Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:38:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548940.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_SRR1548940 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548940.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:38:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,556,545
Mapped reads	6,633,595 / 87.79%
Unmapped reads	922,950 / 12.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	299,130 / 3.96%
Duplication rate	2.66%
Clipped reads	642,348 / 8.5%

2.2. ACGT Content

Number/percentage of A's	74,273,236 / 28.38%
Number/percentage of C's	56,666,436 / 21.65%
Number/percentage of T's	74,707,140 / 28.54%
Number/percentage of G's	56,102,102 / 21.43%
Number/percentage of N's	2,214 / 0%
GC Percentage	43.08%

2.3. Coverage

Mean	0.0846
Standard Deviation	0.9232

2.4. Mapping Quality

Mean Mapping Quality	34.62

2.5. Mismatches and indels

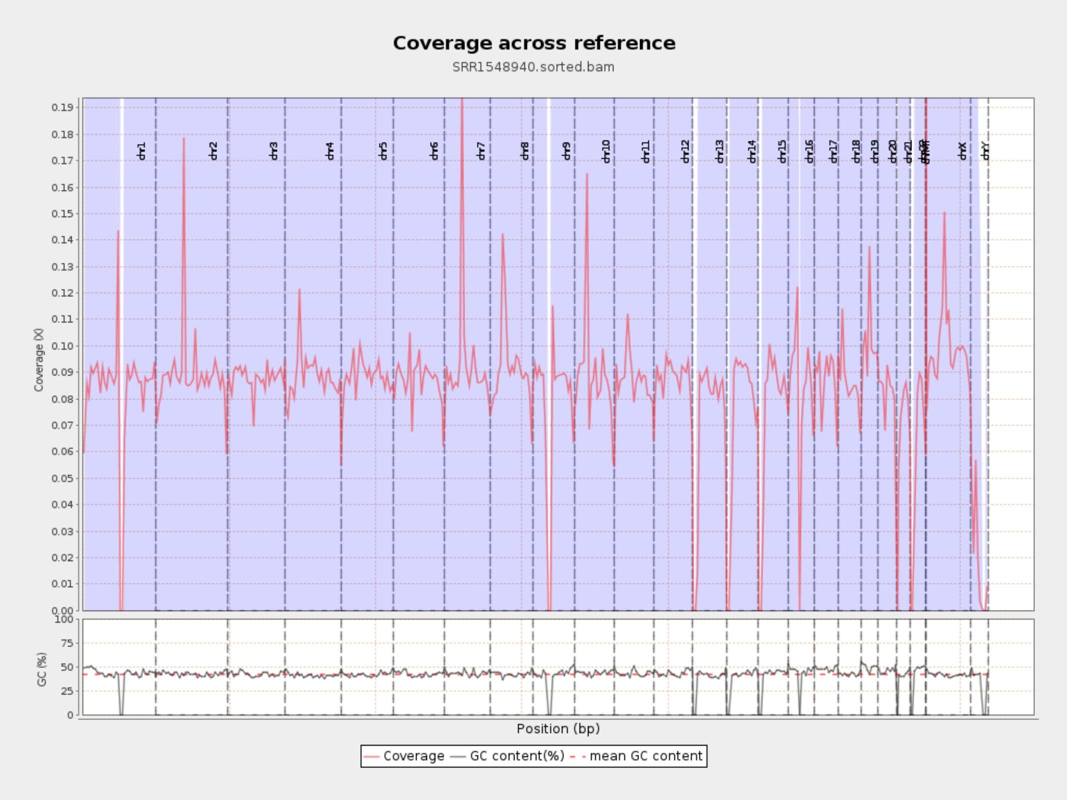
General error rate	0.37%
Mismatches	955,116
Insertions	10,218
Mapped reads with at least one insertion	0.15%
Deletions	21,599
Mapped reads with at least one deletion	0.33%
Homopolymer indels	38.02%

2.6. Chromosome stats

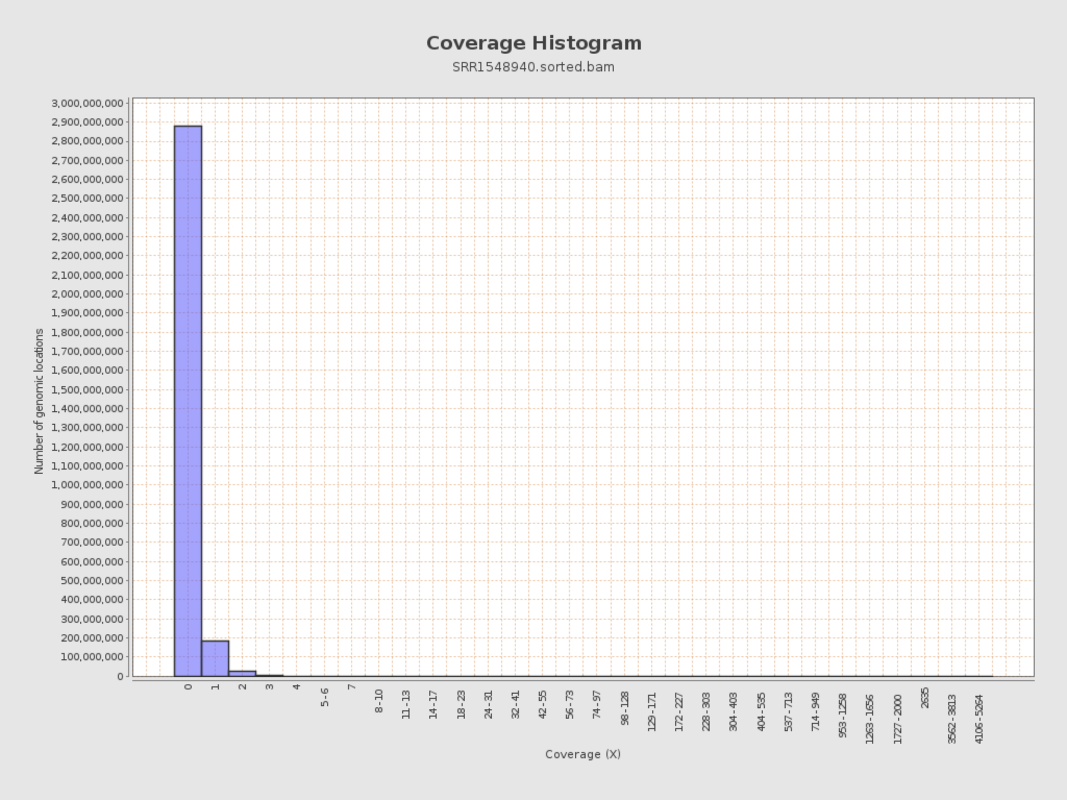
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20605582	0.0827	1.374
chr2	243199373	21845239	0.0898	0.7903
chr3	198022430	17375515	0.0877	0.3512
chr4	191154276	16993089	0.0889	0.3982
chr5	180915260	15984020	0.0884	0.3713
chr6	171115067	14973853	0.0875	0.4155
chr7	159138663	14987203	0.0942	1.1963
chr8	146364022	13498226	0.0922	2.5867

chr9	141213431	10988185	0.0778	0.7799
chr10	135534747	12204090	0.09	0.7122
chr11	135006516	11811660	0.0875	0.686
chr12	133851895	11868865	0.0887	0.3919
chr13	115169878	8119374	0.0705	0.3016
chr14	107349540	7955258	0.0741	0.455
chr15	102531392	7362857	0.0718	0.3158
chr16	90354753	7343640	0.0813	0.4529
chr17	81195210	7162027	0.0882	0.3911
chr18	78077248	6801426	0.0871	1.5864
chr19	59128983	6015098	0.1017	1.4077
chr20	63025520	5144429	0.0816	0.3835
chr21	48129895	3231272	0.0671	0.4226
chr22	51304566	2948954	0.0575	0.3032
chrMT	16571	5295	0.3195	0.6601
chrX	155270560	15430077	0.0994	0.5454
chrY	59373566	1123697	0.0189	0.2687

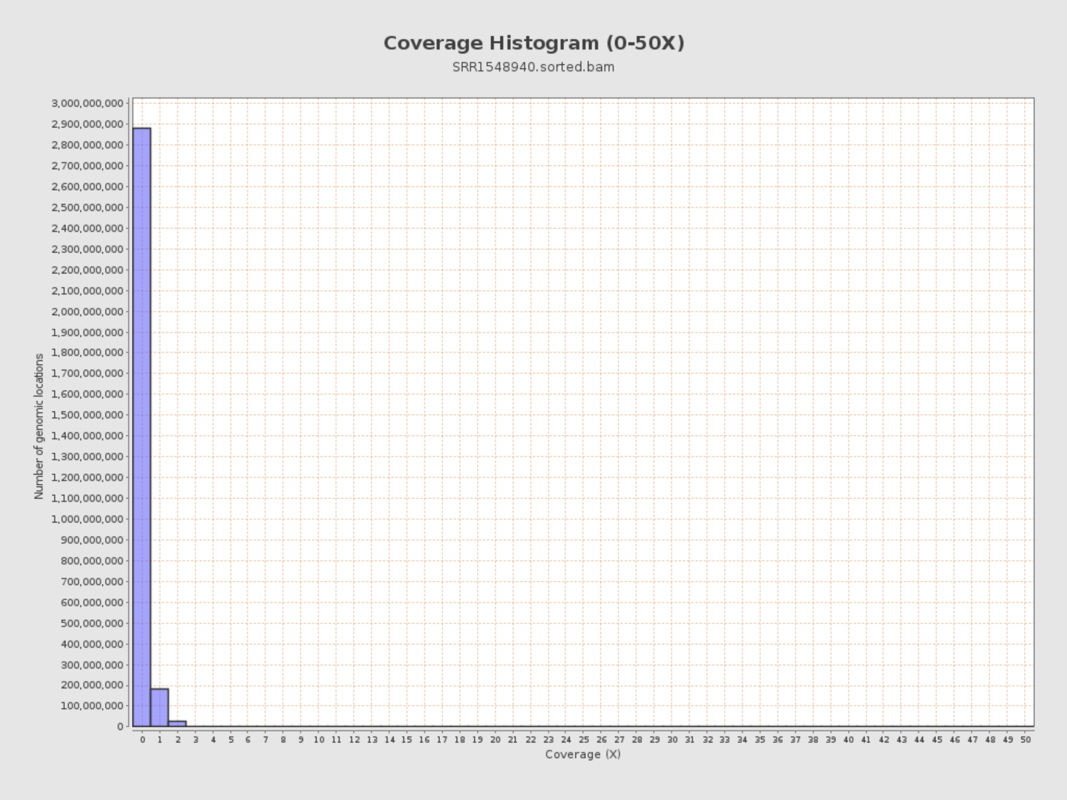
3. Results : Coverage across reference



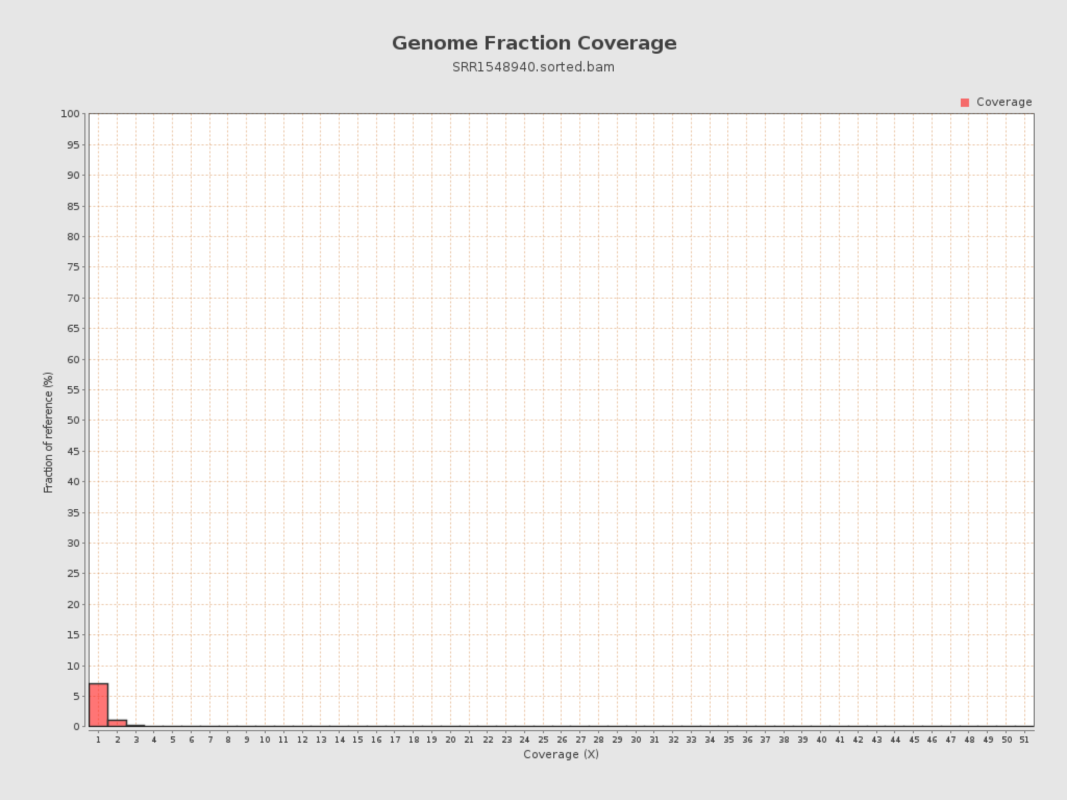
4. Results : Coverage Histogram



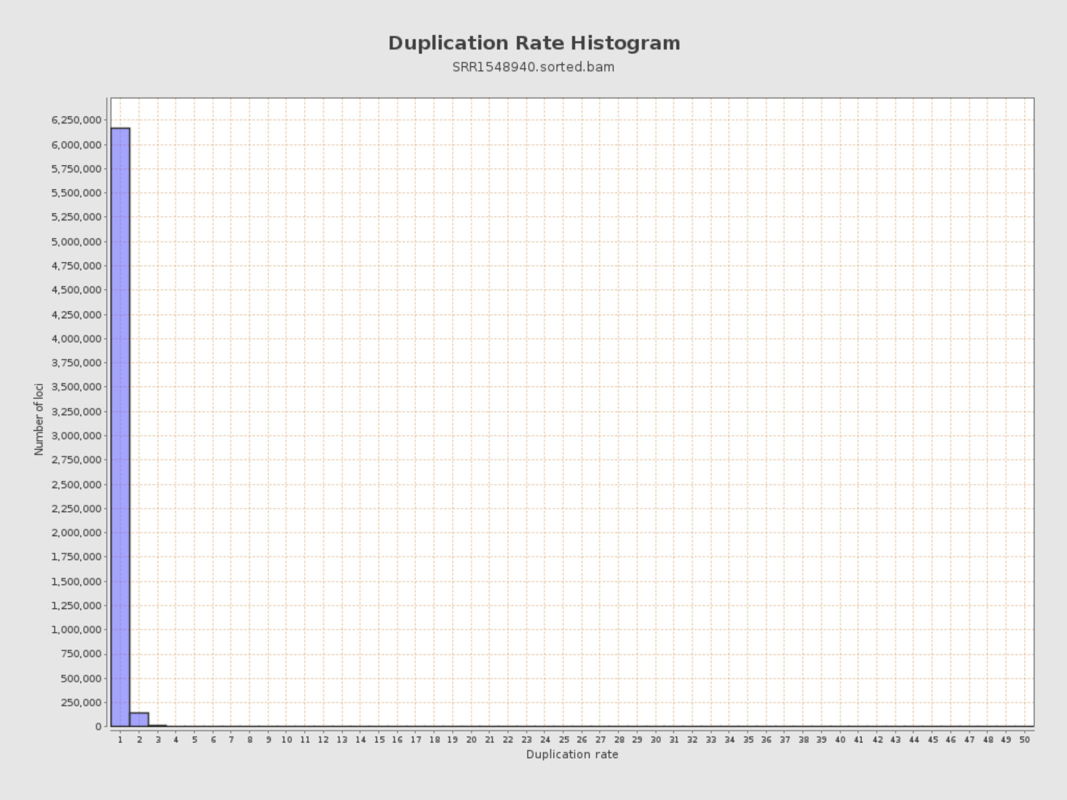
5. Results : Coverage Histogram (0-50X)



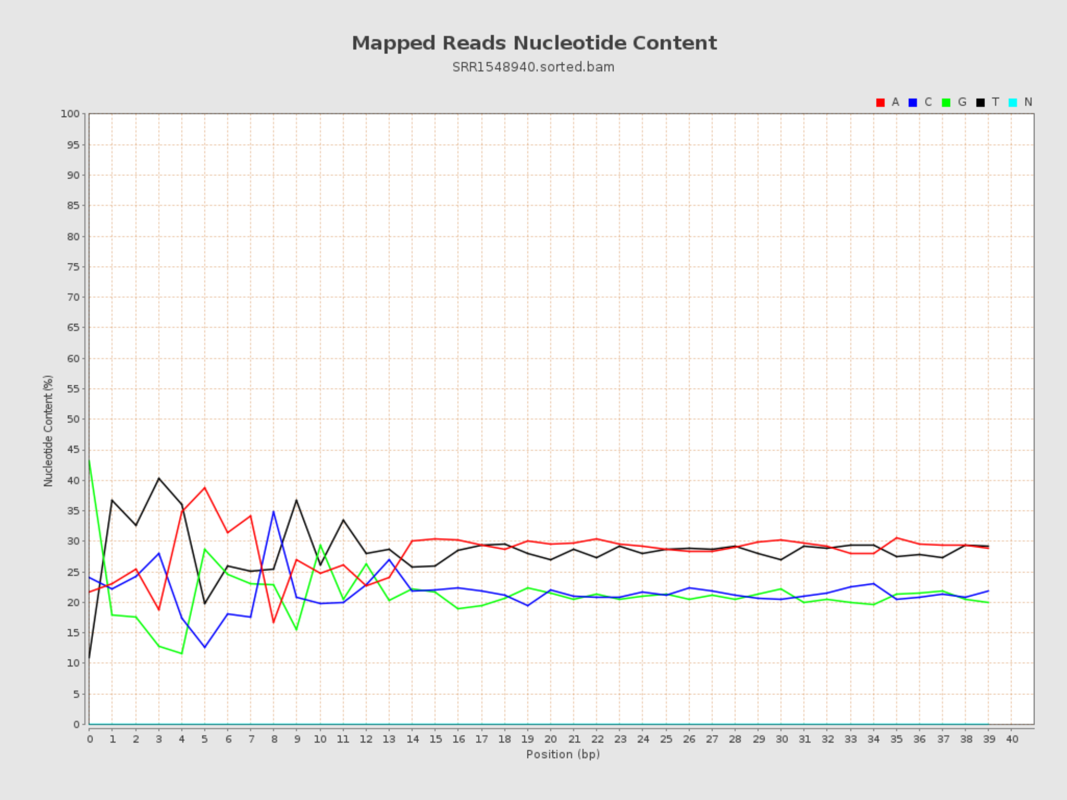
6. Results : Genome Fraction Coverage



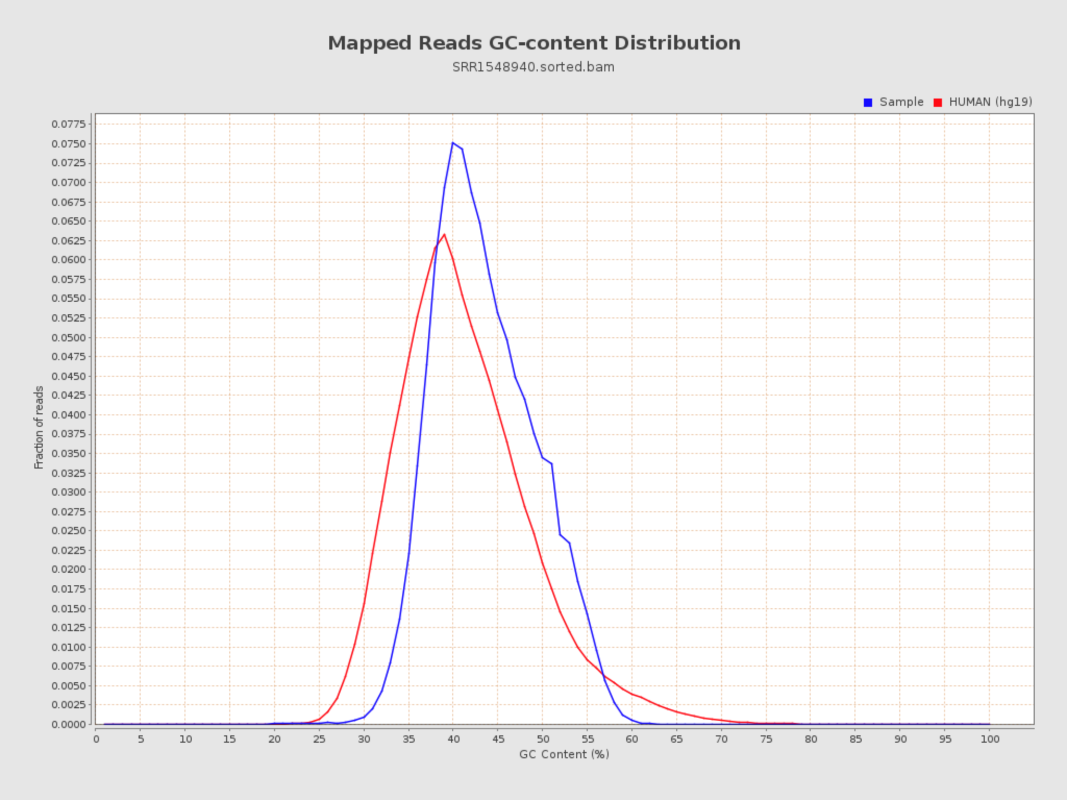
7. Results : Duplication Rate Histogram



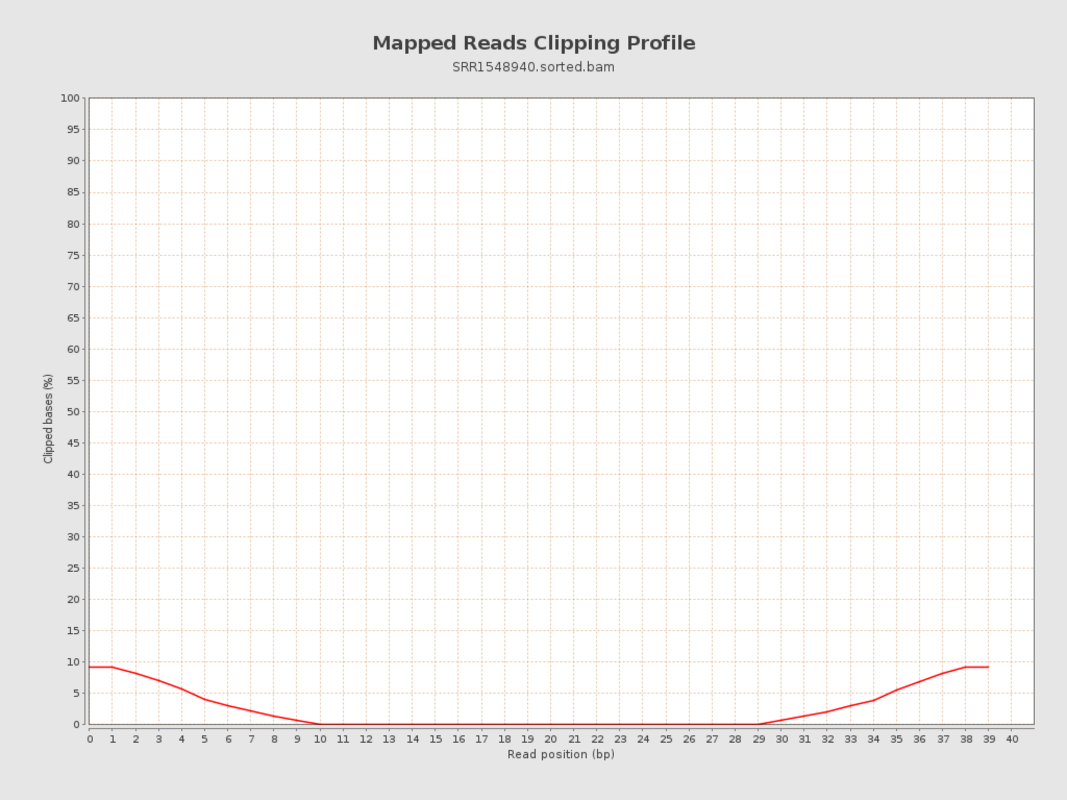
8. Results : Mapped Reads Nucleotide Content



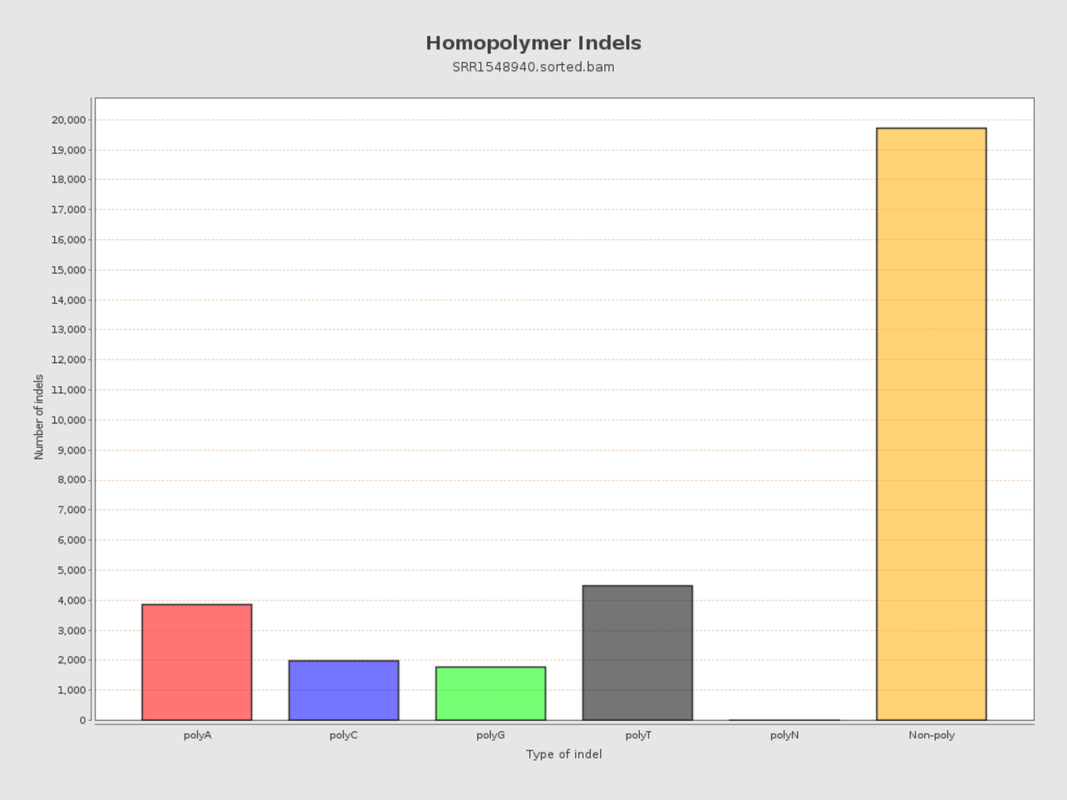
9. Results : Mapped Reads GC-content Distribution



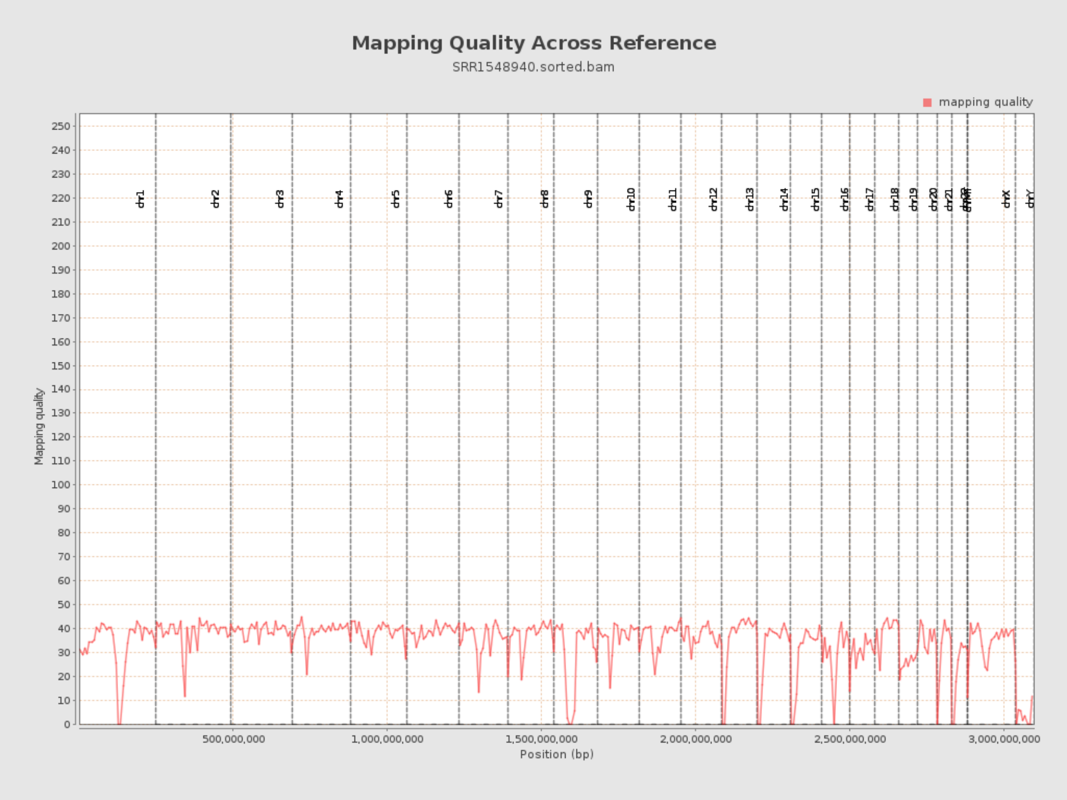
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram