Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:08:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548954.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_SRR1548954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548954.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:08:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,543,467
Mapped reads	7,451,571 / 87.22%
Unmapped reads	1,091,896 / 12.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	418,053 / 4.89%
Duplication rate	3.19%
Clipped reads	716,854 / 8.39%

2.2. ACGT Content

Number/percentage of A's	82,209,663 / 27.96%
Number/percentage of C's	64,213,935 / 21.84%
Number/percentage of T's	83,792,293 / 28.5%
Number/percentage of G's	63,806,866 / 21.7%
Number/percentage of N's	392 / 0%
GC Percentage	43.54%

2.3. Coverage

Mean	0.095
Standard Deviation	1.1968

2.4. Mapping Quality

Mean Mapping Quality	33.82

2.5. Mismatches and indels

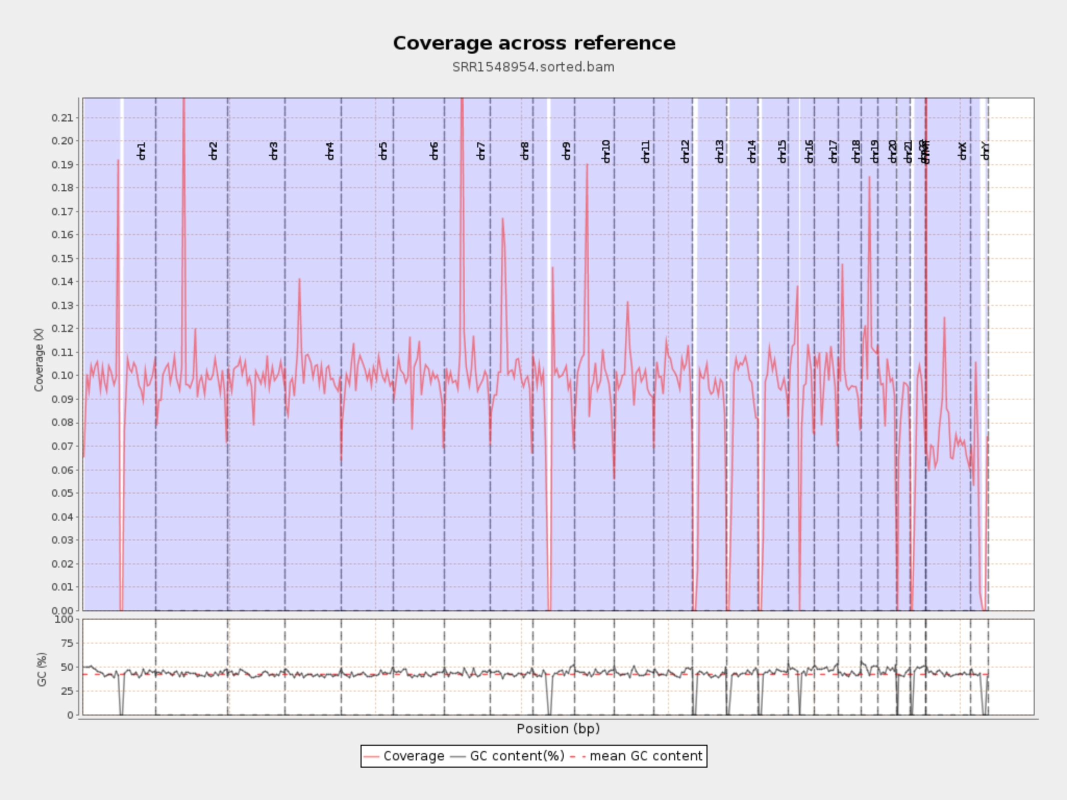
General error rate	0.36%
Mismatches	1,054,851
Insertions	11,381
Mapped reads with at least one insertion	0.15%
Deletions	23,452
Mapped reads with at least one deletion	0.31%
Homopolymer indels	38.04%

2.6. Chromosome stats

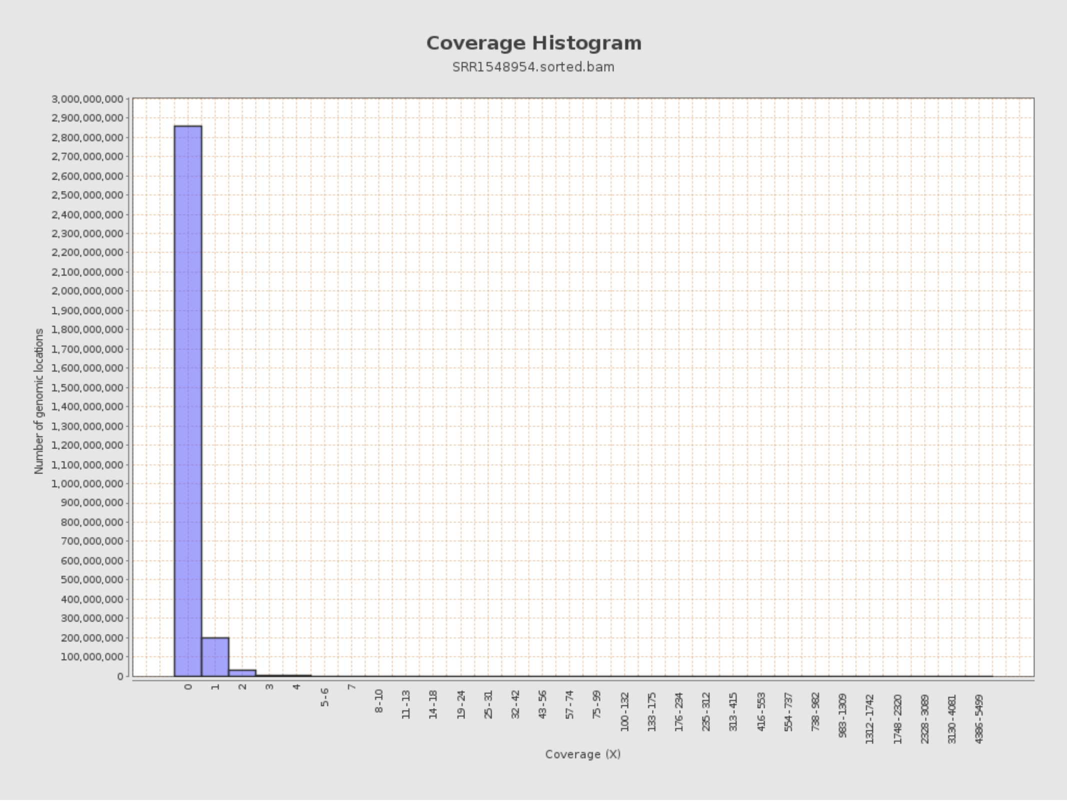
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23654743	0.0949	2.0842
chr2	243199373	24915749	0.1024	1.1149
chr3	198022430	19748235	0.0997	0.3859
chr4	191154276	19398537	0.1015	0.4431
chr5	180915260	18085251	0.1	0.4175
chr6	171115067	17037158	0.0996	0.443
chr7	159138663	17311533	0.1088	1.8204
chr8	146364022	15163584	0.1036	2.7452

chr9	141213431	12510648	0.0886	1.1678
chr10	135534747	13964444	0.103	0.8747
chr11	135006516	13430713	0.0995	0.7553
chr12	133851895	13639481	0.1019	0.454
chr13	115169878	9180594	0.0797	0.325
chr14	107349540	9016261	0.084	0.5607
chr15	102531392	8249697	0.0805	0.35
chr16	90354753	8409358	0.0931	0.5475
chr17	81195210	8160779	0.1005	0.4234
chr18	78077248	7842473	0.1004	2.2641
chr19	59128983	7077718	0.1197	2.1569
chr20	63025520	5914744	0.0938	0.442
chr21	48129895	3720663	0.0773	0.5665
chr22	51304566	3388209	0.066	0.4656
chrMT	16571	12883	0.7774	1.246
chrX	155270560	11431563	0.0736	0.619
chrY	59373566	2788265	0.047	0.4365

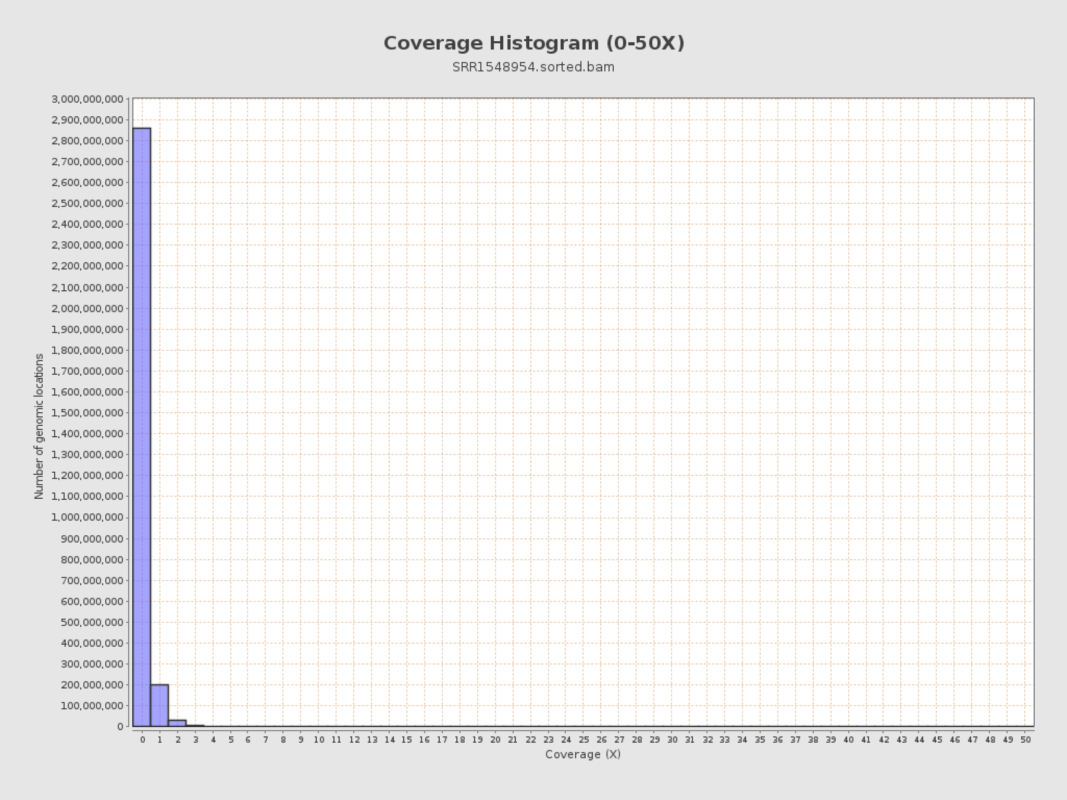
3. Results : Coverage across reference



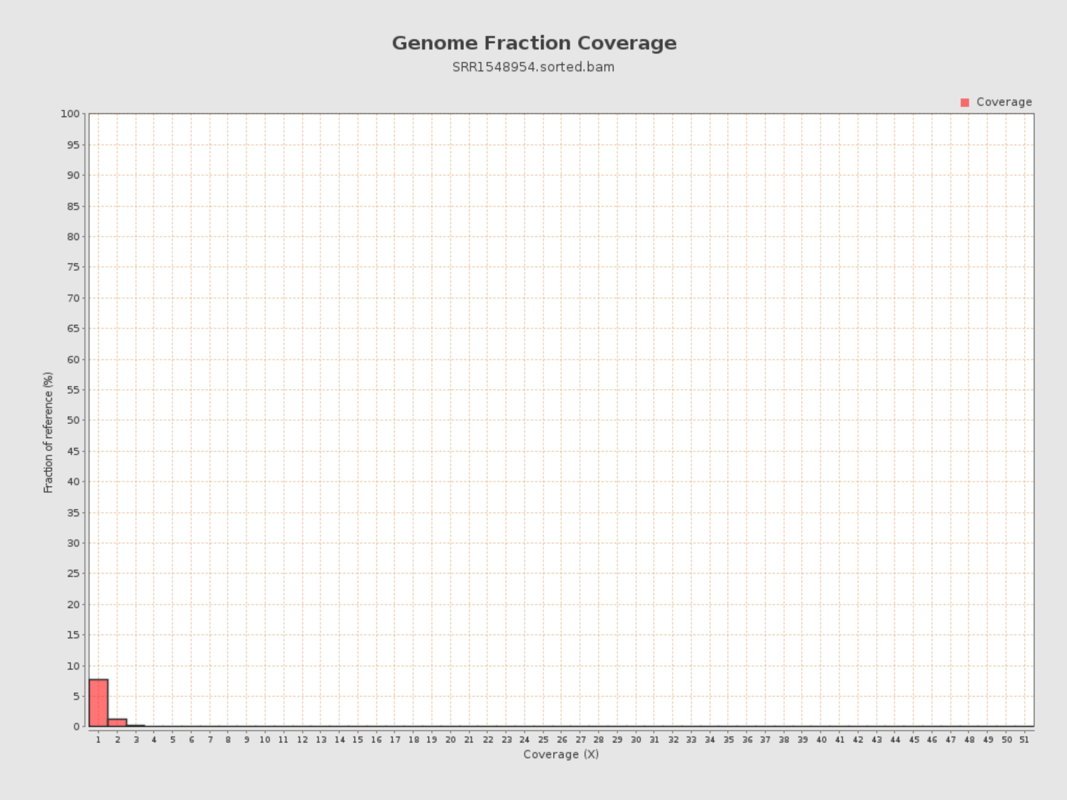
4. Results : Coverage Histogram



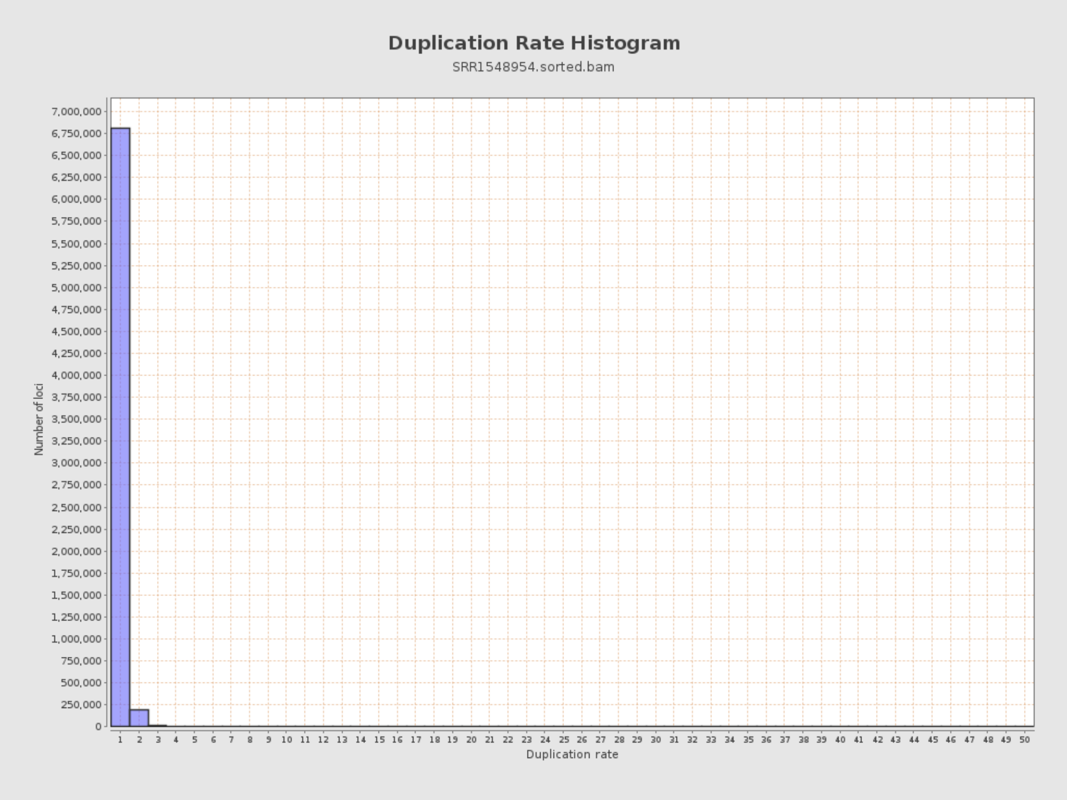
5. Results : Coverage Histogram (0-50X)



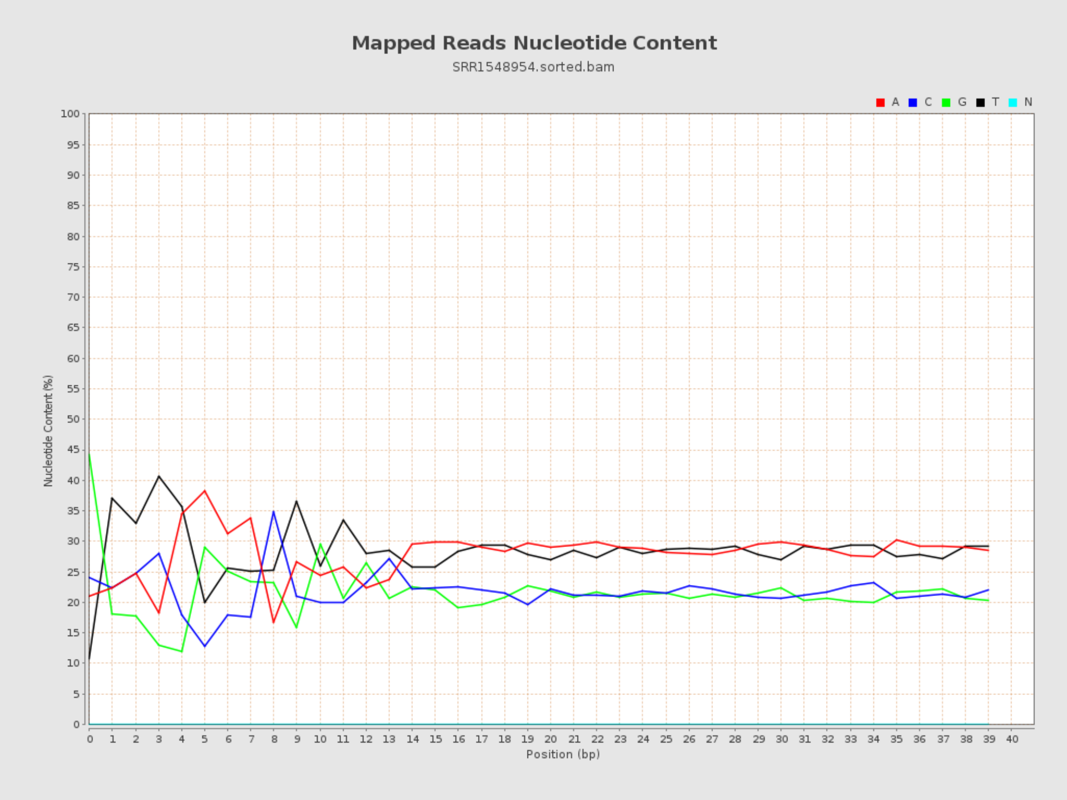
6. Results : Genome Fraction Coverage



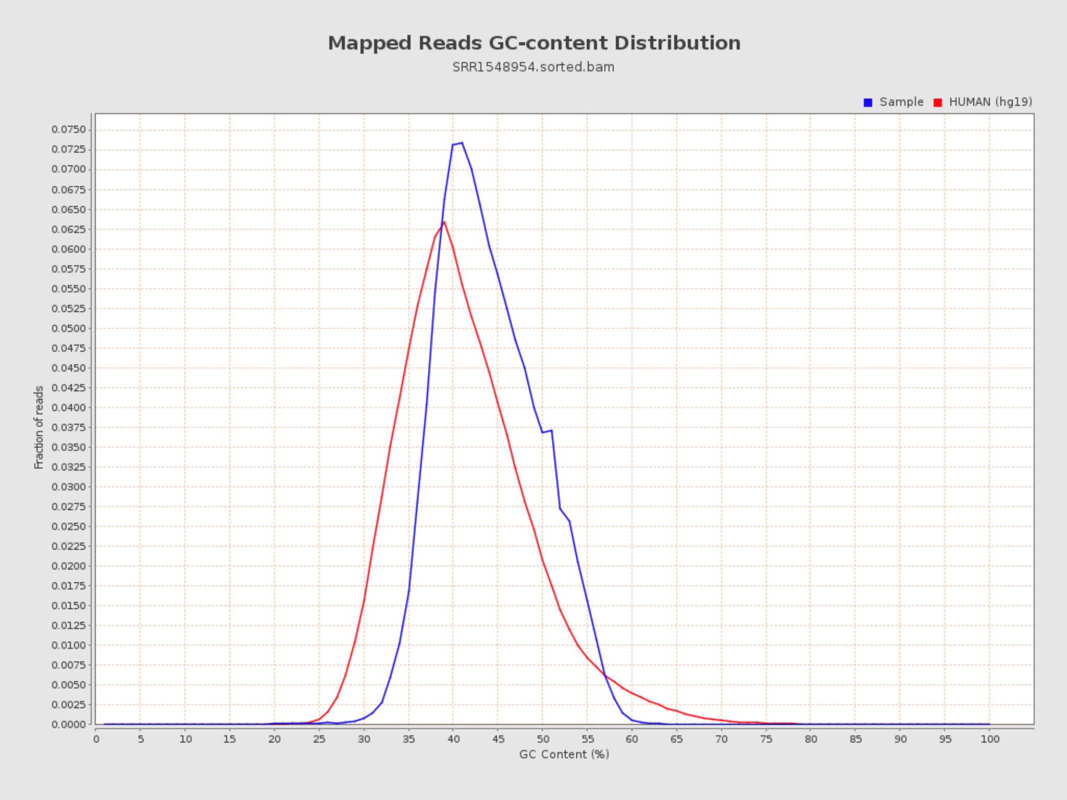
7. Results : Duplication Rate Histogram



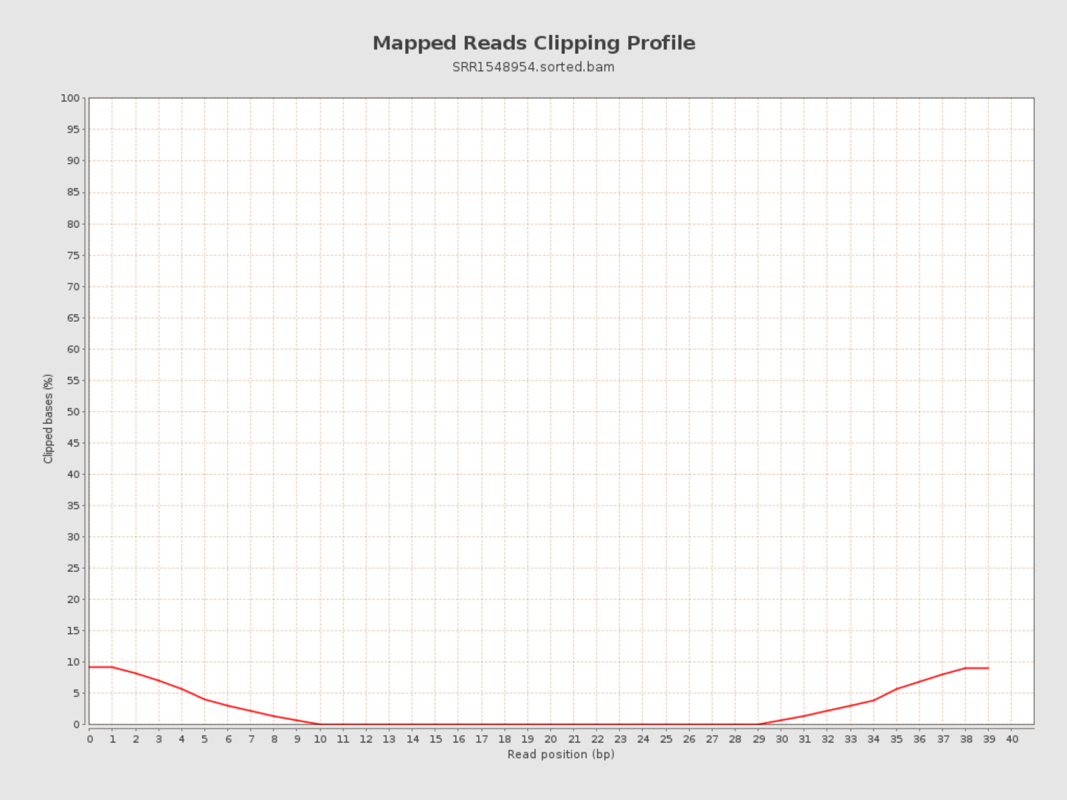
8. Results : Mapped Reads Nucleotide Content



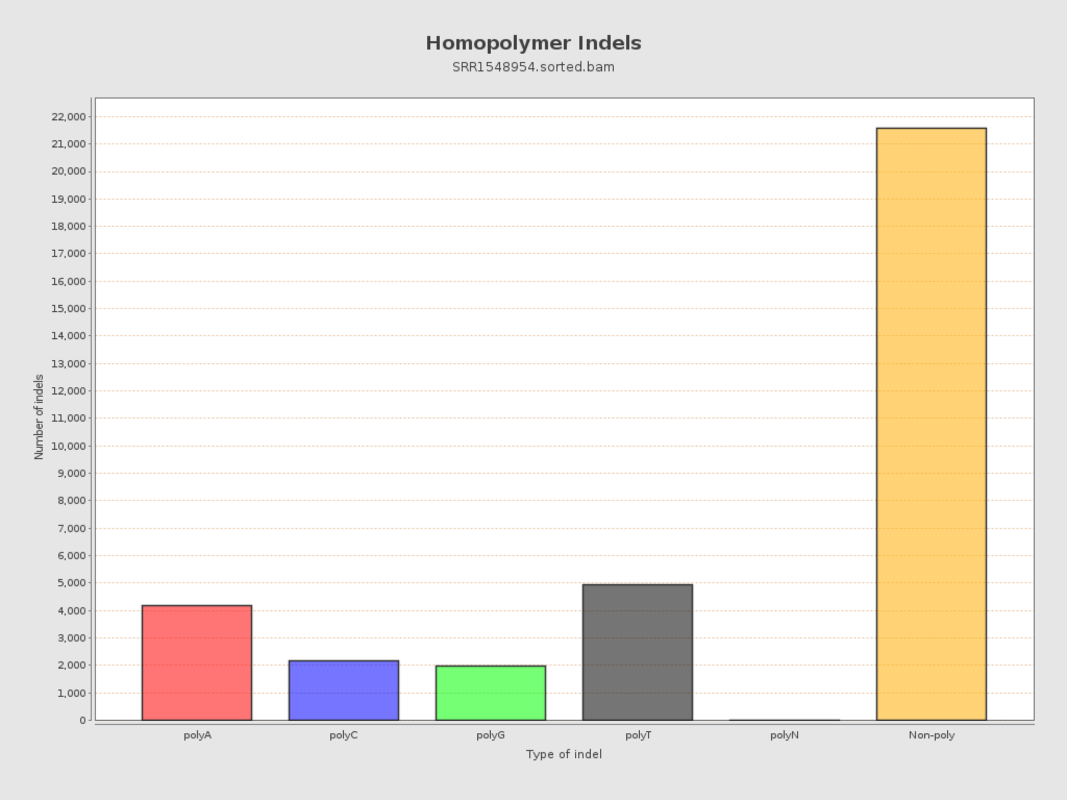
9. Results : Mapped Reads GC-content Distribution



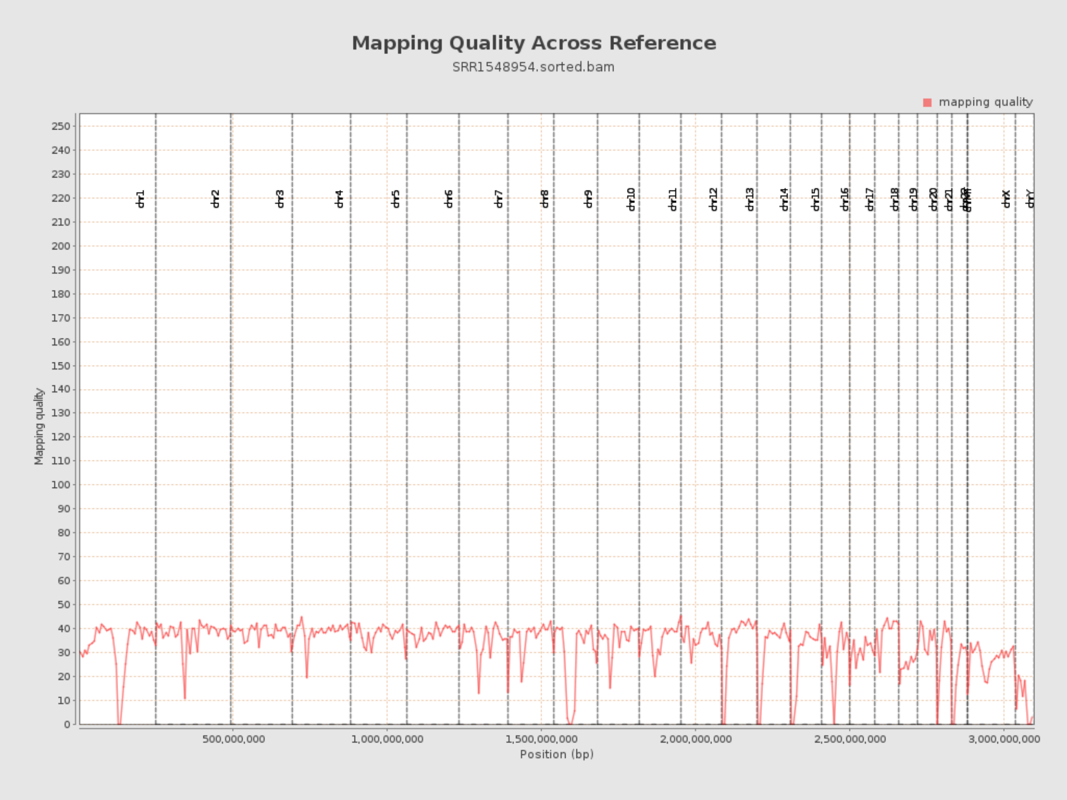
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram