Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:37:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548970.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_SRR1548970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548970.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:37:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,266,879
Mapped reads	2,334,703 / 44.33%
Unmapped reads	2,932,176 / 55.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	53,546 / 1.02%
Duplication rate	1.69%
Clipped reads	254,271 / 4.83%

2.2. ACGT Content

Number/percentage of A's	28,670,487 / 31.14%
Number/percentage of C's	17,360,003 / 18.86%
Number/percentage of T's	28,486,248 / 30.94%
Number/percentage of G's	17,537,069 / 19.05%
Number/percentage of N's	4,082 / 0%
GC Percentage	37.91%

2.3. Coverage

Mean	0.0297
Standard Deviation	0.258

2.4. Mapping Quality

Mean Mapping Quality	43.39

2.5. Mismatches and indels

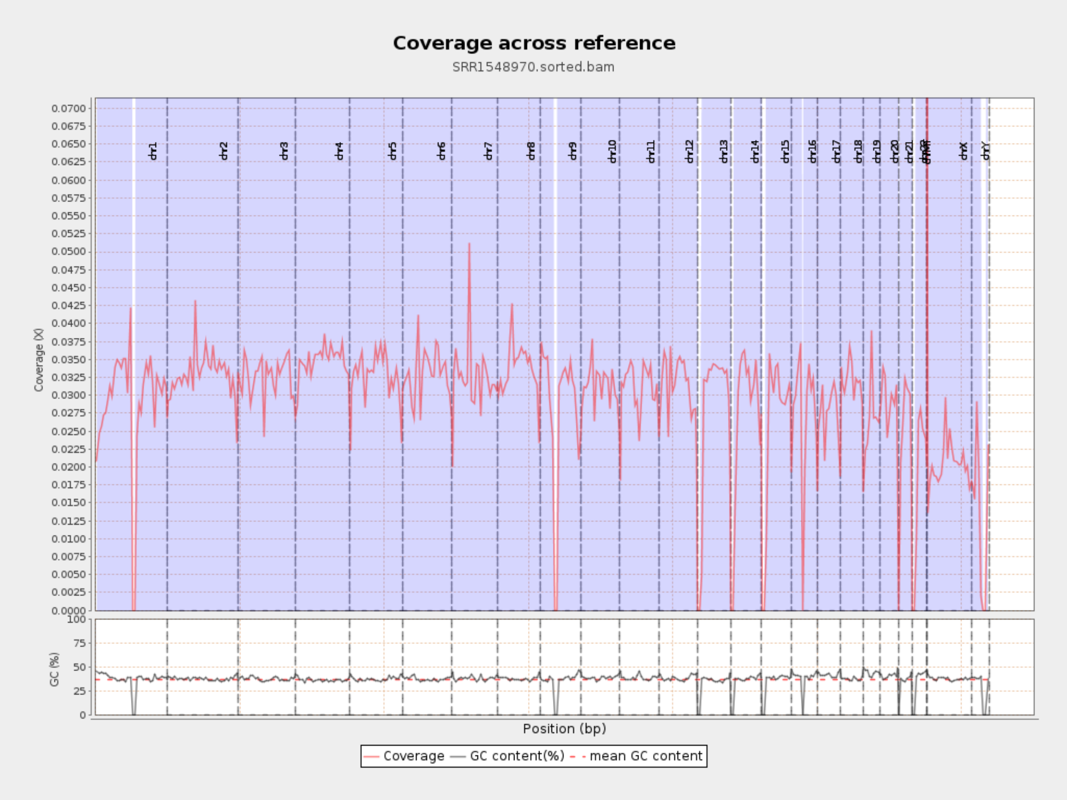
General error rate	0.34%
Mismatches	309,608
Insertions	4,508
Mapped reads with at least one insertion	0.19%
Deletions	10,298
Mapped reads with at least one deletion	0.44%
Homopolymer indels	45.28%

2.6. Chromosome stats

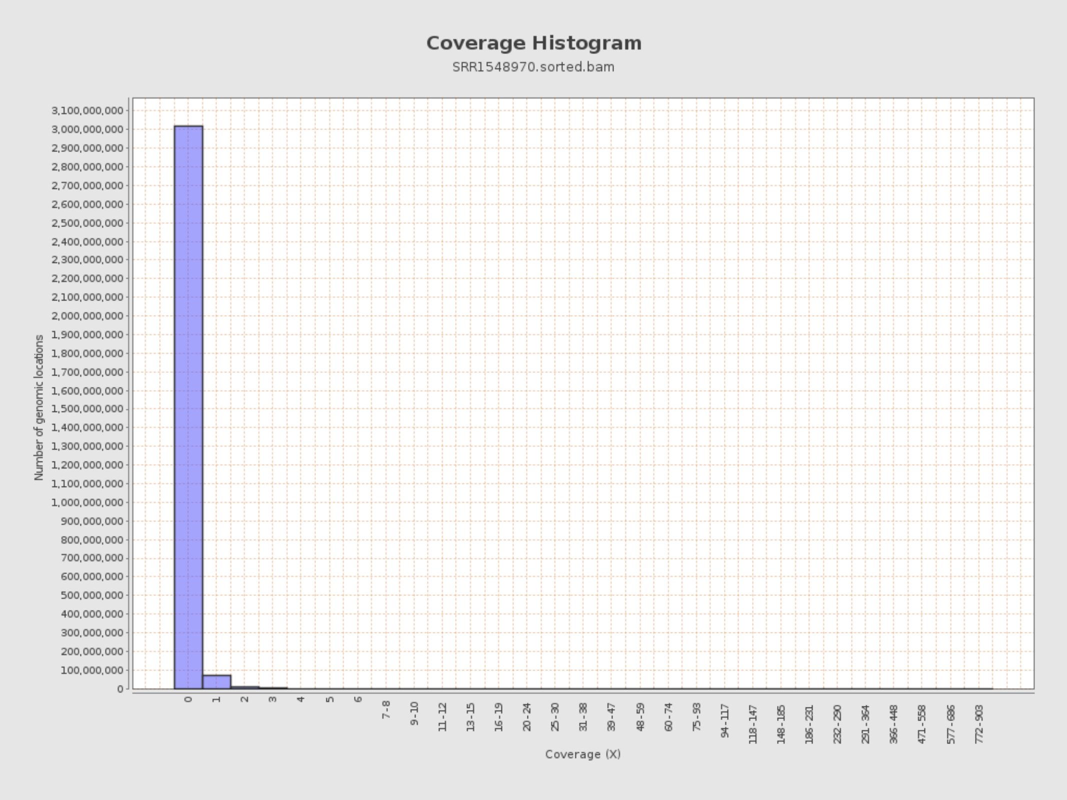
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7220509	0.029	0.3606
chr2	243199373	8037593	0.033	0.2455
chr3	198022430	6453868	0.0326	0.2052
chr4	191154276	6628541	0.0347	0.2151
chr5	180915260	5989491	0.0331	0.2084
chr6	171115067	5649751	0.033	0.2238
chr7	159138663	5208039	0.0327	0.3388
chr8	146364022	4948994	0.0338	0.4861

chr9	141213431	3960868	0.028	0.217
chr10	135534747	4243465	0.0313	0.2231
chr11	135006516	4203224	0.0311	0.2404
chr12	133851895	4233685	0.0316	0.2053
chr13	115169878	3156767	0.0274	0.1881
chr14	107349540	2860980	0.0267	0.201
chr15	102531392	2607691	0.0254	0.1797
chr16	90354753	2428424	0.0269	0.19
chr17	81195210	2225069	0.0274	0.193
chr18	78077248	2522044	0.0323	0.3416
chr19	59128983	1588571	0.0269	0.3331
chr20	63025520	1833367	0.0291	0.1943
chr21	48129895	1185258	0.0246	0.1862
chr22	51304566	921367	0.018	0.1632
chrMT	16571	3027	0.1827	0.4388
chrX	155270560	3177924	0.0205	0.179
chrY	59373566	782204	0.0132	0.1651

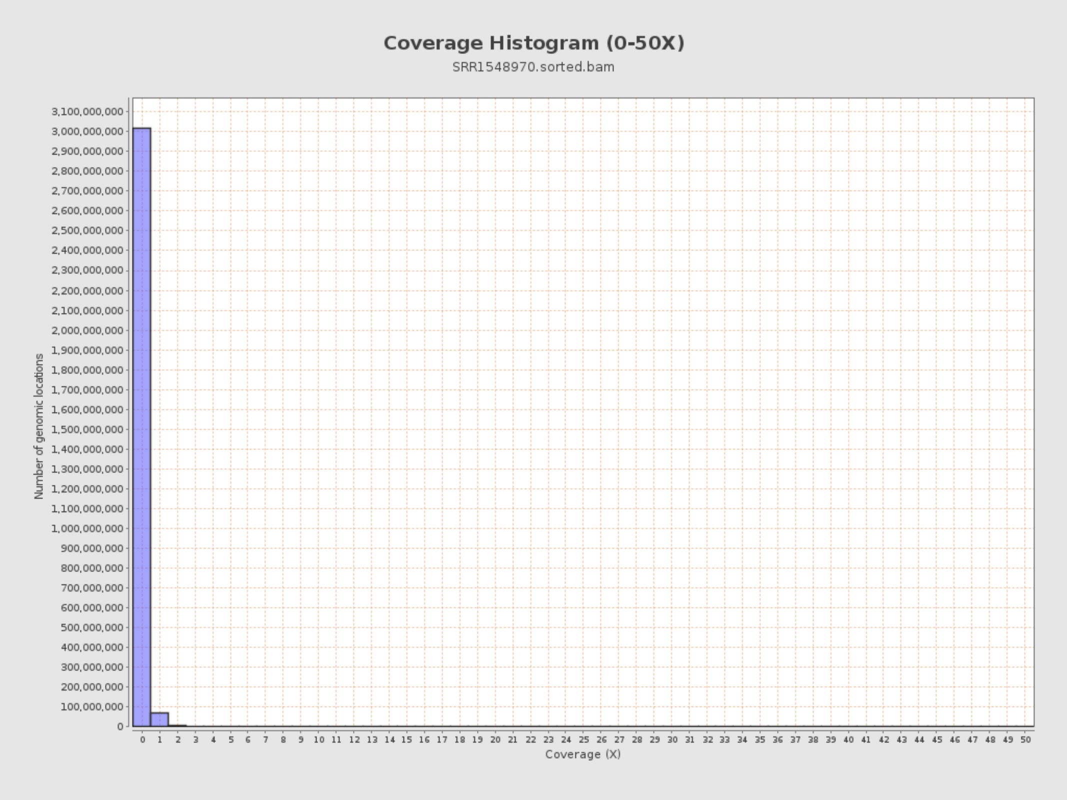
3. Results : Coverage across reference



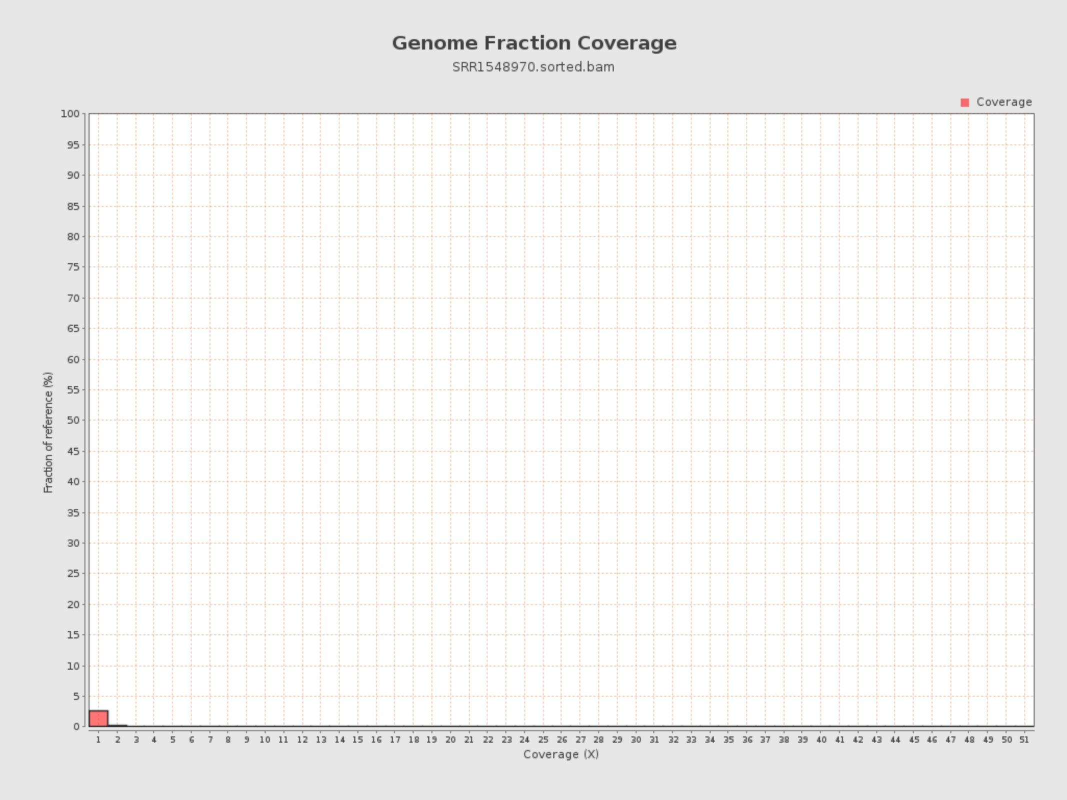
4. Results : Coverage Histogram



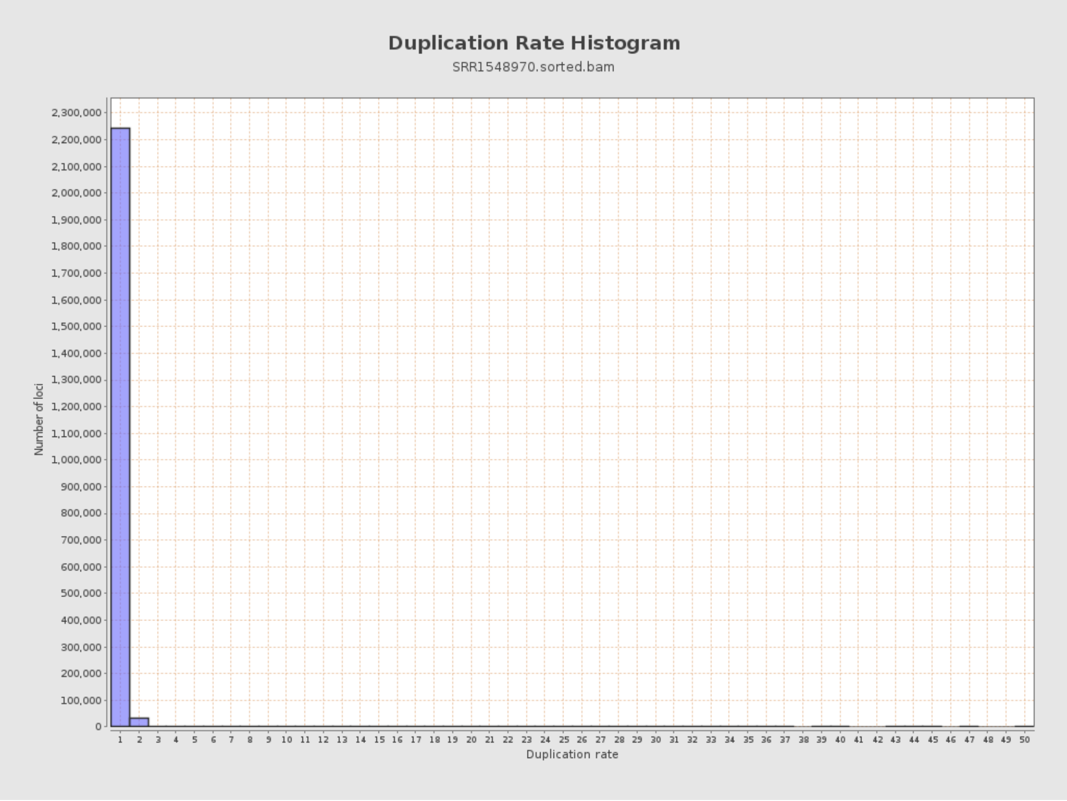
5. Results : Coverage Histogram (0-50X)



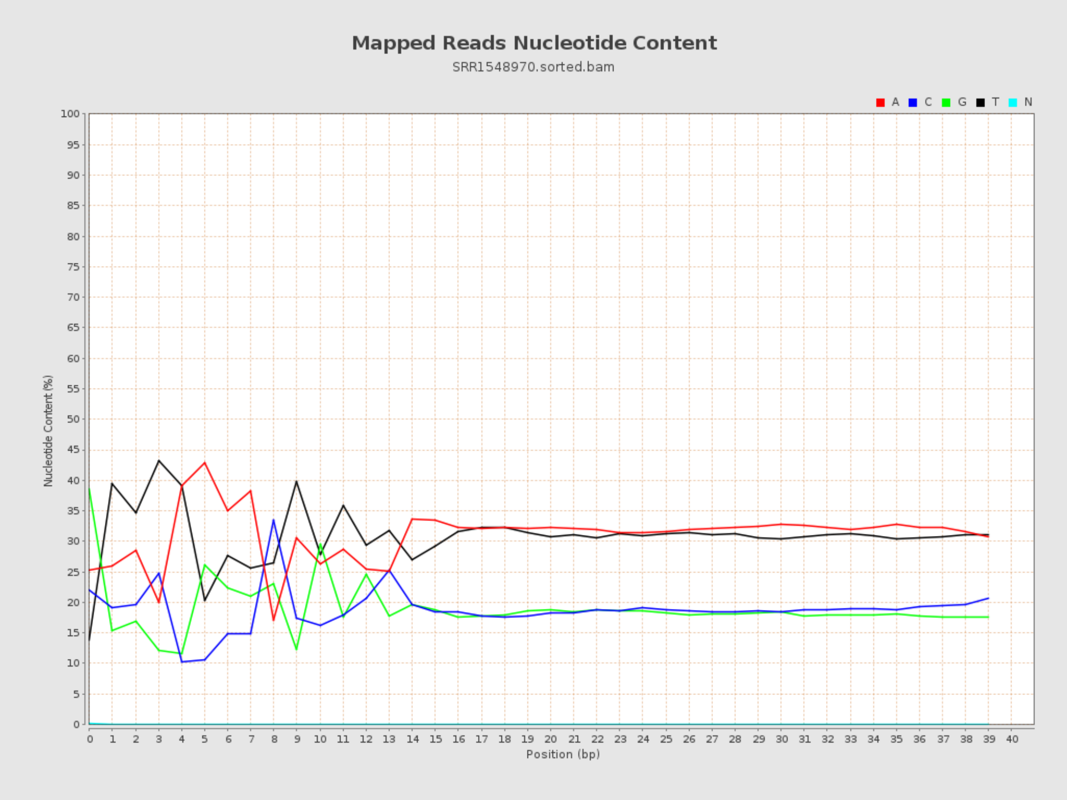
6. Results : Genome Fraction Coverage



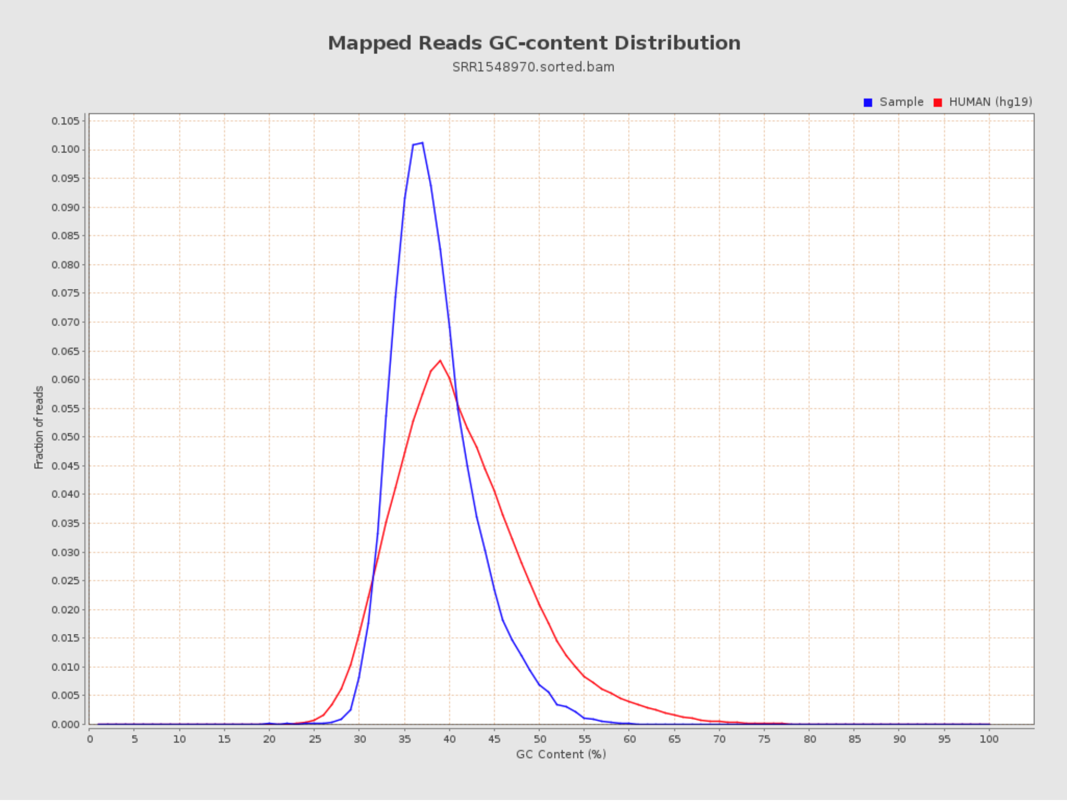
7. Results : Duplication Rate Histogram



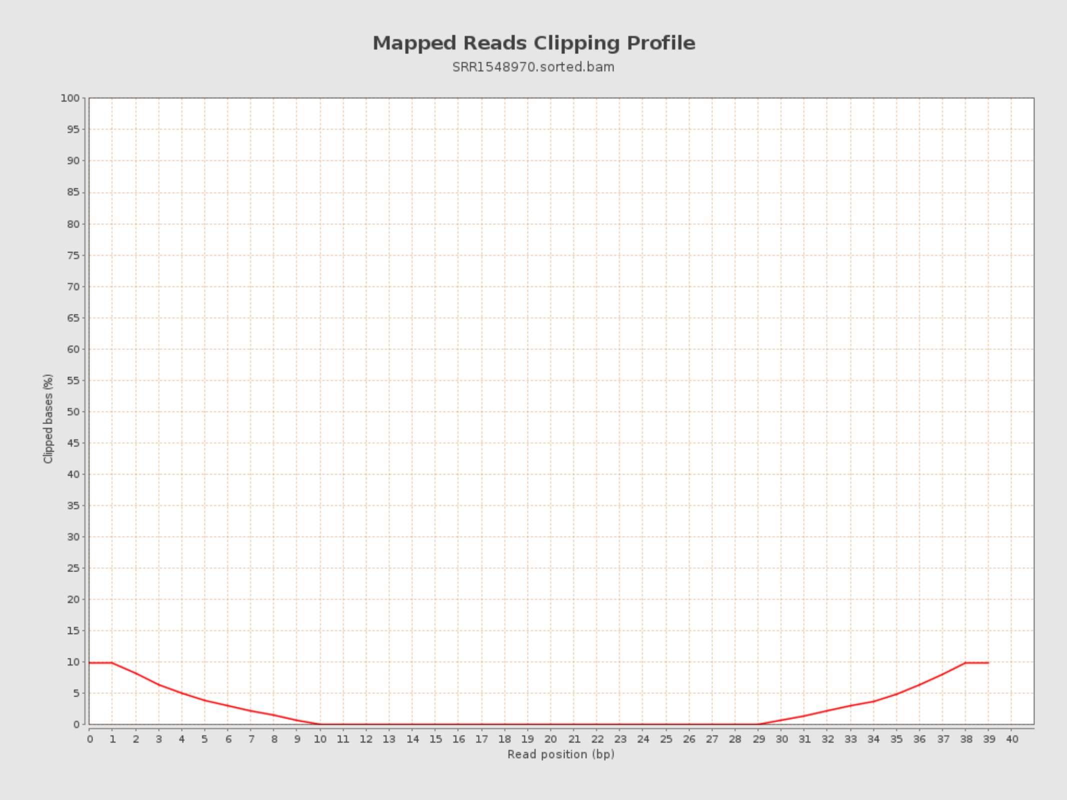
8. Results : Mapped Reads Nucleotide Content



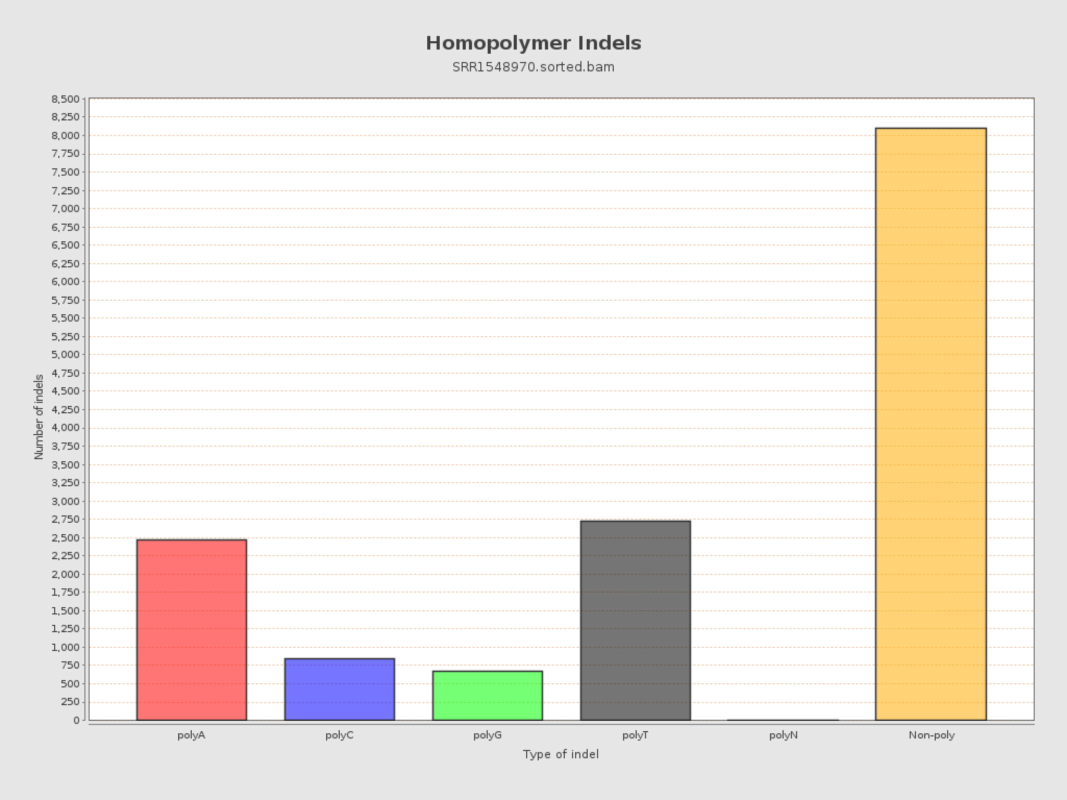
9. Results : Mapped Reads GC-content Distribution



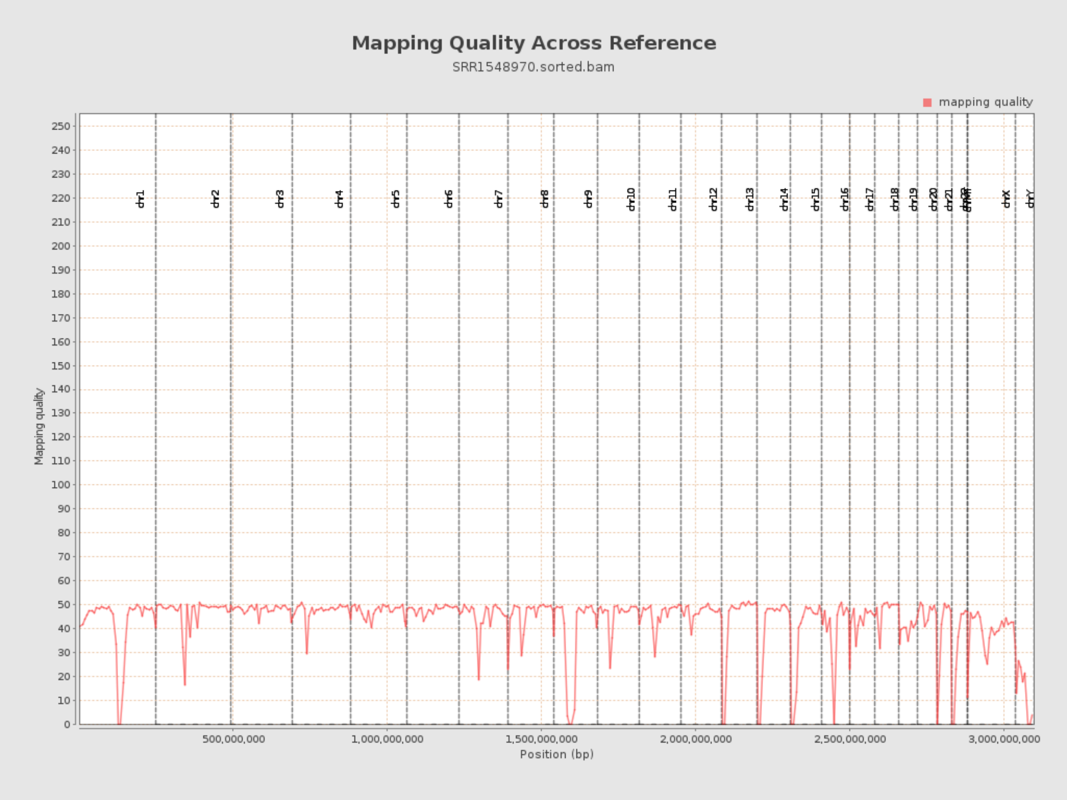
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram