Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:47:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525080.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_SRR10525080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:47:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	491,307
Mapped reads	391,667 / 79.72%
Unmapped reads	99,640 / 20.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,802 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	11,649 / 2.37%
Duplication rate	2.55%
Clipped reads	393,268 / 80.05%

2.2. ACGT Content

Number/percentage of A's	5,861,234 / 25.33%
Number/percentage of C's	4,556,103 / 19.69%
Number/percentage of T's	7,154,511 / 30.92%
Number/percentage of G's	5,562,445 / 24.04%
Number/percentage of N's	2,503 / 0.01%
GC Percentage	43.73%

2.3. Coverage

Mean	0.0075

Standard Deviation	0.1037

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

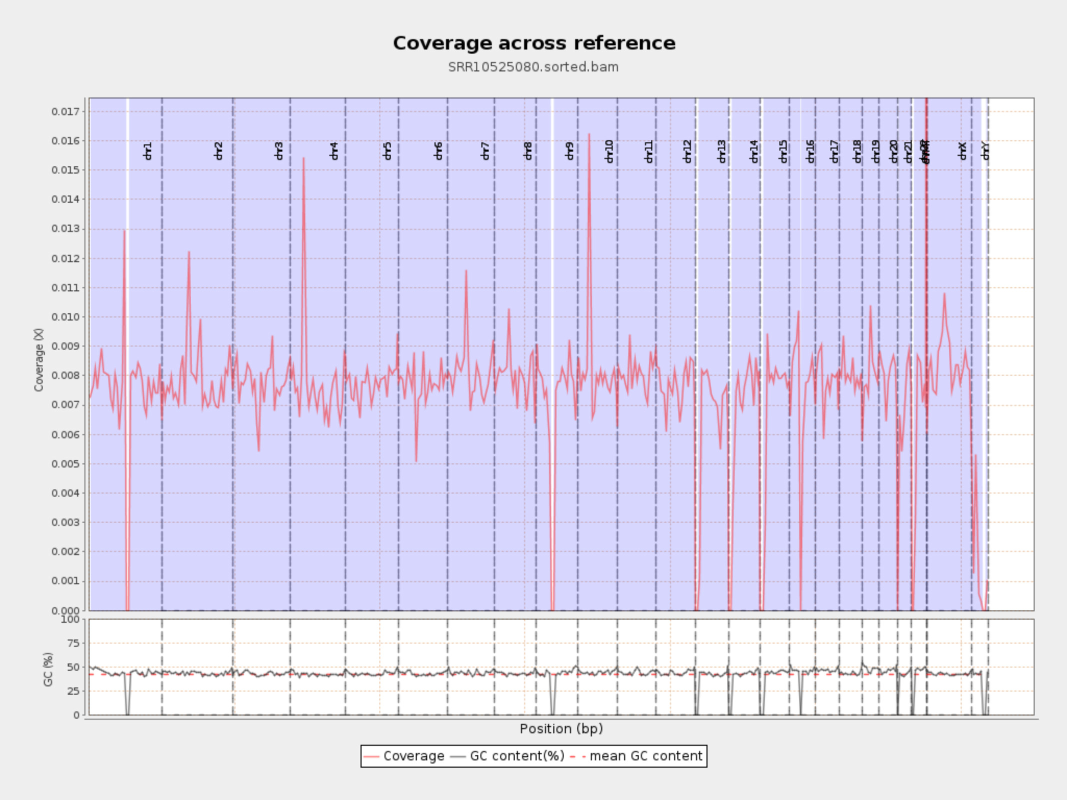
General error rate	0.48%
Mismatches	108,385
Insertions	1,432
Mapped reads with at least one insertion	0.36%
Deletions	4,392
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.2%

2.6. Chromosome stats

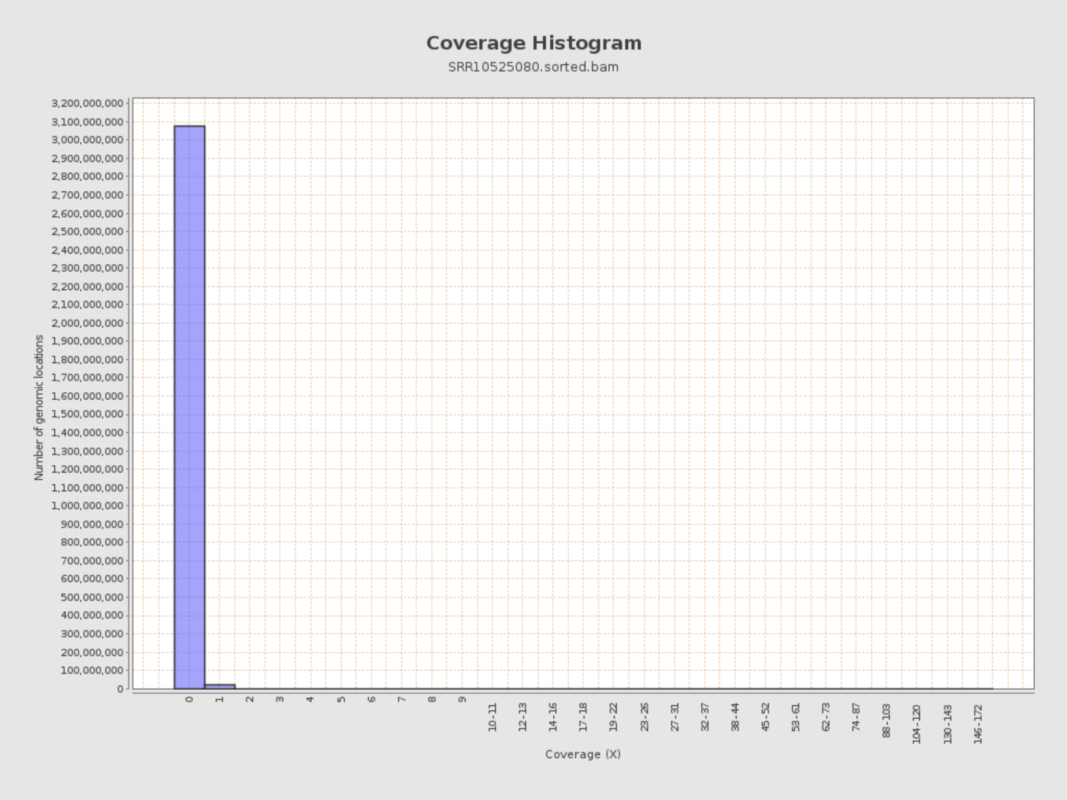
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1845748	0.0074	0.1497
chr2	243199373	1930731	0.0079	0.1161
chr3	198022430	1530178	0.0077	0.0915
chr4	191154276	1470703	0.0077	0.0984
chr5	180915260	1397842	0.0077	0.0921
chr6	171115067	1316277	0.0077	0.0936
chr7	159138663	1292536	0.0081	0.1098

chr8	146364022	1171026	0.008	0.1075
chr9	141213431	969432	0.0069	0.0928
chr10	135534747	1117943	0.0082	0.1152
chr11	135006516	1084598	0.008	0.0996
chr12	133851895	1026787	0.0077	0.0924
chr13	115169878	709671	0.0062	0.082
chr14	107349540	696056	0.0065	0.085
chr15	102531392	670911	0.0065	0.0842
chr16	90354753	674551	0.0075	0.0924
chr17	81195210	633795	0.0078	0.0936
chr18	78077248	630637	0.0081	0.124
chr19	59128983	479423	0.0081	0.1233
chr20	63025520	505574	0.008	0.0941
chr21	48129895	314137	0.0065	0.0885
chr22	51304566	283967	0.0055	0.0778
chrMT	16571	2434	0.1469	0.3952
chrX	155270560	1305512	0.0084	0.0984
chrY	59373566	83500	0.0014	0.0577

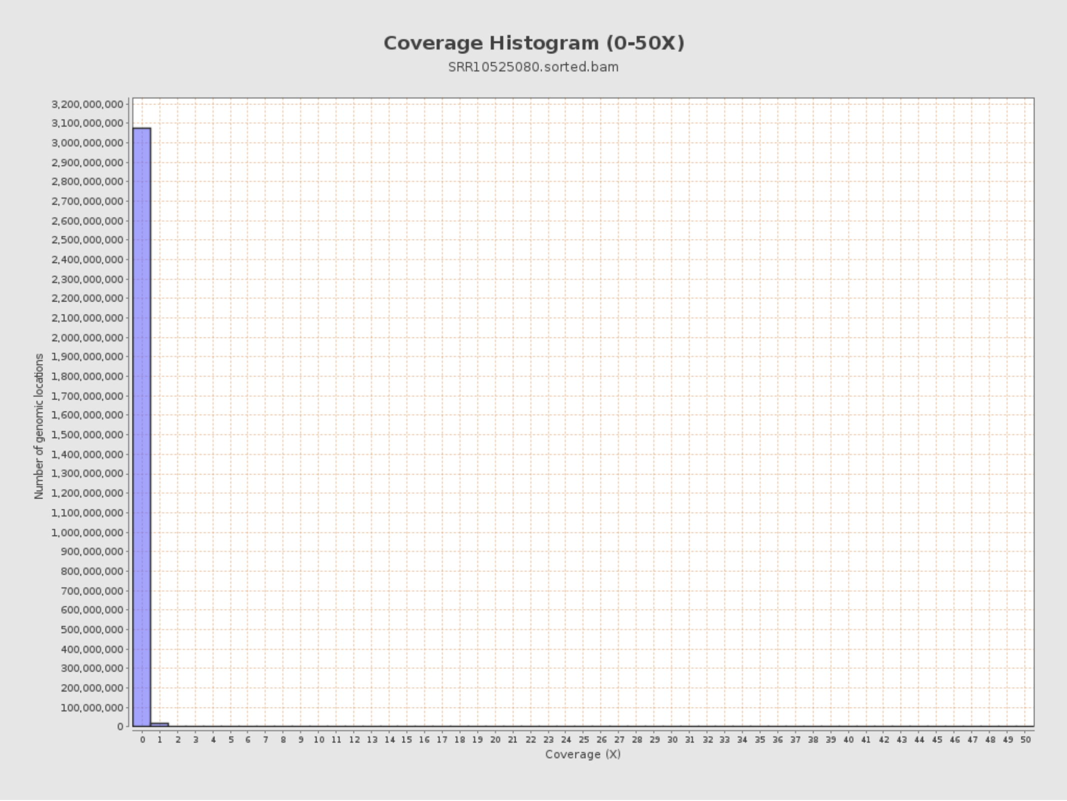
3. Results : Coverage across reference



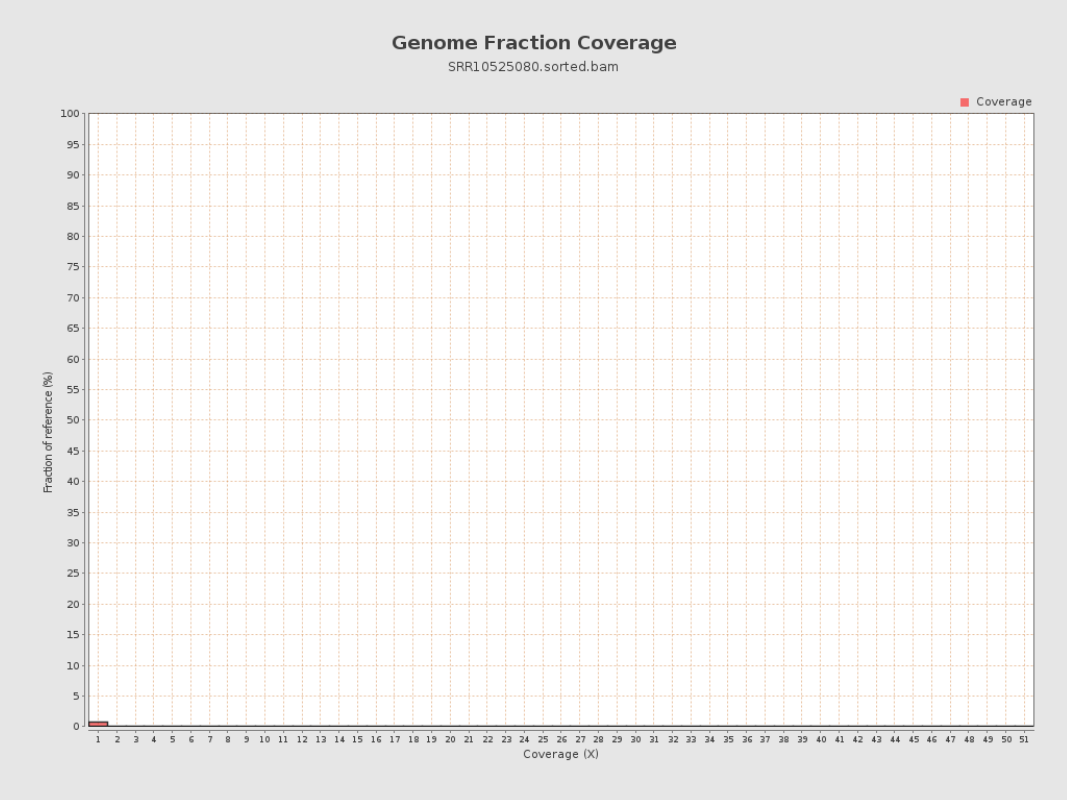
4. Results : Coverage Histogram



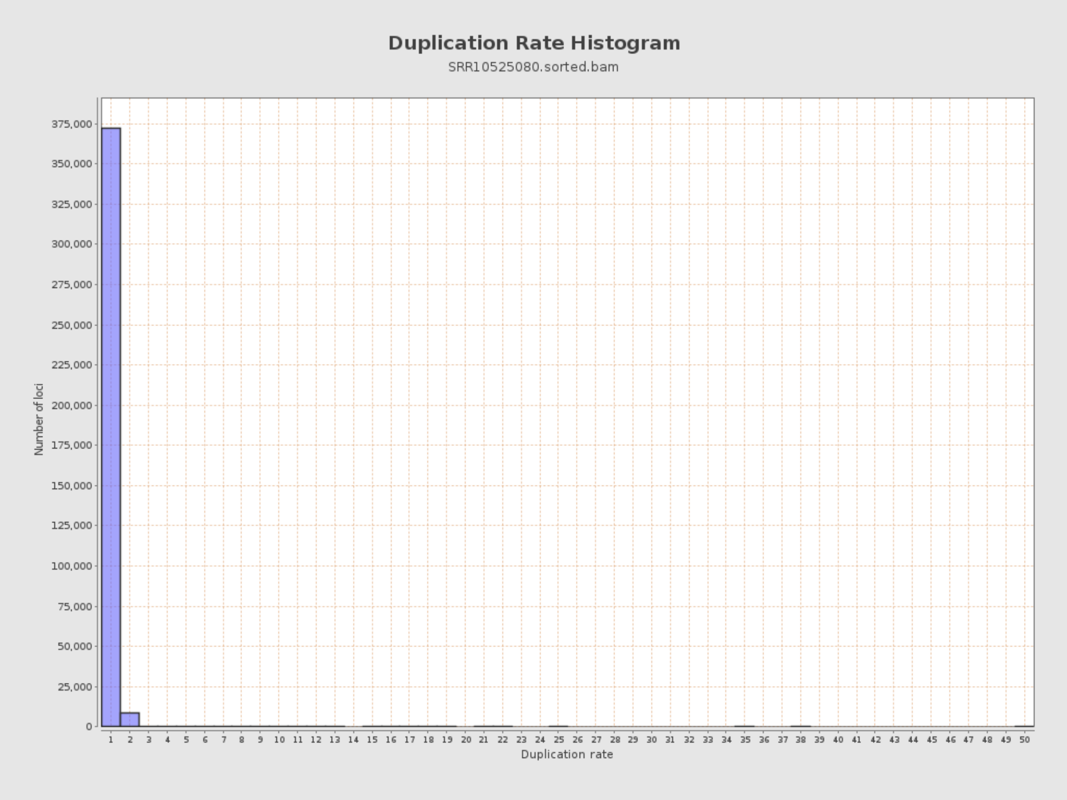
5. Results : Coverage Histogram (0-50X)



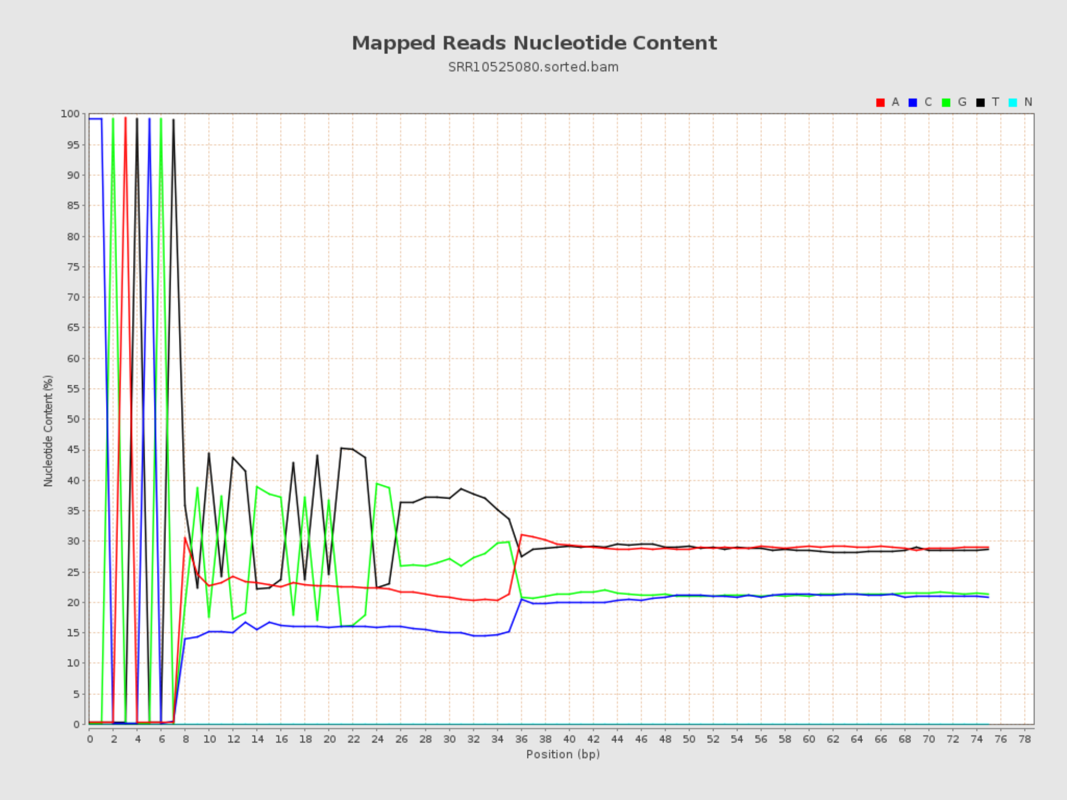
6. Results : Genome Fraction Coverage



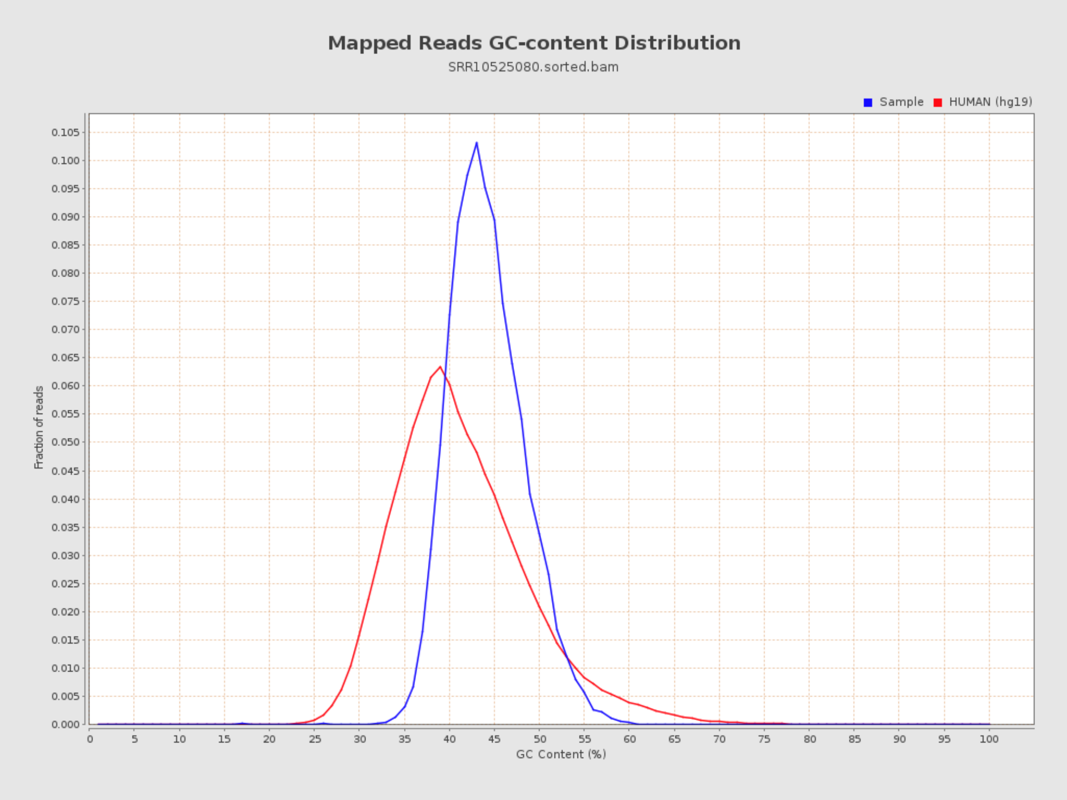
7. Results : Duplication Rate Histogram



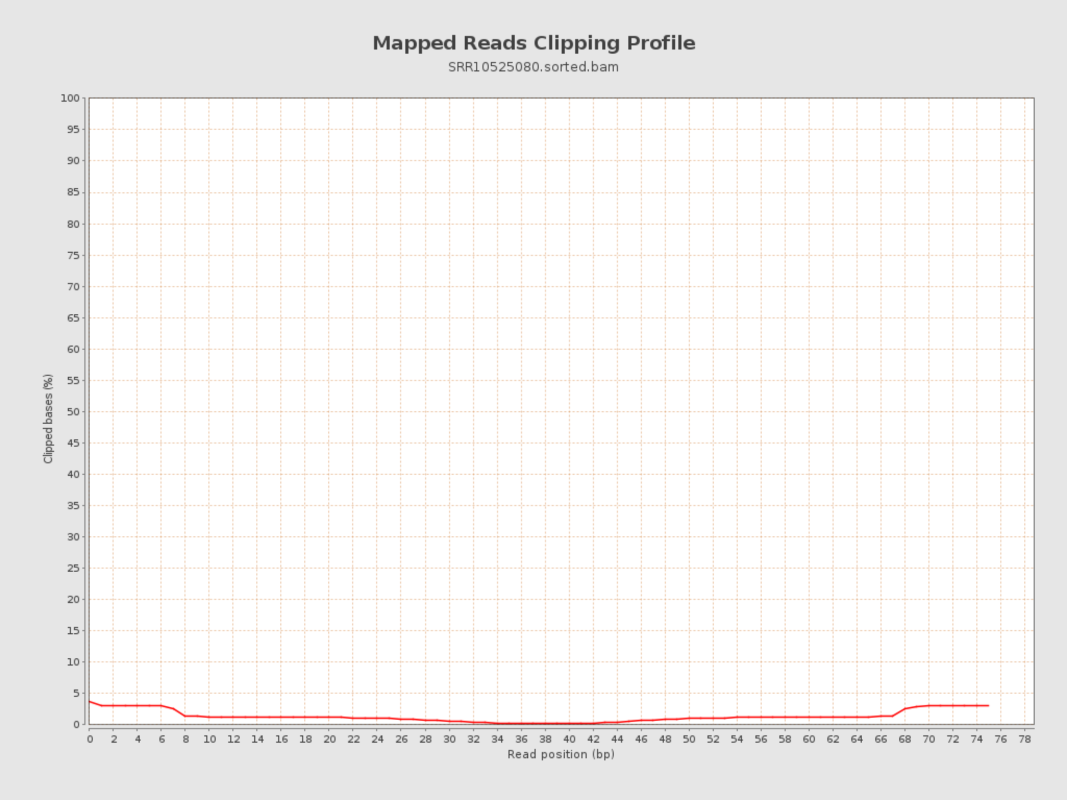
8. Results : Mapped Reads Nucleotide Content



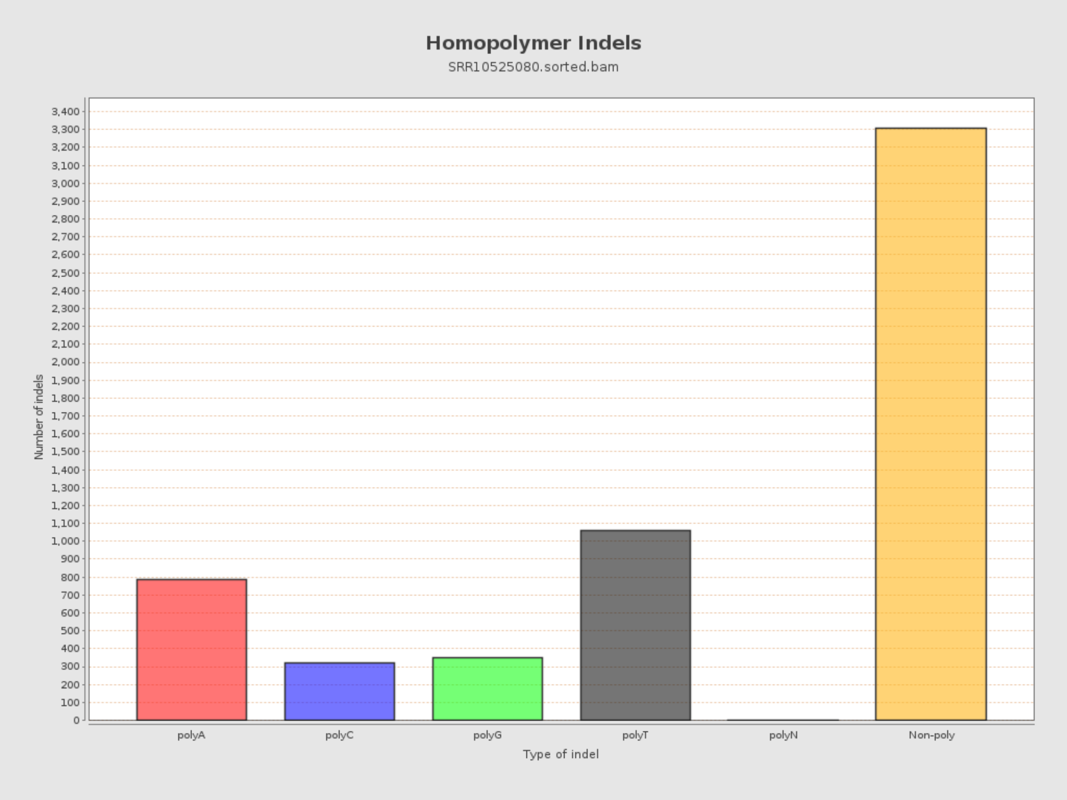
9. Results : Mapped Reads GC-content Distribution



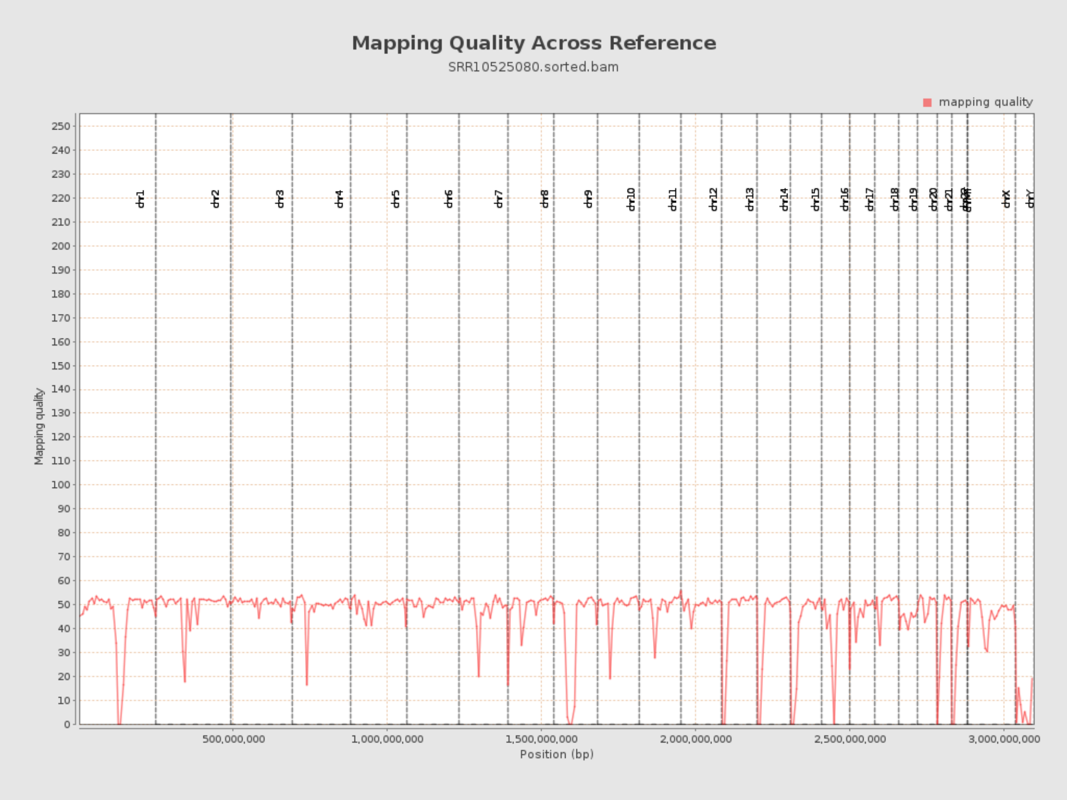
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram