Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:32:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525214.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_SRR10525214 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525214.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:32:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525214.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,130,335
Mapped reads	1,967,187 / 92.34%
Unmapped reads	163,148 / 7.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,998 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	78,762 / 3.7%
Duplication rate	2.87%
Clipped reads	1,970,939 / 92.52%

2.2. ACGT Content

Number/percentage of A's	27,474,255 / 24.01%
Number/percentage of C's	20,083,116 / 17.55%
Number/percentage of T's	37,980,368 / 33.19%
Number/percentage of G's	28,889,033 / 25.25%
Number/percentage of N's	2,674 / 0%
GC Percentage	42.8%

2.3. Coverage

Mean	0.037

Standard Deviation	0.3338

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

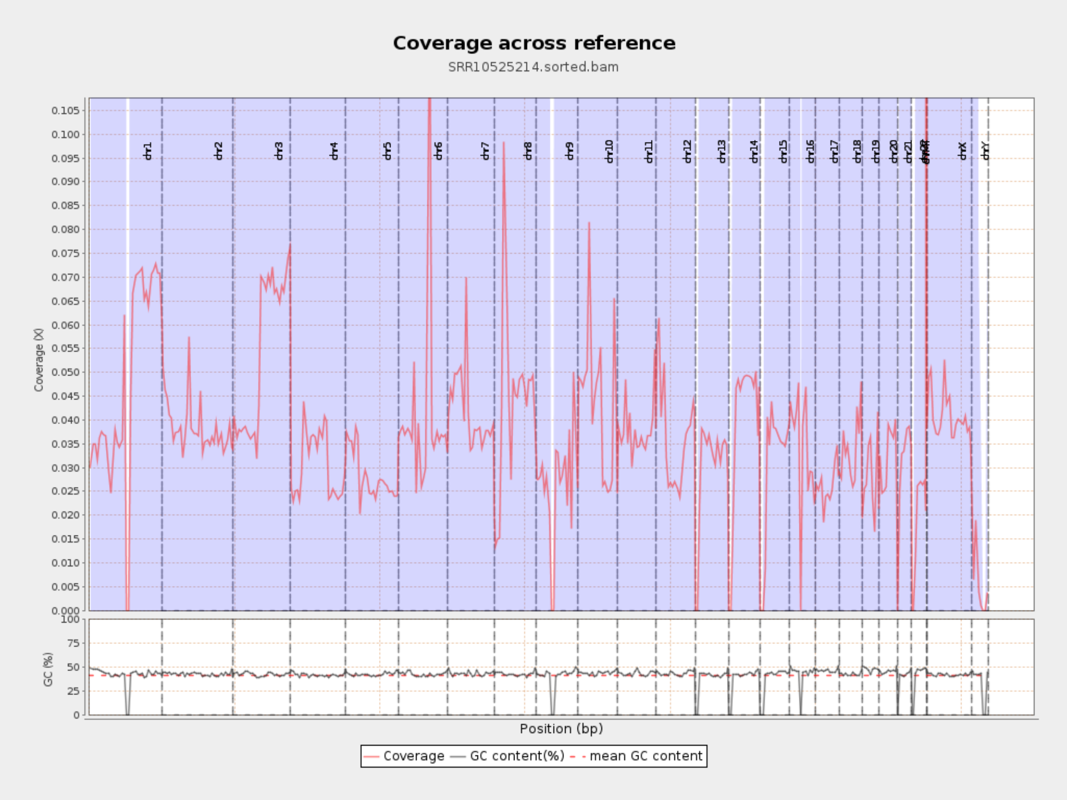
General error rate	0.52%
Mismatches	579,484
Insertions	6,738
Mapped reads with at least one insertion	0.34%
Deletions	22,736
Mapped reads with at least one deletion	1.15%
Homopolymer indels	45.46%

2.6. Chromosome stats

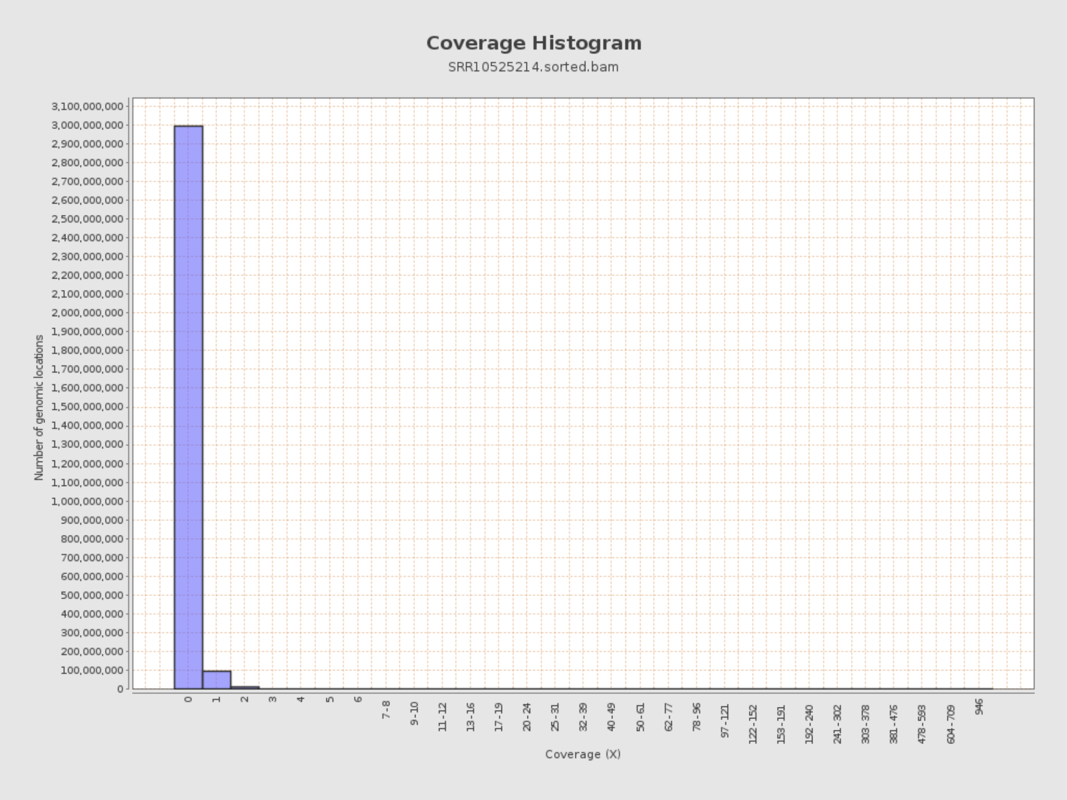
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11854304	0.0476	0.5785
chr2	243199373	9368712	0.0385	0.4542
chr3	198022430	10661356	0.0538	0.2611
chr4	191154276	5819779	0.0304	0.2098
chr5	180915260	5116949	0.0283	0.1869
chr6	171115067	7158565	0.0418	0.2632
chr7	159138663	6731424	0.0423	0.5267

chr8	146364022	6432170	0.0439	0.321
chr9	141213431	3768129	0.0267	0.2496
chr10	135534747	6028893	0.0445	0.381
chr11	135006516	5093936	0.0377	0.27
chr12	133851895	4872689	0.0364	0.2139
chr13	115169878	3460230	0.03	0.1938
chr14	107349540	4211026	0.0392	0.2242
chr15	102531392	3078451	0.03	0.1979
chr16	90354753	3021228	0.0334	0.2285
chr17	81195210	2135183	0.0263	0.1871
chr18	78077248	2620253	0.0336	0.4718
chr19	59128983	1686772	0.0285	0.3985
chr20	63025520	2036421	0.0323	0.2021
chr21	48129895	1475388	0.0307	0.2097
chr22	51304566	950128	0.0185	0.1505
chrMT	16571	167177	10.0885	5.9447
chrX	155270560	6366370	0.041	0.2474
chrY	59373566	350196	0.0059	0.1618

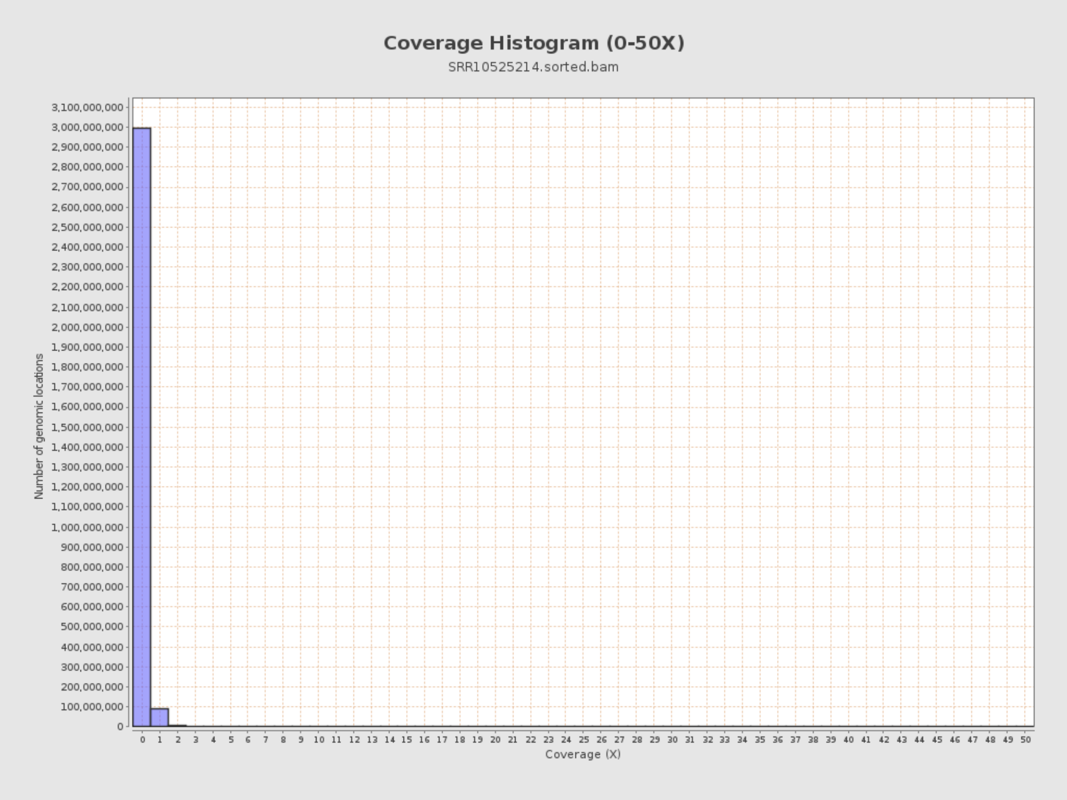
3. Results : Coverage across reference



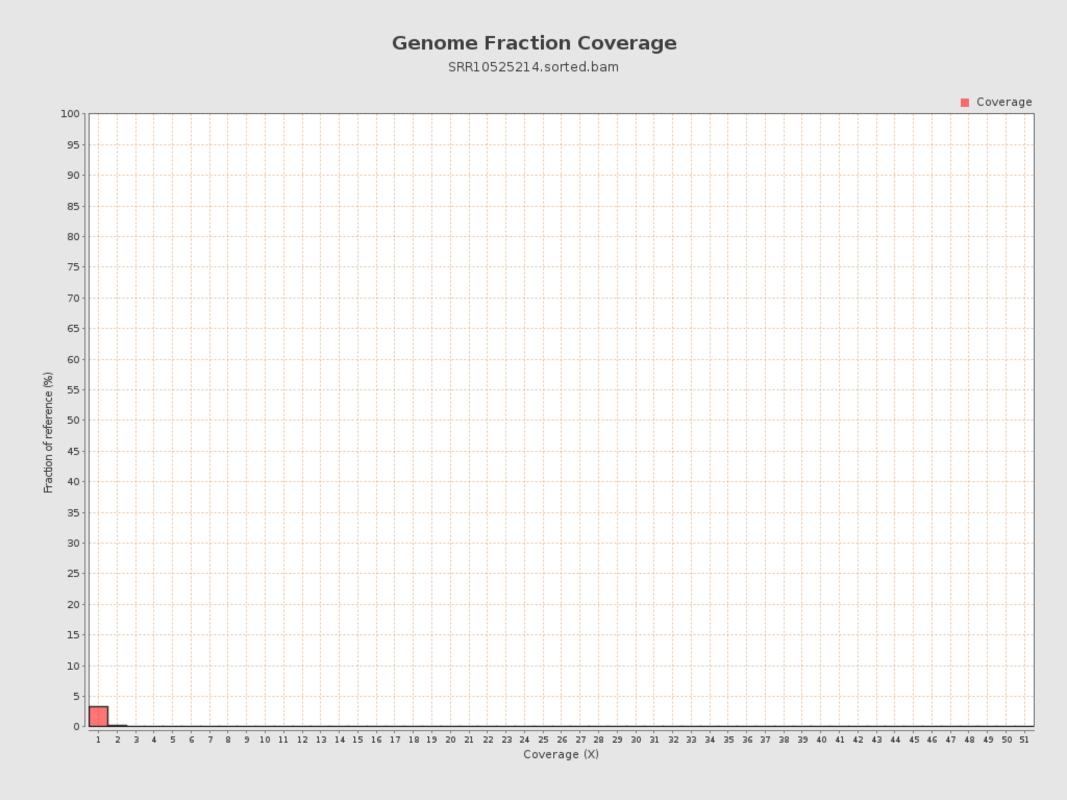
4. Results : Coverage Histogram



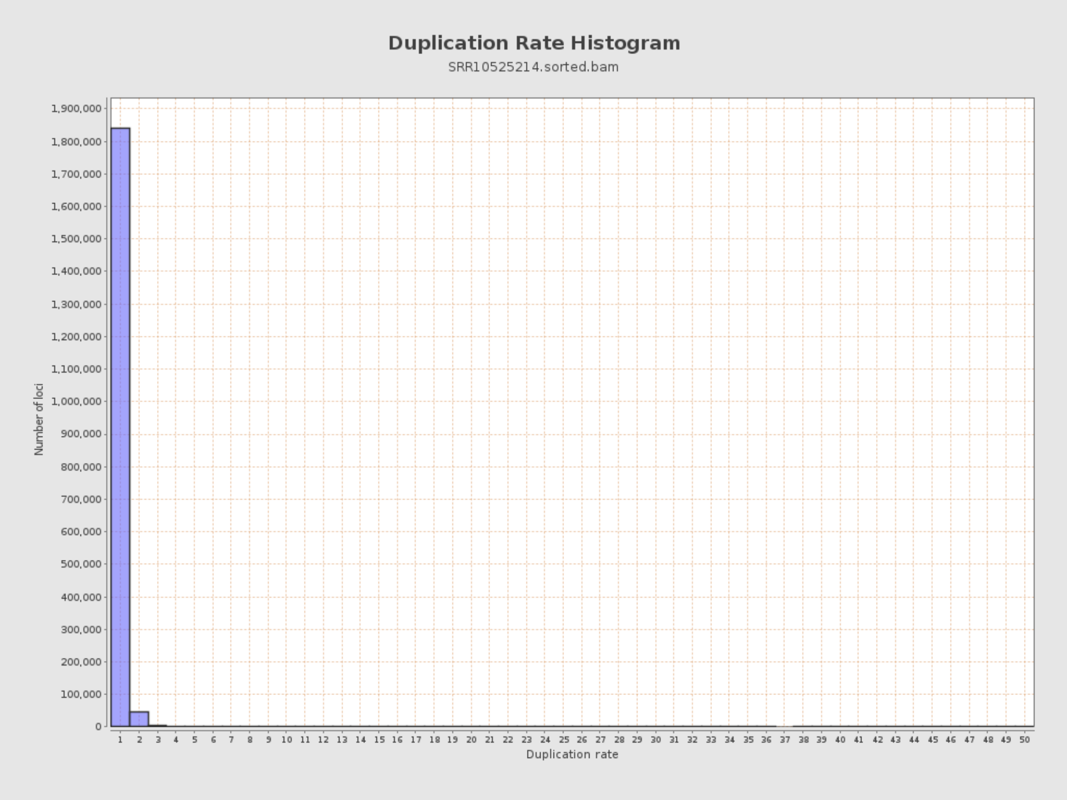
5. Results : Coverage Histogram (0-50X)



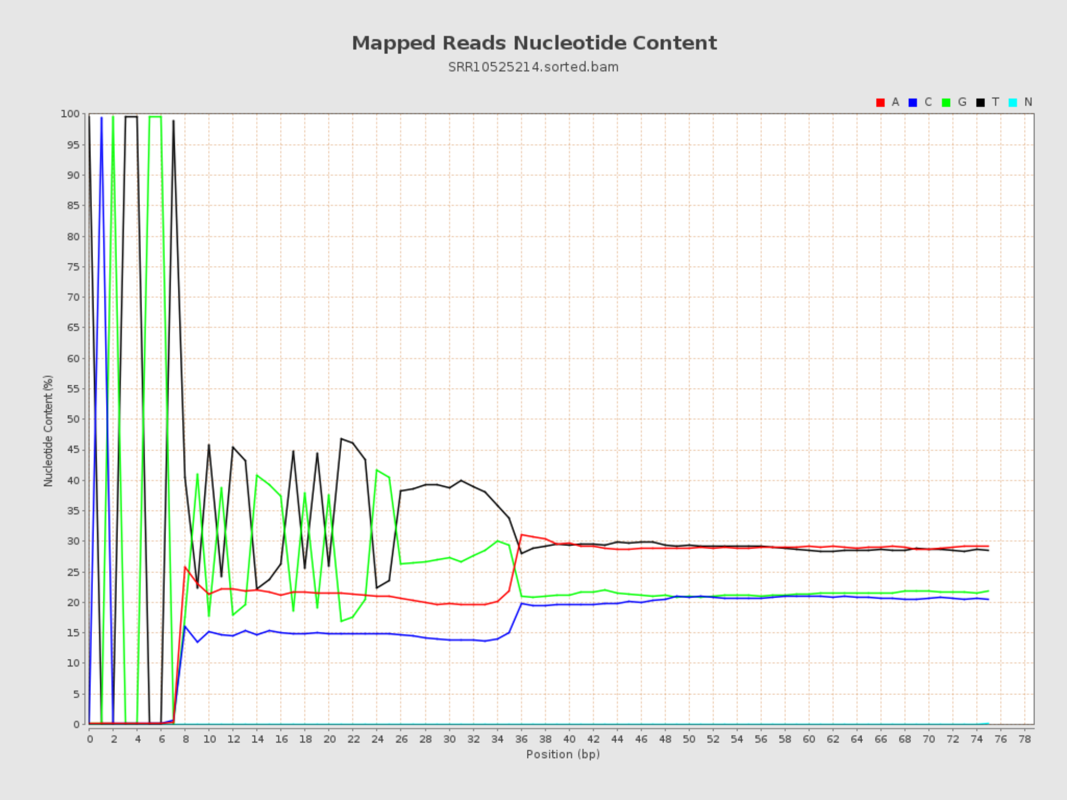
6. Results : Genome Fraction Coverage



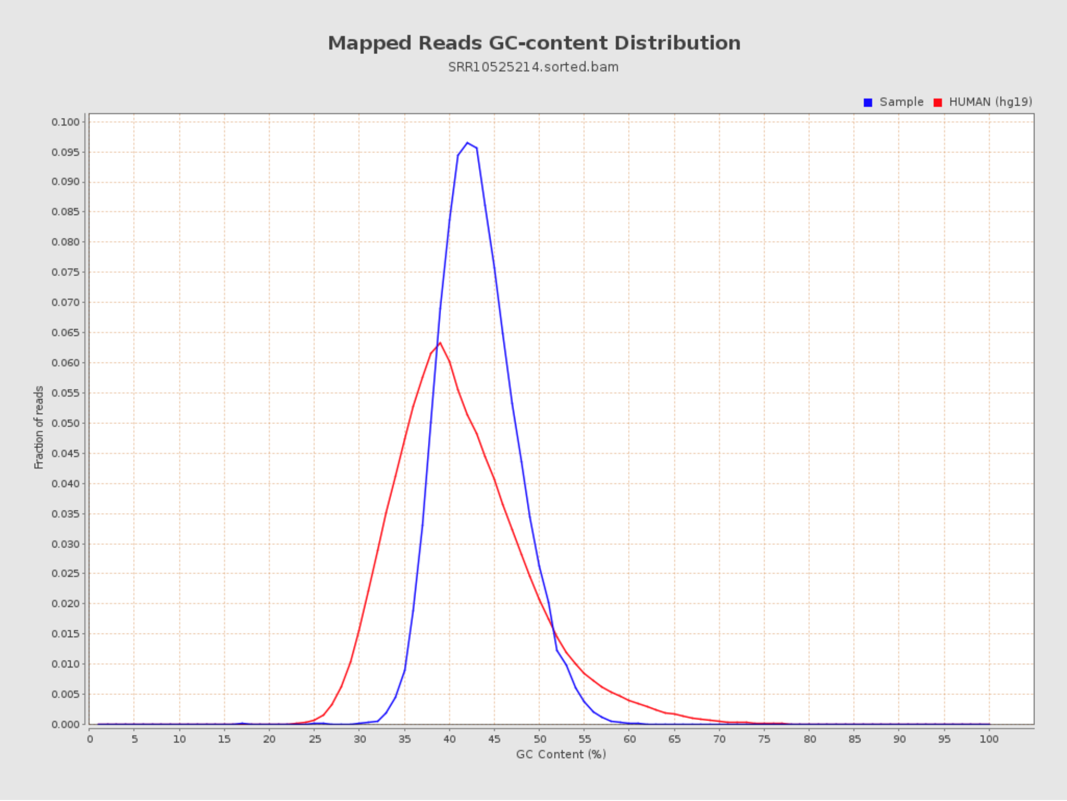
7. Results : Duplication Rate Histogram



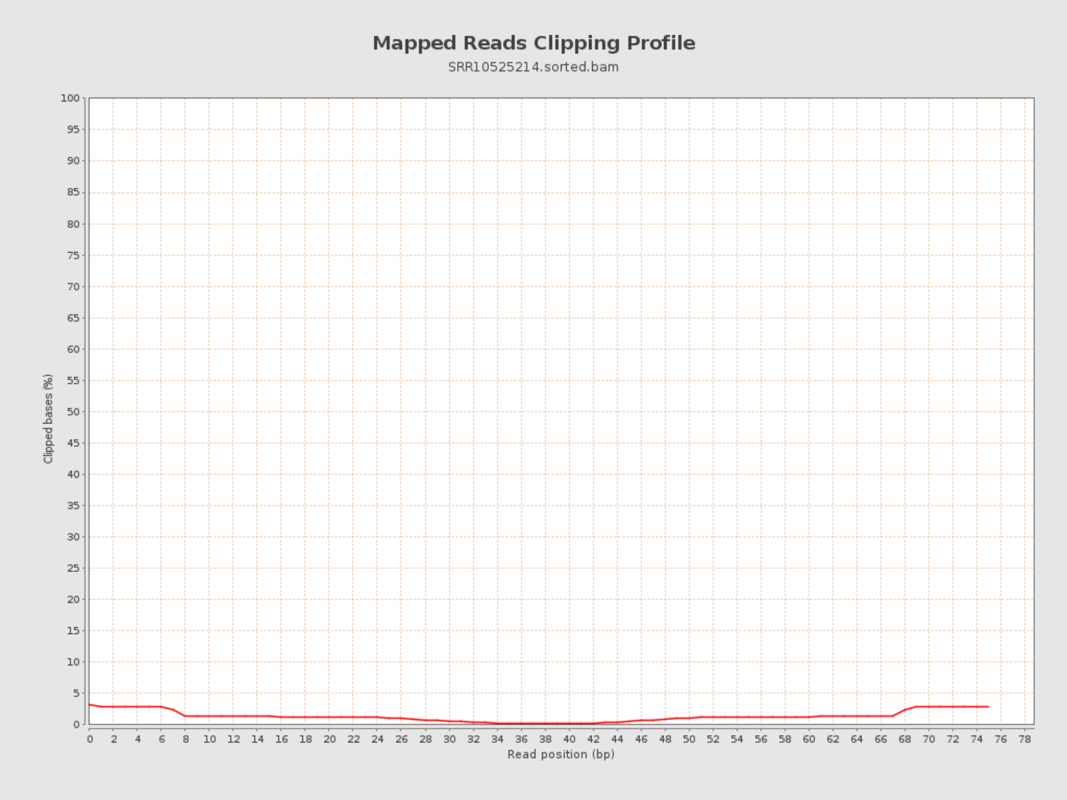
8. Results : Mapped Reads Nucleotide Content



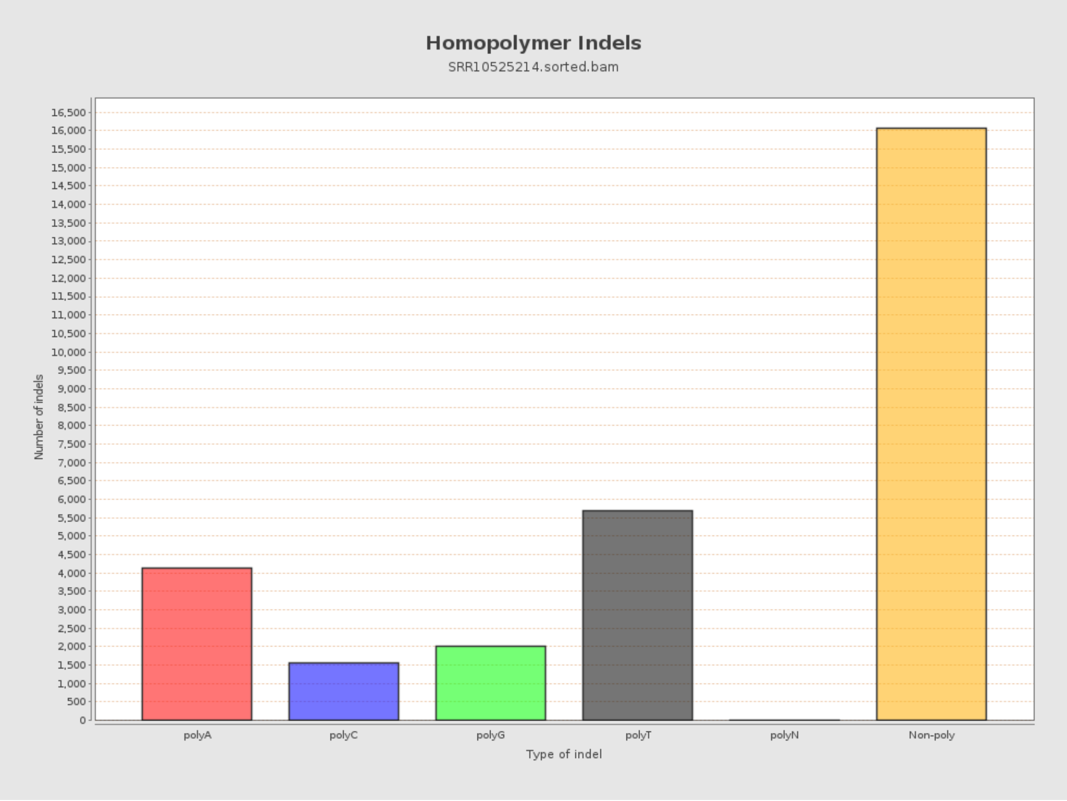
9. Results : Mapped Reads GC-content Distribution



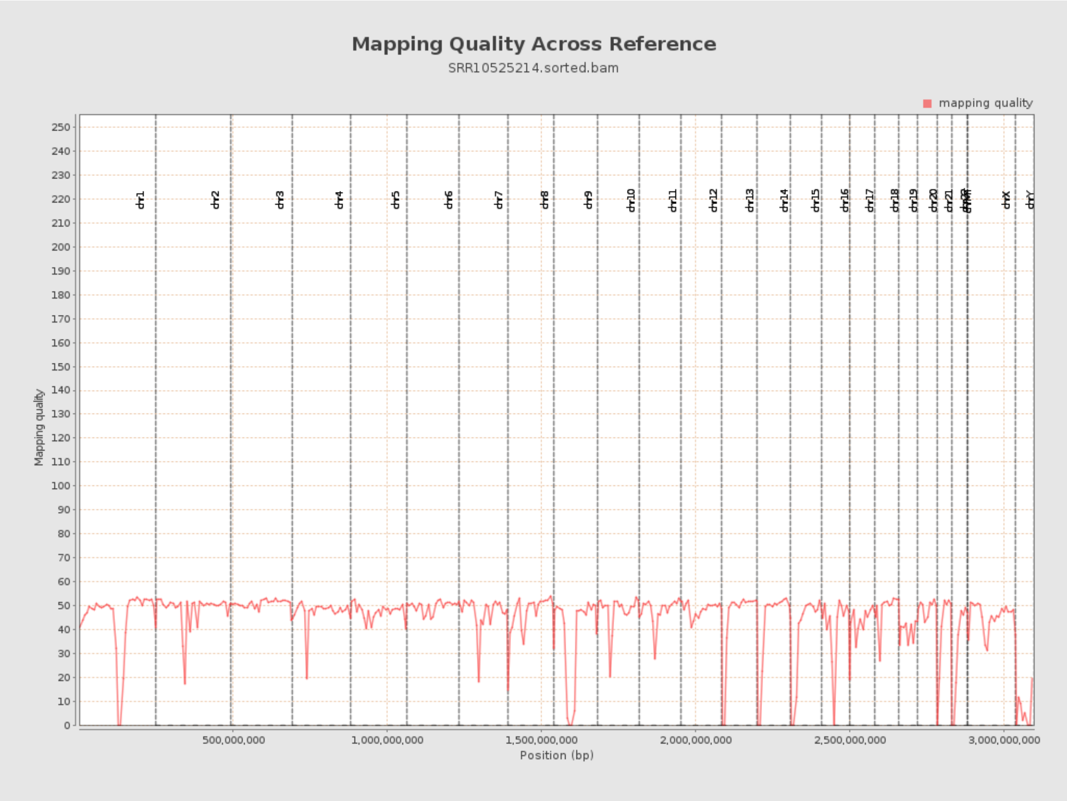
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram