Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:55:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525223.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_SRR10525223 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525223.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:55:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525223.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	686,665
Mapped reads	634,867 / 92.46%
Unmapped reads	51,798 / 7.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,480 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	11,917 / 1.74%
Duplication rate	1.35%
Clipped reads	634,956 / 92.47%

2.2. ACGT Content

Number/percentage of A's	10,817,541 / 27.44%
Number/percentage of C's	7,886,477 / 20%
Number/percentage of T's	11,972,241 / 30.37%
Number/percentage of G's	8,749,791 / 22.19%
Number/percentage of N's	1,059 / 0%
GC Percentage	42.19%

2.3. Coverage

Mean	0.0127

Standard Deviation	0.1523

2.4. Mapping Quality

Mean Mapping Quality	46.63

2.5. Mismatches and indels

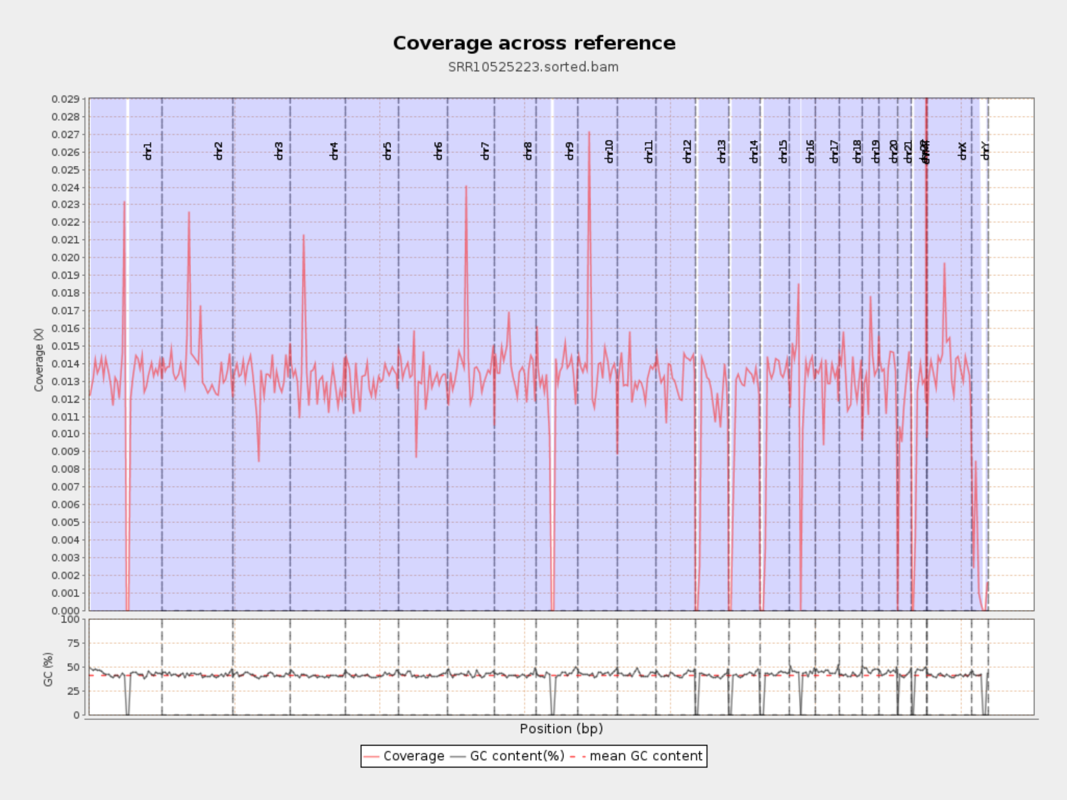
General error rate	0.5%
Mismatches	191,024
Insertions	3,224
Mapped reads with at least one insertion	0.5%
Deletions	8,404
Mapped reads with at least one deletion	1.31%
Homopolymer indels	42.55%

2.6. Chromosome stats

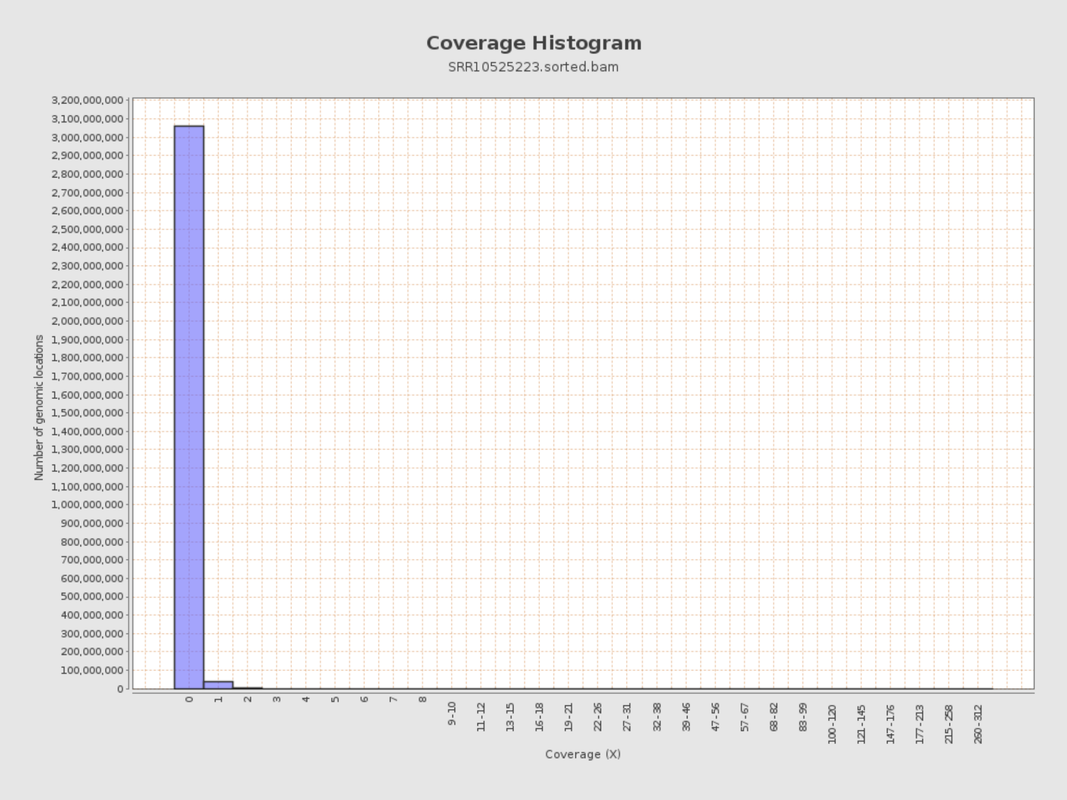
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3206797	0.0129	0.2668
chr2	243199373	3377000	0.0139	0.1617
chr3	198022430	2588172	0.0131	0.1187
chr4	191154276	2517932	0.0132	0.1252
chr5	180915260	2364505	0.0131	0.1188
chr6	171115067	2259088	0.0132	0.1237
chr7	159138663	2212540	0.0139	0.2004

chr8	146364022	2013508	0.0138	0.1446
chr9	141213431	1672057	0.0118	0.132
chr10	135534747	1937134	0.0143	0.1575
chr11	135006516	1768628	0.0131	0.1324
chr12	133851895	1788533	0.0134	0.1212
chr13	115169878	1210592	0.0105	0.1063
chr14	107349540	1181523	0.011	0.1115
chr15	102531392	1128431	0.011	0.1086
chr16	90354753	1164883	0.0129	0.1243
chr17	81195210	1060783	0.0131	0.1218
chr18	78077248	1038538	0.0133	0.2097
chr19	59128983	808792	0.0137	0.1933
chr20	63025520	849262	0.0135	0.1208
chr21	48129895	523652	0.0109	0.1184
chr22	51304566	461440	0.009	0.0984
chrMT	16571	2362	0.1425	0.3918
chrX	155270560	2170225	0.014	0.1274
chrY	59373566	134590	0.0023	0.0827

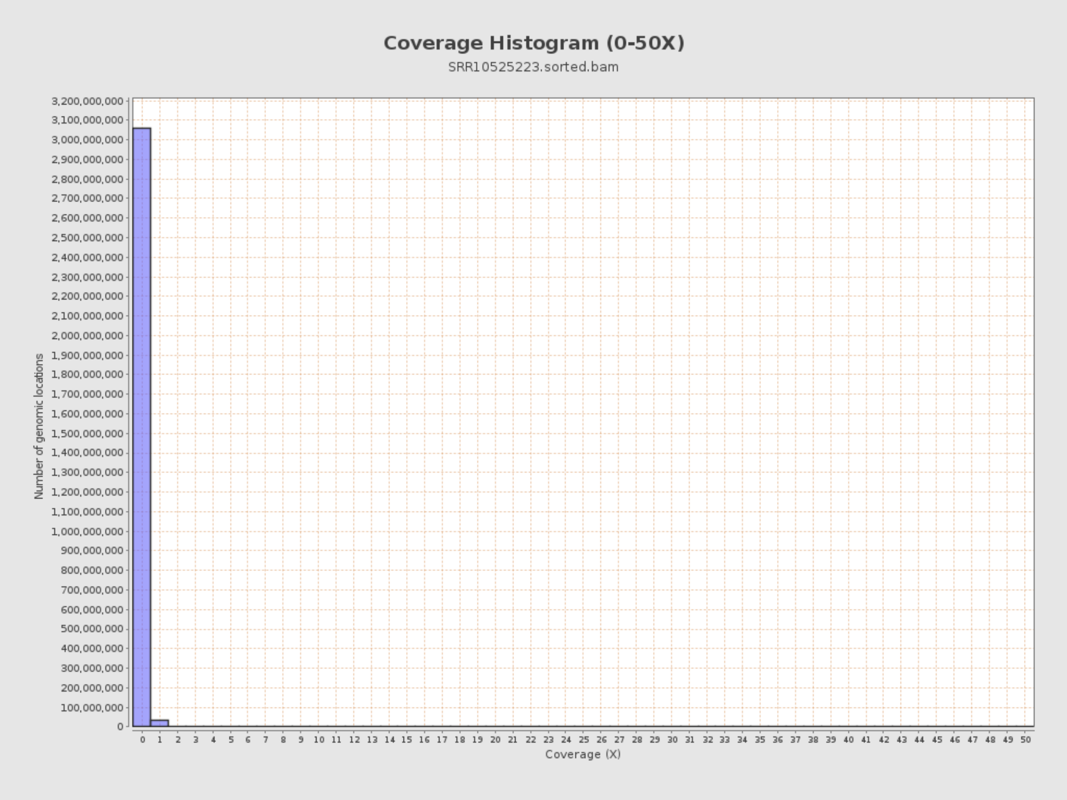
3. Results : Coverage across reference



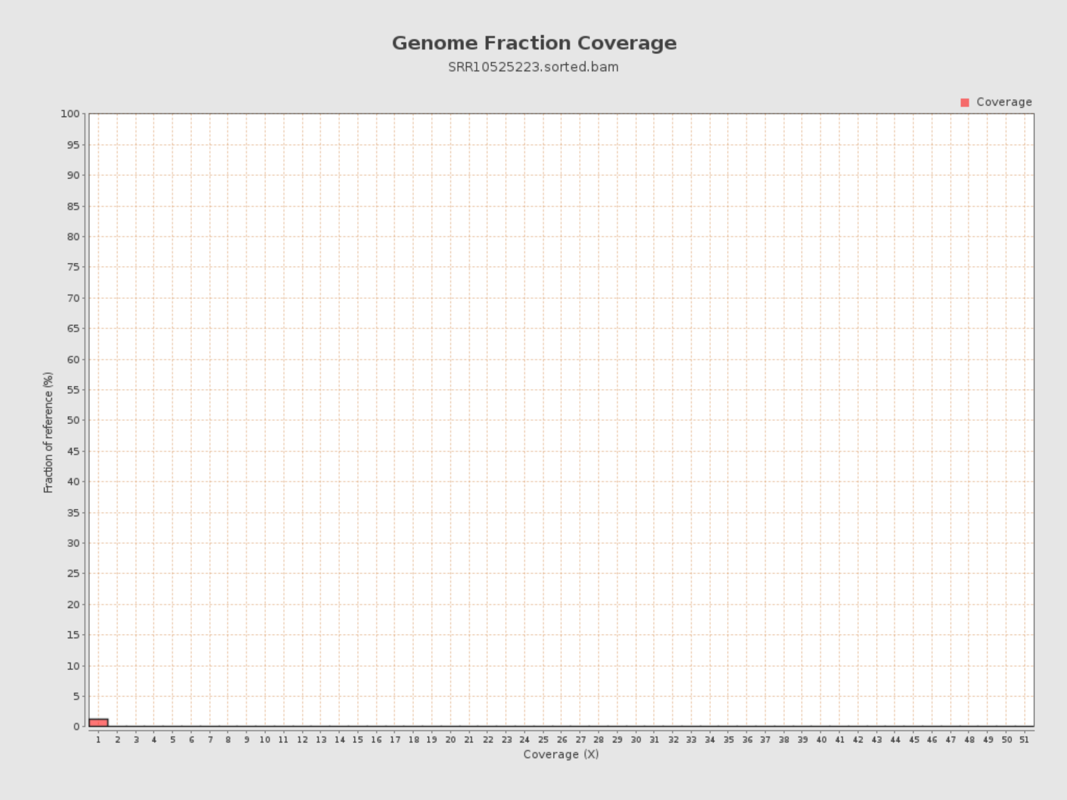
4. Results : Coverage Histogram



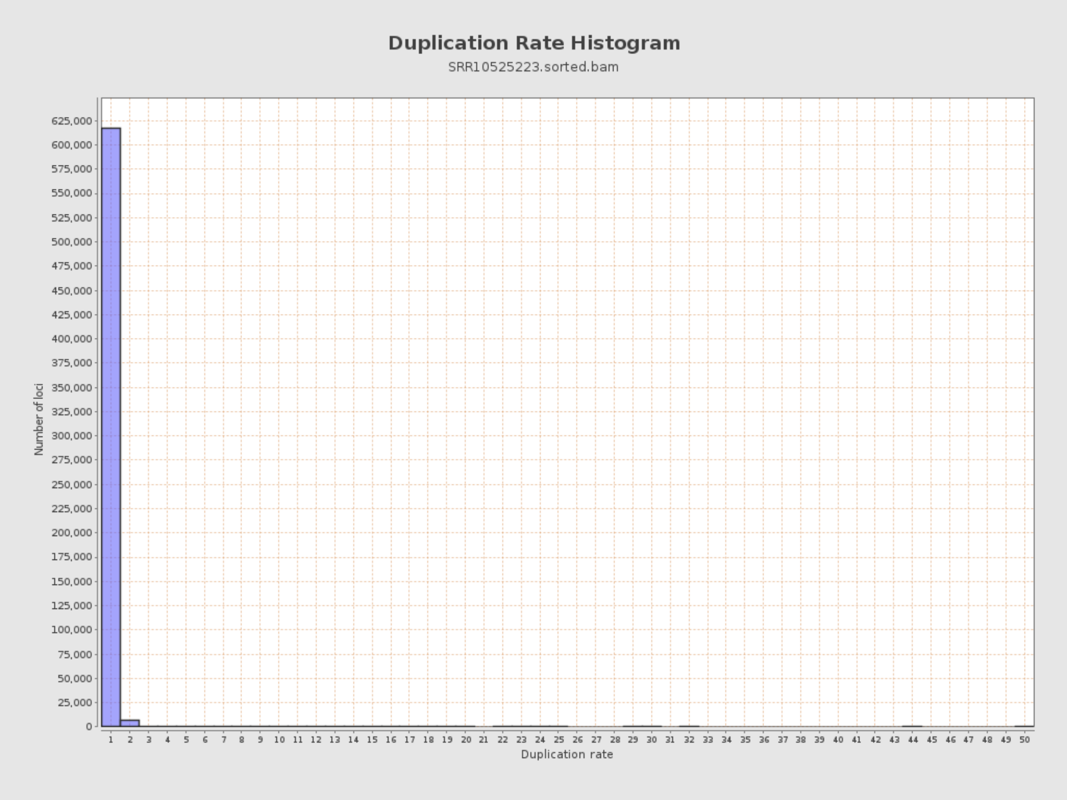
5. Results : Coverage Histogram (0-50X)



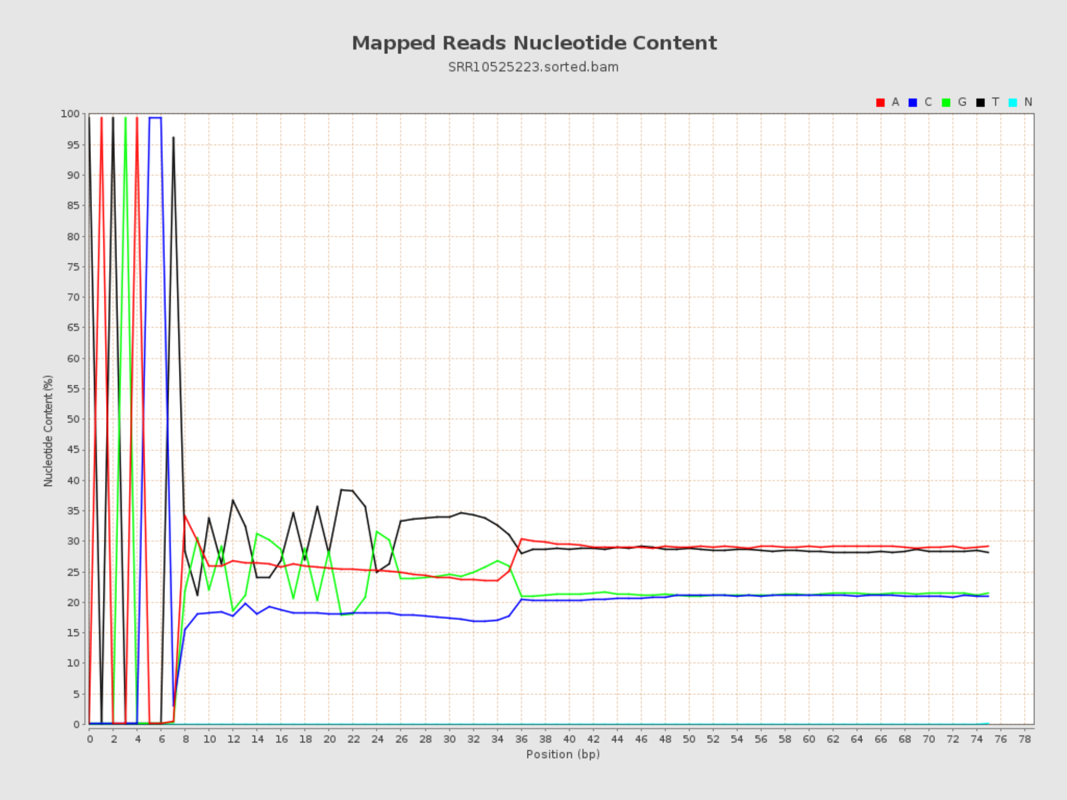
6. Results : Genome Fraction Coverage



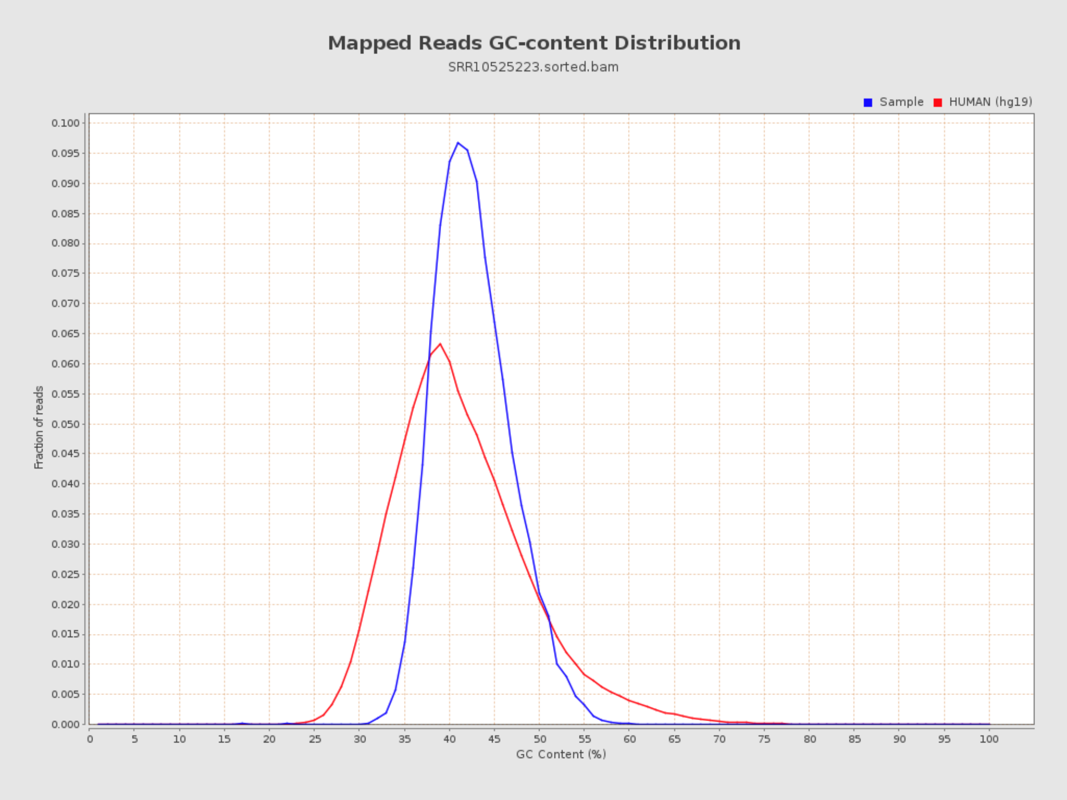
7. Results : Duplication Rate Histogram



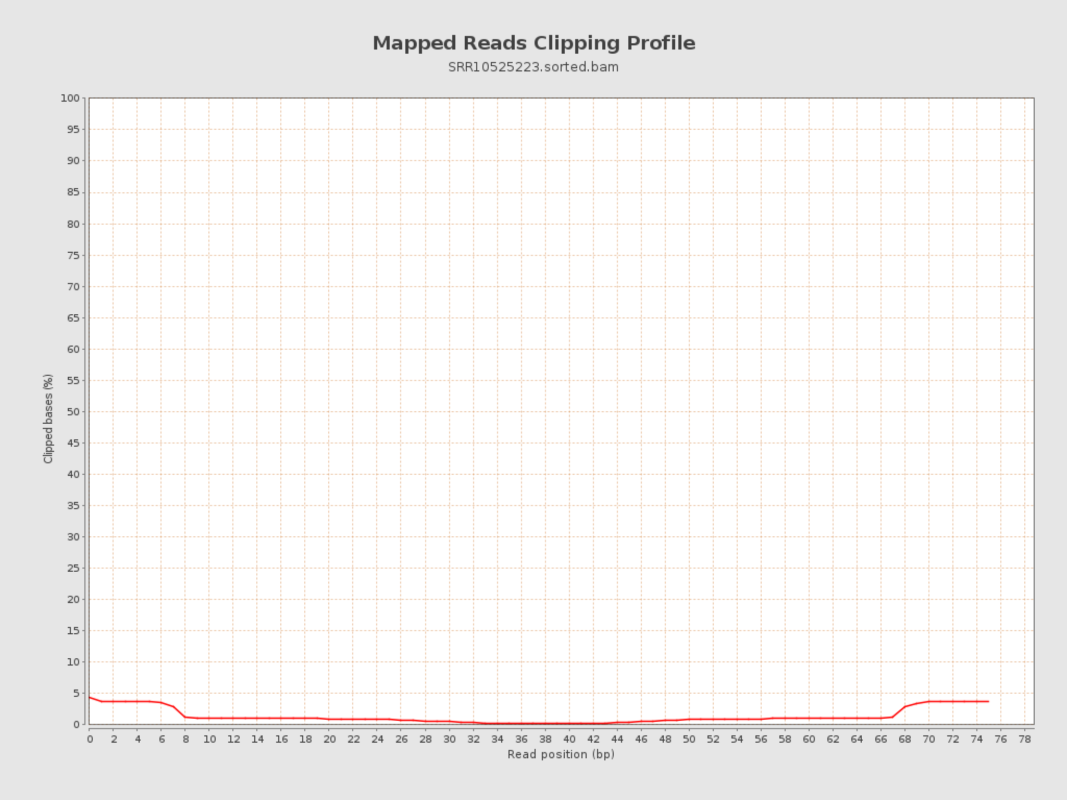
8. Results : Mapped Reads Nucleotide Content



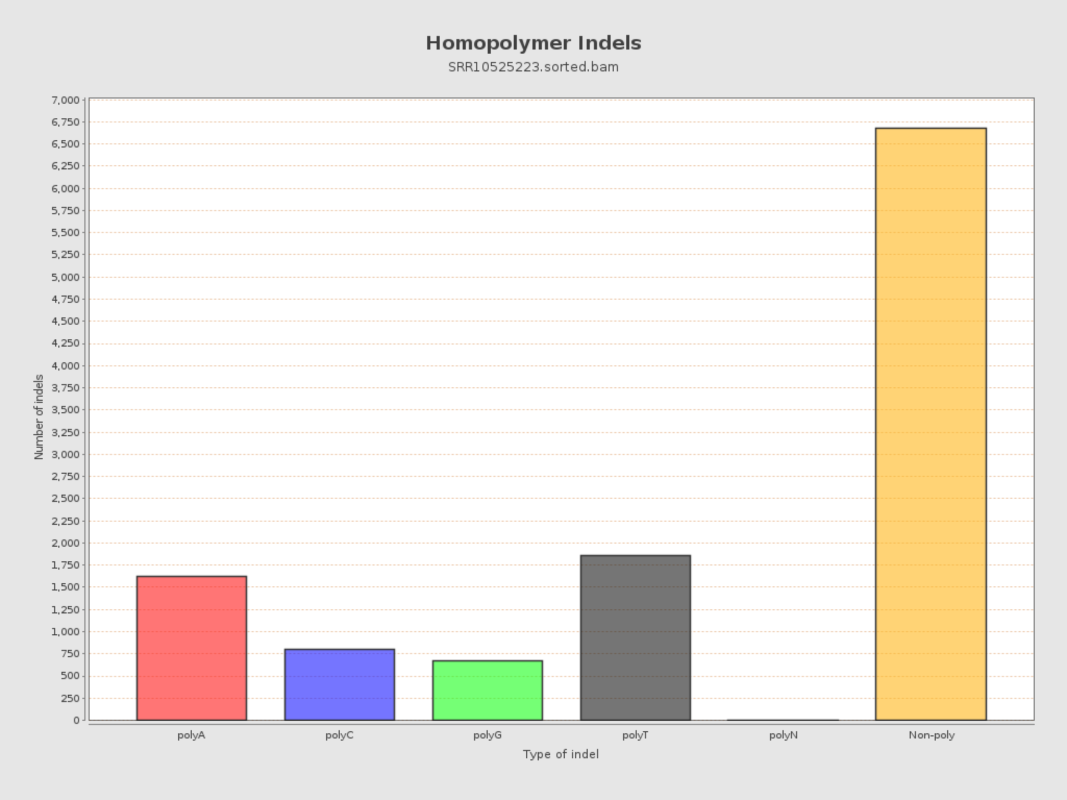
9. Results : Mapped Reads GC-content Distribution



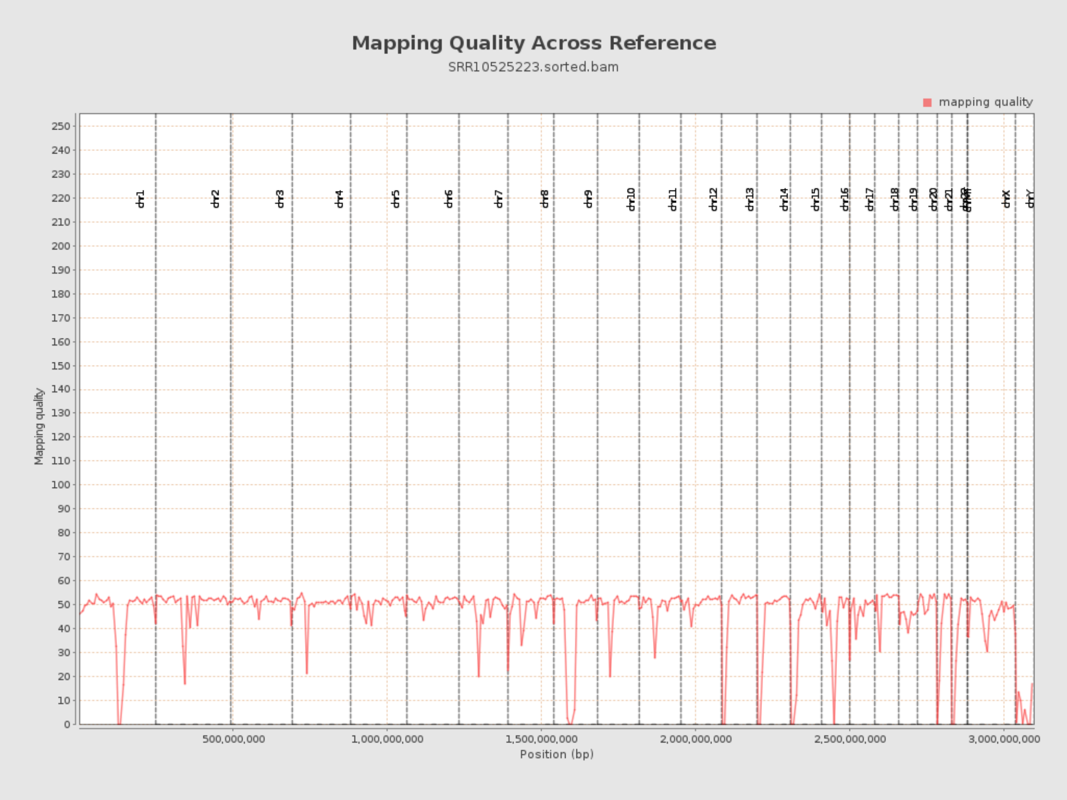
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram