Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:54:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080773.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_SRR3080773 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080773.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:54:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080773.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,930,324
Mapped reads	2,629,152 / 89.72%
Unmapped reads	301,172 / 10.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,360 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	151,855 / 5.18%
Duplication rate	4.55%
Clipped reads	1,162,906 / 39.69%

2.2. ACGT Content

Number/percentage of A's	50,508,429 / 28.51%
Number/percentage of C's	34,637,951 / 19.55%
Number/percentage of T's	53,673,991 / 30.3%
Number/percentage of G's	38,312,690 / 21.63%
Number/percentage of N's	3,774 / 0%
GC Percentage	41.18%

2.3. Coverage

Mean	0.0572

Standard Deviation	0.5

2.4. Mapping Quality

Mean Mapping Quality	46.76

2.5. Mismatches and indels

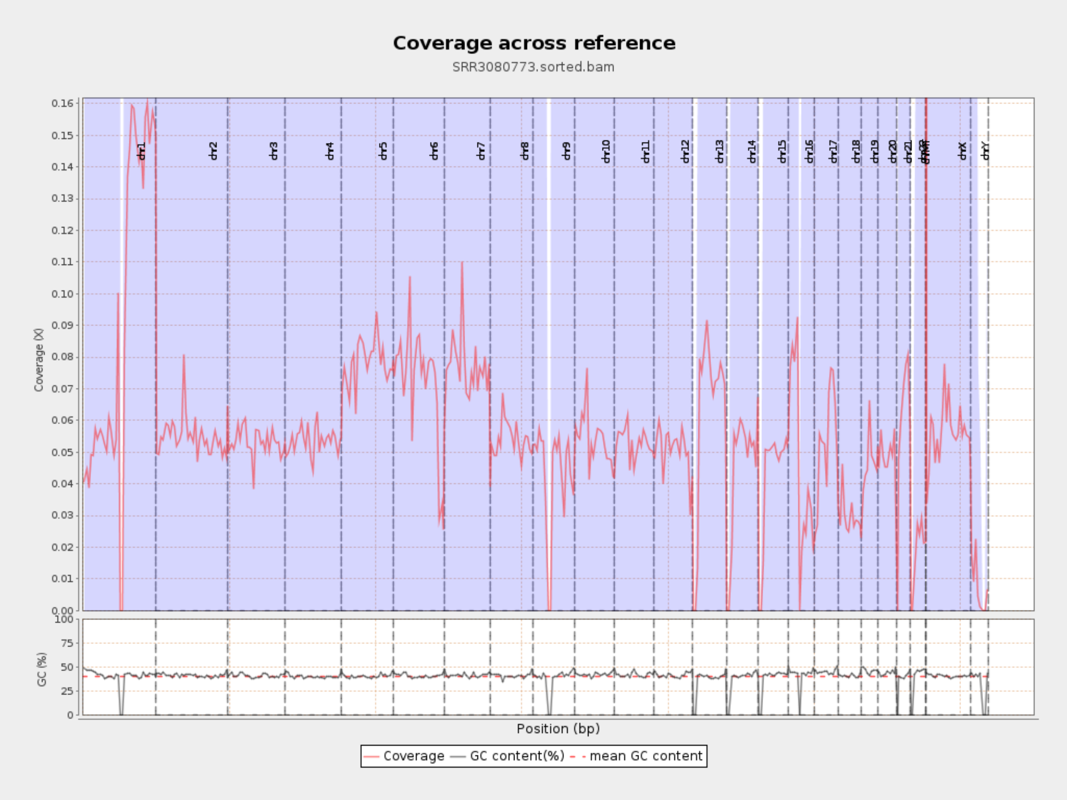
General error rate	0.78%
Mismatches	1,355,829
Insertions	13,577
Mapped reads with at least one insertion	0.51%
Deletions	39,455
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.2%

2.6. Chromosome stats

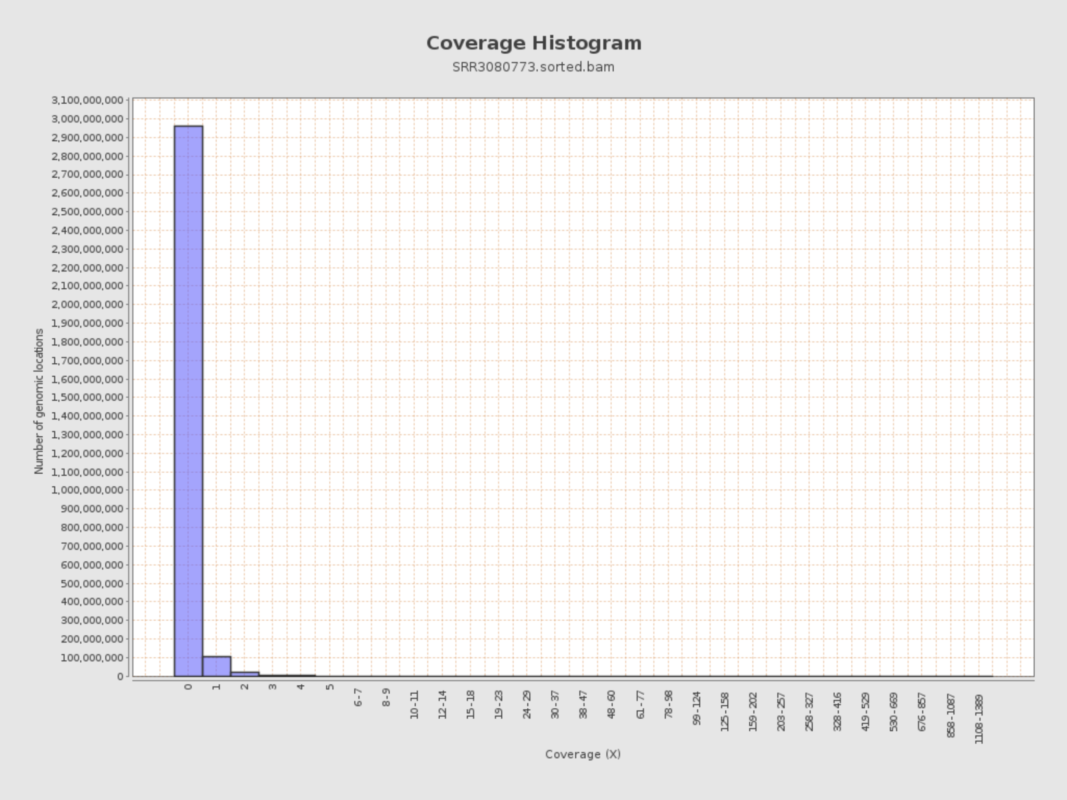
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22674733	0.091	0.953
chr2	243199373	13359299	0.0549	0.4618
chr3	198022430	10529677	0.0532	0.2879
chr4	191154276	10254901	0.0536	0.308
chr5	180915260	14168895	0.0783	0.3522
chr6	171115067	12464650	0.0728	0.4806
chr7	159138663	12311088	0.0774	0.7358

chr8	146364022	7942663	0.0543	0.8843
chr9	141213431	6033324	0.0427	0.3361
chr10	135534747	7331607	0.0541	0.4059
chr11	135006516	7128866	0.0528	0.359
chr12	133851895	6835642	0.0511	0.2872
chr13	115169878	7333243	0.0637	0.3208
chr14	107349540	4805741	0.0448	0.2779
chr15	102531392	4203357	0.041	0.2546
chr16	90354753	4080482	0.0452	0.2828
chr17	81195210	4363127	0.0537	0.3103
chr18	78077248	2348241	0.0301	0.6012
chr19	59128983	2741610	0.0464	0.6848
chr20	63025520	3115727	0.0494	0.2934
chr21	48129895	2899773	0.0602	0.3211
chr22	51304566	914623	0.0178	0.1615
chrMT	16571	166401	10.0417	6.5485
chrX	155270560	8761071	0.0564	0.3376
chrY	59373566	430894	0.0073	0.1606

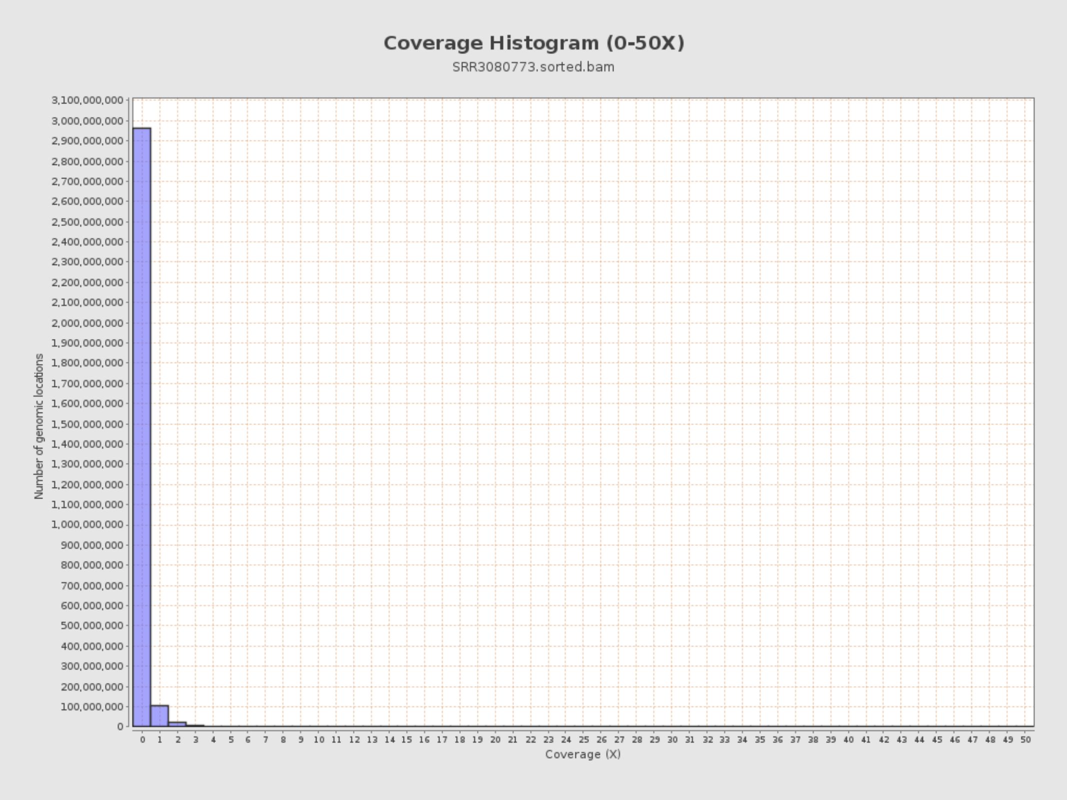
3. Results : Coverage across reference



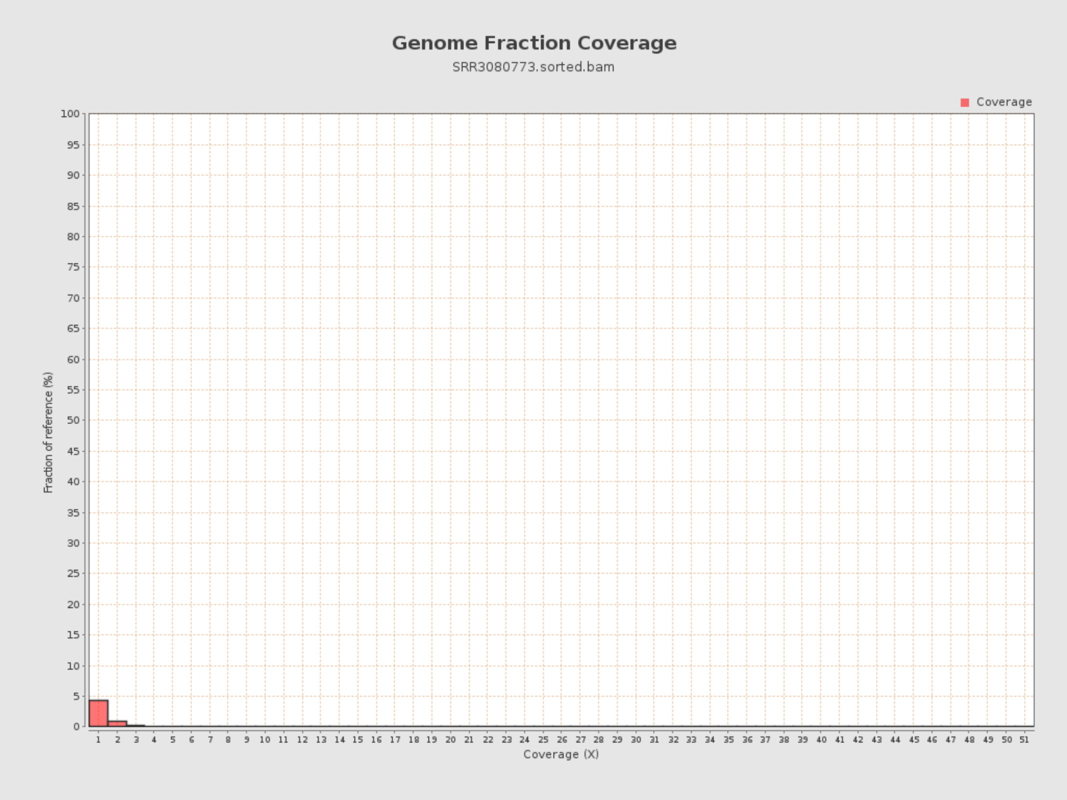
4. Results : Coverage Histogram



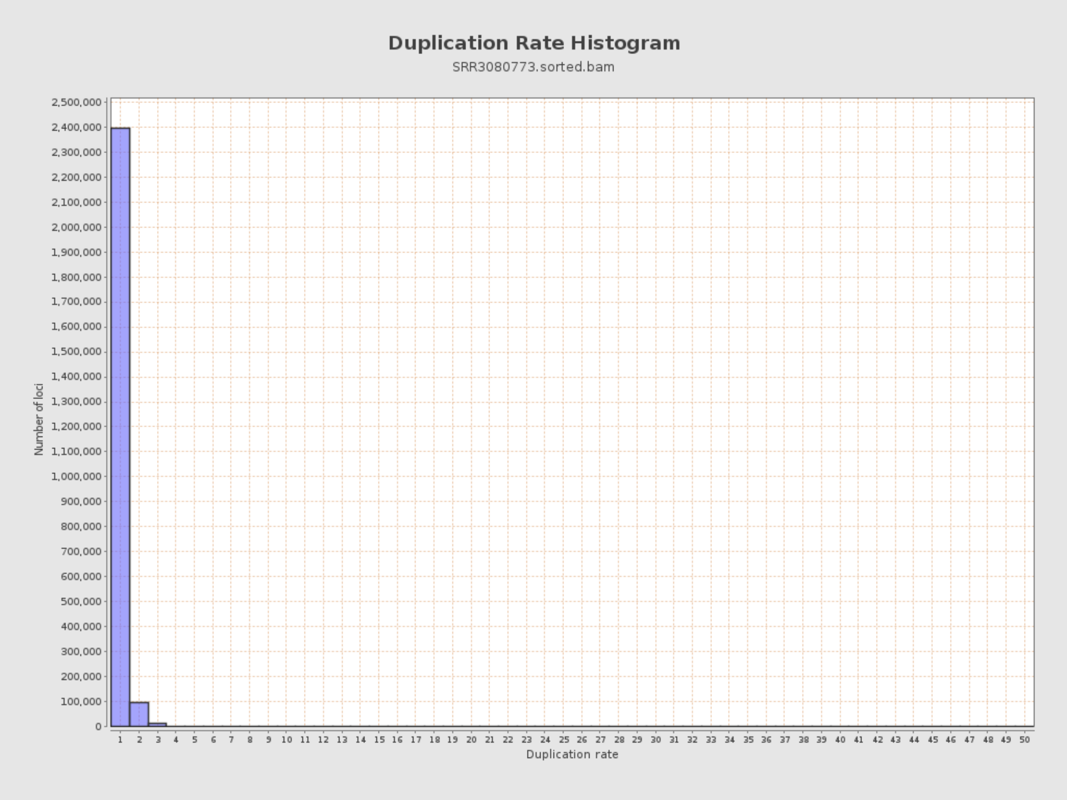
5. Results : Coverage Histogram (0-50X)



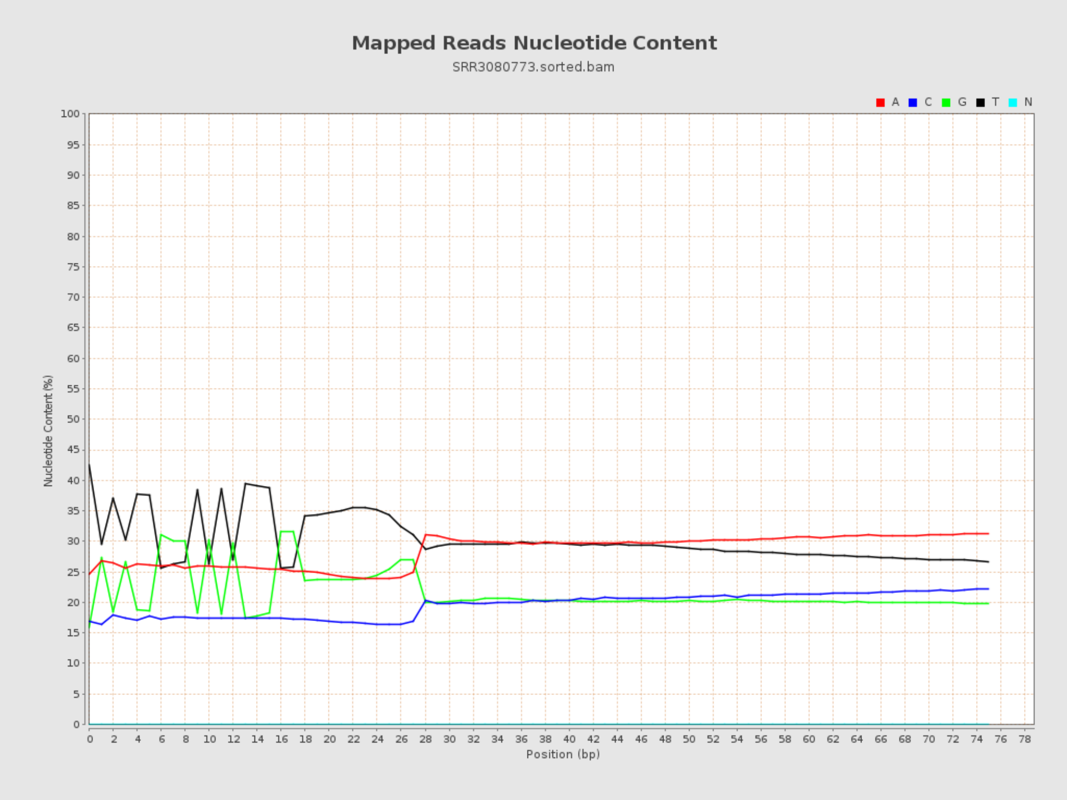
6. Results : Genome Fraction Coverage



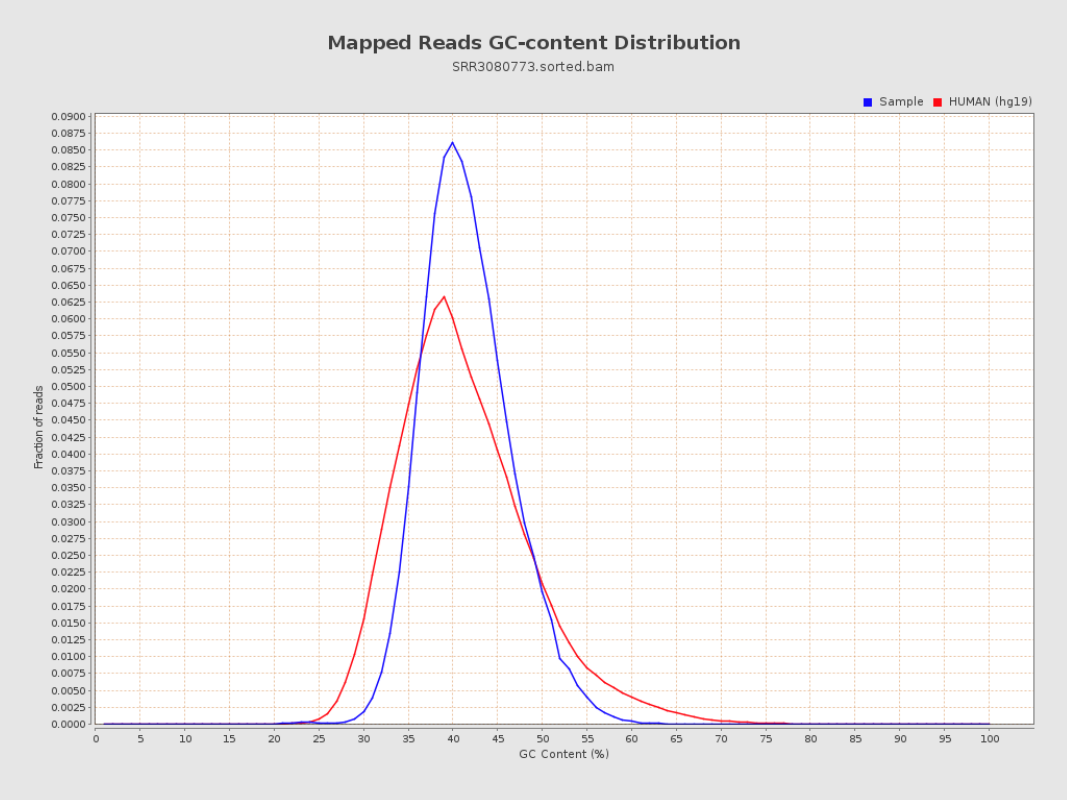
7. Results : Duplication Rate Histogram



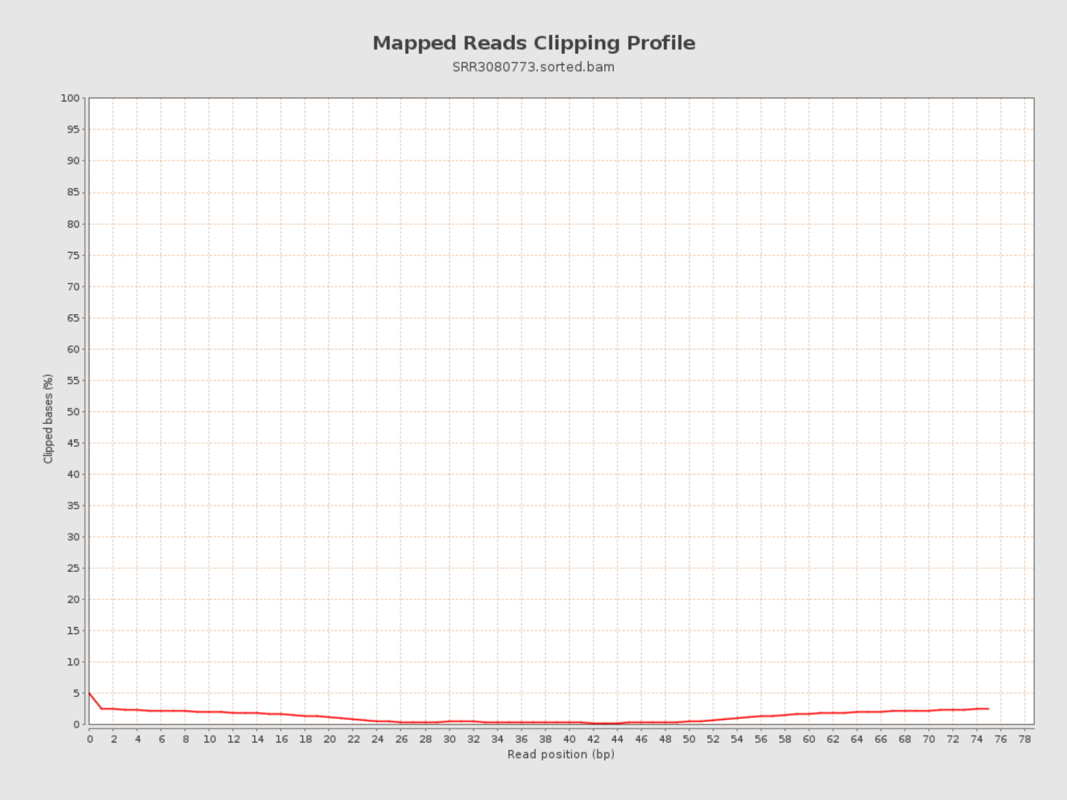
8. Results : Mapped Reads Nucleotide Content



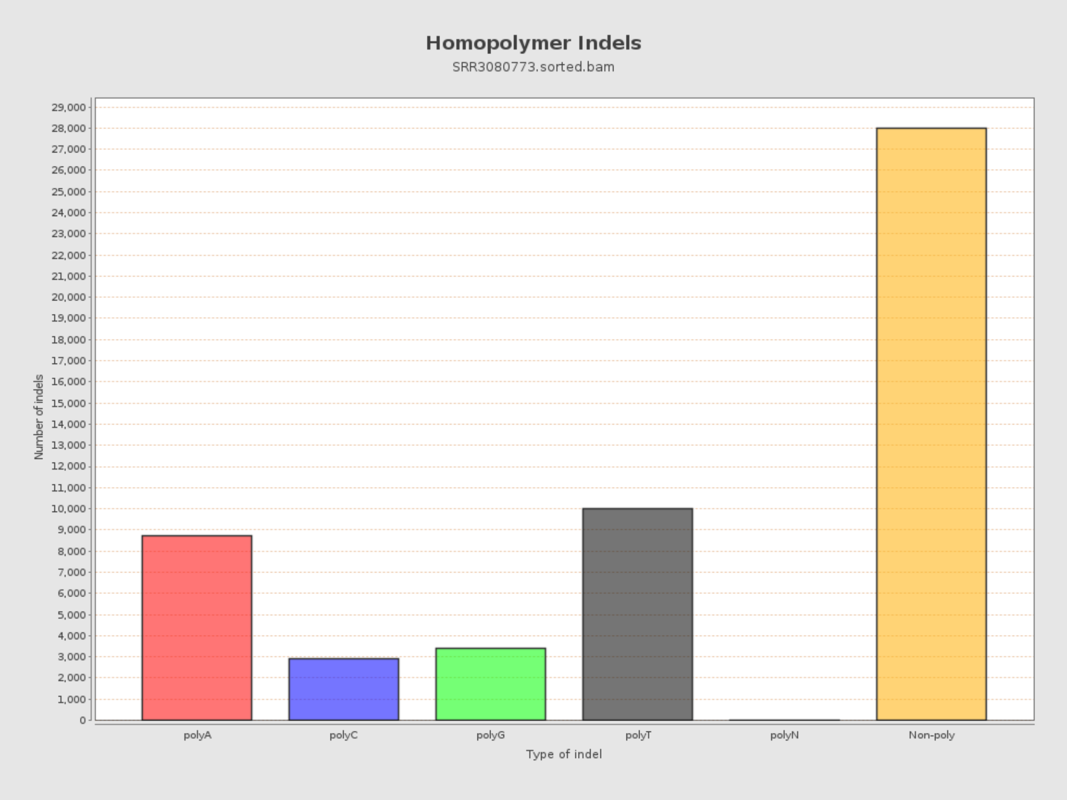
9. Results : Mapped Reads GC-content Distribution



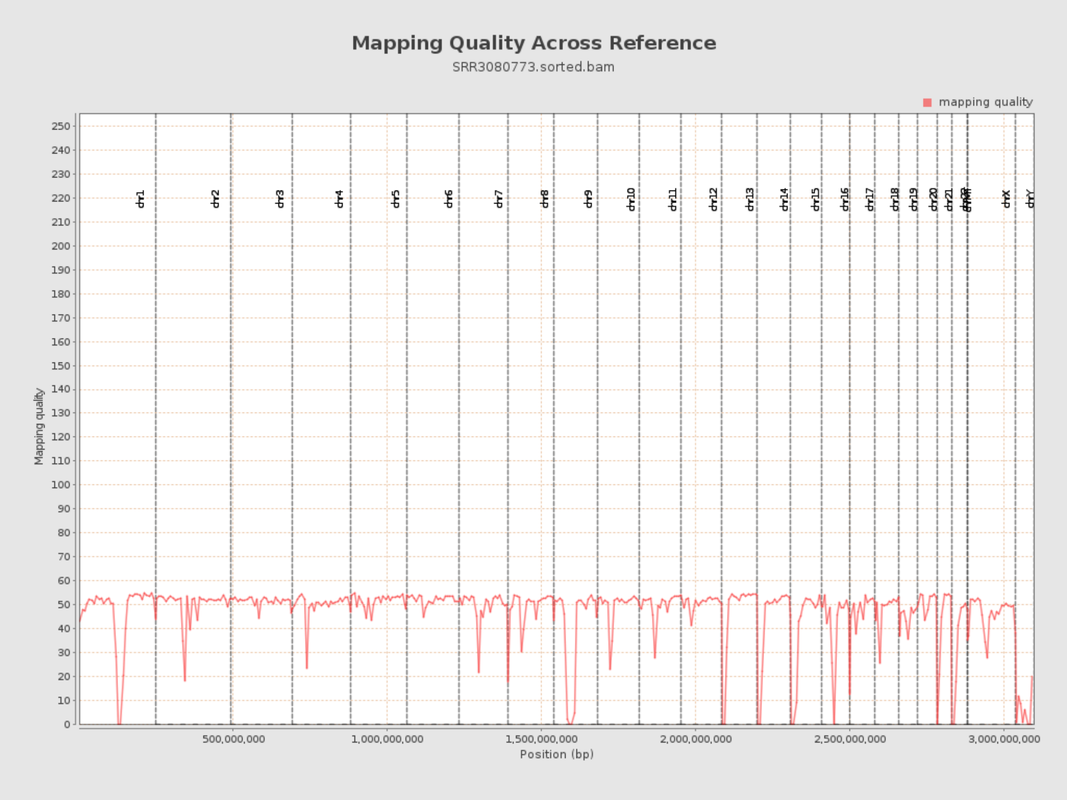
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram