Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:55:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080992.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_SRR3080992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080992.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:55:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,118,966
Mapped reads	2,820,745 / 90.44%
Unmapped reads	298,221 / 9.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,519 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	121,248 / 3.89%
Duplication rate	2.91%
Clipped reads	1,292,493 / 41.44%

2.2. ACGT Content

Number/percentage of A's	51,336,573 / 27.49%
Number/percentage of C's	37,051,004 / 19.84%
Number/percentage of T's	55,846,495 / 29.9%
Number/percentage of G's	42,531,470 / 22.77%
Number/percentage of N's	2,473 / 0%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0604

Standard Deviation	0.5783

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

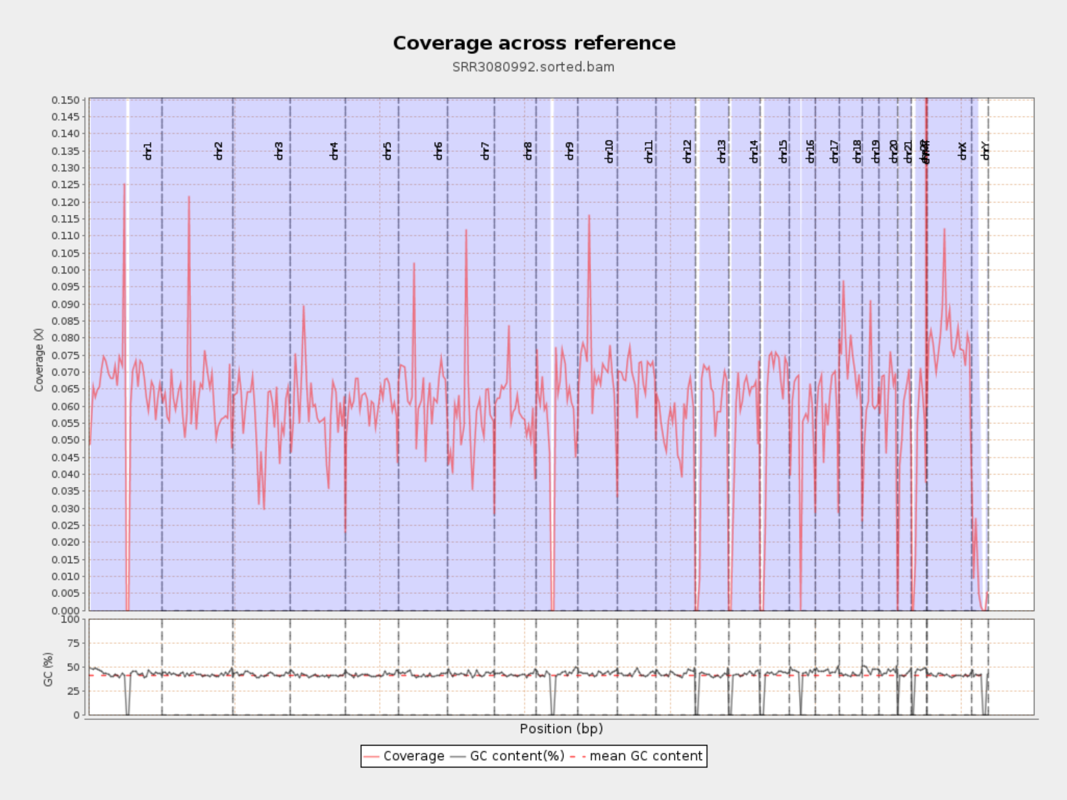
General error rate	0.77%
Mismatches	1,403,473
Insertions	13,628
Mapped reads with at least one insertion	0.48%
Deletions	36,787
Mapped reads with at least one deletion	1.29%
Homopolymer indels	45.95%

2.6. Chromosome stats

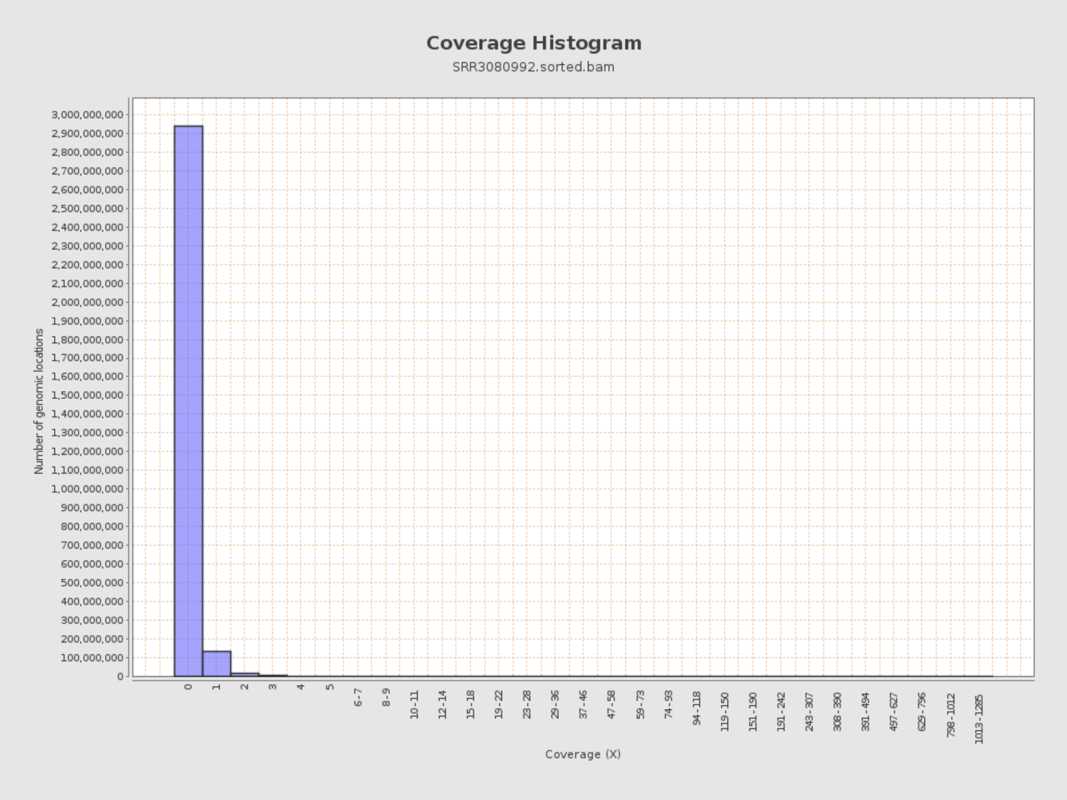
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16092773	0.0646	1.0875
chr2	243199373	15323590	0.063	0.6752
chr3	198022430	11253053	0.0568	0.2754
chr4	191154276	11401227	0.0596	0.3352
chr5	180915260	11095751	0.0613	0.2941
chr6	171115067	11119006	0.065	0.497
chr7	159138663	9101609	0.0572	0.9157

chr8	146364022	8703726	0.0595	0.5232
chr9	141213431	7938174	0.0562	0.541
chr10	135534747	9761697	0.072	0.5351
chr11	135006516	9270526	0.0687	0.5179
chr12	133851895	7386825	0.0552	0.2855
chr13	115169878	6201260	0.0538	0.266
chr14	107349540	5673975	0.0529	0.325
chr15	102531392	5893504	0.0575	0.2992
chr16	90354753	4889171	0.0541	0.3332
chr17	81195210	4808039	0.0592	0.3654
chr18	78077248	5825947	0.0746	1.1514
chr19	59128983	3617921	0.0612	0.7836
chr20	63025520	3985295	0.0632	0.3186
chr21	48129895	2488820	0.0517	0.3286
chr22	51304566	2082324	0.0406	0.2336
chrMT	16571	56331	3.3994	2.522
chrX	155270560	12354239	0.0796	0.4196
chrY	59373566	508391	0.0086	0.2169

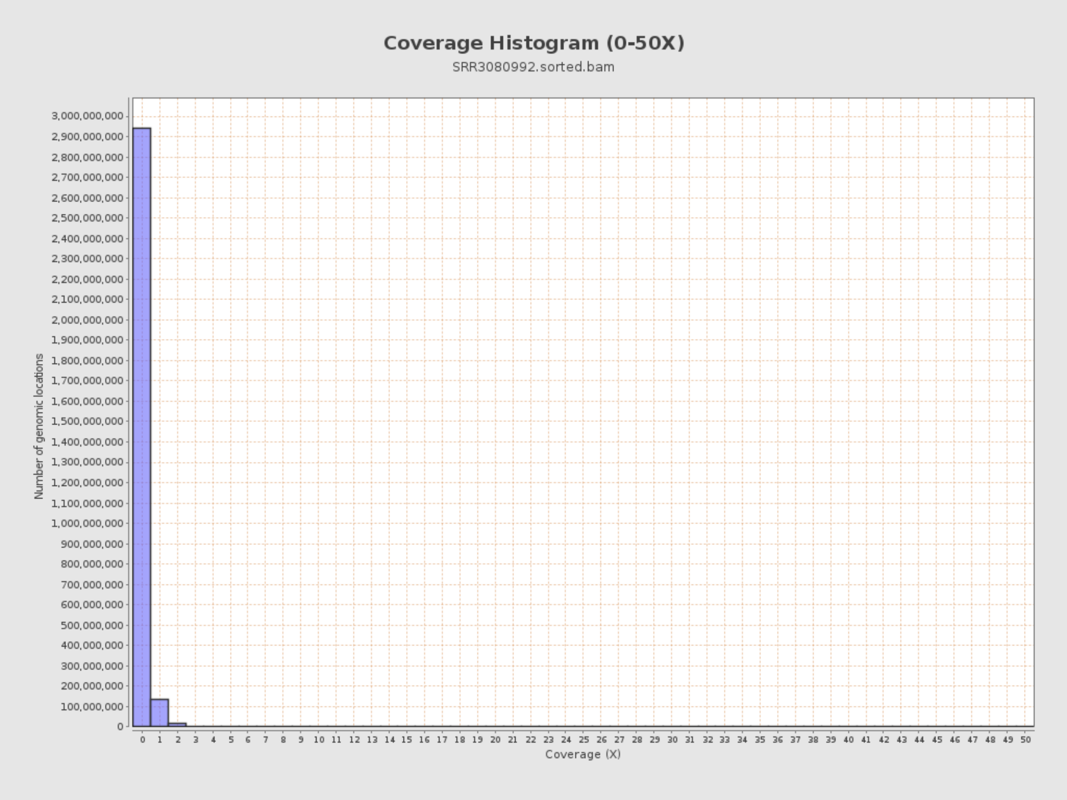
3. Results : Coverage across reference



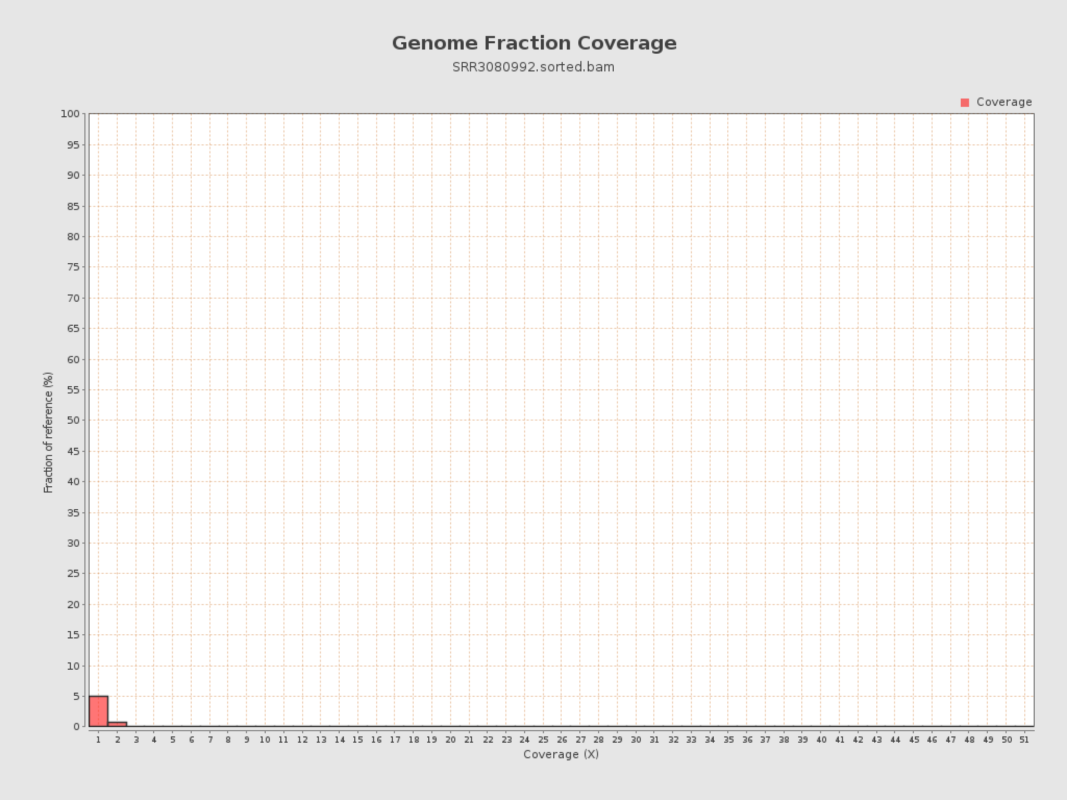
4. Results : Coverage Histogram



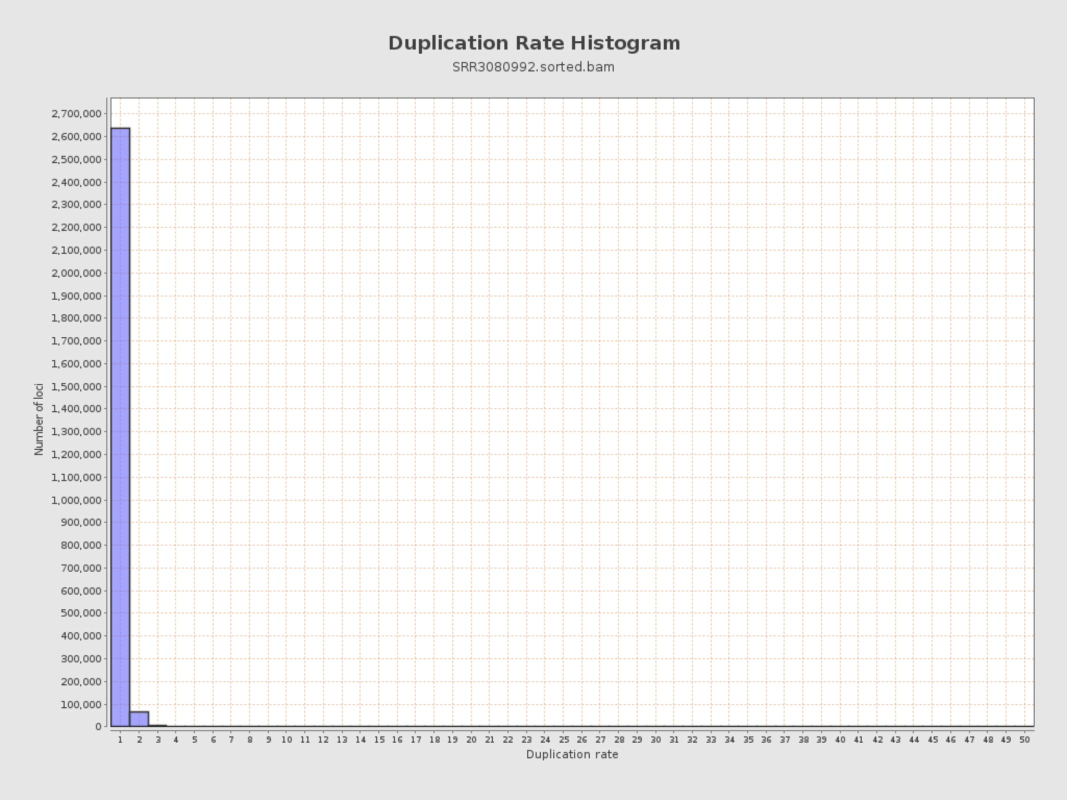
5. Results : Coverage Histogram (0-50X)



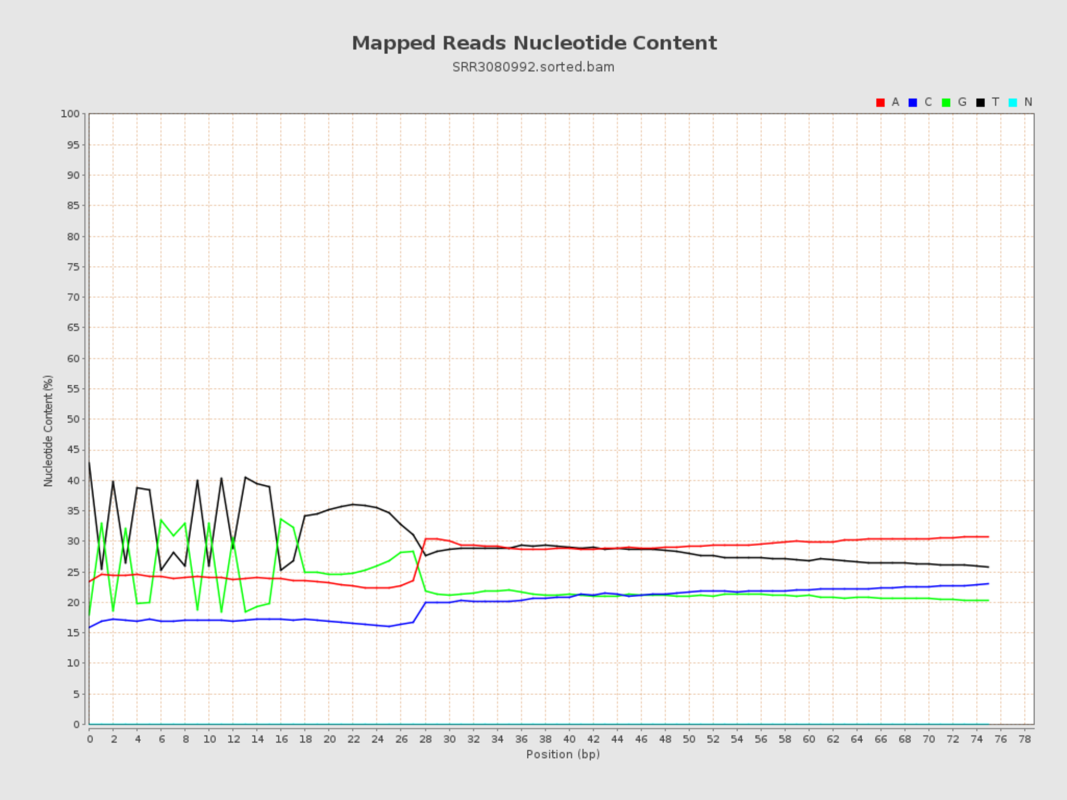
6. Results : Genome Fraction Coverage



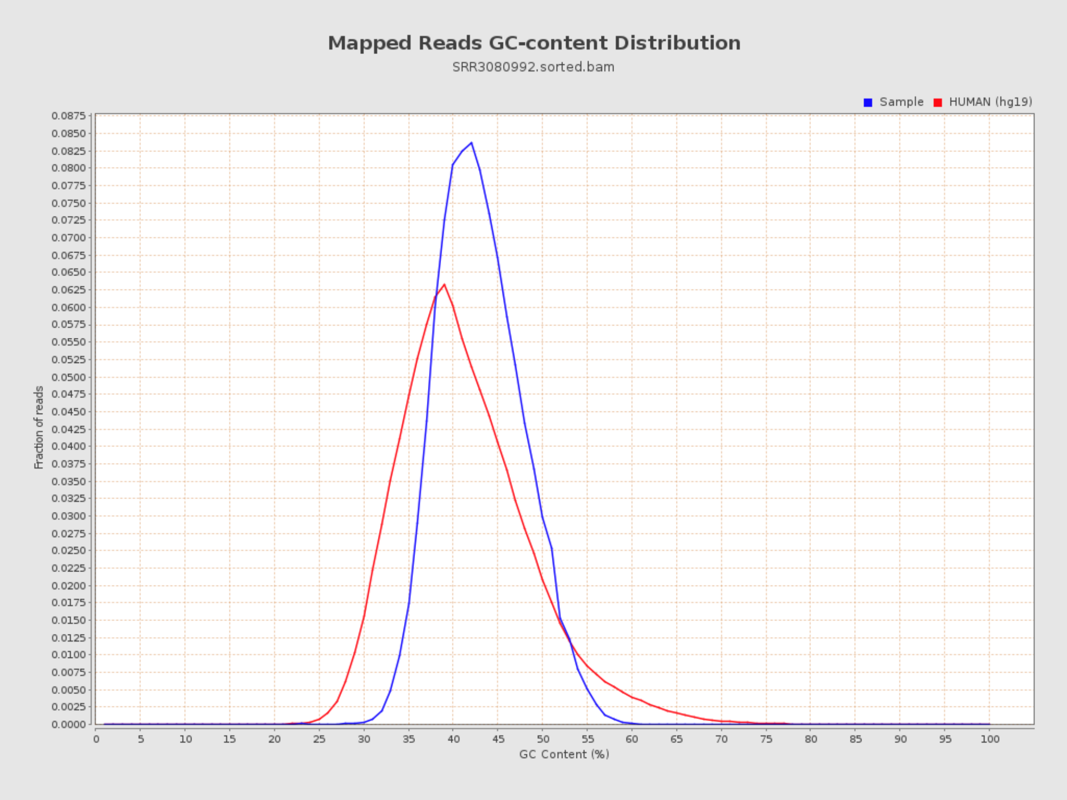
7. Results : Duplication Rate Histogram



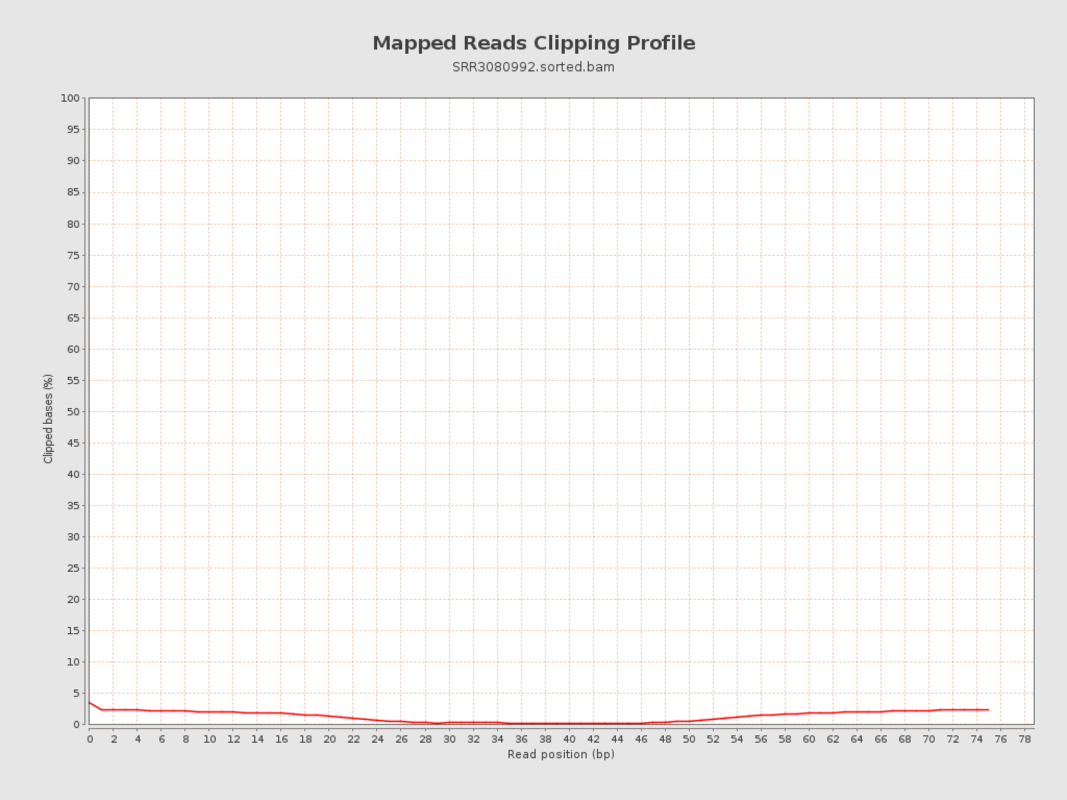
8. Results : Mapped Reads Nucleotide Content



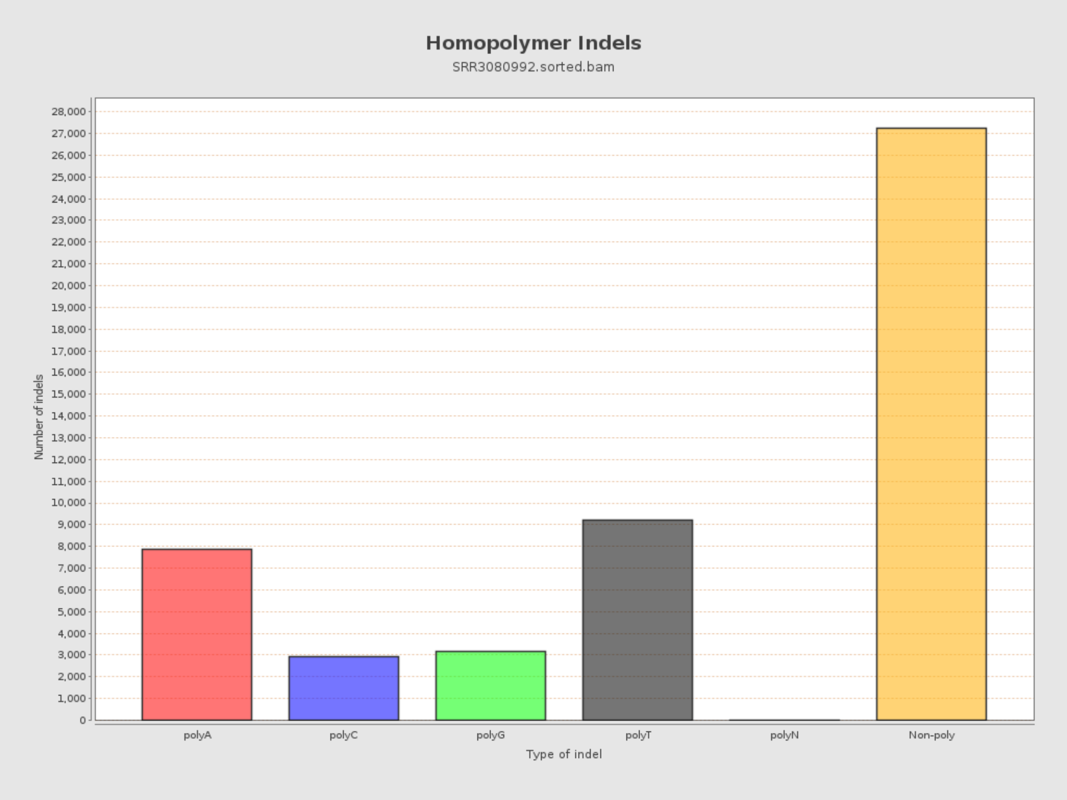
9. Results : Mapped Reads GC-content Distribution



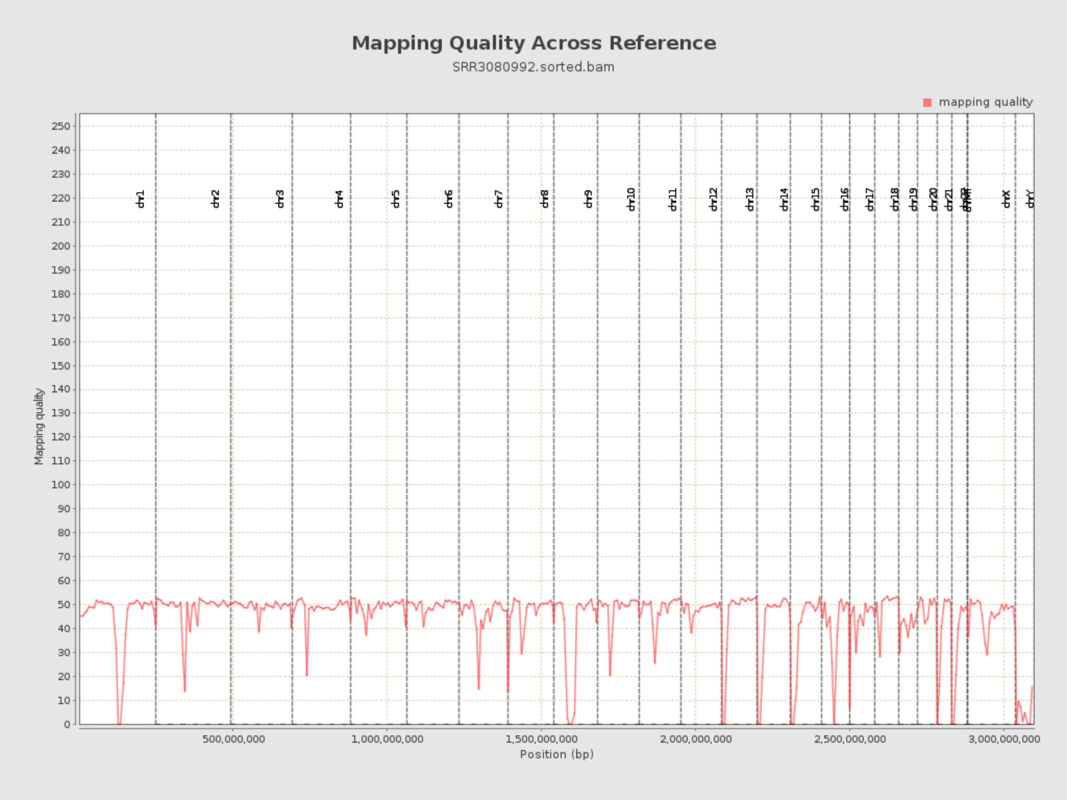
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram