Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:34:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549004.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_SRR1549004 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549004.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:34:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,380,906
Mapped reads	8,980,035 / 86.51%
Unmapped reads	1,400,871 / 13.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	789,094 / 7.6%
Duplication rate	7.98%
Clipped reads	444,394 / 4.28%

2.2. ACGT Content

Number/percentage of A's	107,973,334 / 30.29%
Number/percentage of C's	69,766,771 / 19.57%
Number/percentage of T's	108,428,300 / 30.41%
Number/percentage of G's	70,331,608 / 19.73%
Number/percentage of N's	3,630 / 0%
GC Percentage	39.3%

2.3. Coverage

Mean	0.1152
Standard Deviation	0.9579

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

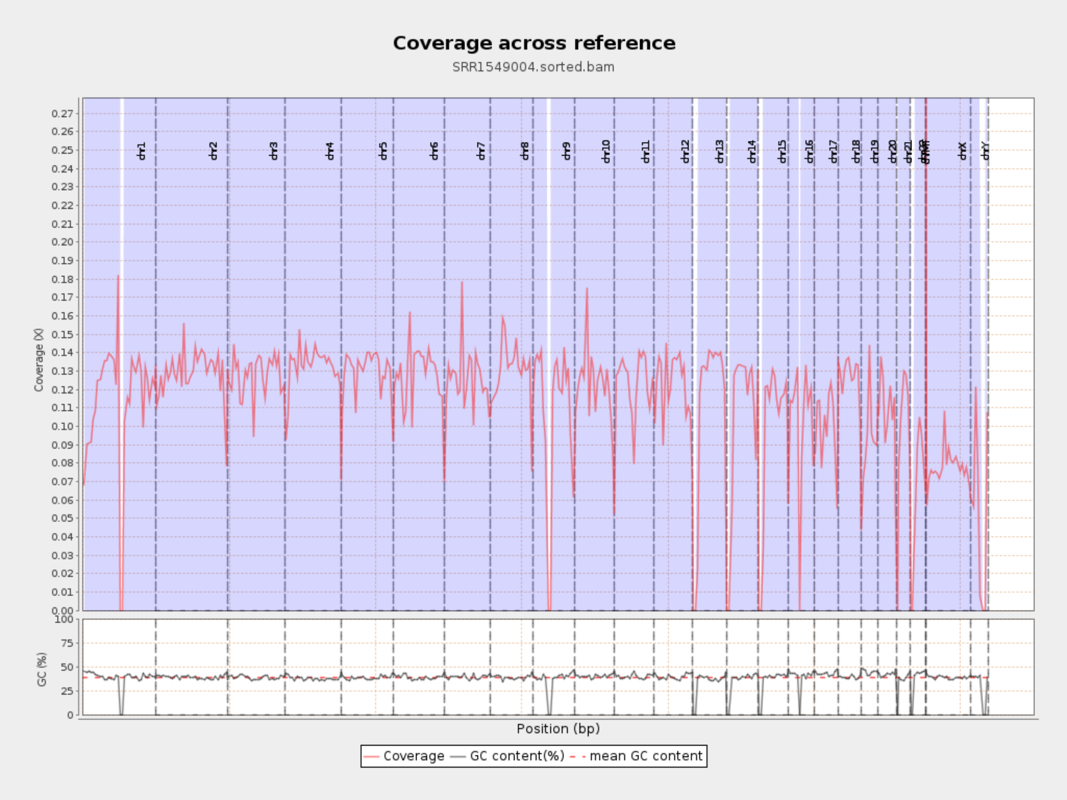
General error rate	0.29%
Mismatches	1,026,682
Insertions	10,705
Mapped reads with at least one insertion	0.12%
Deletions	30,276
Mapped reads with at least one deletion	0.34%
Homopolymer indels	43.81%

2.6. Chromosome stats

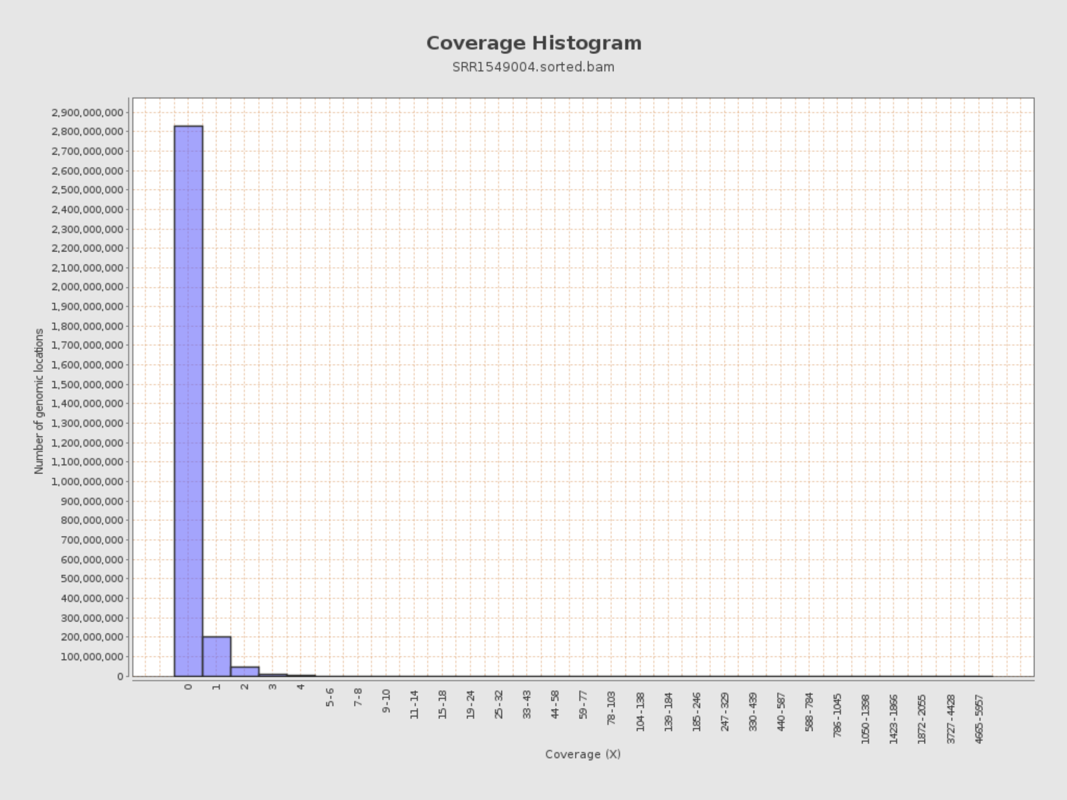
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28423282	0.114	1.5228
chr2	243199373	31412928	0.1292	0.6313
chr3	198022430	25335971	0.1279	0.4504
chr4	191154276	25438703	0.1331	0.4962
chr5	180915260	23398516	0.1293	0.4613
chr6	171115067	22086755	0.1291	0.5528
chr7	159138663	19836712	0.1247	0.9329
chr8	146364022	19106535	0.1305	2.9471

chr9	141213431	15160747	0.1074	0.5997
chr10	135534747	16751723	0.1236	0.6949
chr11	135006516	16608714	0.123	0.6073
chr12	133851895	16435600	0.1228	0.4631
chr13	115169878	12701337	0.1103	0.4139
chr14	107349540	11101560	0.1034	0.4809
chr15	102531392	9827610	0.0958	0.3838
chr16	90354753	8969453	0.0993	0.4505
chr17	81195210	8200932	0.101	0.4492
chr18	78077248	10023311	0.1284	1.2714
chr19	59128983	5555049	0.0939	1.1331
chr20	63025520	6955210	0.1104	0.4519
chr21	48129895	4685638	0.0974	0.4757
chr22	51304566	3272687	0.0638	0.3522
chrMT	16571	5615	0.3388	0.747
chrX	155270560	12069774	0.0777	0.4851
chrY	59373566	3178440	0.0535	0.5693

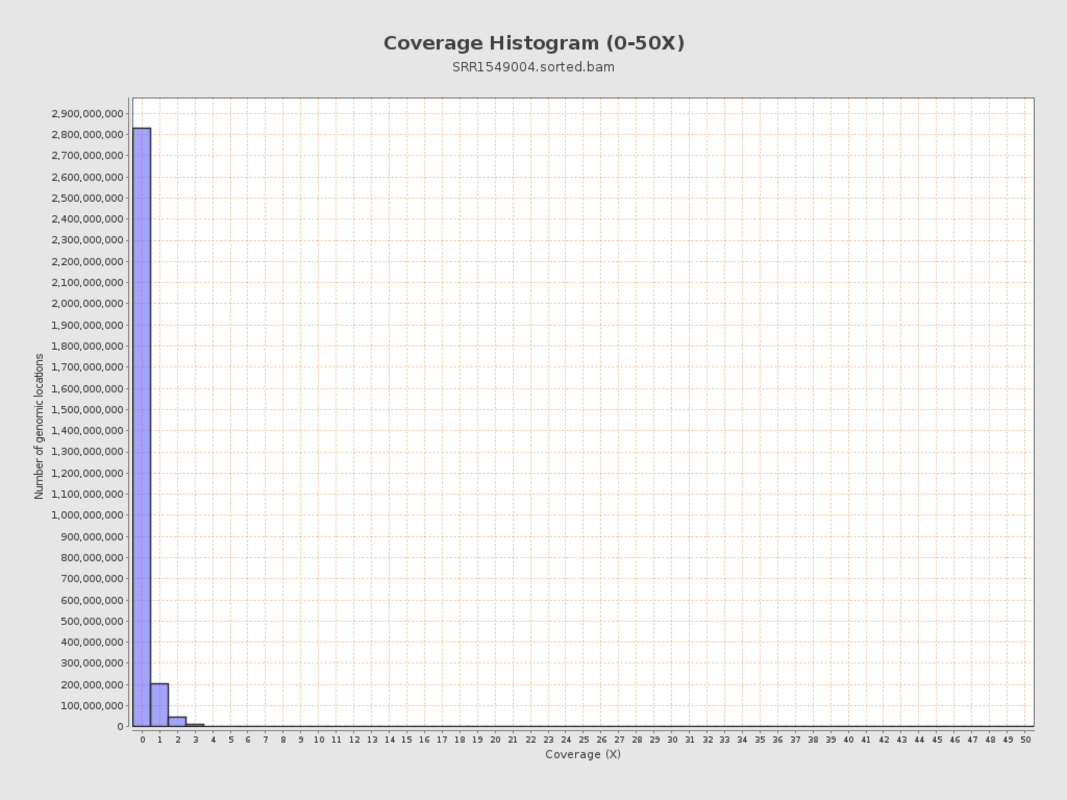
3. Results : Coverage across reference



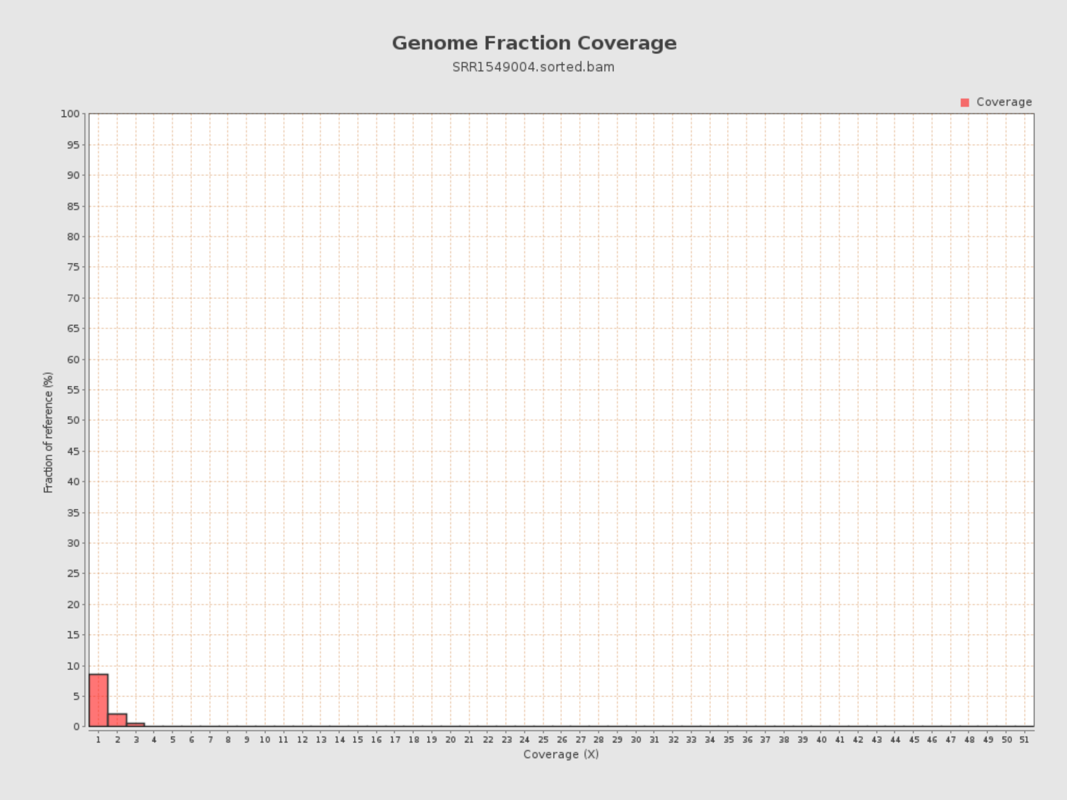
4. Results : Coverage Histogram



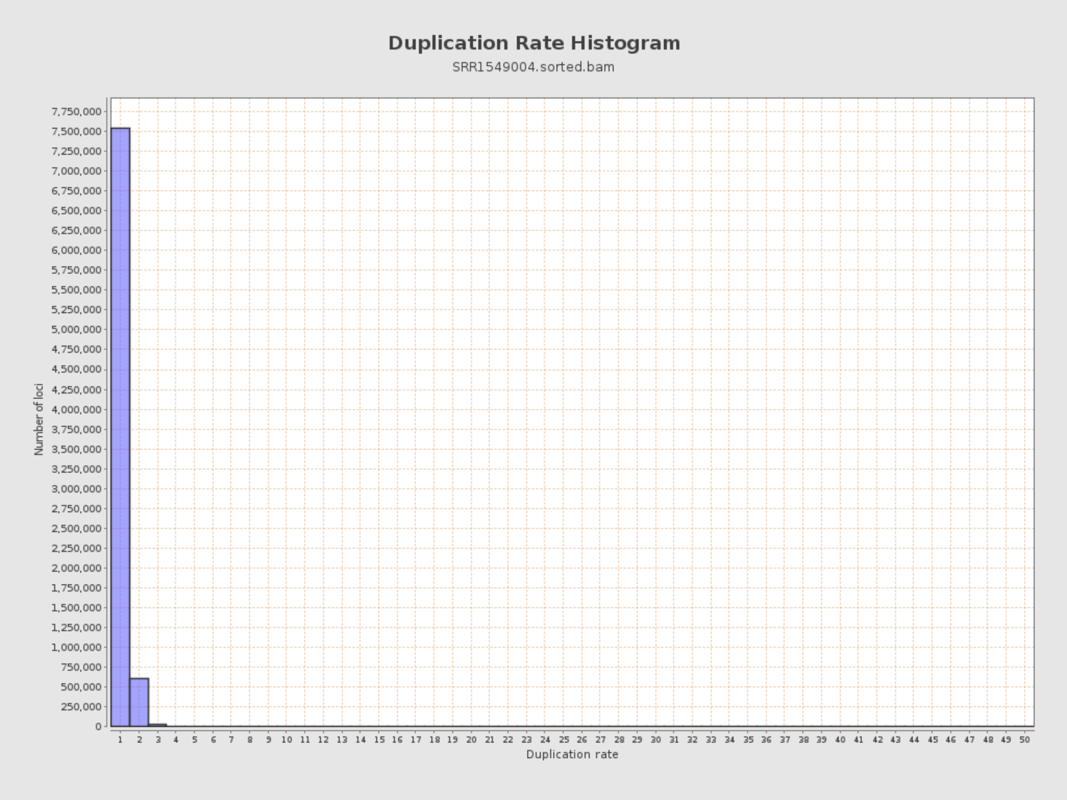
5. Results : Coverage Histogram (0-50X)



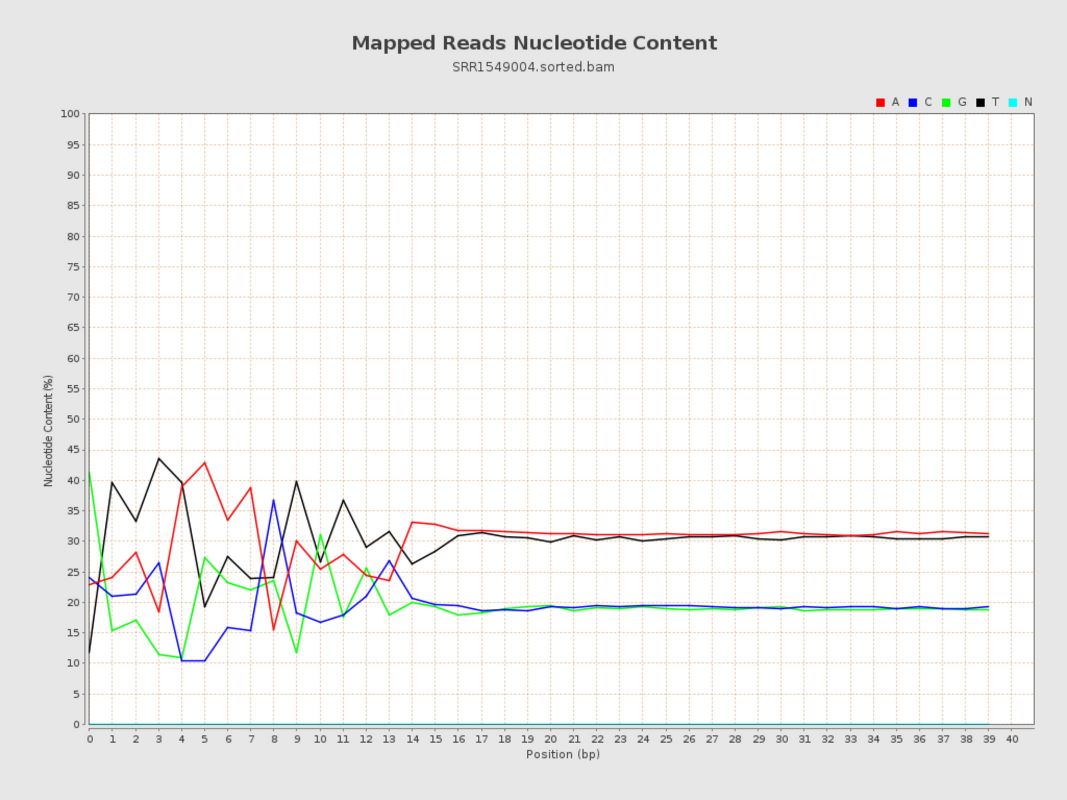
6. Results : Genome Fraction Coverage



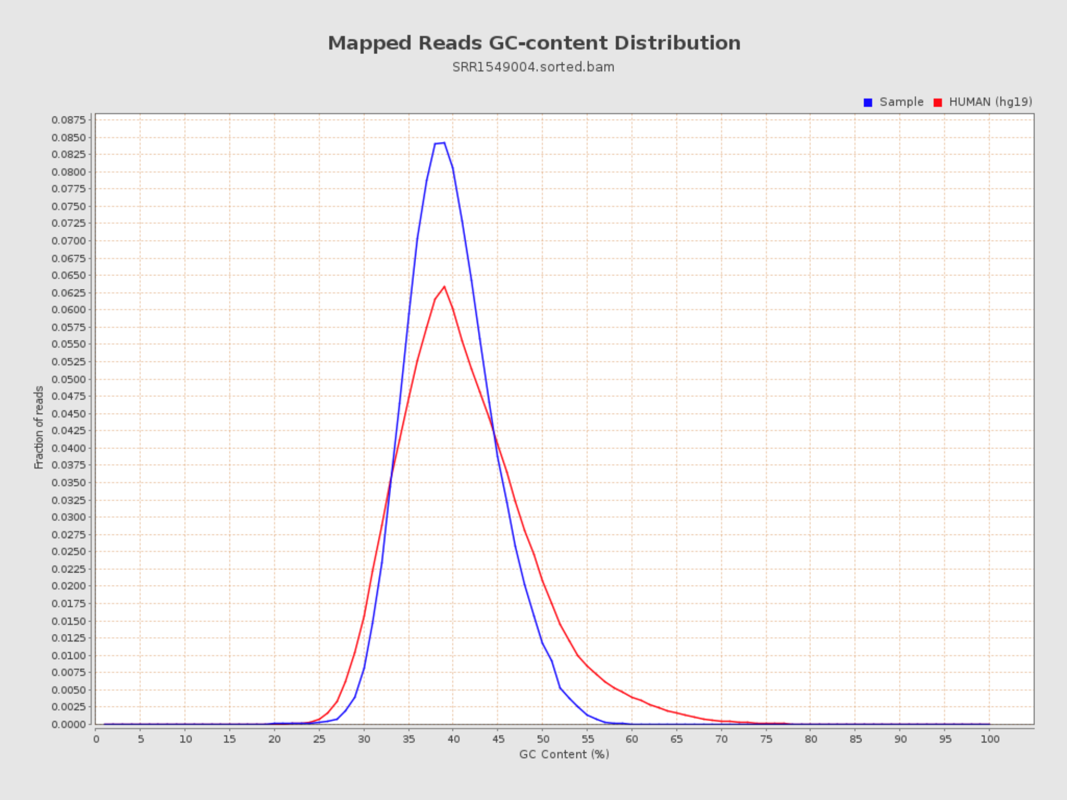
7. Results : Duplication Rate Histogram



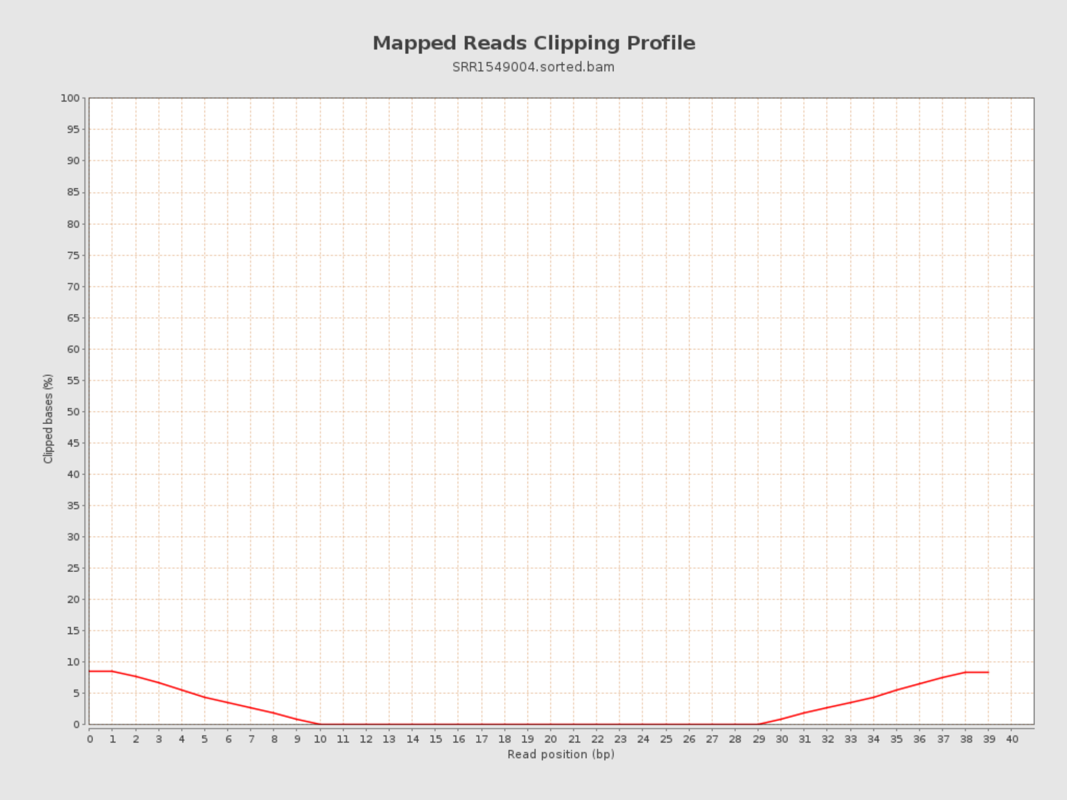
8. Results : Mapped Reads Nucleotide Content



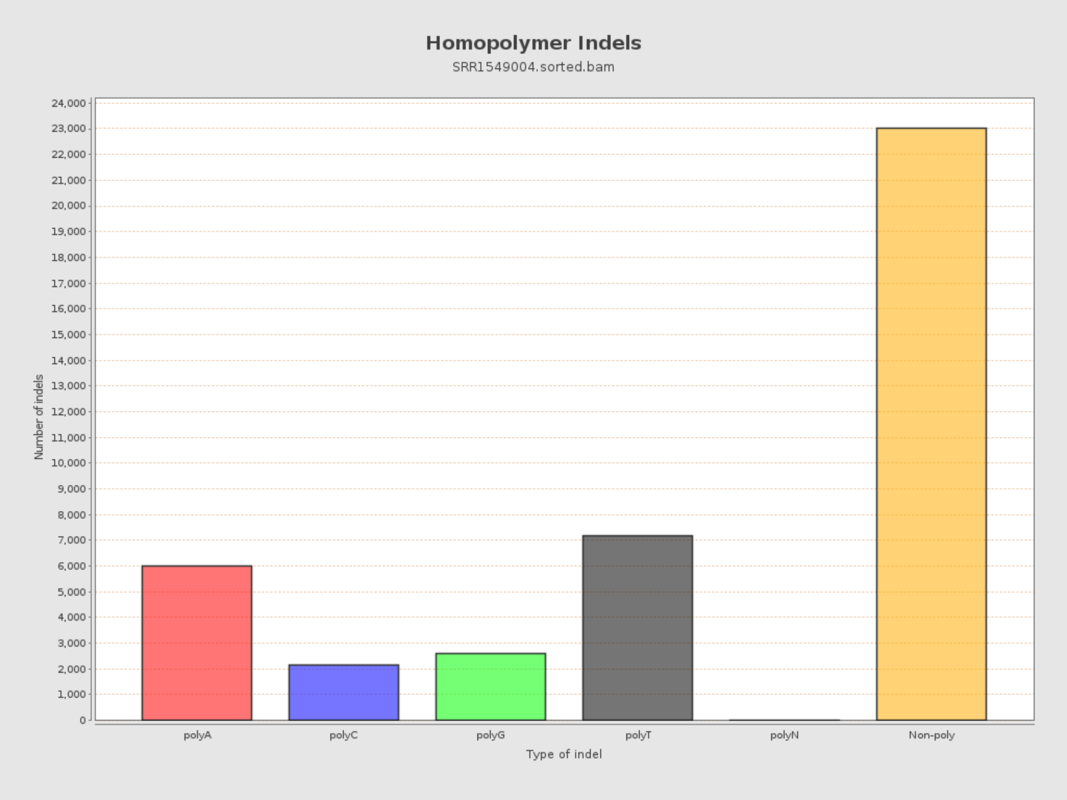
9. Results : Mapped Reads GC-content Distribution



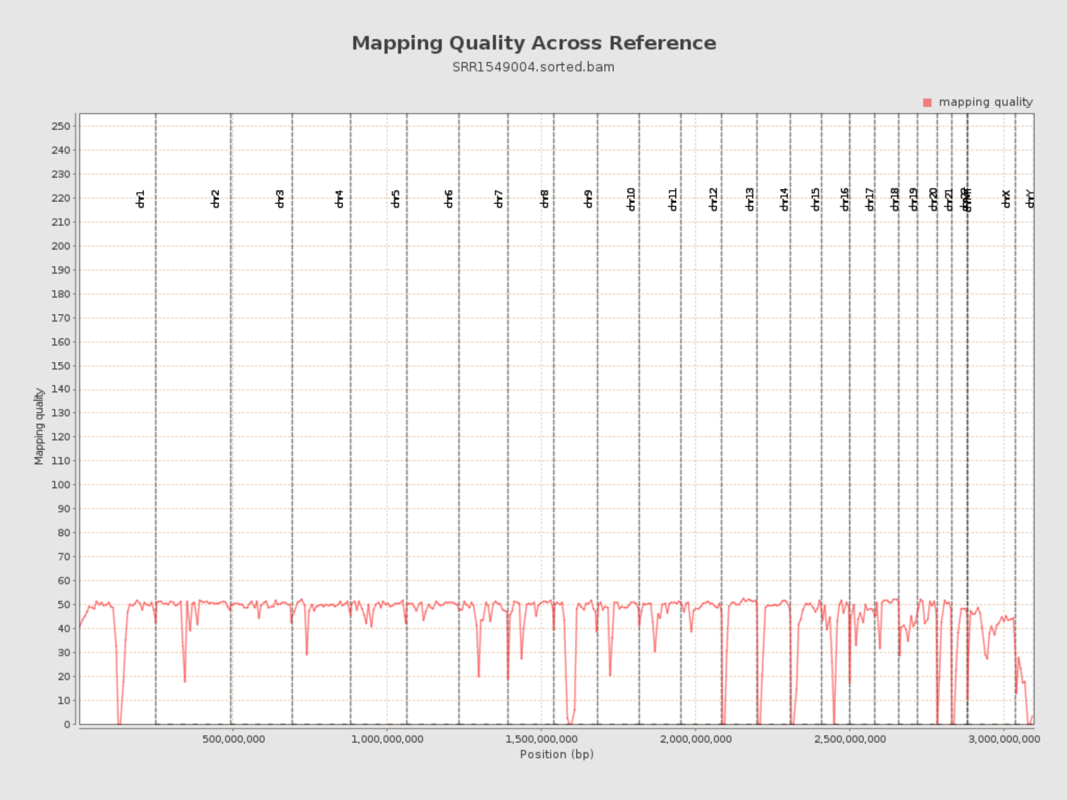
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram