Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:51:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525181.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_SRR10525181 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525181.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:51:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525181.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,501,701
Mapped reads	2,330,416 / 93.15%
Unmapped reads	171,285 / 6.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,842 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	101,756 / 4.07%
Duplication rate	3.22%
Clipped reads	2,328,960 / 93.1%

2.2. ACGT Content

Number/percentage of A's	36,227,623 / 26.5%
Number/percentage of C's	27,812,562 / 20.34%
Number/percentage of T's	41,494,040 / 30.35%
Number/percentage of G's	31,173,387 / 22.8%
Number/percentage of N's	3,182 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0442

Standard Deviation	0.393

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

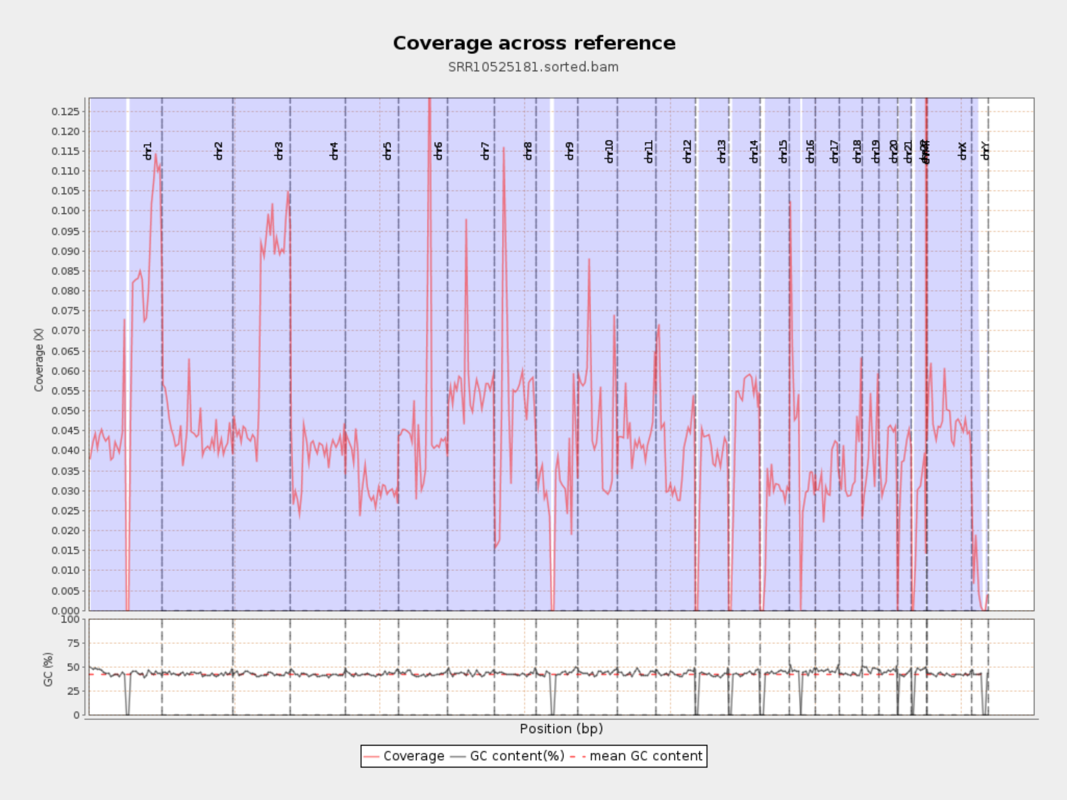
General error rate	0.51%
Mismatches	676,039
Insertions	10,731
Mapped reads with at least one insertion	0.46%
Deletions	27,781
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.55%

2.6. Chromosome stats

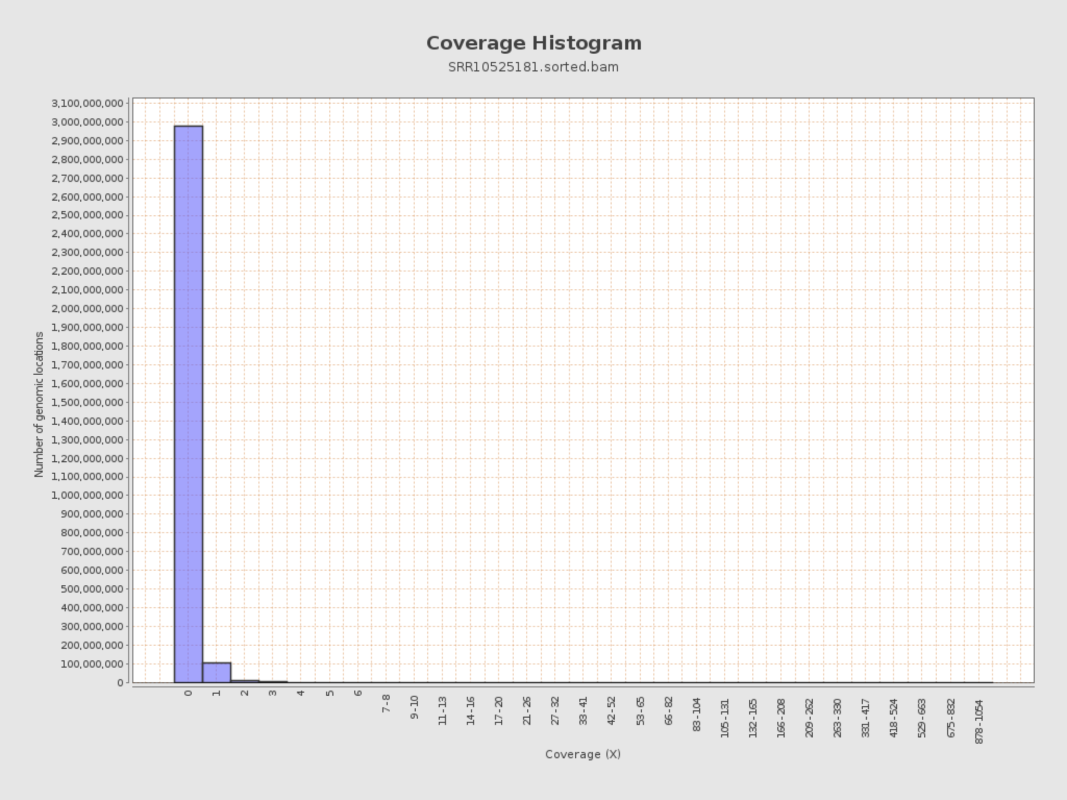
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15127455	0.0607	0.713
chr2	243199373	10837496	0.0446	0.4955
chr3	198022430	13869346	0.07	0.3009
chr4	191154276	7385162	0.0386	0.2334
chr5	180915260	5897576	0.0326	0.2032
chr6	171115067	8269013	0.0483	0.2813
chr7	159138663	9051145	0.0569	0.7609

chr8	146364022	7537142	0.0515	0.3364
chr9	141213431	4274353	0.0303	0.2566
chr10	135534747	6652249	0.0491	0.402
chr11	135006516	5986179	0.0443	0.3059
chr12	133851895	5501366	0.0411	0.2302
chr13	115169878	4086634	0.0355	0.2154
chr14	107349540	4959563	0.0462	0.2487
chr15	102531392	2574344	0.0251	0.1906
chr16	90354753	3592110	0.0398	0.2474
chr17	81195210	2695945	0.0332	0.2143
chr18	78077248	2856180	0.0366	0.529
chr19	59128983	2372101	0.0401	0.4791
chr20	63025520	2437648	0.0387	0.2232
chr21	48129895	1660079	0.0345	0.2205
chr22	51304566	1172000	0.0228	0.1686
chrMT	16571	152335	9.1929	5.7832
chrX	155270560	7436999	0.0479	0.2724
chrY	59373566	370433	0.0062	0.1532

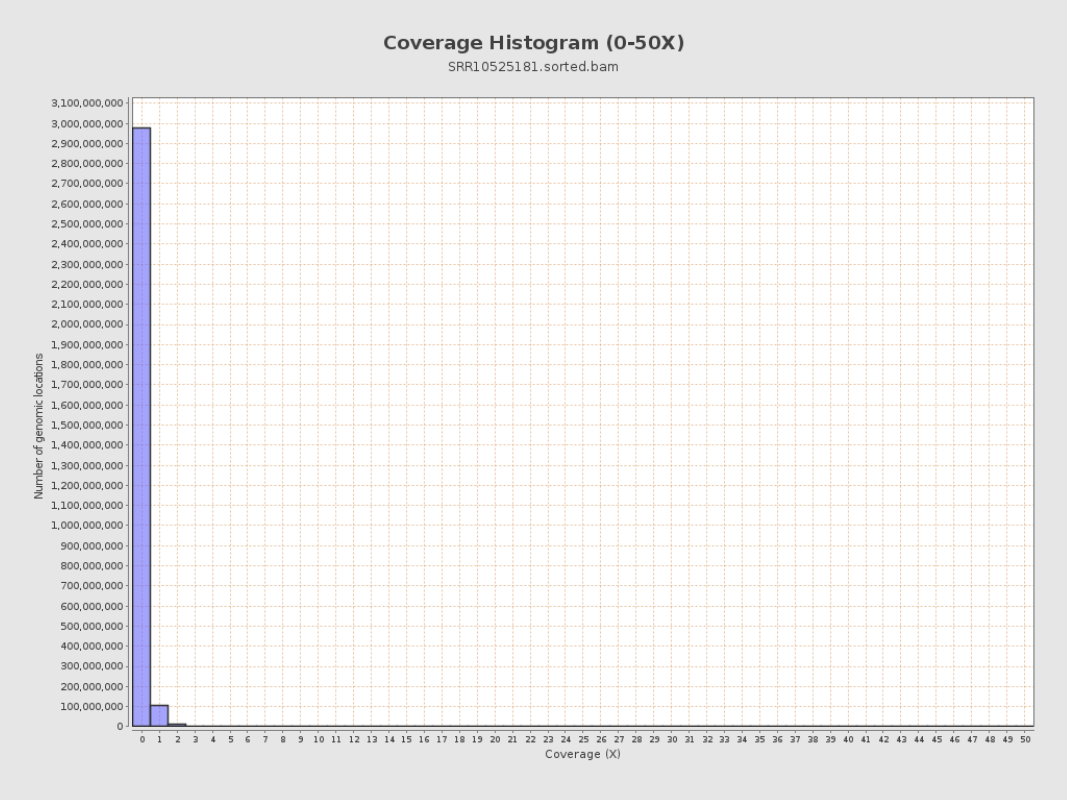
3. Results : Coverage across reference



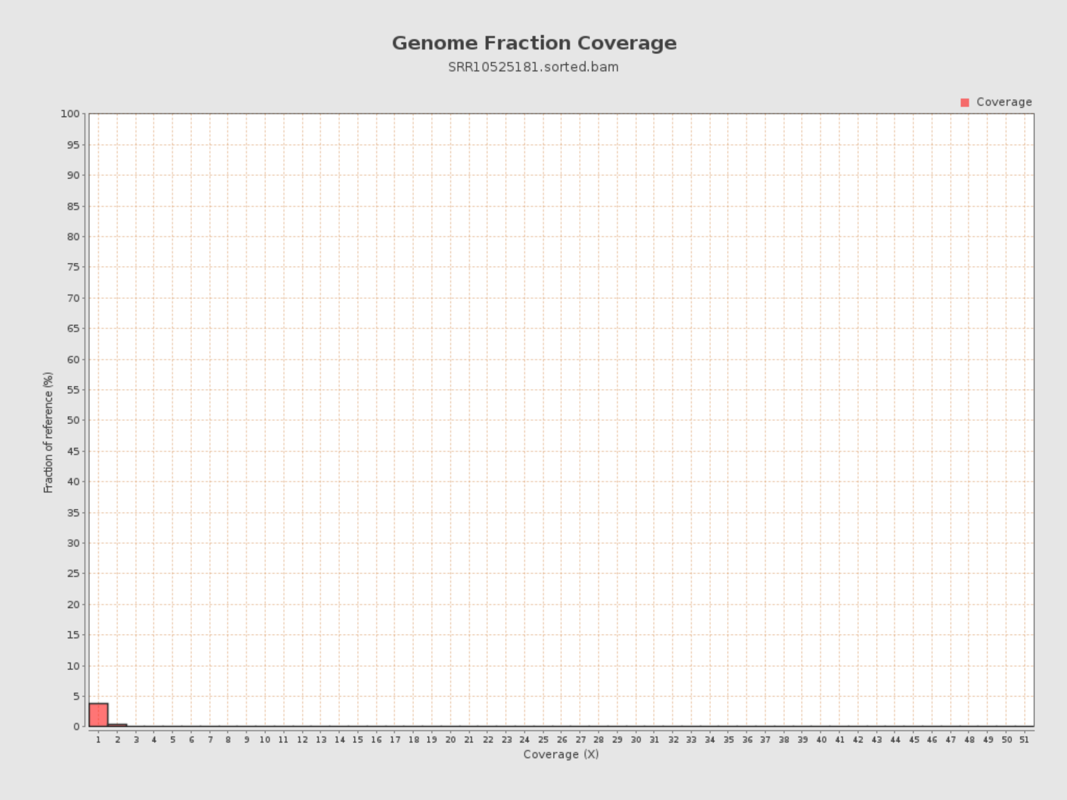
4. Results : Coverage Histogram



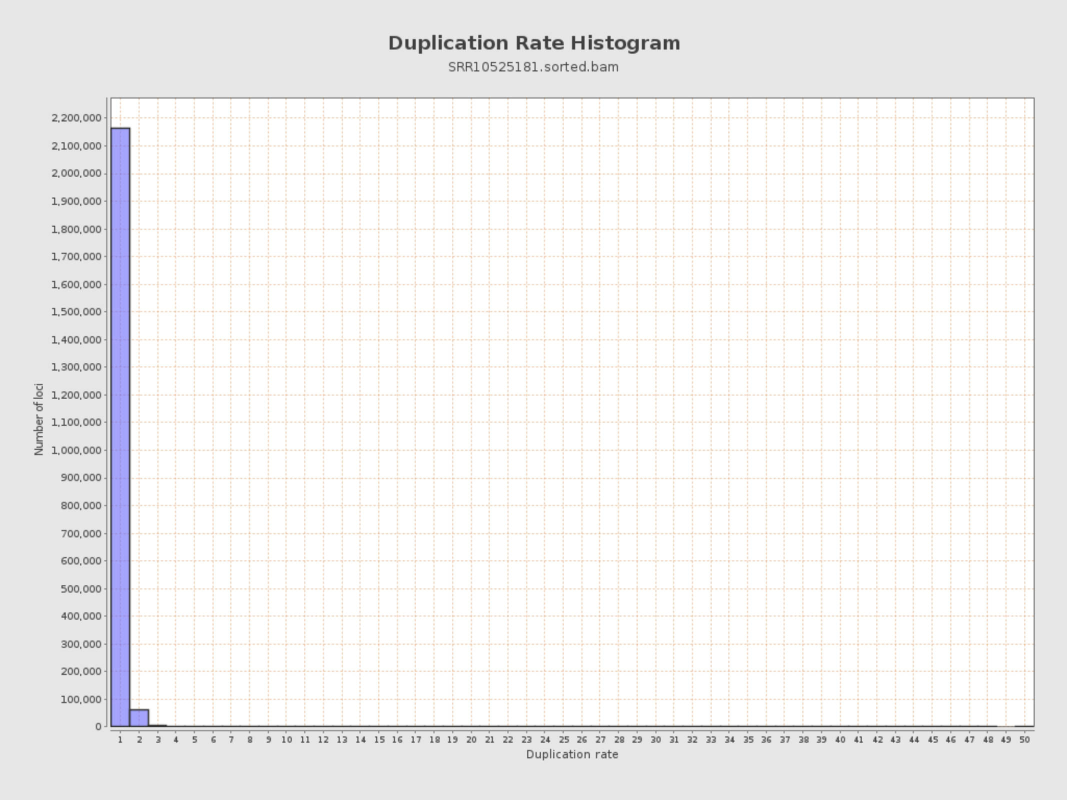
5. Results : Coverage Histogram (0-50X)



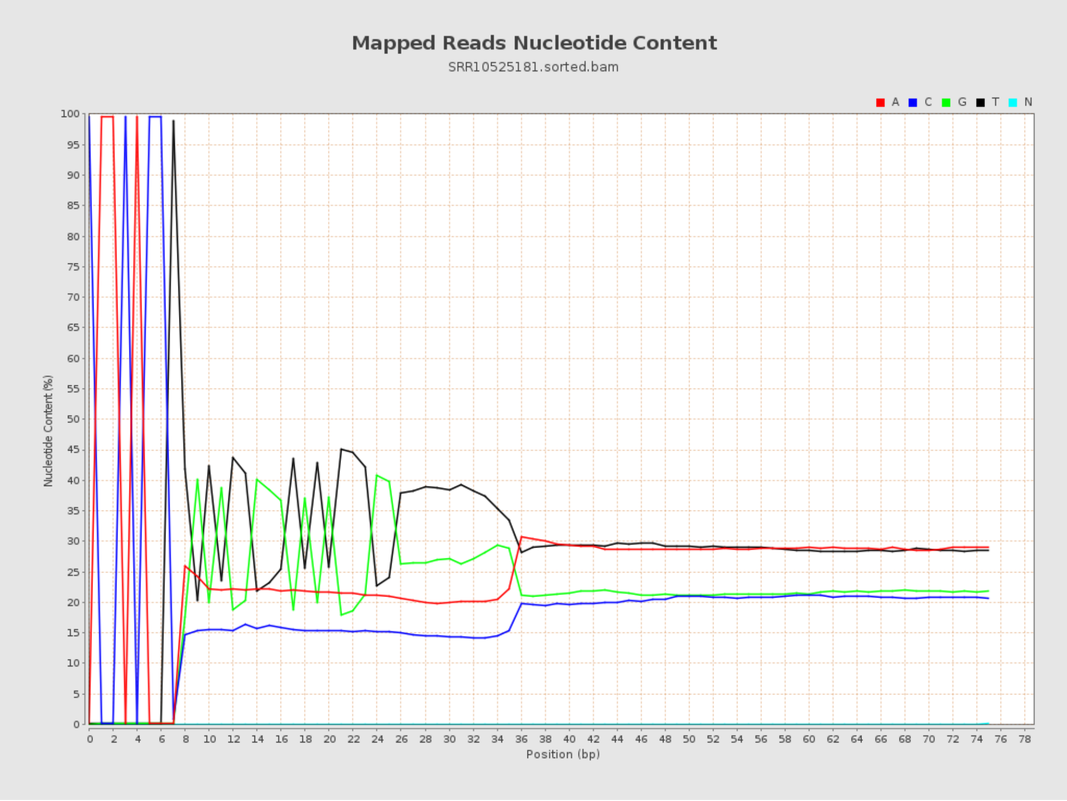
6. Results : Genome Fraction Coverage



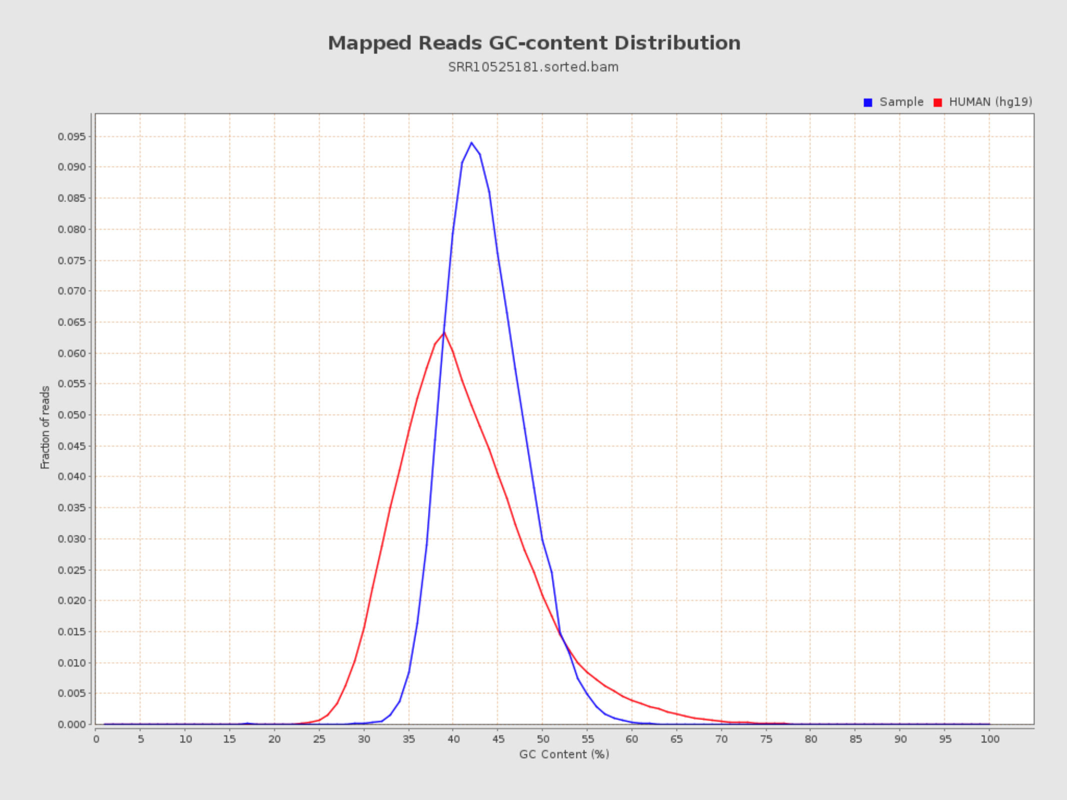
7. Results : Duplication Rate Histogram



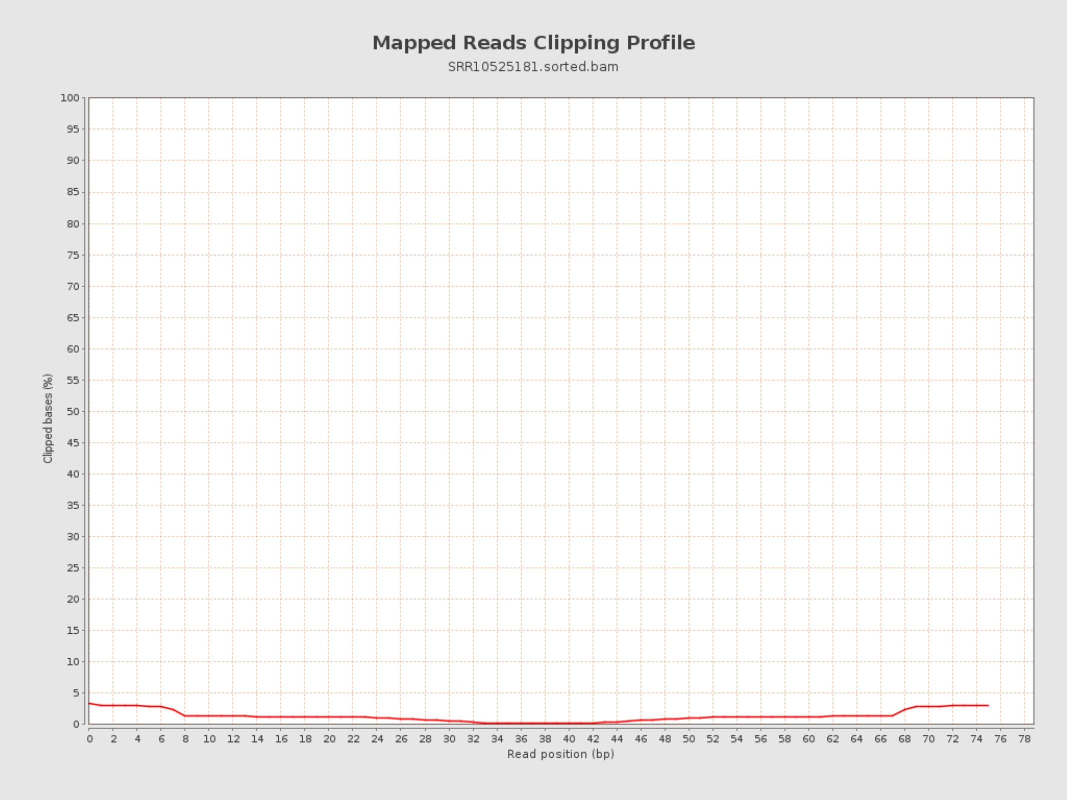
8. Results : Mapped Reads Nucleotide Content



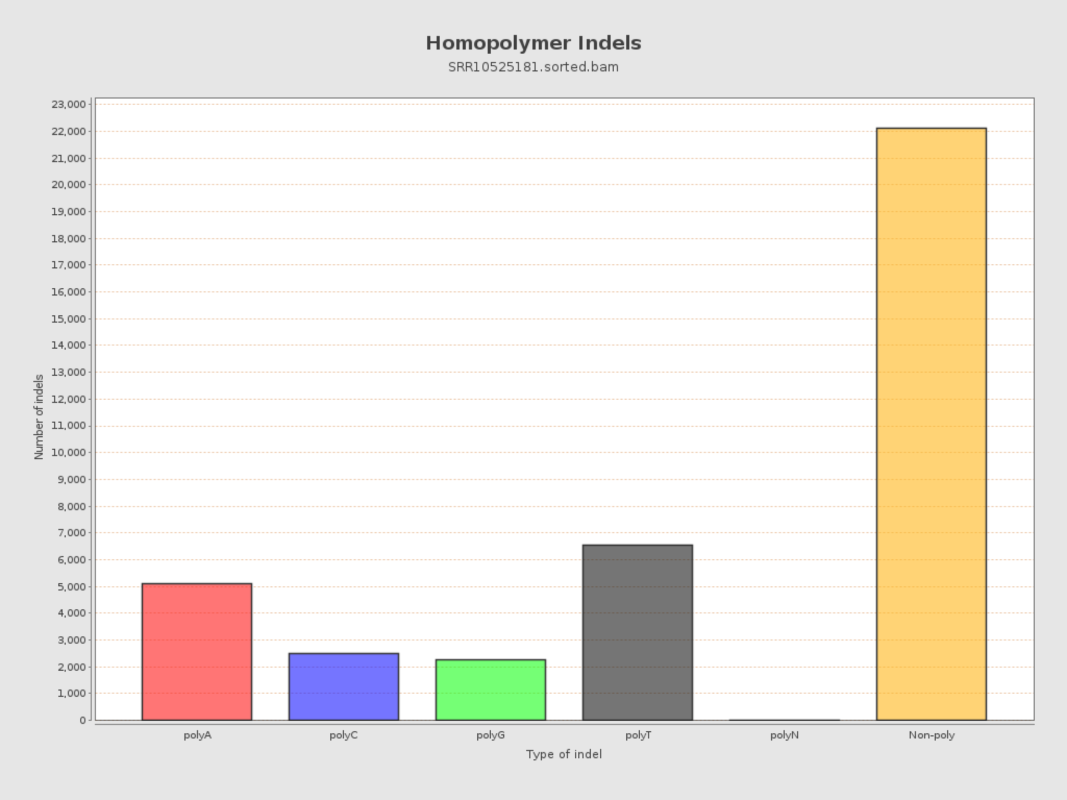
9. Results : Mapped Reads GC-content Distribution



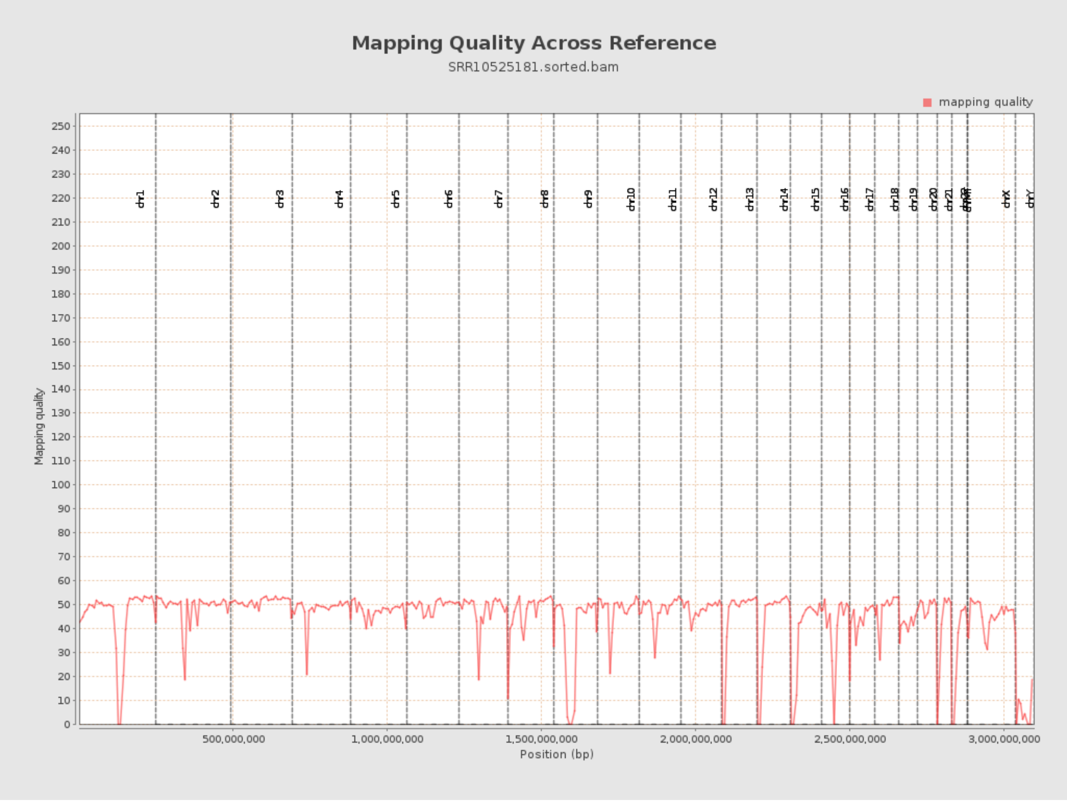
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram