Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:35:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083626.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_SRR3083626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083626.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:35:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,220,211
Mapped reads	1,125,310 / 92.22%
Unmapped reads	94,901 / 7.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,394 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	39,912 / 3.27%
Duplication rate	2.52%
Clipped reads	440,078 / 36.07%

2.2. ACGT Content

Number/percentage of A's	21,267,905 / 27.85%
Number/percentage of C's	14,108,353 / 18.48%
Number/percentage of T's	23,989,814 / 31.42%
Number/percentage of G's	16,985,242 / 22.24%
Number/percentage of N's	4,269 / 0.01%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.3283

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

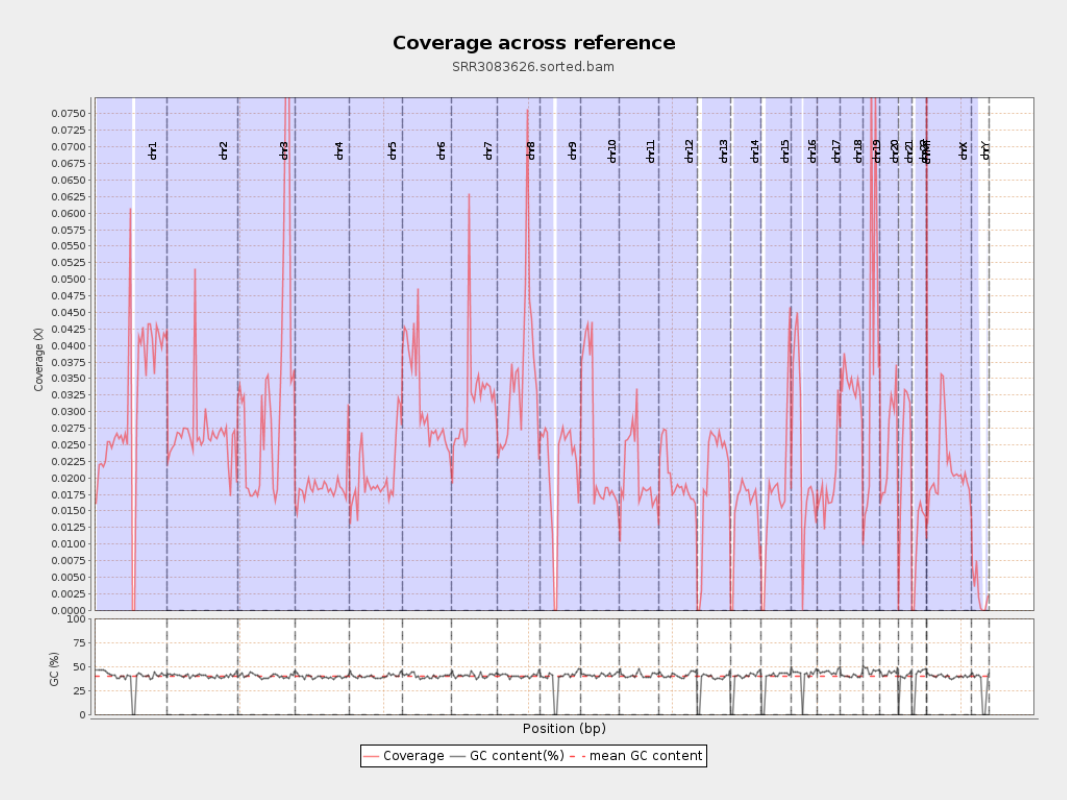
General error rate	0.76%
Mismatches	570,673
Insertions	6,190
Mapped reads with at least one insertion	0.55%
Deletions	19,858
Mapped reads with at least one deletion	1.75%
Homopolymer indels	47.39%

2.6. Chromosome stats

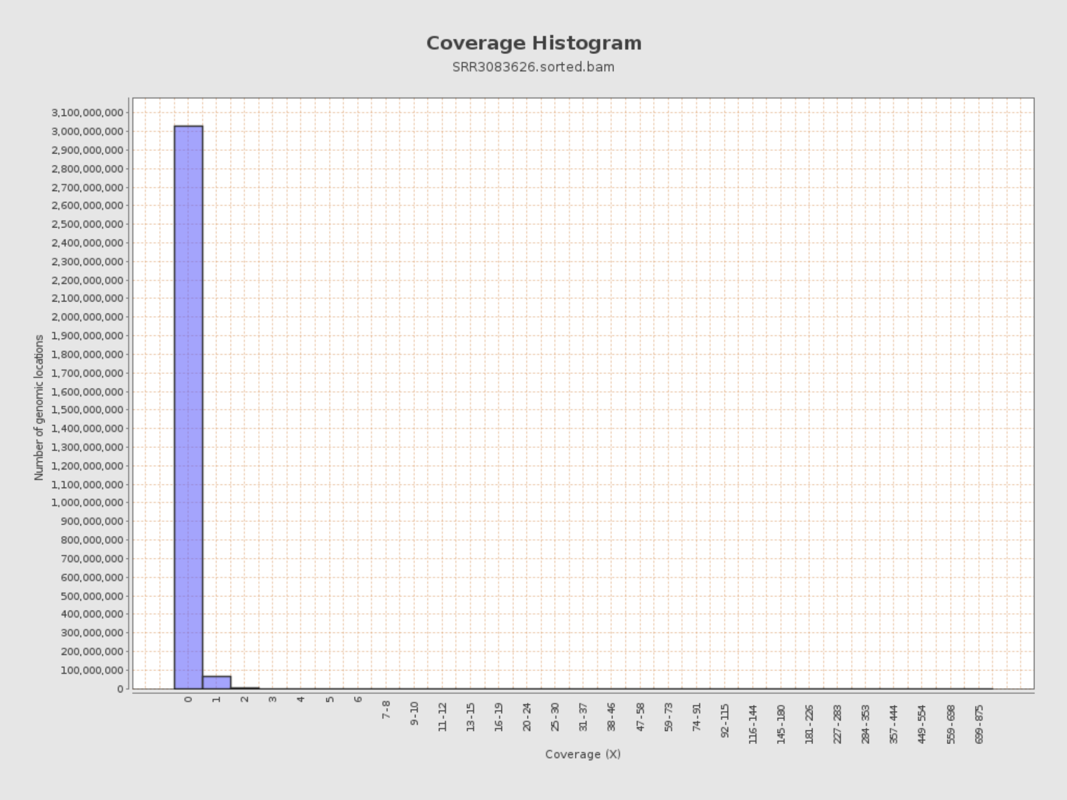
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7667195	0.0308	0.7705
chr2	243199373	6440513	0.0265	0.351
chr3	198022430	6361199	0.0321	0.1926
chr4	191154276	3558386	0.0186	0.1491
chr5	180915260	3657723	0.0202	0.1526
chr6	171115067	5410431	0.0316	0.2329
chr7	159138663	5044458	0.0317	0.5047

chr8	146364022	5203531	0.0356	0.3288
chr9	141213431	3027516	0.0214	0.2248
chr10	135534747	3407277	0.0251	0.2395
chr11	135006516	2804115	0.0208	0.2173
chr12	133851895	2669686	0.0199	0.1532
chr13	115169878	2297760	0.02	0.1515
chr14	107349540	1553996	0.0145	0.1351
chr15	102531392	1867343	0.0182	0.1492
chr16	90354753	2064151	0.0228	0.1739
chr17	81195210	1558363	0.0192	0.1571
chr18	78077248	2656925	0.034	0.4483
chr19	59128983	2297392	0.0389	0.4805
chr20	63025520	1588014	0.0252	0.1737
chr21	48129895	1196601	0.0249	0.1702
chr22	51304566	553146	0.0108	0.1098
chrMT	16571	1480	0.0893	0.3097
chrX	155270560	3344061	0.0215	0.1706
chrY	59373566	156158	0.0026	0.0694

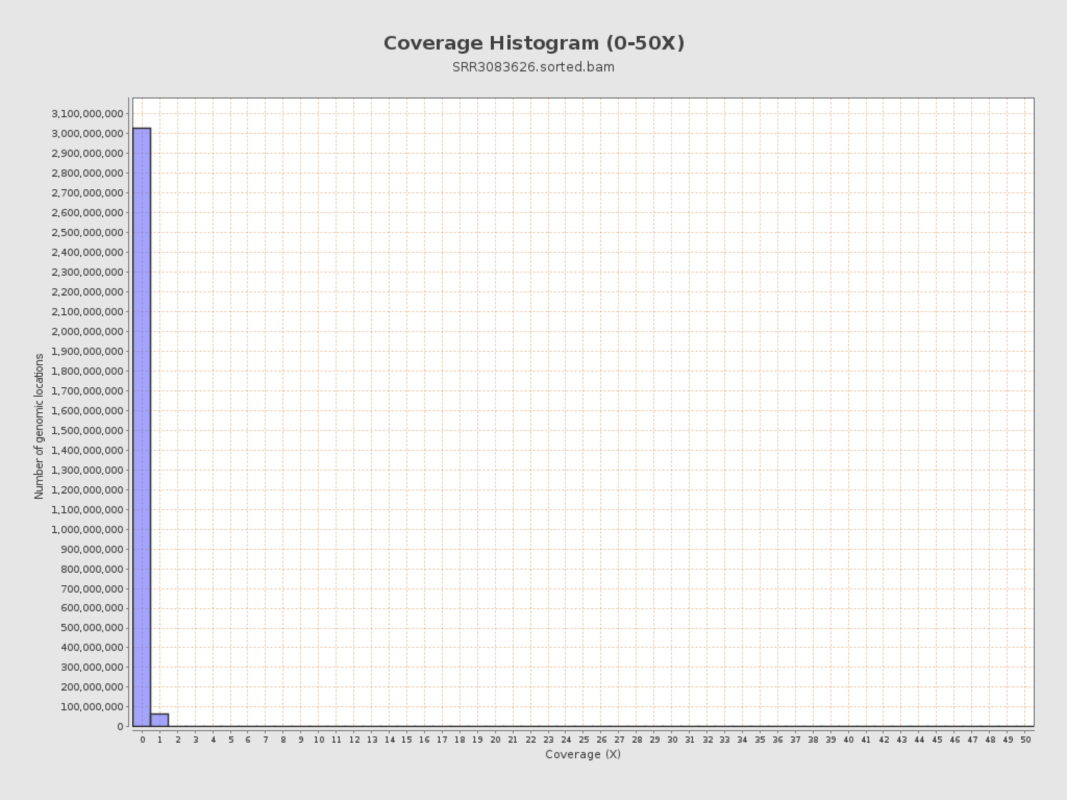
3. Results : Coverage across reference



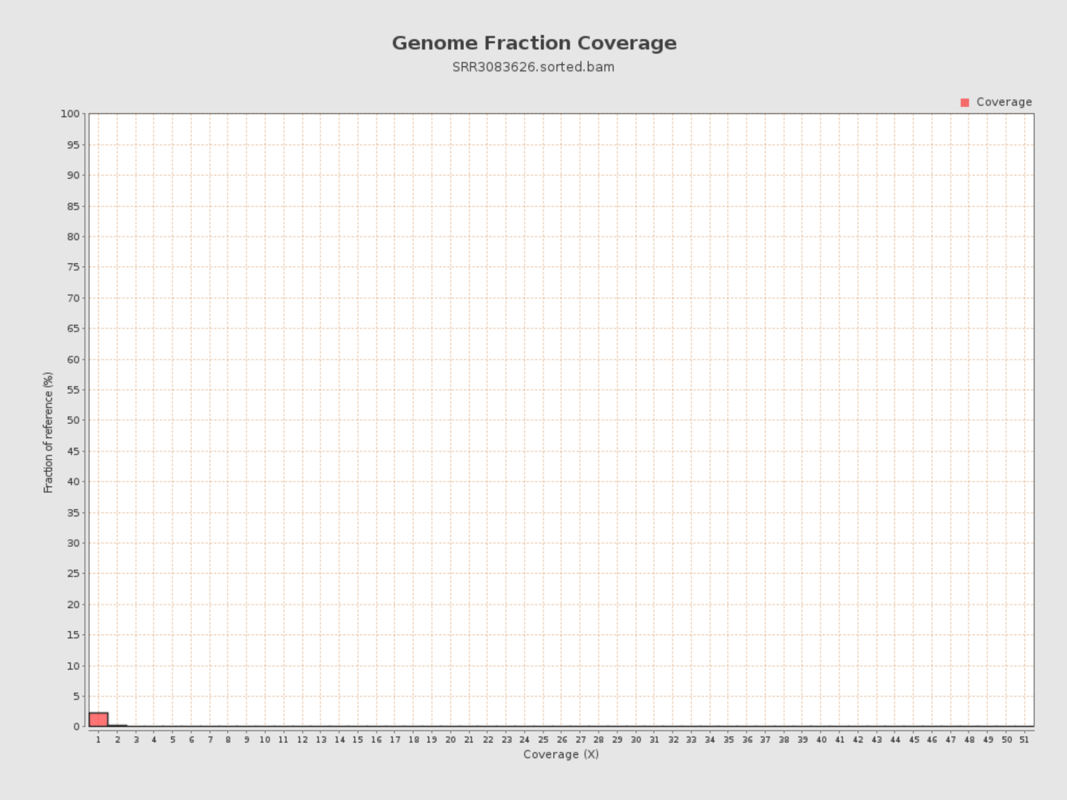
4. Results : Coverage Histogram



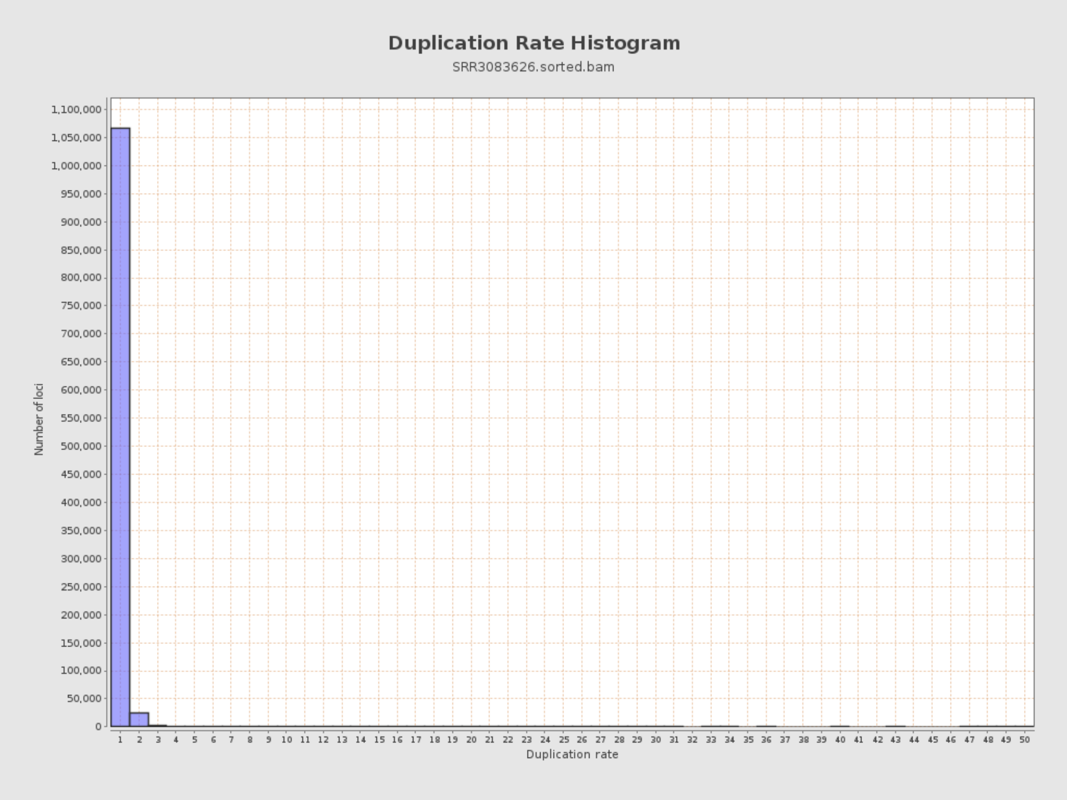
5. Results : Coverage Histogram (0-50X)



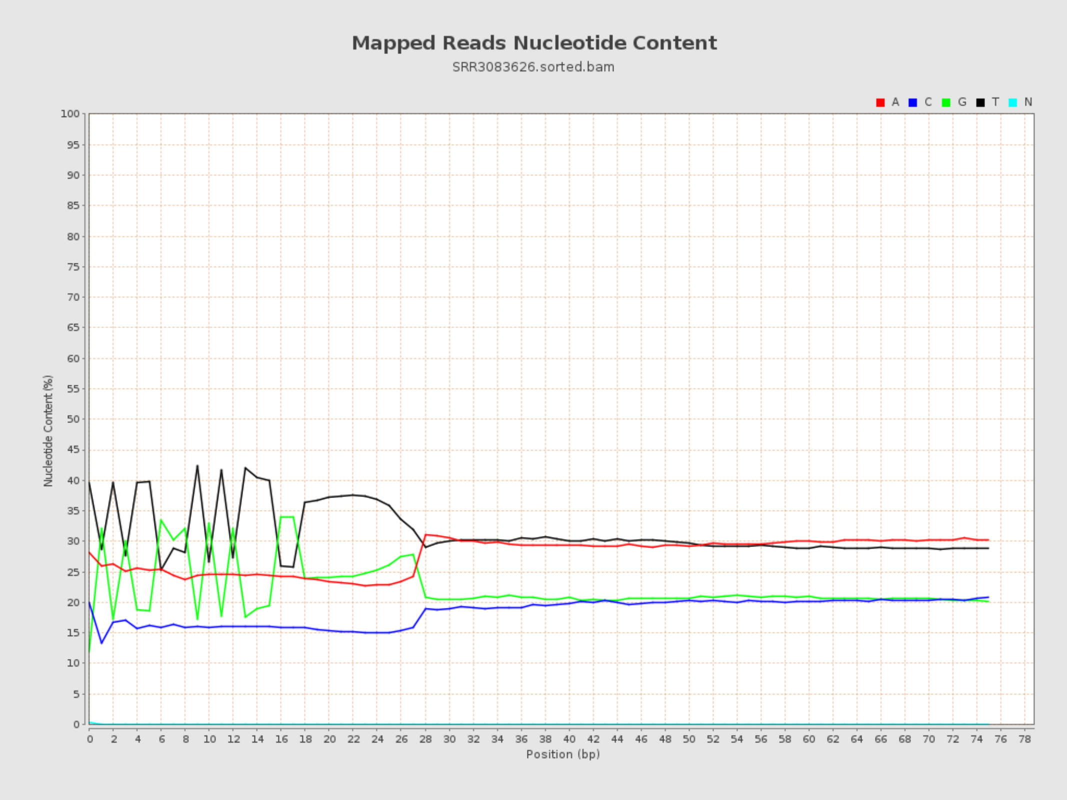
6. Results : Genome Fraction Coverage



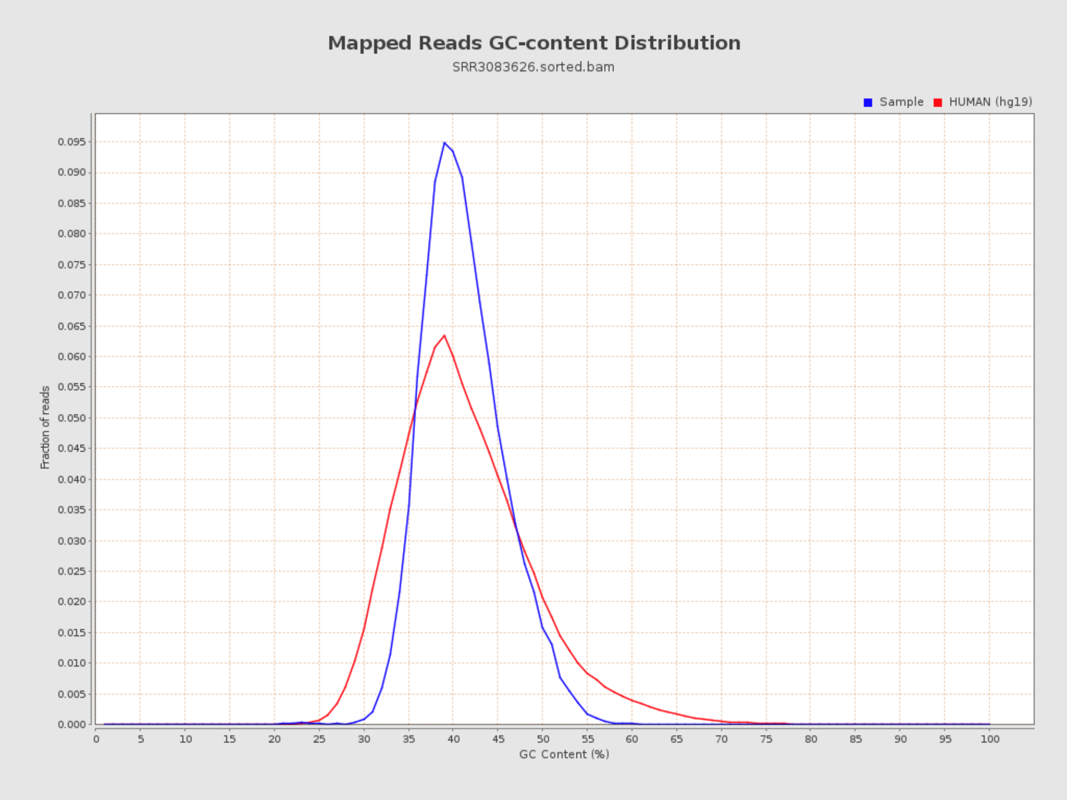
7. Results : Duplication Rate Histogram



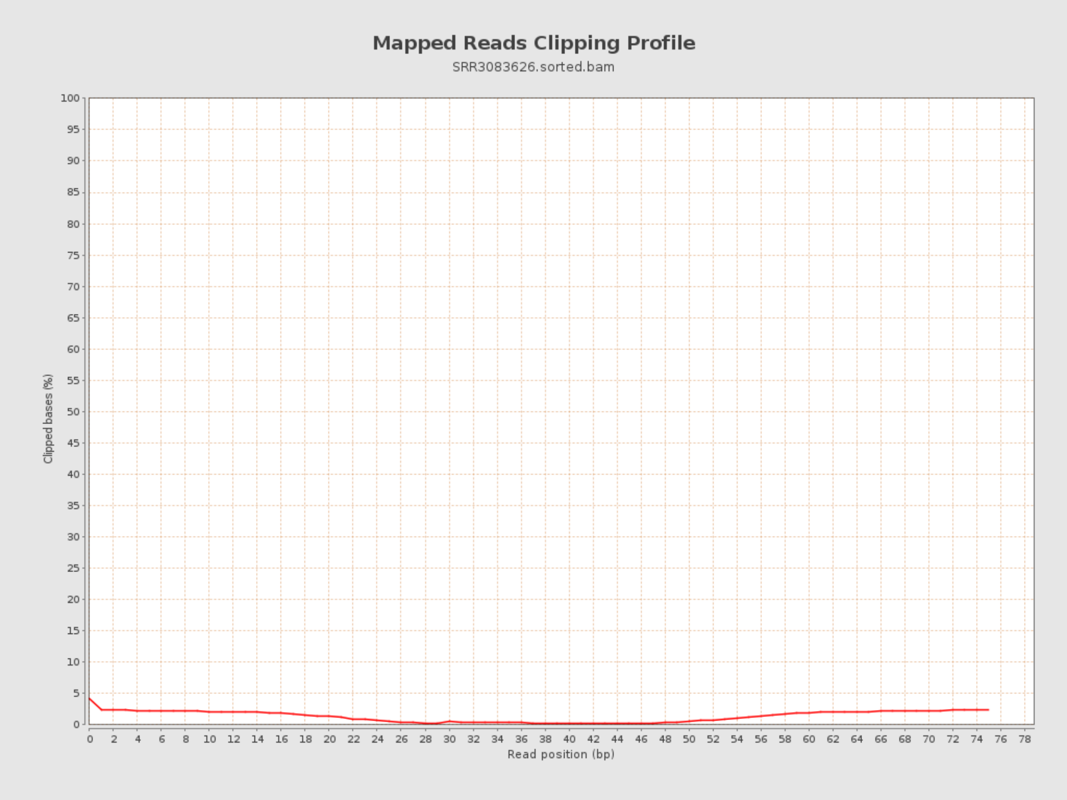
8. Results : Mapped Reads Nucleotide Content



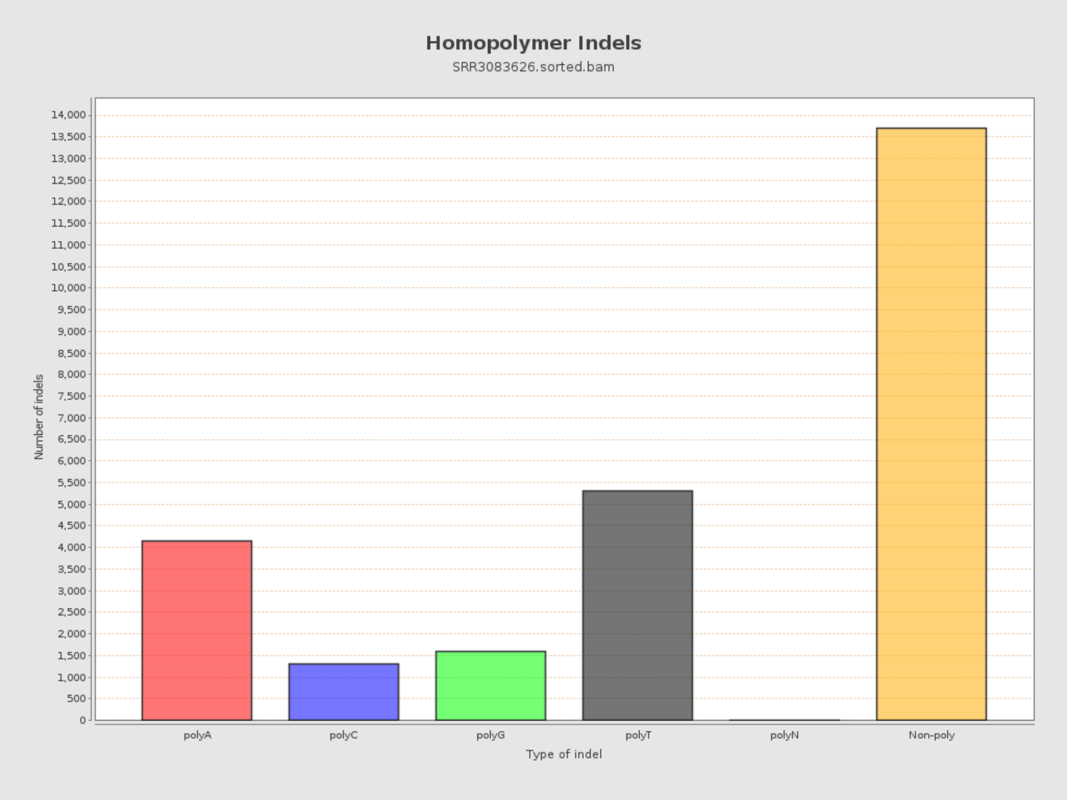
9. Results : Mapped Reads GC-content Distribution



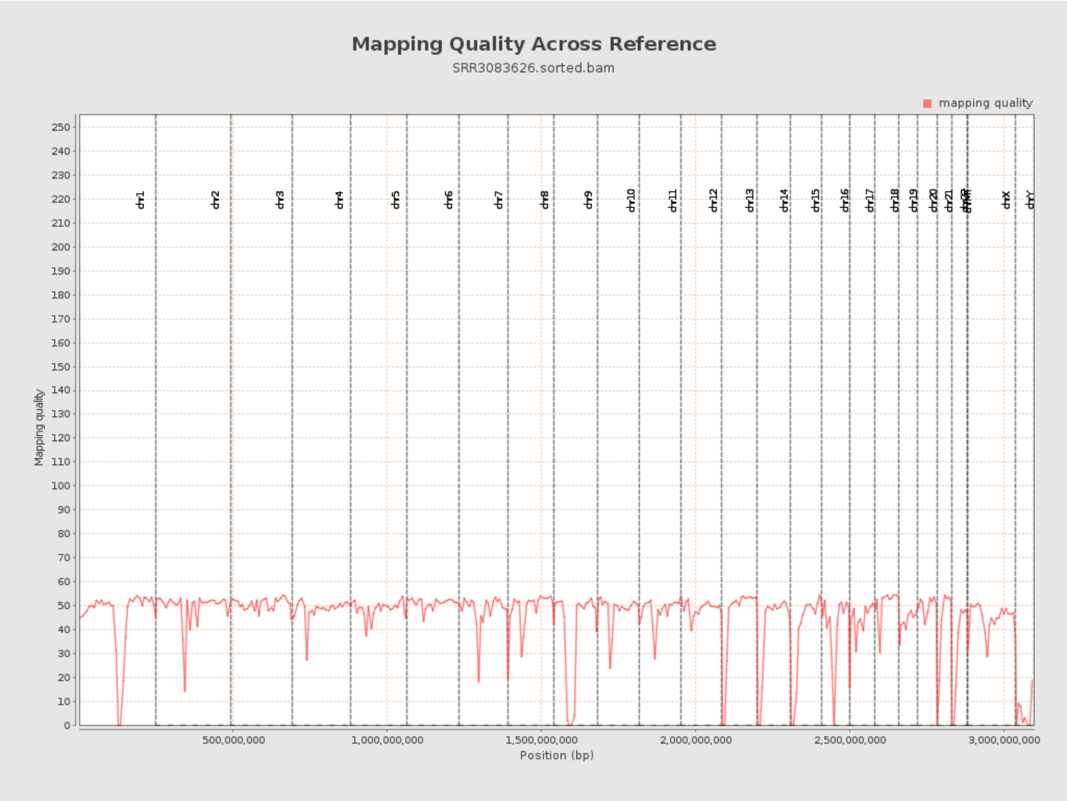
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram