Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:17:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525034.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_SRR10525034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:17:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	542,170
Mapped reads	500,794 / 92.37%
Unmapped reads	41,376 / 7.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,004 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	9,352 / 1.72%
Duplication rate	1.41%
Clipped reads	500,941 / 92.4%

2.2. ACGT Content

Number/percentage of A's	7,798,012 / 26.57%
Number/percentage of C's	5,542,066 / 18.89%
Number/percentage of T's	8,887,018 / 30.29%
Number/percentage of G's	7,116,481 / 24.25%
Number/percentage of N's	320 / 0%
GC Percentage	43.14%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.1174

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

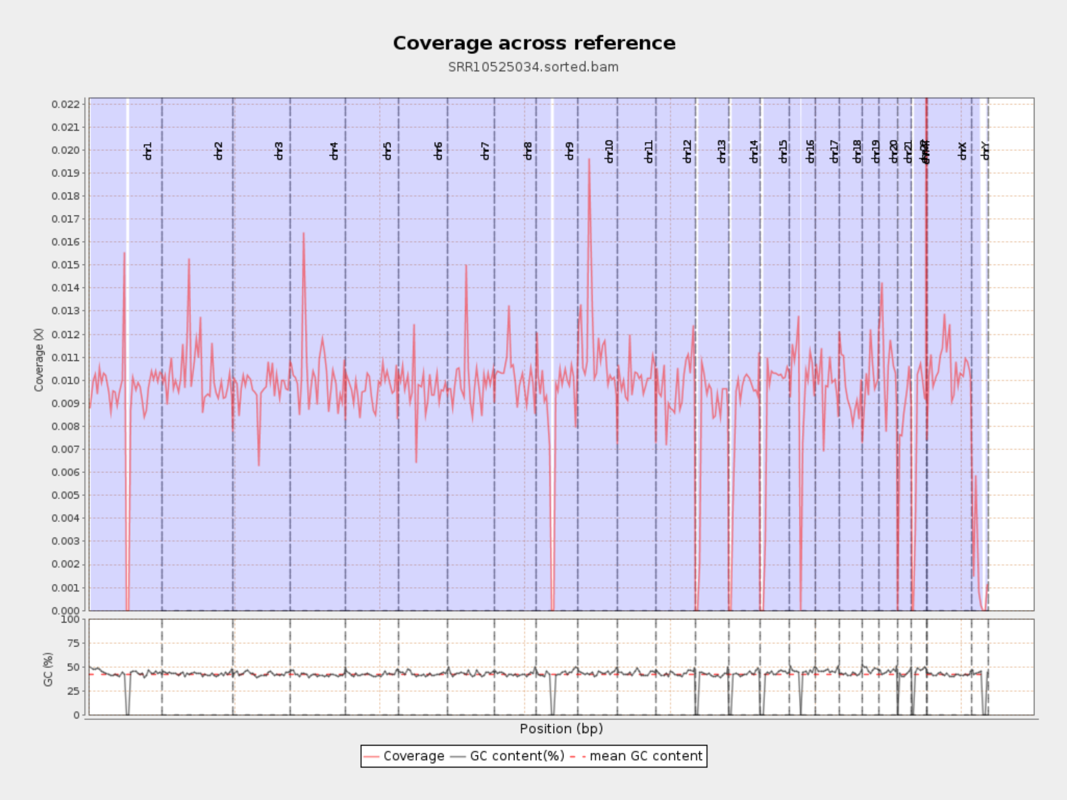
General error rate	0.51%
Mismatches	143,840
Insertions	2,332
Mapped reads with at least one insertion	0.46%
Deletions	5,774
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.98%

2.6. Chromosome stats

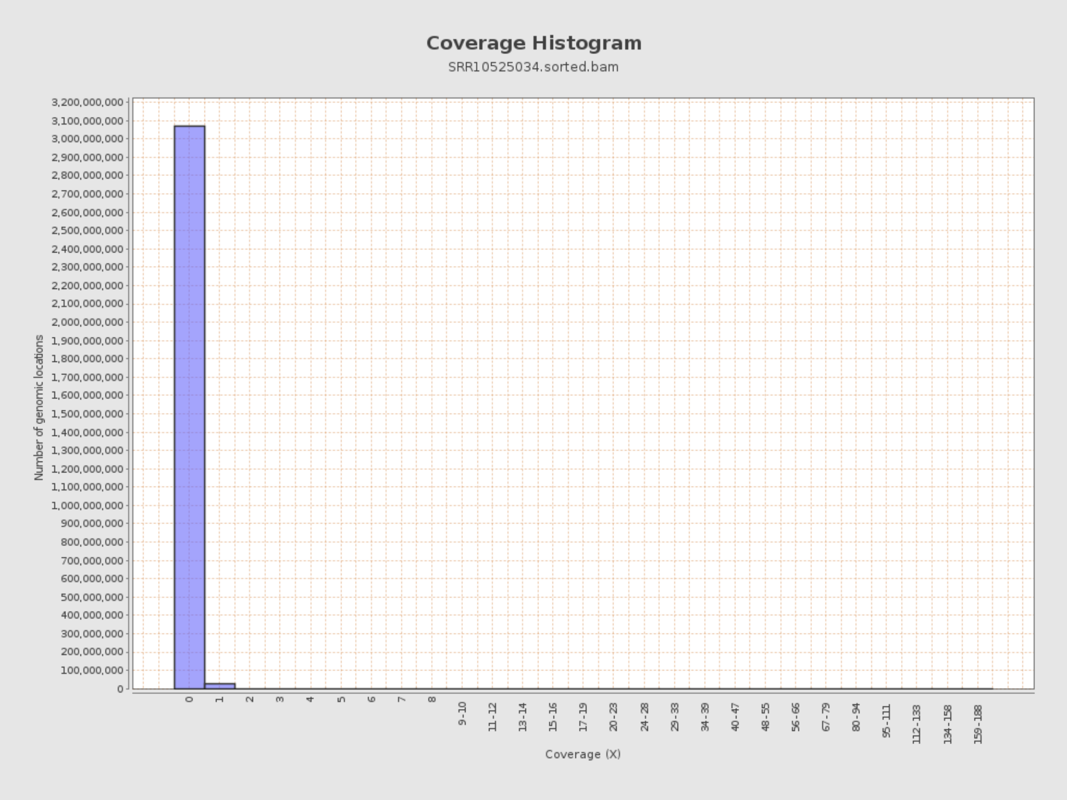
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2304464	0.0092	0.1685
chr2	243199373	2496817	0.0103	0.1311
chr3	198022430	1907008	0.0096	0.1014
chr4	191154276	1948734	0.0102	0.1093
chr5	180915260	1748310	0.0097	0.1018
chr6	171115067	1652075	0.0097	0.109
chr7	159138663	1586256	0.01	0.13

chr8	146364022	1488981	0.0102	0.1285
chr9	141213431	1216608	0.0086	0.1042
chr10	135534747	1554533	0.0115	0.1315
chr11	135006516	1356474	0.01	0.1156
chr12	133851895	1303111	0.0097	0.1024
chr13	115169878	911253	0.0079	0.0922
chr14	107349540	875686	0.0082	0.0938
chr15	102531392	850530	0.0083	0.0945
chr16	90354753	867497	0.0096	0.1035
chr17	81195210	793408	0.0098	0.1053
chr18	78077248	742959	0.0095	0.1456
chr19	59128983	595751	0.0101	0.1307
chr20	63025520	684905	0.0109	0.1086
chr21	48129895	385106	0.008	0.0968
chr22	51304566	356267	0.0069	0.0859
chrMT	16571	1473	0.0889	0.3011
chrX	155270560	1631980	0.0105	0.109
chrY	59373566	93167	0.0016	0.0591

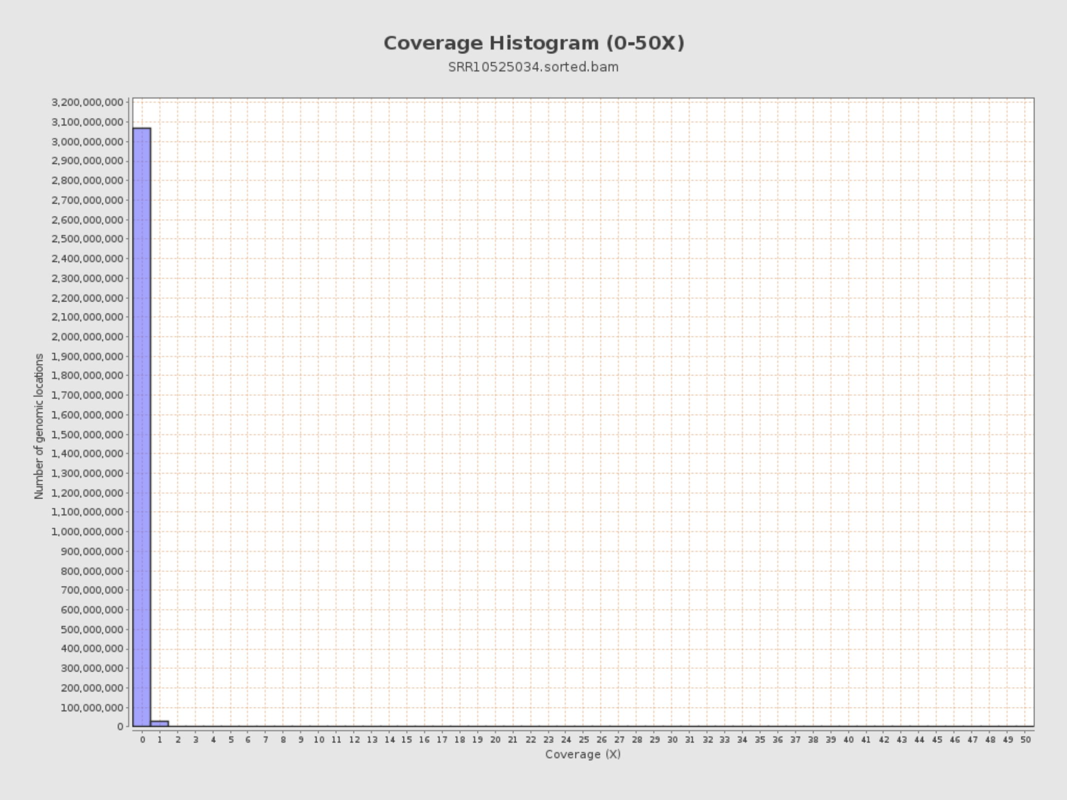
3. Results : Coverage across reference



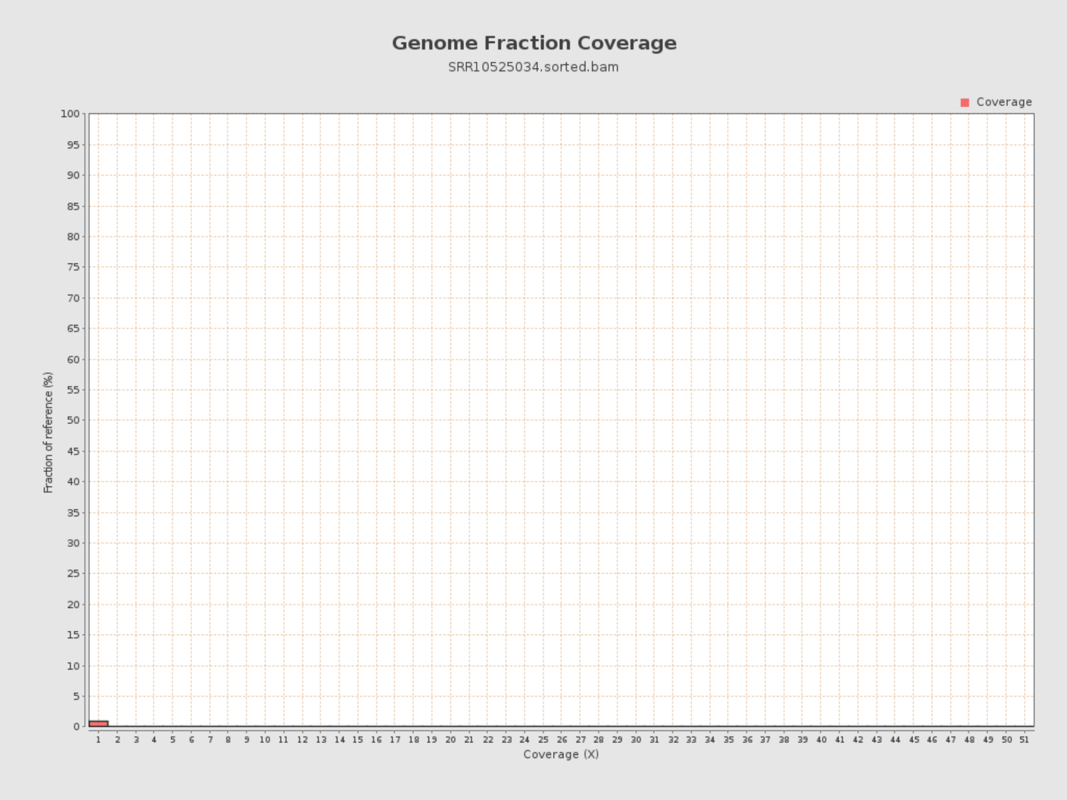
4. Results : Coverage Histogram



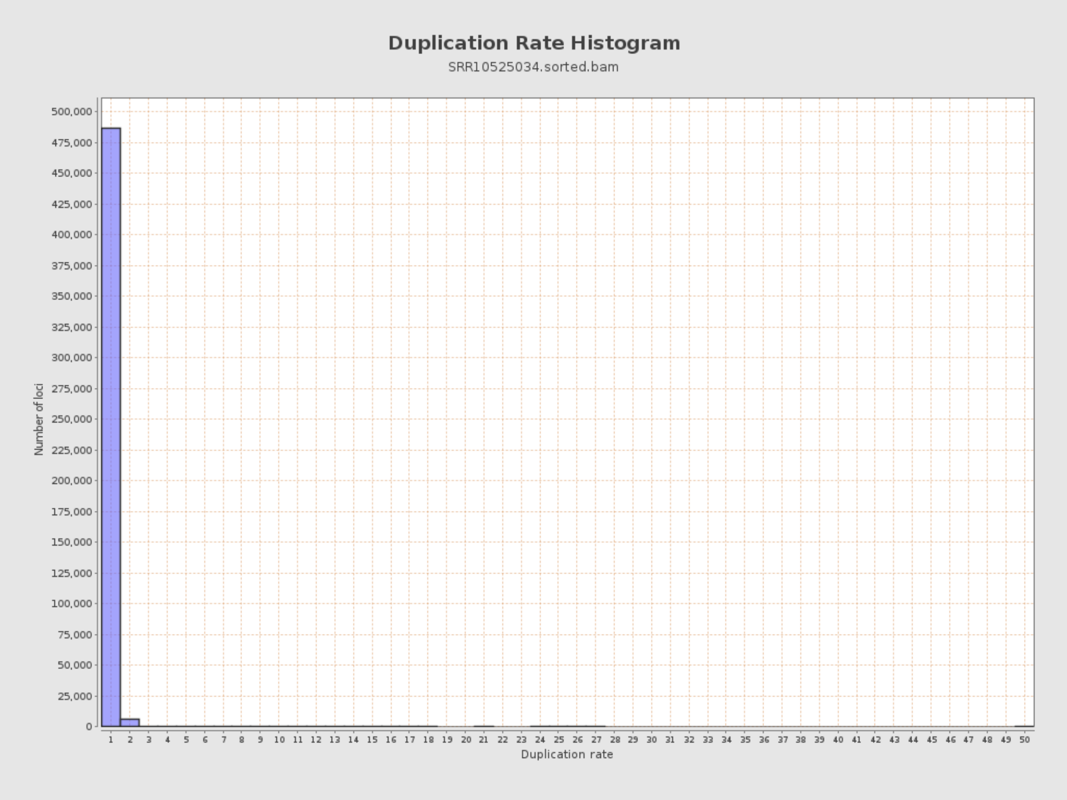
5. Results : Coverage Histogram (0-50X)



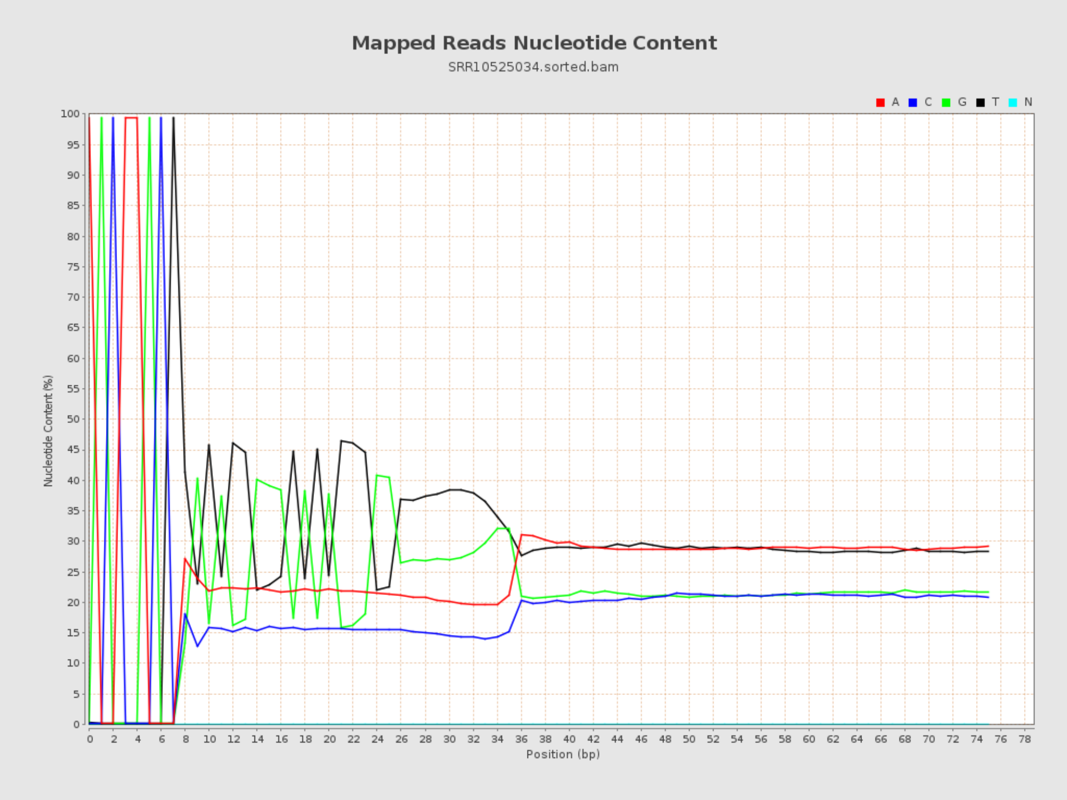
6. Results : Genome Fraction Coverage



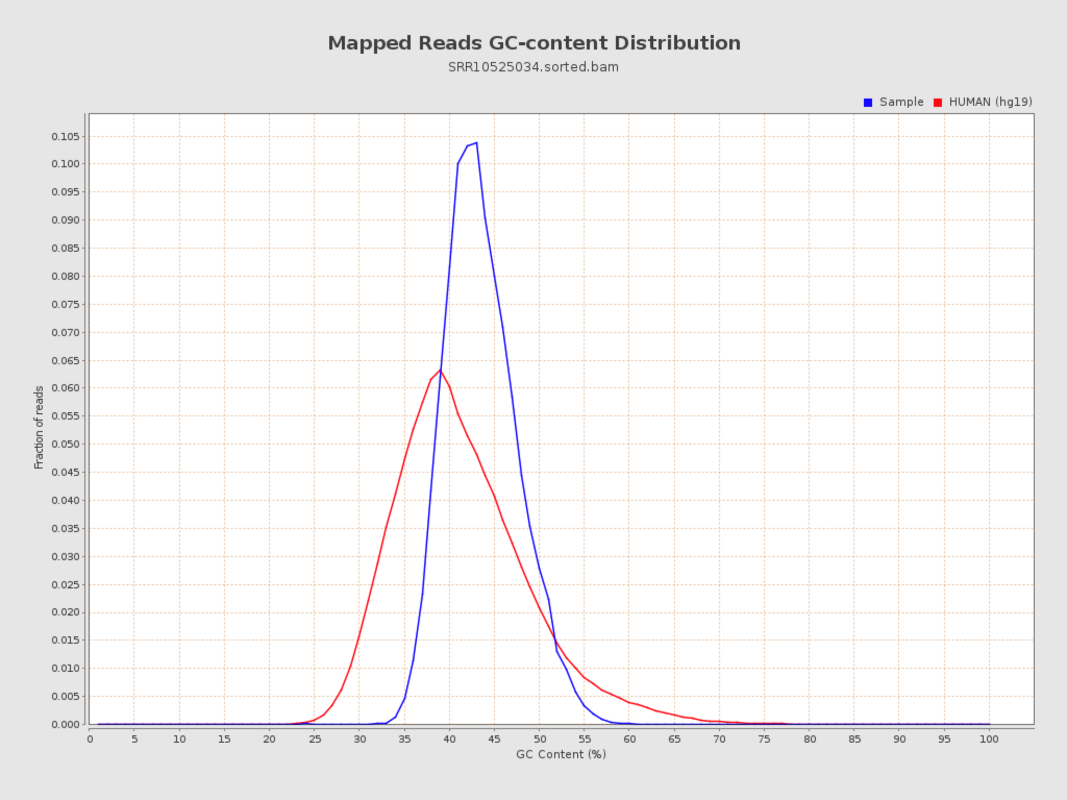
7. Results : Duplication Rate Histogram



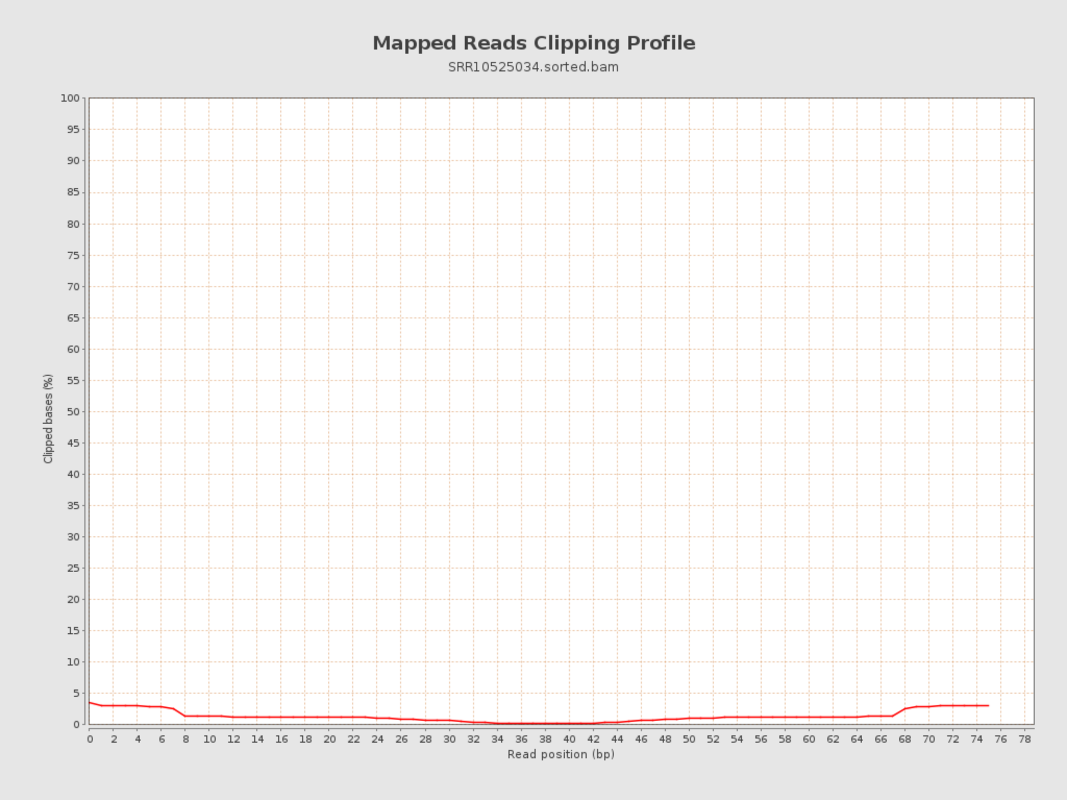
8. Results : Mapped Reads Nucleotide Content



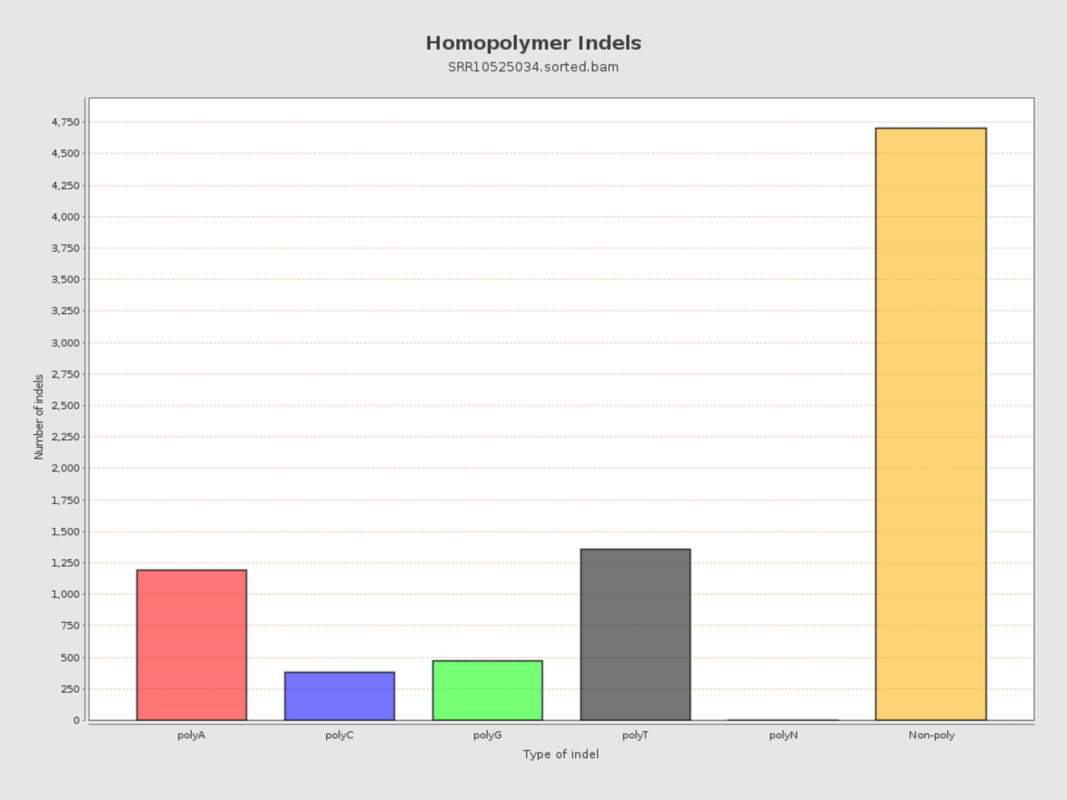
9. Results : Mapped Reads GC-content Distribution



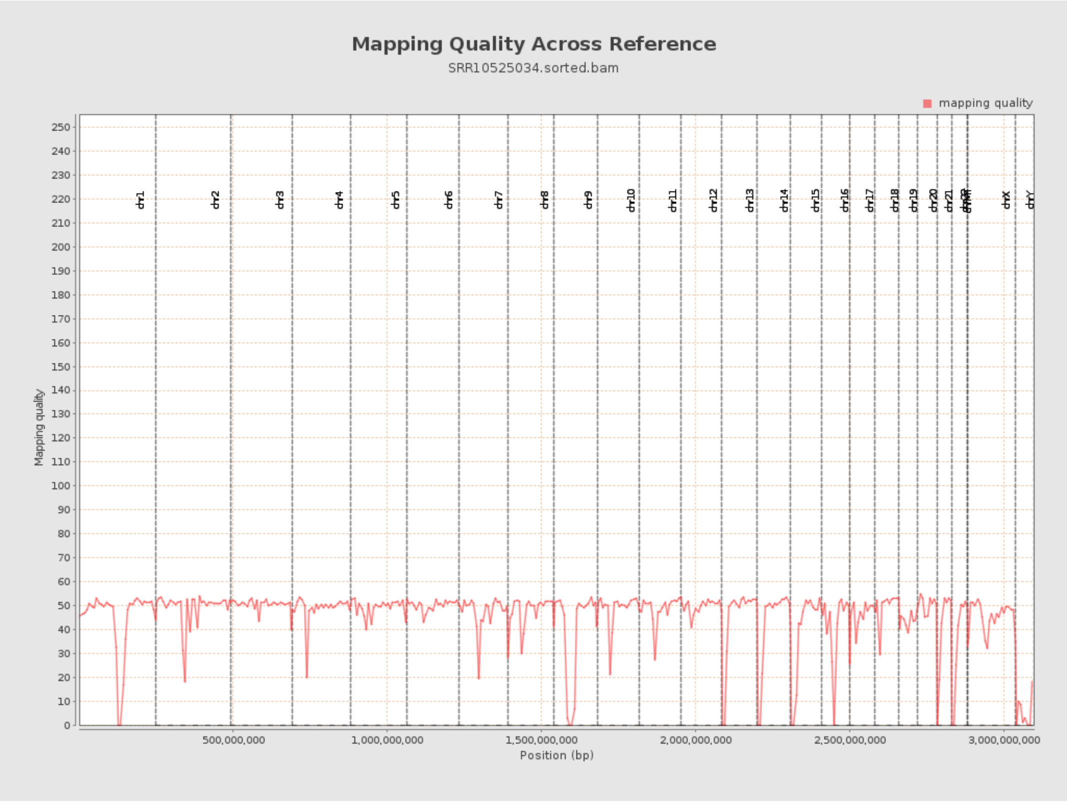
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram