Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:43:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080784.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_SRR3080784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080784.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:43:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080784.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,580,615
Mapped reads	2,298,946 / 89.09%
Unmapped reads	281,669 / 10.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,546 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	96,545 / 3.74%
Duplication rate	3.56%
Clipped reads	1,078,792 / 41.8%

2.2. ACGT Content

Number/percentage of A's	43,730,512 / 28.57%
Number/percentage of C's	29,653,595 / 19.37%
Number/percentage of T's	46,606,740 / 30.45%
Number/percentage of G's	33,086,022 / 21.61%
Number/percentage of N's	3,194 / 0%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0495

Standard Deviation	0.334

2.4. Mapping Quality

Mean Mapping Quality	46.33

2.5. Mismatches and indels

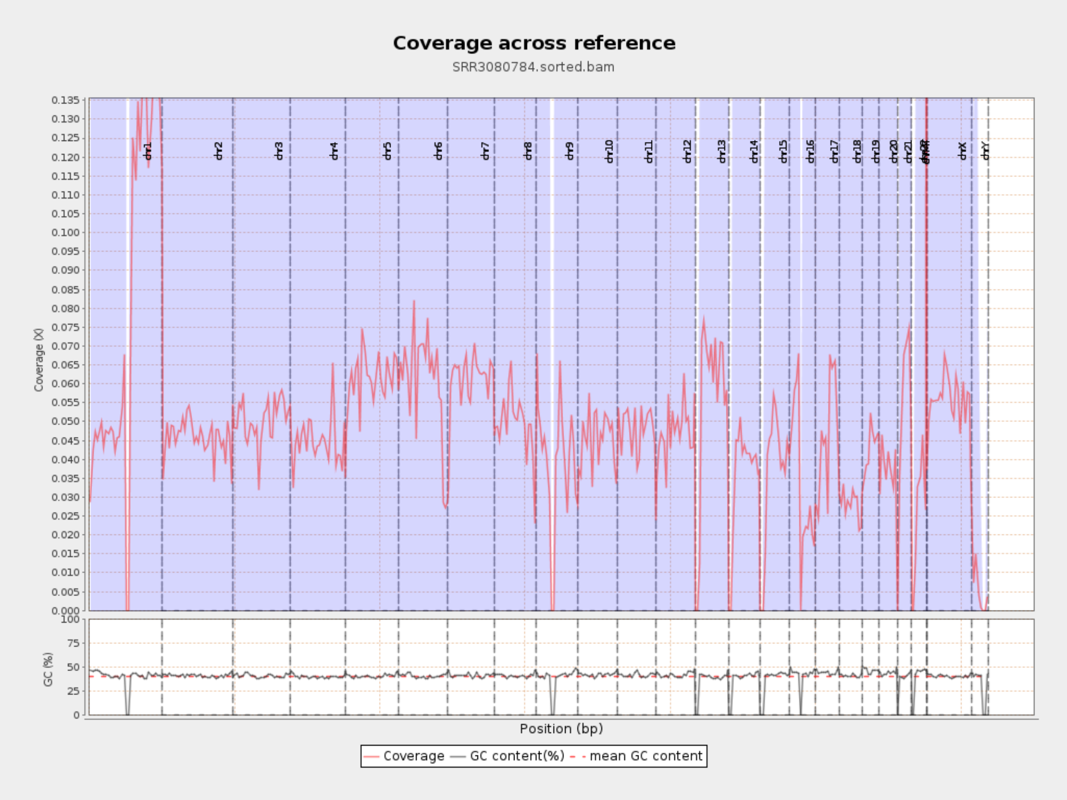
General error rate	0.75%
Mismatches	1,129,828
Insertions	11,440
Mapped reads with at least one insertion	0.49%
Deletions	33,261
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.42%

2.6. Chromosome stats

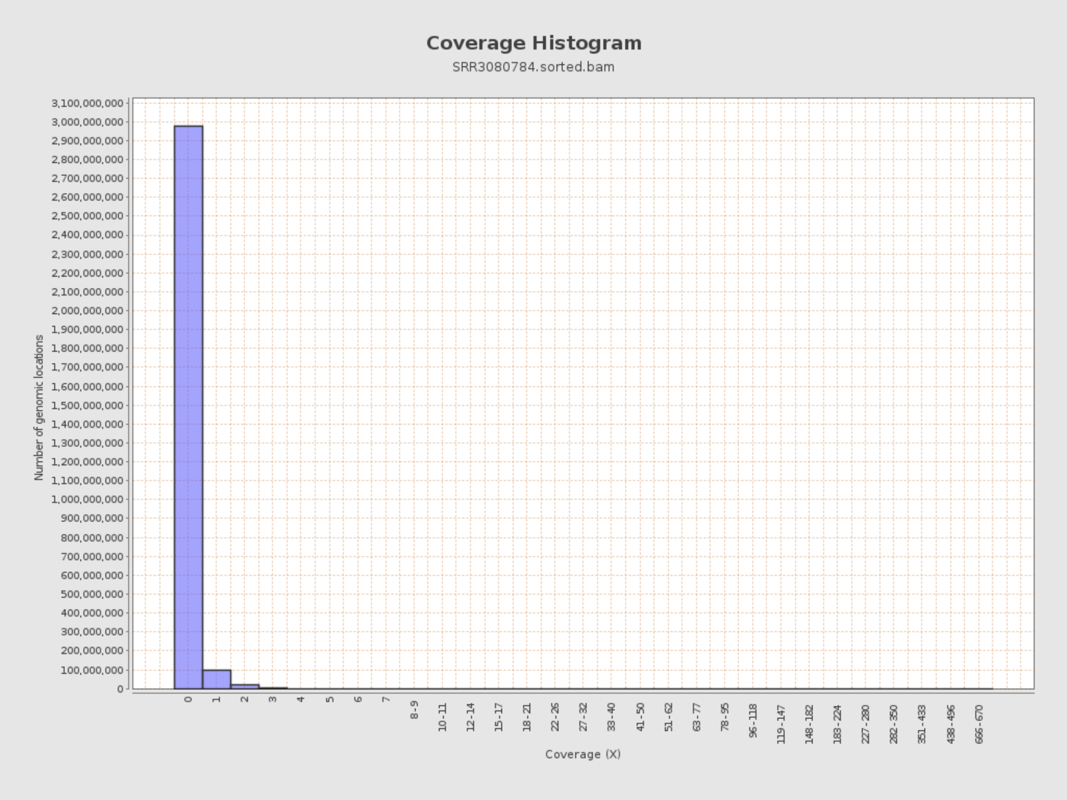
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19797651	0.0794	0.5374
chr2	243199373	11166883	0.0459	0.3925
chr3	198022430	10005836	0.0505	0.2721
chr4	191154276	8554218	0.0448	0.2624
chr5	180915260	11142529	0.0616	0.3027
chr6	171115067	10396196	0.0608	0.3659
chr7	159138663	9837093	0.0618	0.3832

chr8	146364022	7232755	0.0494	0.3933
chr9	141213431	5468343	0.0387	0.2816
chr10	135534747	6150758	0.0454	0.3117
chr11	135006516	6481033	0.048	0.2906
chr12	133851895	6335917	0.0473	0.266
chr13	115169878	6319197	0.0549	0.2892
chr14	107349540	3807464	0.0355	0.2372
chr15	102531392	3699815	0.0361	0.241
chr16	90354753	3058452	0.0338	0.2338
chr17	81195210	3745299	0.0461	0.274
chr18	78077248	2203809	0.0282	0.4091
chr19	59128983	2537229	0.0429	0.3513
chr20	63025520	2368923	0.0376	0.2376
chr21	48129895	2571545	0.0534	0.2871
chr22	51304566	1282186	0.025	0.1909
chrMT	16571	11309	0.6825	0.9793
chrX	155270560	8633606	0.0556	0.2962
chrY	59373566	325198	0.0055	0.1076

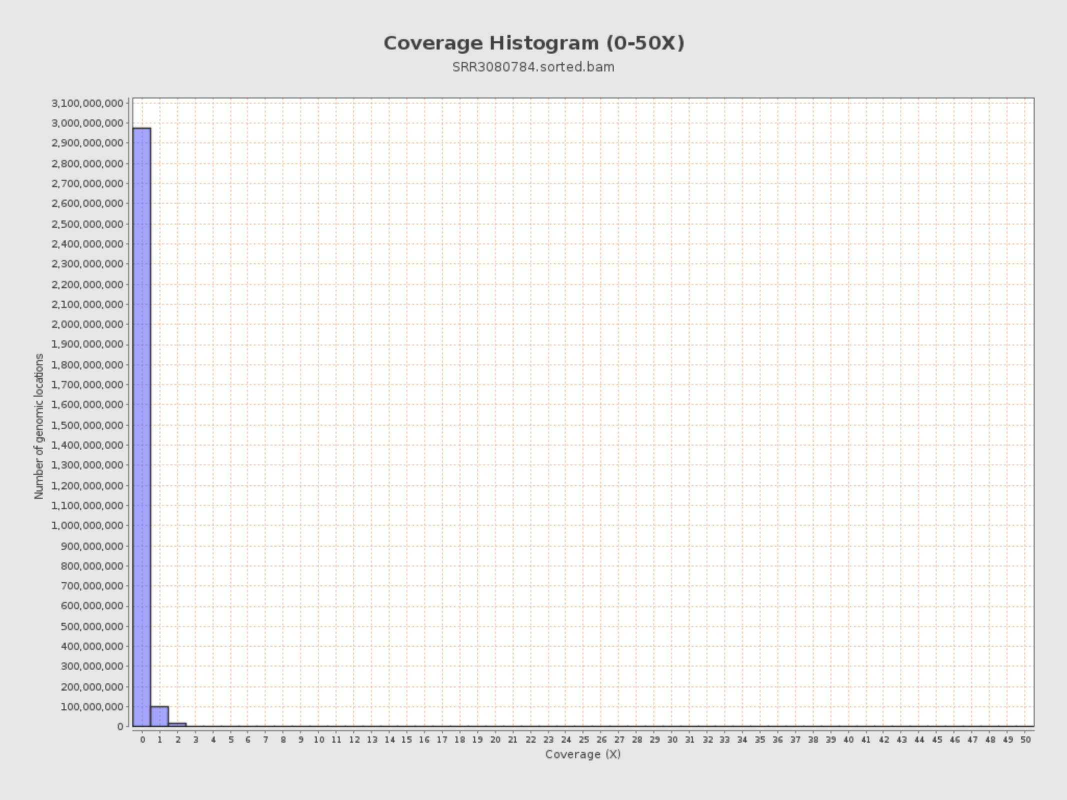
3. Results : Coverage across reference



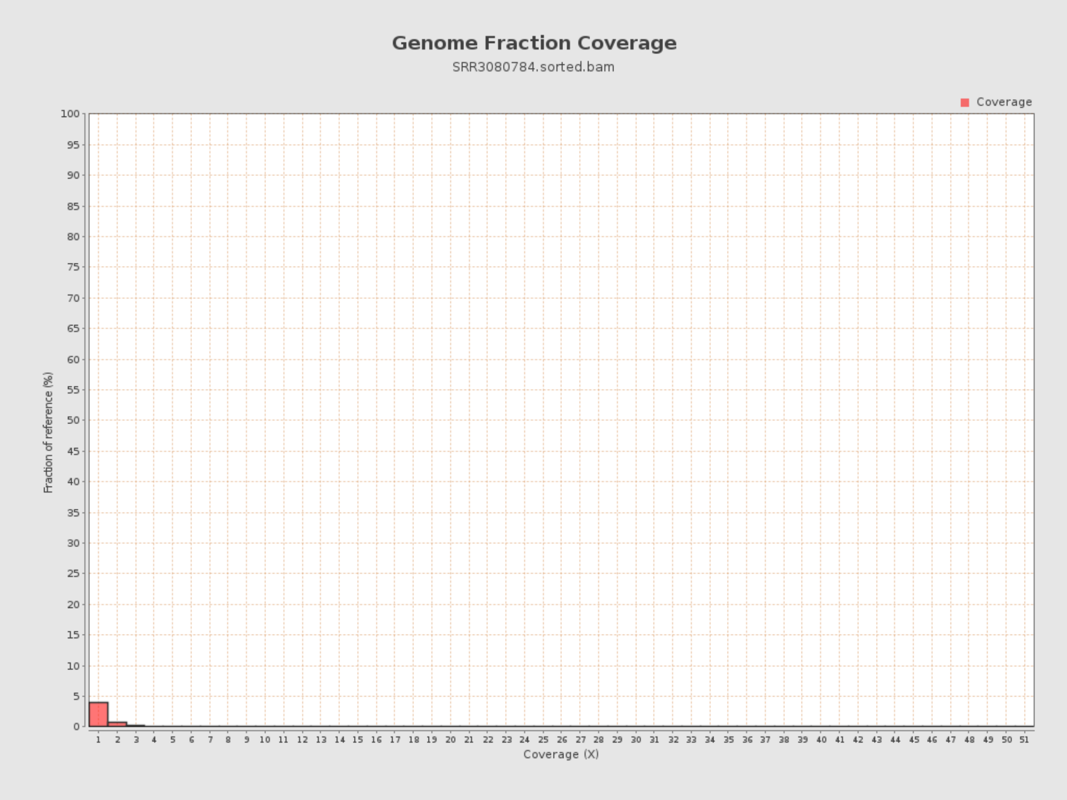
4. Results : Coverage Histogram



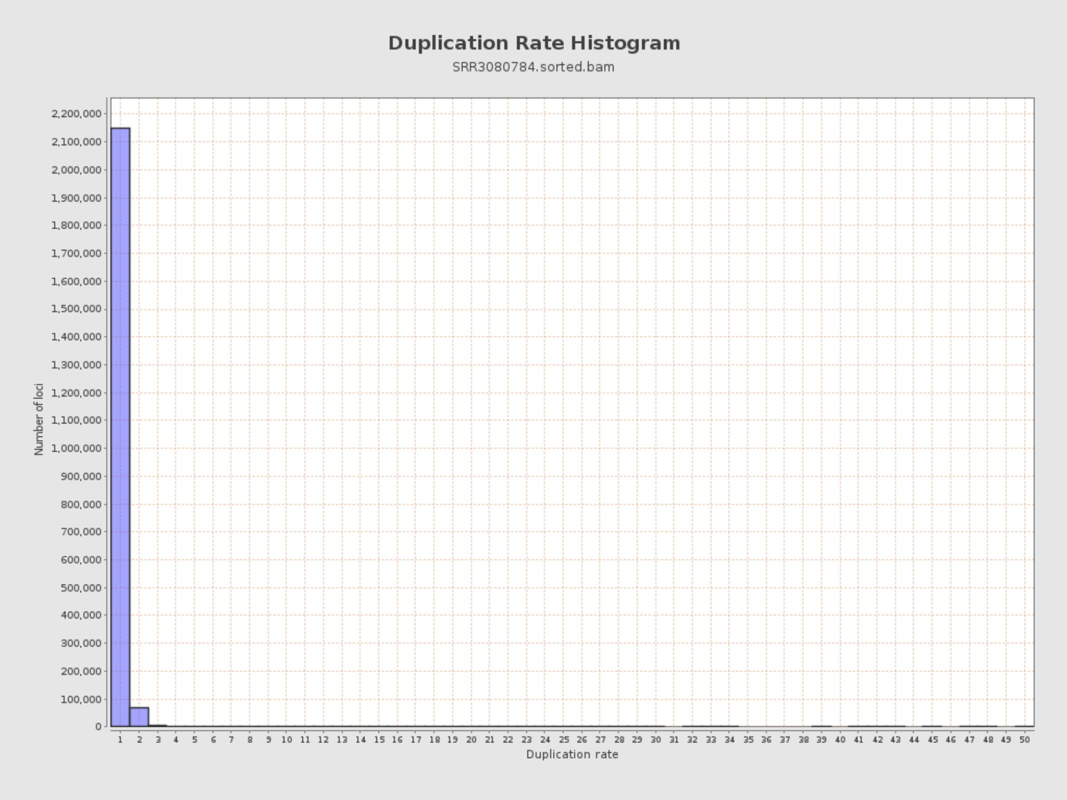
5. Results : Coverage Histogram (0-50X)



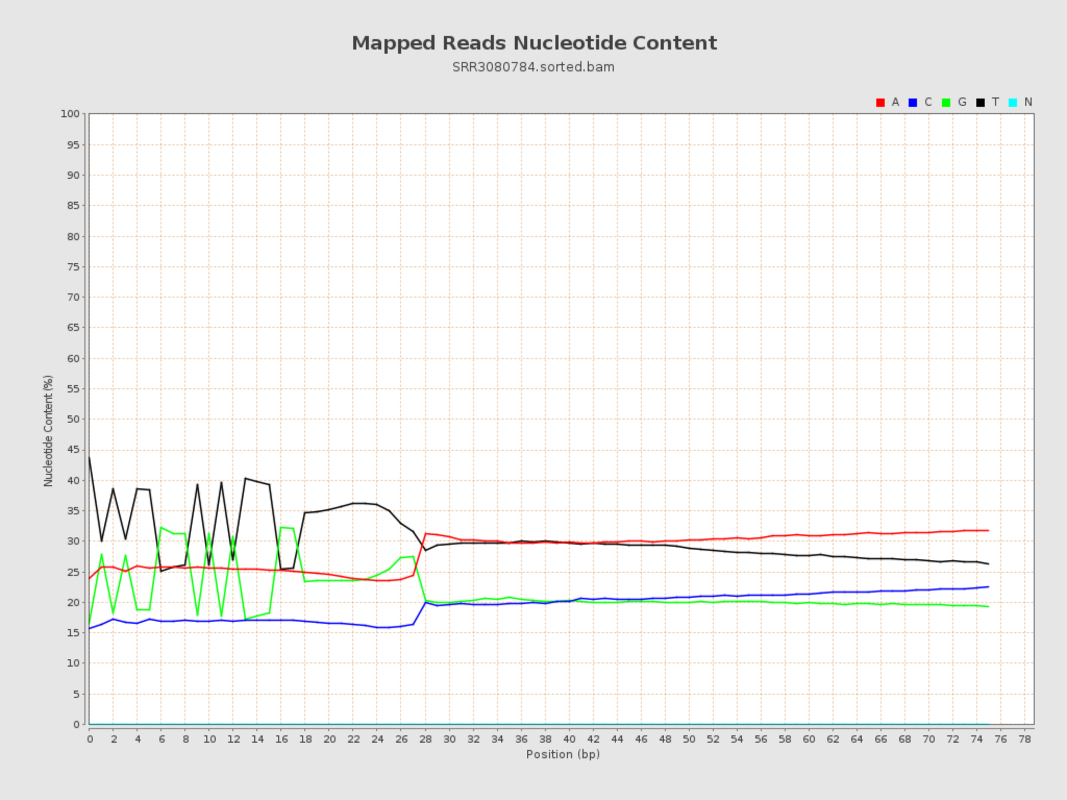
6. Results : Genome Fraction Coverage



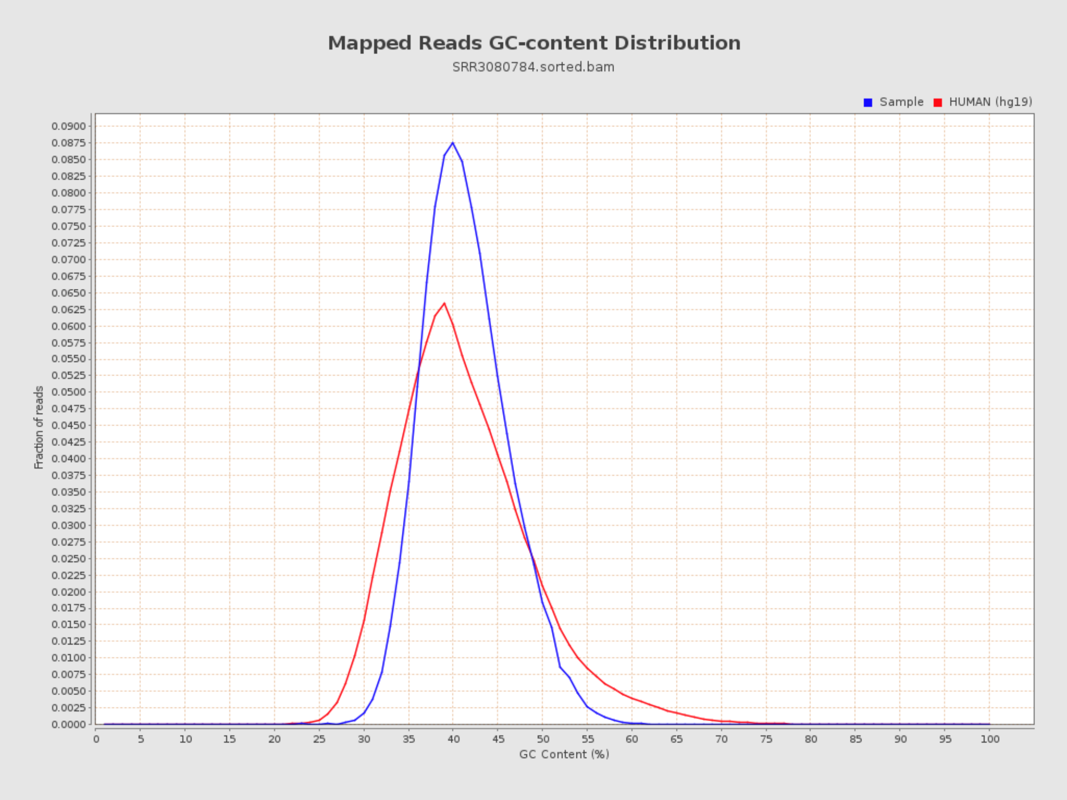
7. Results : Duplication Rate Histogram



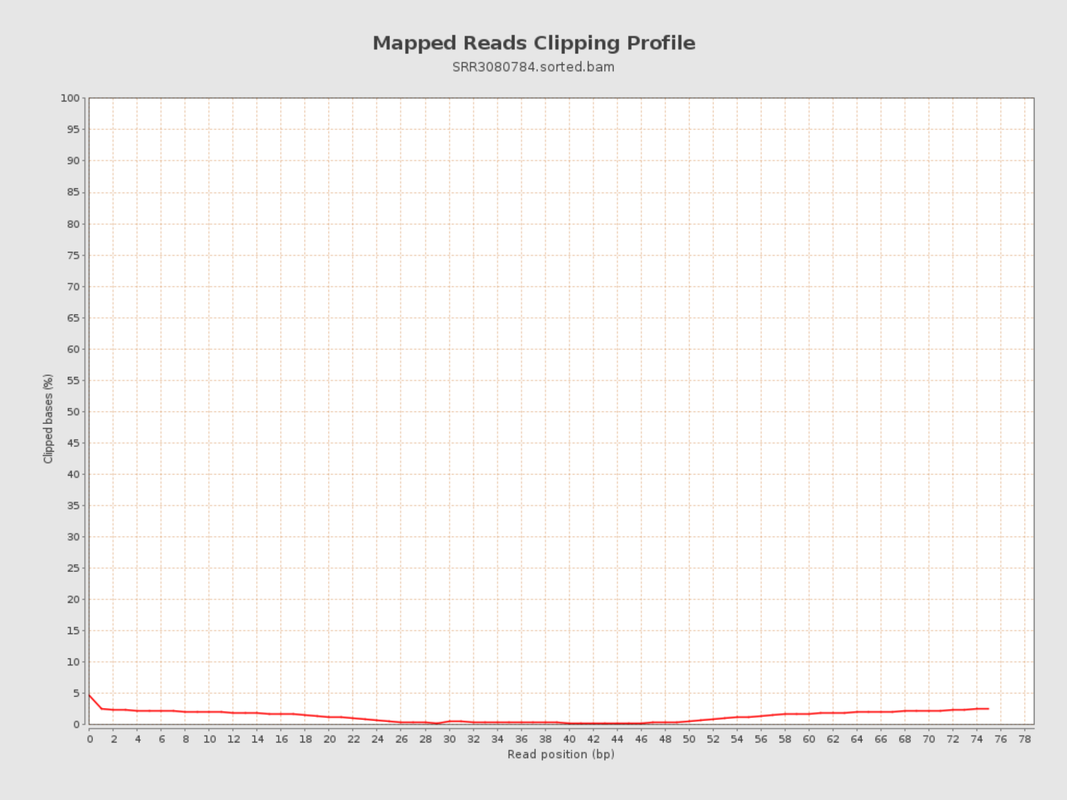
8. Results : Mapped Reads Nucleotide Content



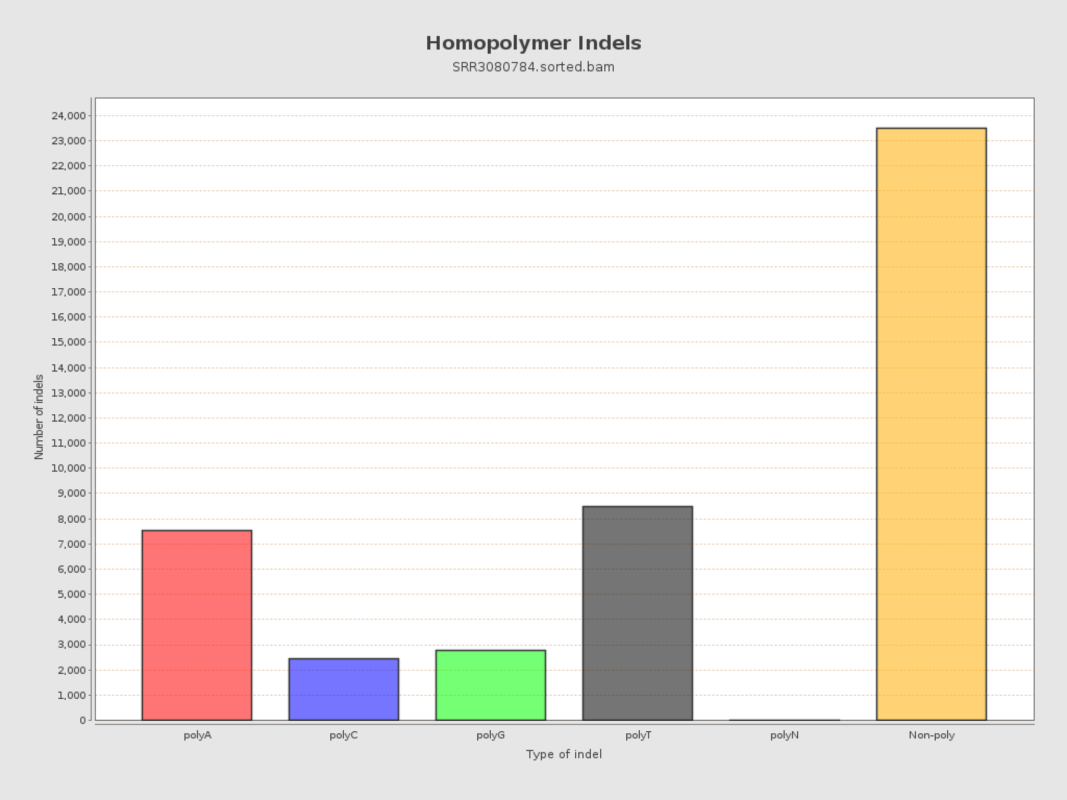
9. Results : Mapped Reads GC-content Distribution



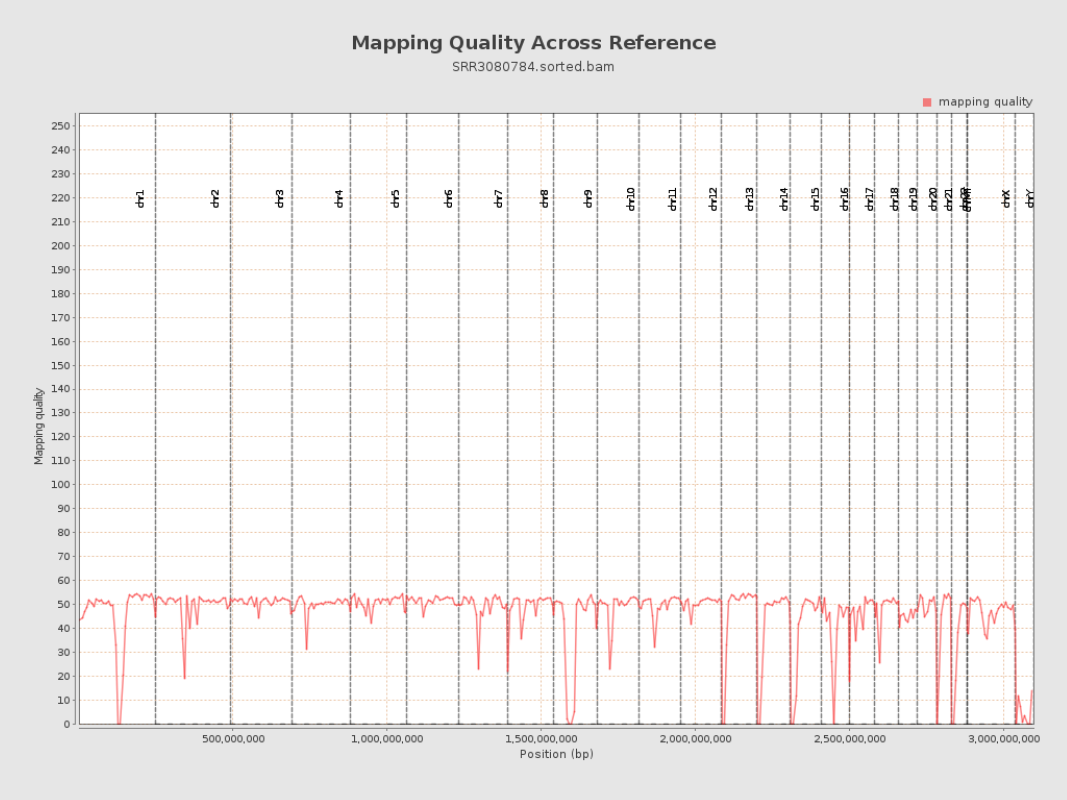
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram