Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:50:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080990.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_SRR3080990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080990.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:50:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,232,312
Mapped reads	2,879,201 / 89.08%
Unmapped reads	353,111 / 10.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,290 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	122,303 / 3.78%
Duplication rate	2.89%
Clipped reads	1,404,057 / 43.44%

2.2. ACGT Content

Number/percentage of A's	52,892,739 / 27.97%
Number/percentage of C's	37,274,239 / 19.71%
Number/percentage of T's	56,738,668 / 30.01%
Number/percentage of G's	42,169,449 / 22.3%
Number/percentage of N's	2,536 / 0%
GC Percentage	42.02%

2.3. Coverage

Mean	0.0611

Standard Deviation	0.5766

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

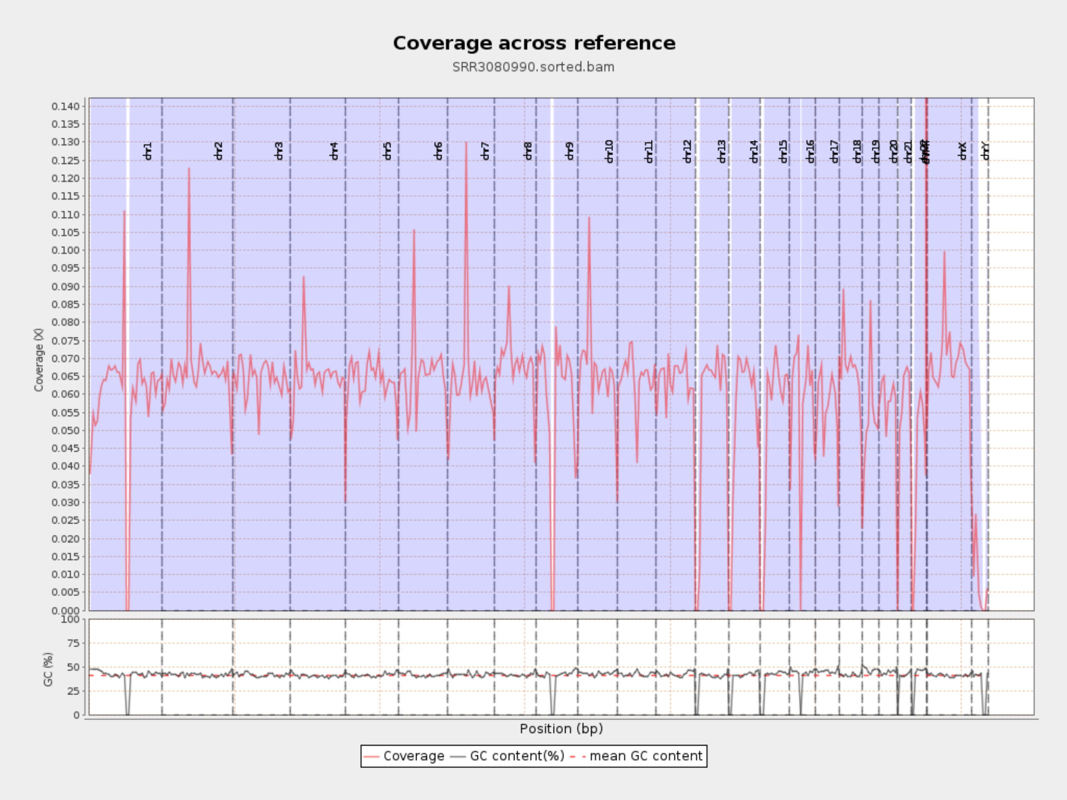
General error rate	0.78%
Mismatches	1,457,278
Insertions	13,895
Mapped reads with at least one insertion	0.48%
Deletions	36,680
Mapped reads with at least one deletion	1.26%
Homopolymer indels	45.79%

2.6. Chromosome stats

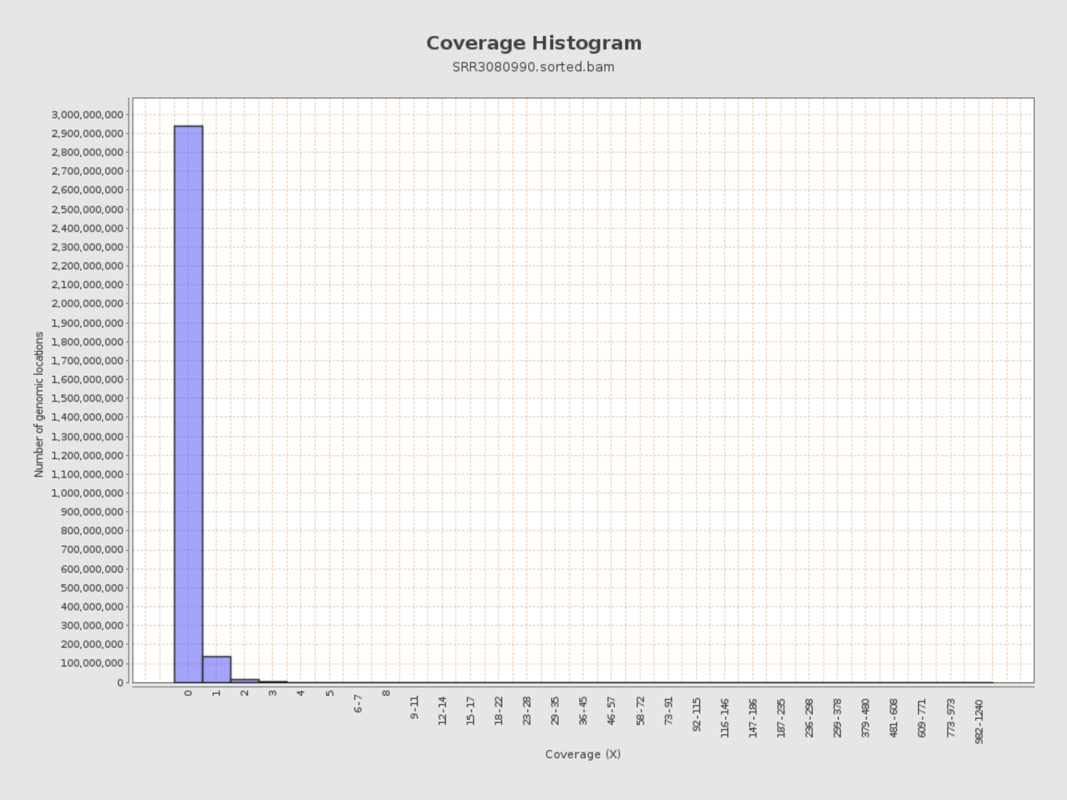
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14785895	0.0593	1.0333
chr2	243199373	16281165	0.0669	0.6419
chr3	198022430	12779603	0.0645	0.291
chr4	191154276	12492974	0.0654	0.3366
chr5	180915260	11597906	0.0641	0.2953
chr6	171115067	11331104	0.0662	0.48
chr7	159138663	10442189	0.0656	0.9673

chr8	146364022	10011114	0.0684	0.5617
chr9	141213431	8138749	0.0576	0.5763
chr10	135534747	9105508	0.0672	0.5111
chr11	135006516	8628005	0.0639	0.5539
chr12	133851895	8528965	0.0637	0.303
chr13	115169878	6340242	0.0551	0.2682
chr14	107349540	5718826	0.0533	0.3272
chr15	102531392	5319362	0.0519	0.2815
chr16	90354753	5223392	0.0578	0.3474
chr17	81195210	4532119	0.0558	0.3575
chr18	78077248	5316631	0.0681	1.2131
chr19	59128983	3179696	0.0538	0.7569
chr20	63025520	3630304	0.0576	0.3062
chr21	48129895	2545739	0.0529	0.3136
chr22	51304566	1930738	0.0376	0.2236
chrMT	16571	49548	2.99	2.2606
chrX	155270560	10736743	0.0691	0.3954
chrY	59373566	494808	0.0083	0.1987

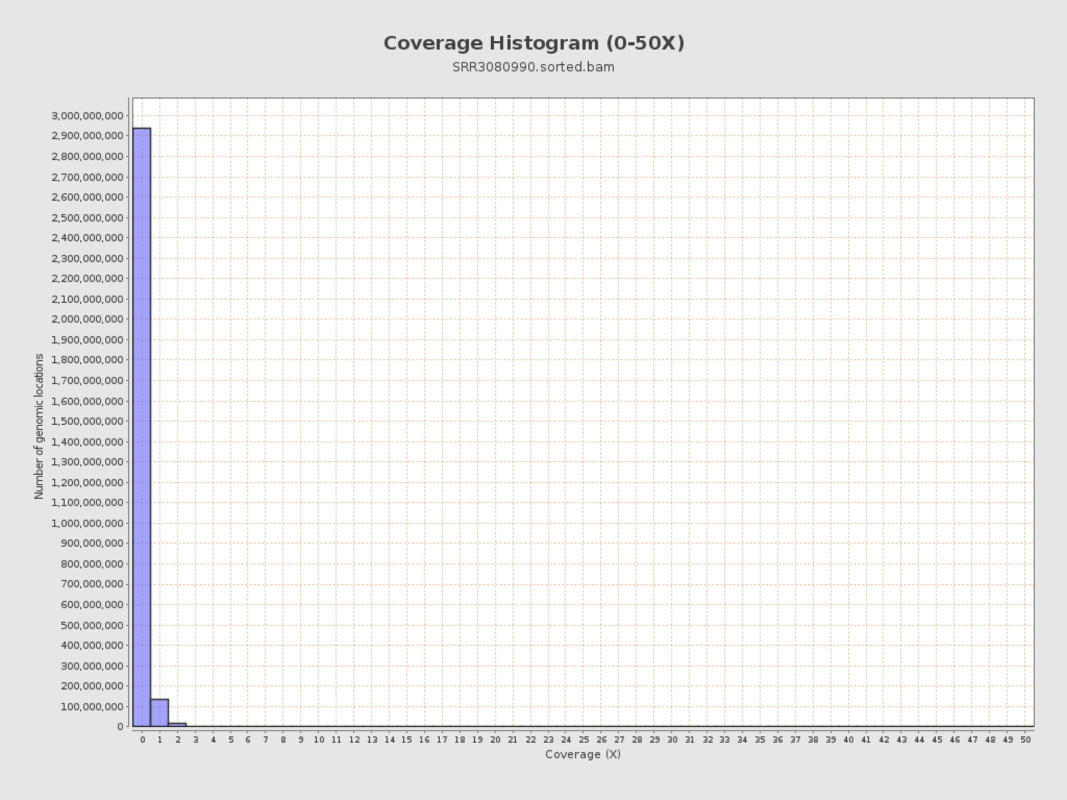
3. Results : Coverage across reference



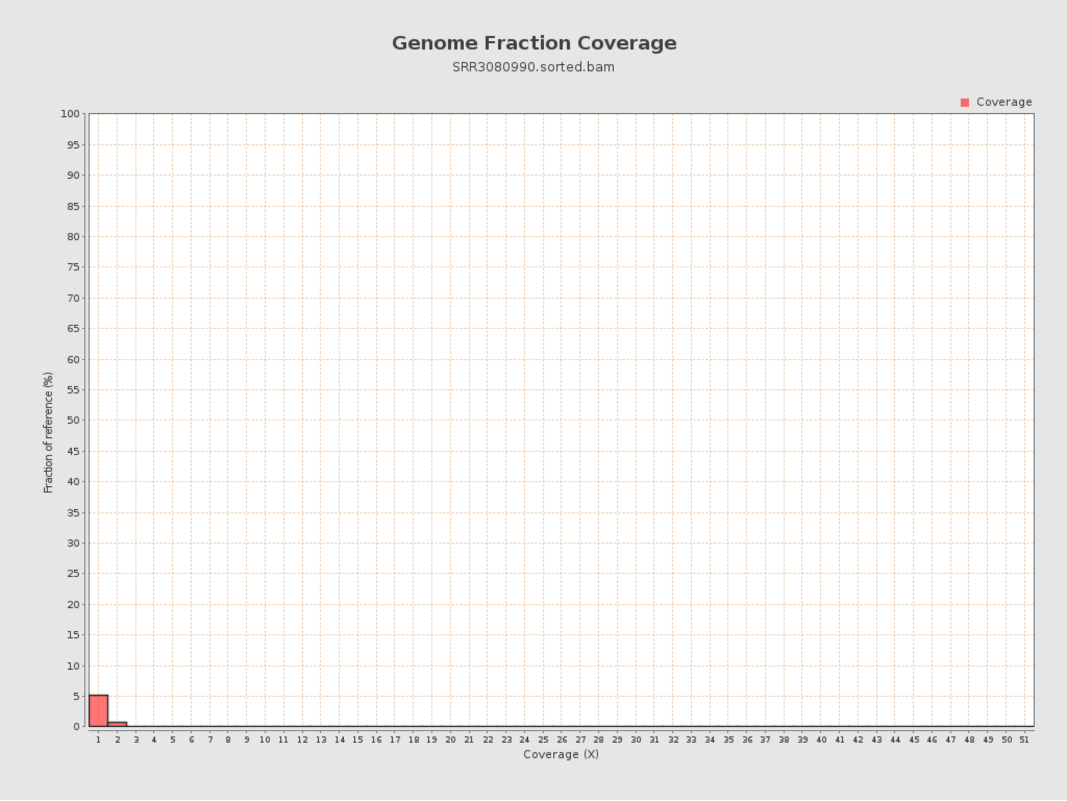
4. Results : Coverage Histogram



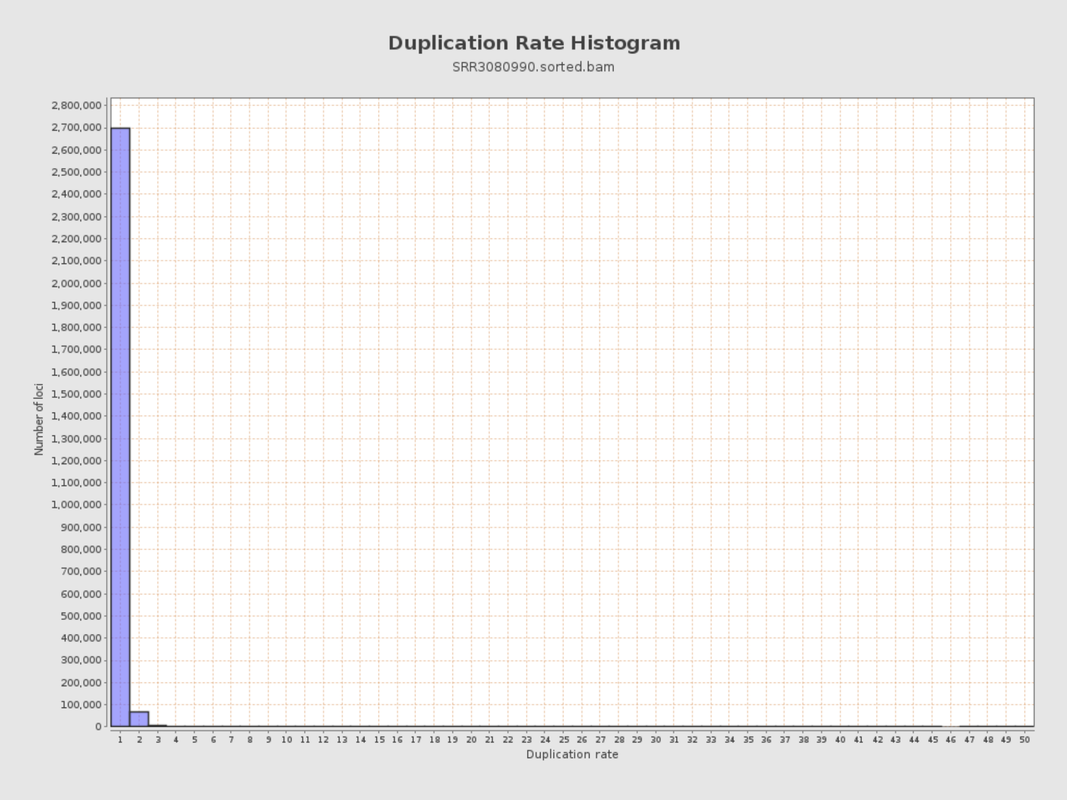
5. Results : Coverage Histogram (0-50X)



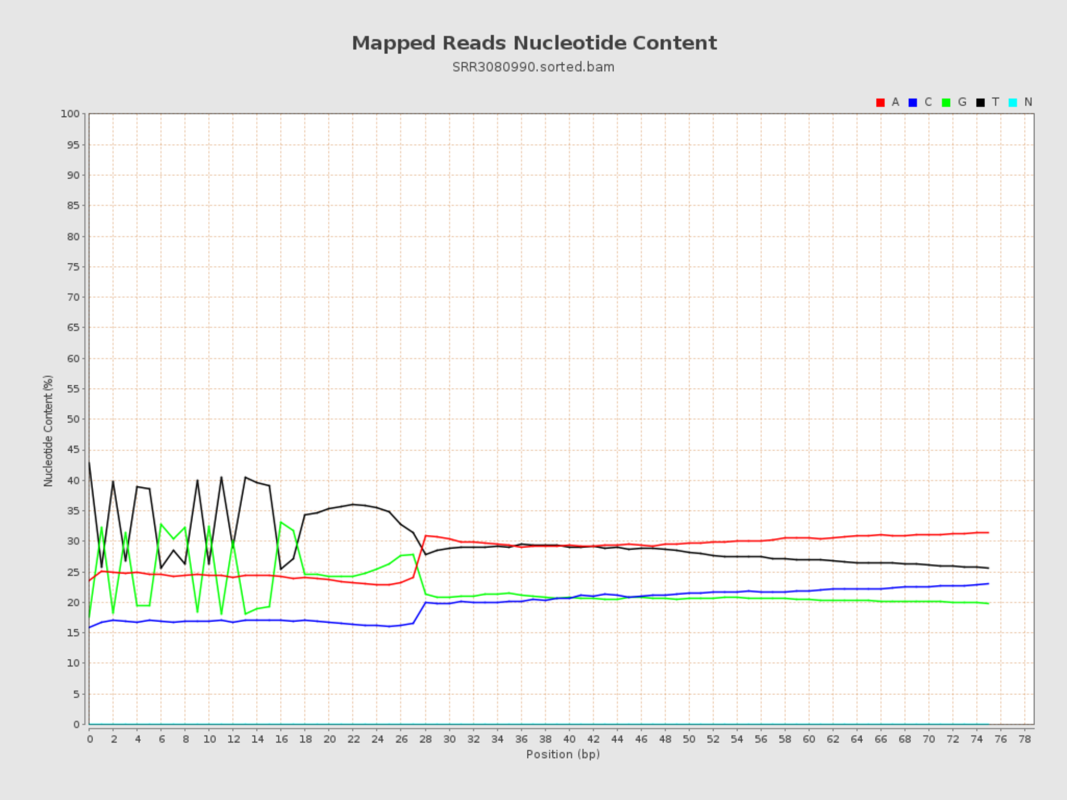
6. Results : Genome Fraction Coverage



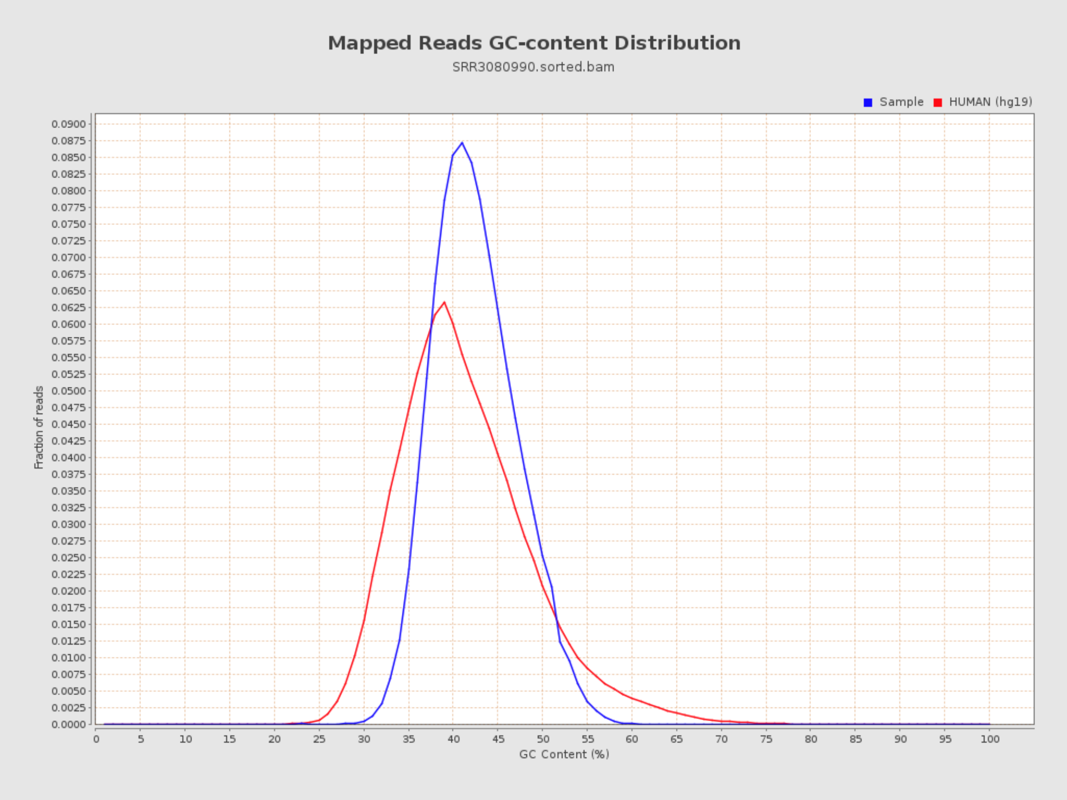
7. Results : Duplication Rate Histogram



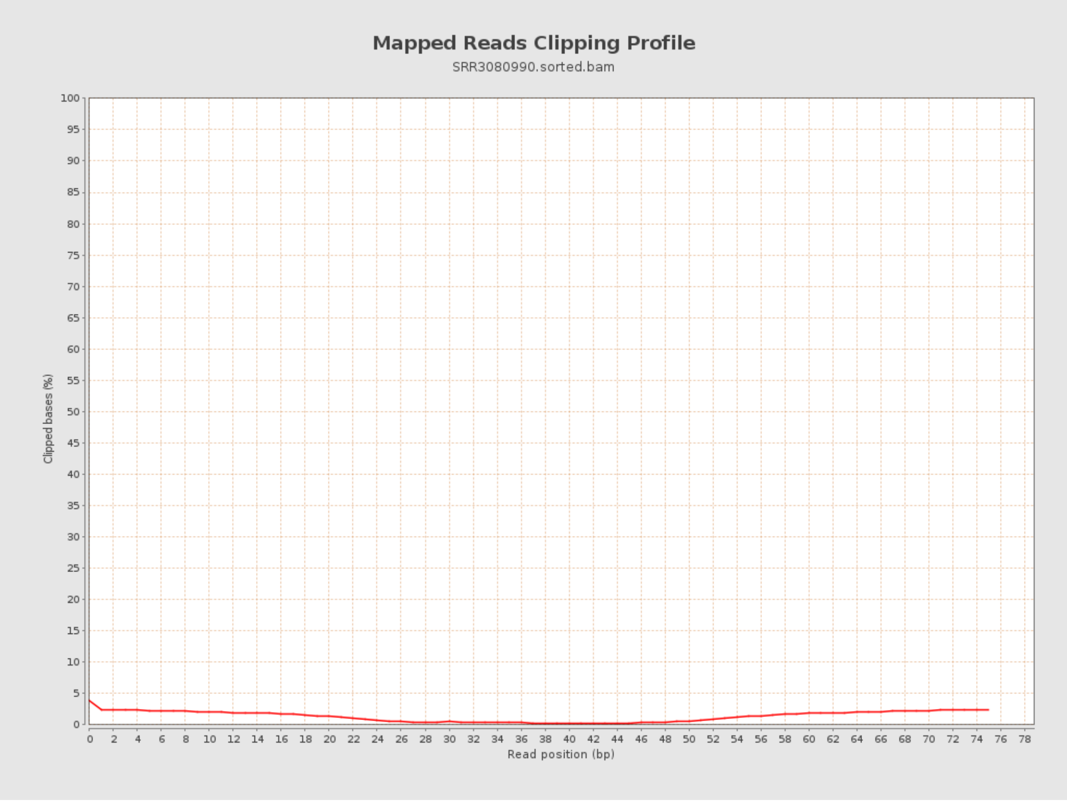
8. Results : Mapped Reads Nucleotide Content



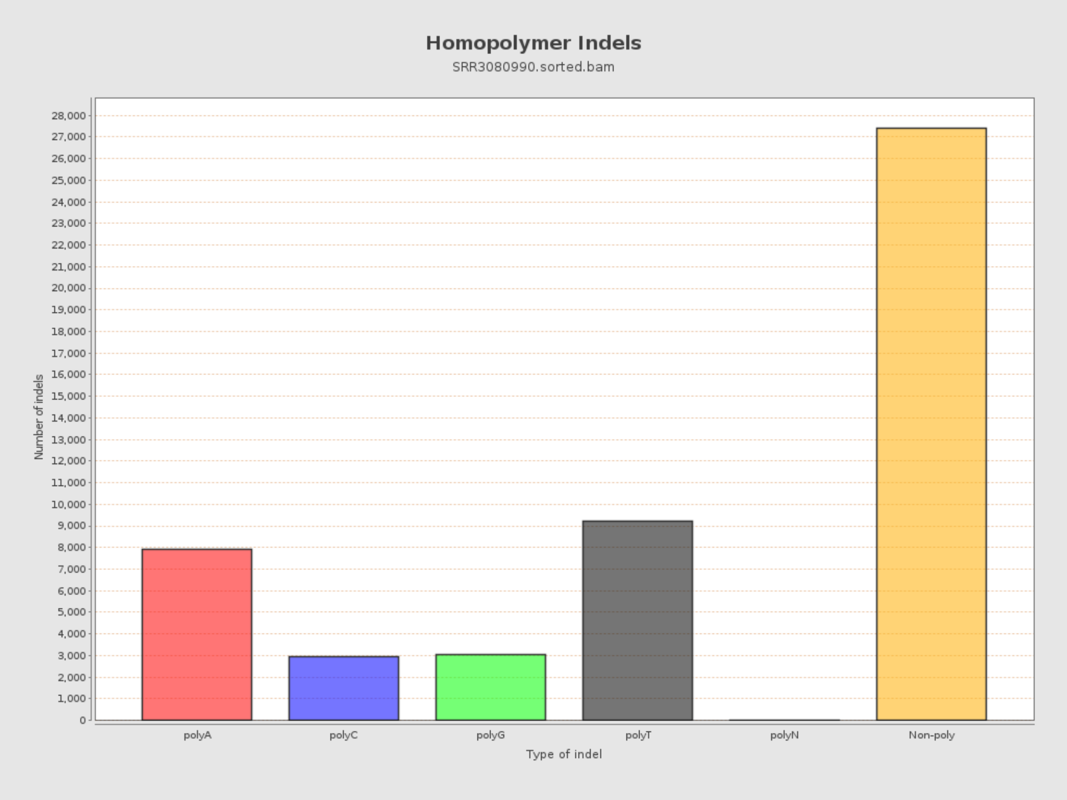
9. Results : Mapped Reads GC-content Distribution



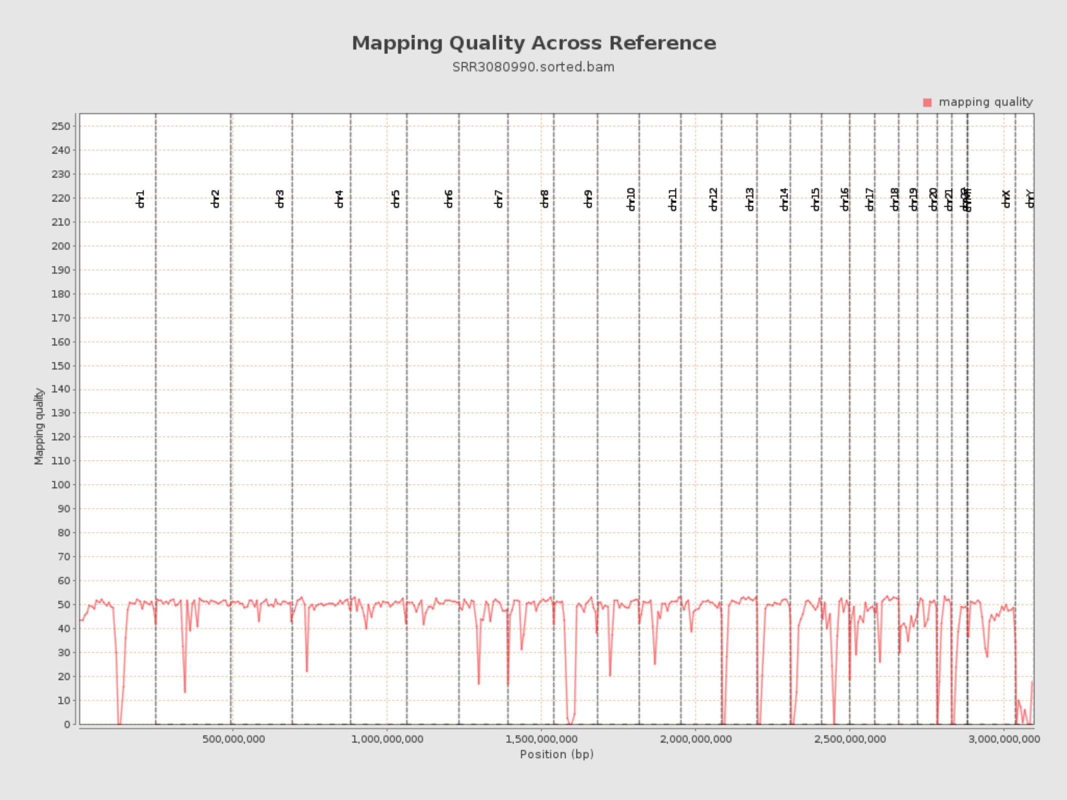
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram