Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:09:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080769.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_SRR3080769 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080769.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:09:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080769.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,343,122
Mapped reads	3,499,178 / 65.49%
Unmapped reads	1,843,944 / 34.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,302 / 0.45%
Read min/max/mean length	30 / 66 / 66.15
Duplicated reads (estimated)	368,246 / 6.89%
Duplication rate	8.19%
Clipped reads	629,464 / 11.78%

2.2. ACGT Content

Number/percentage of A's	65,825,586 / 29.73%
Number/percentage of C's	45,524,962 / 20.56%
Number/percentage of T's	60,594,655 / 27.37%
Number/percentage of G's	49,393,322 / 22.31%
Number/percentage of N's	70,773 / 0.03%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0715

Standard Deviation	0.4682

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

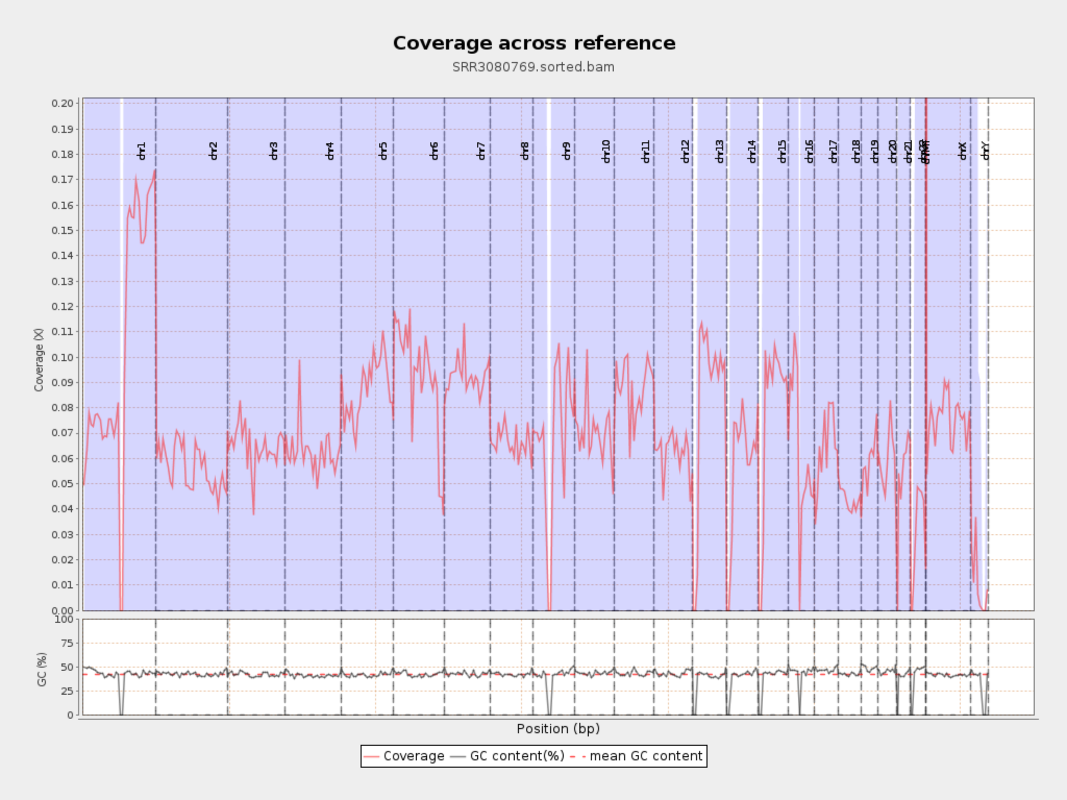
General error rate	0.9%
Mismatches	1,954,136
Insertions	16,313
Mapped reads with at least one insertion	0.46%
Deletions	40,439
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.48%

2.6. Chromosome stats

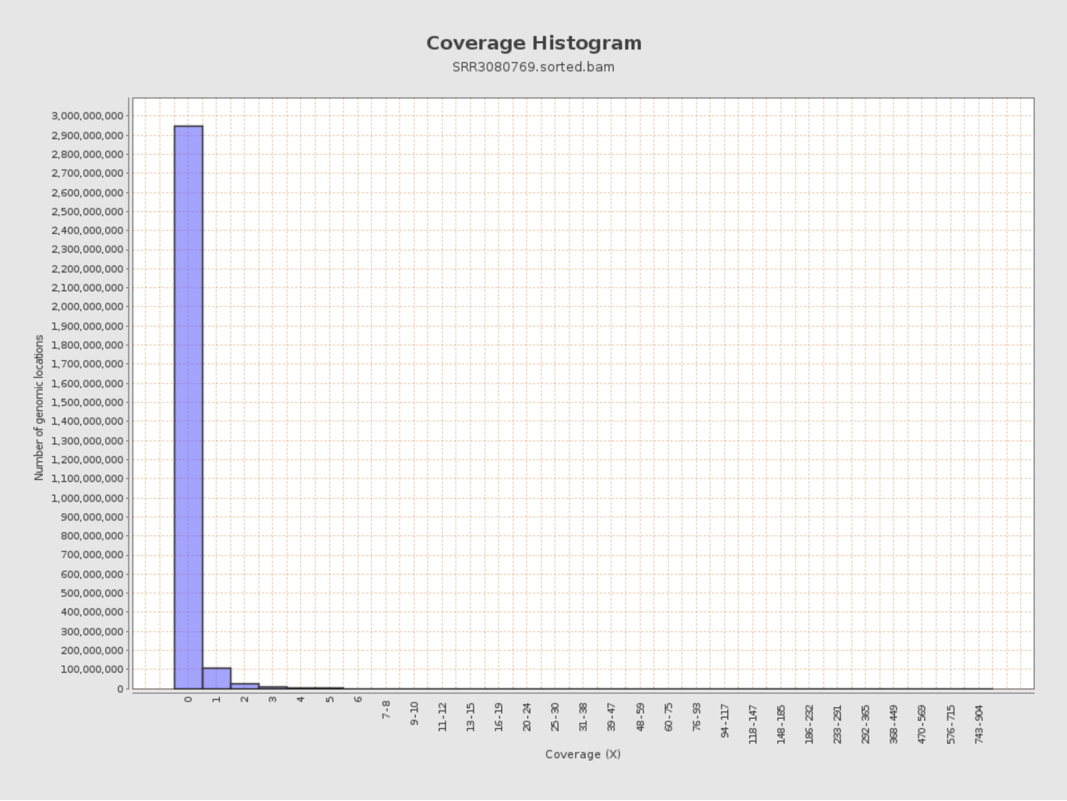
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25829930	0.1036	0.6084
chr2	243199373	13710603	0.0564	0.4306
chr3	198022430	12809447	0.0647	0.359
chr4	191154276	12029940	0.0629	0.4077
chr5	180915260	15857737	0.0877	0.4223
chr6	171115067	15986118	0.0934	0.6565
chr7	159138663	14770733	0.0928	0.5917

chr8	146364022	9704335	0.0663	0.5439
chr9	141213431	9567634	0.0678	0.4163
chr10	135534747	9462806	0.0698	0.5341
chr11	135006516	11806235	0.0874	0.4797
chr12	133851895	8359219	0.0625	0.3637
chr13	115169878	9625463	0.0836	0.4146
chr14	107349540	6072256	0.0566	0.3669
chr15	102531392	7868111	0.0767	0.4012
chr16	90354753	5544693	0.0614	0.382
chr17	81195210	5239391	0.0645	0.3801
chr18	78077248	3423354	0.0438	0.4921
chr19	59128983	3485835	0.059	0.5991
chr20	63025520	3737730	0.0593	0.3622
chr21	48129895	2590982	0.0538	0.3932
chr22	51304566	1610215	0.0314	0.2508
chrMT	16571	39899	2.4078	2.9483
chrX	155270560	11725736	0.0755	0.4073
chrY	59373566	625104	0.0105	0.2986

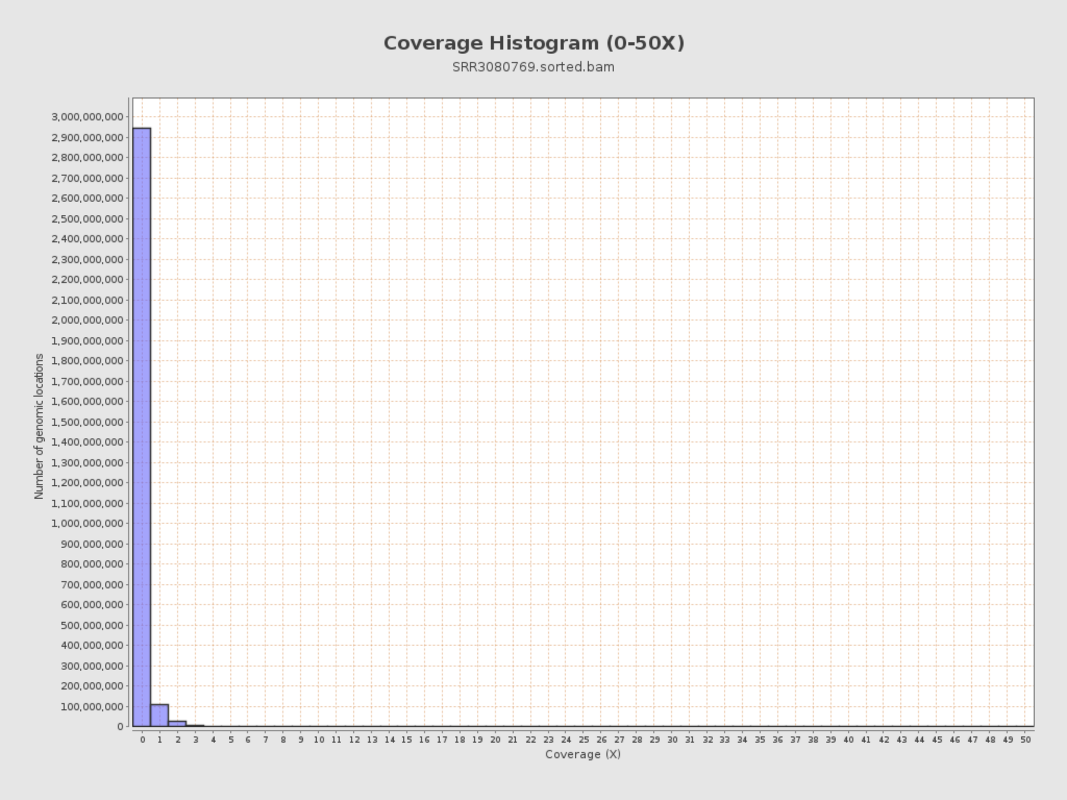
3. Results : Coverage across reference



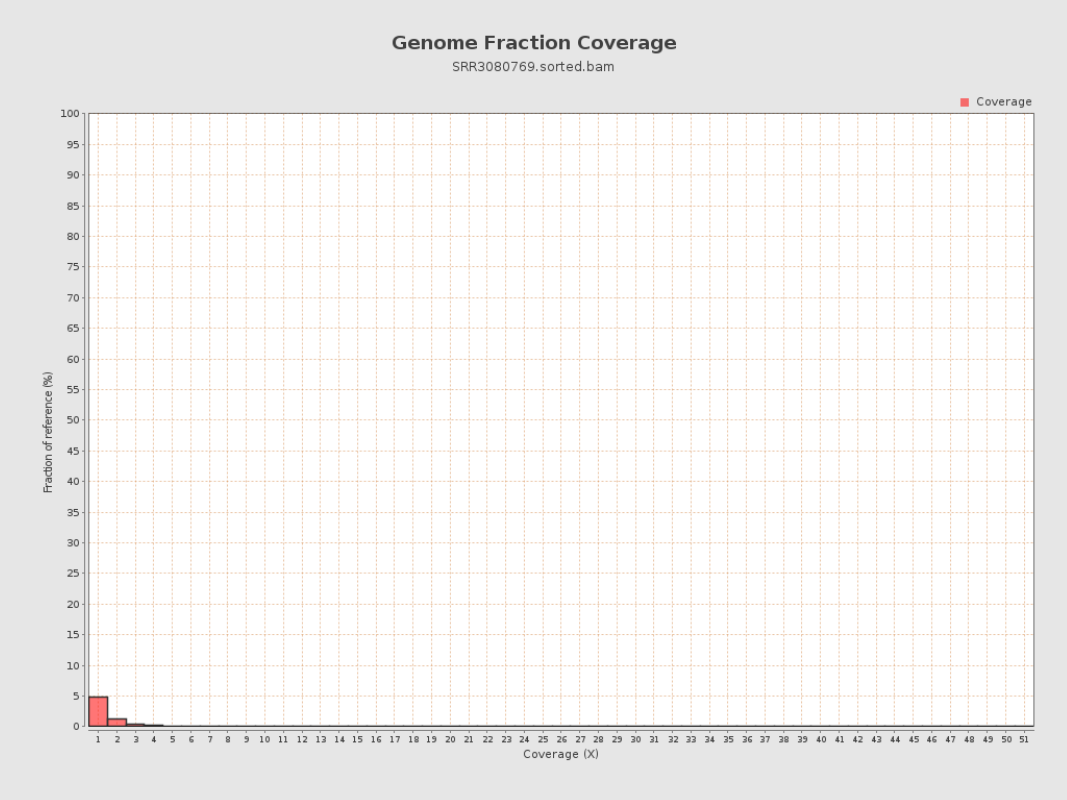
4. Results : Coverage Histogram



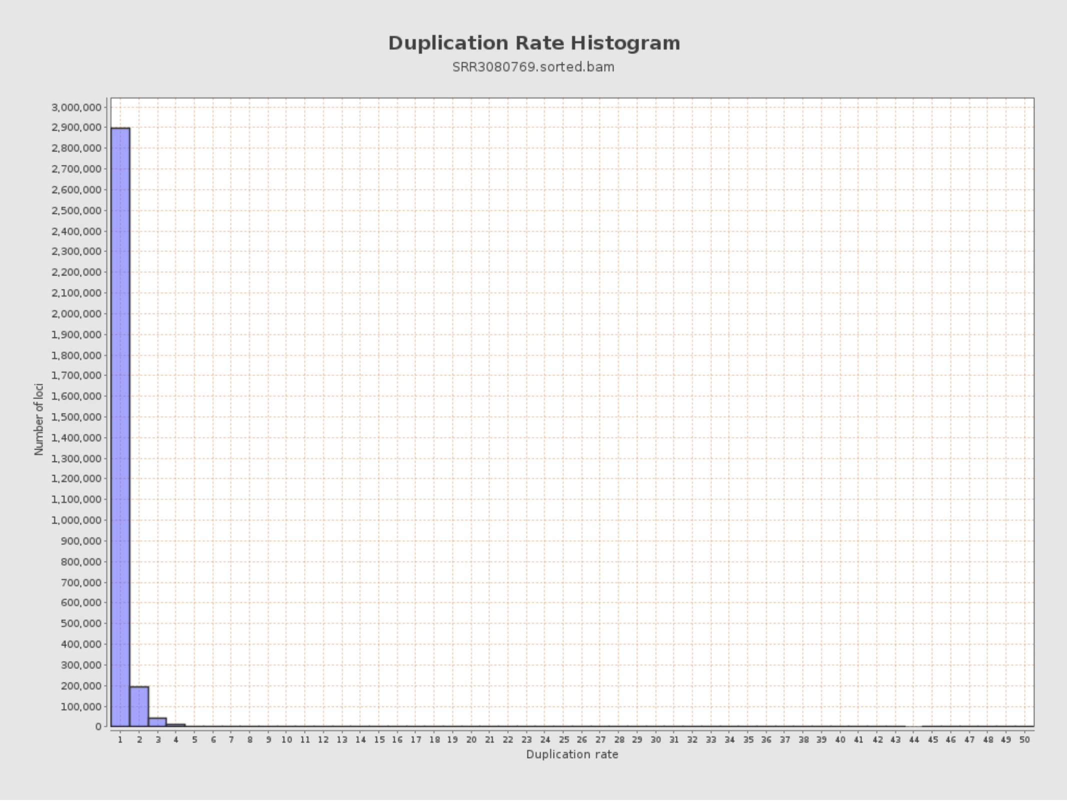
5. Results : Coverage Histogram (0-50X)



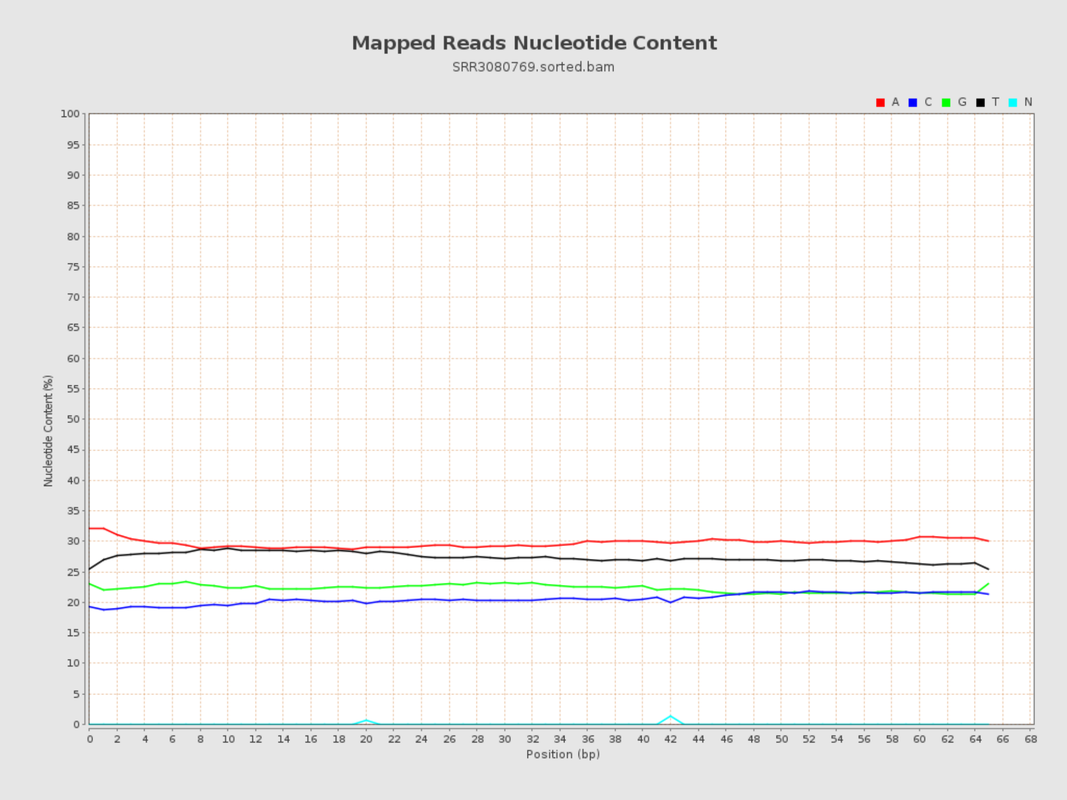
6. Results : Genome Fraction Coverage



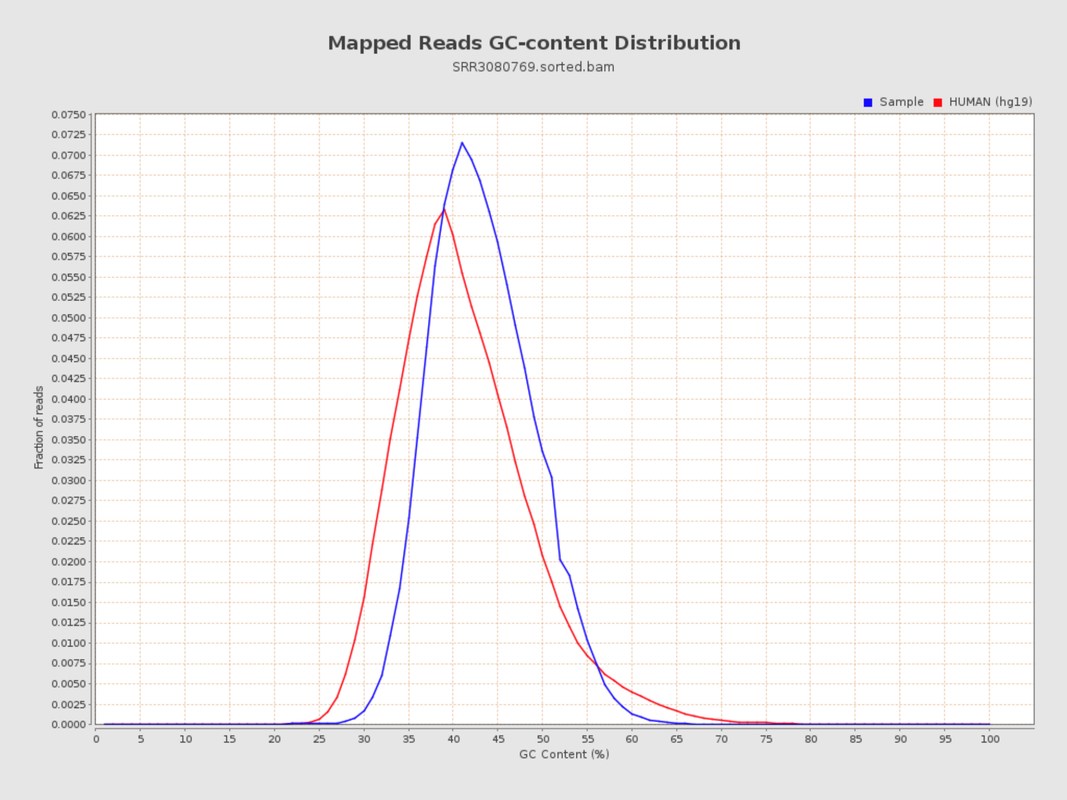
7. Results : Duplication Rate Histogram



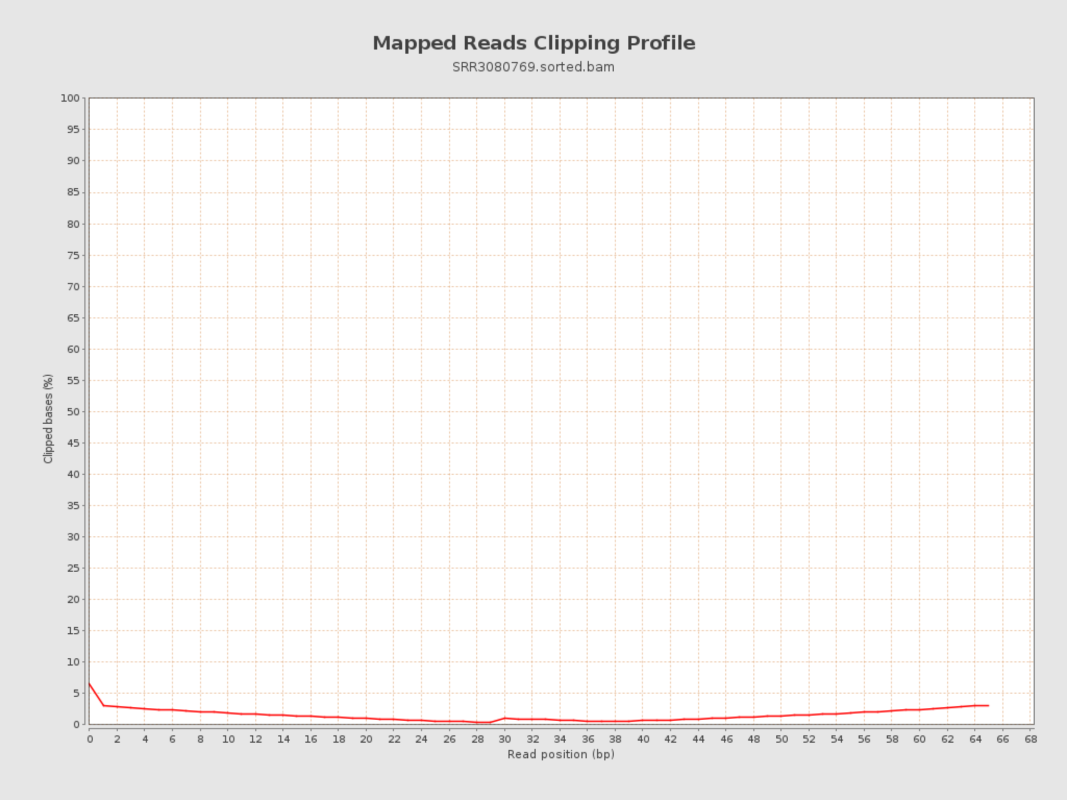
8. Results : Mapped Reads Nucleotide Content



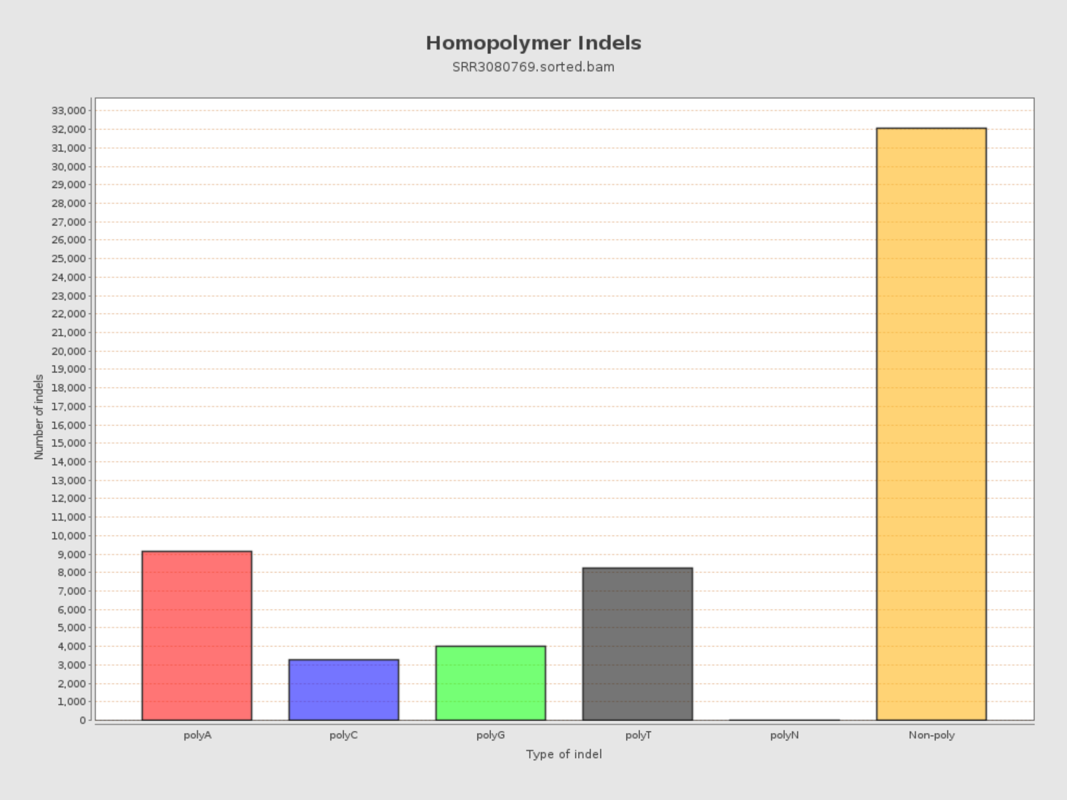
9. Results : Mapped Reads GC-content Distribution



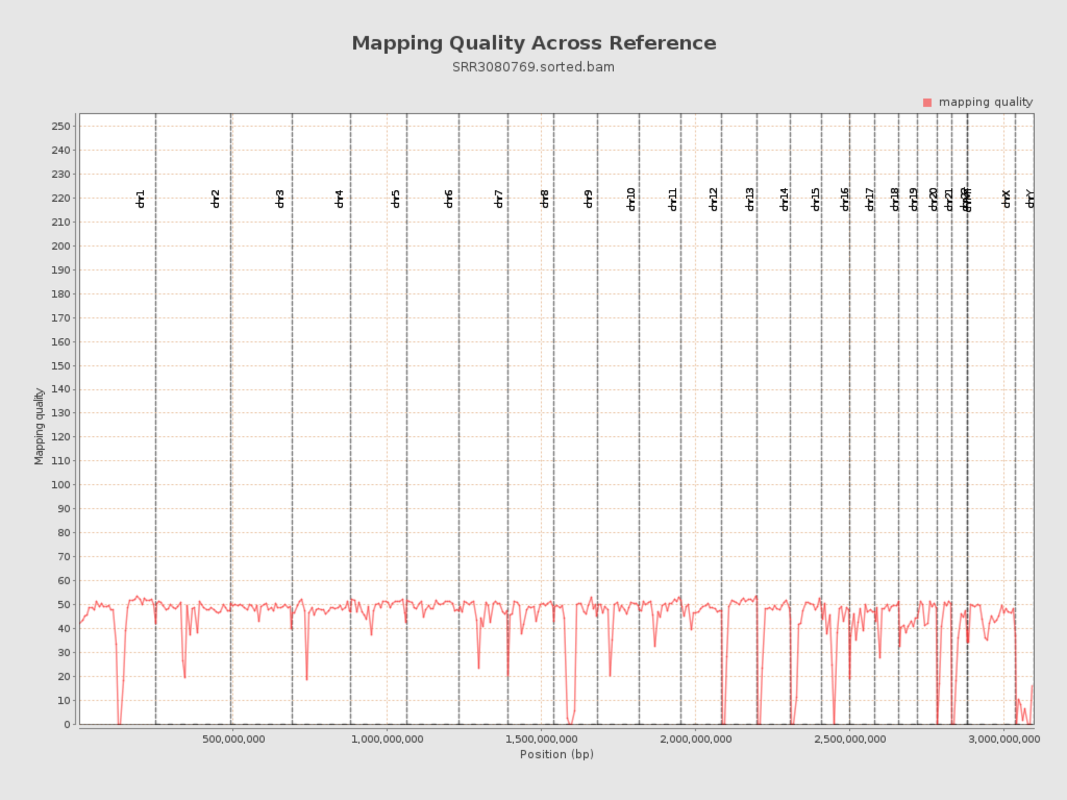
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram