Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:06:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548920.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_SRR1548920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548920.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:06:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,886,925
Mapped reads	8,579,420 / 86.78%
Unmapped reads	1,307,505 / 13.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	338,358 / 3.42%
Duplication rate	2.89%
Clipped reads	692,131 / 7%

2.2. ACGT Content

Number/percentage of A's	99,095,207 / 29.2%
Number/percentage of C's	70,334,031 / 20.72%
Number/percentage of T's	99,695,919 / 29.38%
Number/percentage of G's	70,256,467 / 20.7%
Number/percentage of N's	3,364 / 0%
GC Percentage	41.43%

2.3. Coverage

Mean	0.1096
Standard Deviation	1.3972

2.4. Mapping Quality

Mean Mapping Quality	42.06

2.5. Mismatches and indels

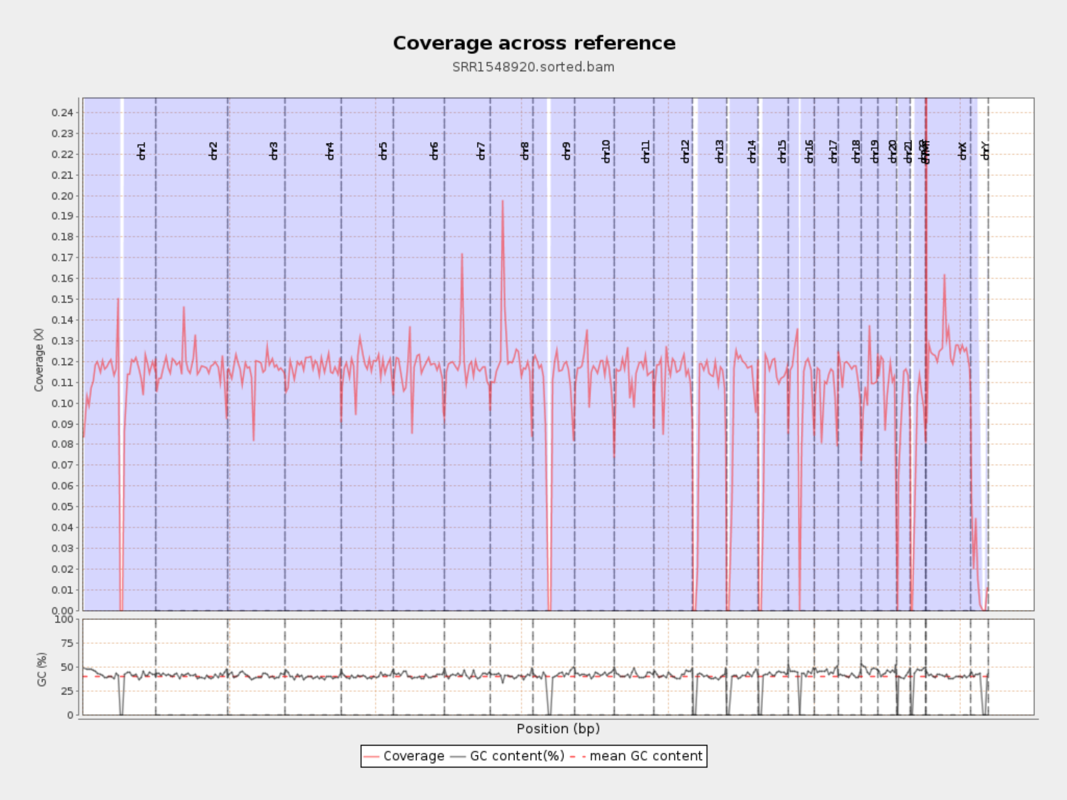
General error rate	0.28%
Mismatches	923,724
Insertions	11,430
Mapped reads with at least one insertion	0.13%
Deletions	28,467
Mapped reads with at least one deletion	0.33%
Homopolymer indels	39.94%

2.6. Chromosome stats

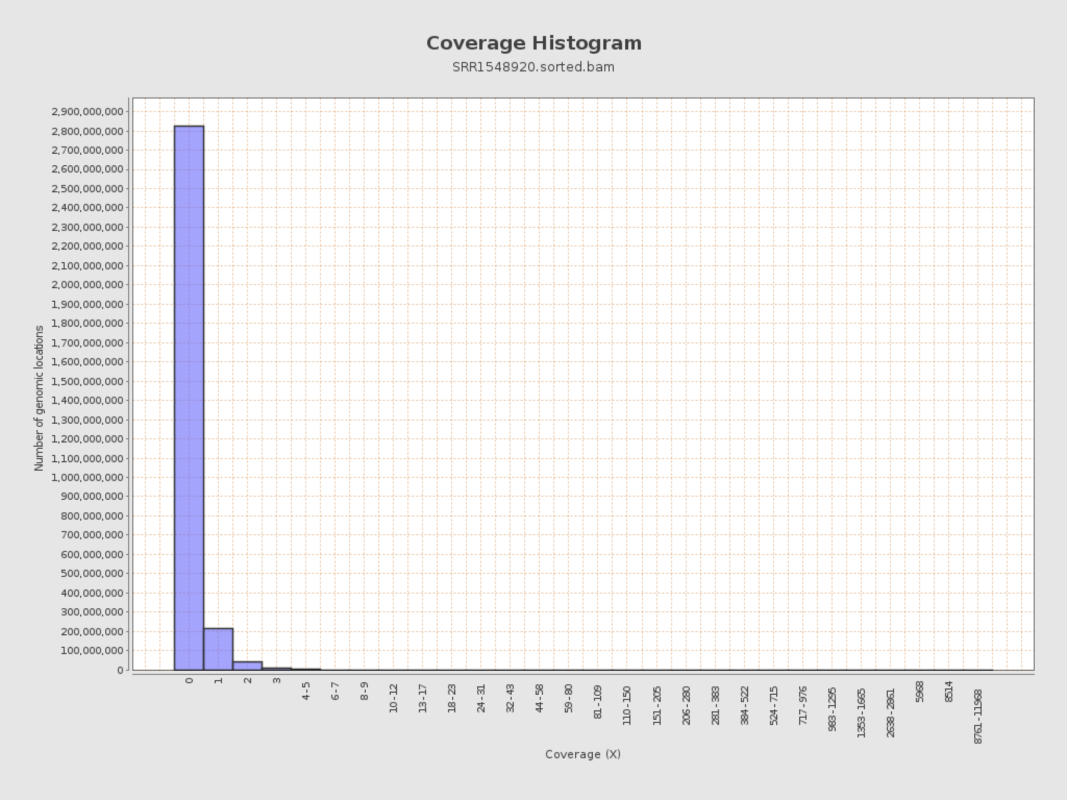
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26772992	0.1074	1.1413
chr2	243199373	28596196	0.1176	0.5955
chr3	198022430	22985659	0.1161	0.4117
chr4	191154276	22441264	0.1174	0.4265
chr5	180915260	21190215	0.1171	0.4205
chr6	171115067	19902895	0.1163	0.469
chr7	159138663	18849036	0.1184	0.8891
chr8	146364022	17861717	0.122	5.7859

chr9	141213431	14251303	0.1009	0.5737
chr10	135534747	15700197	0.1158	0.5331
chr11	135006516	15432763	0.1143	0.6604
chr12	133851895	15413908	0.1152	0.424
chr13	115169878	11038692	0.0958	0.3693
chr14	107349540	10429371	0.0972	0.4631
chr15	102531392	9712886	0.0947	0.3703
chr16	90354753	9271412	0.1026	0.4243
chr17	81195210	8695646	0.1071	0.4381
chr18	78077248	9055196	0.116	1.0269
chr19	59128983	6426134	0.1087	1.0091
chr20	63025520	6870209	0.109	0.4123
chr21	48129895	4308092	0.0895	0.41
chr22	51304566	3720292	0.0725	0.4039
chrMT	16571	19677	1.1874	1.612
chrX	155270560	19480615	0.1255	0.5236
chrY	59373566	996559	0.0168	0.2214

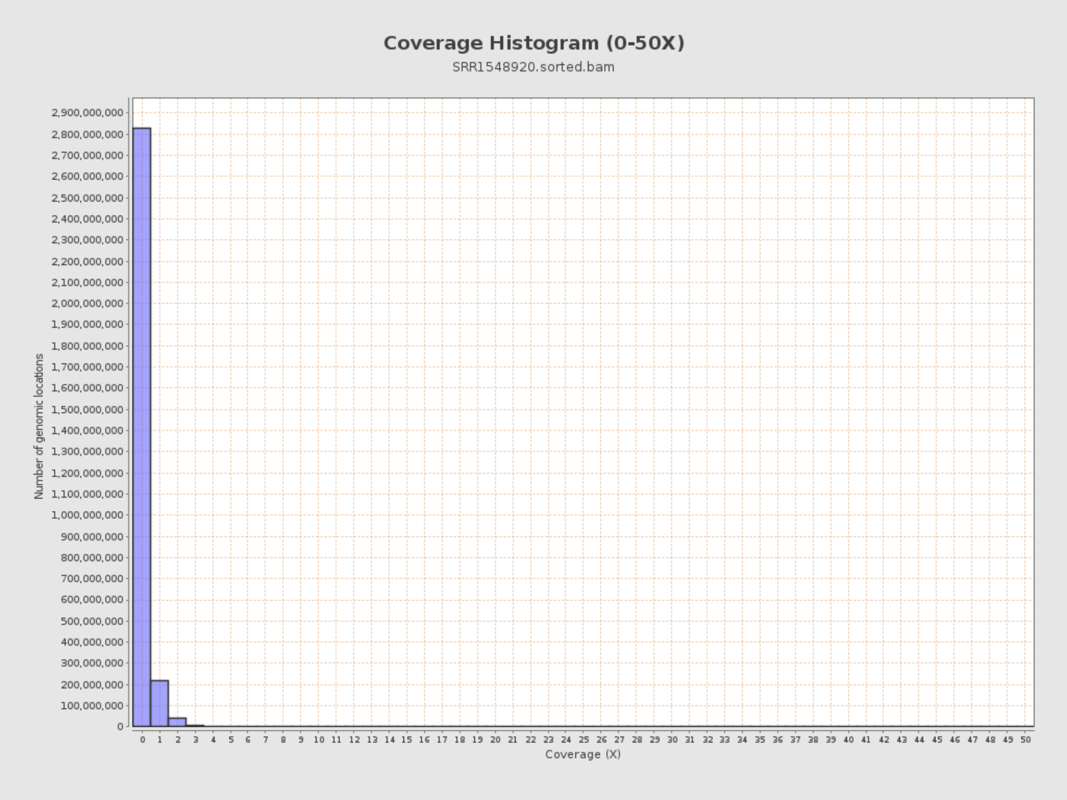
3. Results : Coverage across reference



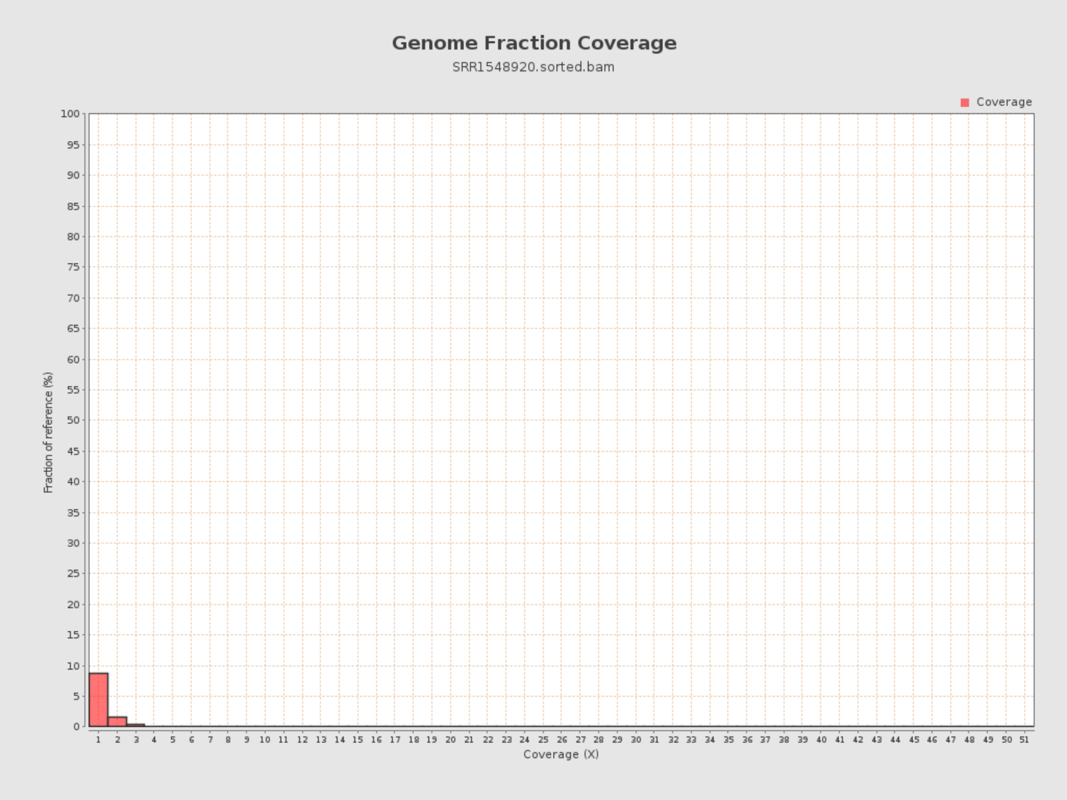
4. Results : Coverage Histogram



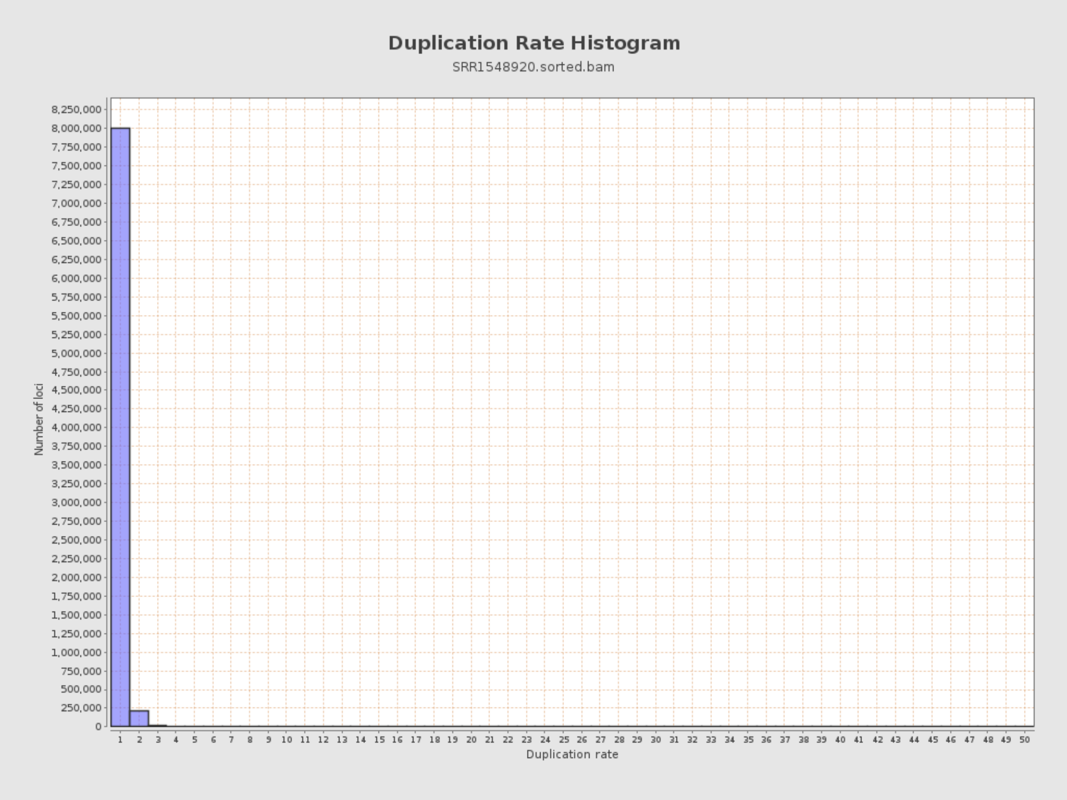
5. Results : Coverage Histogram (0-50X)



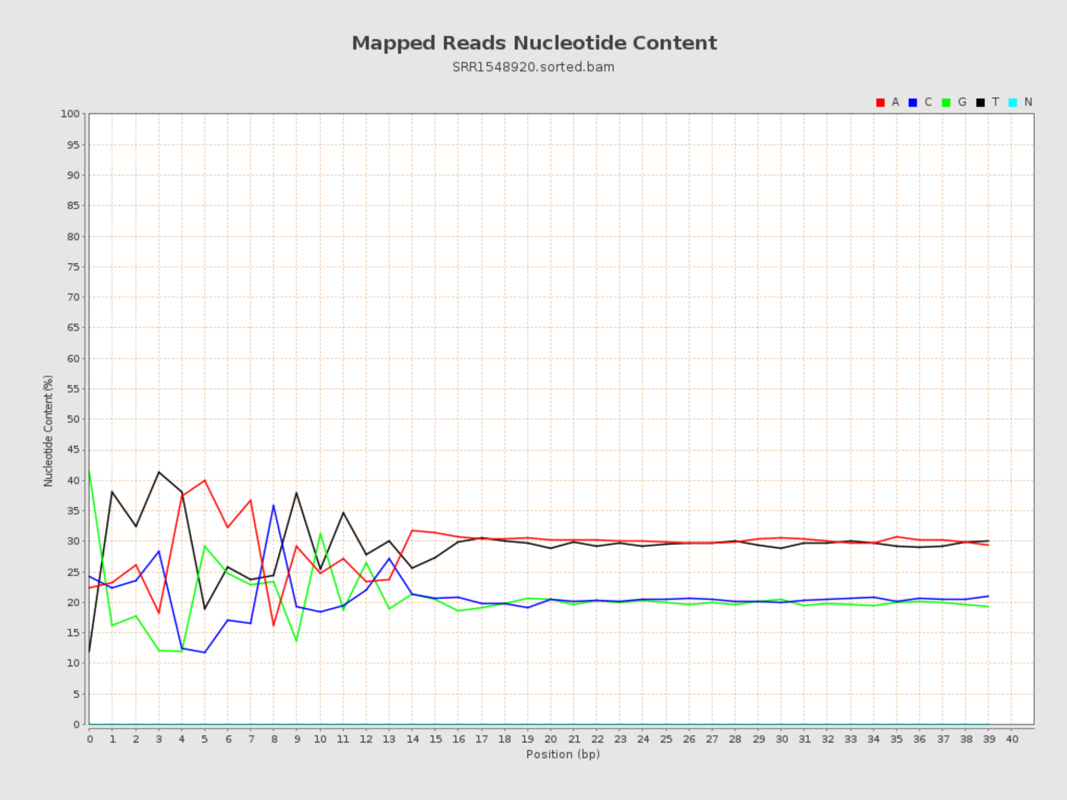
6. Results : Genome Fraction Coverage



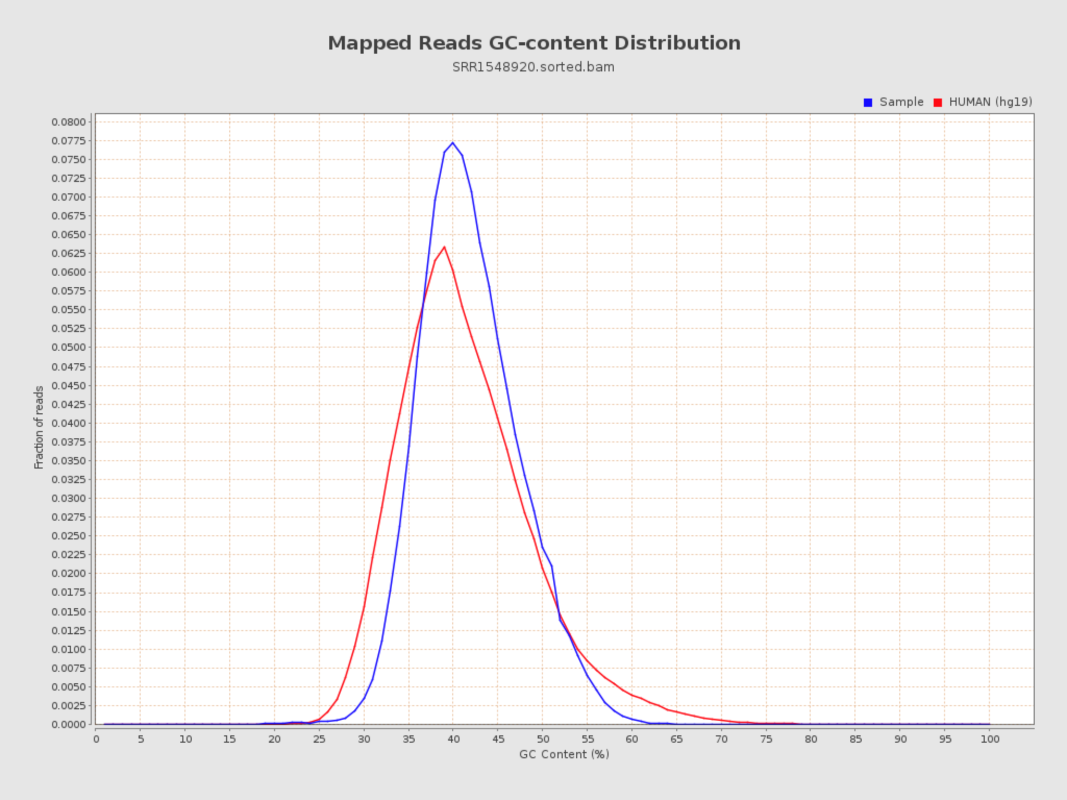
7. Results : Duplication Rate Histogram



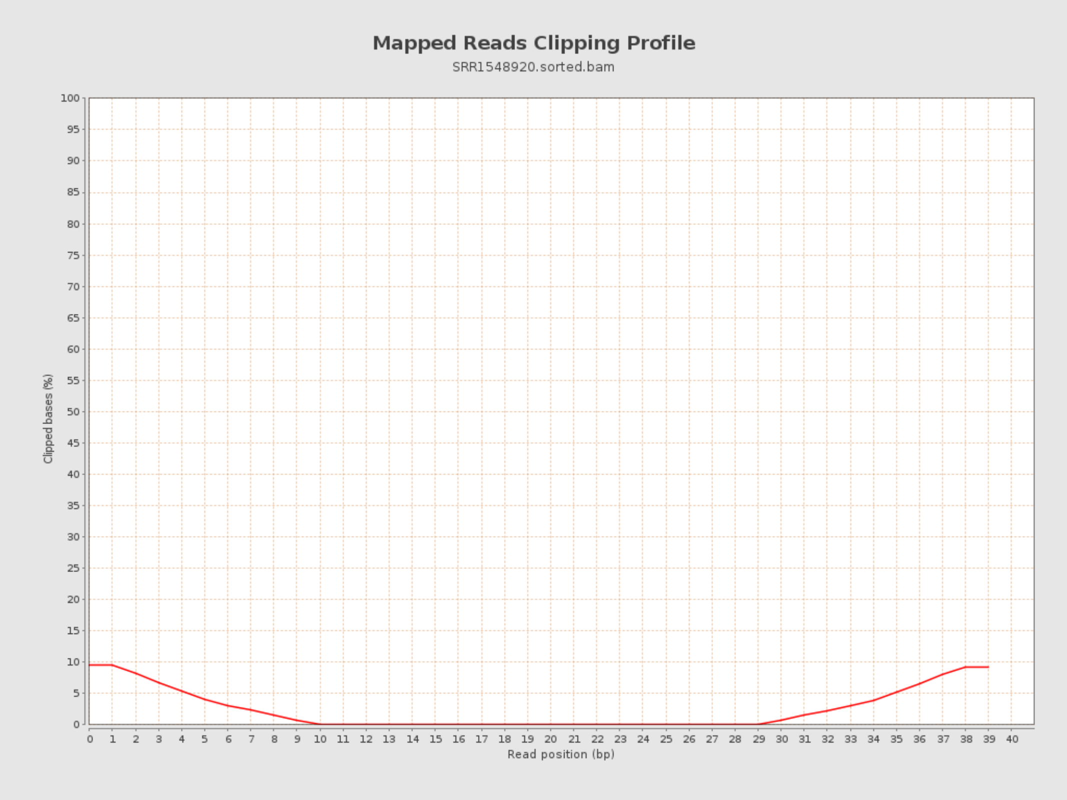
8. Results : Mapped Reads Nucleotide Content



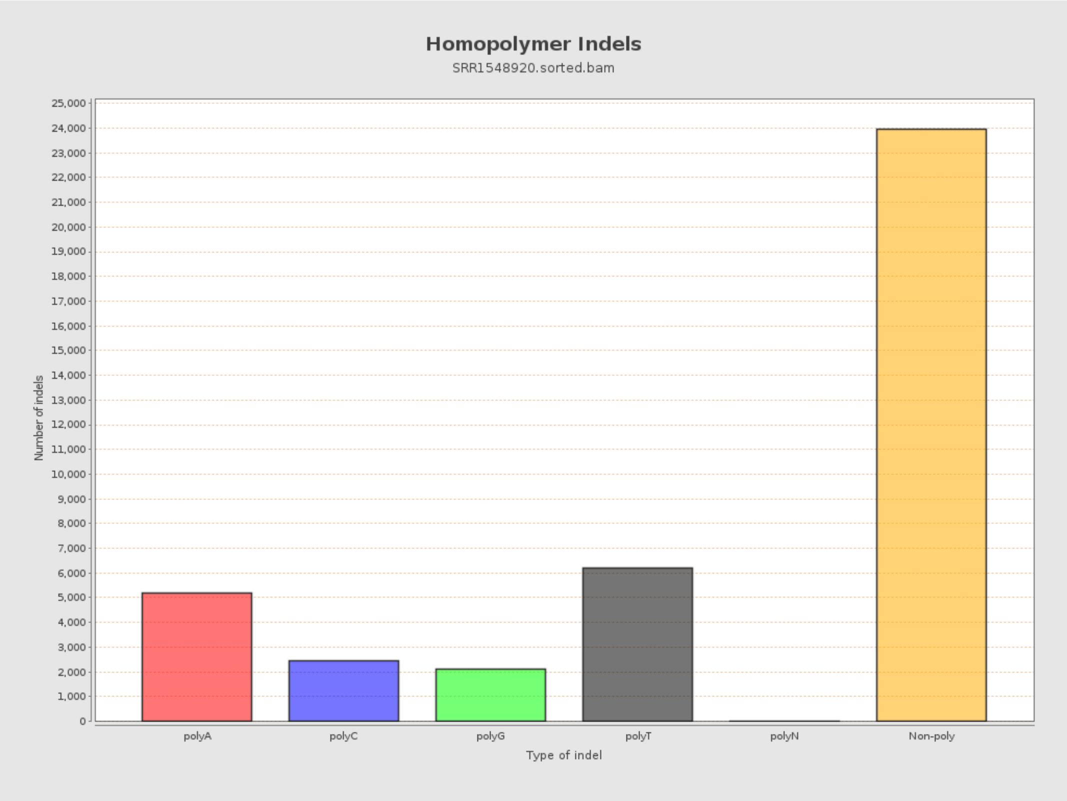
9. Results : Mapped Reads GC-content Distribution



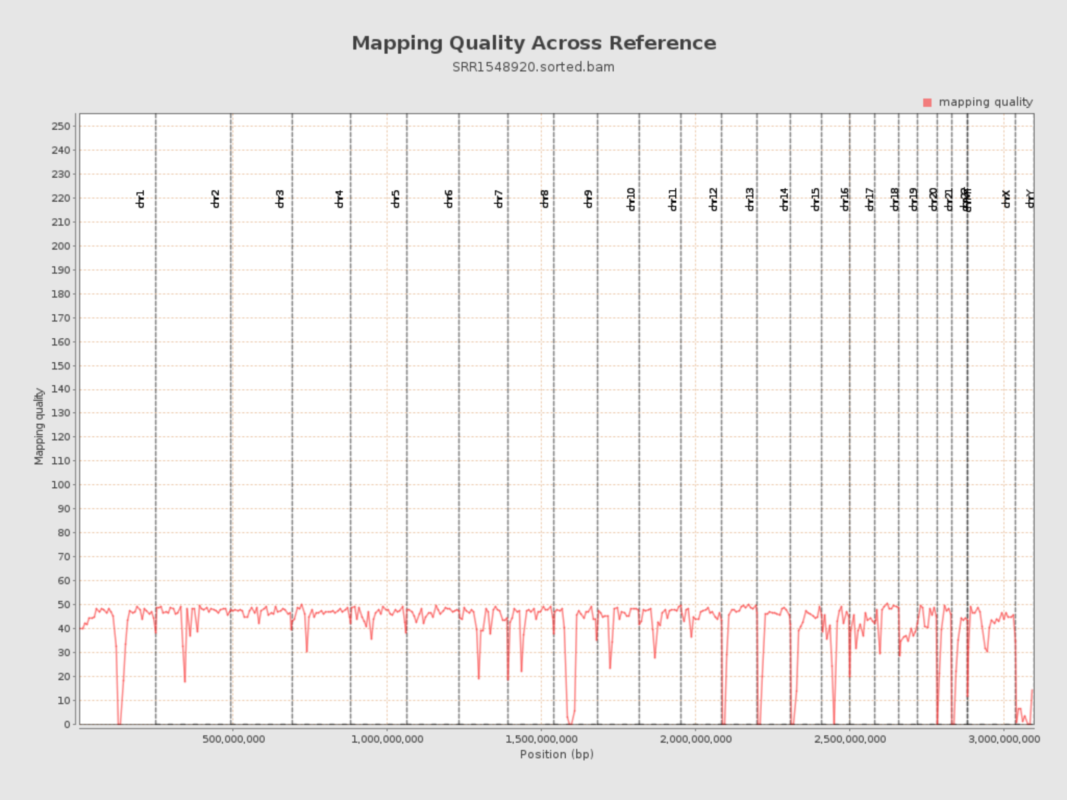
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram