Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:19:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525209.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_SRR10525209 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525209.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:19:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525209.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	371,447
Mapped reads	346,879 / 93.39%
Unmapped reads	24,568 / 6.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,053 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	4,530 / 1.22%
Duplication rate	0.94%
Clipped reads	347,354 / 93.51%

2.2. ACGT Content

Number/percentage of A's	5,604,676 / 26.37%
Number/percentage of C's	4,152,353 / 19.54%
Number/percentage of T's	6,235,653 / 29.34%
Number/percentage of G's	5,261,901 / 24.76%
Number/percentage of N's	518 / 0%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0069

Standard Deviation	0.1003

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

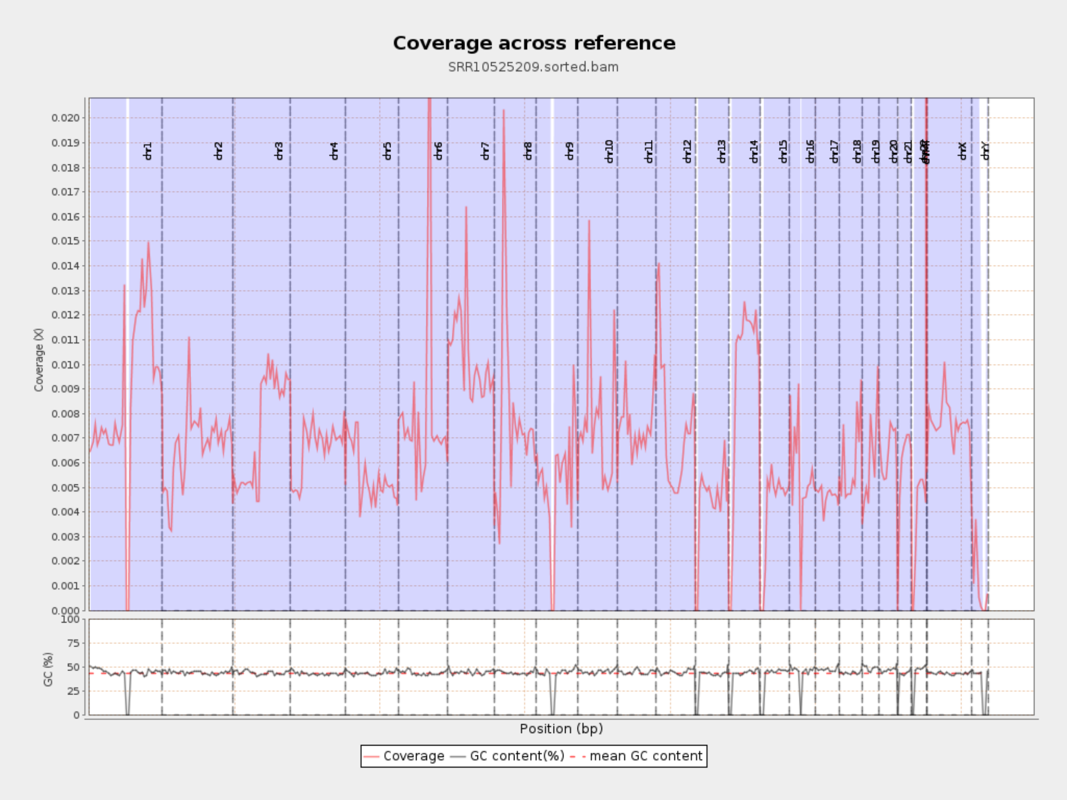
General error rate	0.55%
Mismatches	113,893
Insertions	1,255
Mapped reads with at least one insertion	0.36%
Deletions	4,408
Mapped reads with at least one deletion	1.26%
Homopolymer indels	46.07%

2.6. Chromosome stats

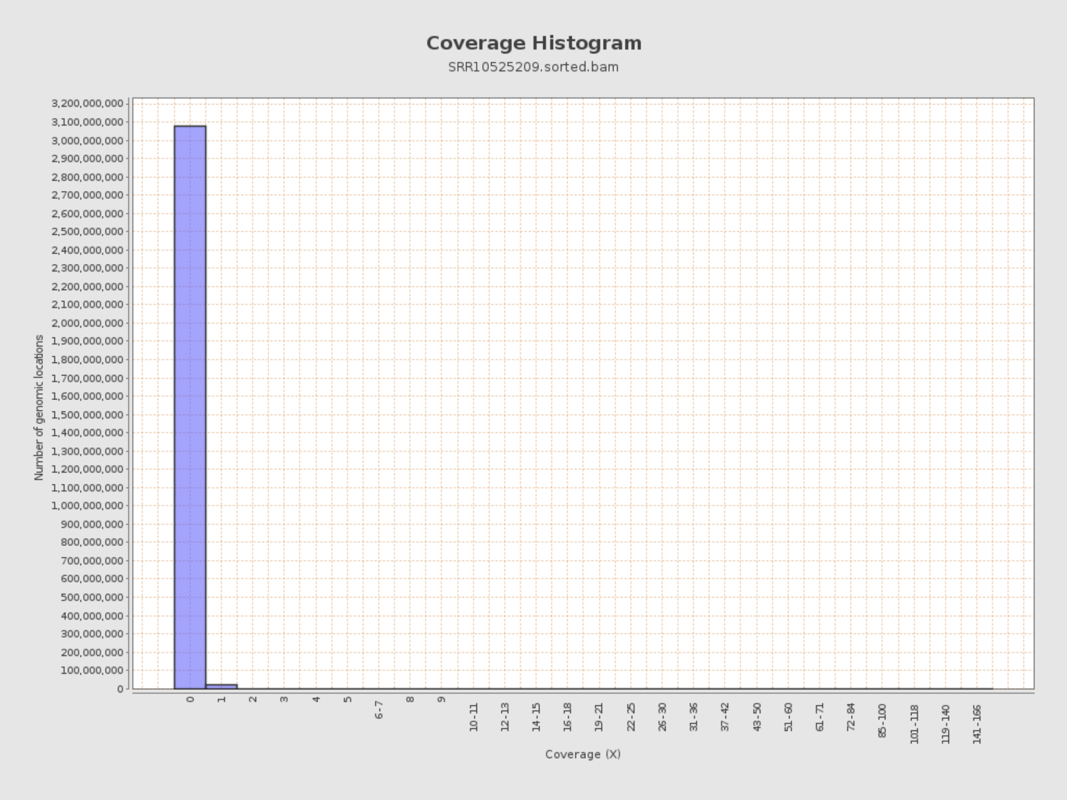
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2189907	0.0088	0.153
chr2	243199373	1626452	0.0067	0.1055
chr3	198022430	1449430	0.0073	0.0881
chr4	191154276	1258010	0.0066	0.084
chr5	180915260	992699	0.0055	0.0756
chr6	171115067	1401034	0.0082	0.0956
chr7	159138663	1658190	0.0104	0.1498

chr8	146364022	1125843	0.0077	0.0992
chr9	141213431	731126	0.0052	0.0789
chr10	135534747	1037323	0.0077	0.1118
chr11	135006516	1017533	0.0075	0.0931
chr12	133851895	997480	0.0075	0.0884
chr13	115169878	508708	0.0044	0.0678
chr14	107349540	1012116	0.0094	0.0999
chr15	102531392	420439	0.0041	0.0651
chr16	90354753	489166	0.0054	0.0784
chr17	81195210	377363	0.0046	0.0705
chr18	78077248	467948	0.006	0.1183
chr19	59128983	365062	0.0062	0.1207
chr20	63025520	405757	0.0064	0.0824
chr21	48129895	278063	0.0058	0.0785
chr22	51304566	183504	0.0036	0.0609
chrMT	16571	19844	1.1975	1.2795
chrX	155270560	1187272	0.0076	0.0913
chrY	59373566	62019	0.001	0.0421

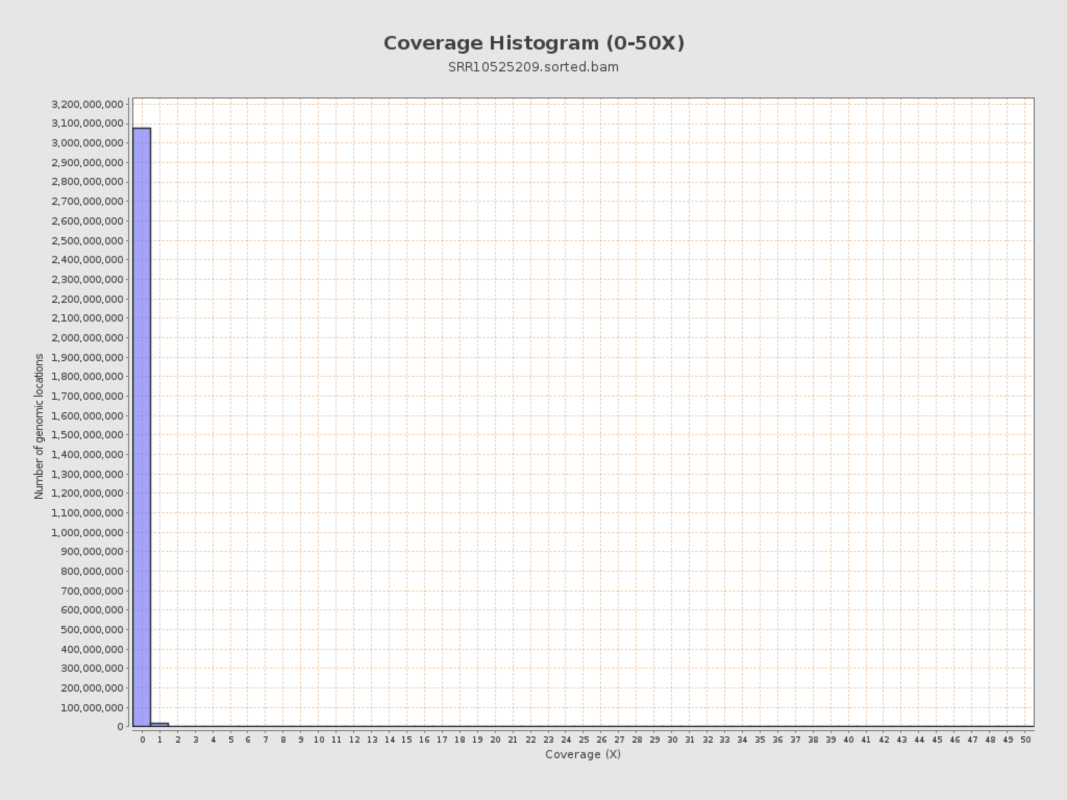
3. Results : Coverage across reference



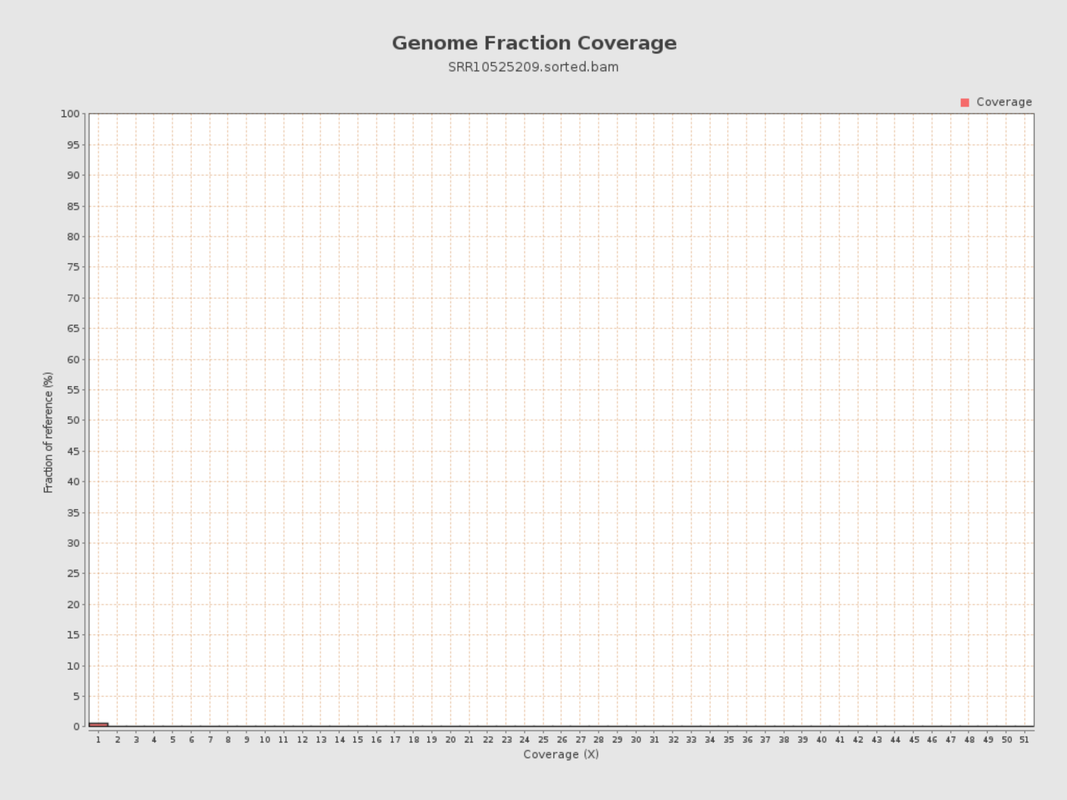
4. Results : Coverage Histogram



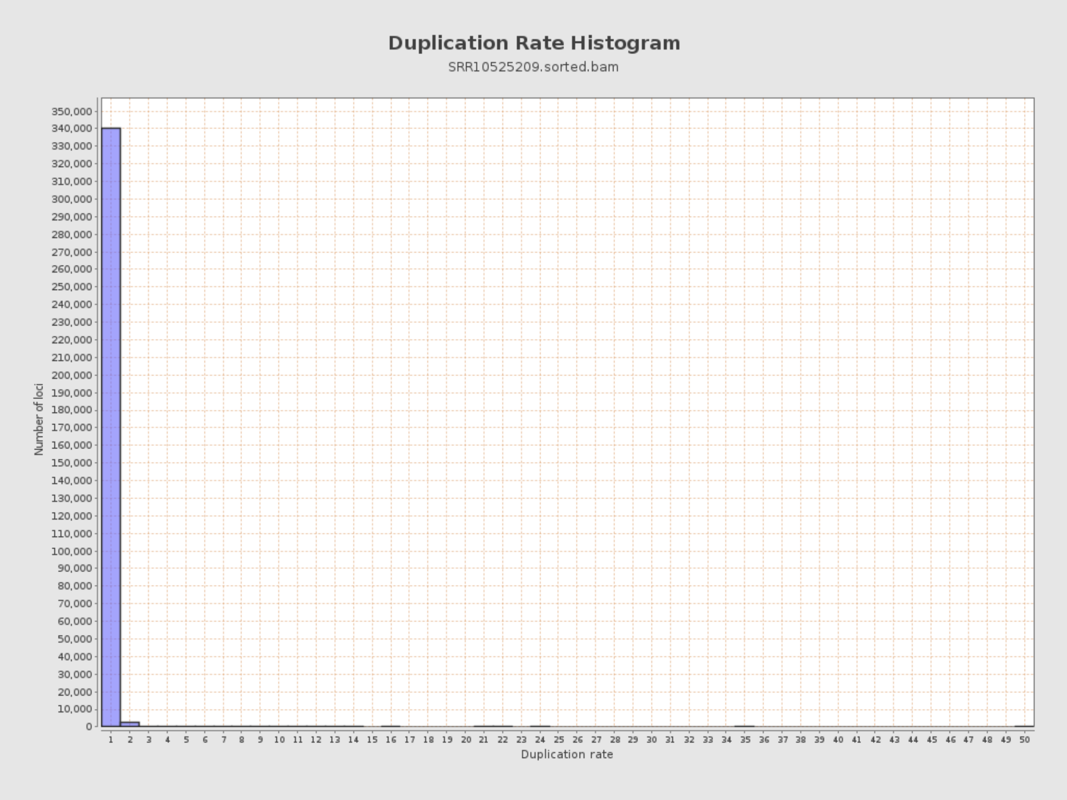
5. Results : Coverage Histogram (0-50X)



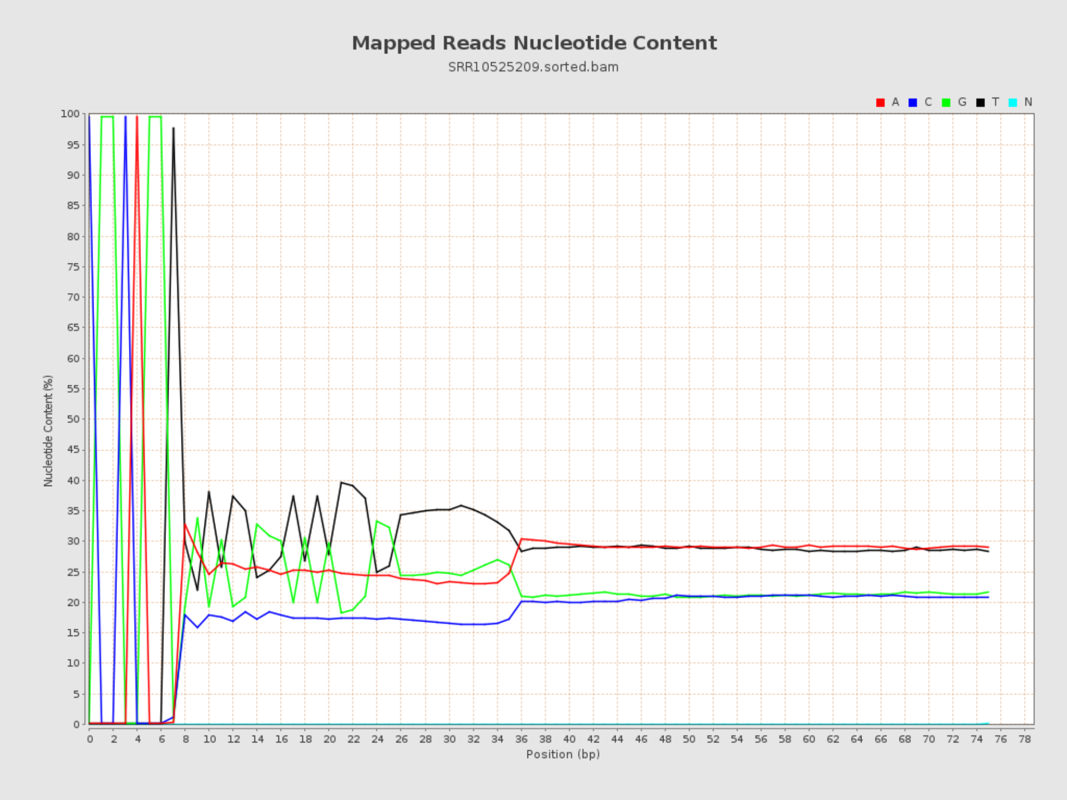
6. Results : Genome Fraction Coverage



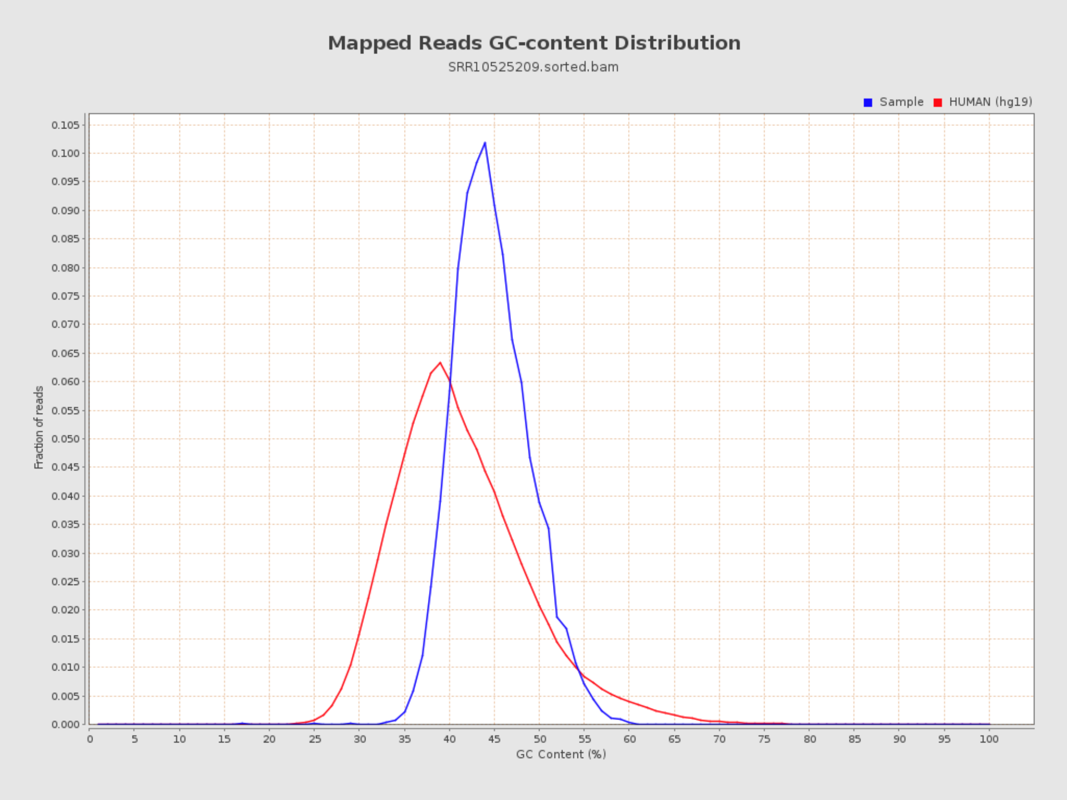
7. Results : Duplication Rate Histogram



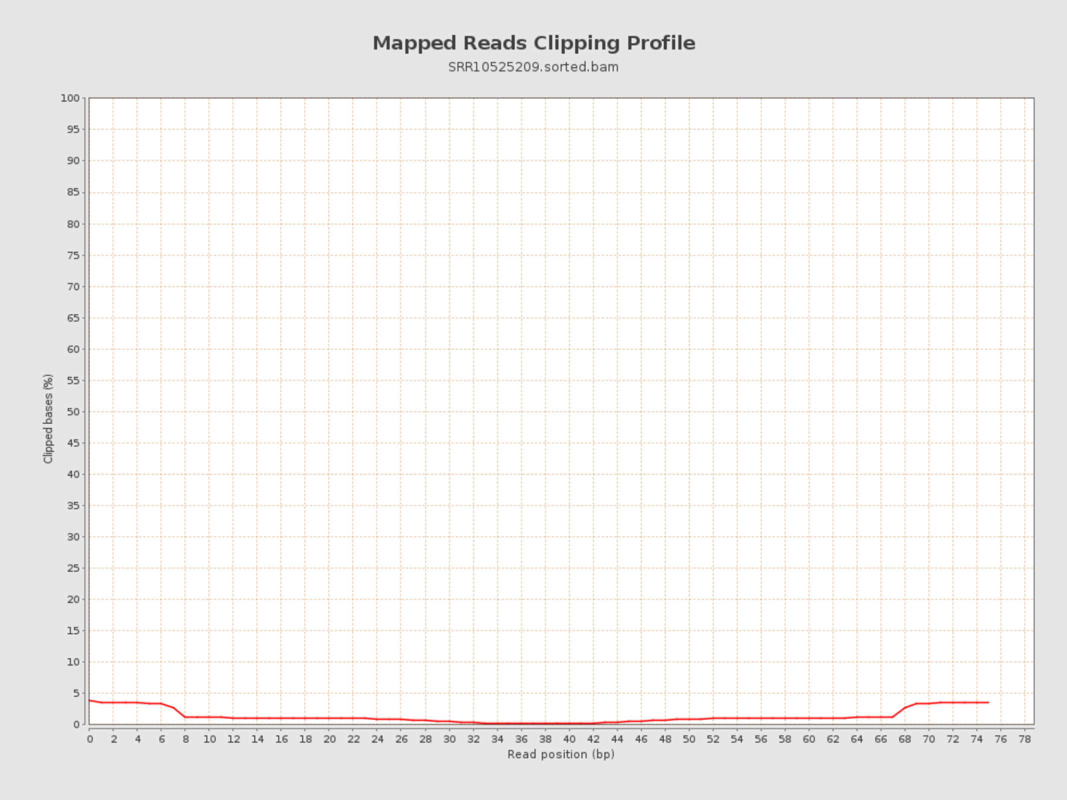
8. Results : Mapped Reads Nucleotide Content



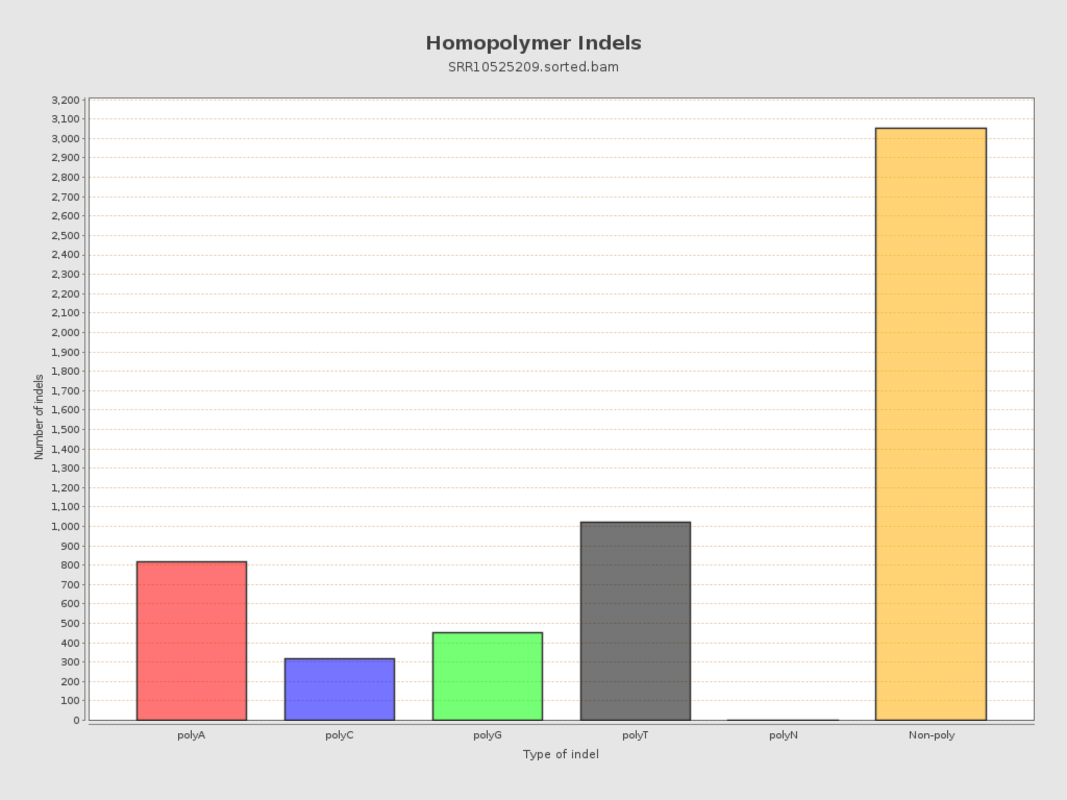
9. Results : Mapped Reads GC-content Distribution



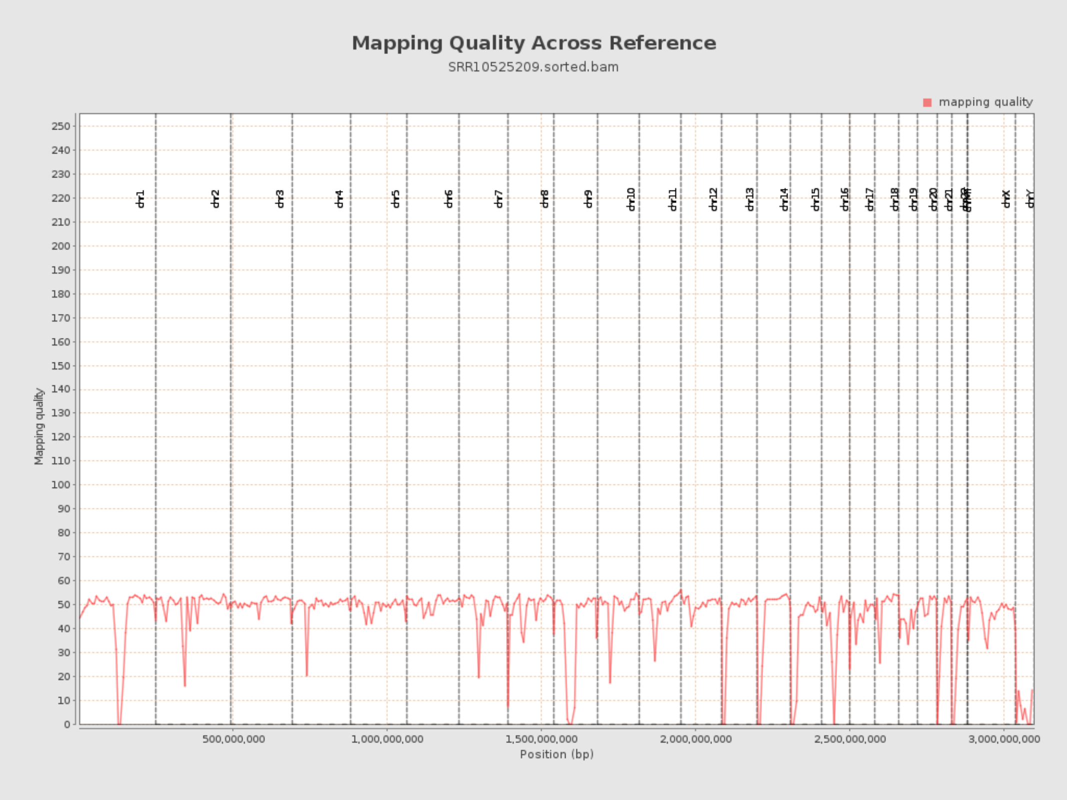
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram