Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:48:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525180.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_SRR10525180 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525180.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:48:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525180.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,081,958
Mapped reads	1,916,851 / 92.07%
Unmapped reads	165,107 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,333 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	76,670 / 3.68%
Duplication rate	2.93%
Clipped reads	1,918,860 / 92.17%

2.2. ACGT Content

Number/percentage of A's	27,710,799 / 24.7%
Number/percentage of C's	20,934,828 / 18.66%
Number/percentage of T's	36,026,363 / 32.11%
Number/percentage of G's	27,512,605 / 24.52%
Number/percentage of N's	2,552 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.3332

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

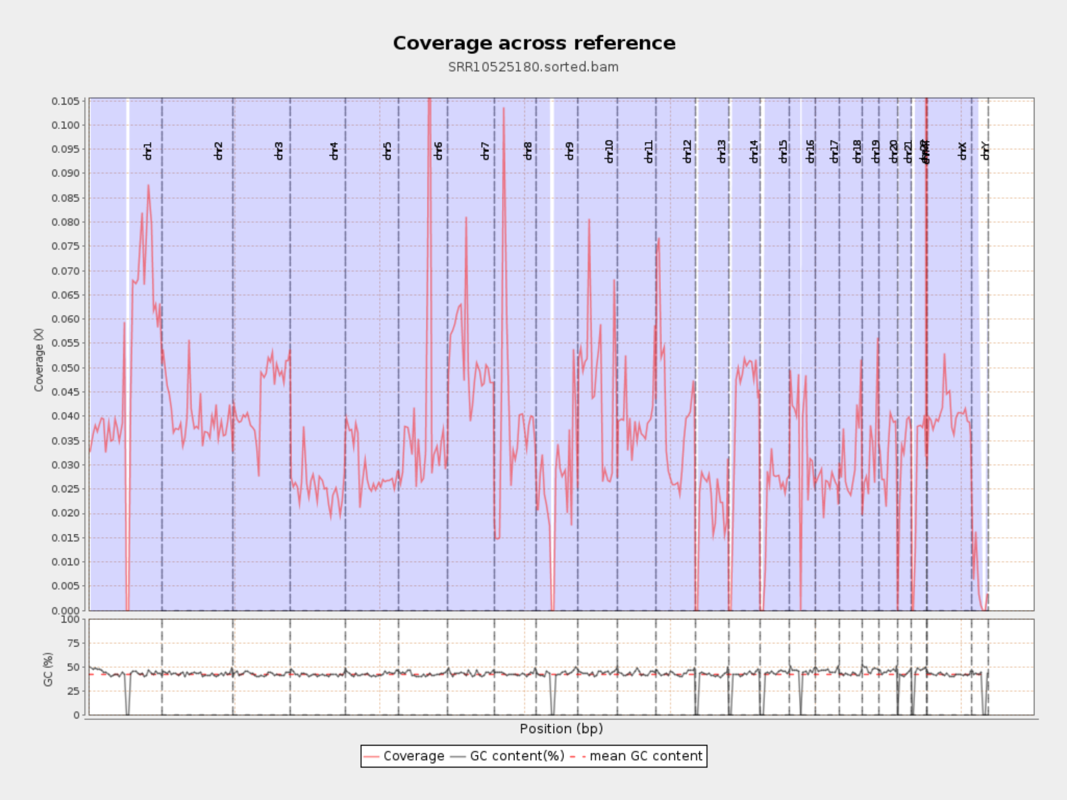
General error rate	0.51%
Mismatches	562,080
Insertions	7,519
Mapped reads with at least one insertion	0.39%
Deletions	22,321
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.83%

2.6. Chromosome stats

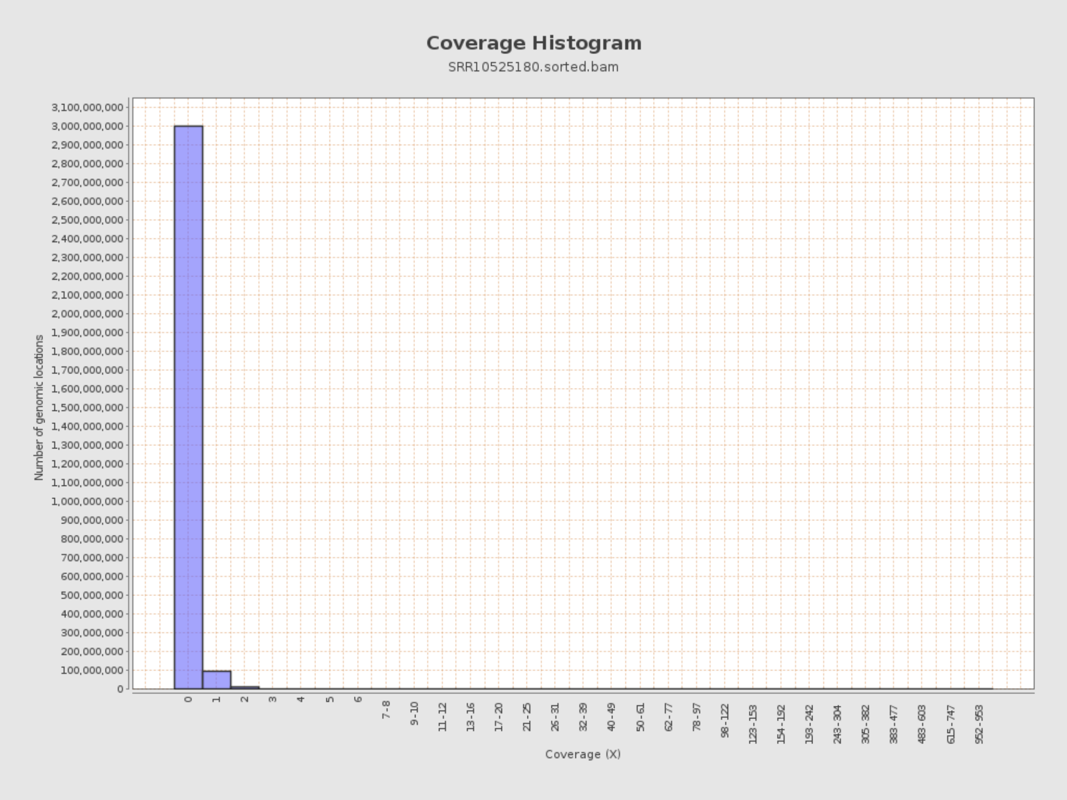
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12275455	0.0492	0.5728
chr2	243199373	9700119	0.0399	0.451
chr3	198022430	8714433	0.044	0.2321
chr4	191154276	4827311	0.0253	0.187
chr5	180915260	5253823	0.029	0.1873
chr6	171115067	6635137	0.0388	0.2462
chr7	159138663	8372518	0.0526	0.5951

chr8	146364022	5574633	0.0381	0.2734
chr9	141213431	3647283	0.0258	0.2347
chr10	135534747	6336009	0.0467	0.3733
chr11	135006516	5310075	0.0393	0.2772
chr12	133851895	5336357	0.0399	0.223
chr13	115169878	2369493	0.0206	0.1648
chr14	107349540	4373737	0.0407	0.2276
chr15	102531392	2269618	0.0221	0.1657
chr16	90354753	3130448	0.0346	0.2316
chr17	81195210	2103947	0.0259	0.1865
chr18	78077248	2492112	0.0319	0.5092
chr19	59128983	1934102	0.0327	0.4066
chr20	63025520	2040591	0.0324	0.2028
chr21	48129895	1482815	0.0308	0.2049
chr22	51304566	1353746	0.0264	0.1784
chrMT	16571	126388	7.6271	4.8899
chrX	155270560	6253046	0.0403	0.242
chrY	59373566	309484	0.0052	0.1399

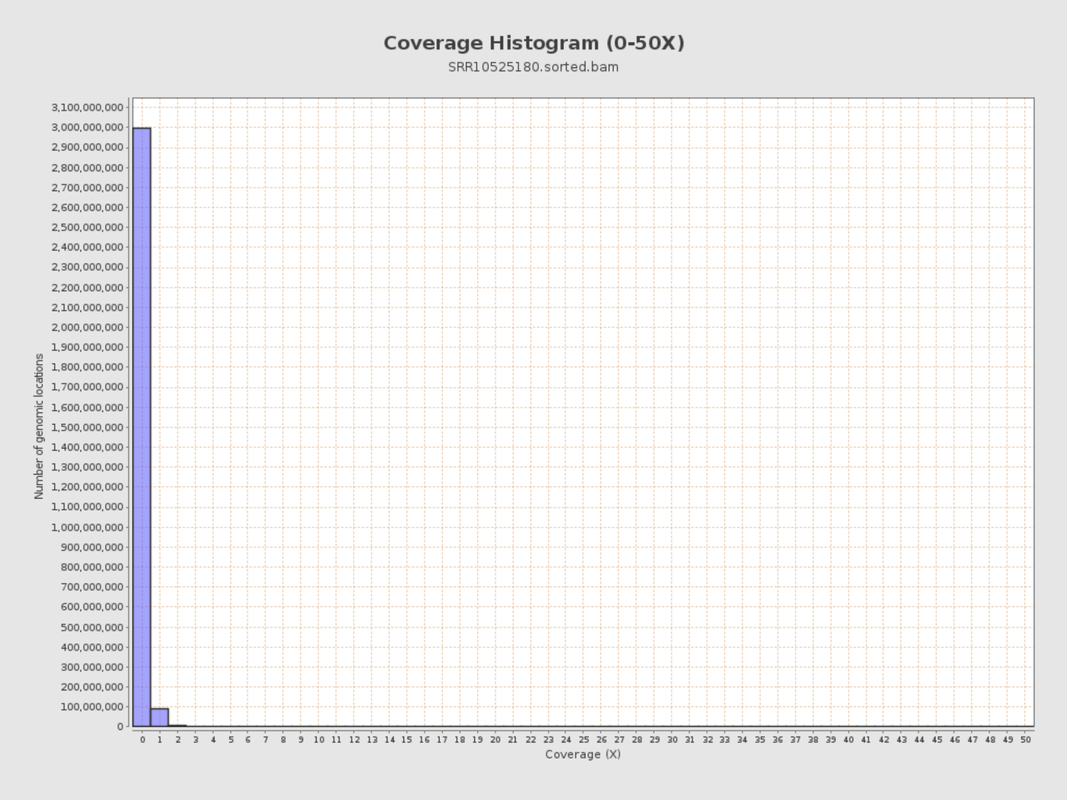
3. Results : Coverage across reference



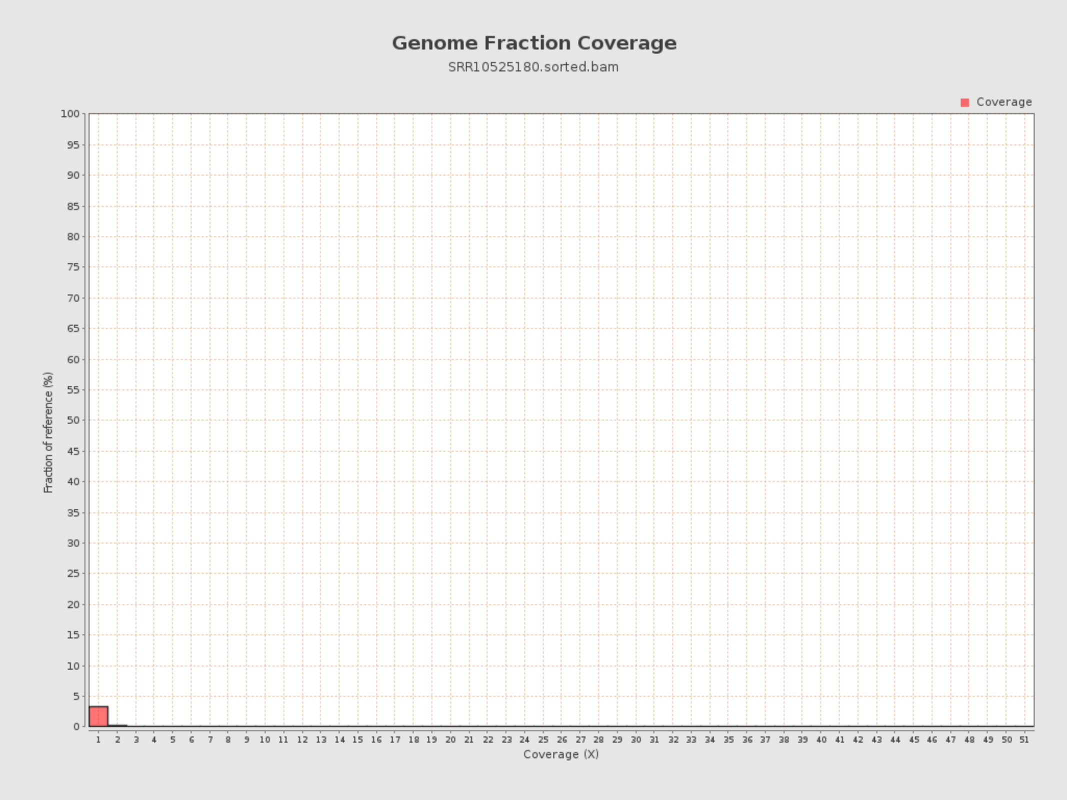
4. Results : Coverage Histogram



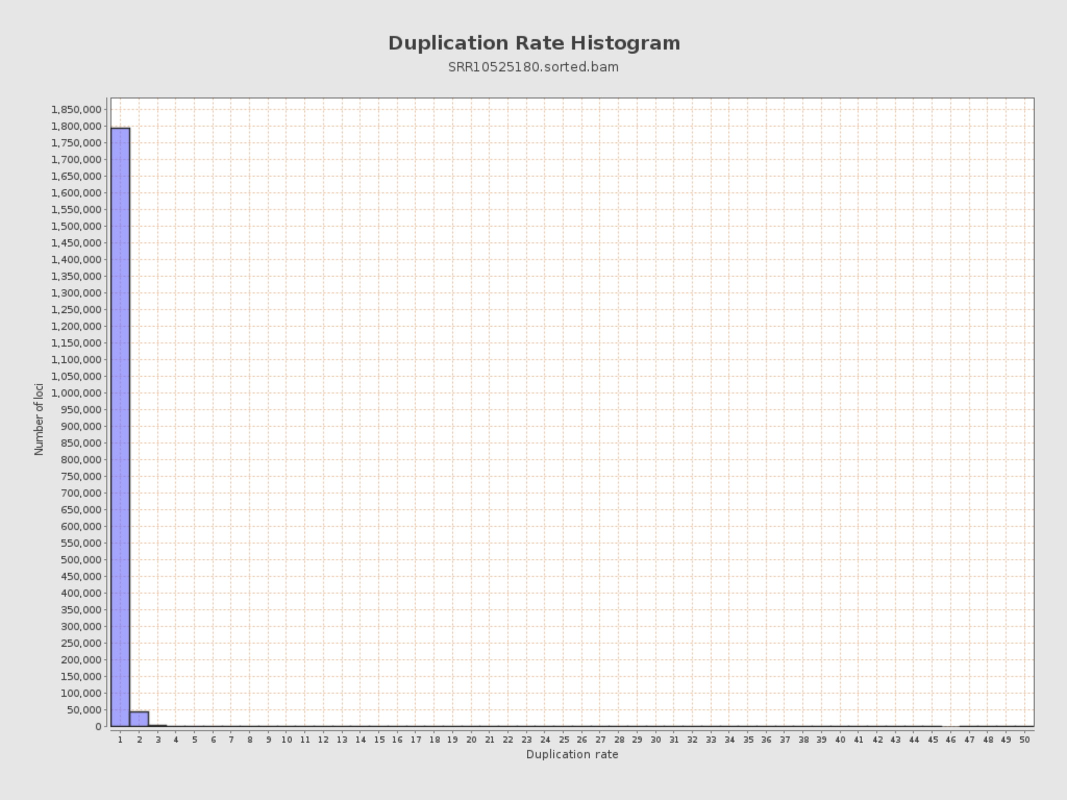
5. Results : Coverage Histogram (0-50X)



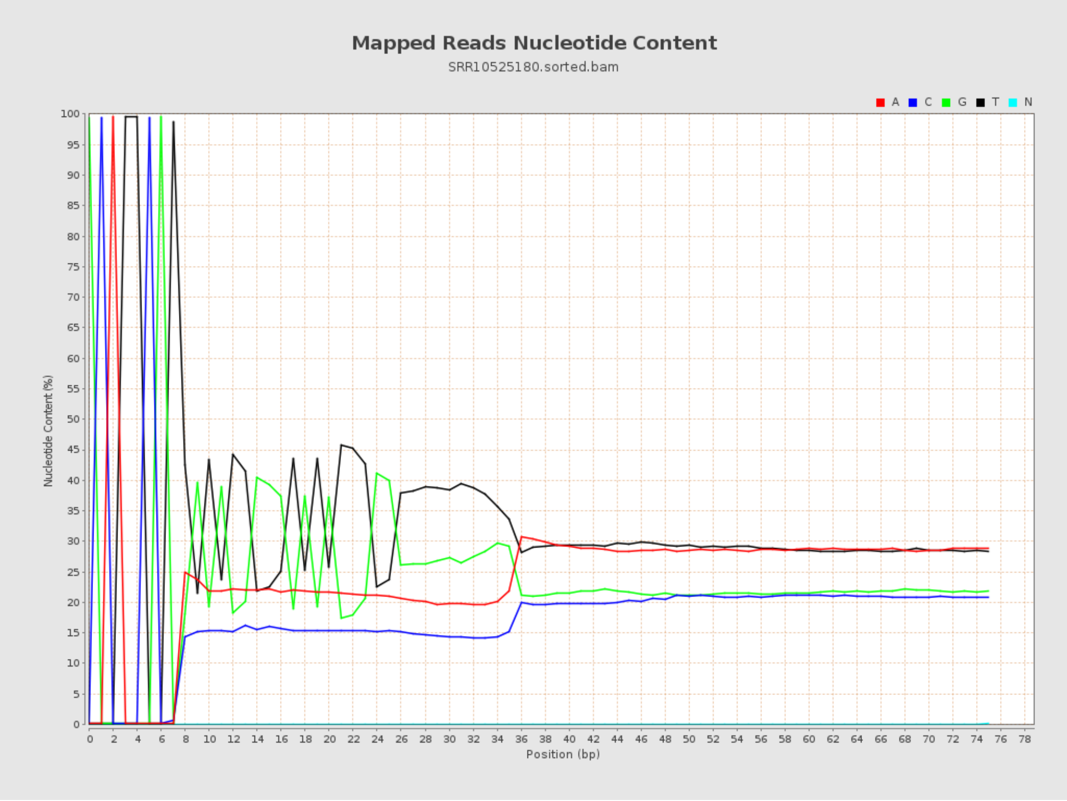
6. Results : Genome Fraction Coverage



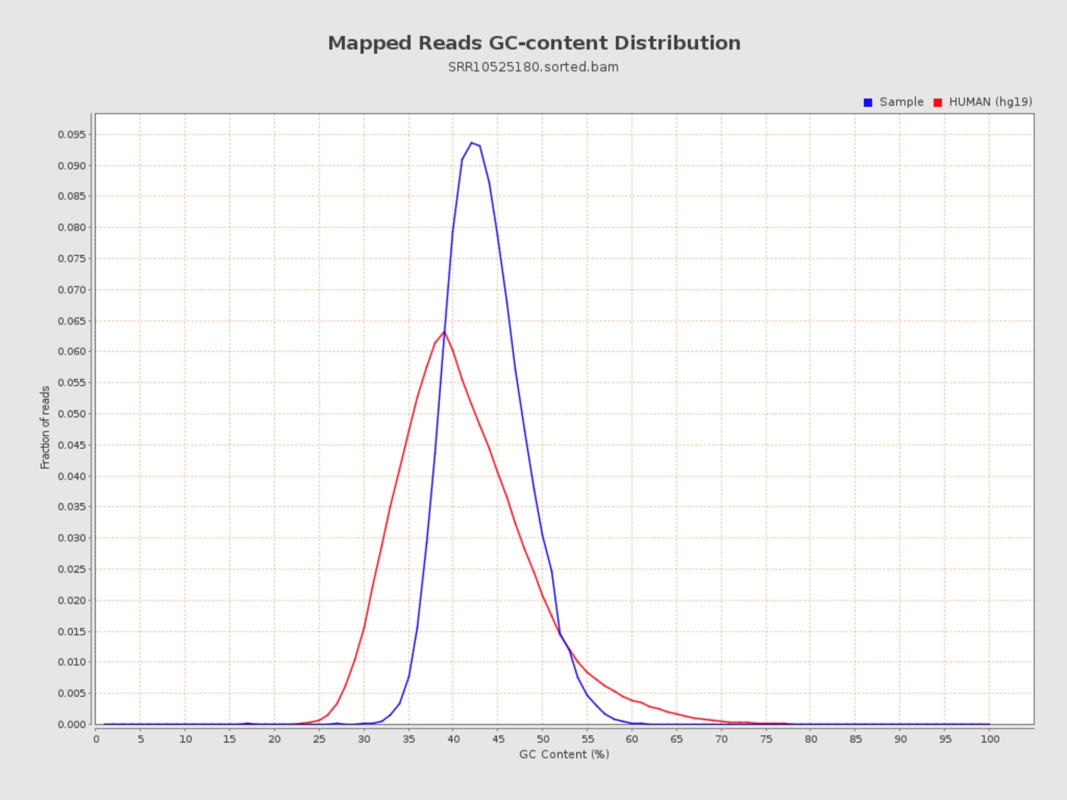
7. Results : Duplication Rate Histogram



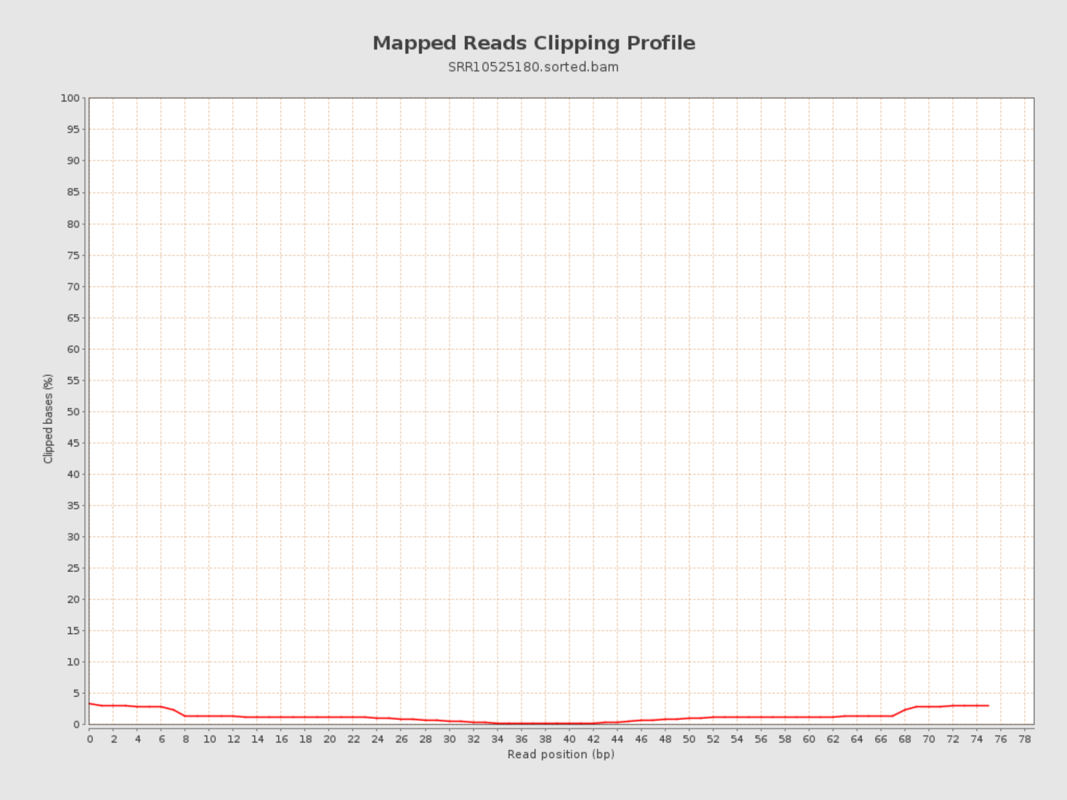
8. Results : Mapped Reads Nucleotide Content



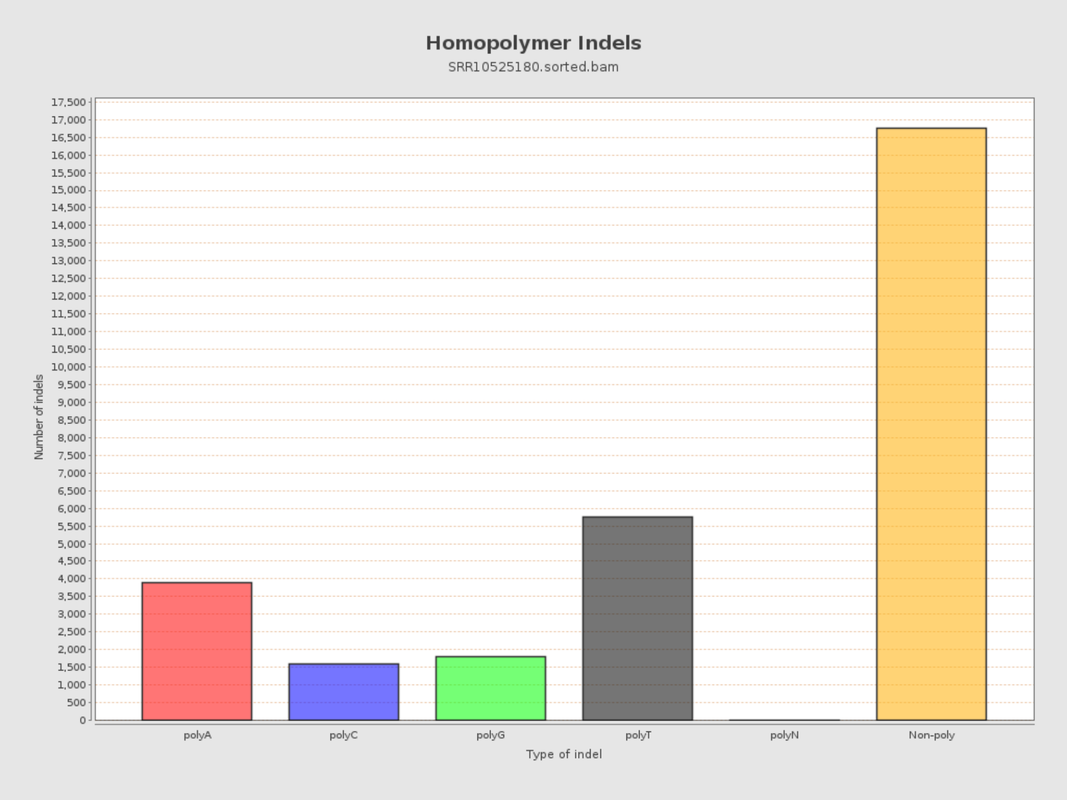
9. Results : Mapped Reads GC-content Distribution



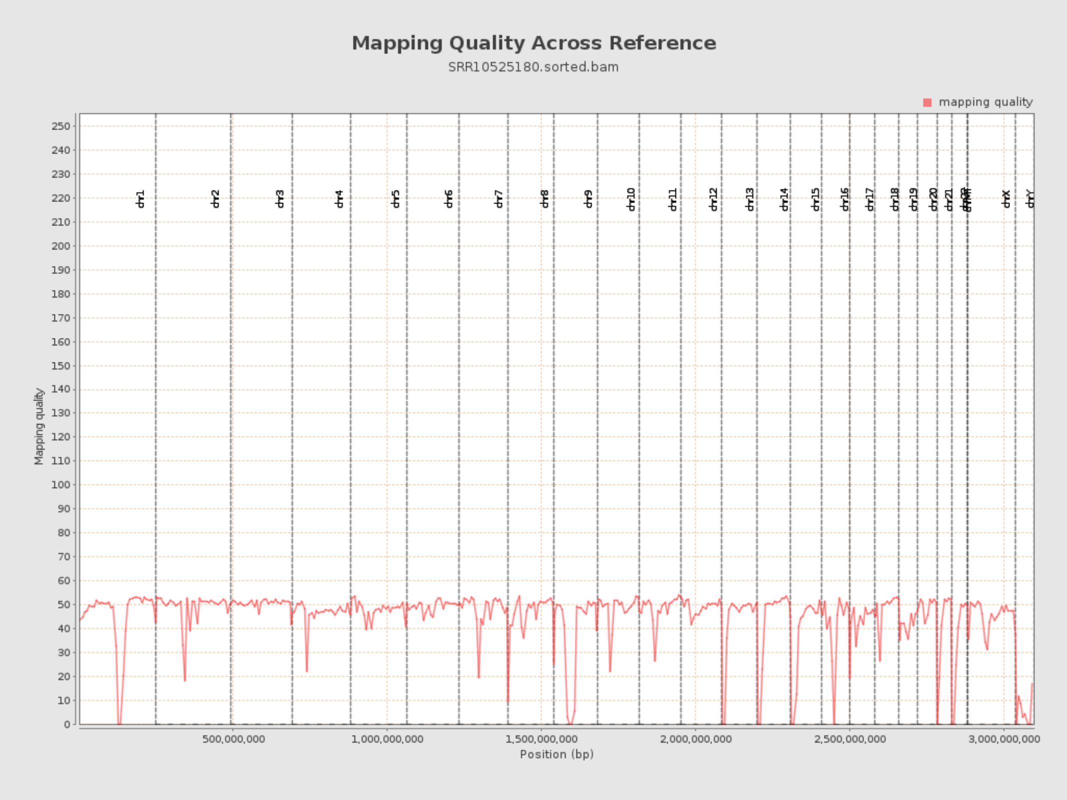
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram