Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:59:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525007.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_SRR10525007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525007.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:59:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,314,452
Mapped reads	1,212,278 / 92.23%
Unmapped reads	102,174 / 7.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,080 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	33,461 / 2.55%
Duplication rate	1.95%
Clipped reads	1,214,009 / 92.36%

2.2. ACGT Content

Number/percentage of A's	16,525,807 / 23.54%
Number/percentage of C's	13,167,211 / 18.75%
Number/percentage of T's	22,504,899 / 32.05%
Number/percentage of G's	18,013,768 / 25.66%
Number/percentage of N's	616 / 0%
GC Percentage	44.41%

2.3. Coverage

Mean	0.0227

Standard Deviation	0.2225

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

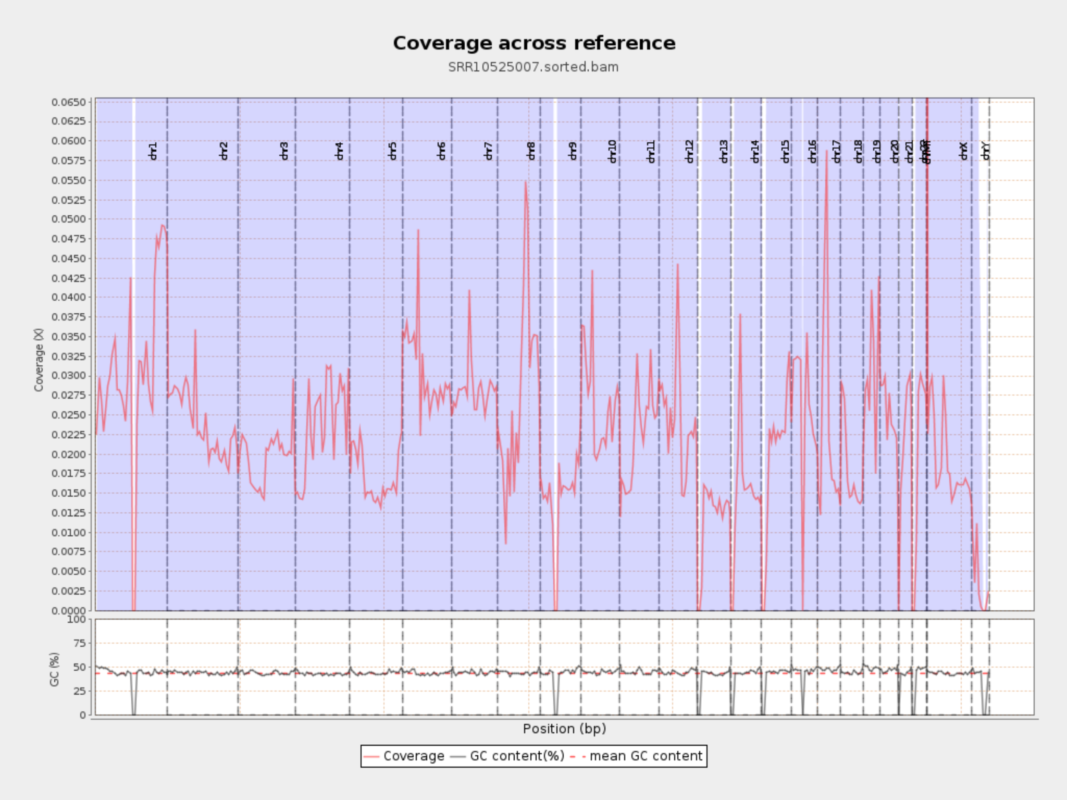
General error rate	0.49%
Mismatches	333,997
Insertions	4,284
Mapped reads with at least one insertion	0.35%
Deletions	13,878
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.01%

2.6. Chromosome stats

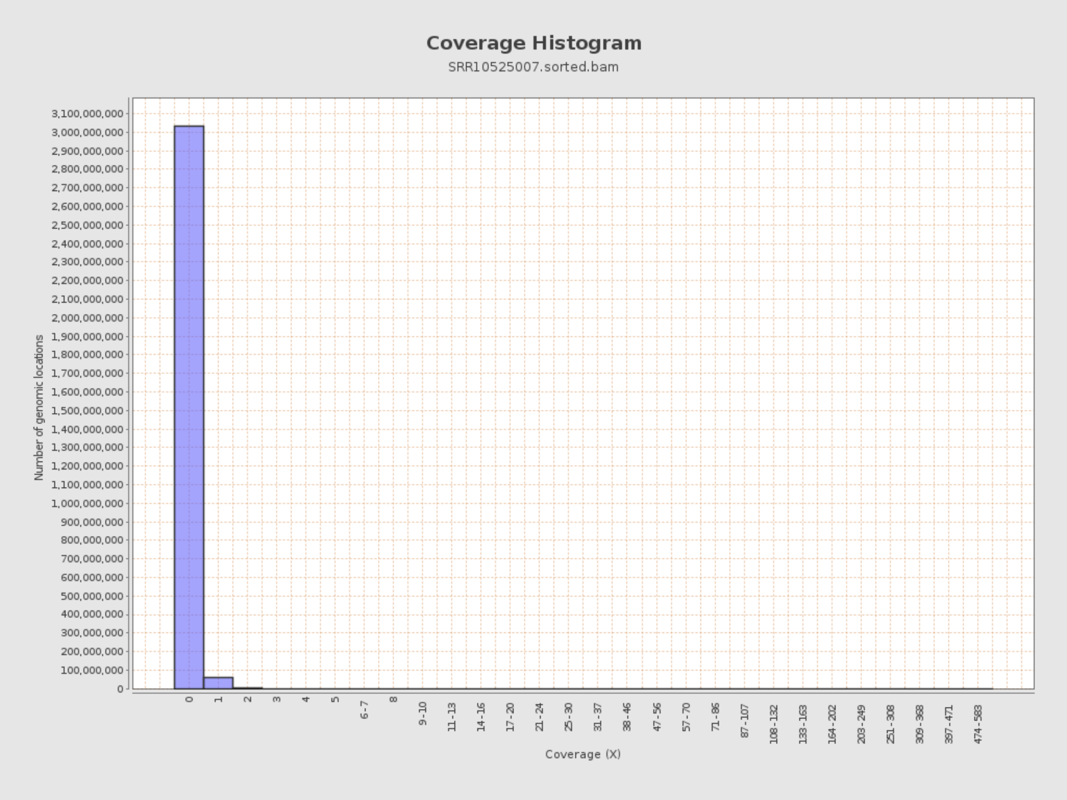
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7626155	0.0306	0.4204
chr2	243199373	5830267	0.024	0.2377
chr3	198022430	3904404	0.0197	0.1507
chr4	191154276	4557616	0.0238	0.1753
chr5	180915260	3103995	0.0172	0.1408
chr6	171115067	5251025	0.0307	0.2543
chr7	159138663	4519087	0.0284	0.282

chr8	146364022	4113464	0.0281	0.2235
chr9	141213431	2001423	0.0142	0.1668
chr10	135534747	3652035	0.0269	0.2199
chr11	135006516	3046658	0.0226	0.1992
chr12	133851895	3264625	0.0244	0.1676
chr13	115169878	1343175	0.0117	0.1165
chr14	107349540	1618134	0.0151	0.1336
chr15	102531392	2016720	0.0197	0.153
chr16	90354753	2324138	0.0257	0.1764
chr17	81195210	1988827	0.0245	0.2133
chr18	78077248	1410299	0.0181	0.2572
chr19	59128983	1818588	0.0308	0.2615
chr20	63025520	1588090	0.0252	0.1704
chr21	48129895	1042319	0.0217	0.1653
chr22	51304566	1005260	0.0196	0.1482
chrMT	16571	12996	0.7843	1.0532
chrX	155270560	2994477	0.0193	0.1667
chrY	59373566	201606	0.0034	0.0943

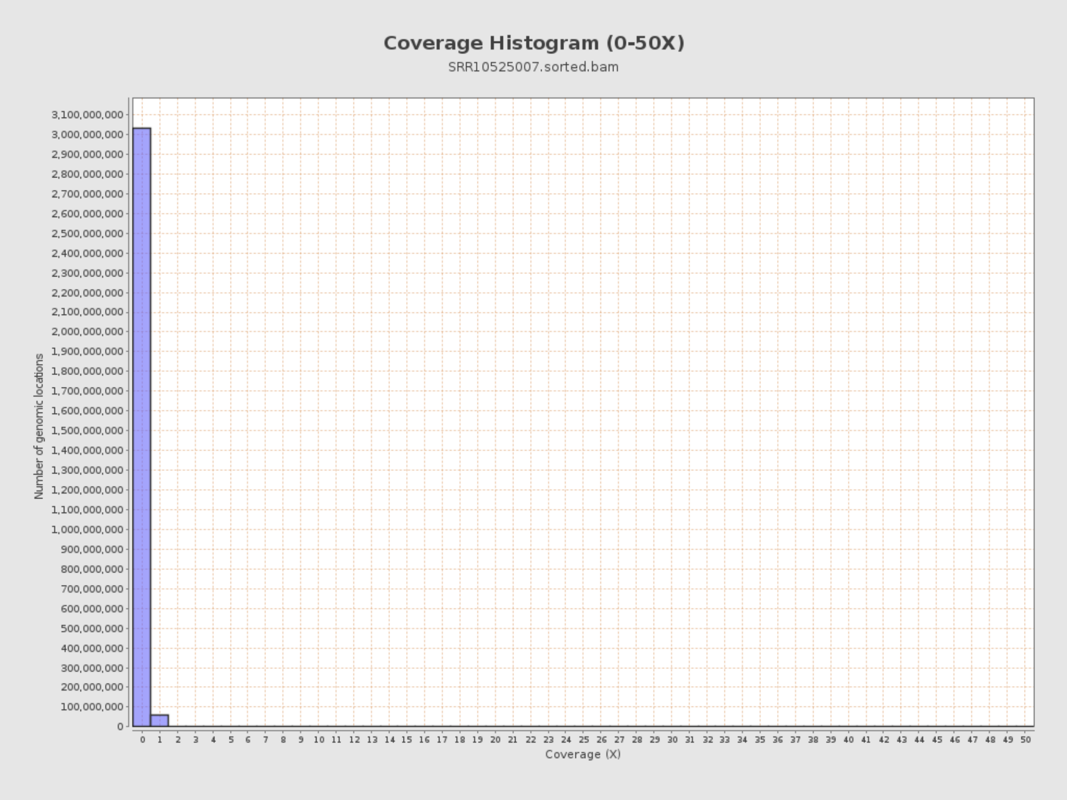
3. Results : Coverage across reference



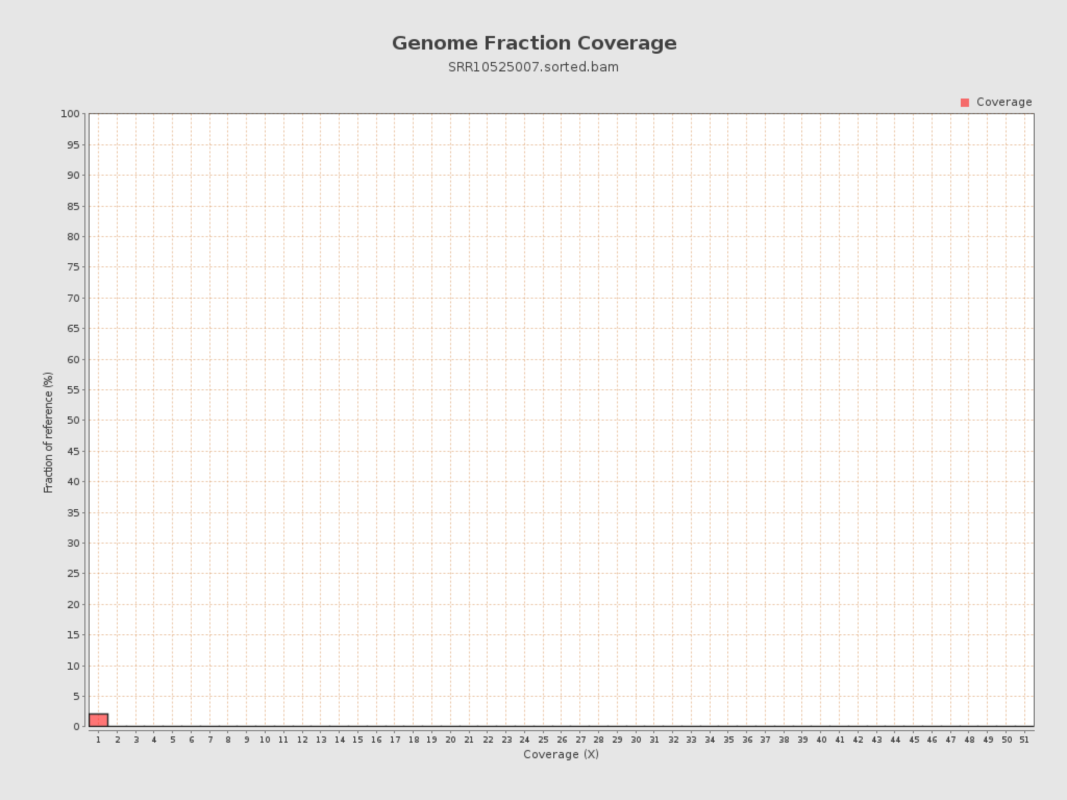
4. Results : Coverage Histogram



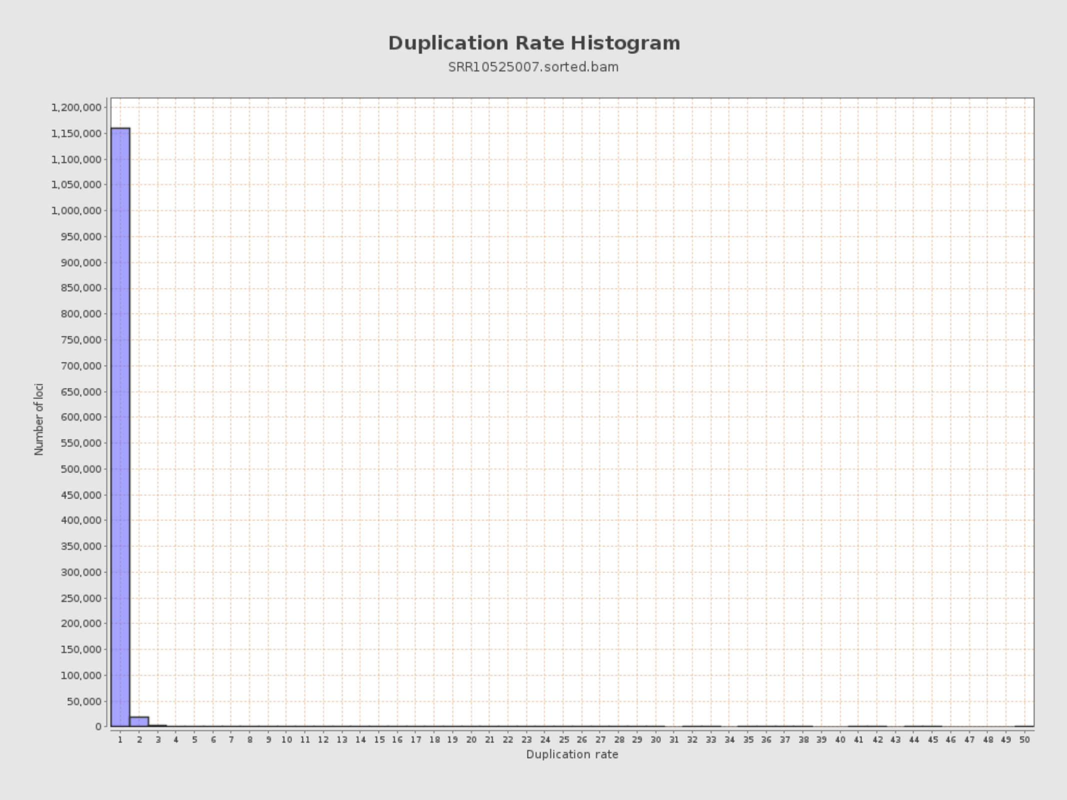
5. Results : Coverage Histogram (0-50X)



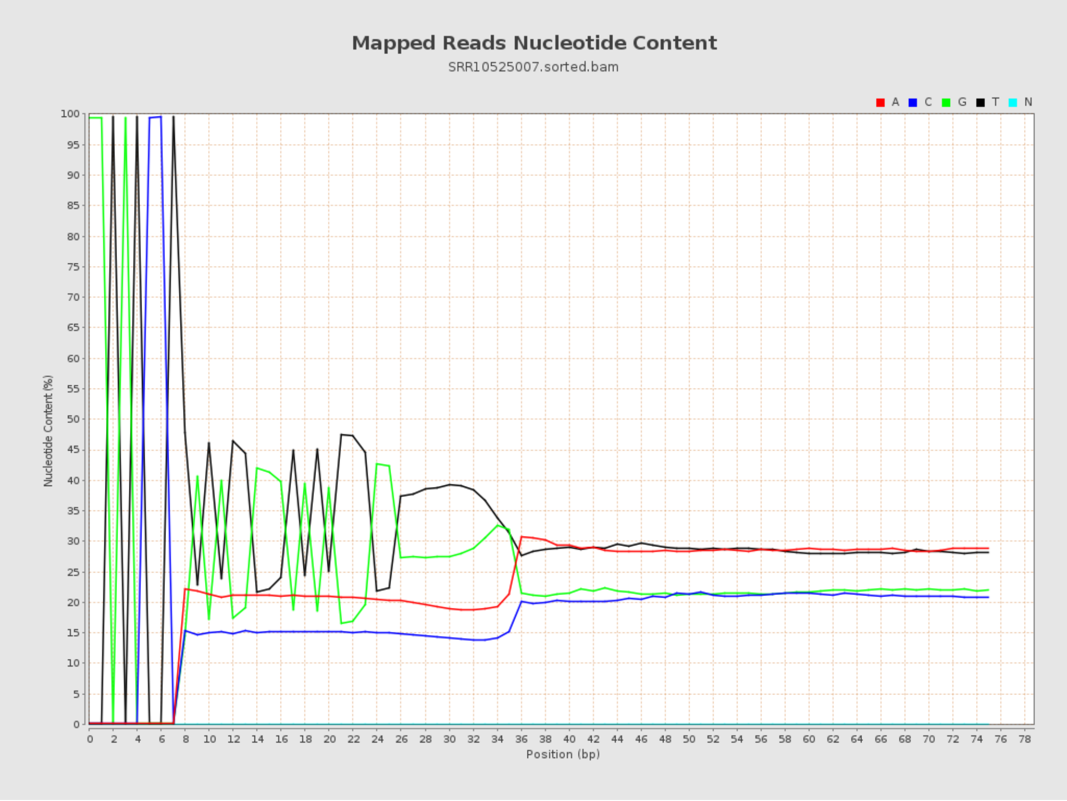
6. Results : Genome Fraction Coverage



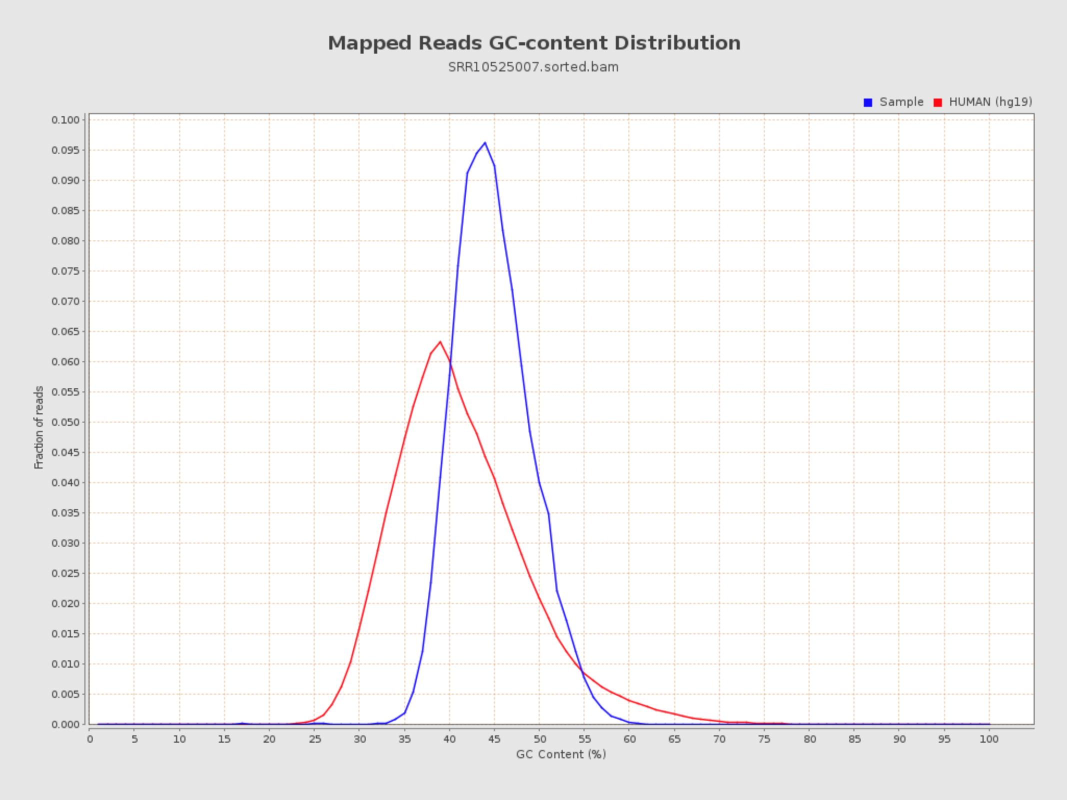
7. Results : Duplication Rate Histogram



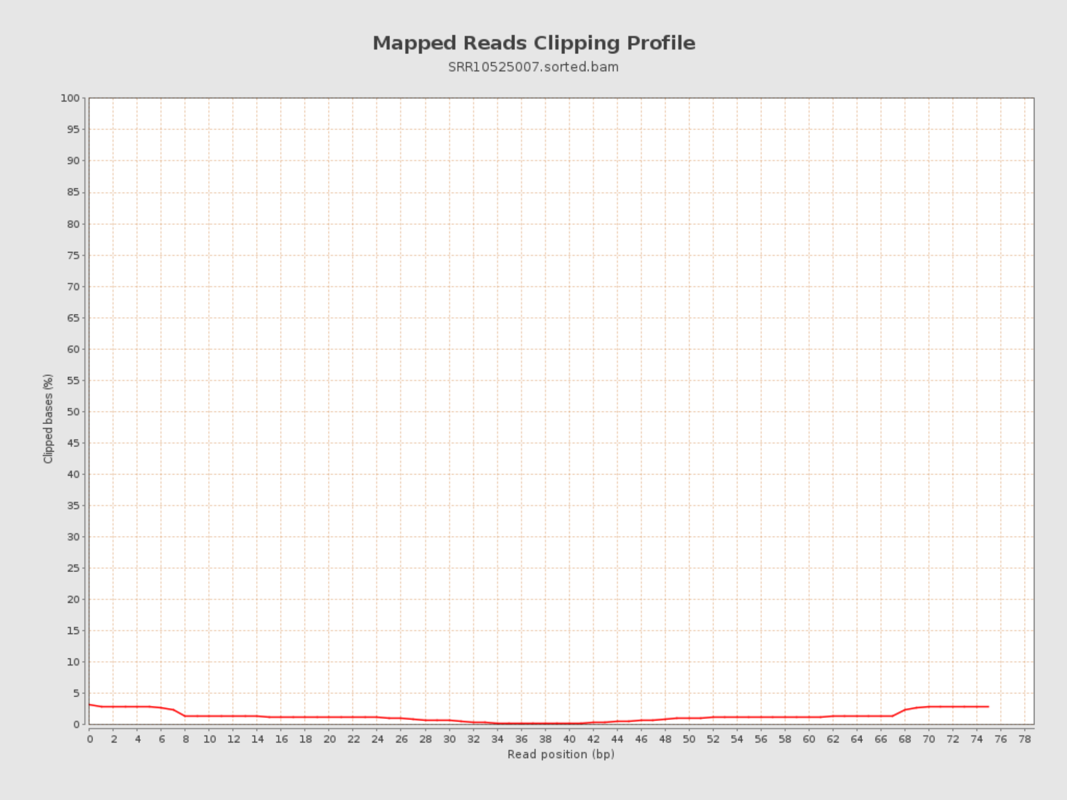
8. Results : Mapped Reads Nucleotide Content



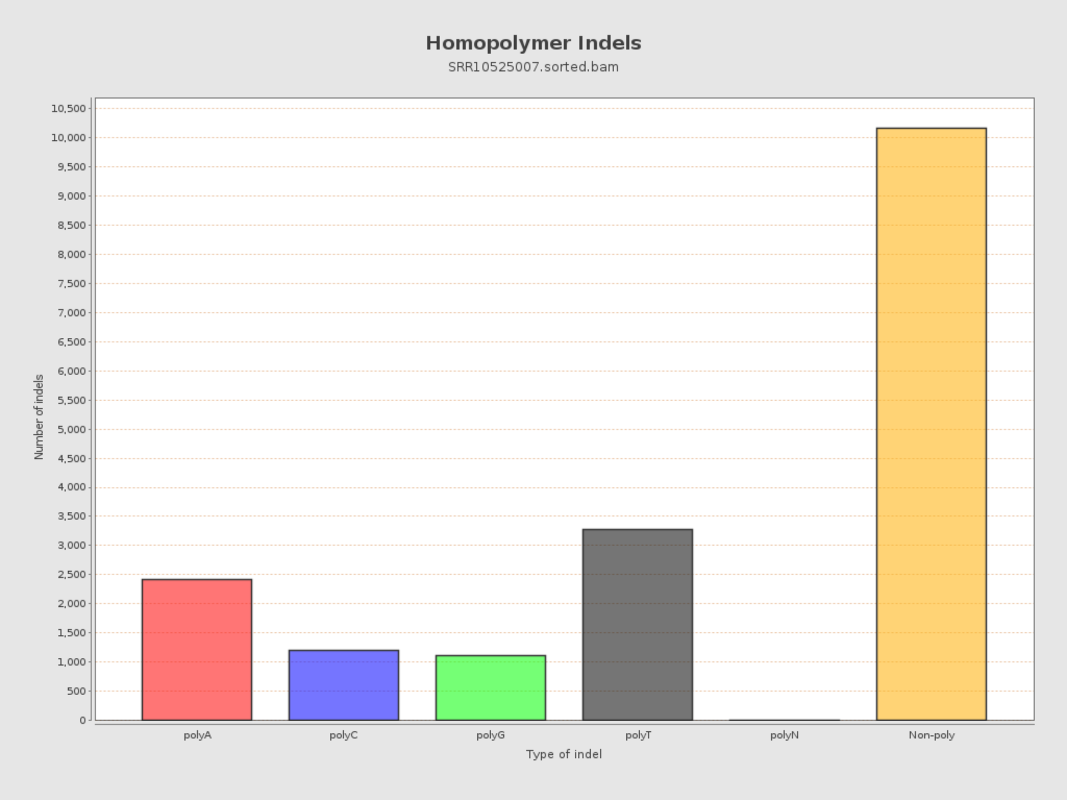
9. Results : Mapped Reads GC-content Distribution



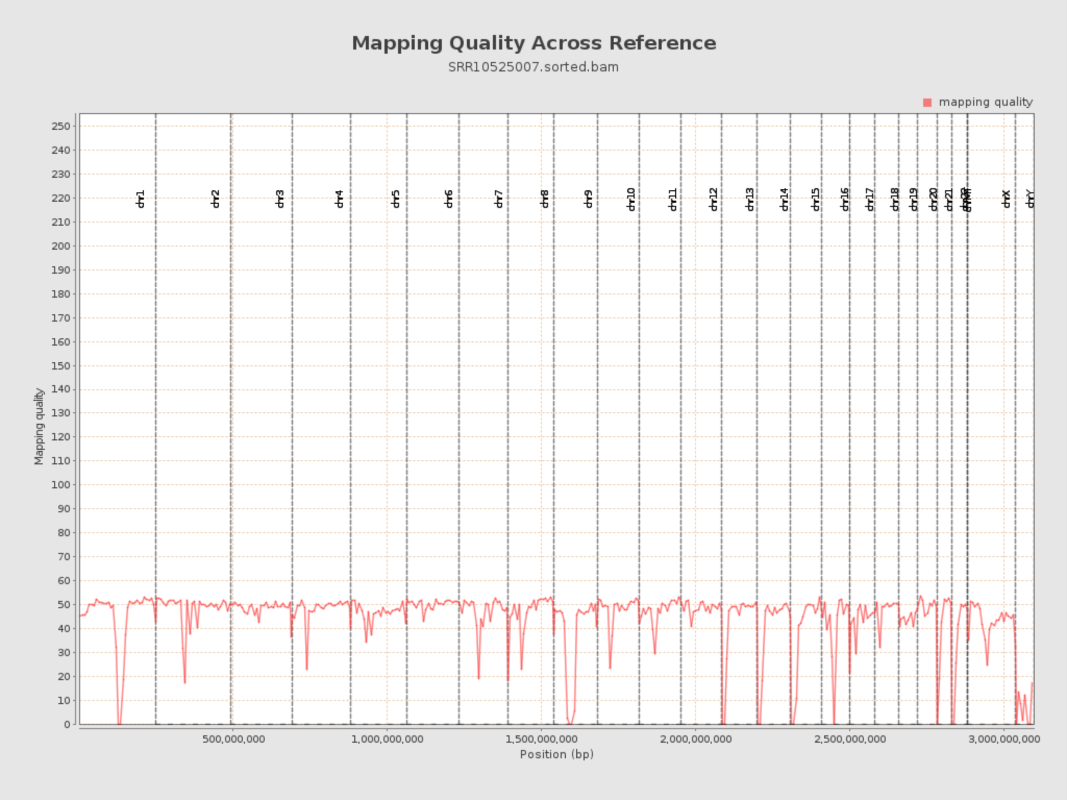
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram