Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:18:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080793.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_SRR3080793 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080793.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:18:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080793.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,411,839
Mapped reads	2,175,645 / 90.21%
Unmapped reads	236,194 / 9.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,181 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	87,113 / 3.61%
Duplication rate	3.24%
Clipped reads	1,123,150 / 46.57%

2.2. ACGT Content

Number/percentage of A's	41,470,749 / 29.06%
Number/percentage of C's	27,542,652 / 19.3%
Number/percentage of T's	43,455,109 / 30.45%
Number/percentage of G's	30,228,812 / 21.18%
Number/percentage of N's	2,768 / 0%
GC Percentage	40.48%

2.3. Coverage

Mean	0.0461

Standard Deviation	0.3749

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

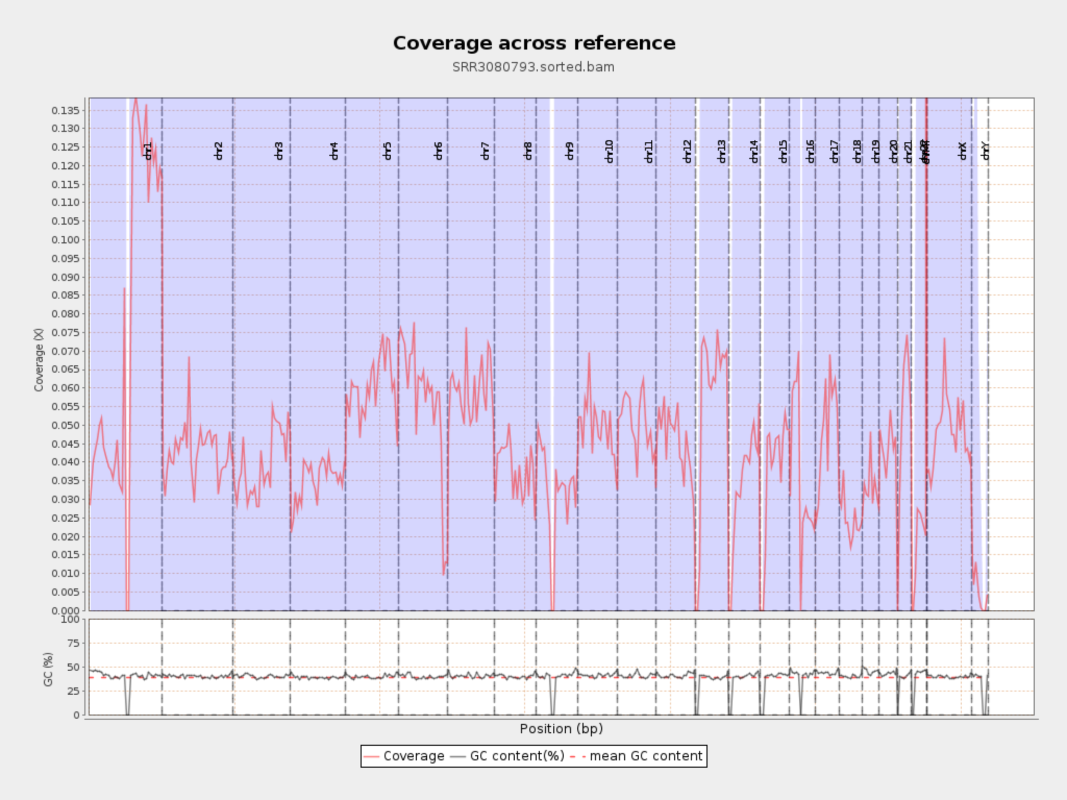
General error rate	0.78%
Mismatches	1,094,234
Insertions	11,002
Mapped reads with at least one insertion	0.5%
Deletions	32,312
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.12%

2.6. Chromosome stats

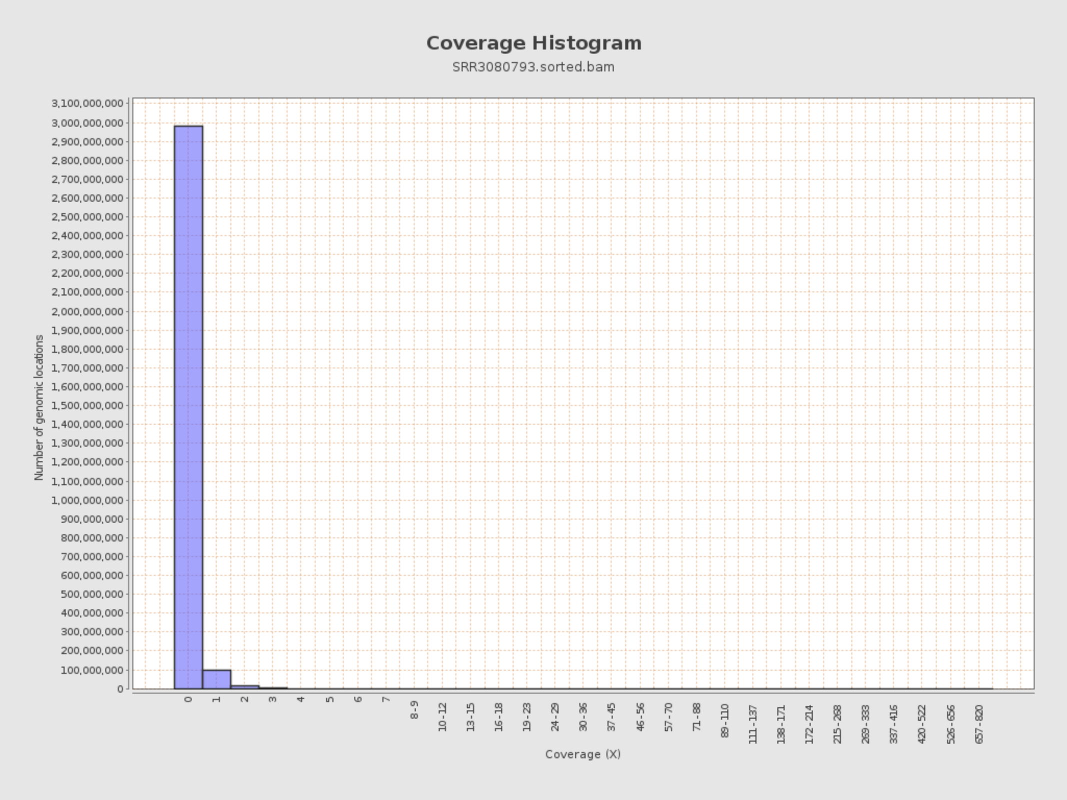
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18848524	0.0756	0.7628
chr2	243199373	10494577	0.0432	0.3853
chr3	198022430	7798172	0.0394	0.2362
chr4	191154276	6679607	0.0349	0.2257
chr5	180915260	11017462	0.0609	0.2917
chr6	171115067	9795161	0.0572	0.3368
chr7	159138663	9502057	0.0597	0.4339

chr8	146364022	5548229	0.0379	0.4516
chr9	141213431	4490729	0.0318	0.255
chr10	135534747	6789169	0.0501	0.38
chr11	135006516	6850954	0.0507	0.3391
chr12	133851895	6091440	0.0455	0.2522
chr13	115169878	6432680	0.0559	0.2805
chr14	107349540	3576104	0.0333	0.2241
chr15	102531392	3747486	0.0365	0.2286
chr16	90354753	3257621	0.0361	0.2364
chr17	81195210	3996256	0.0492	0.2928
chr18	78077248	1935813	0.0248	0.4242
chr19	59128983	1974164	0.0334	0.5462
chr20	63025520	2755085	0.0437	0.2531
chr21	48129895	2487670	0.0517	0.2726
chr22	51304566	875606	0.0171	0.1492
chrMT	16571	23763	1.434	1.5405
chrX	155270560	7495479	0.0483	0.28
chrY	59373566	287122	0.0048	0.0956

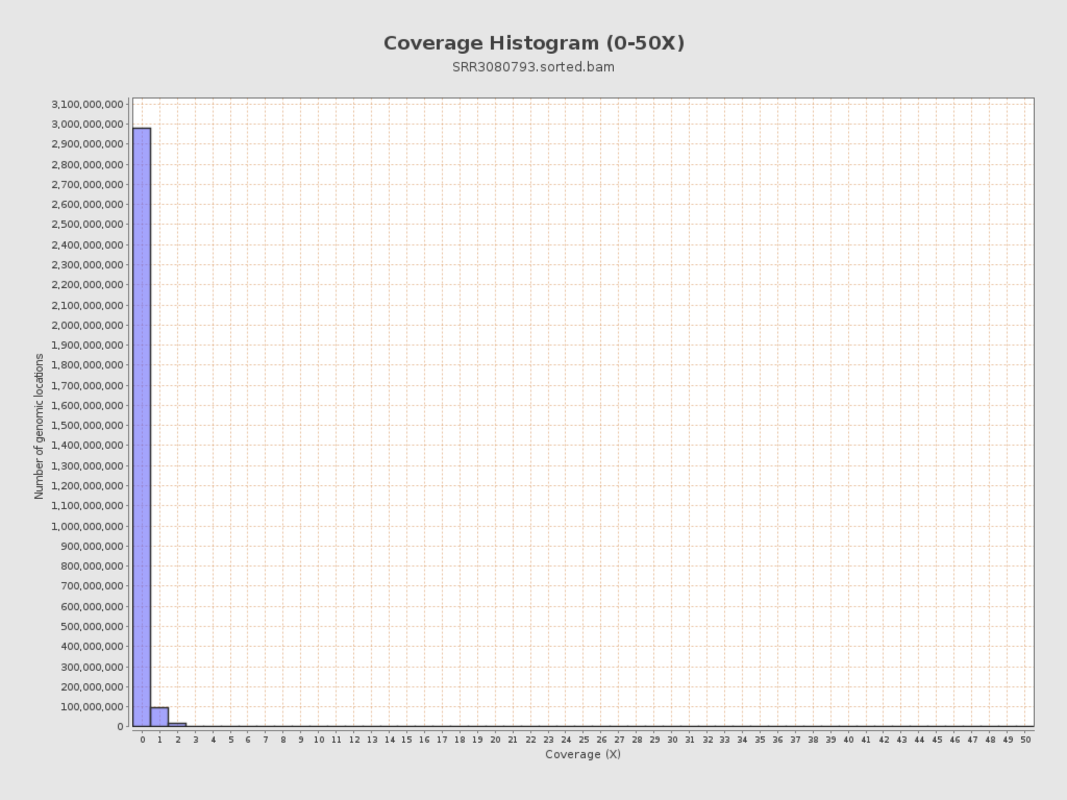
3. Results : Coverage across reference



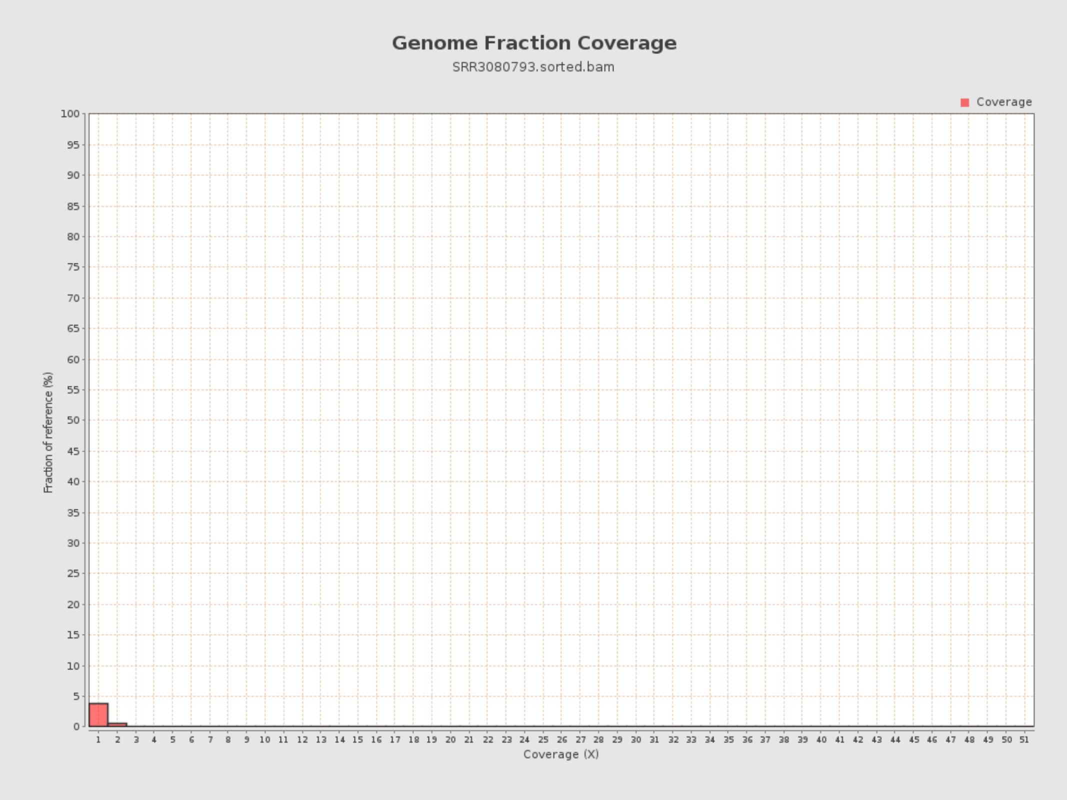
4. Results : Coverage Histogram



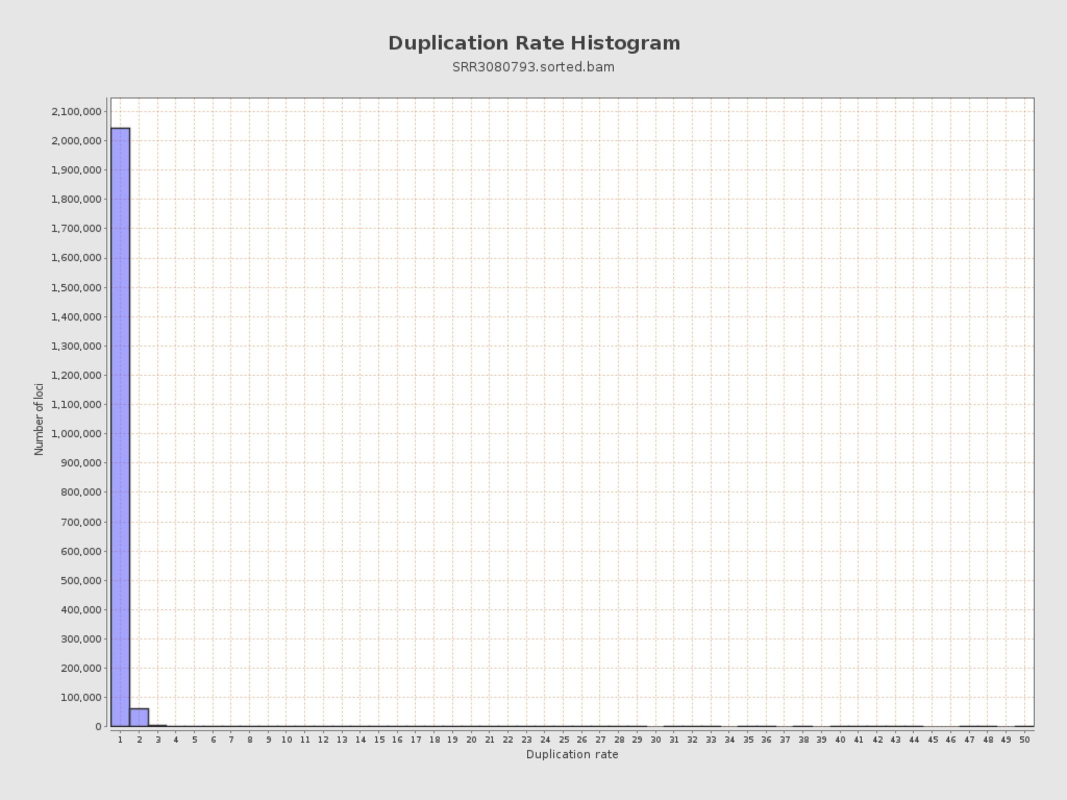
5. Results : Coverage Histogram (0-50X)



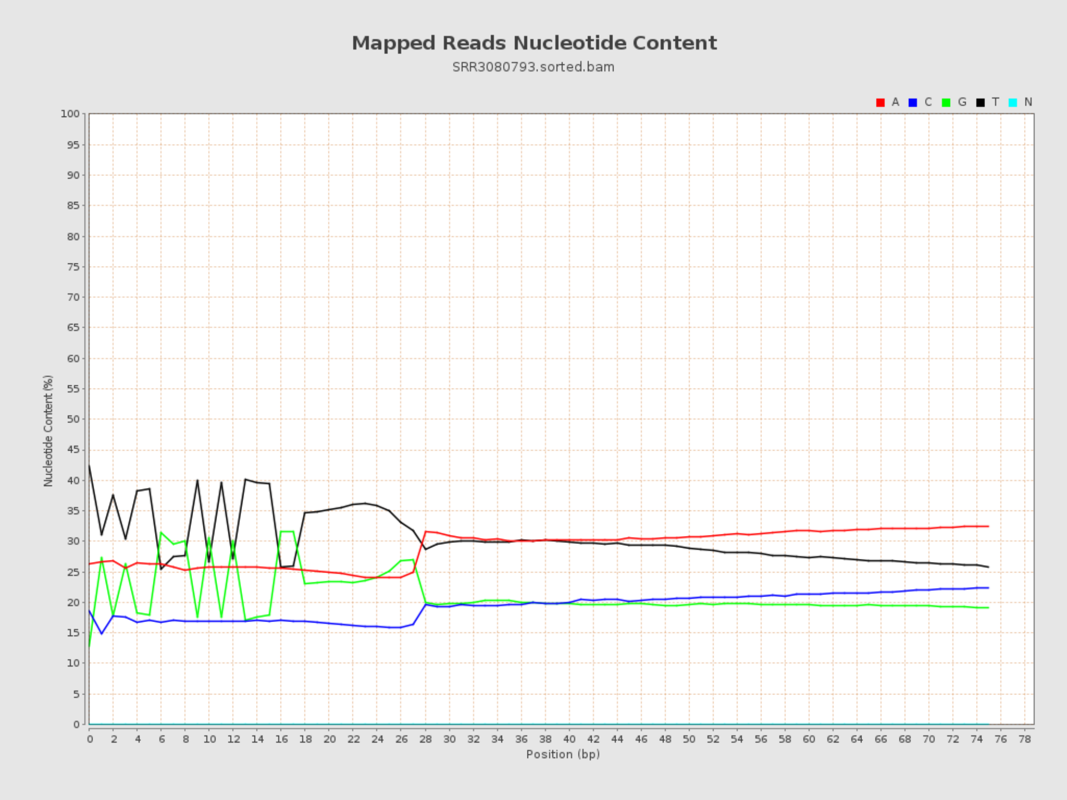
6. Results : Genome Fraction Coverage



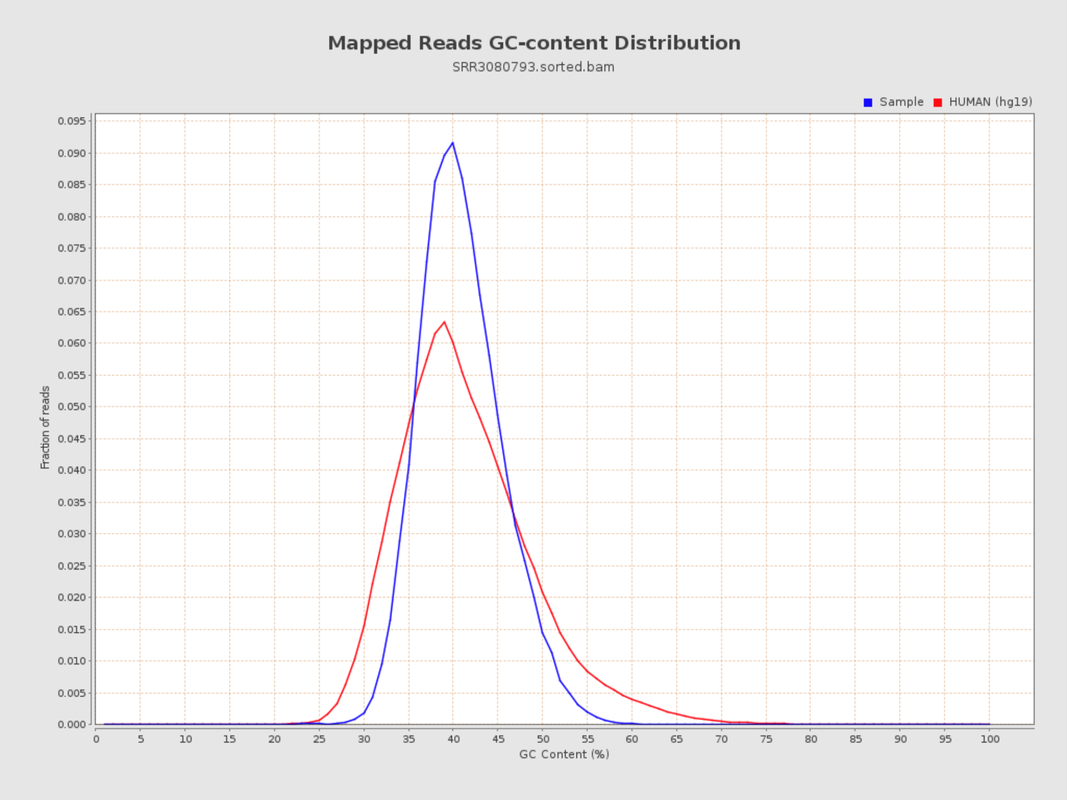
7. Results : Duplication Rate Histogram



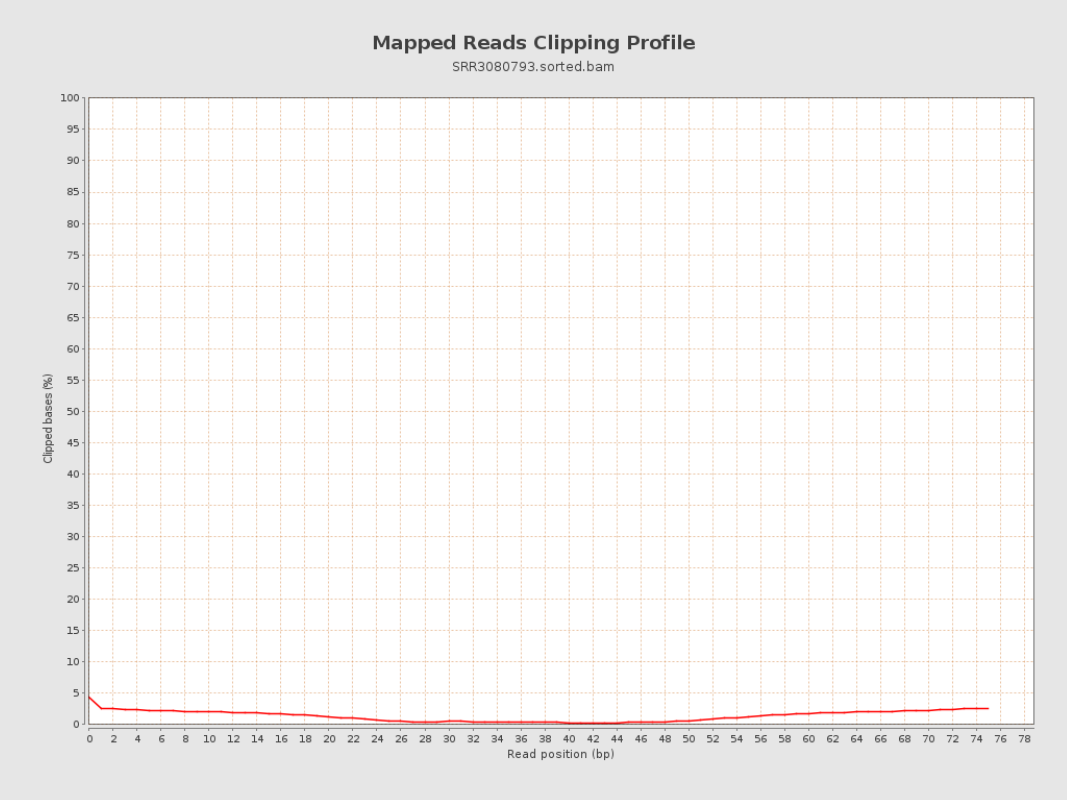
8. Results : Mapped Reads Nucleotide Content



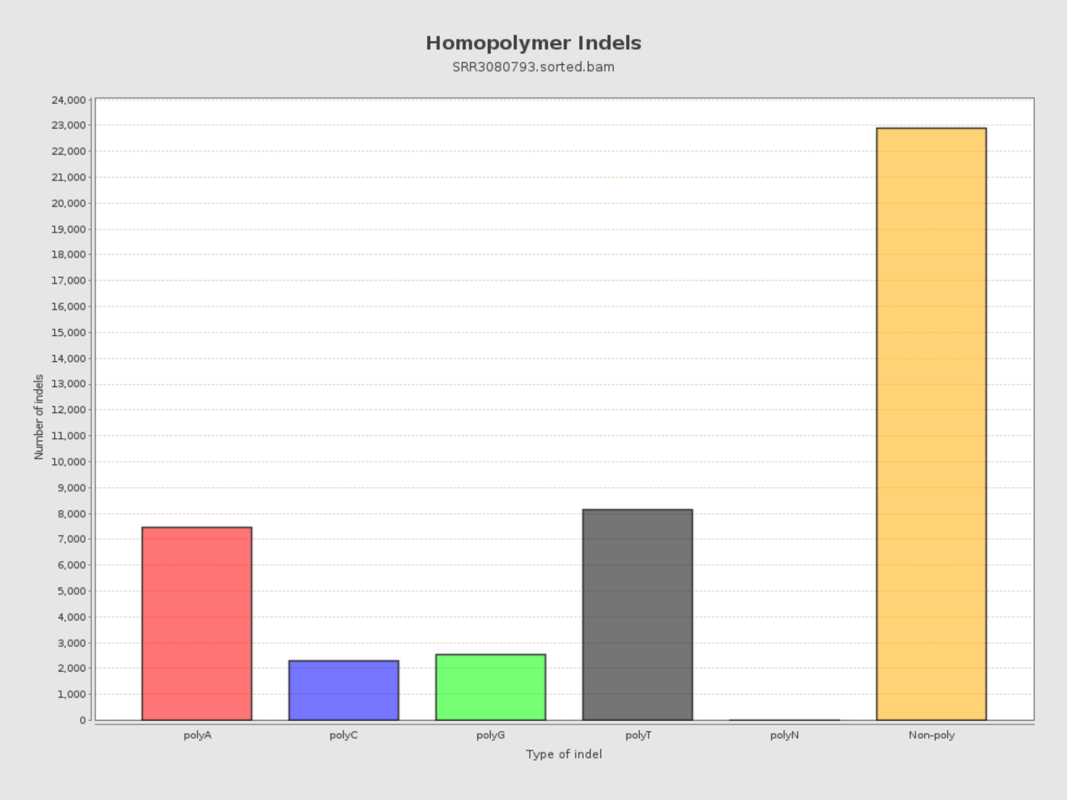
9. Results : Mapped Reads GC-content Distribution



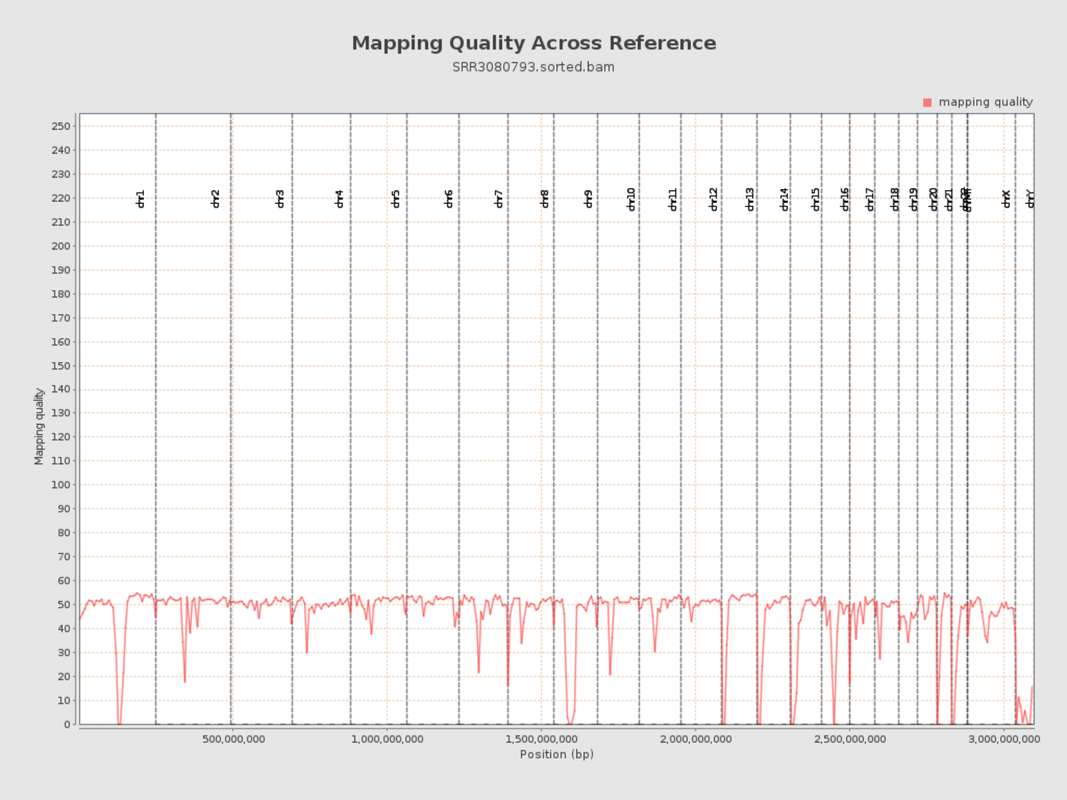
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram