Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:08:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080775.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_SRR3080775 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080775.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:08:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080775.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,376,849
Mapped reads	2,095,618 / 88.17%
Unmapped reads	281,231 / 11.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,418 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	97,460 / 4.1%
Duplication rate	3.78%
Clipped reads	951,664 / 40.04%

2.2. ACGT Content

Number/percentage of A's	39,183,746 / 27.98%
Number/percentage of C's	27,274,799 / 19.48%
Number/percentage of T's	42,501,693 / 30.35%
Number/percentage of G's	31,062,654 / 22.18%
Number/percentage of N's	2,822 / 0%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0452

Standard Deviation	0.3685

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

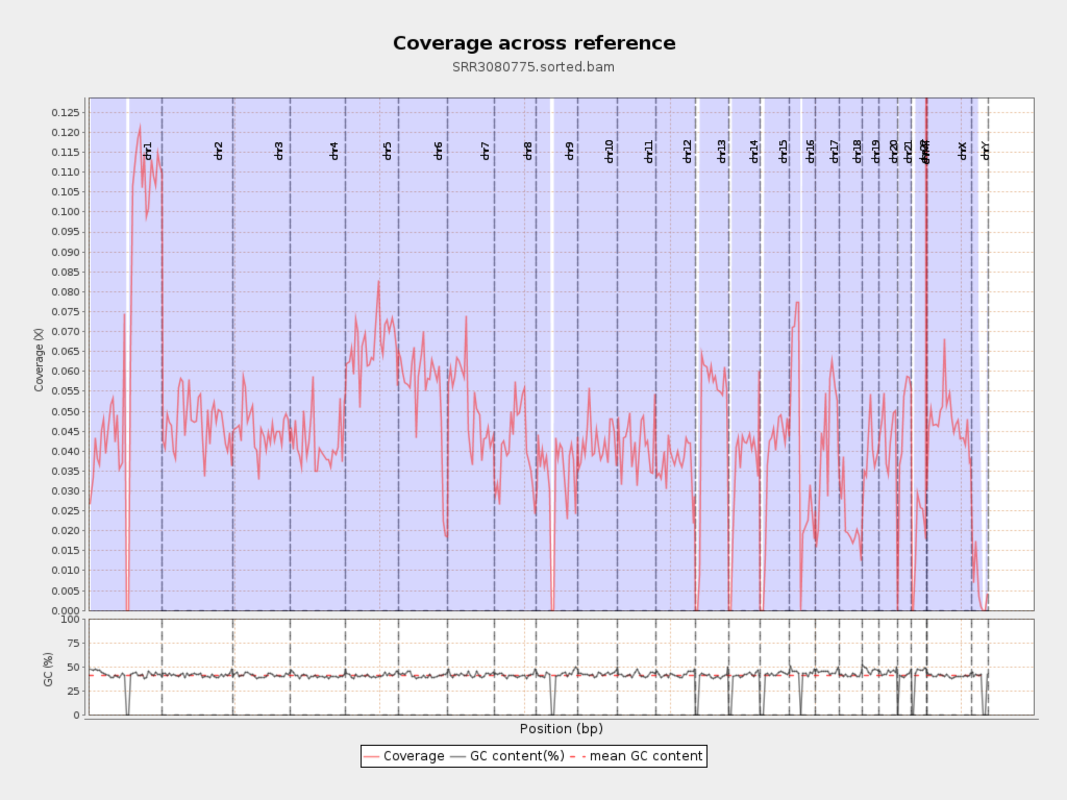
General error rate	0.78%
Mismatches	1,074,608
Insertions	10,867
Mapped reads with at least one insertion	0.51%
Deletions	31,195
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.62%

2.6. Chromosome stats

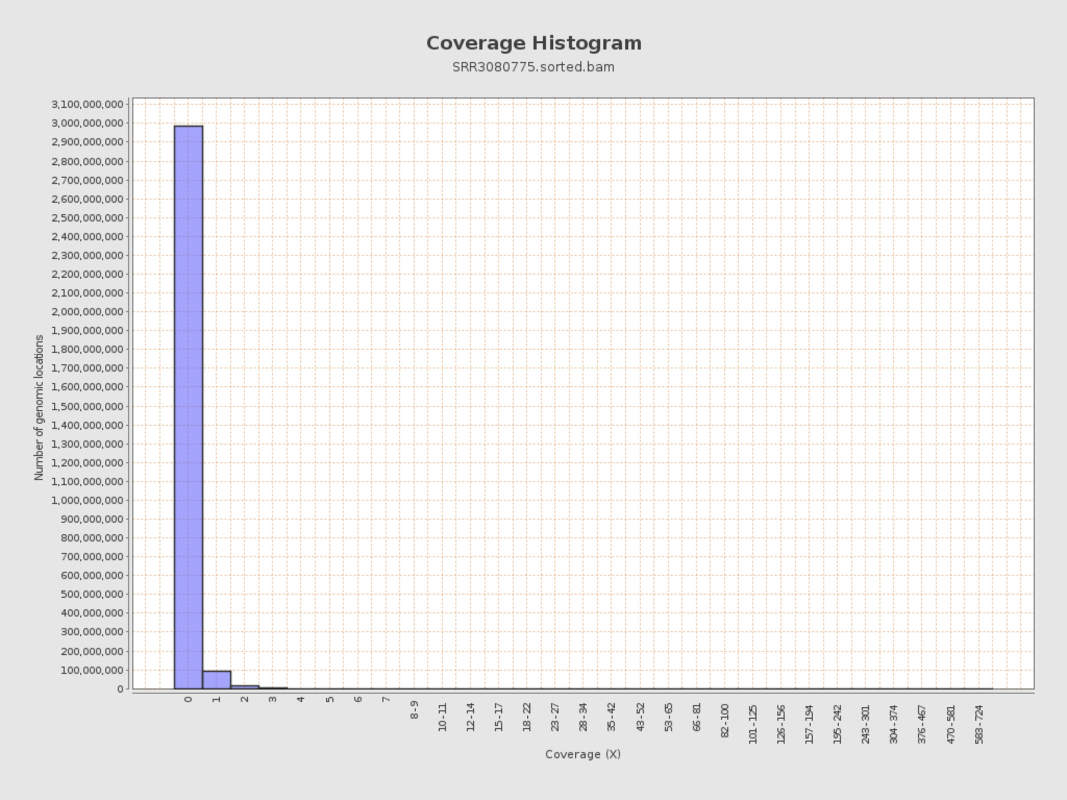
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17236574	0.0692	0.6821
chr2	243199373	11484782	0.0472	0.4108
chr3	198022430	9022813	0.0456	0.2558
chr4	191154276	8031858	0.042	0.2637
chr5	180915260	12077512	0.0668	0.3131
chr6	171115067	9403057	0.055	0.3345
chr7	159138663	8189550	0.0515	0.5213

chr8	146364022	6010051	0.0411	0.4017
chr9	141213431	4601203	0.0326	0.2946
chr10	135534747	5703891	0.0421	0.3033
chr11	135006516	5683564	0.0421	0.2892
chr12	133851895	4947626	0.037	0.2344
chr13	115169878	5582678	0.0485	0.2667
chr14	107349540	3689272	0.0344	0.2409
chr15	102531392	3650486	0.0356	0.2355
chr16	90354753	3622594	0.0401	0.2594
chr17	81195210	3520235	0.0434	0.2669
chr18	78077248	1713112	0.0219	0.53
chr19	59128983	2345558	0.0397	0.476
chr20	63025520	2777167	0.0441	0.2588
chr21	48129895	2186768	0.0454	0.2701
chr22	51304566	915151	0.0178	0.1556
chrMT	16571	14427	0.8706	1.1503
chrX	155270560	7329716	0.0472	0.2791
chrY	59373566	336143	0.0057	0.1329

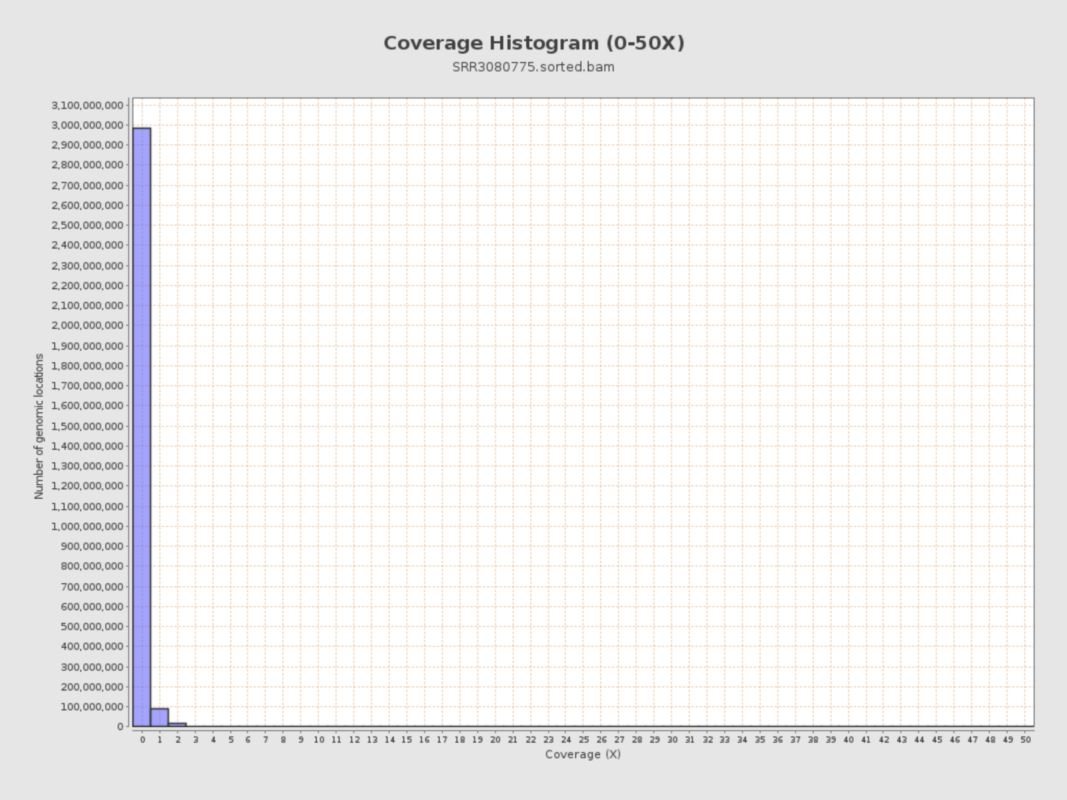
3. Results : Coverage across reference



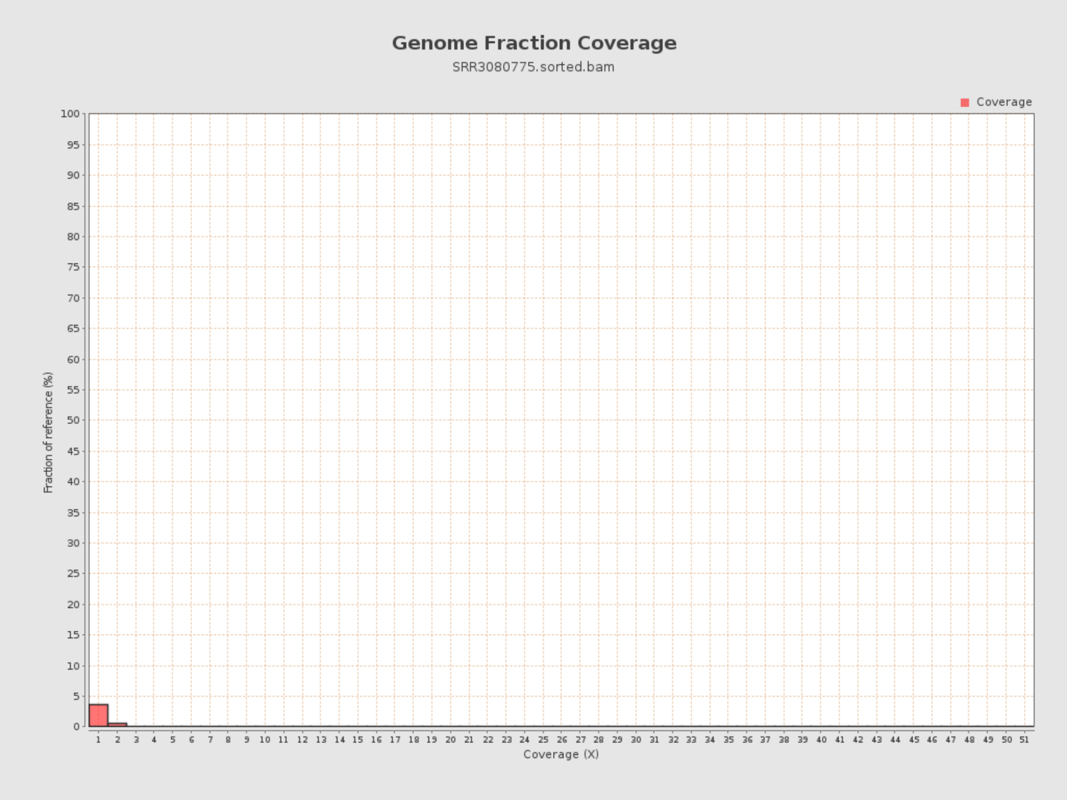
4. Results : Coverage Histogram



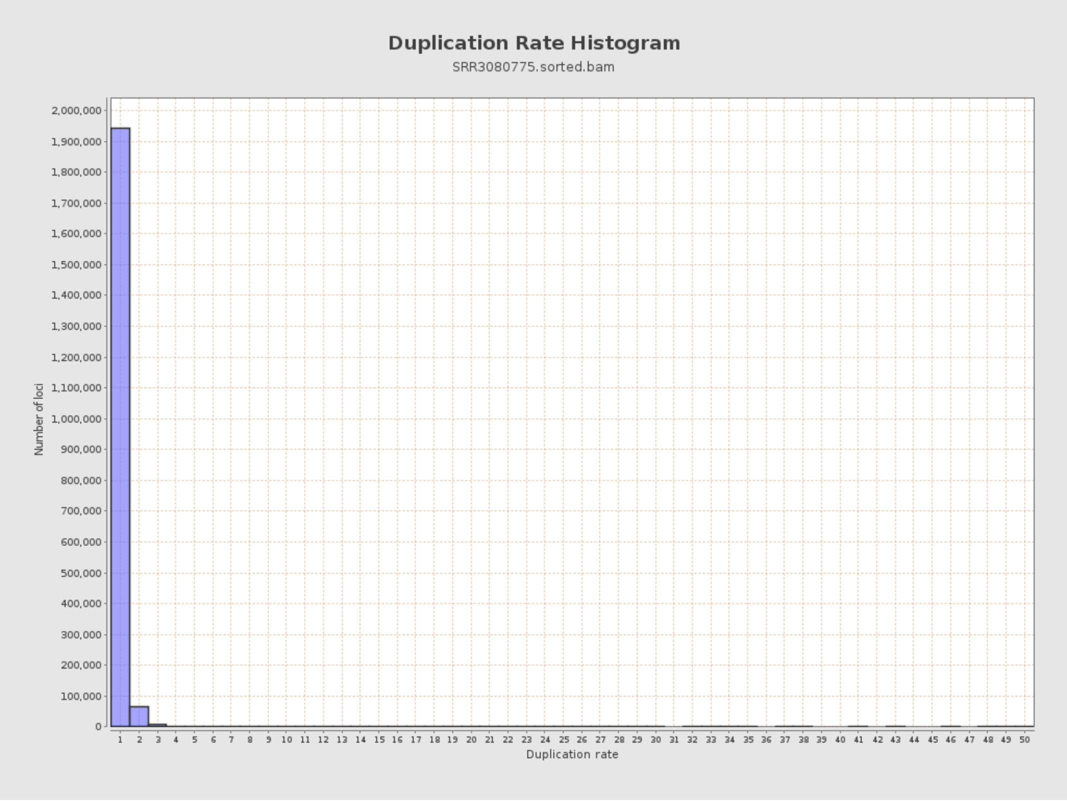
5. Results : Coverage Histogram (0-50X)



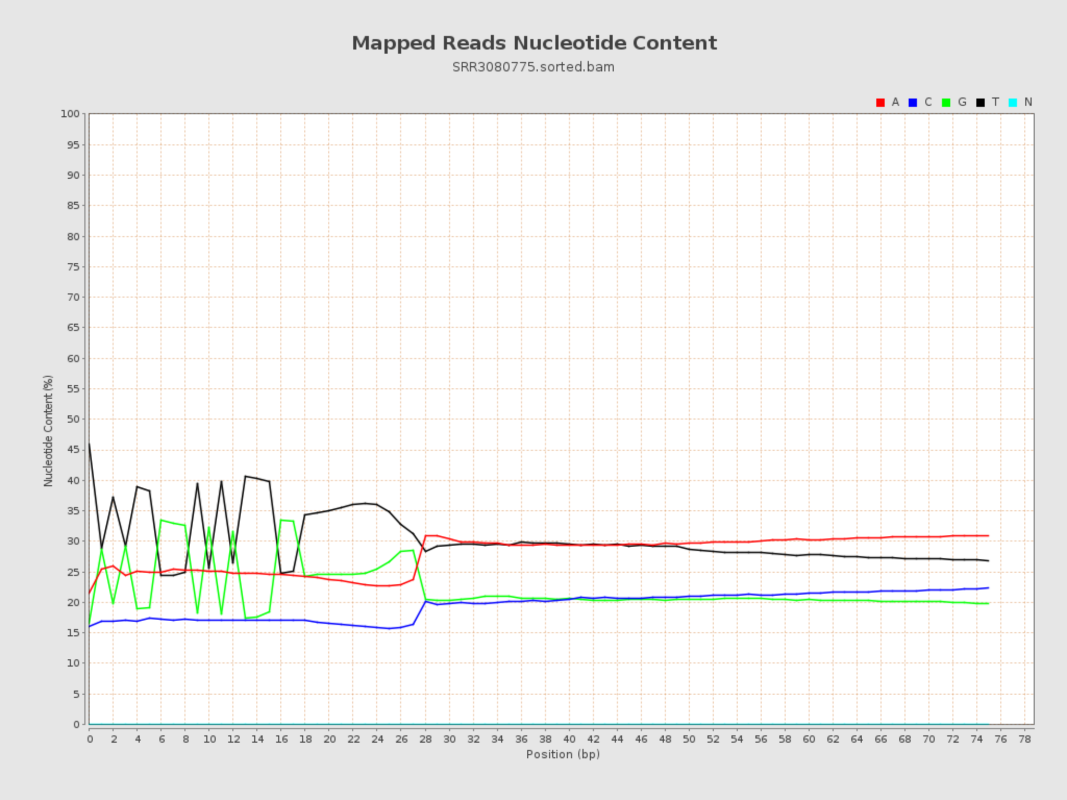
6. Results : Genome Fraction Coverage



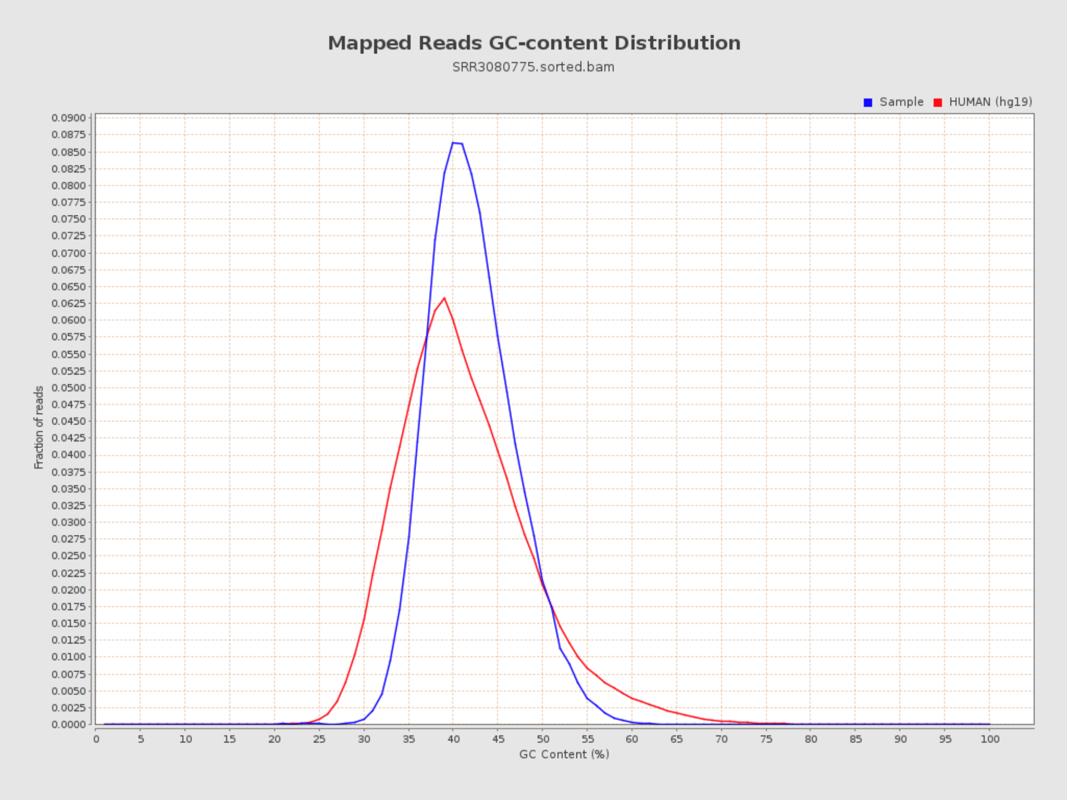
7. Results : Duplication Rate Histogram



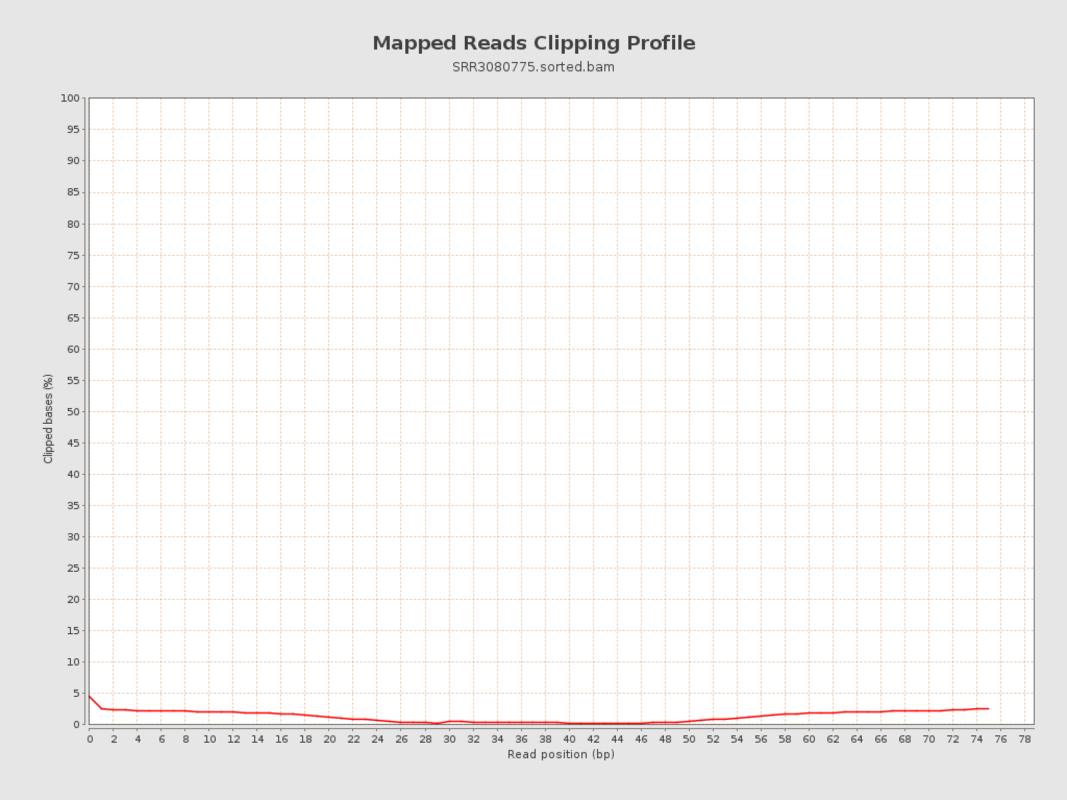
8. Results : Mapped Reads Nucleotide Content



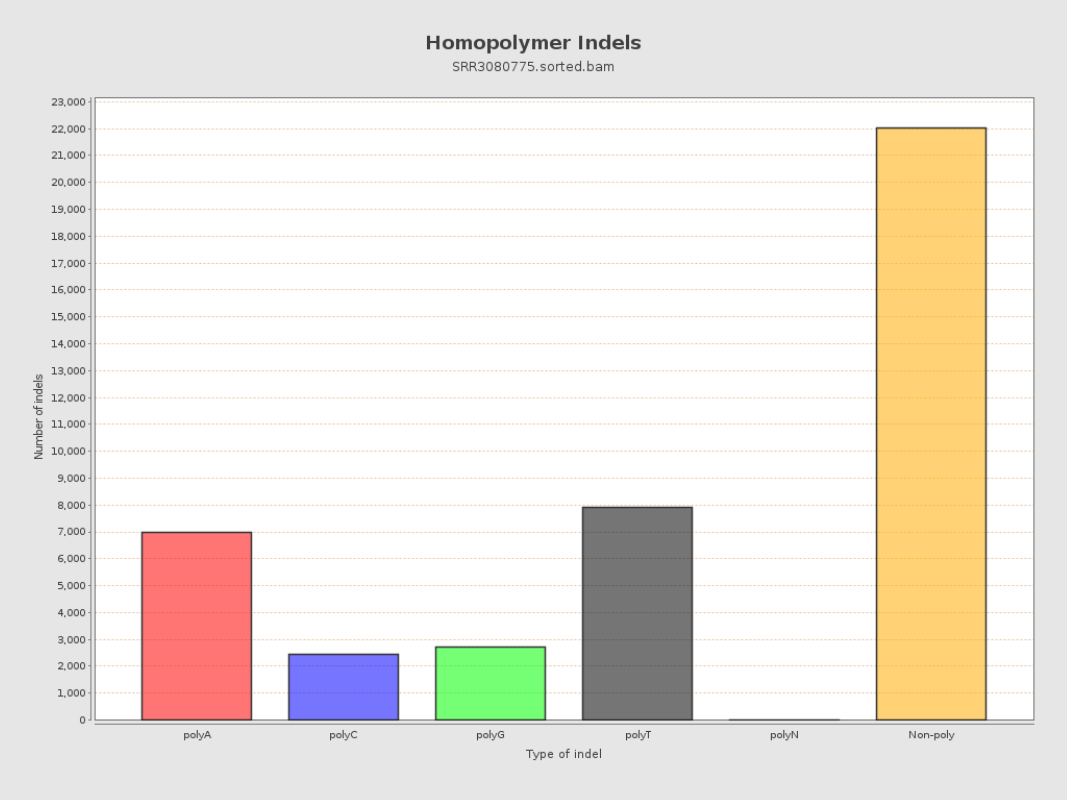
9. Results : Mapped Reads GC-content Distribution



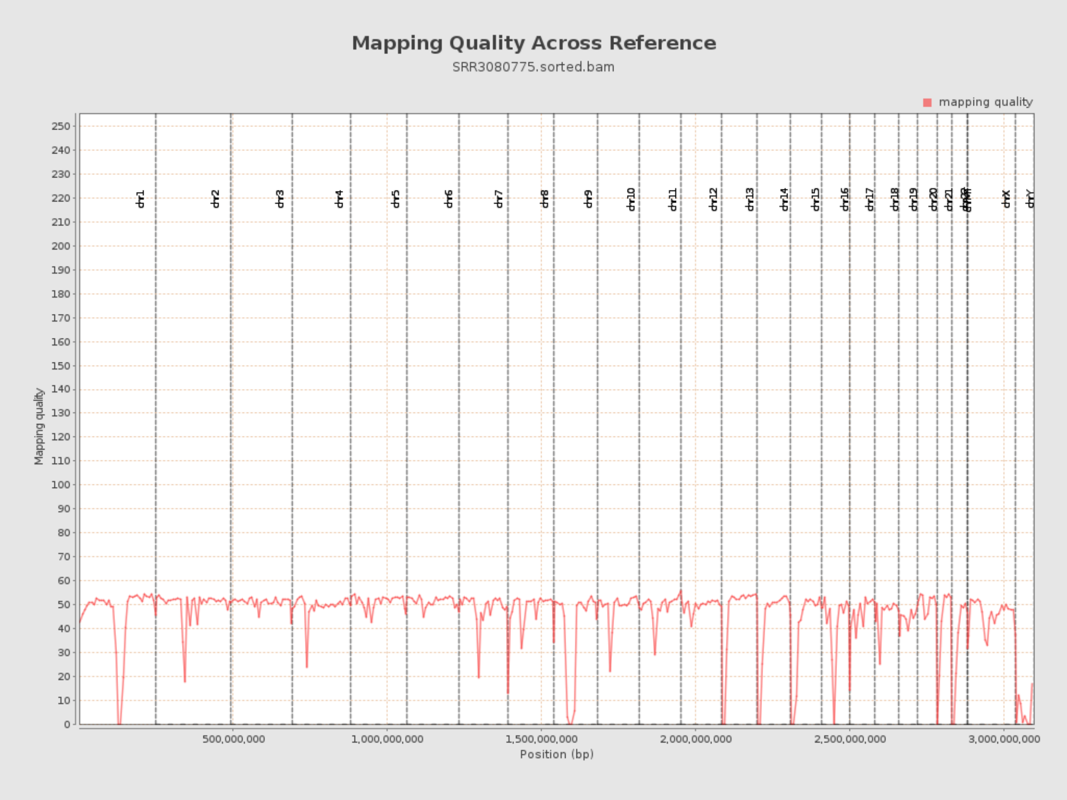
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram