Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:02:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003984.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_SRR6003984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003984.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:02:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,634,913
Mapped reads	3,072,254 / 84.52%
Unmapped reads	562,659 / 15.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,396 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	193,137 / 5.31%
Duplication rate	4.84%
Clipped reads	1,505,584 / 41.42%

2.2. ACGT Content

Number/percentage of A's	54,959,527 / 27.23%
Number/percentage of C's	35,435,437 / 17.56%
Number/percentage of T's	66,830,083 / 33.12%
Number/percentage of G's	44,554,179 / 22.08%
Number/percentage of N's	21,104 / 0.01%
GC Percentage	39.64%

2.3. Coverage

Mean	0.0652

Standard Deviation	0.6311

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

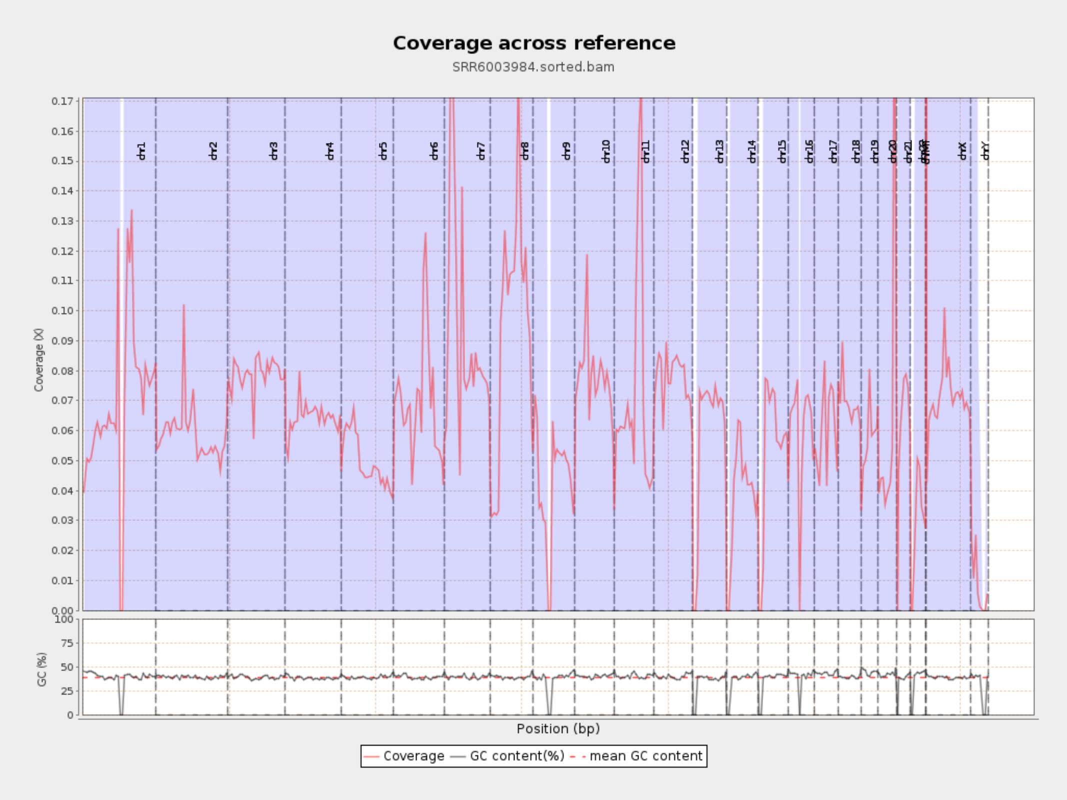
General error rate	0.91%
Mismatches	1,813,517
Insertions	17,310
Mapped reads with at least one insertion	0.56%
Deletions	52,052
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.88%

2.6. Chromosome stats

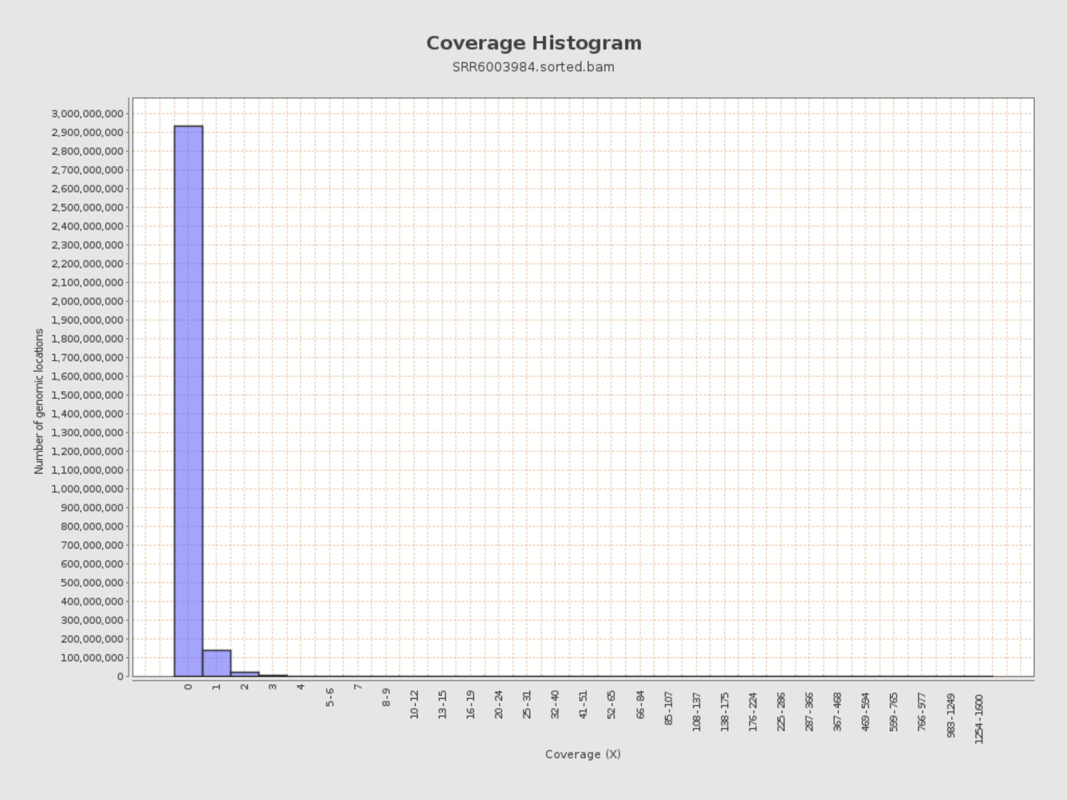
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17348379	0.0696	1.2299
chr2	243199373	14334755	0.0589	0.7896
chr3	198022430	15632657	0.0789	0.3361
chr4	191154276	12323198	0.0645	0.3332
chr5	180915260	8998937	0.0497	0.2735
chr6	171115067	11935299	0.0698	0.3844
chr7	159138663	14679736	0.0922	1.0635

chr8	146364022	13979289	0.0955	0.8782
chr9	141213431	6030950	0.0427	0.5019
chr10	135534747	10635284	0.0785	0.5571
chr11	135006516	9682732	0.0717	0.4794
chr12	133851895	10452913	0.0781	0.3469
chr13	115169878	6726211	0.0584	0.2909
chr14	107349540	4170374	0.0388	0.2669
chr15	102531392	5346553	0.0521	0.2829
chr16	90354753	5261965	0.0582	0.3272
chr17	81195210	4887939	0.0602	0.3324
chr18	78077248	5459398	0.0699	1.0409
chr19	59128983	3420447	0.0578	0.7592
chr20	63025520	4527392	0.0718	0.3547
chr21	48129895	2925972	0.0608	0.3128
chr22	51304566	1469539	0.0286	0.1932
chrMT	16571	136028	8.2088	5.5167
chrX	155270560	11027313	0.071	0.3819
chrY	59373566	492145	0.0083	0.1756

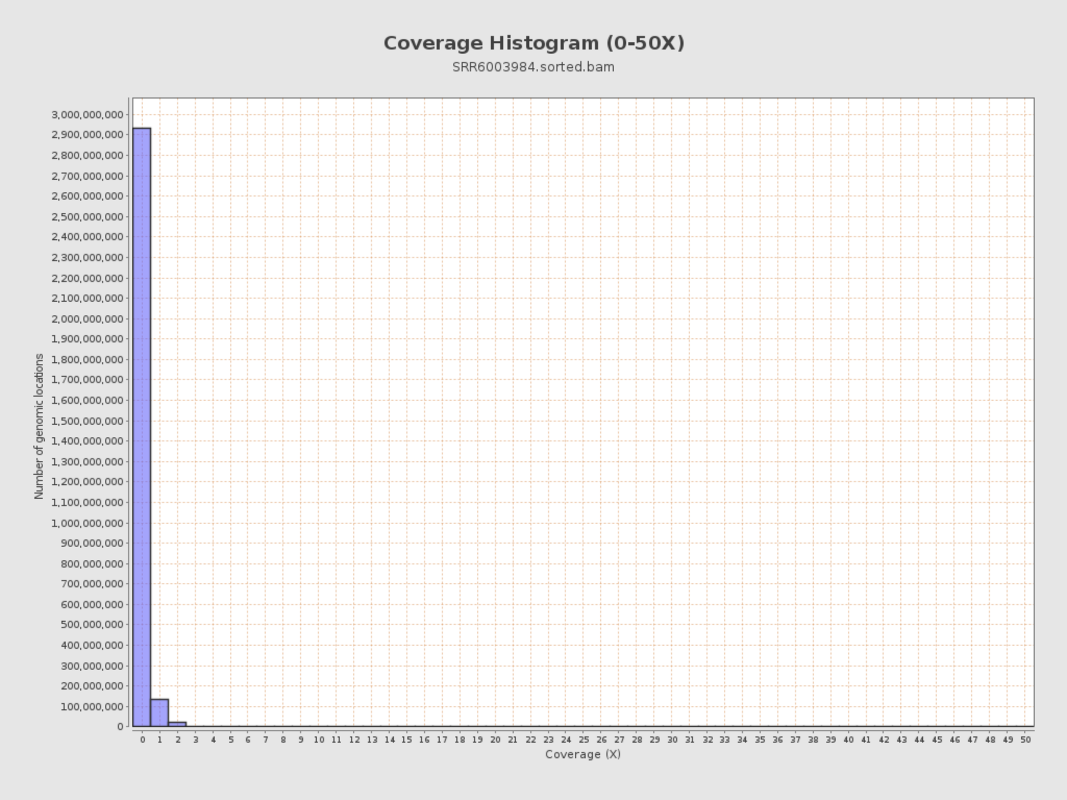
3. Results : Coverage across reference



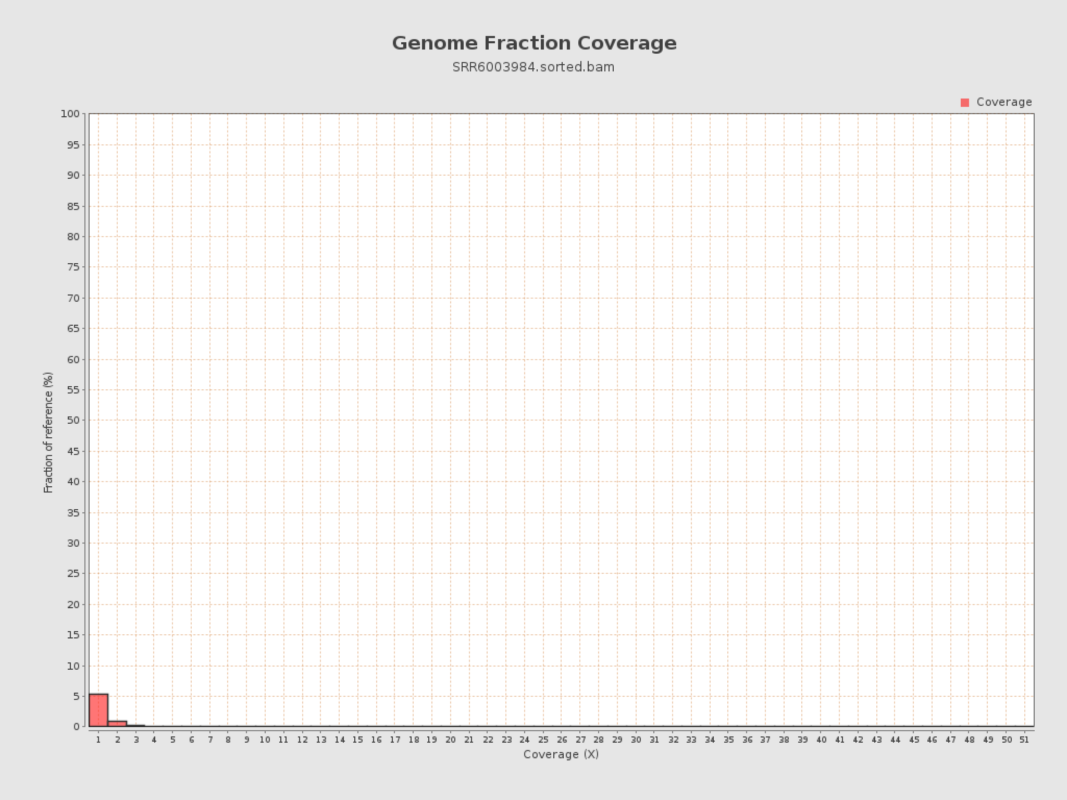
4. Results : Coverage Histogram



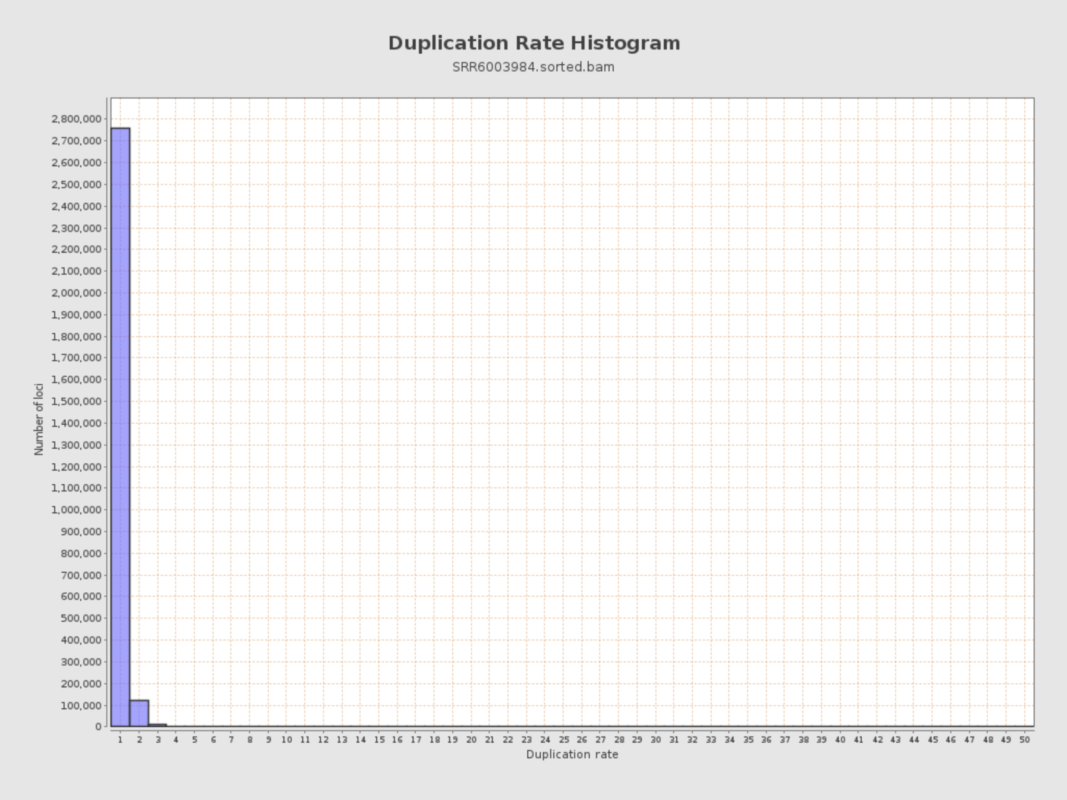
5. Results : Coverage Histogram (0-50X)



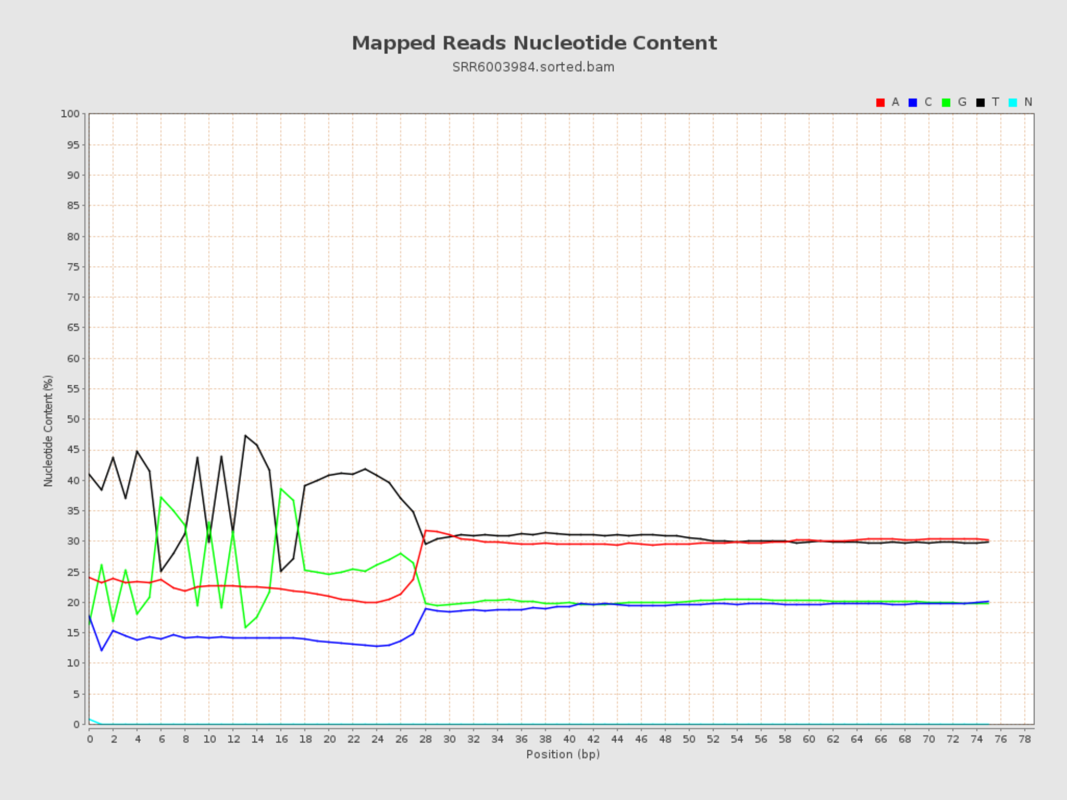
6. Results : Genome Fraction Coverage



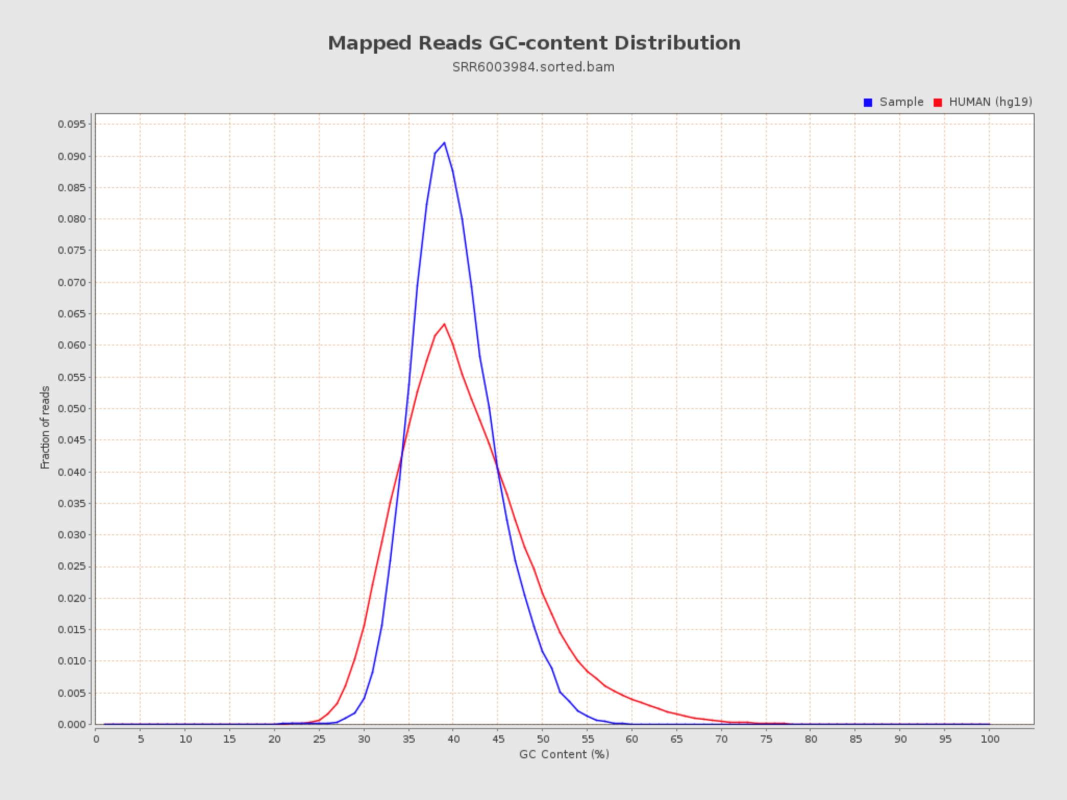
7. Results : Duplication Rate Histogram



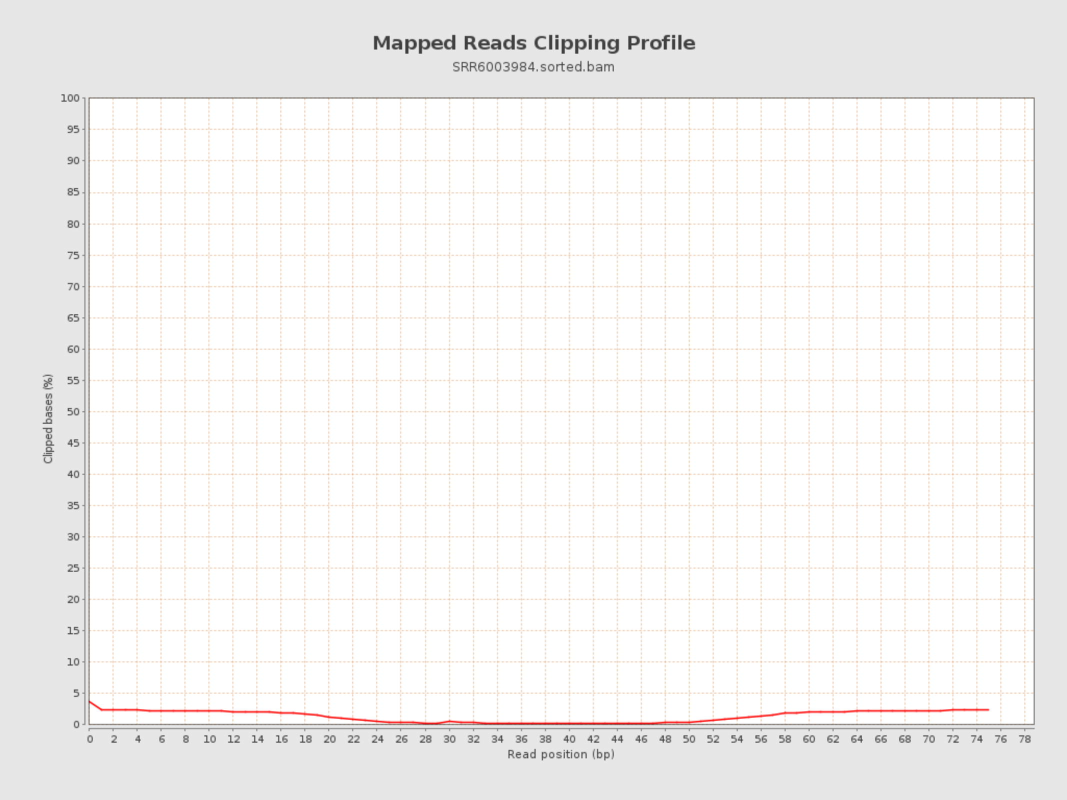
8. Results : Mapped Reads Nucleotide Content



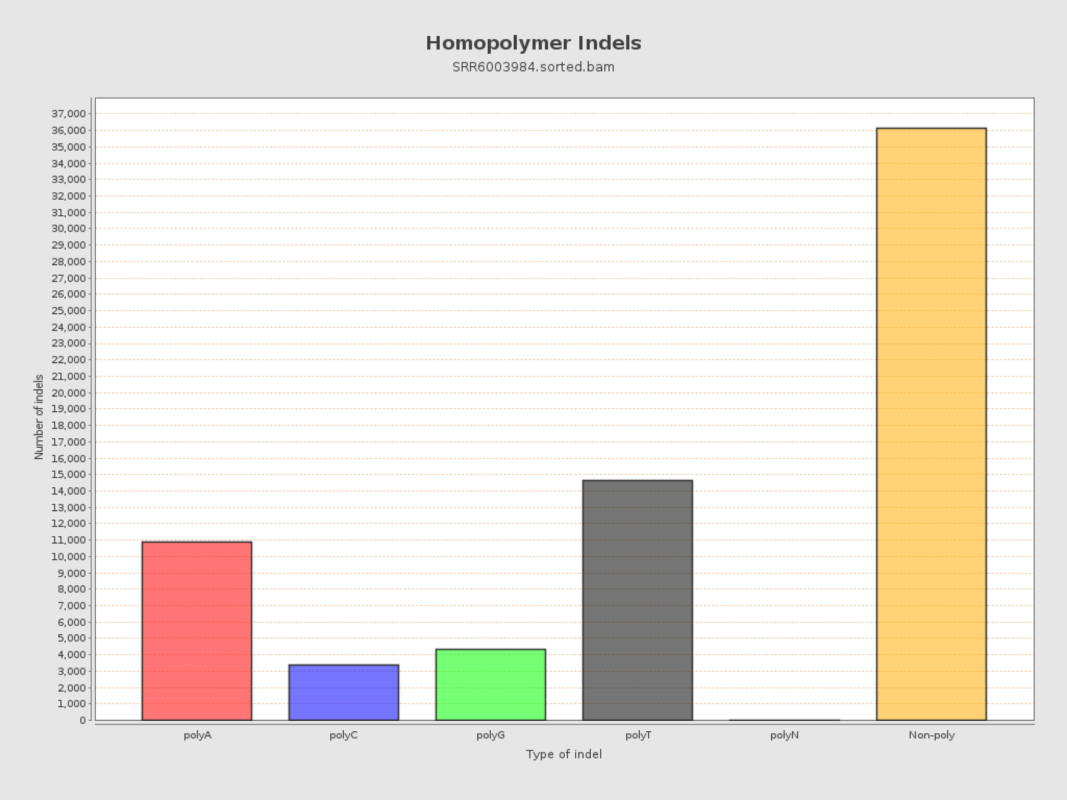
9. Results : Mapped Reads GC-content Distribution



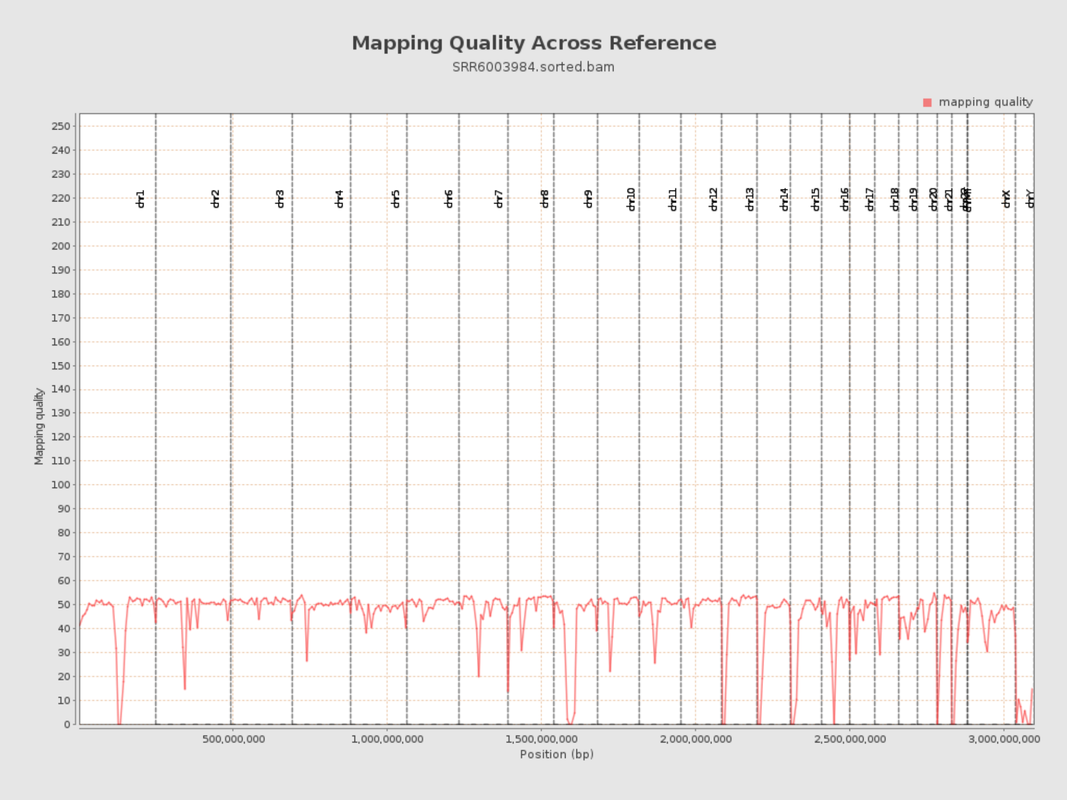
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram