Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:52:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063586.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_SRR6063586 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063586.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:52:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063586.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,751,239
Mapped reads	2,386,412 / 86.74%
Unmapped reads	364,827 / 13.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,072 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	298,893 / 10.86%
Duplication rate	9.6%
Clipped reads	1,100,144 / 39.99%

2.2. ACGT Content

Number/percentage of A's	44,472,231 / 28.04%
Number/percentage of C's	28,868,884 / 18.2%
Number/percentage of T's	50,779,150 / 32.02%
Number/percentage of G's	34,462,737 / 21.73%
Number/percentage of N's	4,156 / 0%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0512

Standard Deviation	0.5595

2.4. Mapping Quality

Mean Mapping Quality	41.56

2.5. Mismatches and indels

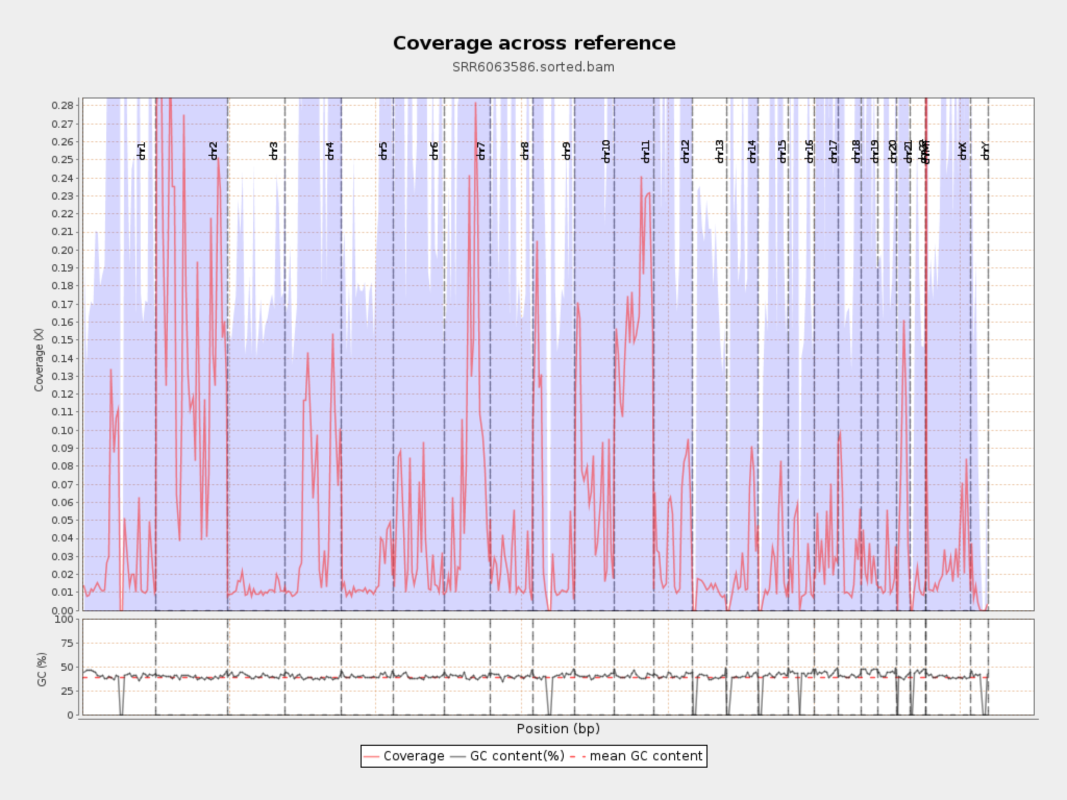
General error rate	0.79%
Mismatches	1,236,505
Insertions	11,891
Mapped reads with at least one insertion	0.49%
Deletions	41,500
Mapped reads with at least one deletion	1.72%
Homopolymer indels	47.26%

2.6. Chromosome stats

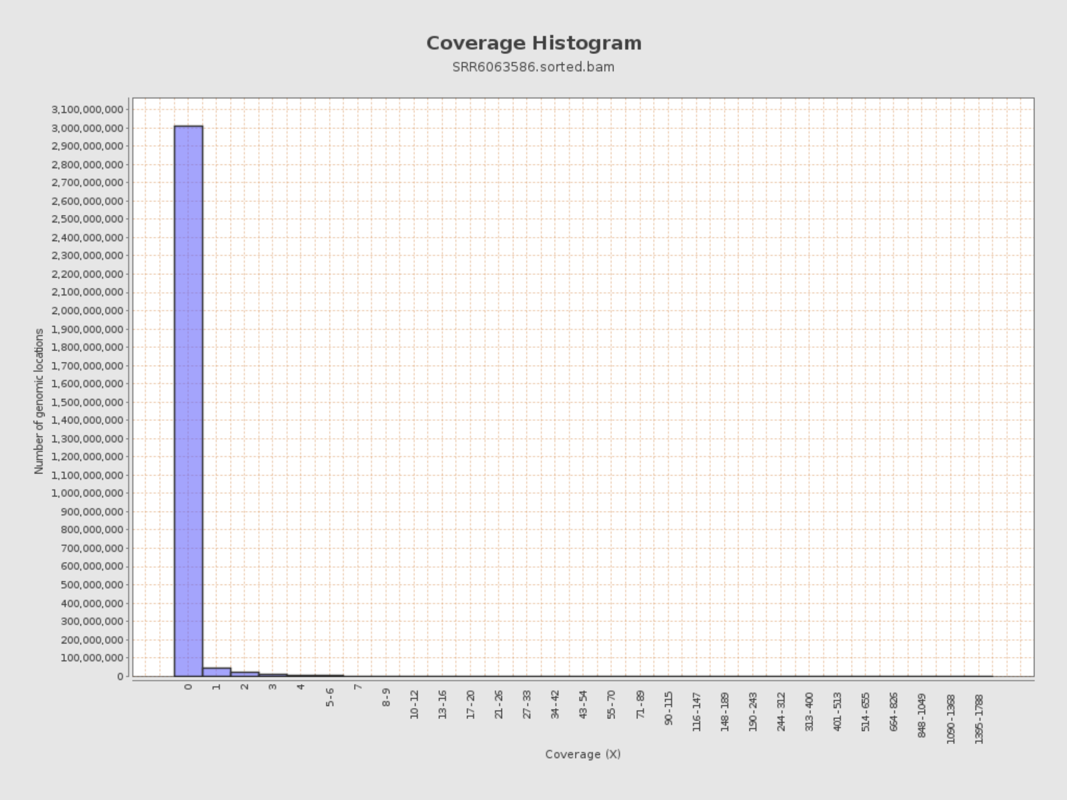
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7319048	0.0294	0.5821
chr2	243199373	40392211	0.1661	0.9062
chr3	198022430	2321341	0.0117	0.1694
chr4	191154276	11396309	0.0596	0.4009
chr5	180915260	3315322	0.0183	0.2171
chr6	171115067	6322158	0.0369	0.3274
chr7	159138663	13803366	0.0867	0.7987

chr8	146364022	3226279	0.022	0.5903
chr9	141213431	6353545	0.045	0.3829
chr10	135534747	9918221	0.0732	0.4791
chr11	135006516	22713041	0.1682	1.3777
chr12	133851895	6074601	0.0454	0.3487
chr13	115169878	1306260	0.0113	0.1735
chr14	107349540	3103094	0.0289	0.2957
chr15	102531392	2179328	0.0213	0.237
chr16	90354753	1812583	0.0201	0.2522
chr17	81195210	2780379	0.0342	0.5199
chr18	78077248	2799236	0.0359	0.7351
chr19	59128983	1450963	0.0245	0.3648
chr20	63025520	1182697	0.0188	0.2834
chr21	48129895	3337248	0.0693	0.4484
chr22	51304566	538234	0.0105	0.1535
chrMT	16571	103839	6.2663	5.1109
chrX	155270560	4488374	0.0289	0.3878
chrY	59373566	415194	0.007	0.1191

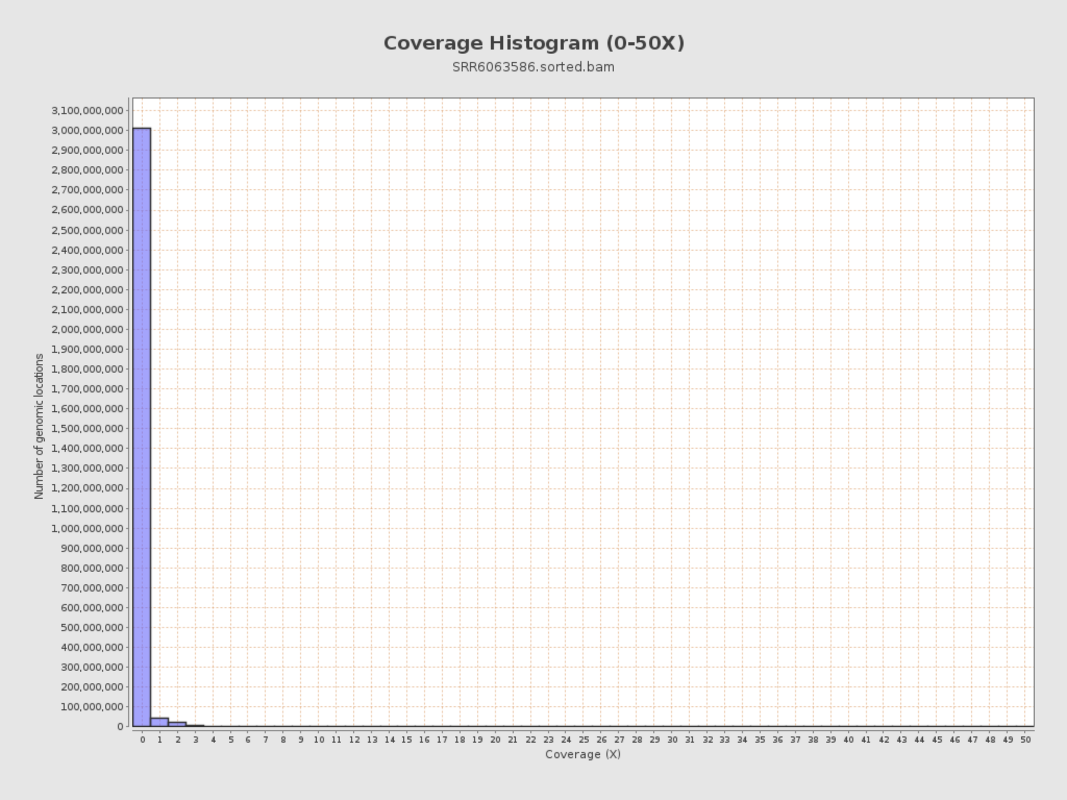
3. Results : Coverage across reference



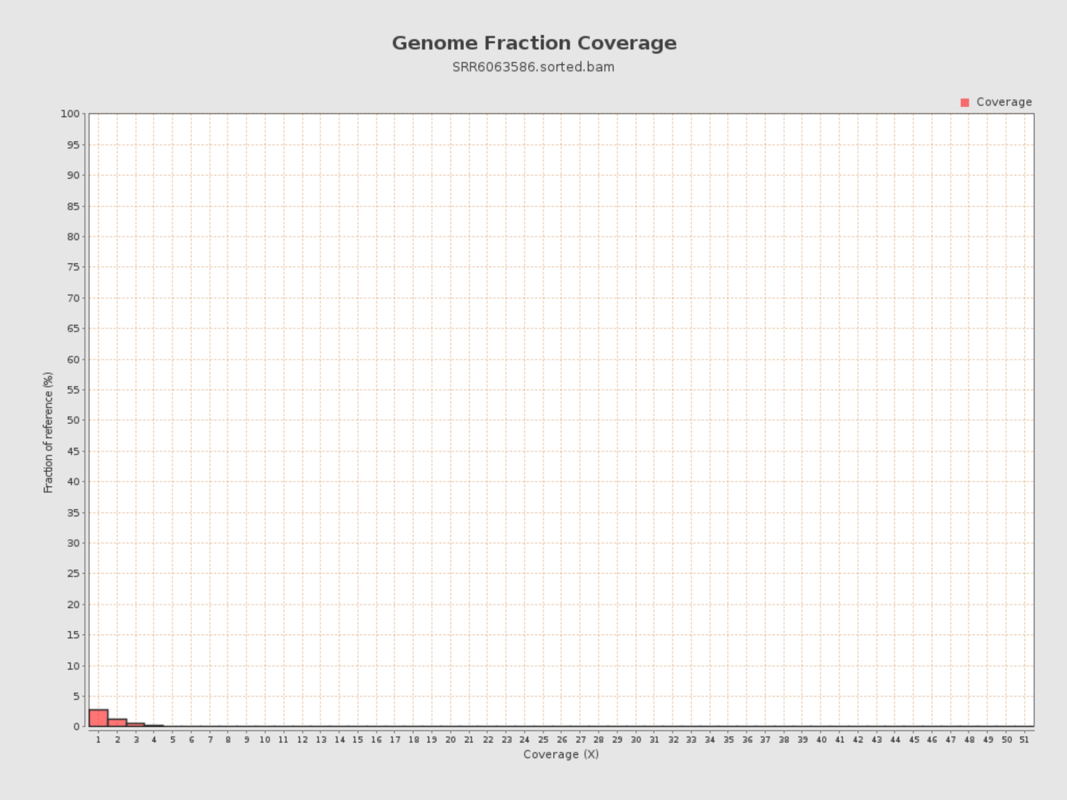
4. Results : Coverage Histogram



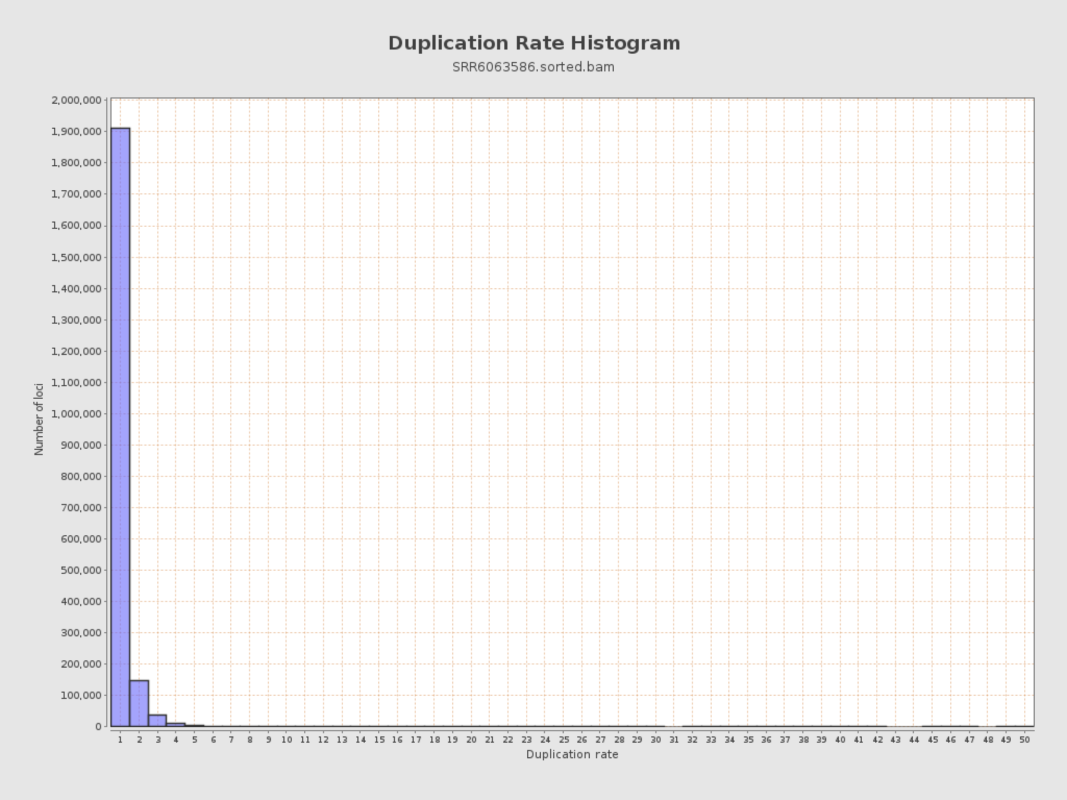
5. Results : Coverage Histogram (0-50X)



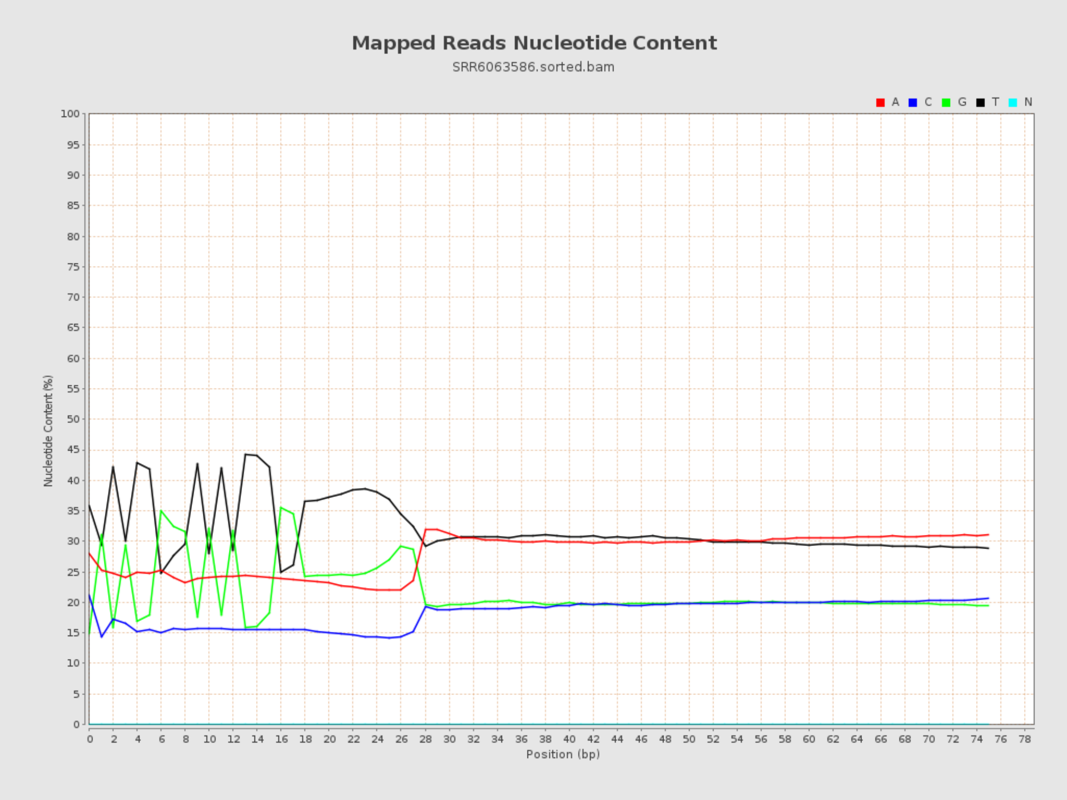
6. Results : Genome Fraction Coverage



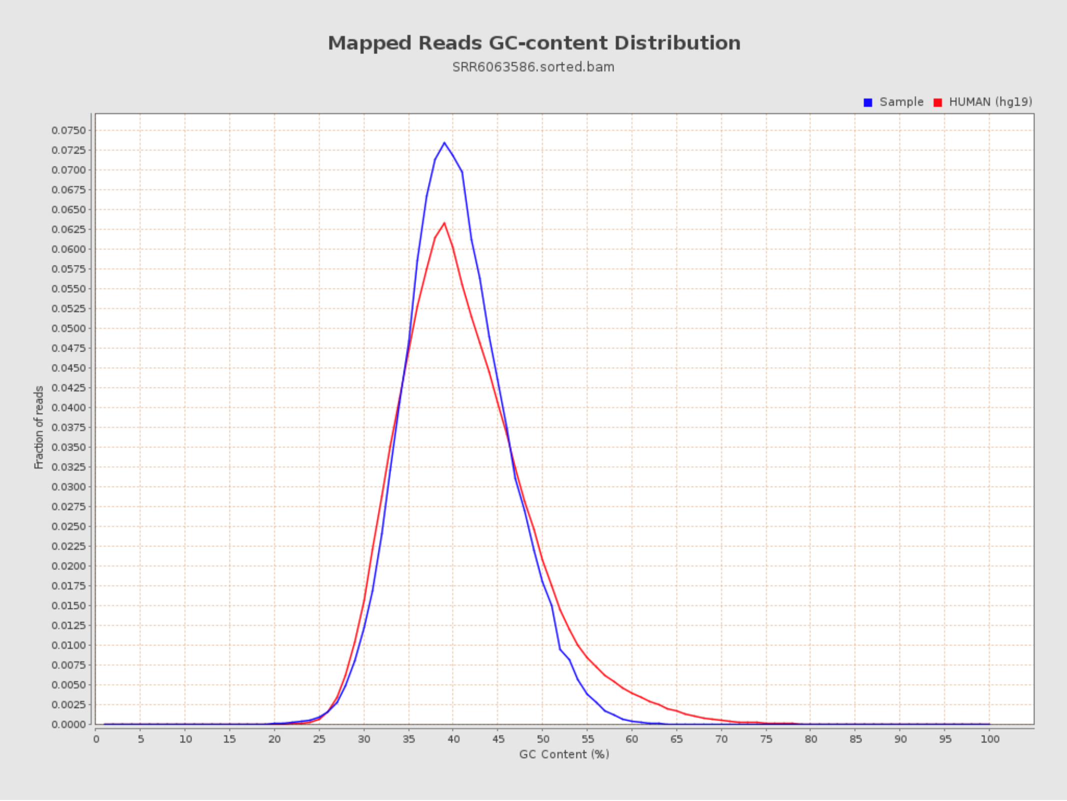
7. Results : Duplication Rate Histogram



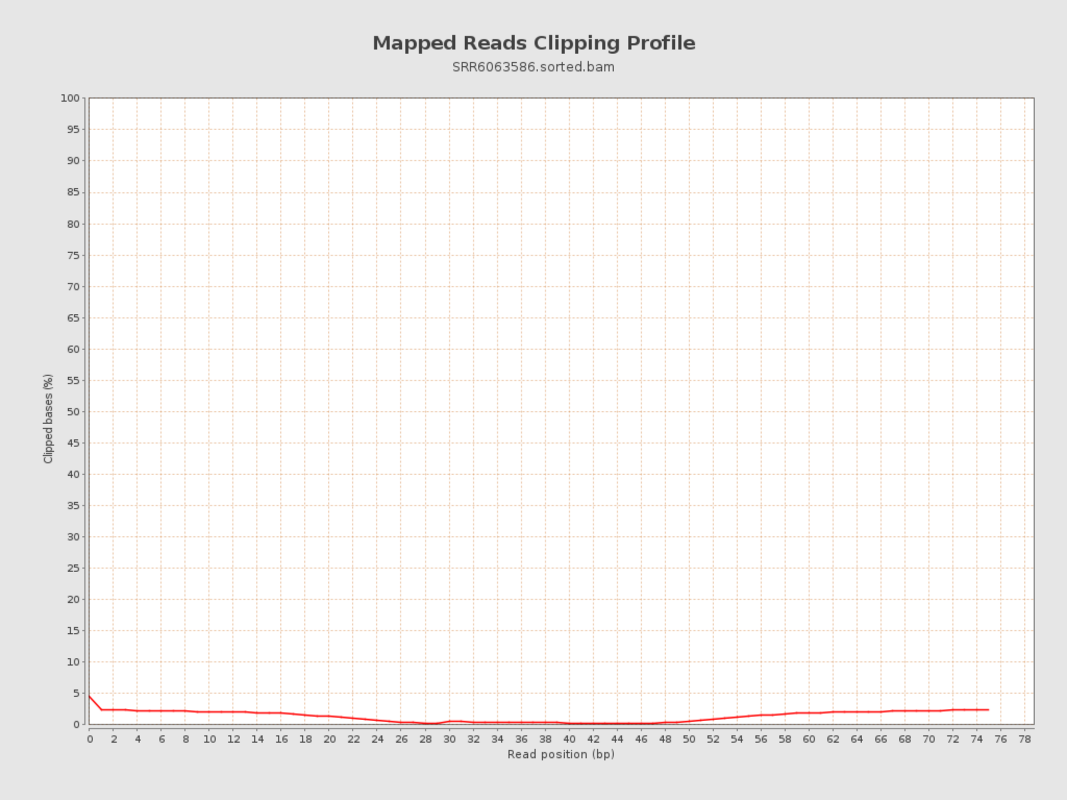
8. Results : Mapped Reads Nucleotide Content



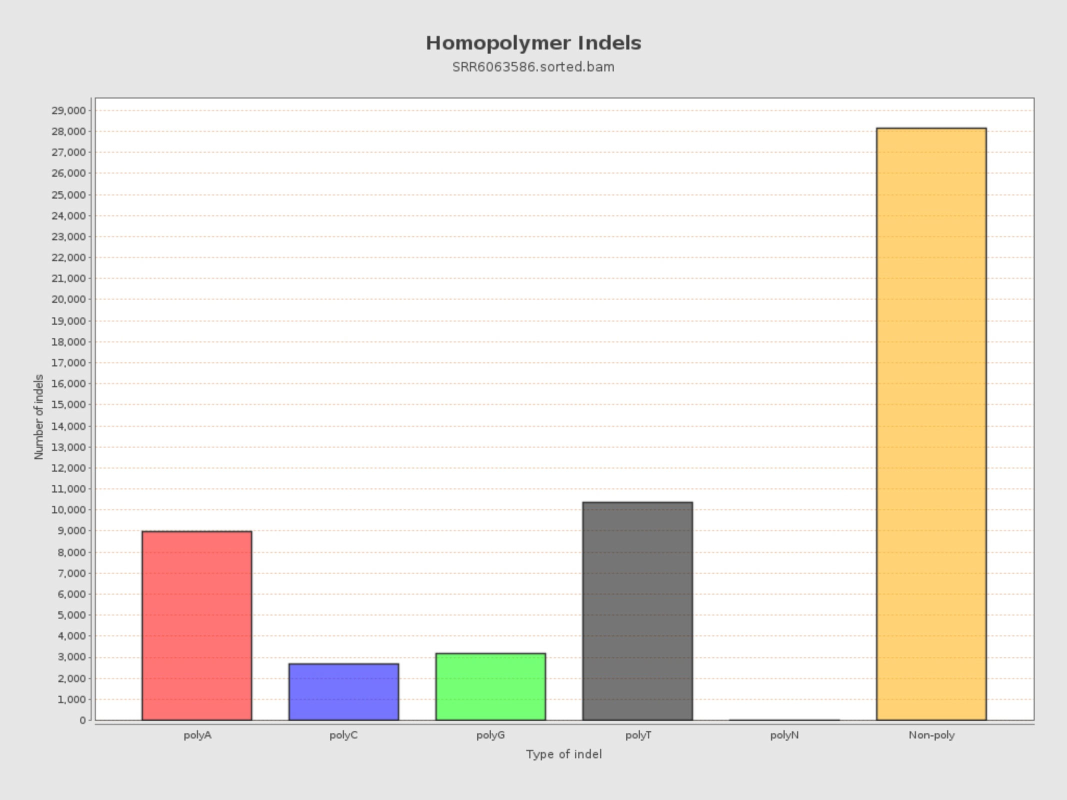
9. Results : Mapped Reads GC-content Distribution



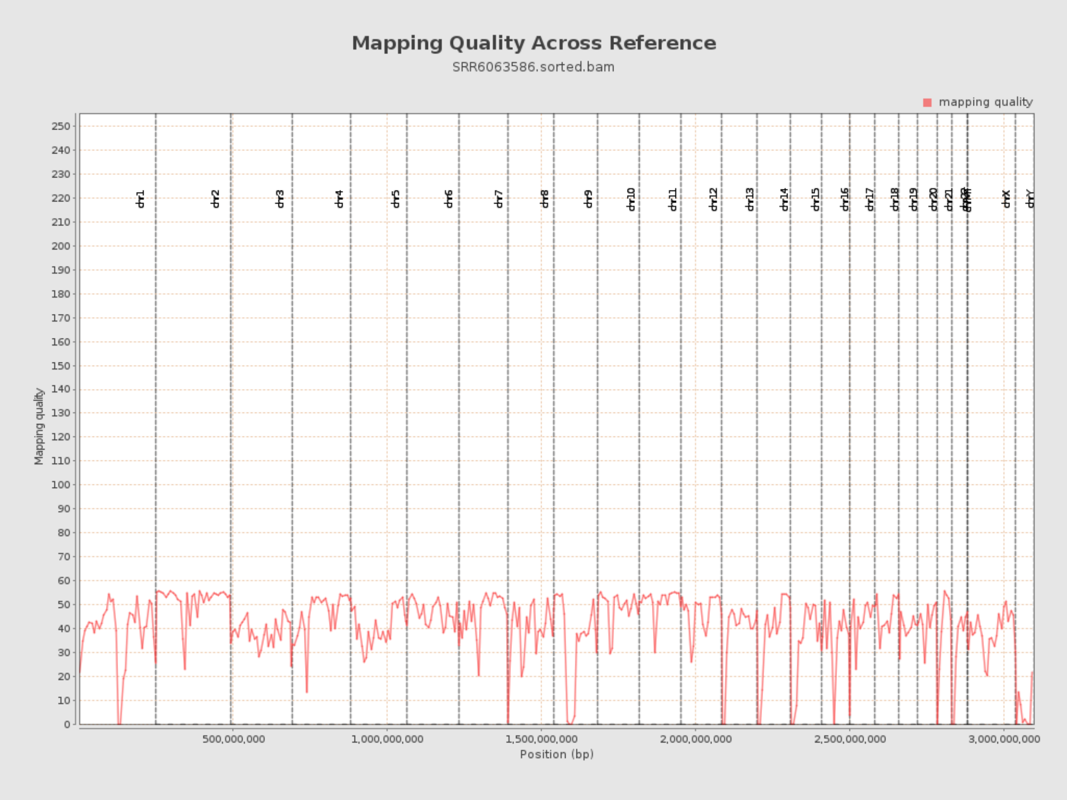
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram