Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:34:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525064.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_SRR10525064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:34:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	557,886
Mapped reads	485,435 / 87.01%
Unmapped reads	72,451 / 12.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,542 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	15,025 / 2.69%
Duplication rate	2.64%
Clipped reads	485,699 / 87.06%

2.2. ACGT Content

Number/percentage of A's	7,279,907 / 25.84%
Number/percentage of C's	5,370,763 / 19.06%
Number/percentage of T's	8,981,001 / 31.87%
Number/percentage of G's	6,541,811 / 23.22%
Number/percentage of N's	3,053 / 0.01%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0091

Standard Deviation	0.1169

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

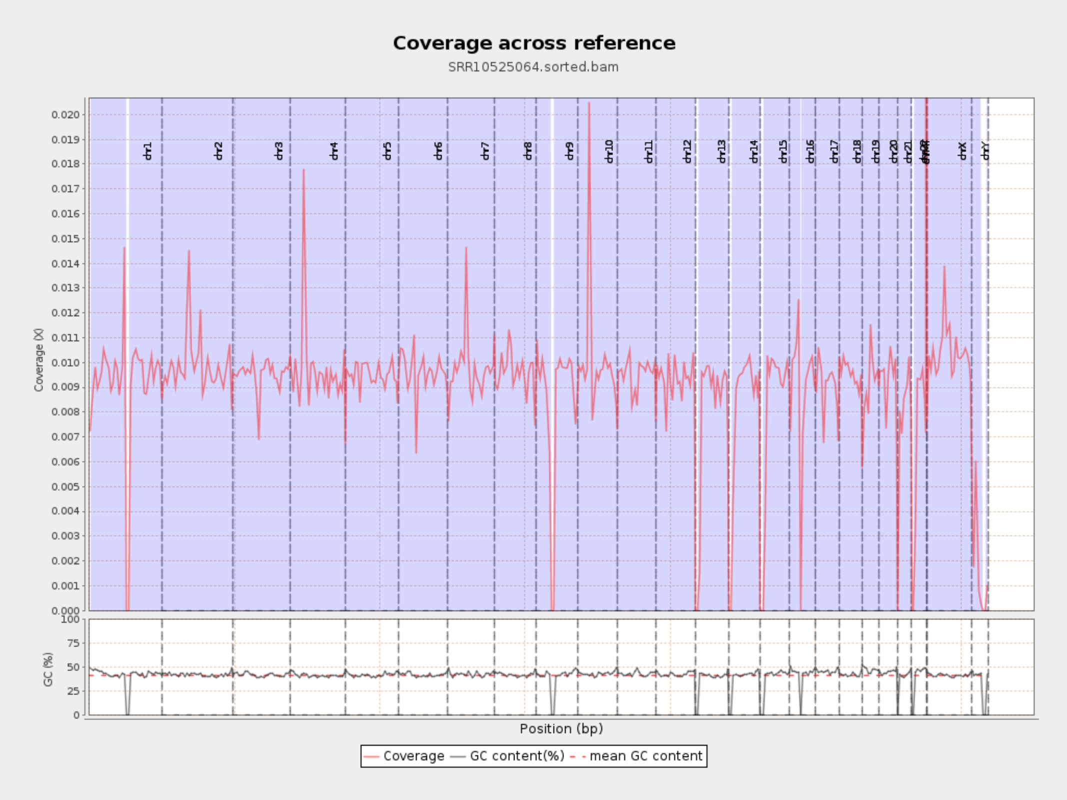
General error rate	0.5%
Mismatches	135,127
Insertions	2,159
Mapped reads with at least one insertion	0.44%
Deletions	5,624
Mapped reads with at least one deletion	1.15%
Homopolymer indels	44.66%

2.6. Chromosome stats

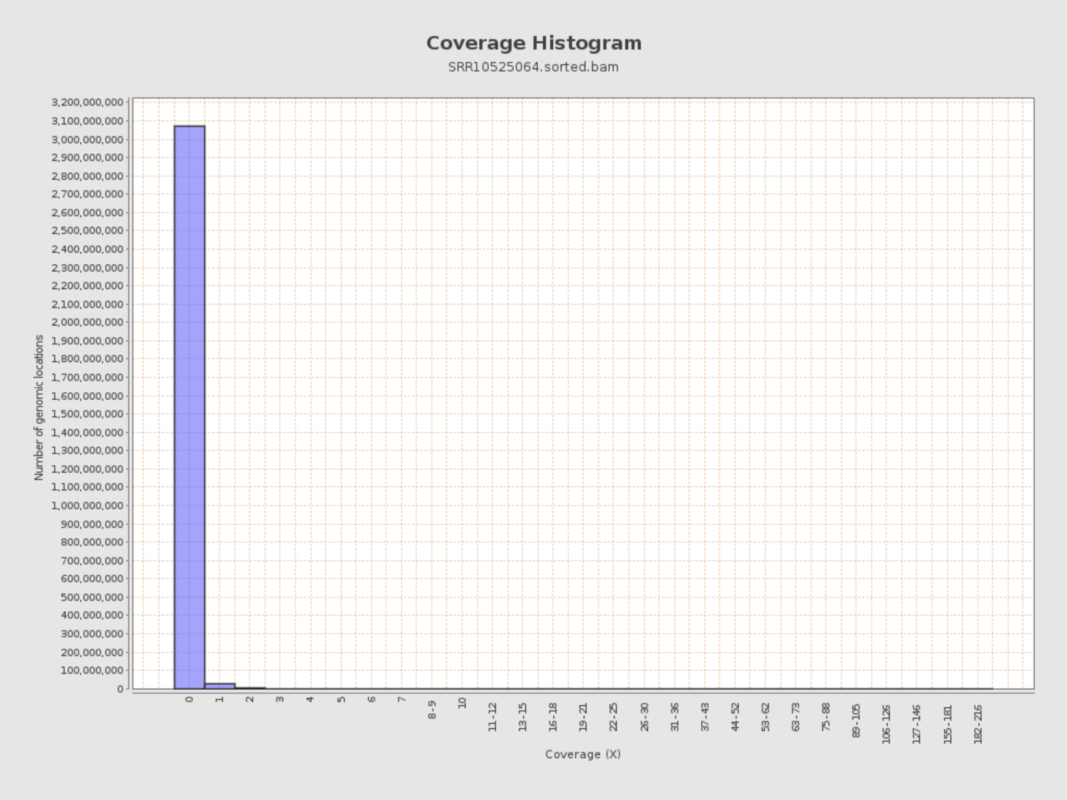
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2270411	0.0091	0.1717
chr2	243199373	2410852	0.0099	0.134
chr3	198022430	1885868	0.0095	0.1024
chr4	191154276	1854299	0.0097	0.1085
chr5	180915260	1717699	0.0095	0.1021
chr6	171115067	1647518	0.0096	0.1058
chr7	159138663	1552383	0.0098	0.1304

chr8	146364022	1404962	0.0096	0.1202
chr9	141213431	1176145	0.0083	0.1037
chr10	135534747	1364404	0.0101	0.1335
chr11	135006516	1285132	0.0095	0.1075
chr12	133851895	1248348	0.0093	0.1021
chr13	115169878	890699	0.0077	0.0919
chr14	107349540	844771	0.0079	0.0932
chr15	102531392	809544	0.0079	0.093
chr16	90354753	806921	0.0089	0.1022
chr17	81195210	727927	0.009	0.1005
chr18	78077248	748021	0.0096	0.1415
chr19	59128983	541764	0.0092	0.1335
chr20	63025520	590454	0.0094	0.1024
chr21	48129895	372592	0.0077	0.0955
chr22	51304566	324942	0.0063	0.0832
chrMT	16571	5655	0.3413	0.6322
chrX	155270560	1611092	0.0104	0.1106
chrY	59373566	93148	0.0016	0.0627

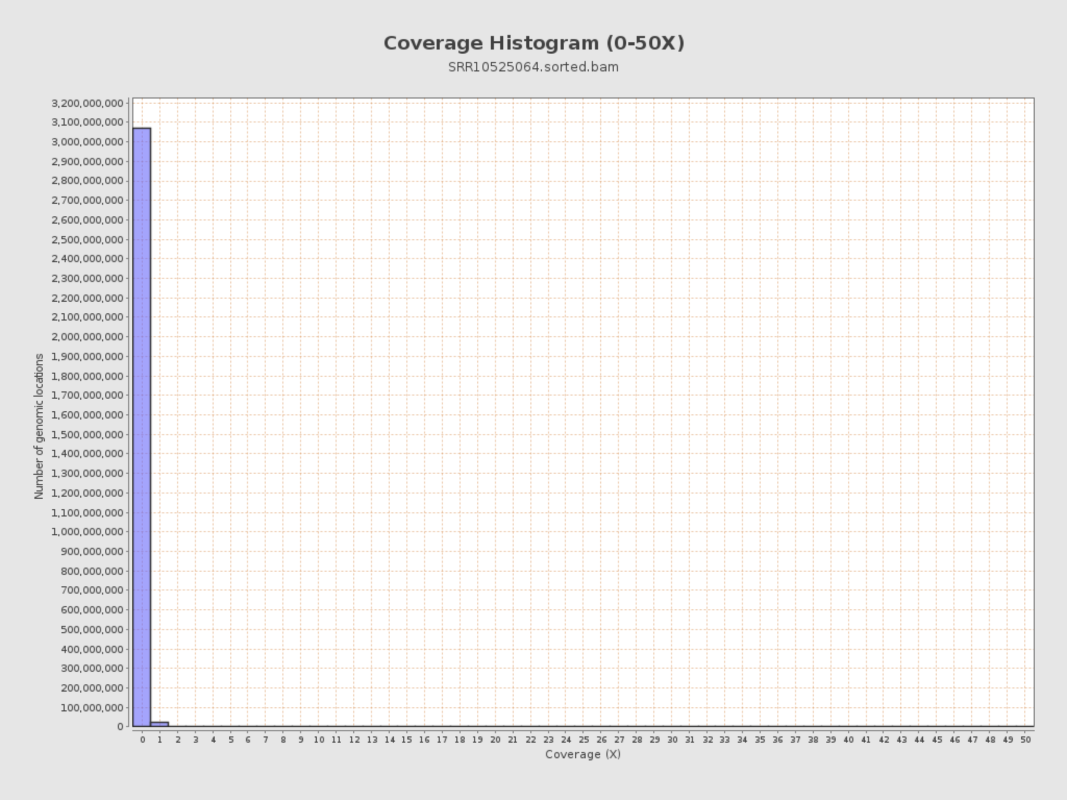
3. Results : Coverage across reference



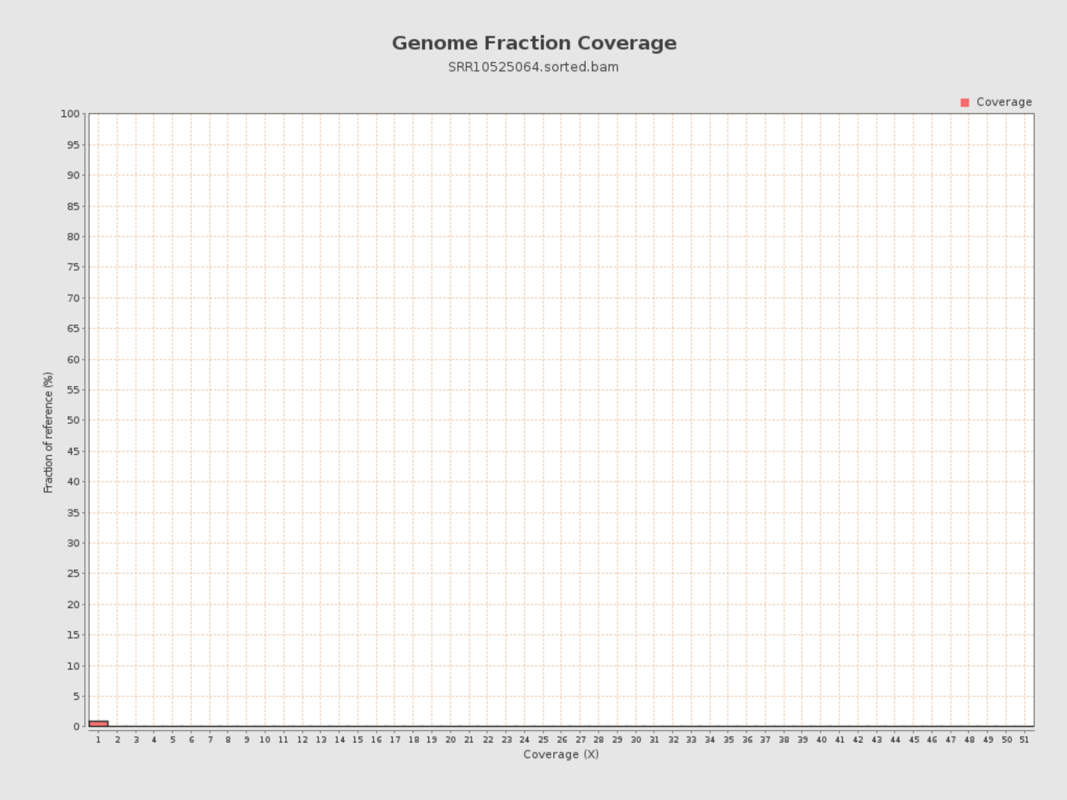
4. Results : Coverage Histogram



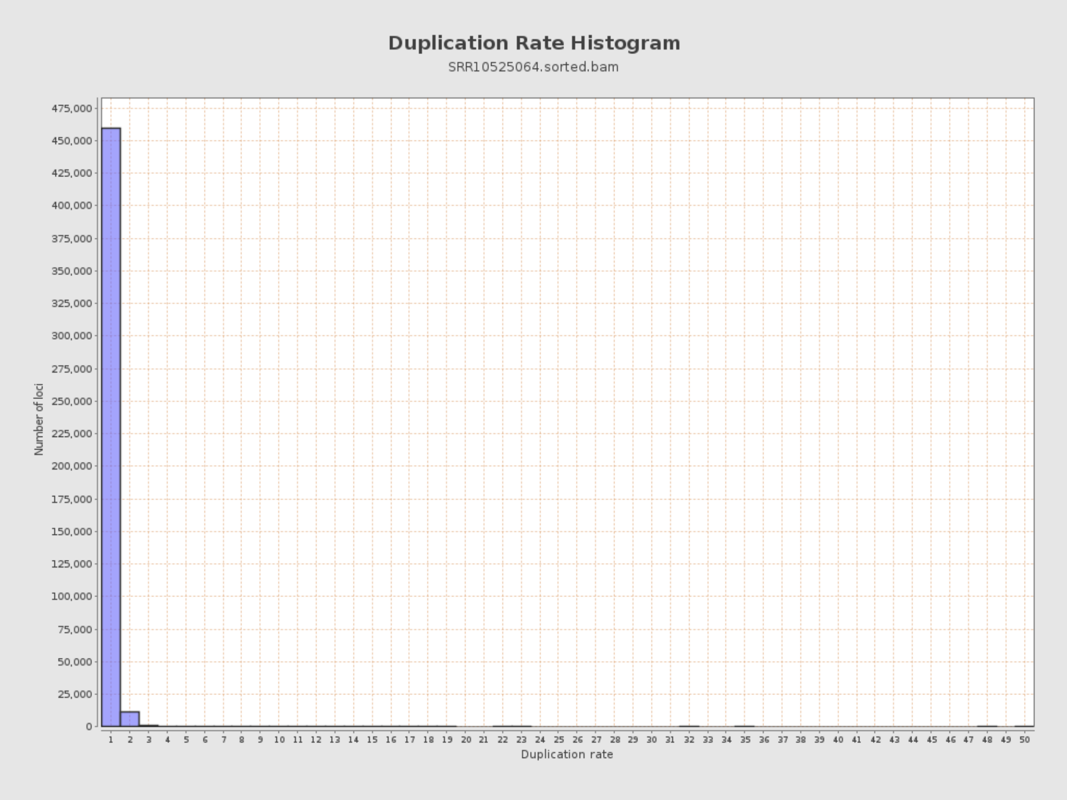
5. Results : Coverage Histogram (0-50X)



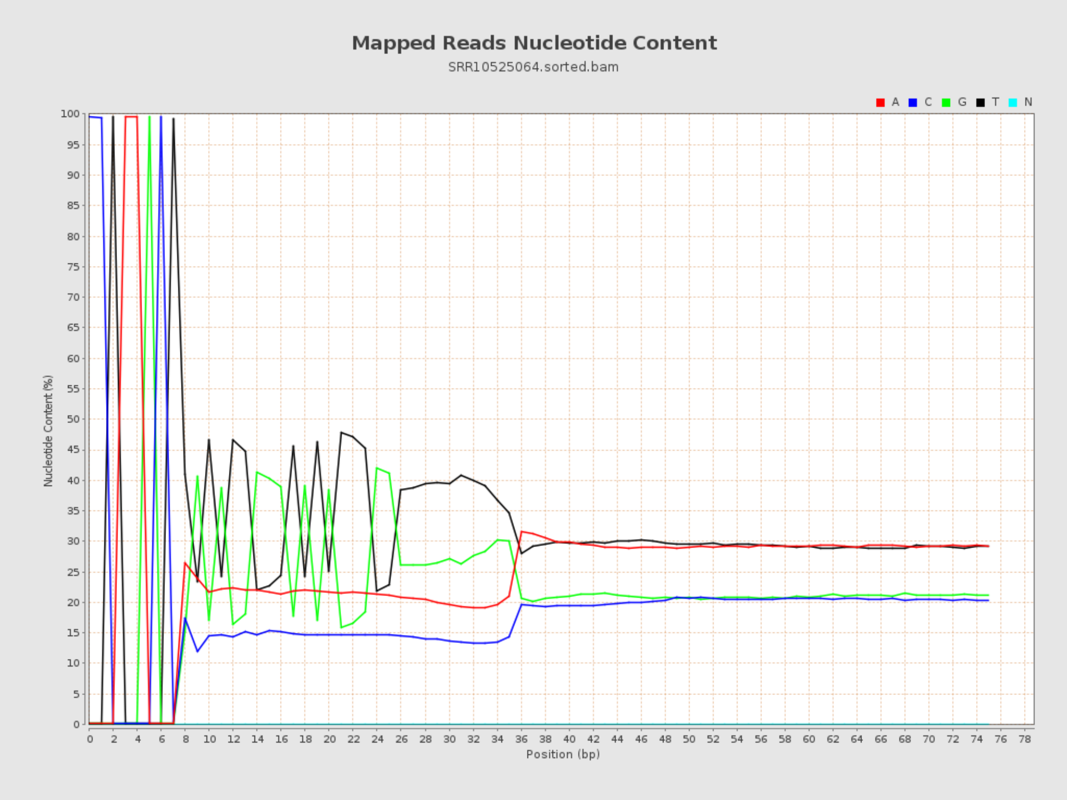
6. Results : Genome Fraction Coverage



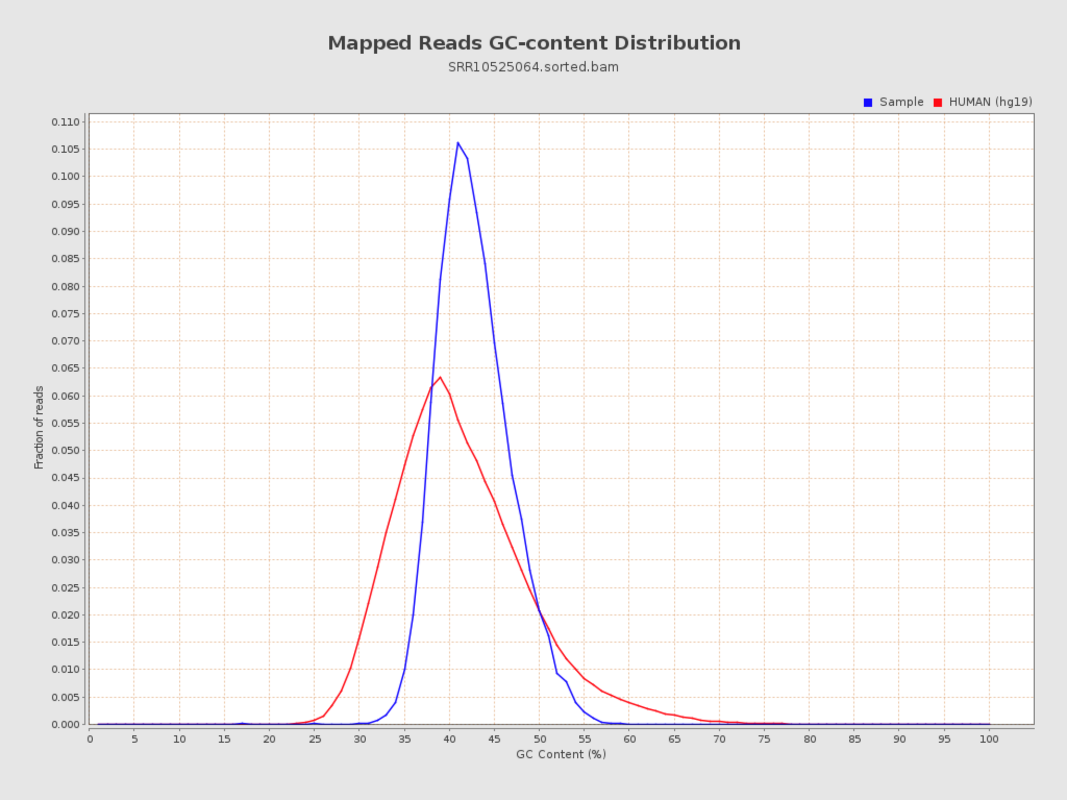
7. Results : Duplication Rate Histogram



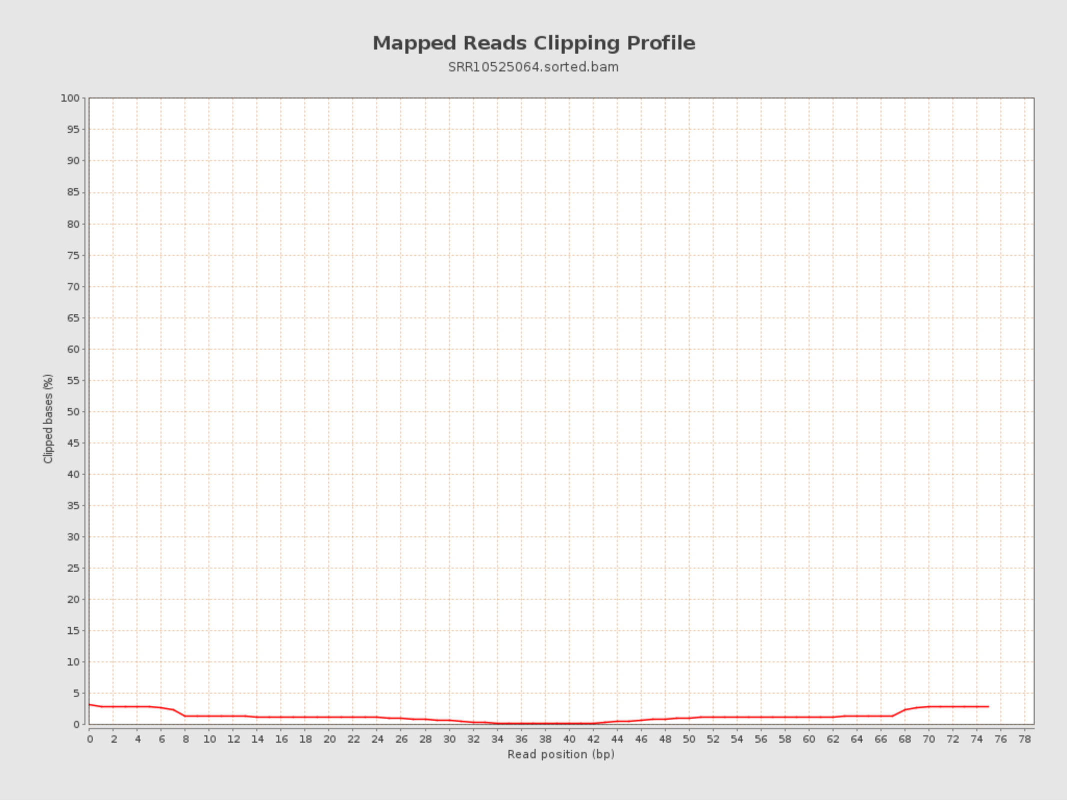
8. Results : Mapped Reads Nucleotide Content



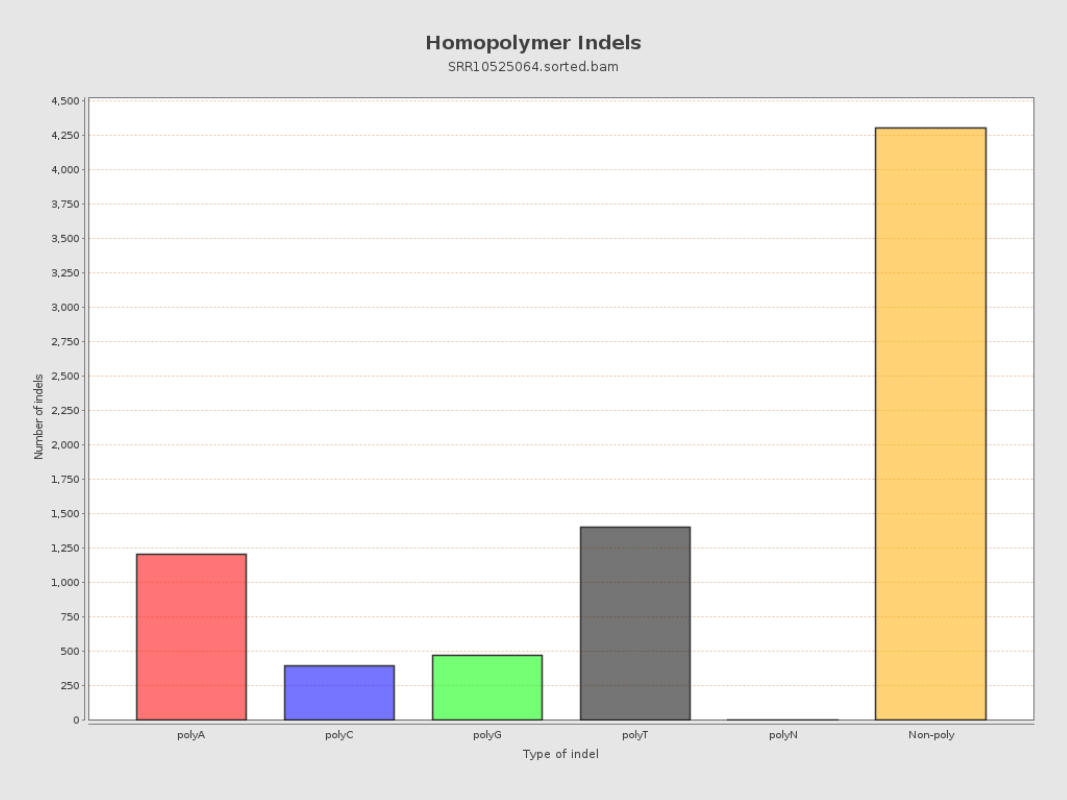
9. Results : Mapped Reads GC-content Distribution



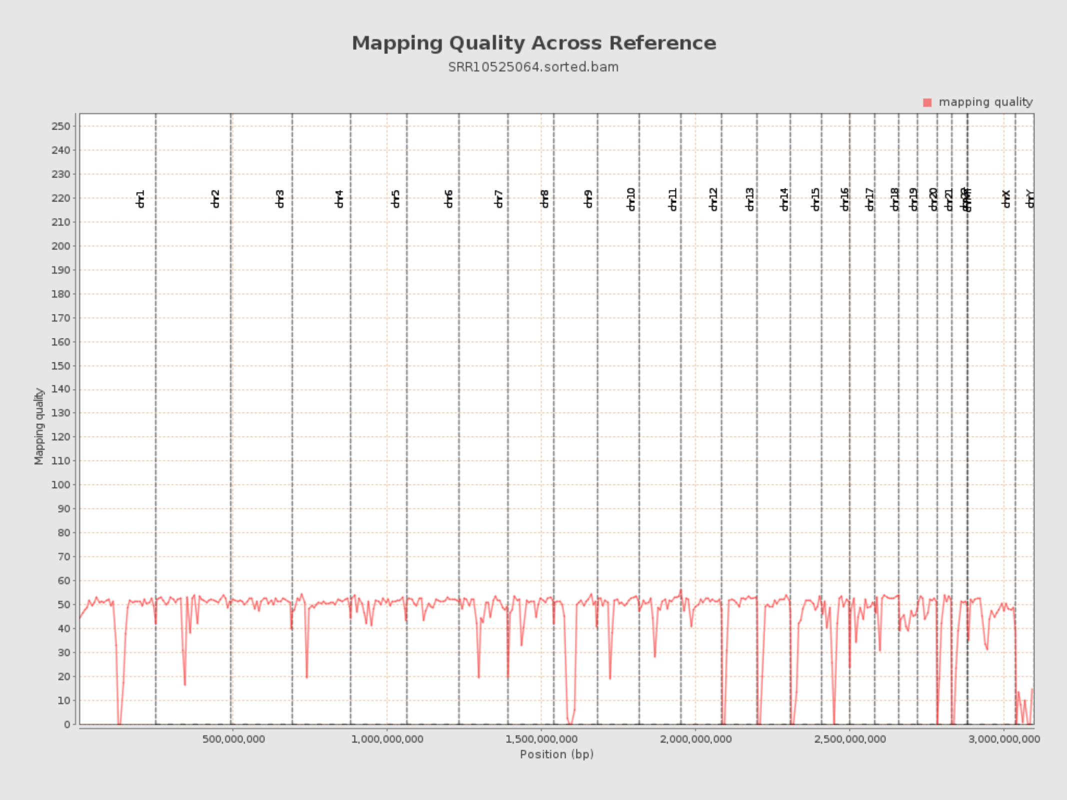
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram