Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:15:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525233.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_SRR10525233 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525233.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:15:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525233.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	402,525
Mapped reads	365,110 / 90.7%
Unmapped reads	37,415 / 9.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,434 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	5,222 / 1.3%
Duplication rate	1.09%
Clipped reads	364,376 / 90.52%

2.2. ACGT Content

Number/percentage of A's	6,065,512 / 26.39%
Number/percentage of C's	4,853,440 / 21.12%
Number/percentage of T's	7,032,634 / 30.6%
Number/percentage of G's	5,028,355 / 21.88%
Number/percentage of N's	558 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0074

Standard Deviation	0.1058

2.4. Mapping Quality

Mean Mapping Quality	46.87

2.5. Mismatches and indels

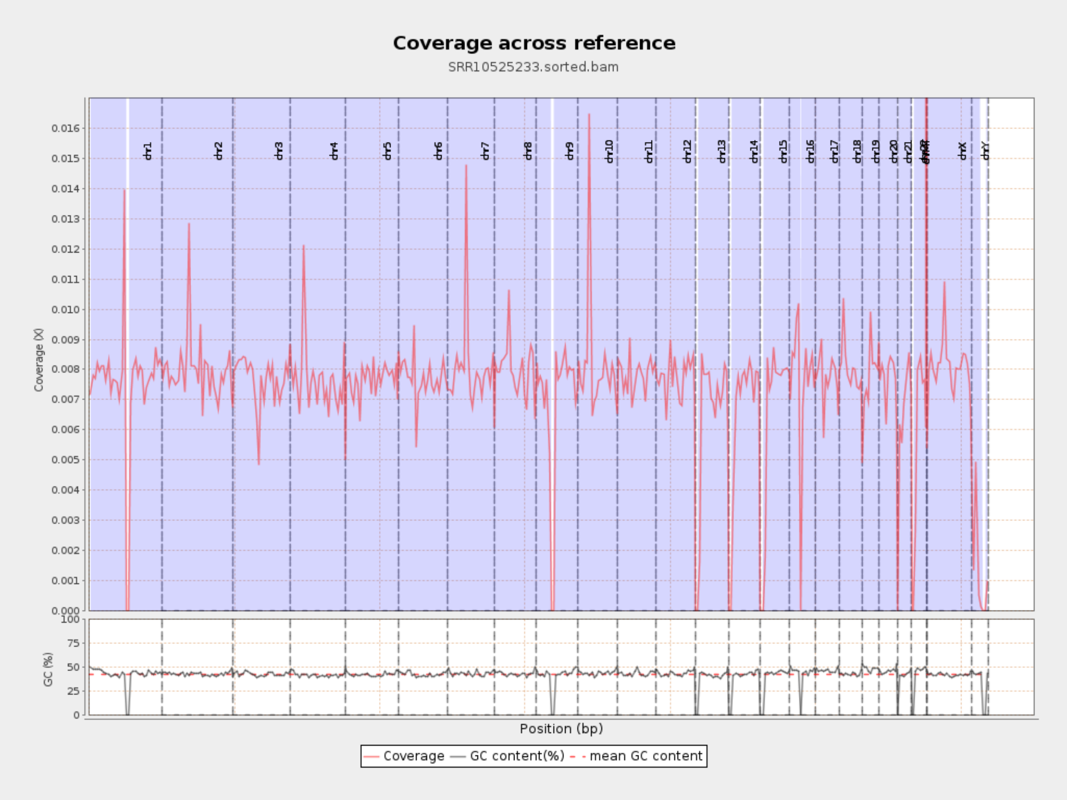
General error rate	0.51%
Mismatches	113,272
Insertions	2,029
Mapped reads with at least one insertion	0.55%
Deletions	5,190
Mapped reads with at least one deletion	1.41%
Homopolymer indels	40.07%

2.6. Chromosome stats

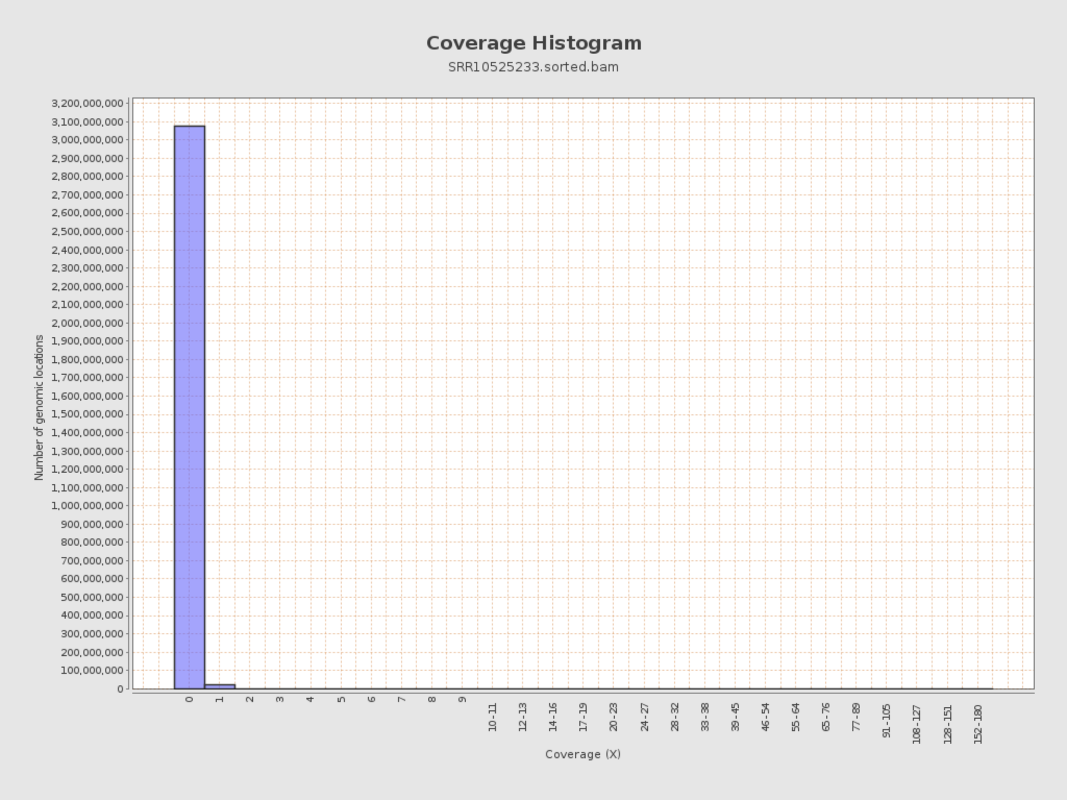
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1869104	0.0075	0.1685
chr2	243199373	1947182	0.008	0.1059
chr3	198022430	1511627	0.0076	0.0896
chr4	191154276	1459689	0.0076	0.0922
chr5	180915260	1388599	0.0077	0.0902
chr6	171115067	1320994	0.0077	0.0933
chr7	159138663	1287448	0.0081	0.1348

chr8	146364022	1171861	0.008	0.1017
chr9	141213431	960391	0.0068	0.0935
chr10	135534747	1104753	0.0082	0.1113
chr11	135006516	1053420	0.0078	0.0961
chr12	133851895	1038847	0.0078	0.0907
chr13	115169878	722603	0.0063	0.0809
chr14	107349540	687754	0.0064	0.0837
chr15	102531392	654180	0.0064	0.0817
chr16	90354753	685484	0.0076	0.0923
chr17	81195210	623006	0.0077	0.0915
chr18	78077248	632060	0.0081	0.1496
chr19	59128983	463553	0.0078	0.1236
chr20	63025520	485771	0.0077	0.0905
chr21	48129895	307568	0.0064	0.0847
chr22	51304566	277056	0.0054	0.0753
chrMT	16571	4718	0.2847	0.5551
chrX	155270560	1256194	0.0081	0.0943
chrY	59373566	75380	0.0013	0.0554

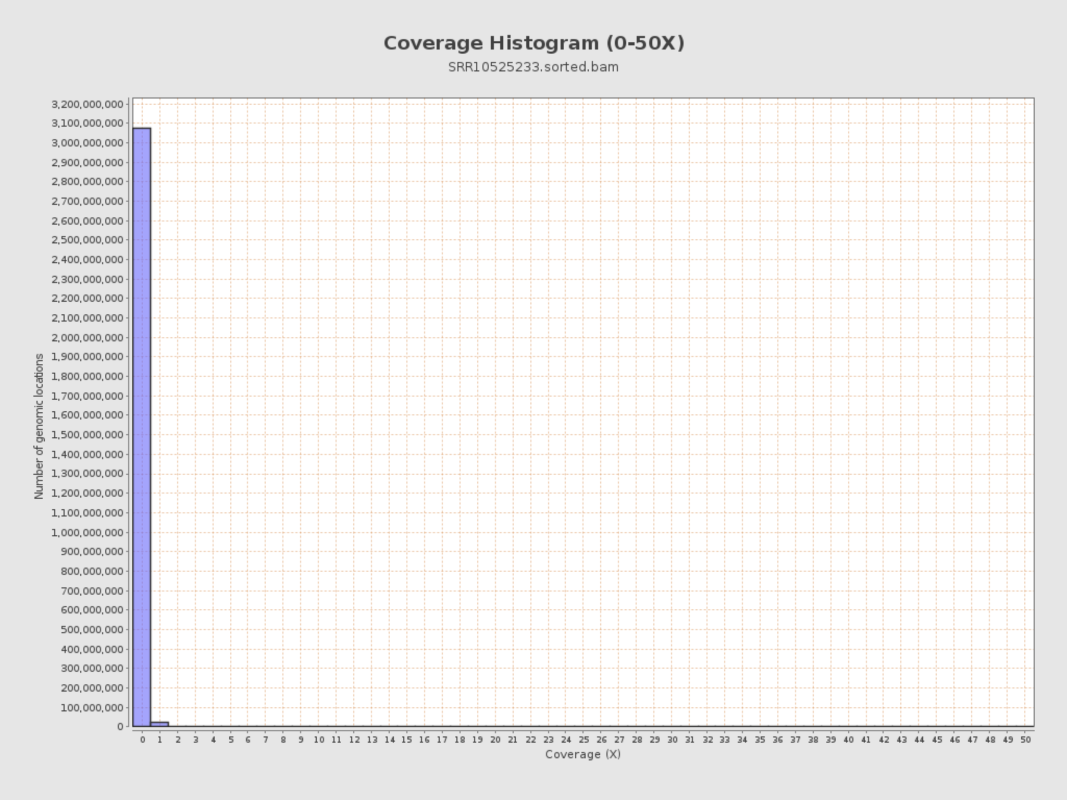
3. Results : Coverage across reference



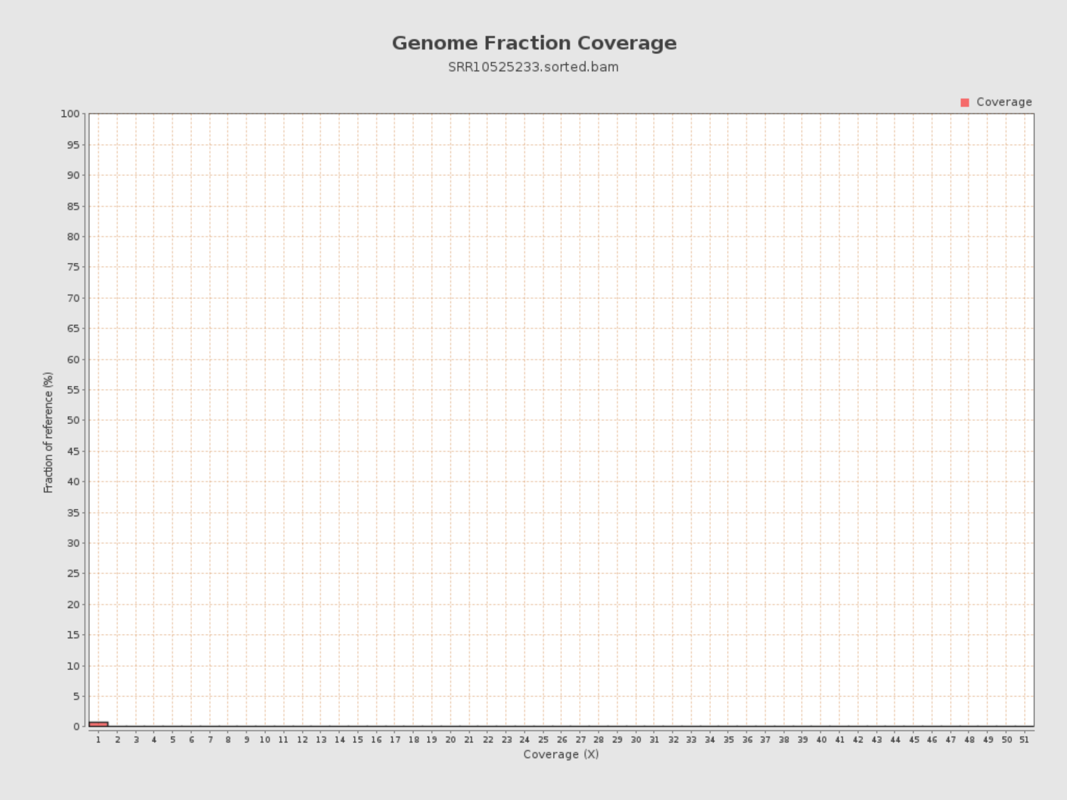
4. Results : Coverage Histogram



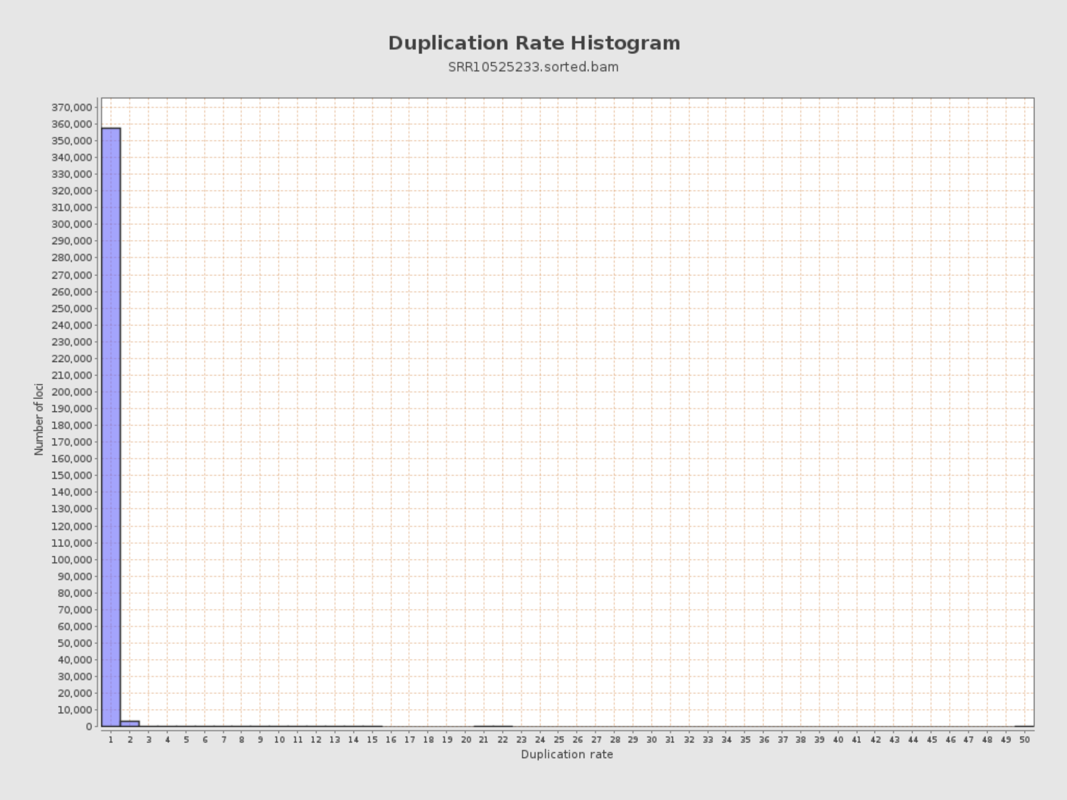
5. Results : Coverage Histogram (0-50X)



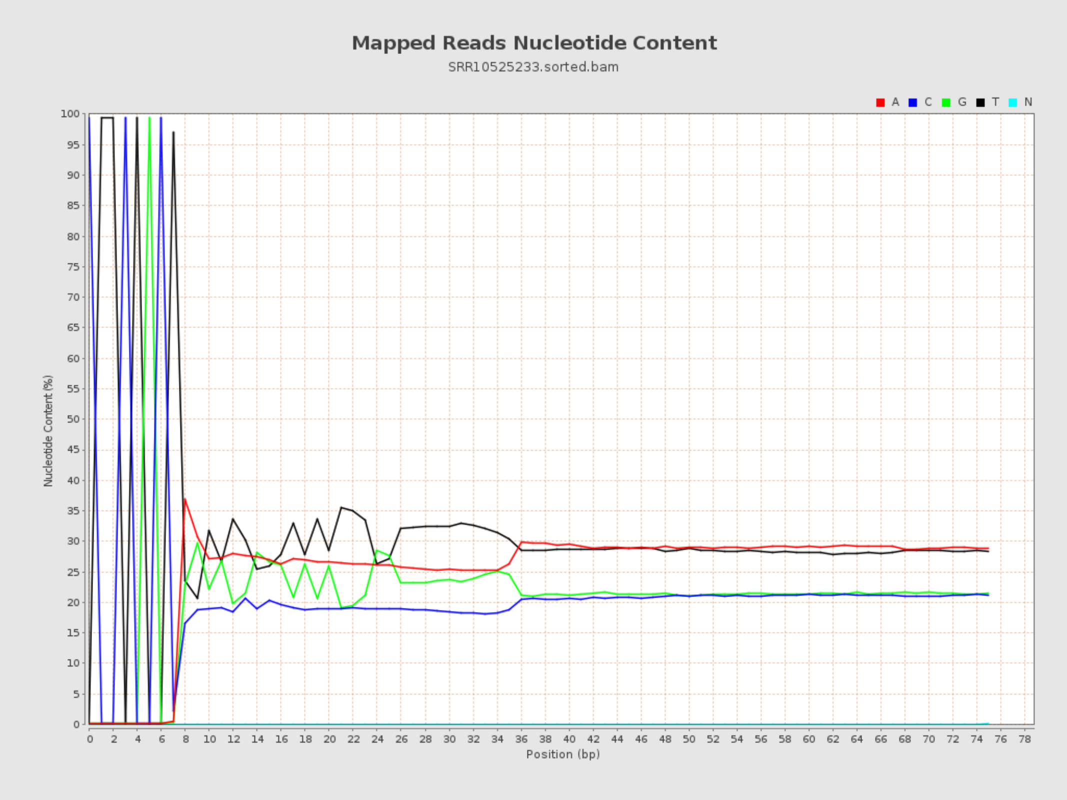
6. Results : Genome Fraction Coverage



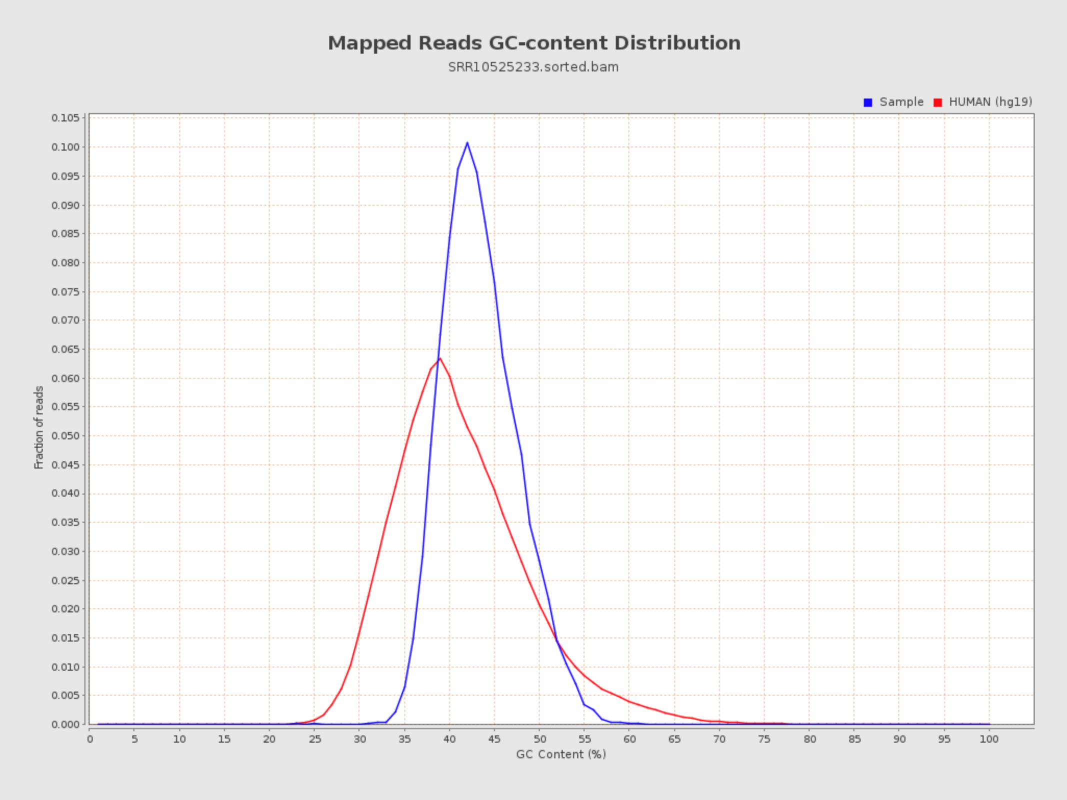
7. Results : Duplication Rate Histogram



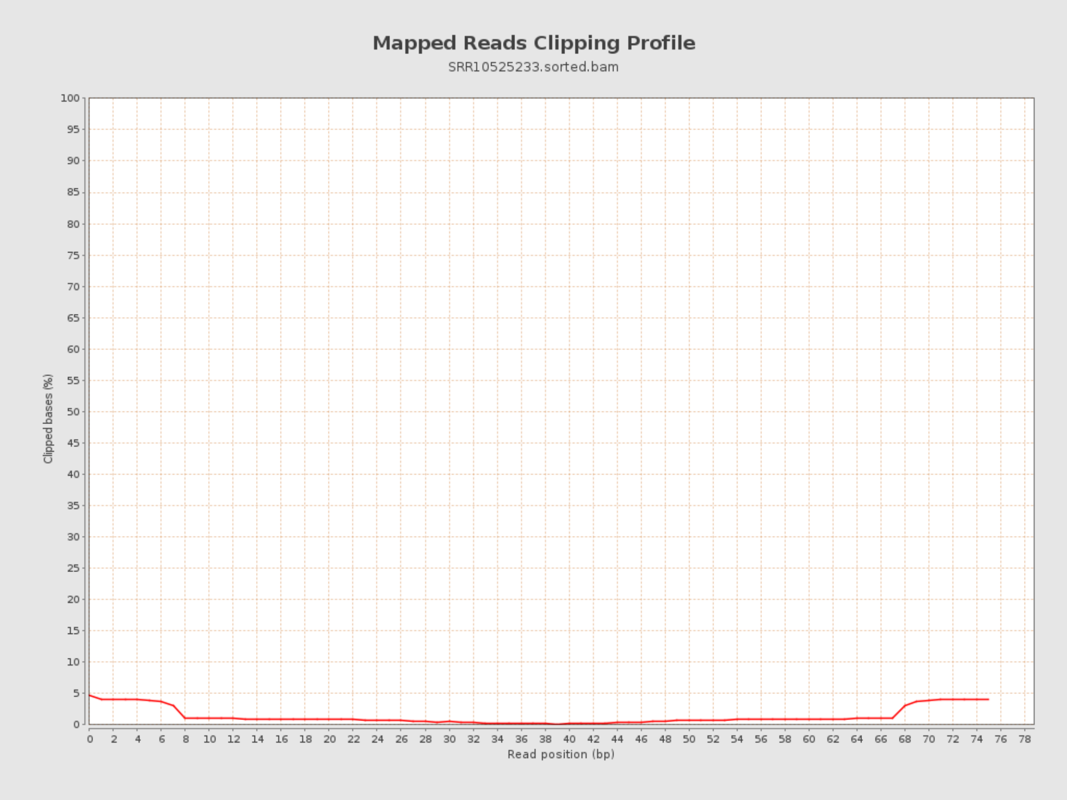
8. Results : Mapped Reads Nucleotide Content



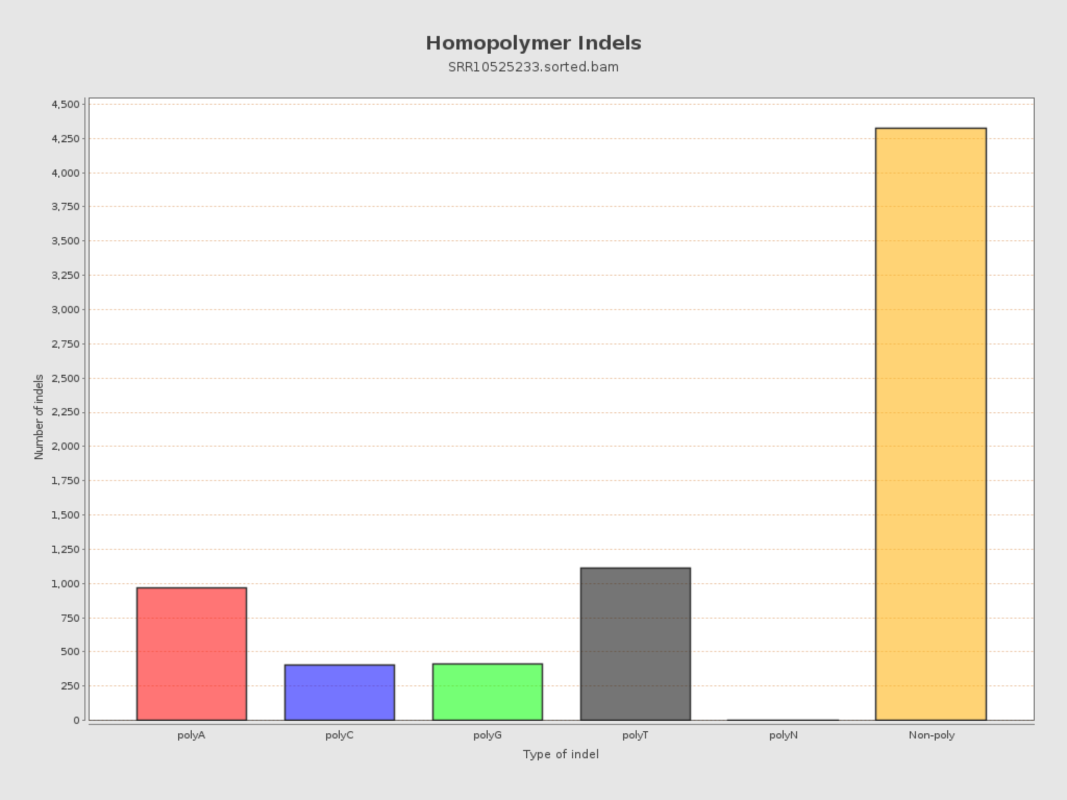
9. Results : Mapped Reads GC-content Distribution



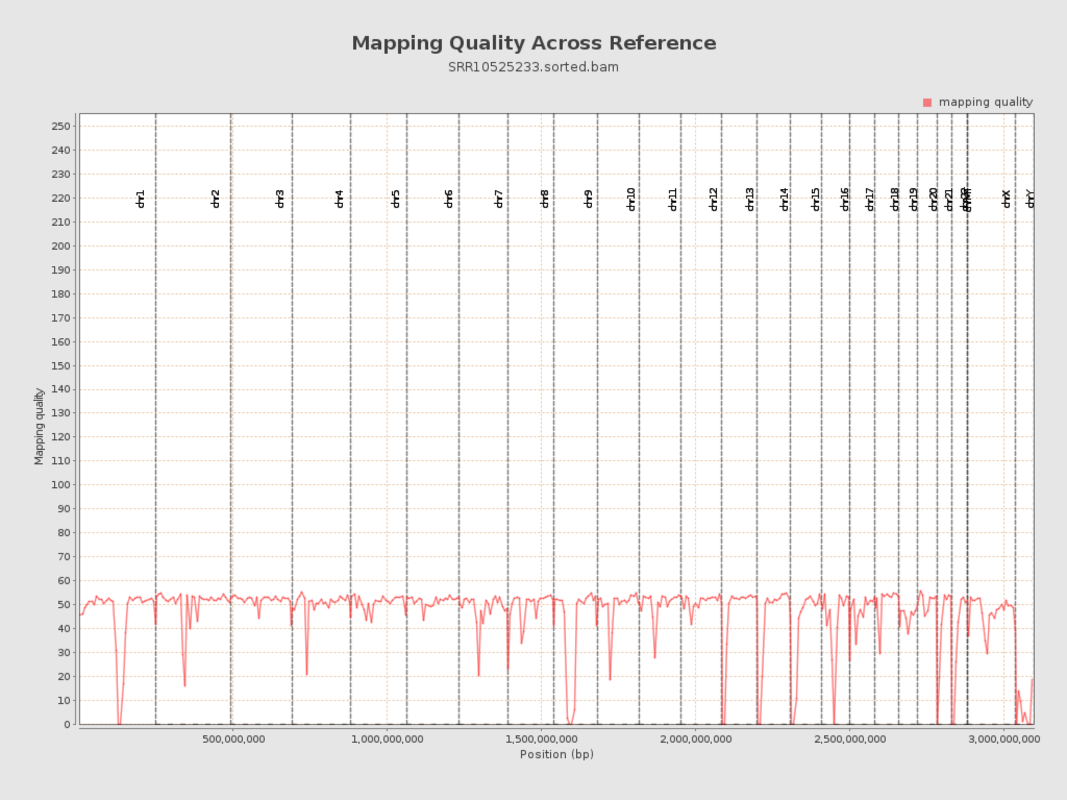
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram