Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:30:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525062.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_SRR10525062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:30:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	645,239
Mapped reads	535,914 / 83.06%
Unmapped reads	109,325 / 16.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,512 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	19,422 / 3.01%
Duplication rate	3.02%
Clipped reads	535,668 / 83.02%

2.2. ACGT Content

Number/percentage of A's	7,619,893 / 24.76%
Number/percentage of C's	5,808,641 / 18.87%
Number/percentage of T's	10,401,543 / 33.79%
Number/percentage of G's	6,946,436 / 22.57%
Number/percentage of N's	2,965 / 0.01%
GC Percentage	41.44%

2.3. Coverage

Mean	0.0099

Standard Deviation	0.1307

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

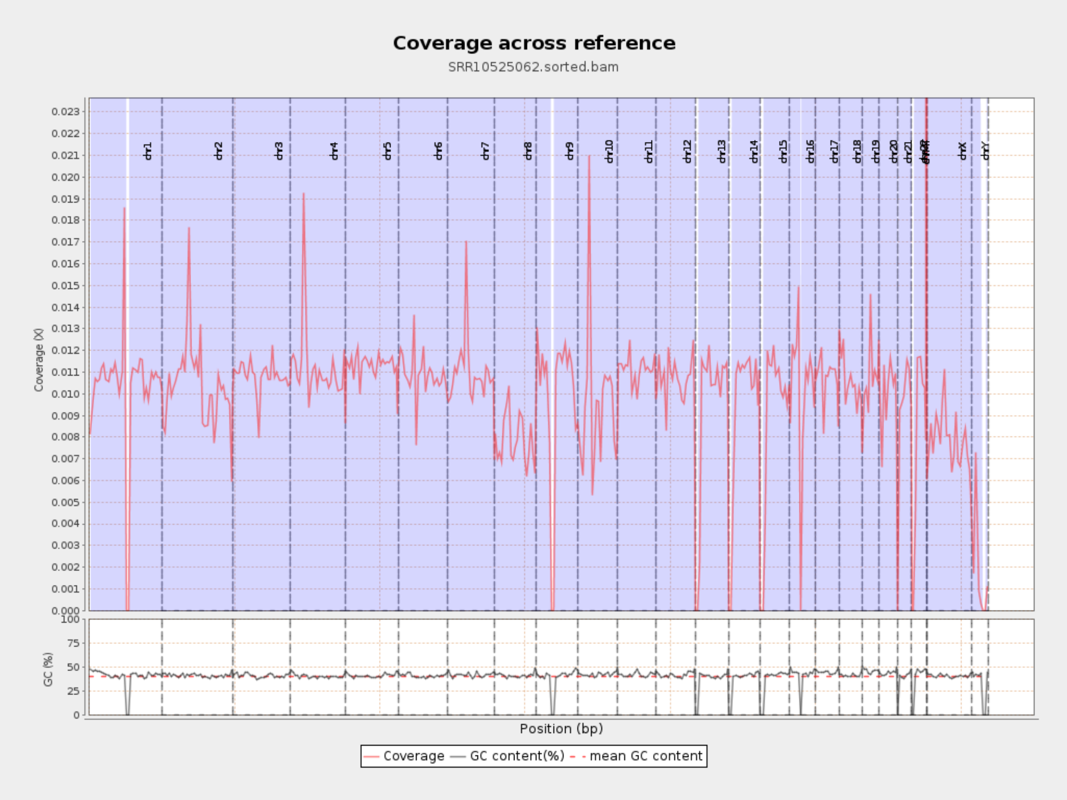
General error rate	0.52%
Mismatches	156,089
Insertions	2,178
Mapped reads with at least one insertion	0.4%
Deletions	6,144
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.93%

2.6. Chromosome stats

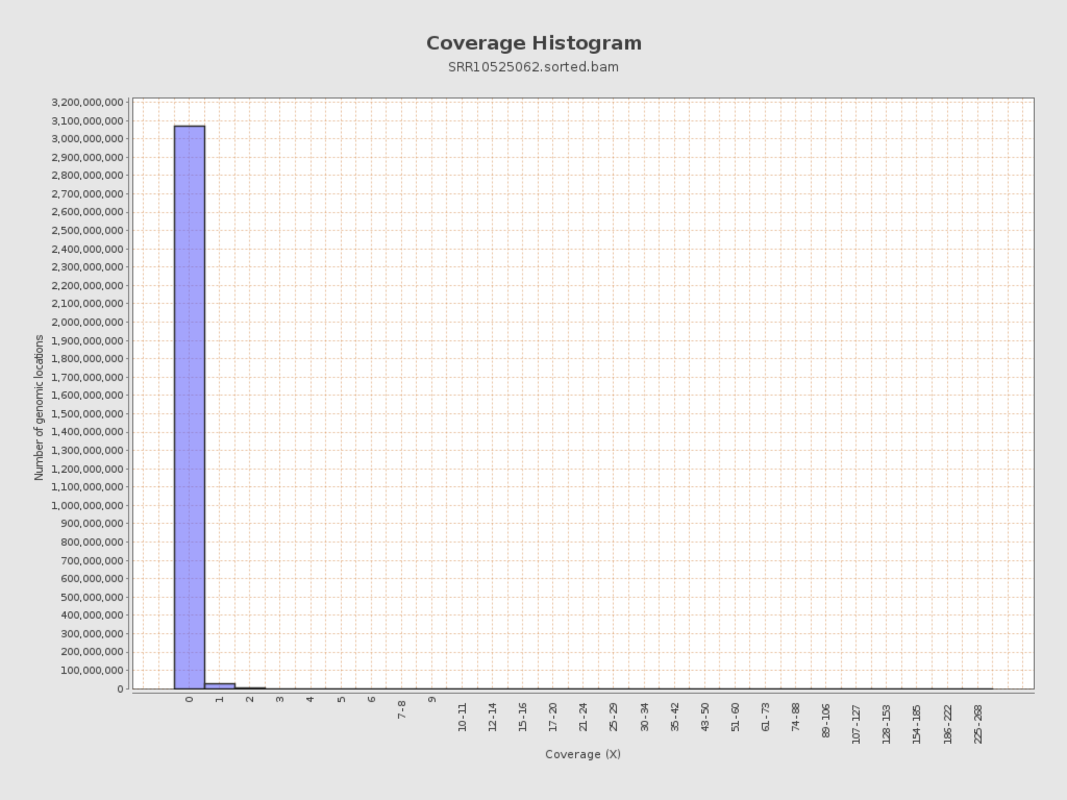
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2560069	0.0103	0.2151
chr2	243199373	2534155	0.0104	0.1553
chr3	198022430	2139370	0.0108	0.1095
chr4	191154276	2143910	0.0112	0.1185
chr5	180915260	2047834	0.0113	0.1122
chr6	171115067	1864750	0.0109	0.1173
chr7	159138663	1759909	0.0111	0.1402

chr8	146364022	1144874	0.0078	0.1261
chr9	141213431	1388468	0.0098	0.1129
chr10	135534747	1282415	0.0095	0.1333
chr11	135006516	1499363	0.0111	0.1182
chr12	133851895	1428209	0.0107	0.1102
chr13	115169878	1058711	0.0092	0.1011
chr14	107349540	985435	0.0092	0.102
chr15	102531392	904567	0.0088	0.099
chr16	90354753	920440	0.0102	0.1117
chr17	81195210	866594	0.0107	0.1109
chr18	78077248	828866	0.0106	0.1653
chr19	59128983	635460	0.0107	0.1578
chr20	63025520	626505	0.0099	0.107
chr21	48129895	445270	0.0093	0.107
chr22	51304566	389906	0.0076	0.092
chrMT	16571	9364	0.5651	0.8489
chrX	155270560	1221914	0.0079	0.0997
chrY	59373566	102983	0.0017	0.0756

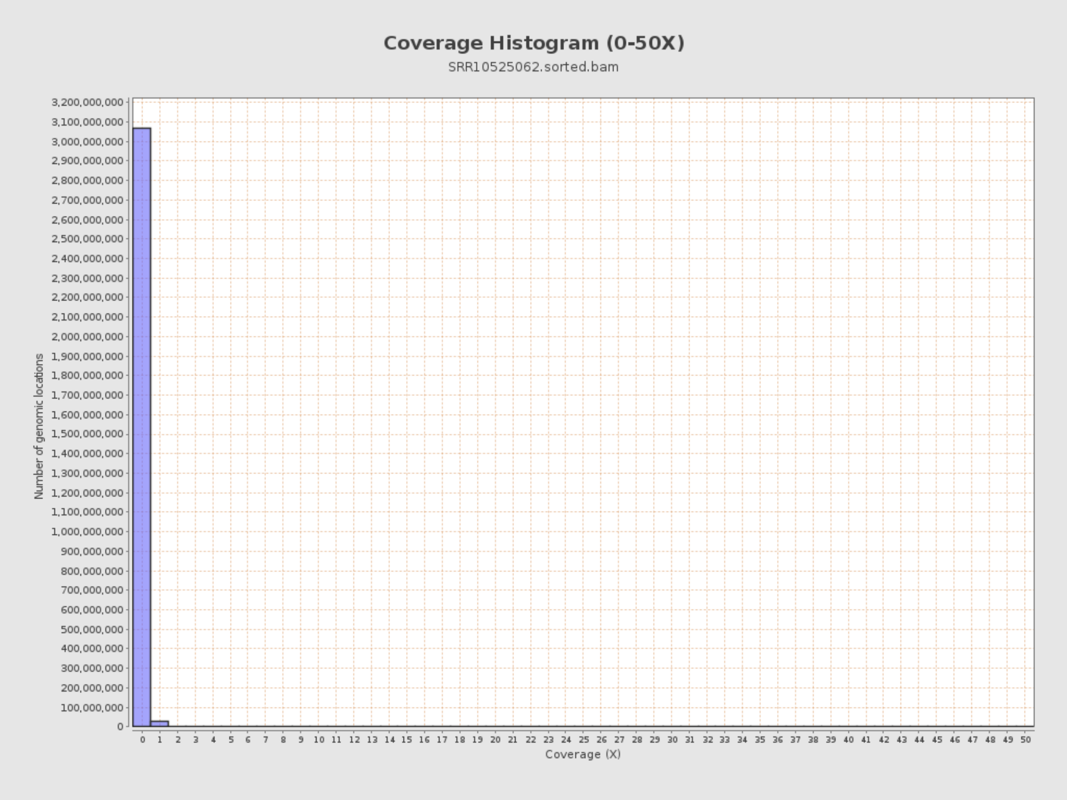
3. Results : Coverage across reference



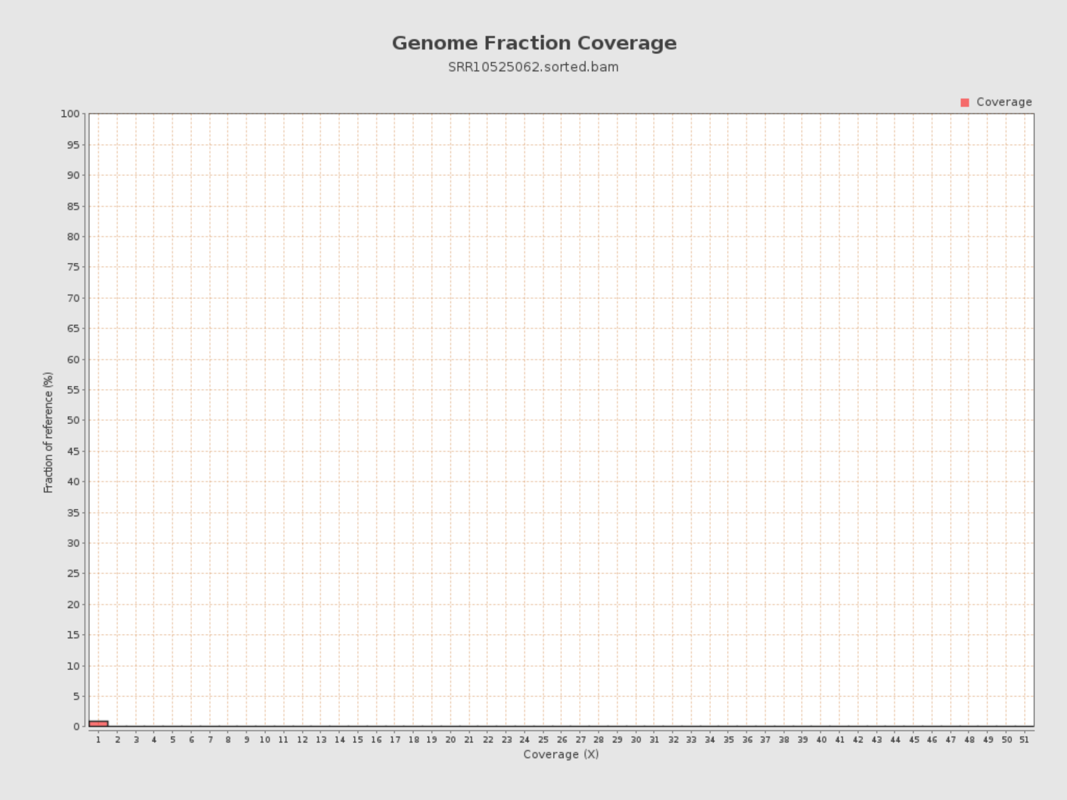
4. Results : Coverage Histogram



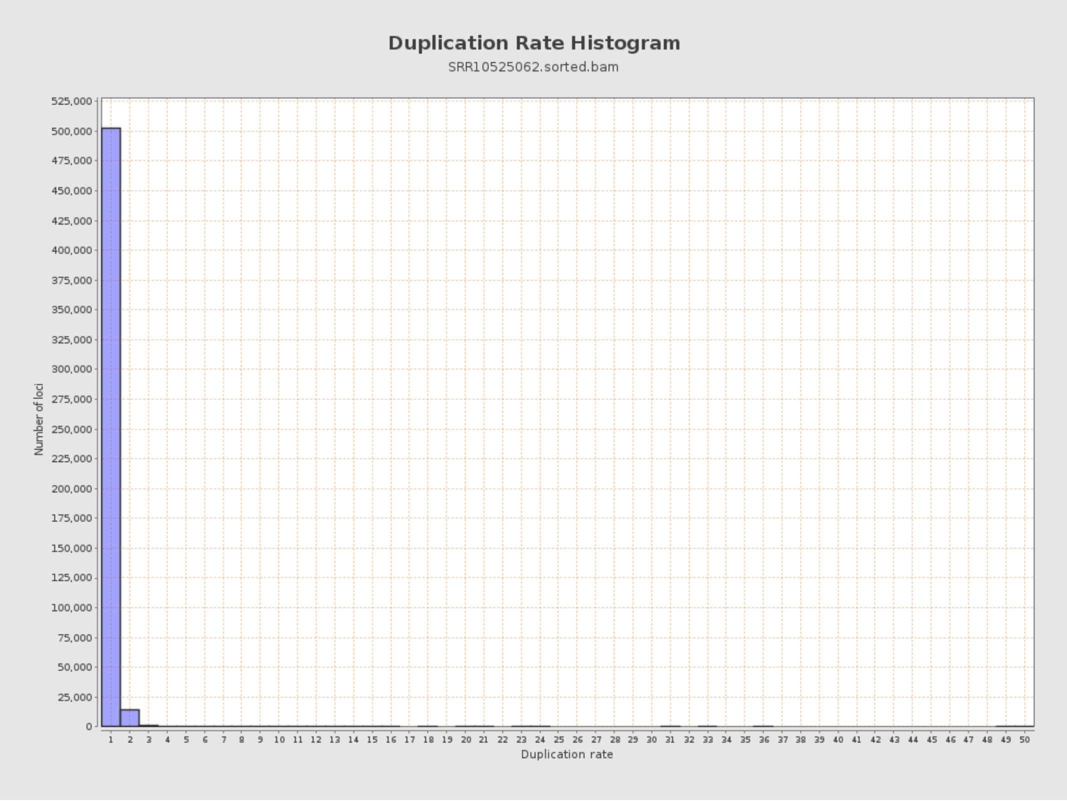
5. Results : Coverage Histogram (0-50X)



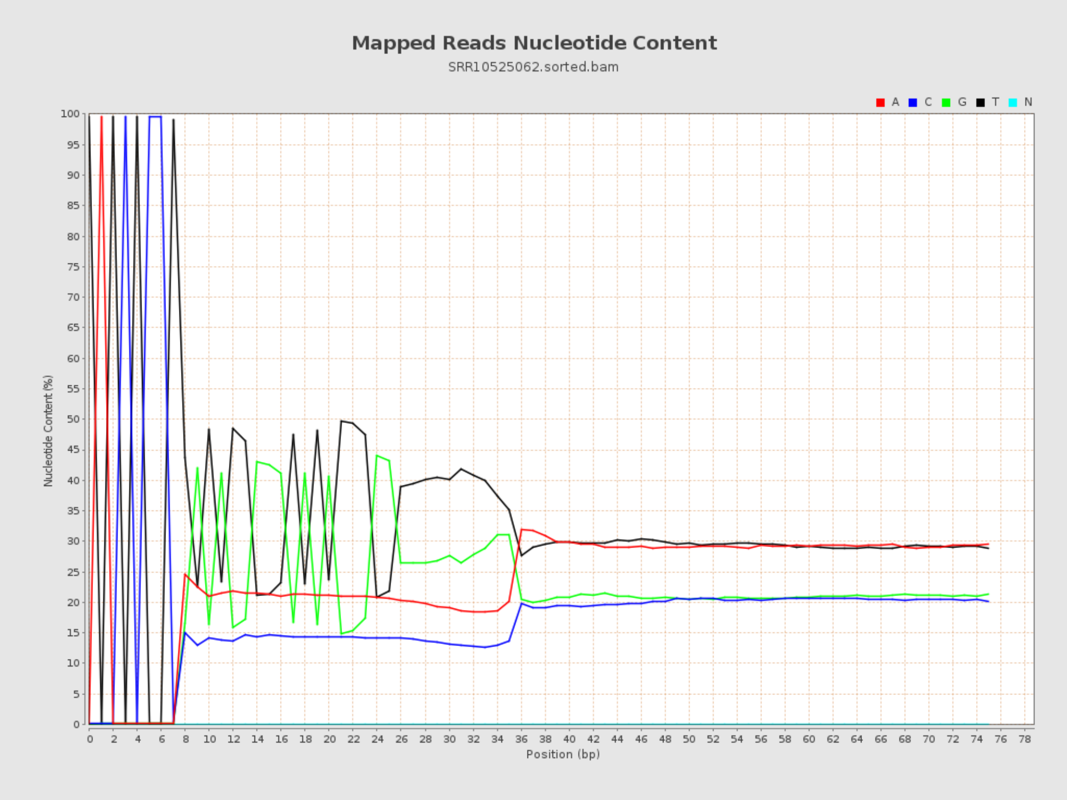
6. Results : Genome Fraction Coverage



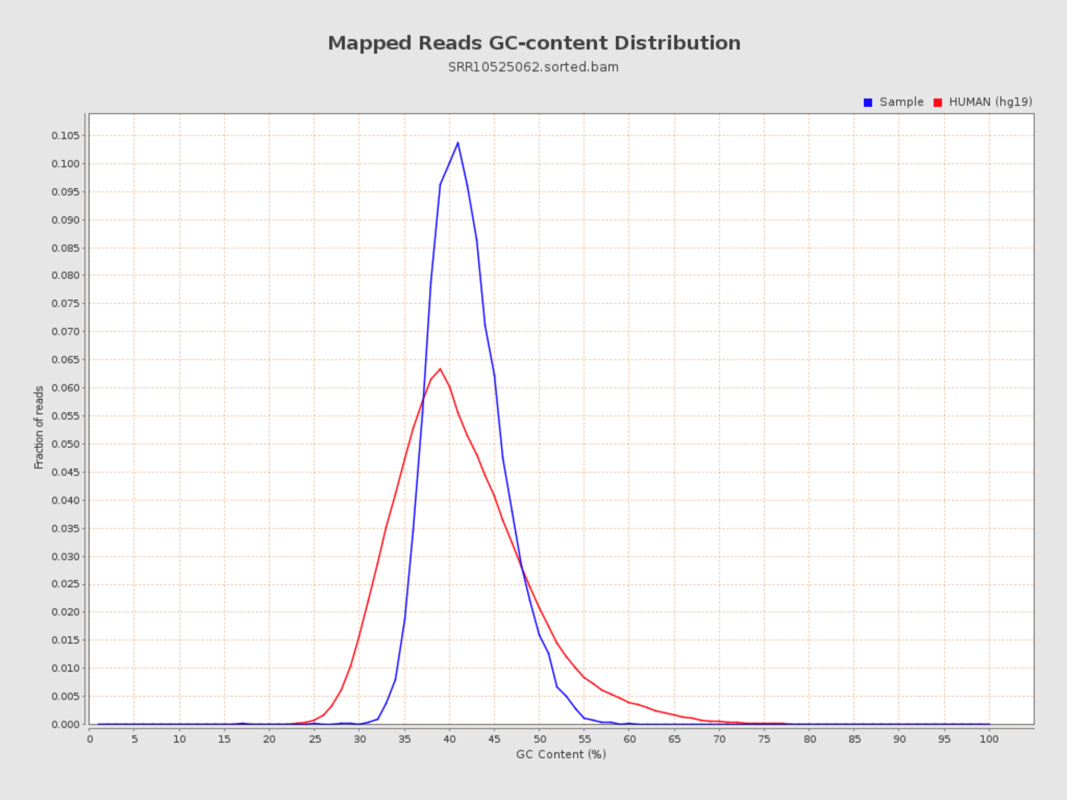
7. Results : Duplication Rate Histogram



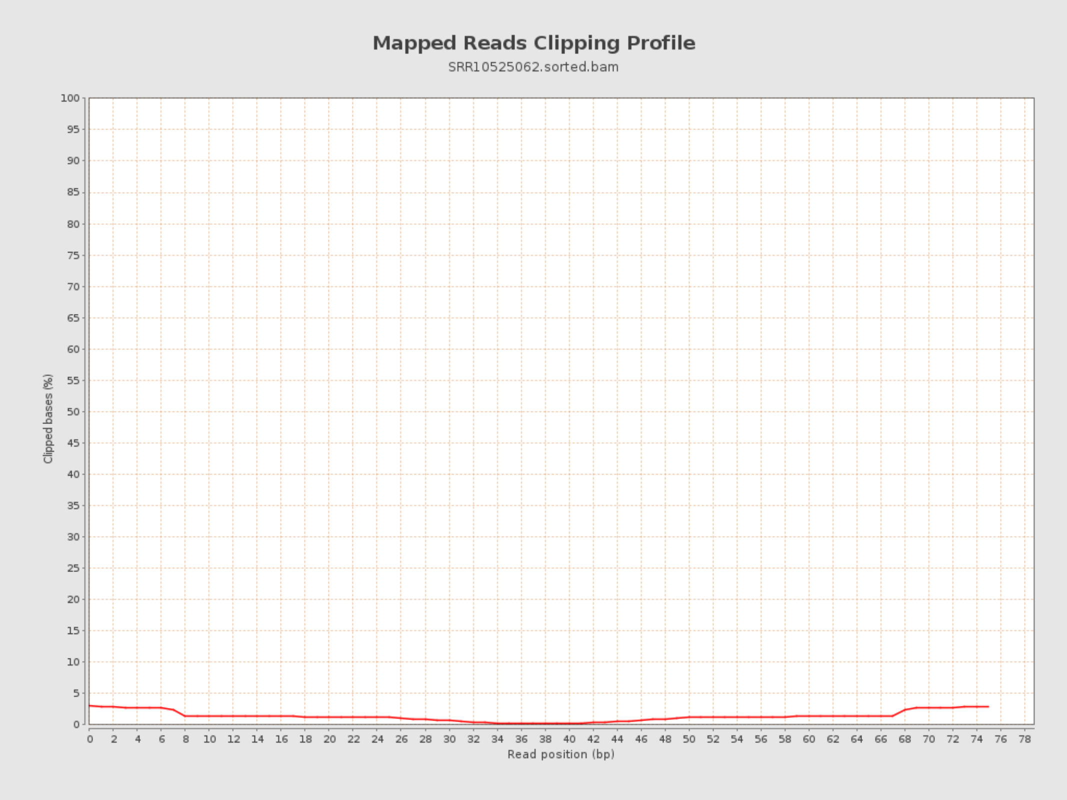
8. Results : Mapped Reads Nucleotide Content



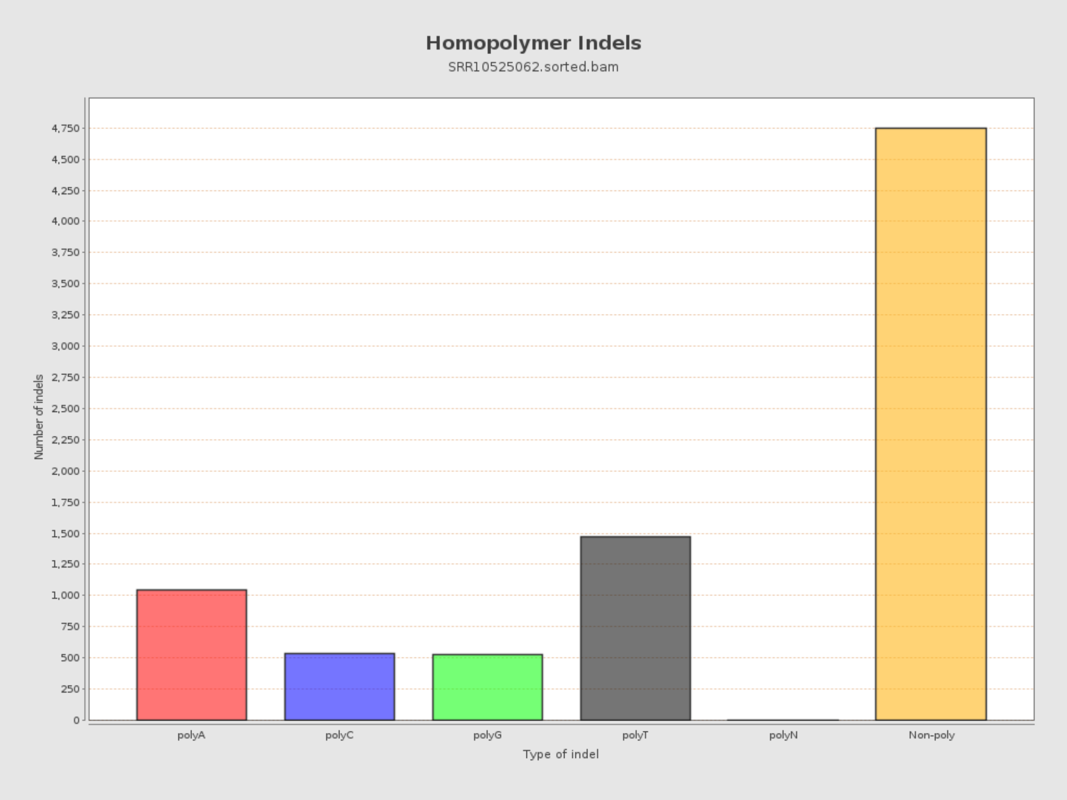
9. Results : Mapped Reads GC-content Distribution



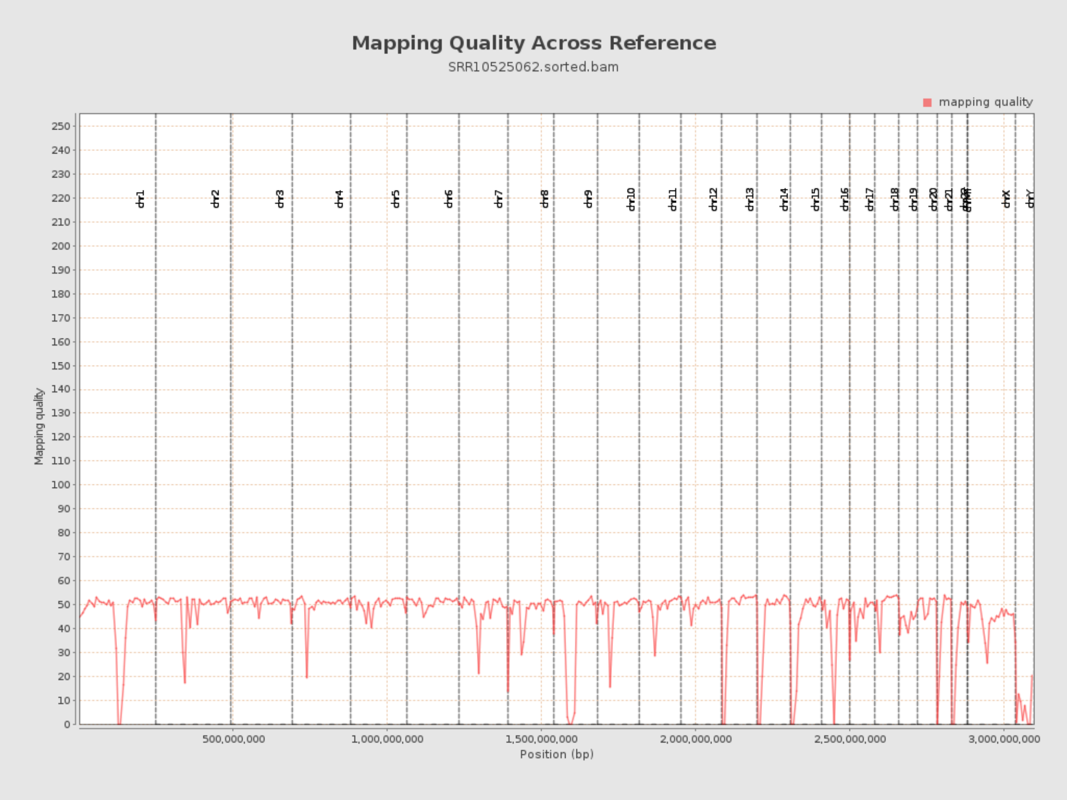
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram