Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:07:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525186.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_SRR10525186 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525186.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:07:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525186.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	936,719
Mapped reads	855,411 / 91.32%
Unmapped reads	81,308 / 8.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,629 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	20,303 / 2.17%
Duplication rate	1.67%
Clipped reads	857,362 / 91.53%

2.2. ACGT Content

Number/percentage of A's	13,309,884 / 26.2%
Number/percentage of C's	9,242,469 / 18.19%
Number/percentage of T's	15,653,362 / 30.81%
Number/percentage of G's	12,599,444 / 24.8%
Number/percentage of N's	1,248 / 0%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0164

Standard Deviation	0.1873

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

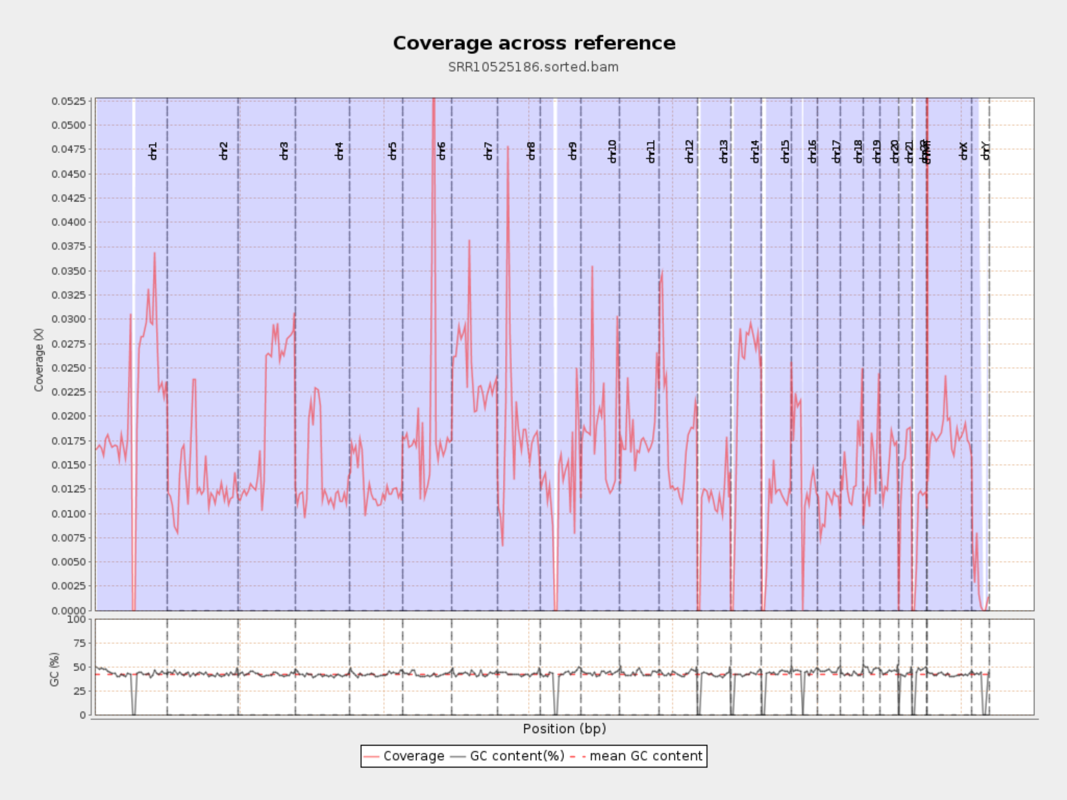
General error rate	0.5%
Mismatches	249,339
Insertions	2,966
Mapped reads with at least one insertion	0.35%
Deletions	10,372
Mapped reads with at least one deletion	1.2%
Homopolymer indels	44.53%

2.6. Chromosome stats

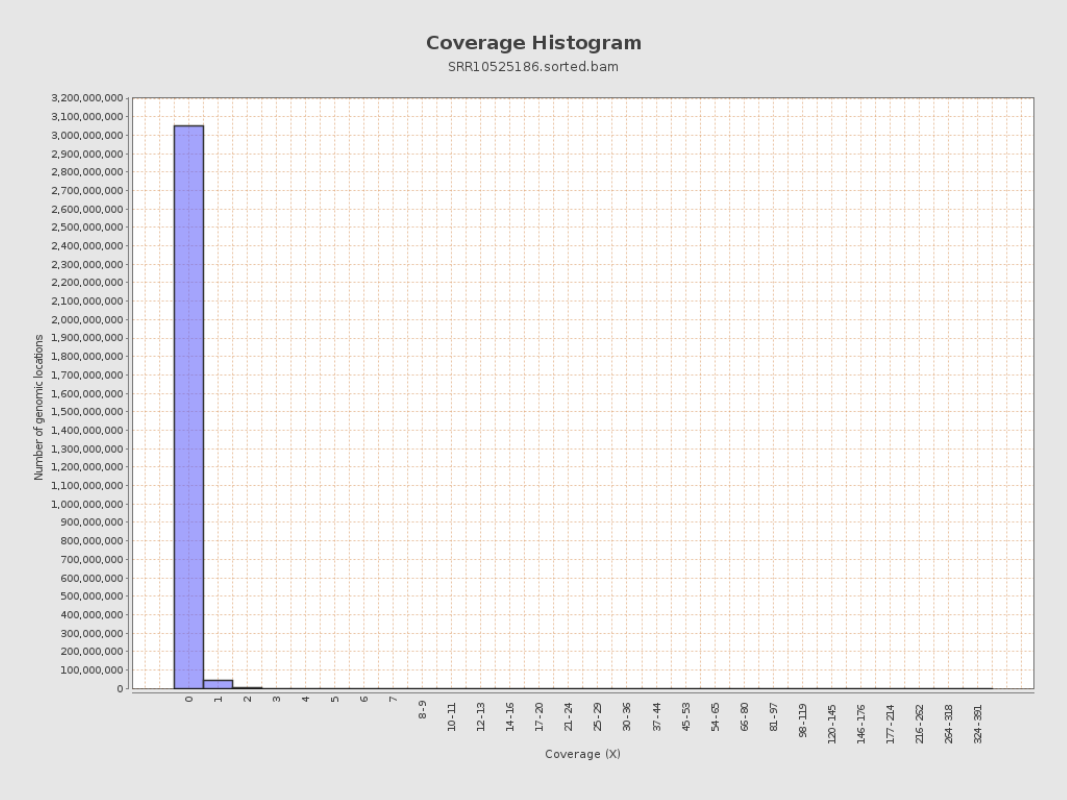
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5198399	0.0209	0.327
chr2	243199373	3190092	0.0131	0.2068
chr3	198022430	4032881	0.0204	0.1515
chr4	191154276	2666488	0.0139	0.1282
chr5	180915260	2354442	0.013	0.1189
chr6	171115067	3352493	0.0196	0.1554
chr7	159138663	3976884	0.025	0.3128

chr8	146364022	2731716	0.0187	0.1694
chr9	141213431	1795529	0.0127	0.1353
chr10	135534747	2572297	0.019	0.1992
chr11	135006516	2429159	0.018	0.1588
chr12	133851895	2442317	0.0182	0.1425
chr13	115169878	1240225	0.0108	0.1097
chr14	107349540	2427851	0.0226	0.1591
chr15	102531392	1019443	0.0099	0.1049
chr16	90354753	1337190	0.0148	0.1366
chr17	81195210	869893	0.0107	0.1117
chr18	78077248	1142062	0.0146	0.2357
chr19	59128983	880750	0.0149	0.2361
chr20	63025520	932172	0.0148	0.1282
chr21	48129895	691640	0.0144	0.1296
chr22	51304566	428658	0.0084	0.0955
chrMT	16571	141882	8.5621	4.7679
chrX	155270560	2823831	0.0182	0.1487
chrY	59373566	144978	0.0024	0.0778

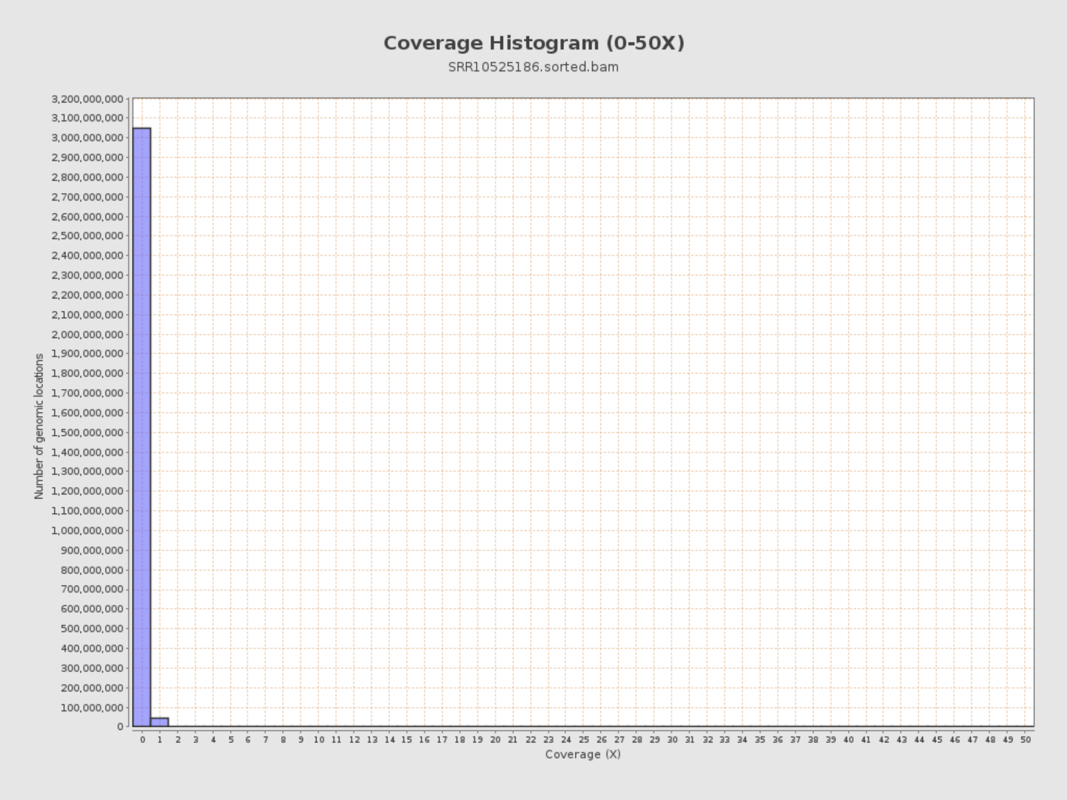
3. Results : Coverage across reference



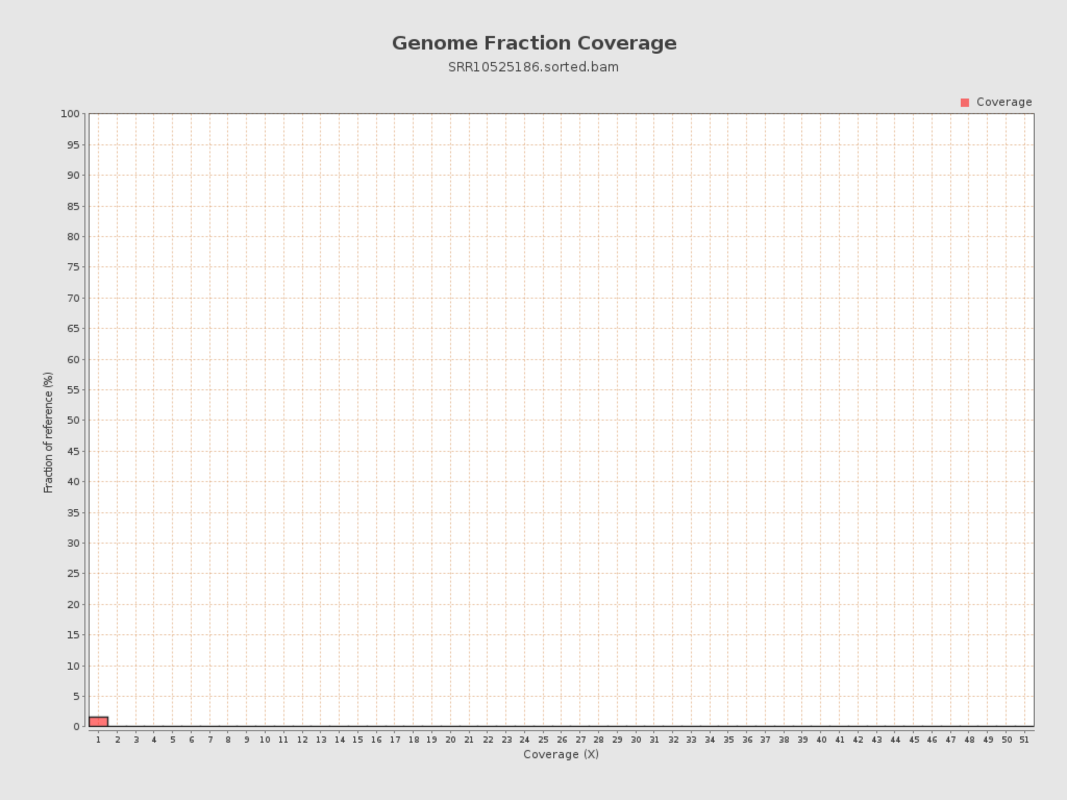
4. Results : Coverage Histogram



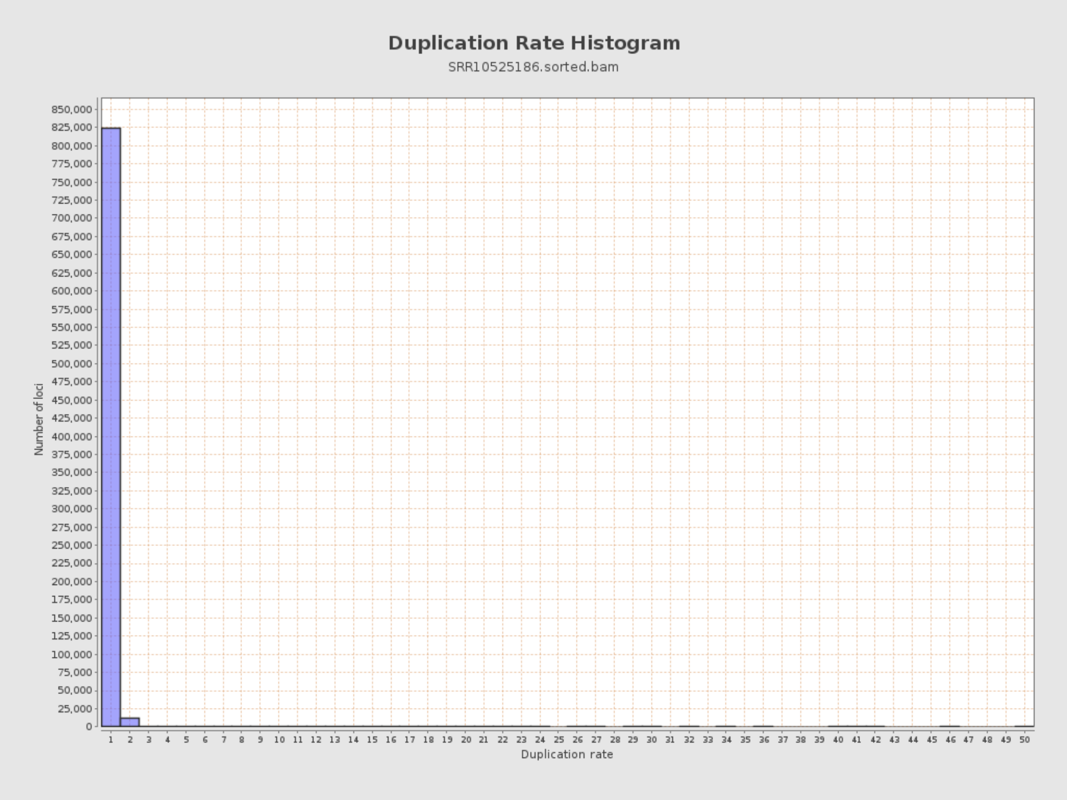
5. Results : Coverage Histogram (0-50X)



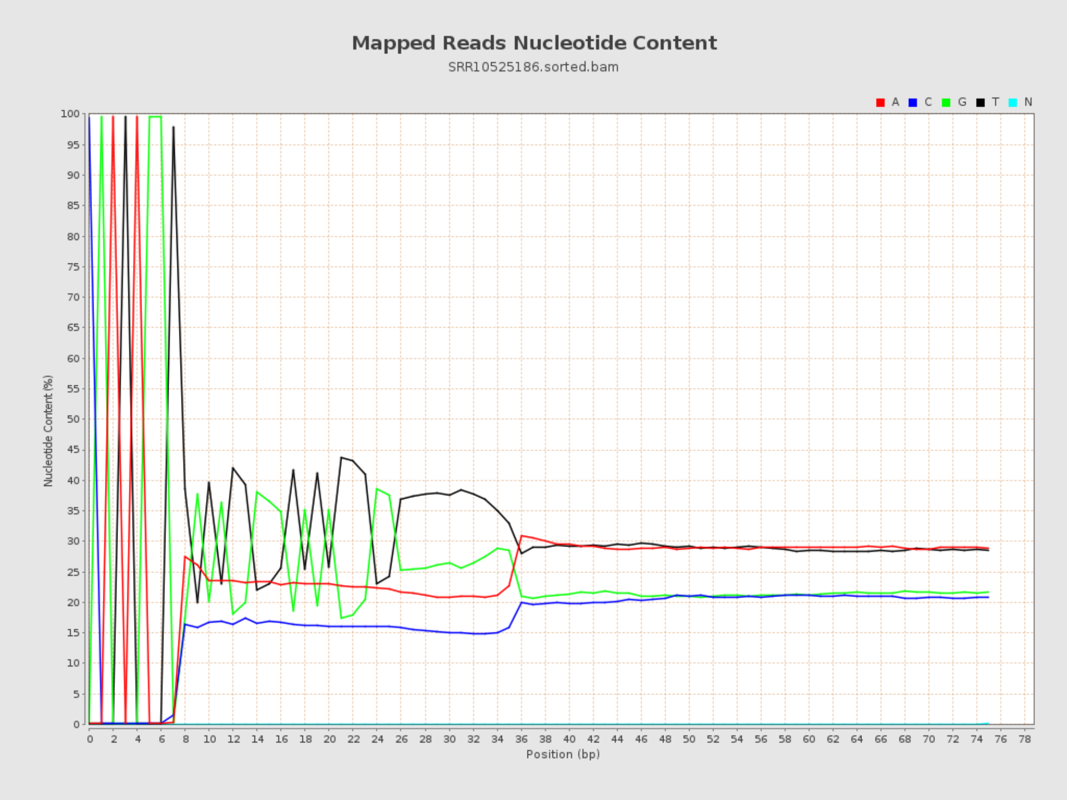
6. Results : Genome Fraction Coverage



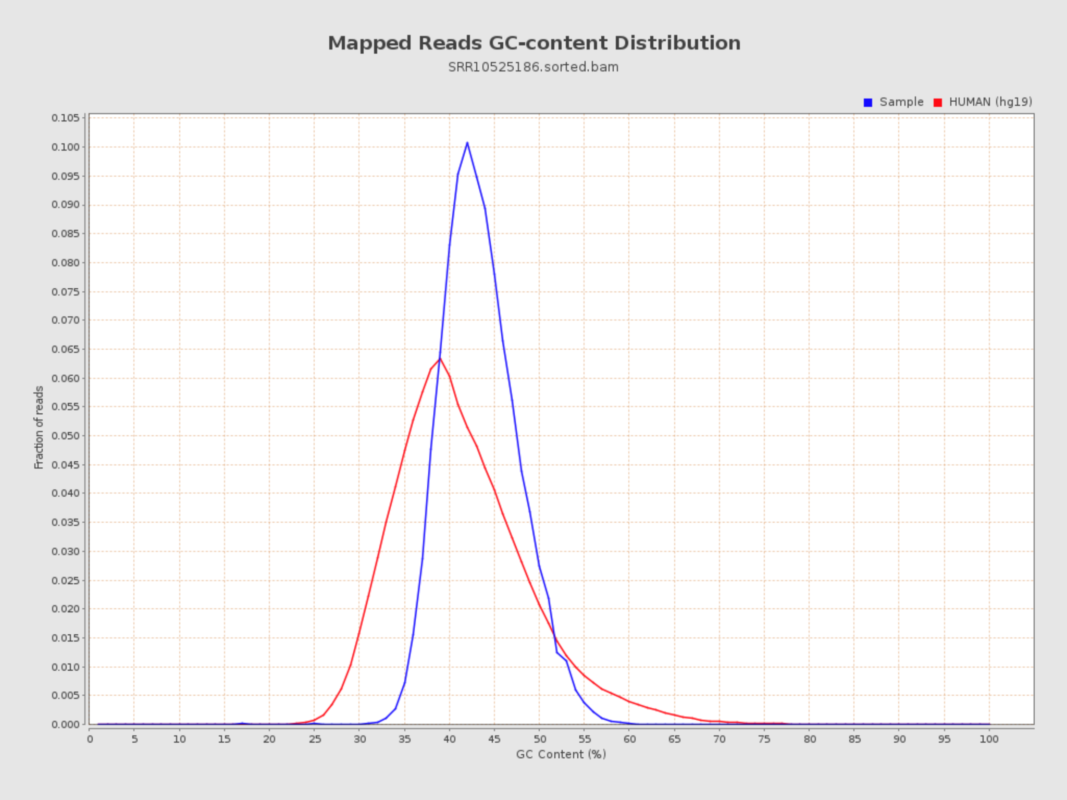
7. Results : Duplication Rate Histogram



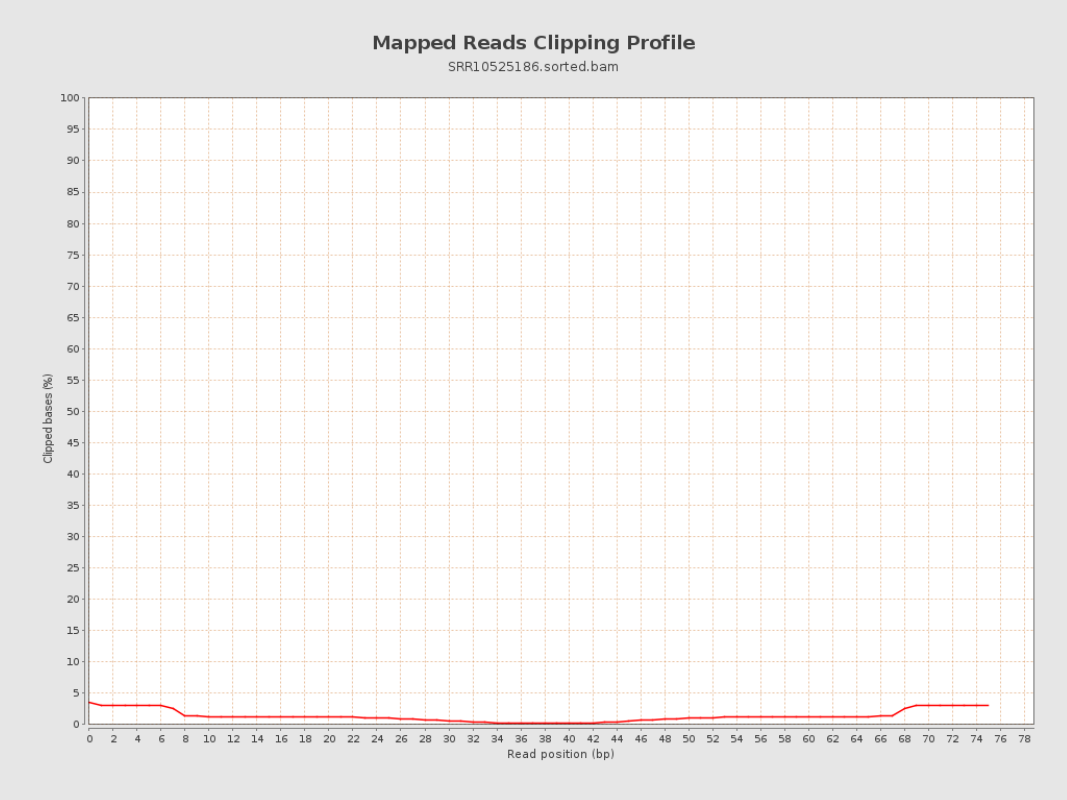
8. Results : Mapped Reads Nucleotide Content



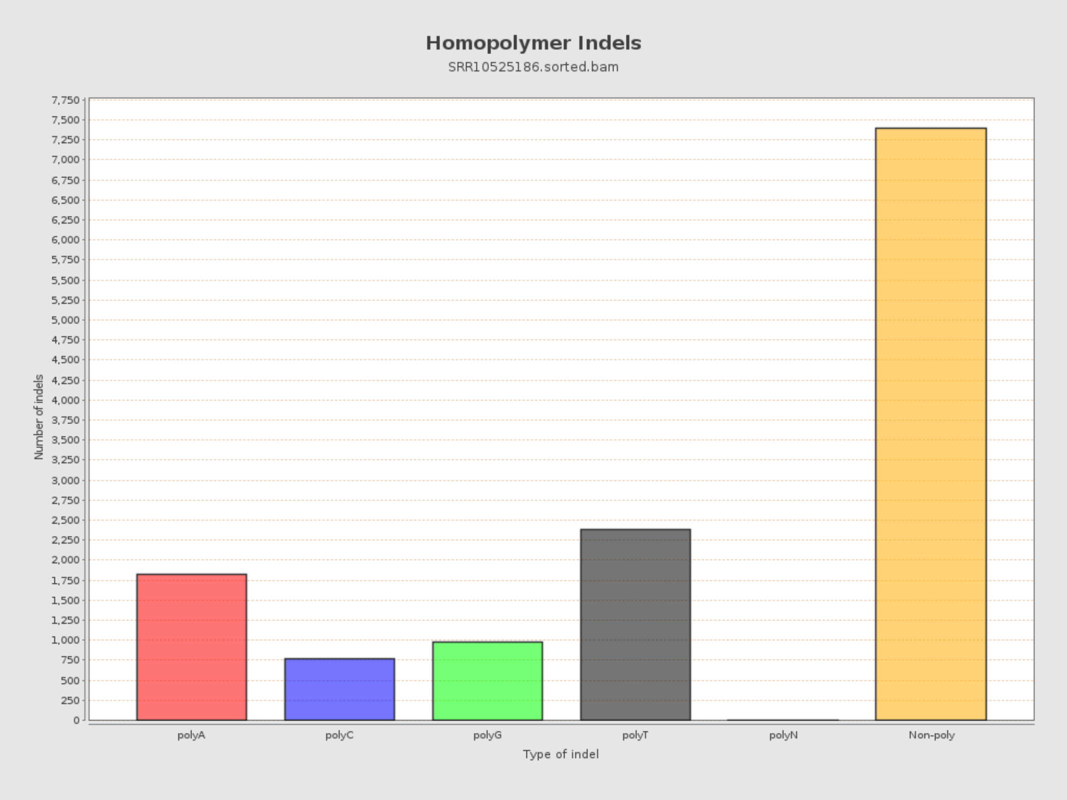
9. Results : Mapped Reads GC-content Distribution



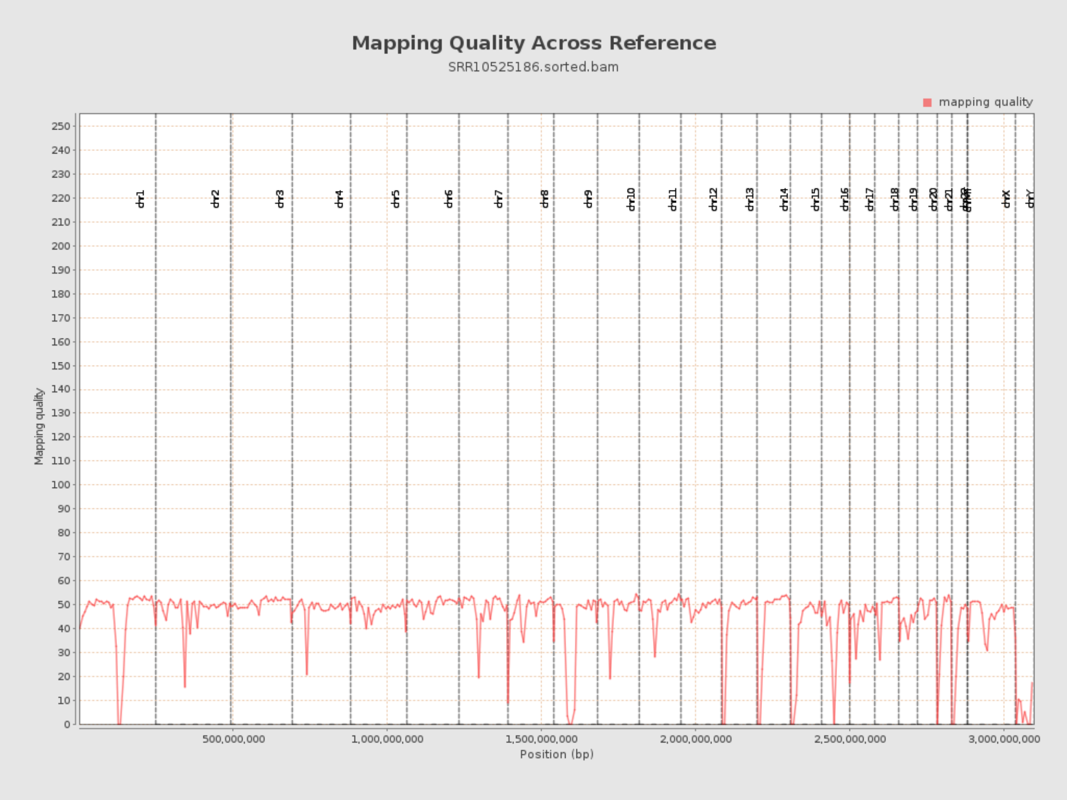
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram