Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:41:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063582.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_SRR6063582 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063582.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:41:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063582.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,096,989
Mapped reads	2,730,805 / 88.18%
Unmapped reads	366,184 / 11.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,855 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	186,921 / 6.04%
Duplication rate	5.25%
Clipped reads	1,313,667 / 42.42%

2.2. ACGT Content

Number/percentage of A's	51,213,979 / 28.32%
Number/percentage of C's	34,059,588 / 18.83%
Number/percentage of T's	56,515,599 / 31.25%
Number/percentage of G's	39,051,199 / 21.59%
Number/percentage of N's	3,779 / 0%
GC Percentage	40.43%

2.3. Coverage

Mean	0.0584

Standard Deviation	0.6326

2.4. Mapping Quality

Mean Mapping Quality	39

2.5. Mismatches and indels

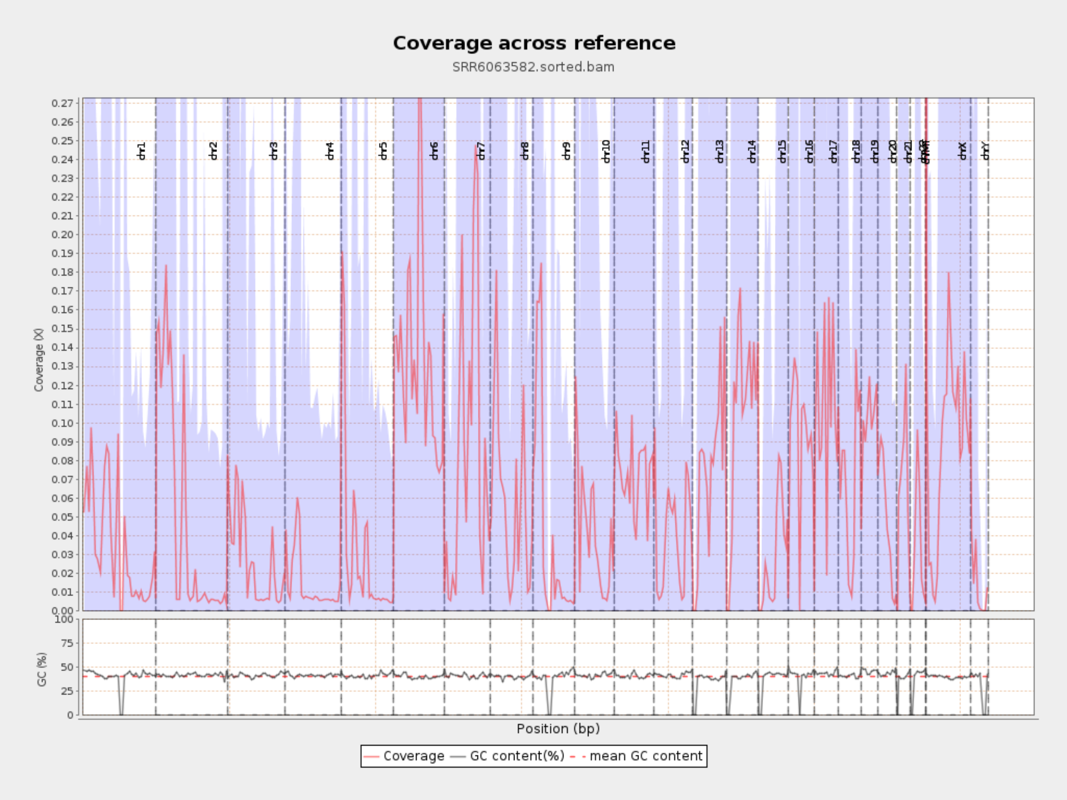
General error rate	0.81%
Mismatches	1,437,949
Insertions	14,084
Mapped reads with at least one insertion	0.51%
Deletions	46,817
Mapped reads with at least one deletion	1.7%
Homopolymer indels	46.18%

2.6. Chromosome stats

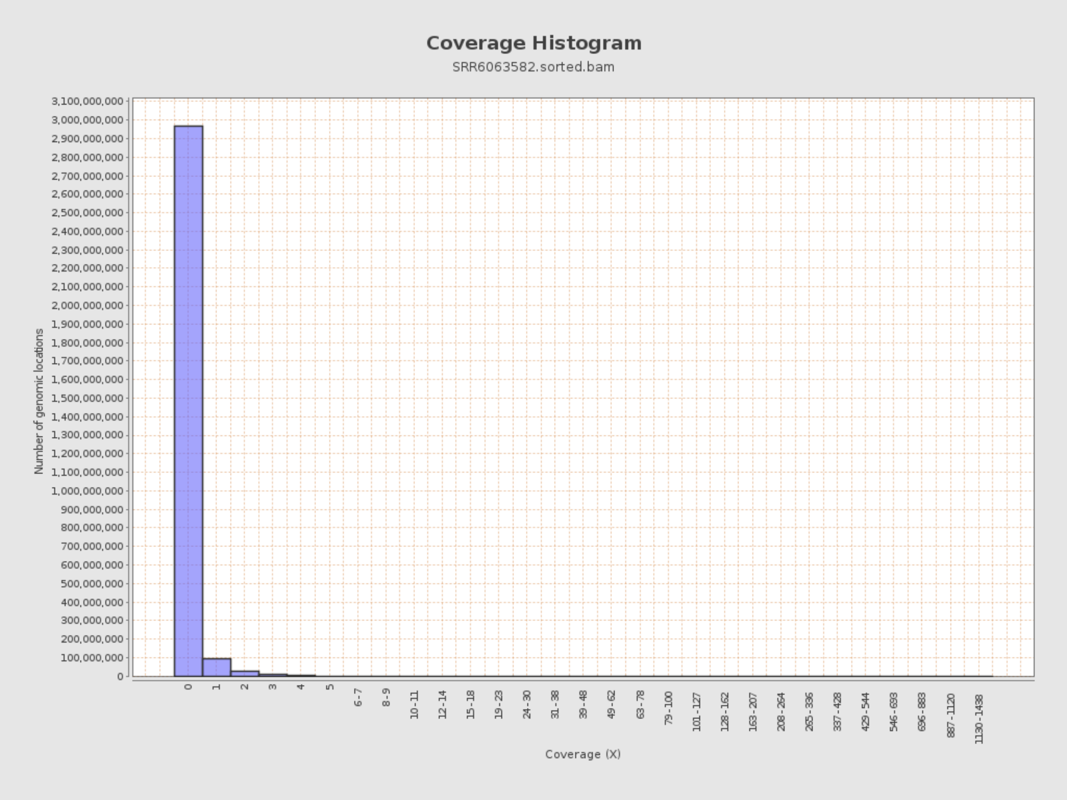
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8644868	0.0347	1.2294
chr2	243199373	12068006	0.0496	0.6264
chr3	198022430	5251700	0.0265	0.2152
chr4	191154276	2652354	0.0139	0.1893
chr5	180915260	5659437	0.0313	0.2438
chr6	171115067	23548324	0.1376	0.6421
chr7	159138663	13907074	0.0874	1.2389

chr8	146364022	8560056	0.0585	0.8833
chr9	141213431	5848868	0.0414	0.3758
chr10	135534747	5578644	0.0412	0.3259
chr11	135006516	9906987	0.0734	0.4031
chr12	133851895	5352044	0.04	0.2668
chr13	115169878	8671521	0.0753	0.3613
chr14	107349540	11357117	0.1058	0.4342
chr15	102531392	2926243	0.0285	0.2275
chr16	90354753	8115981	0.0898	0.4694
chr17	81195210	8993373	0.1108	0.4856
chr18	78077248	5445455	0.0697	0.6942
chr19	59128983	6016432	0.1018	1.1078
chr20	63025520	3001707	0.0476	0.3012
chr21	48129895	3167076	0.0658	0.3513
chr22	51304566	1682105	0.0328	0.233
chrMT	16571	33024	1.9929	1.9503
chrX	155270560	13775865	0.0887	0.4589
chrY	59373566	757104	0.0128	0.279

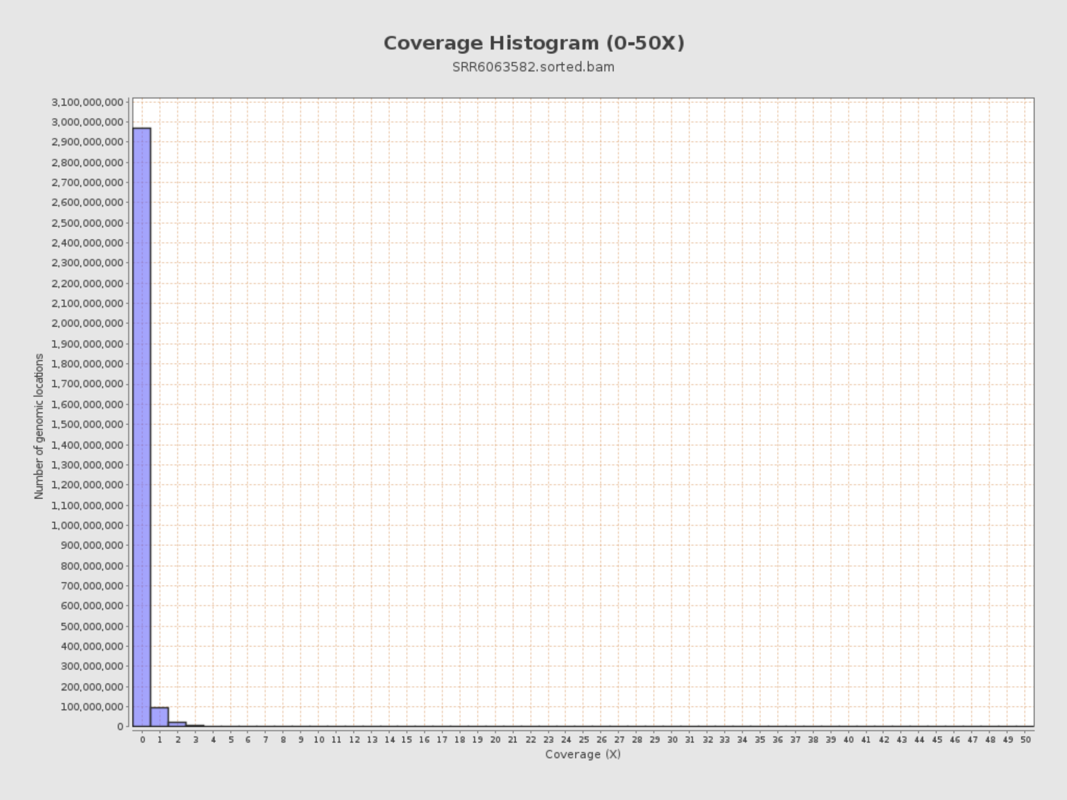
3. Results : Coverage across reference



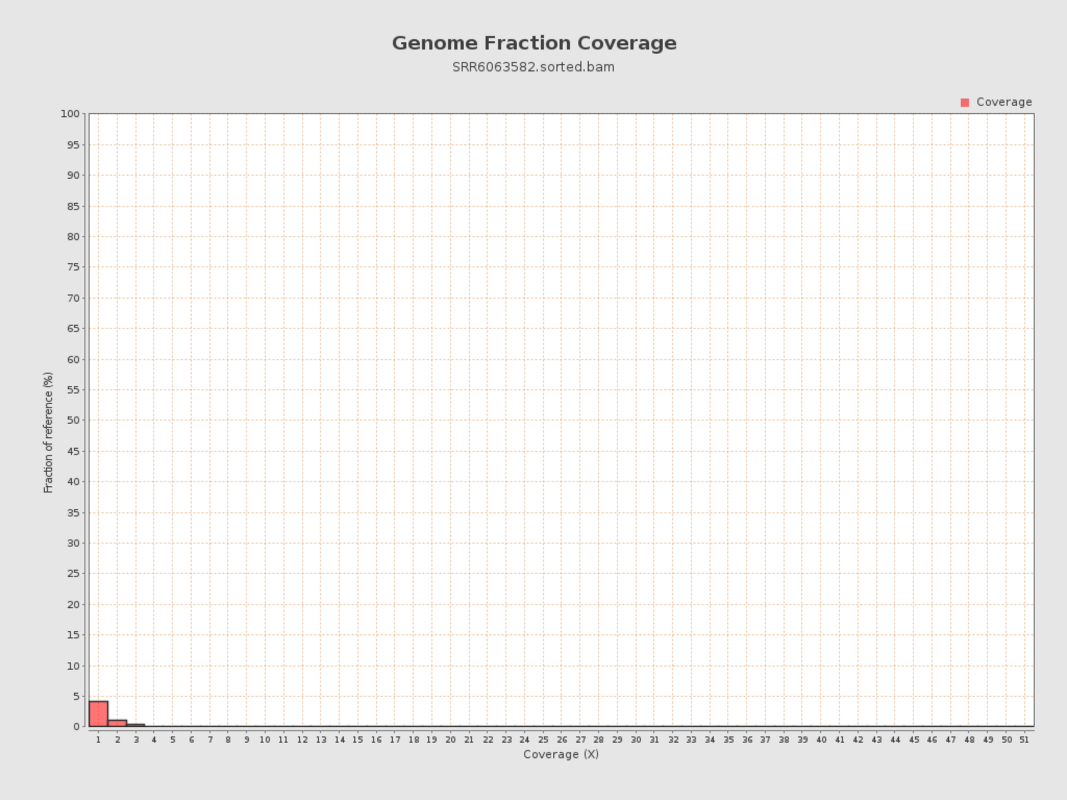
4. Results : Coverage Histogram



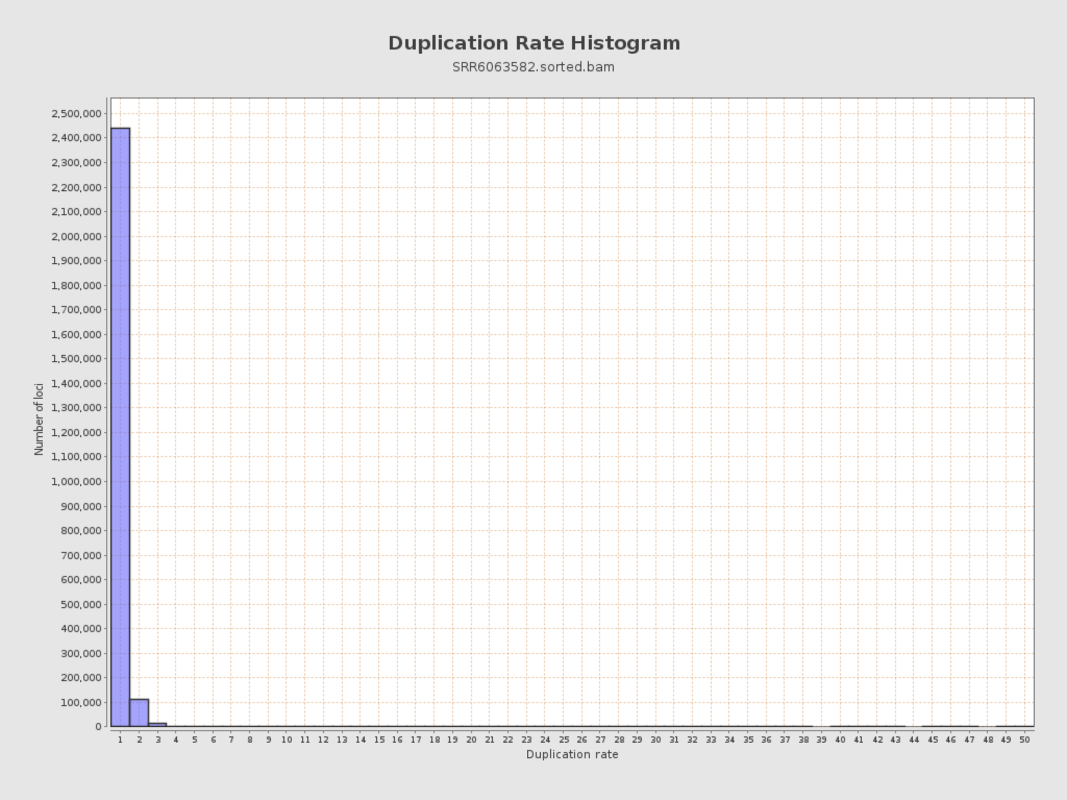
5. Results : Coverage Histogram (0-50X)



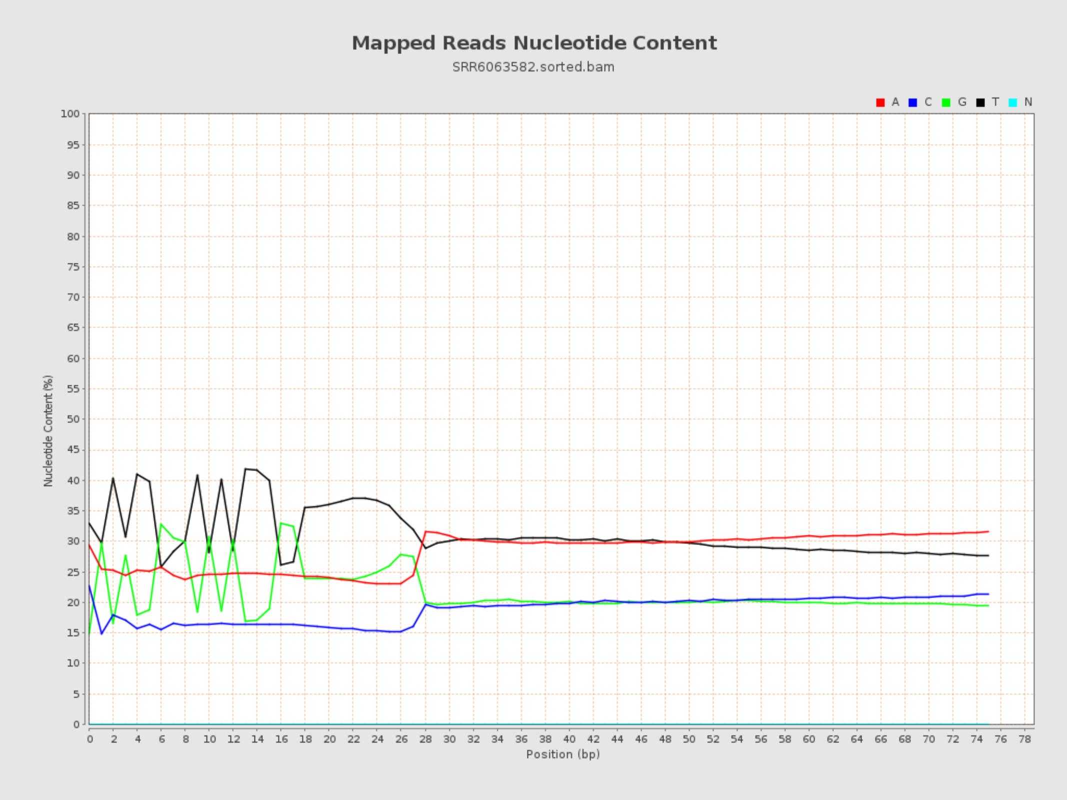
6. Results : Genome Fraction Coverage



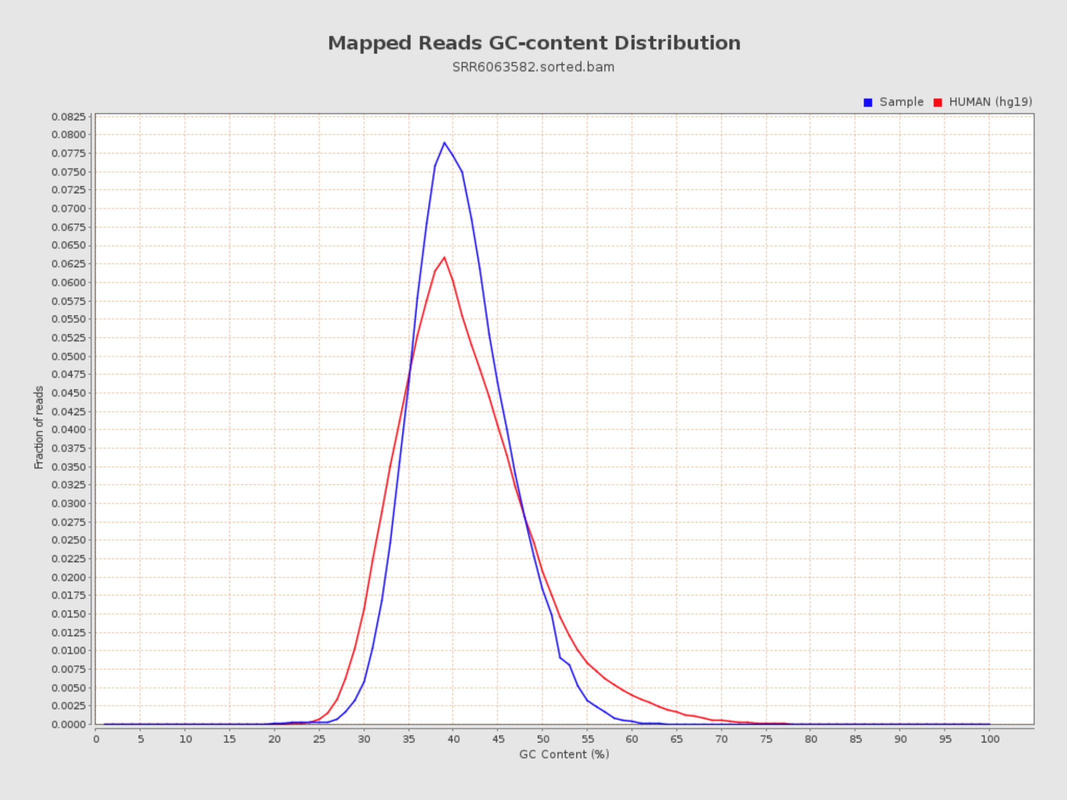
7. Results : Duplication Rate Histogram



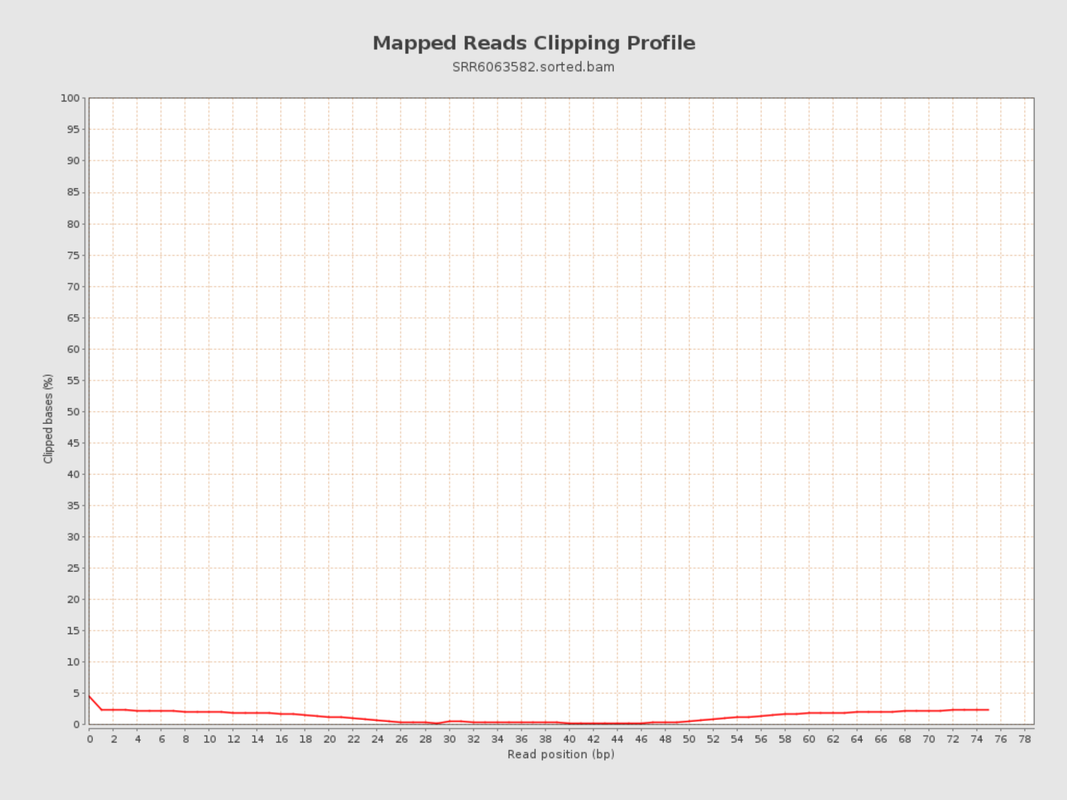
8. Results : Mapped Reads Nucleotide Content



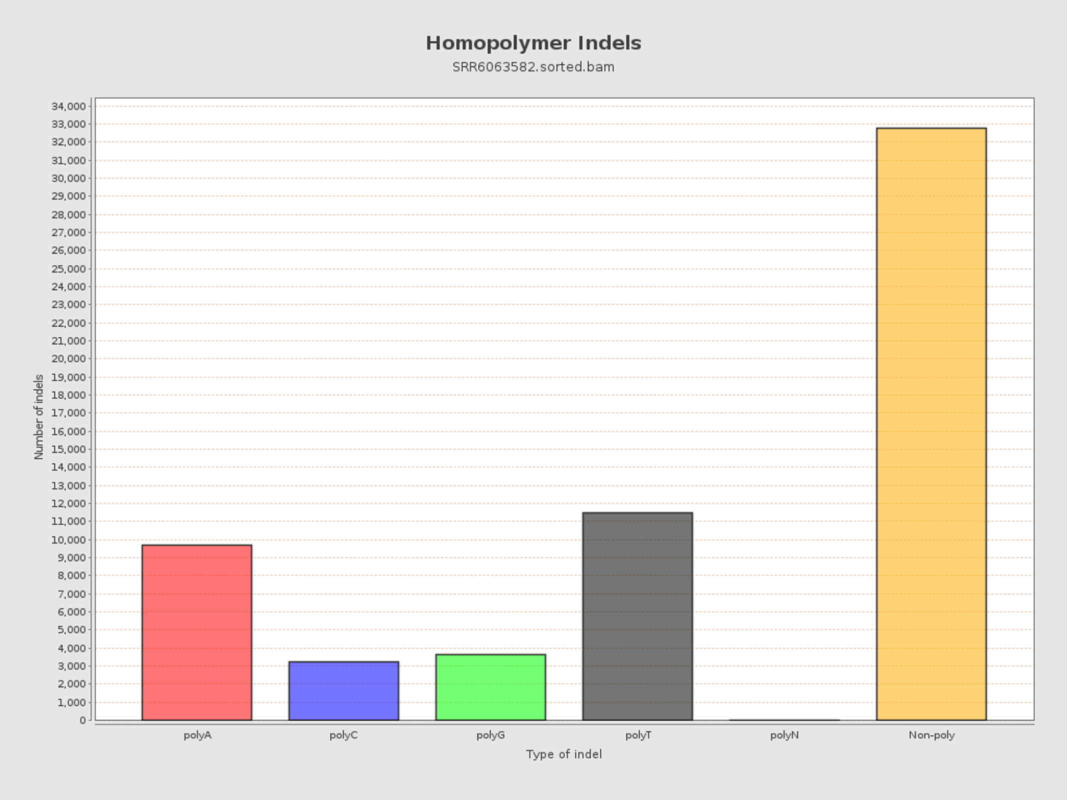
9. Results : Mapped Reads GC-content Distribution



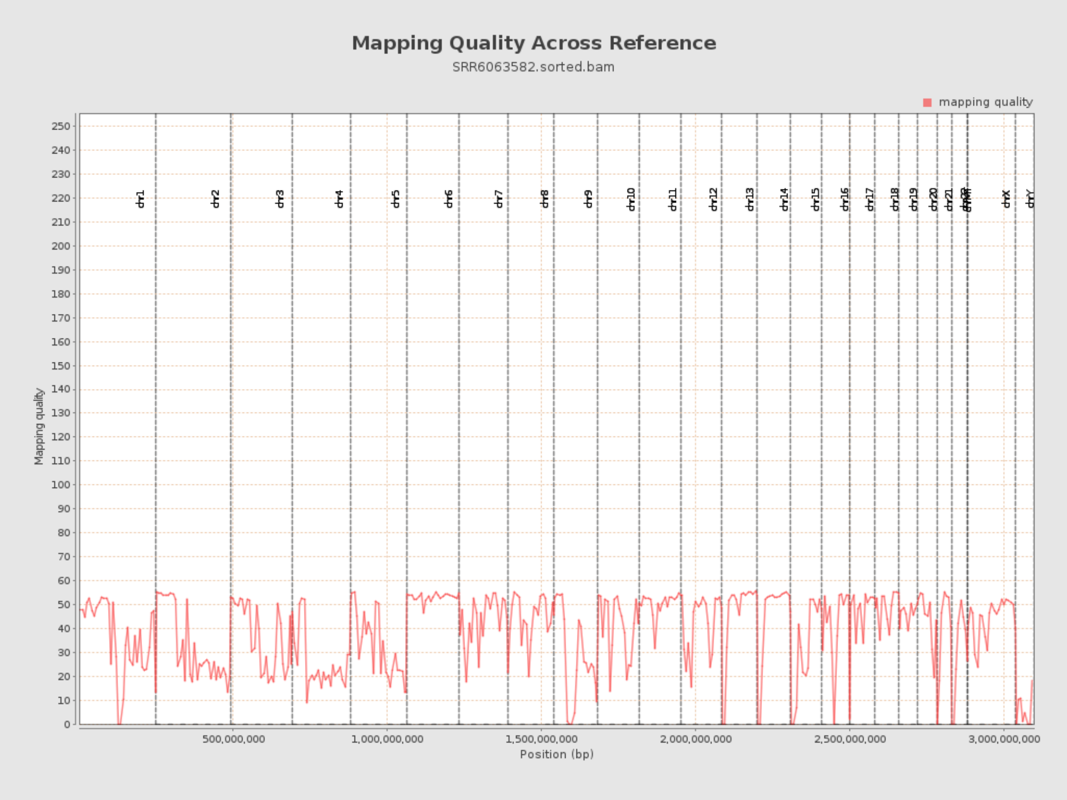
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram