Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:19:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525015.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_SRR10525015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525015.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:19:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,410,226
Mapped reads	1,295,951 / 91.9%
Unmapped reads	114,275 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,234 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	36,595 / 2.59%
Duplication rate	1.82%
Clipped reads	1,296,444 / 91.93%

2.2. ACGT Content

Number/percentage of A's	18,487,368 / 24.8%
Number/percentage of C's	14,452,061 / 19.39%
Number/percentage of T's	23,318,992 / 31.29%
Number/percentage of G's	18,274,025 / 24.52%
Number/percentage of N's	668 / 0%
GC Percentage	43.91%

2.3. Coverage

Mean	0.0241

Standard Deviation	0.246

2.4. Mapping Quality

Mean Mapping Quality	42.62

2.5. Mismatches and indels

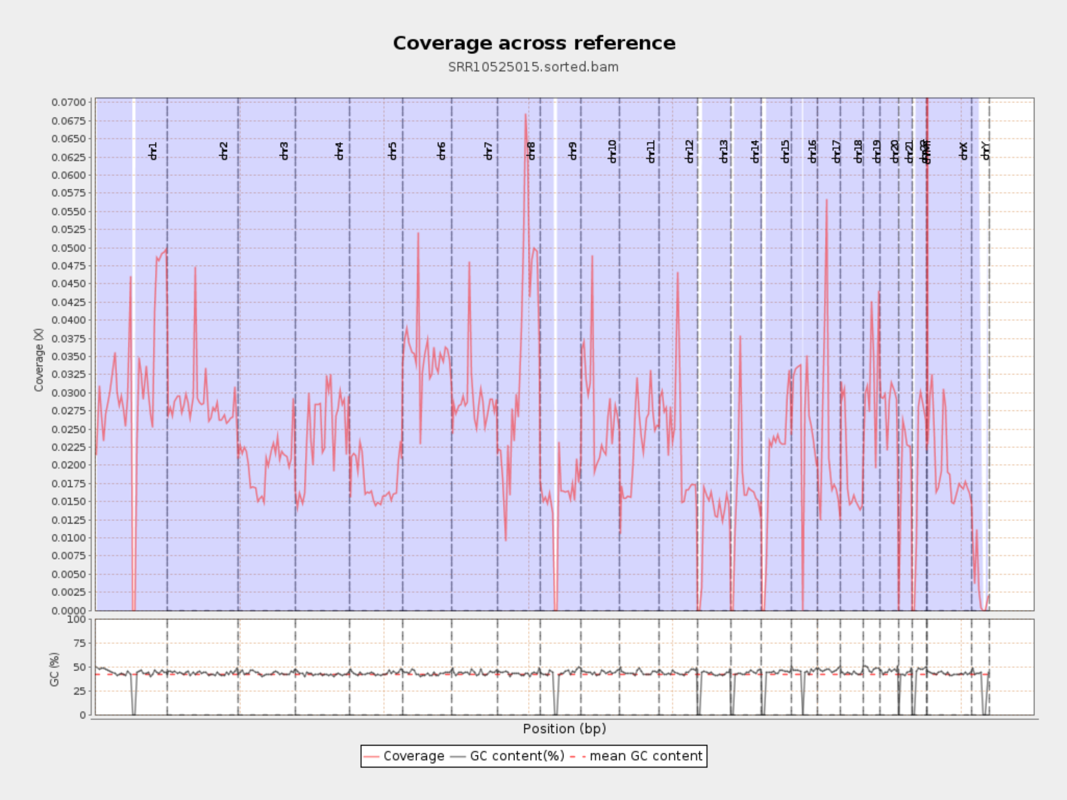
General error rate	0.52%
Mismatches	378,180
Insertions	5,579
Mapped reads with at least one insertion	0.43%
Deletions	14,803
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.95%

2.6. Chromosome stats

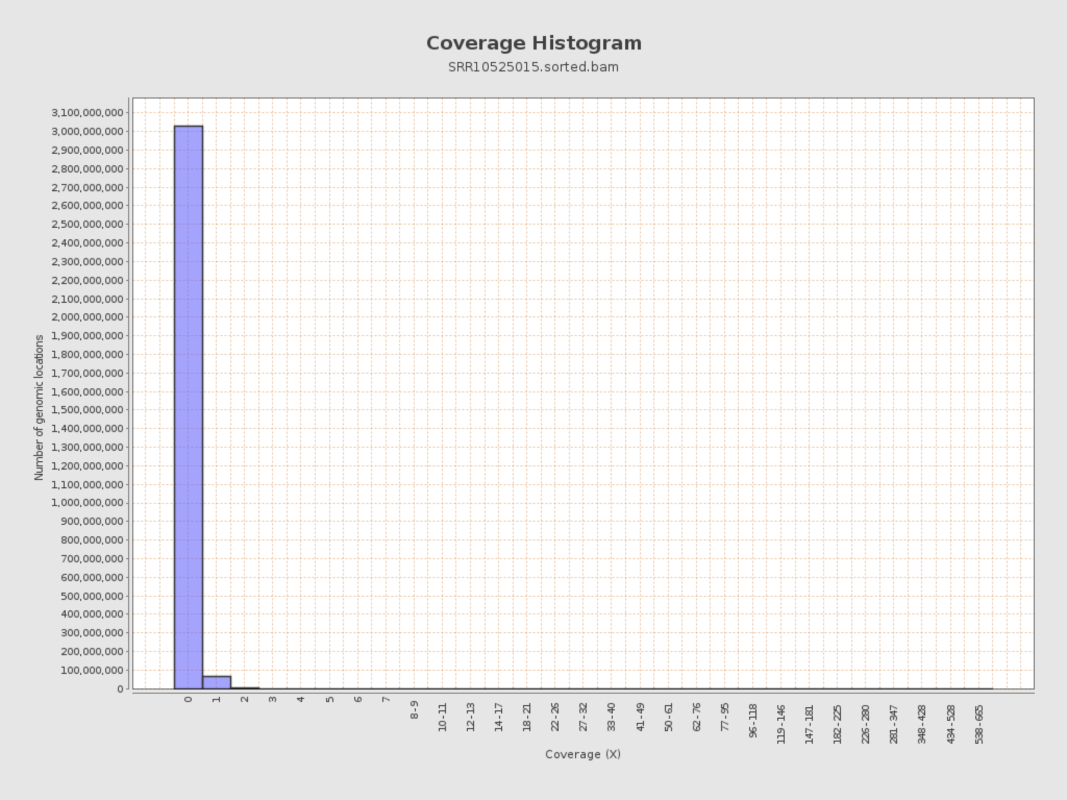
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7766293	0.0312	0.4732
chr2	243199373	6948445	0.0286	0.2819
chr3	198022430	4032309	0.0204	0.1551
chr4	191154276	4692645	0.0245	0.1795
chr5	180915260	3215883	0.0178	0.1465
chr6	171115067	6031836	0.0353	0.2794
chr7	159138663	4633848	0.0291	0.324

chr8	146364022	5140165	0.0351	0.2321
chr9	141213431	2106876	0.0149	0.1869
chr10	135534747	3767628	0.0278	0.2404
chr11	135006516	3111588	0.023	0.2149
chr12	133851895	3176436	0.0237	0.1671
chr13	115169878	1417032	0.0123	0.1224
chr14	107349540	1680466	0.0157	0.1372
chr15	102531392	2067708	0.0202	0.1675
chr16	90354753	2382671	0.0264	0.185
chr17	81195210	1907018	0.0235	0.2179
chr18	78077248	1463238	0.0187	0.3091
chr19	59128983	1908332	0.0323	0.3034
chr20	63025520	1787514	0.0284	0.1811
chr21	48129895	954452	0.0198	0.1567
chr22	51304566	992040	0.0193	0.1472
chrMT	16571	21632	1.3054	1.4416
chrX	155270560	3142619	0.0202	0.1842
chrY	59373566	209000	0.0035	0.0886

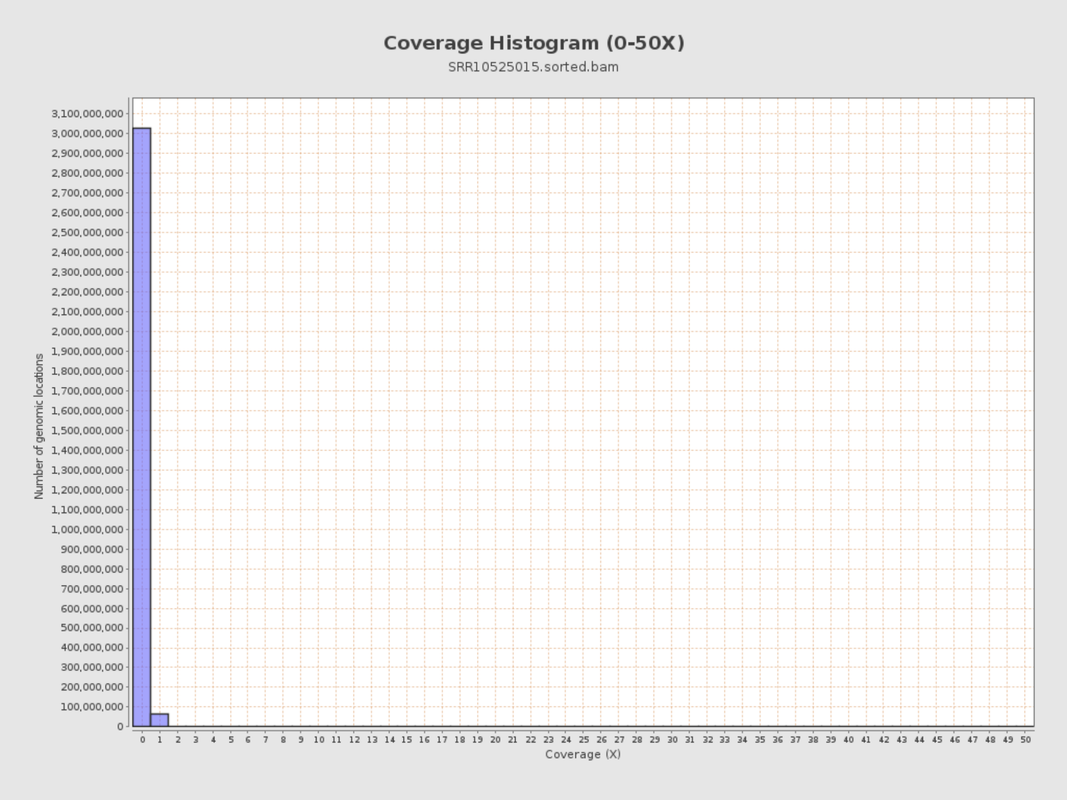
3. Results : Coverage across reference



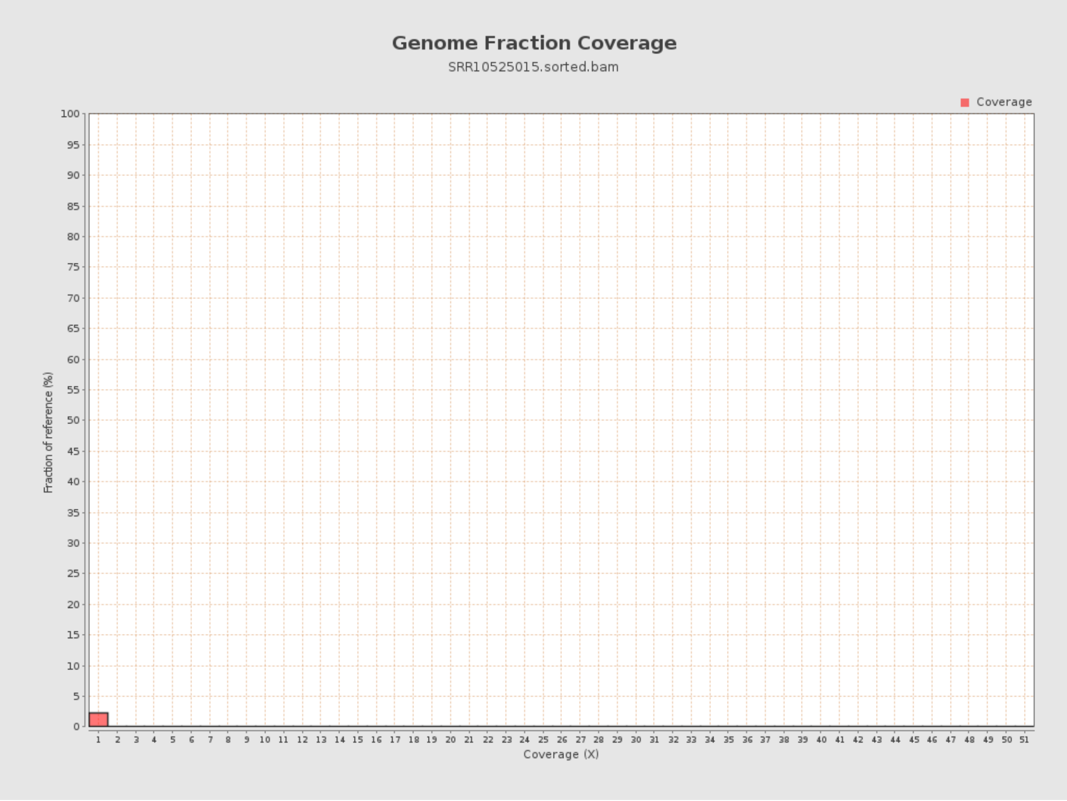
4. Results : Coverage Histogram



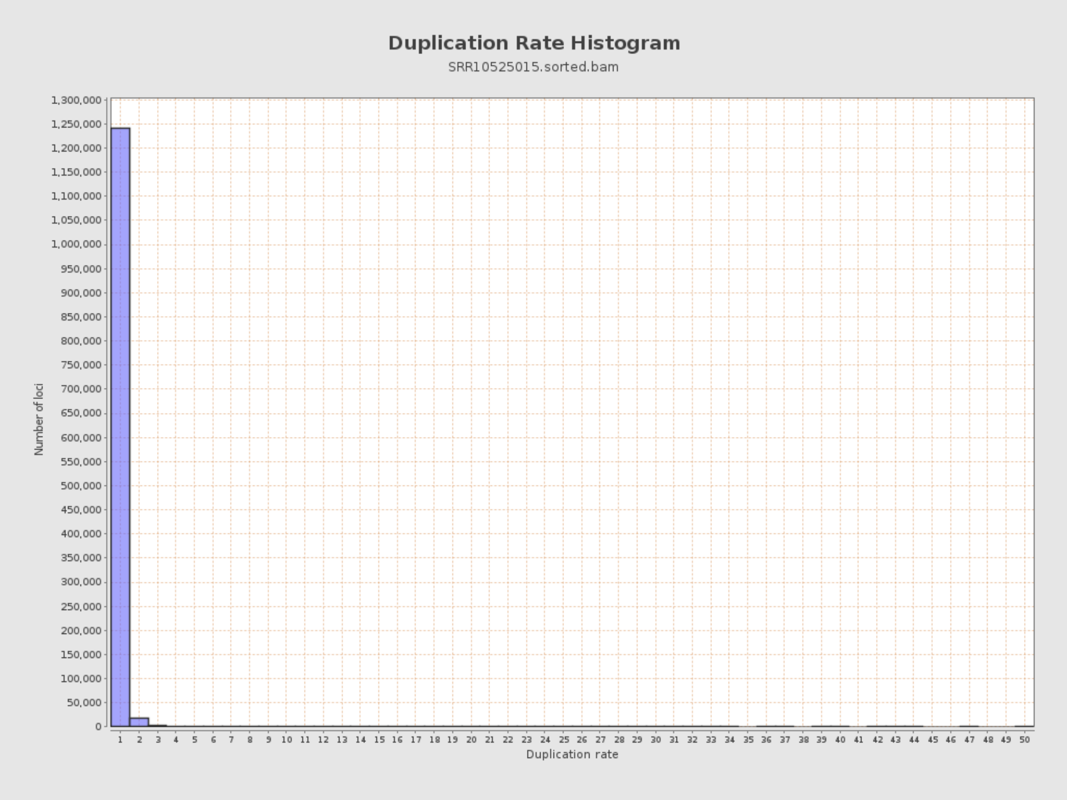
5. Results : Coverage Histogram (0-50X)



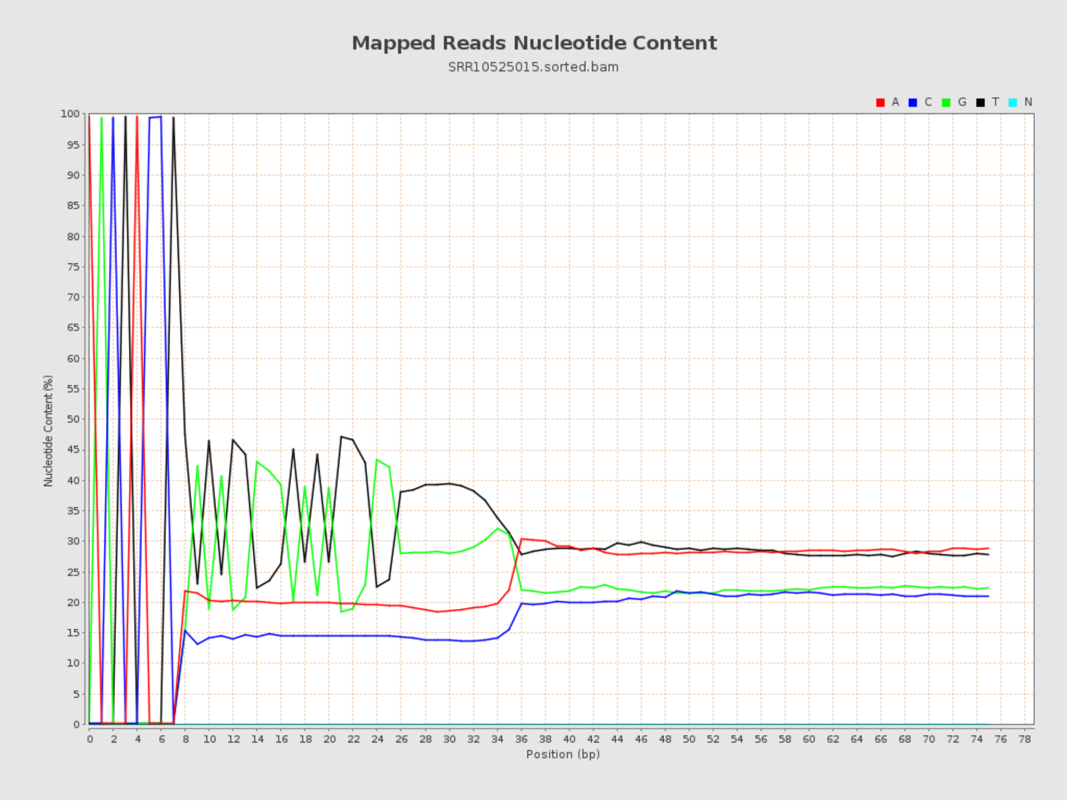
6. Results : Genome Fraction Coverage



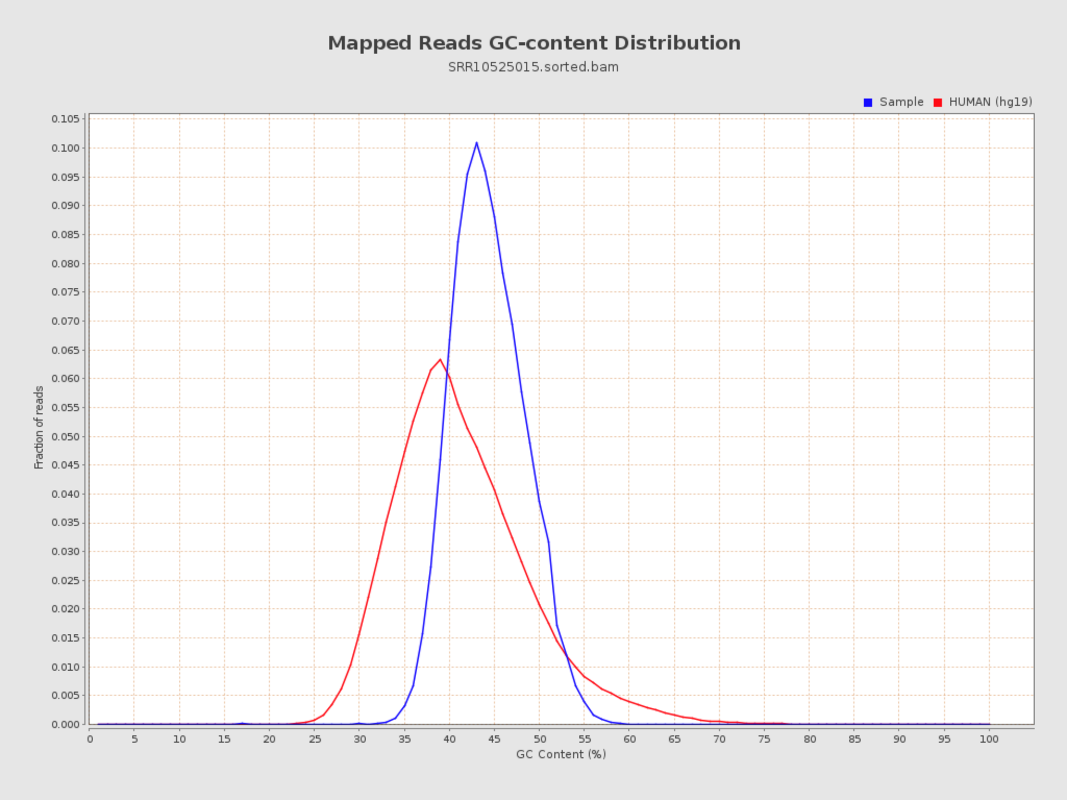
7. Results : Duplication Rate Histogram



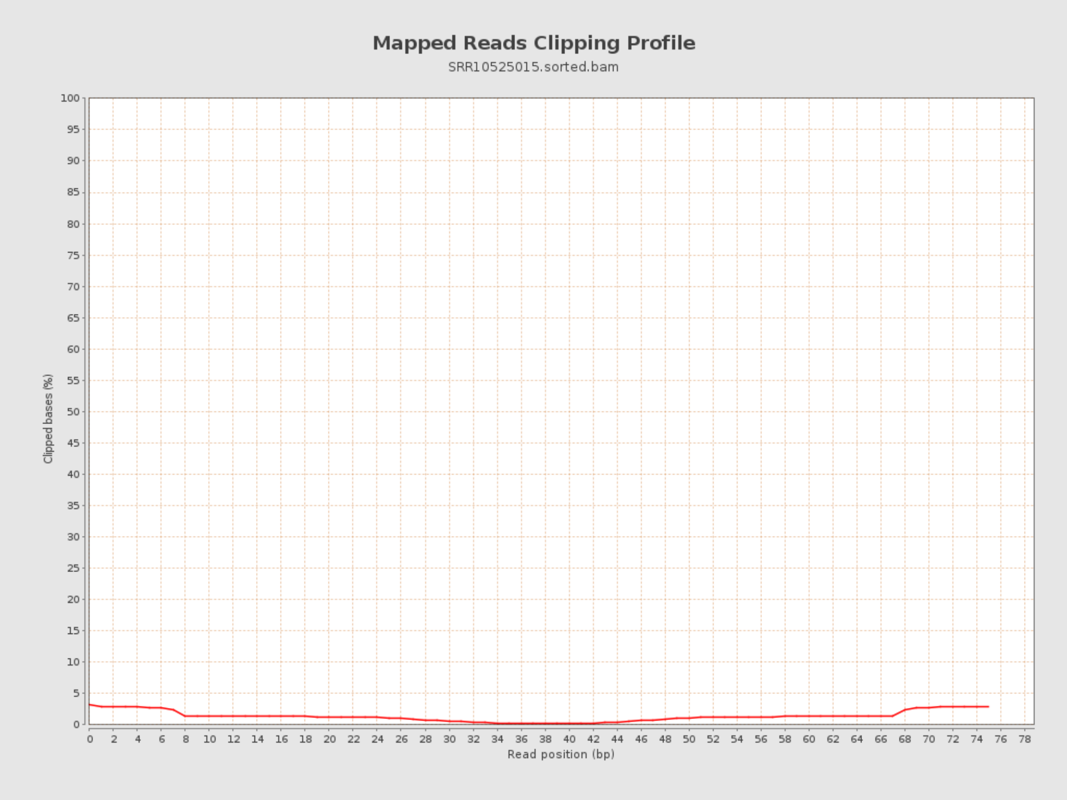
8. Results : Mapped Reads Nucleotide Content



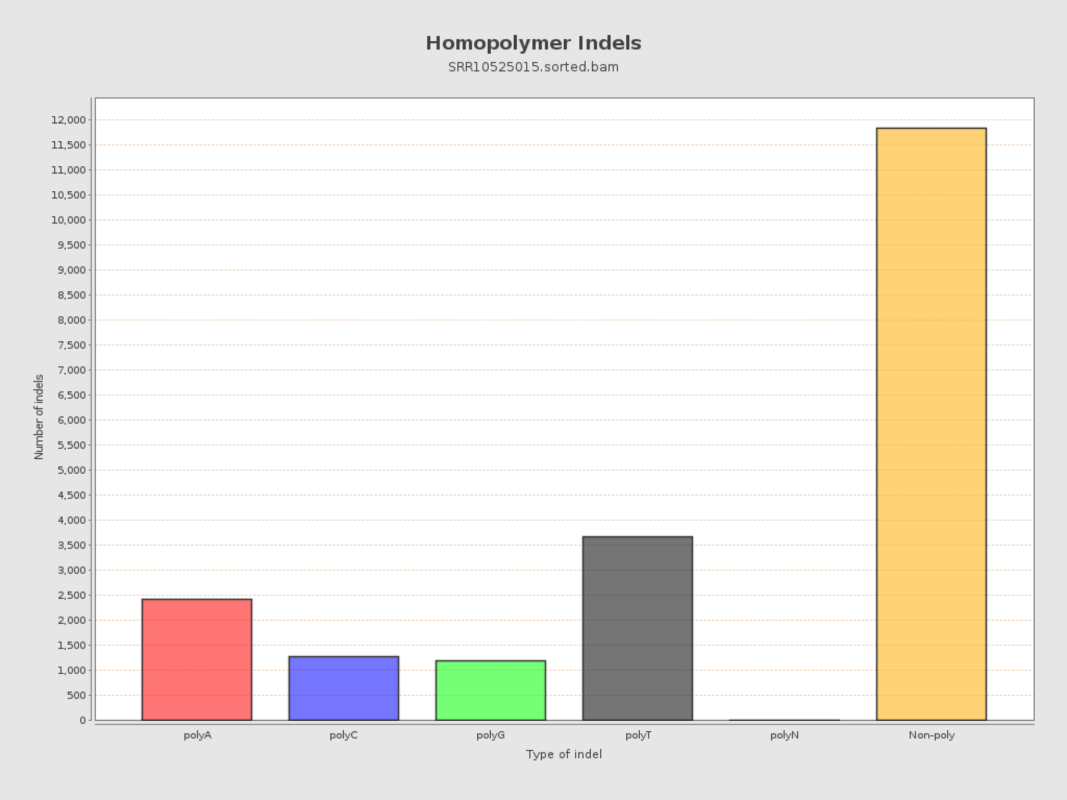
9. Results : Mapped Reads GC-content Distribution



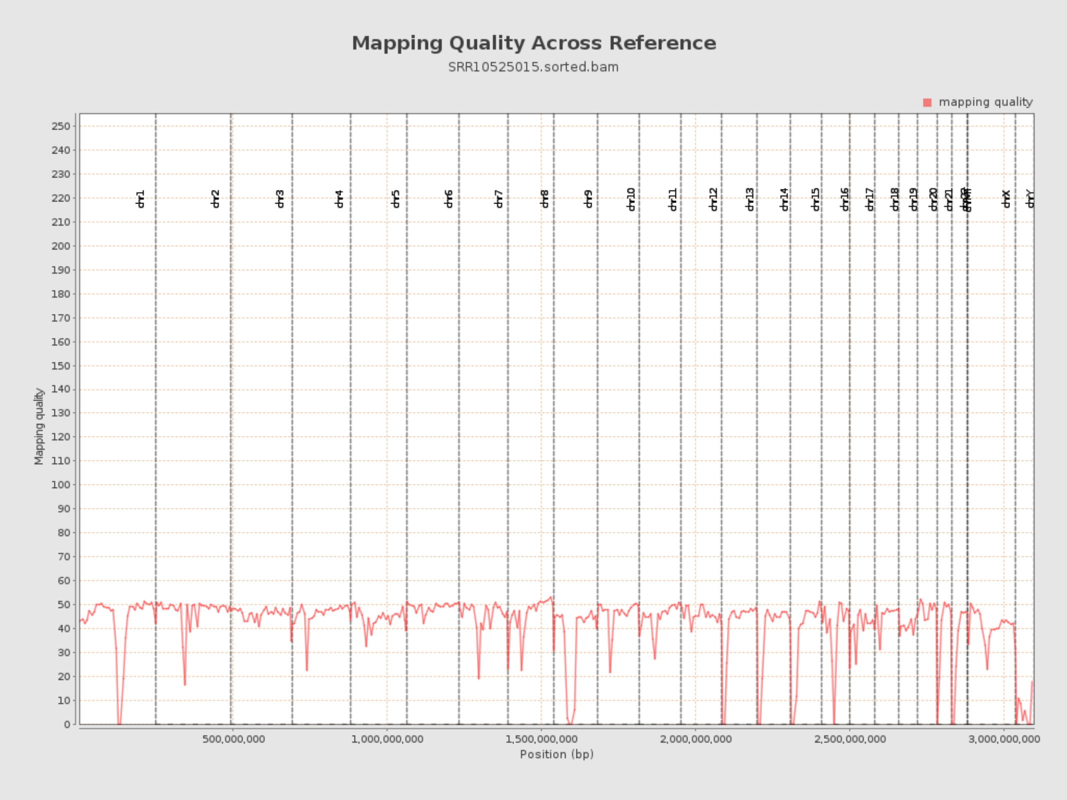
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram