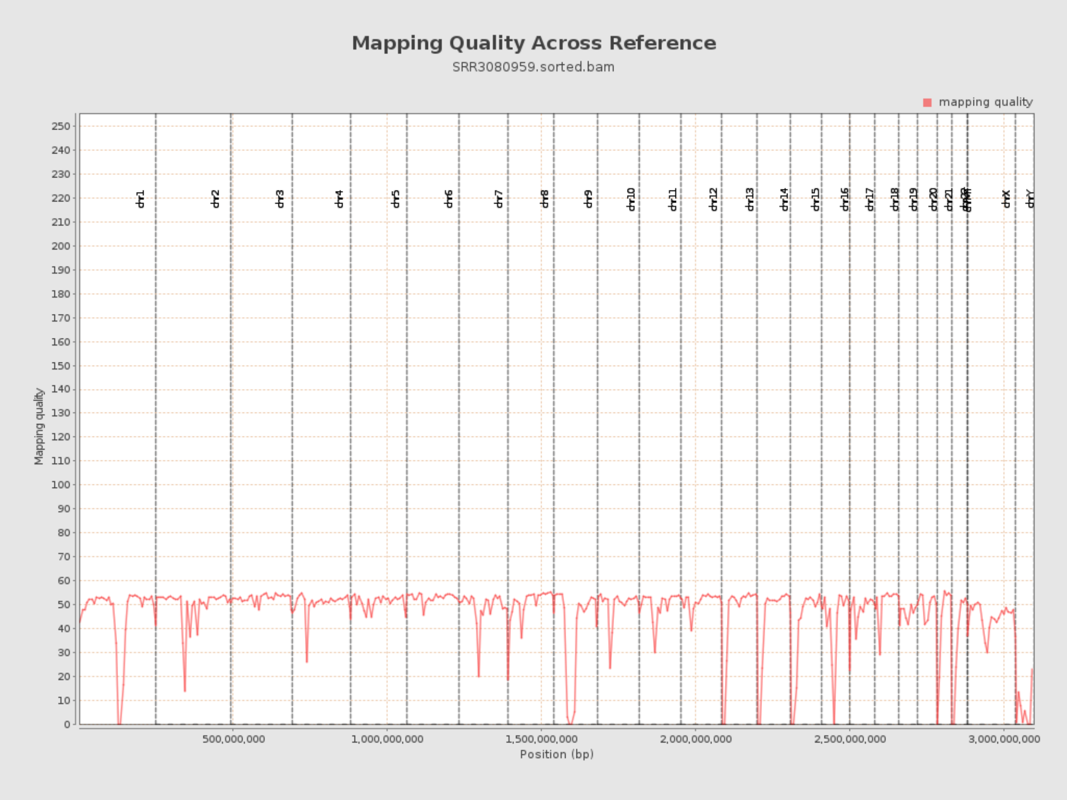
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram