Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:02:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525008.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_SRR10525008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525008.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:02:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,931,177
Mapped reads	1,773,181 / 91.82%
Unmapped reads	157,996 / 8.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,551 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	57,771 / 2.99%
Duplication rate	2.2%
Clipped reads	1,774,103 / 91.87%

2.2. ACGT Content

Number/percentage of A's	25,903,247 / 25.13%
Number/percentage of C's	20,120,112 / 19.52%
Number/percentage of T's	32,196,782 / 31.24%
Number/percentage of G's	24,839,110 / 24.1%
Number/percentage of N's	840 / 0%
GC Percentage	43.62%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.3179

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

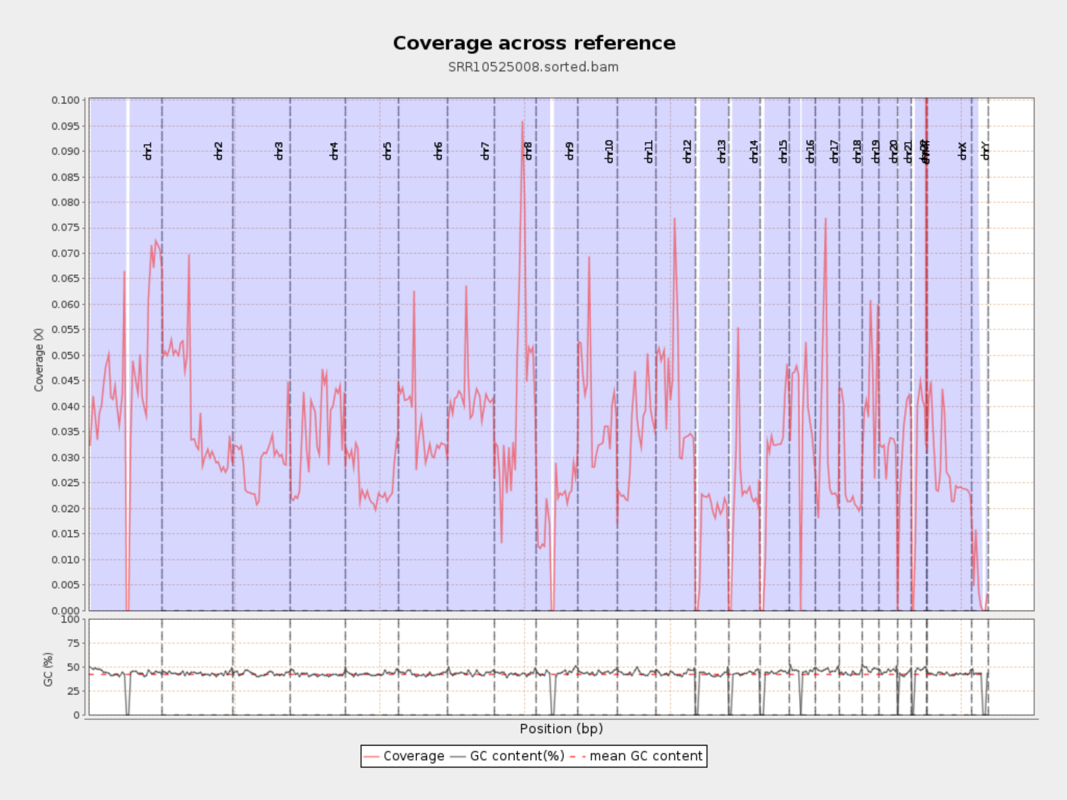
General error rate	0.51%
Mismatches	517,857
Insertions	6,320
Mapped reads with at least one insertion	0.35%
Deletions	20,339
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.35%

2.6. Chromosome stats

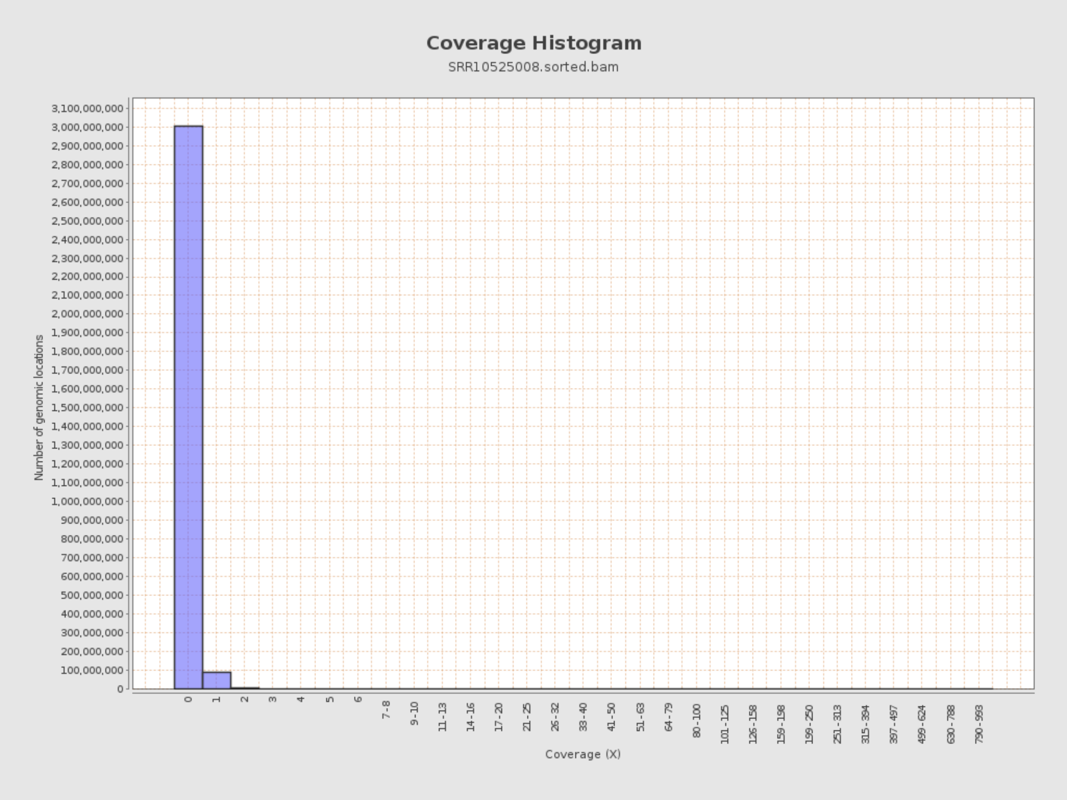
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11208614	0.045	0.6715
chr2	243199373	9594368	0.0395	0.3491
chr3	198022430	5797529	0.0293	0.1886
chr4	191154276	6732213	0.0352	0.2212
chr5	180915260	4576743	0.0253	0.1754
chr6	171115067	6212406	0.0363	0.3135
chr7	159138663	6689745	0.042	0.4222

chr8	146364022	6220336	0.0425	0.2947
chr9	141213431	2618107	0.0185	0.2201
chr10	135534747	5391607	0.0398	0.3124
chr11	135006516	4461657	0.033	0.2668
chr12	133851895	5755737	0.043	0.2266
chr13	115169878	2007717	0.0174	0.1435
chr14	107349540	2424709	0.0226	0.1681
chr15	102531392	2932754	0.0286	0.1966
chr16	90354753	3412519	0.0378	0.223
chr17	81195210	2723227	0.0335	0.2723
chr18	78077248	2054862	0.0263	0.3676
chr19	59128983	2599278	0.044	0.3883
chr20	63025520	1980389	0.0314	0.1954
chr21	48129895	1510518	0.0314	0.2019
chr22	51304566	1452782	0.0283	0.1804
chrMT	16571	19061	1.1503	1.3089
chrX	155270560	4428514	0.0285	0.2233
chrY	59373566	288384	0.0049	0.1248

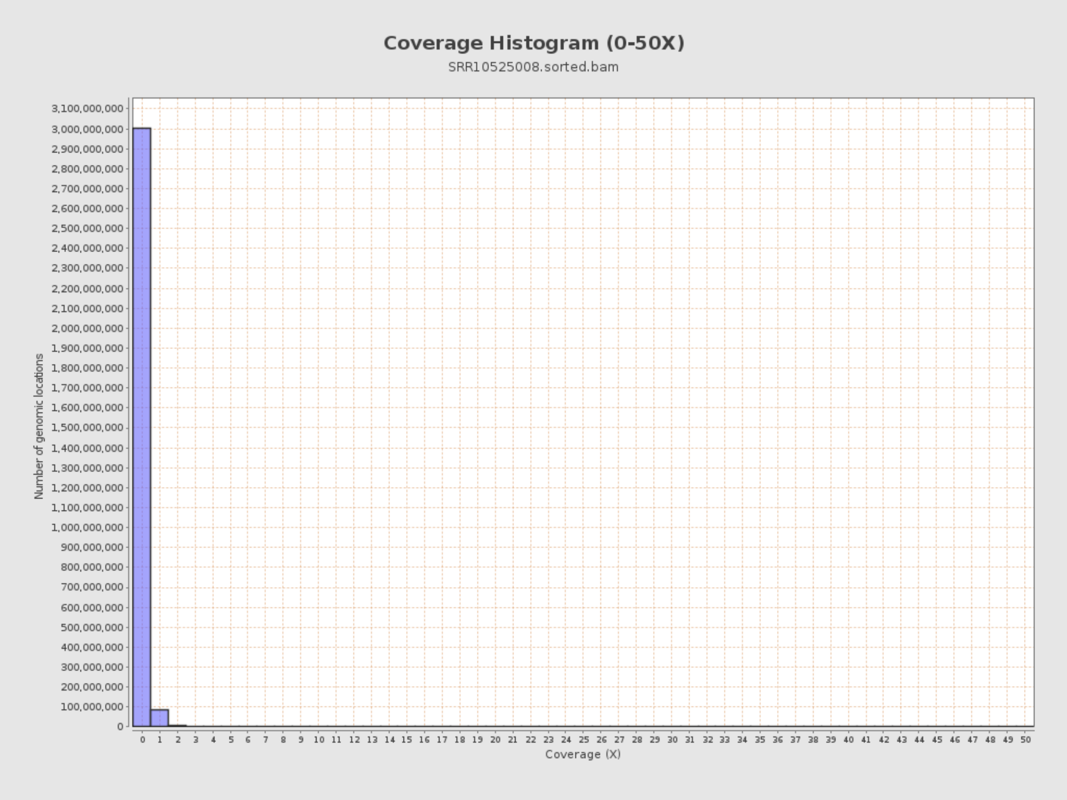
3. Results : Coverage across reference



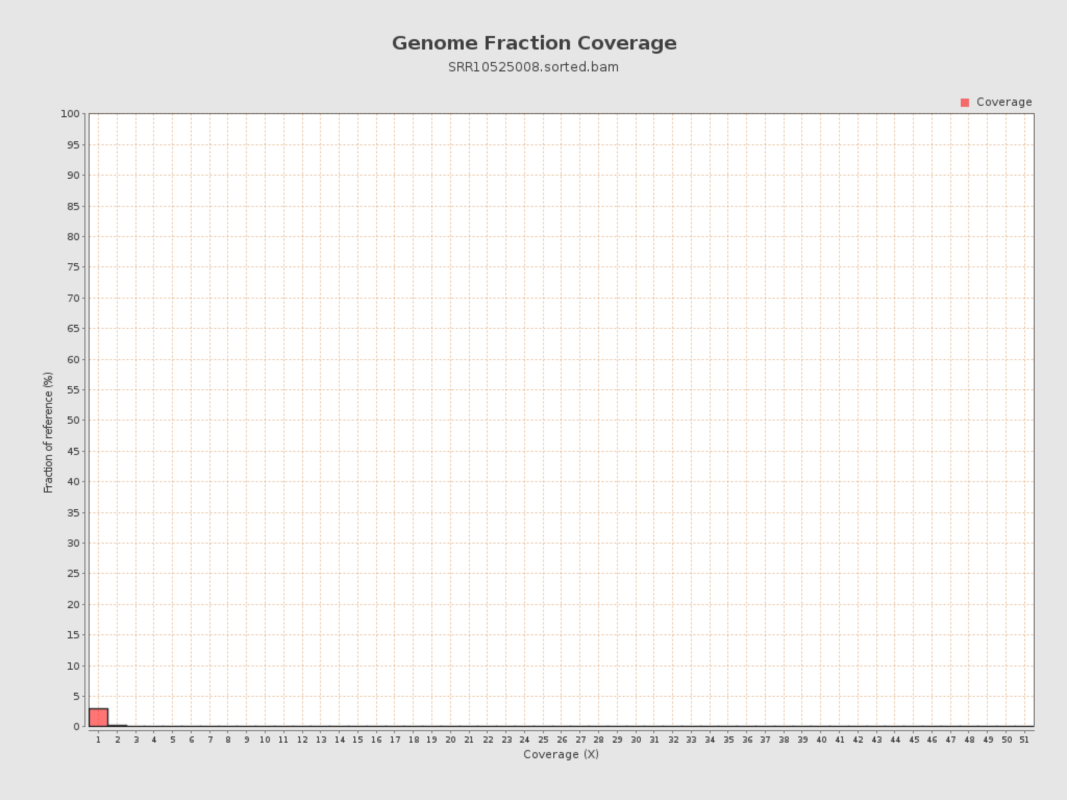
4. Results : Coverage Histogram



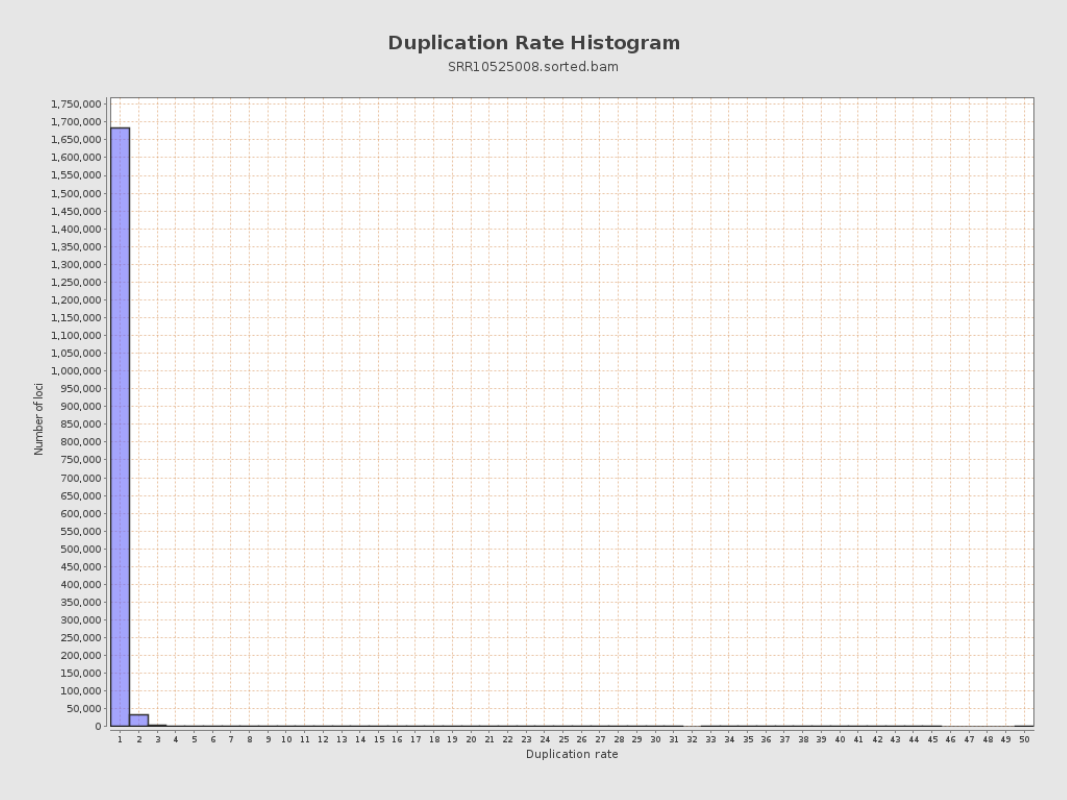
5. Results : Coverage Histogram (0-50X)



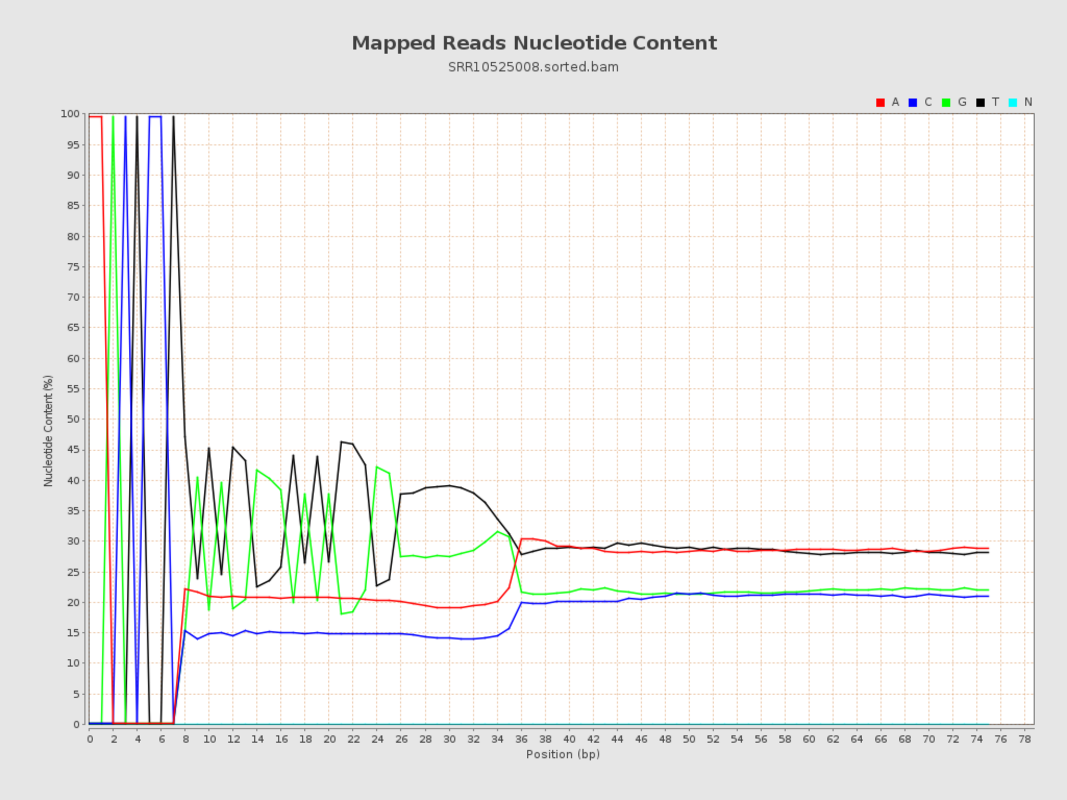
6. Results : Genome Fraction Coverage



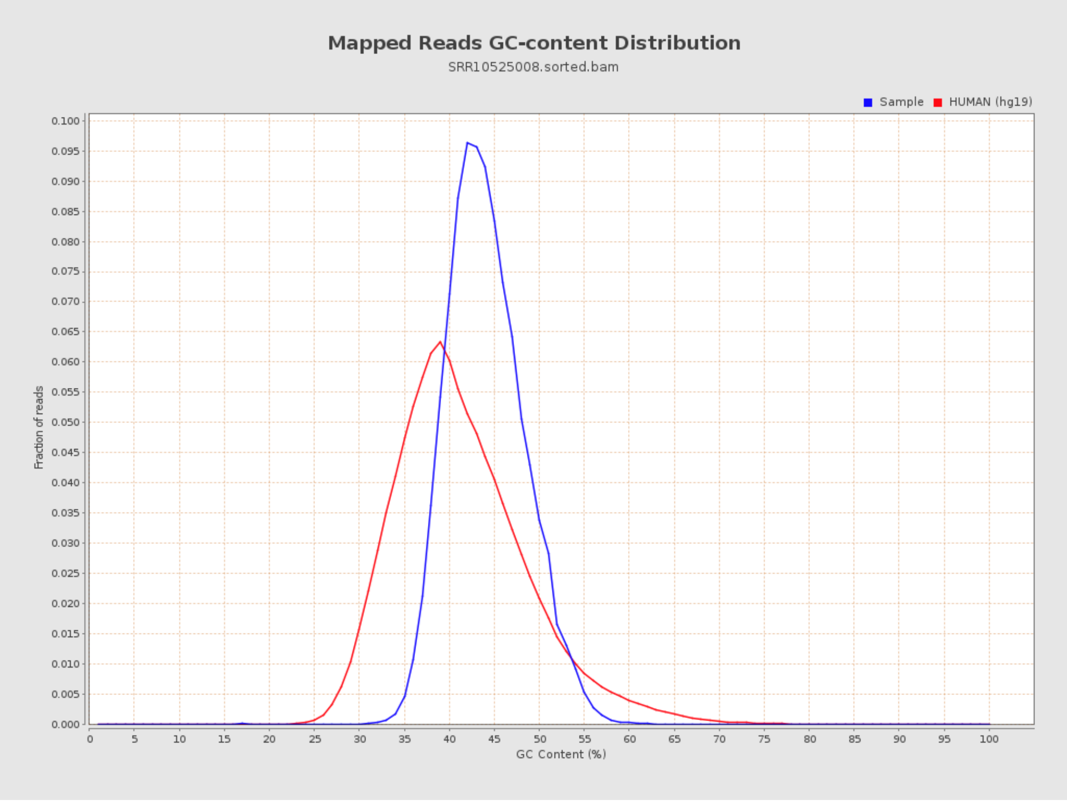
7. Results : Duplication Rate Histogram



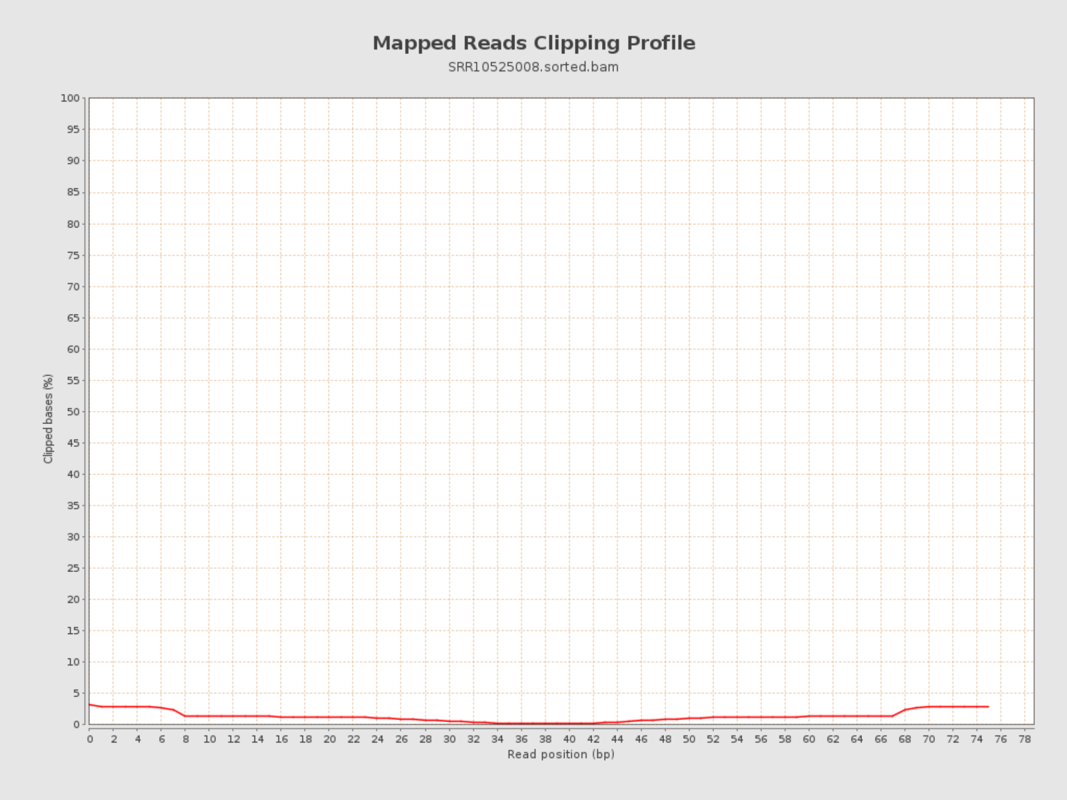
8. Results : Mapped Reads Nucleotide Content



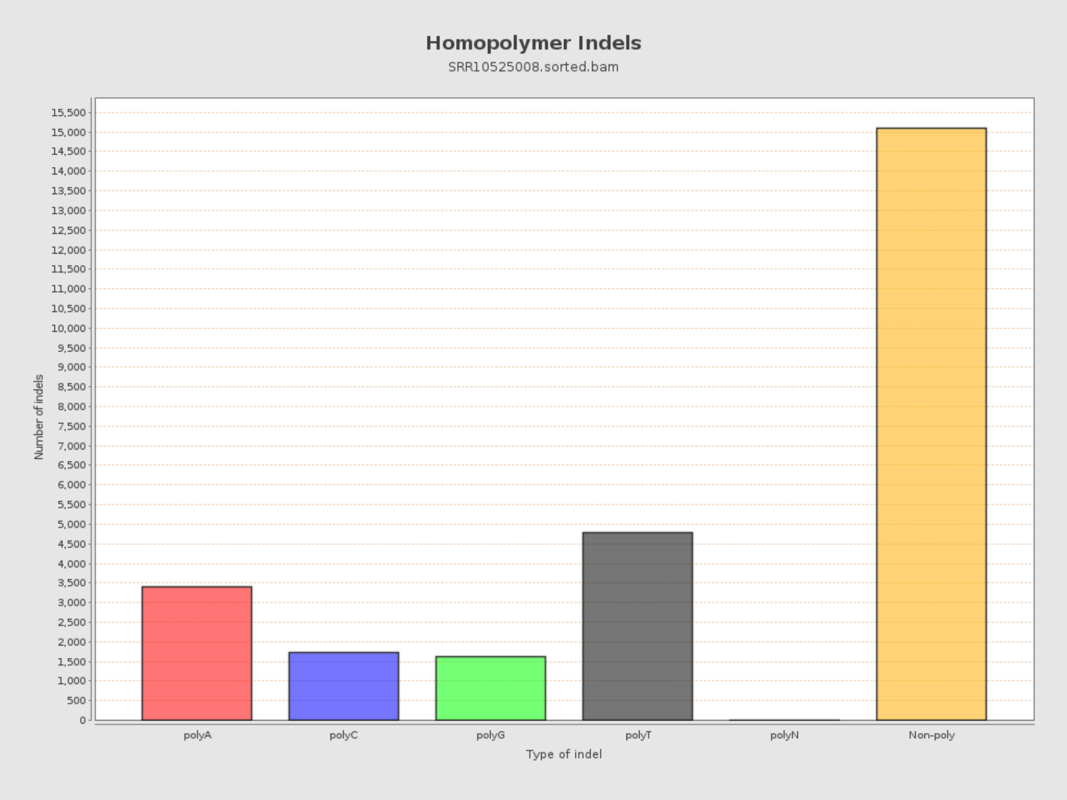
9. Results : Mapped Reads GC-content Distribution



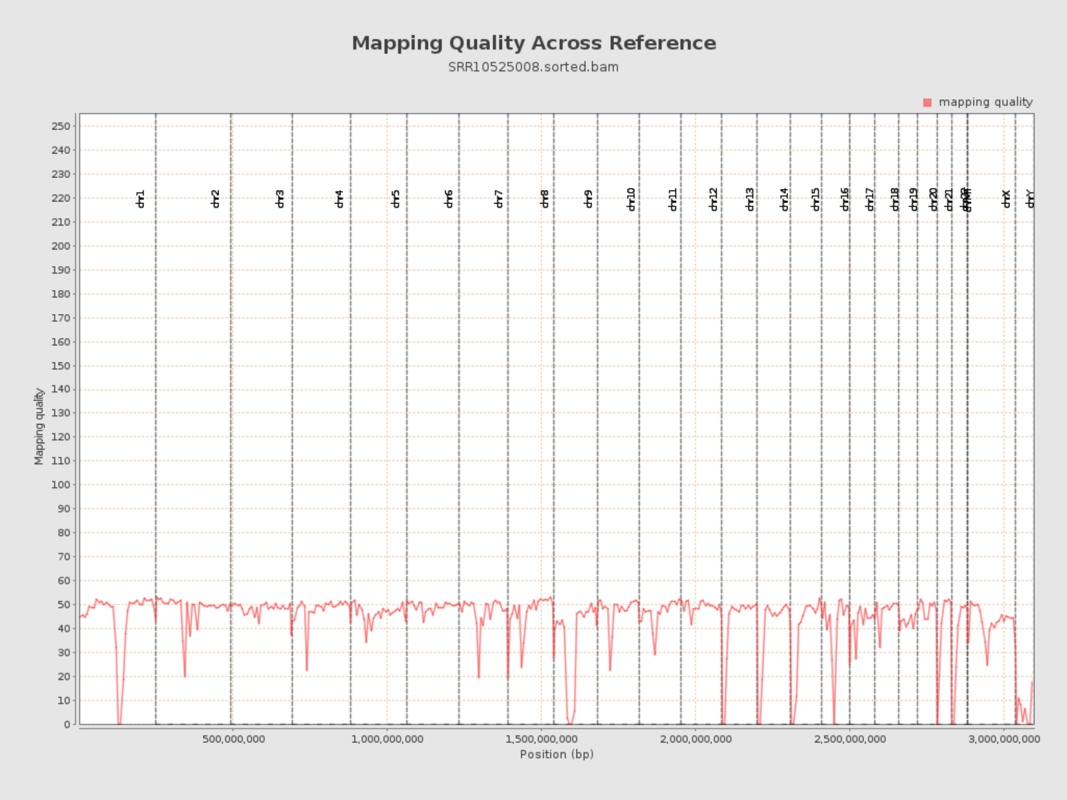
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram