Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:52:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063604.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_SRR6063604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063604.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:52:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,525,199
Mapped reads	3,352,769 / 95.11%
Unmapped reads	172,430 / 4.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,855 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	342,212 / 9.71%
Duplication rate	8.44%
Clipped reads	1,790,215 / 50.78%

2.2. ACGT Content

Number/percentage of A's	55,577,725 / 25.84%
Number/percentage of C's	38,958,206 / 18.11%
Number/percentage of T's	69,790,466 / 32.45%
Number/percentage of G's	50,729,971 / 23.59%
Number/percentage of N's	25,087 / 0.01%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0695

Standard Deviation	0.7133

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

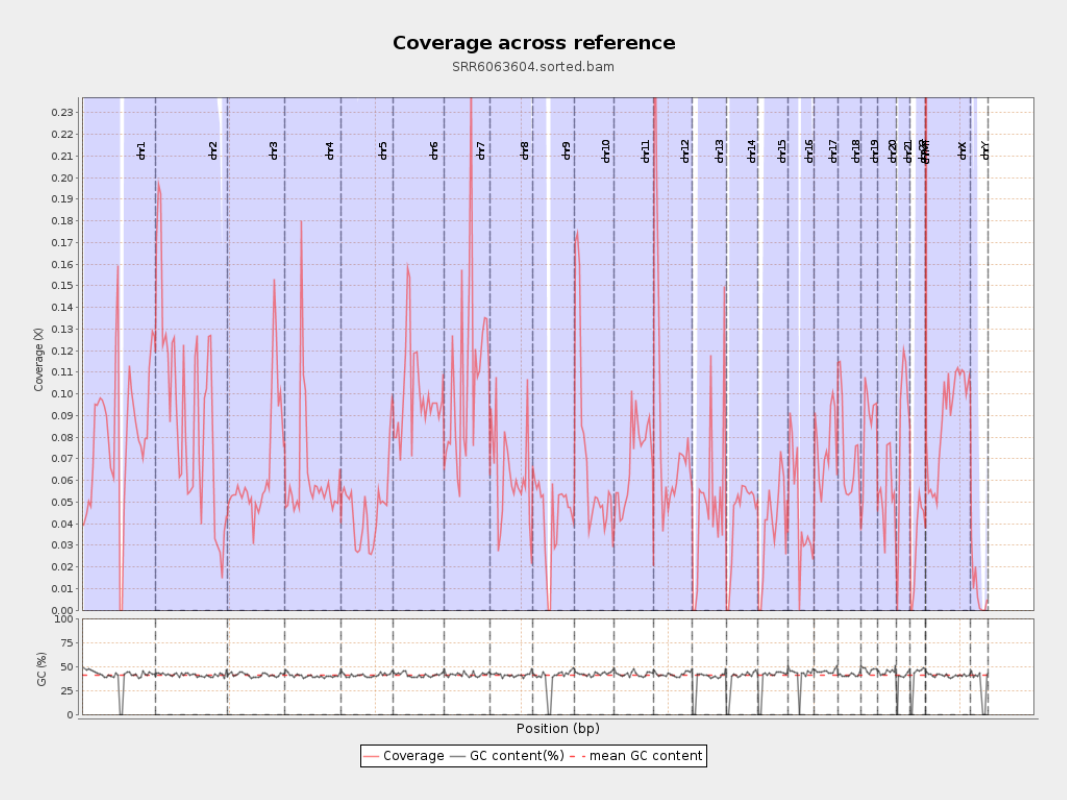
General error rate	0.53%
Mismatches	1,114,546
Insertions	12,698
Mapped reads with at least one insertion	0.38%
Deletions	47,470
Mapped reads with at least one deletion	1.4%
Homopolymer indels	44.43%

2.6. Chromosome stats

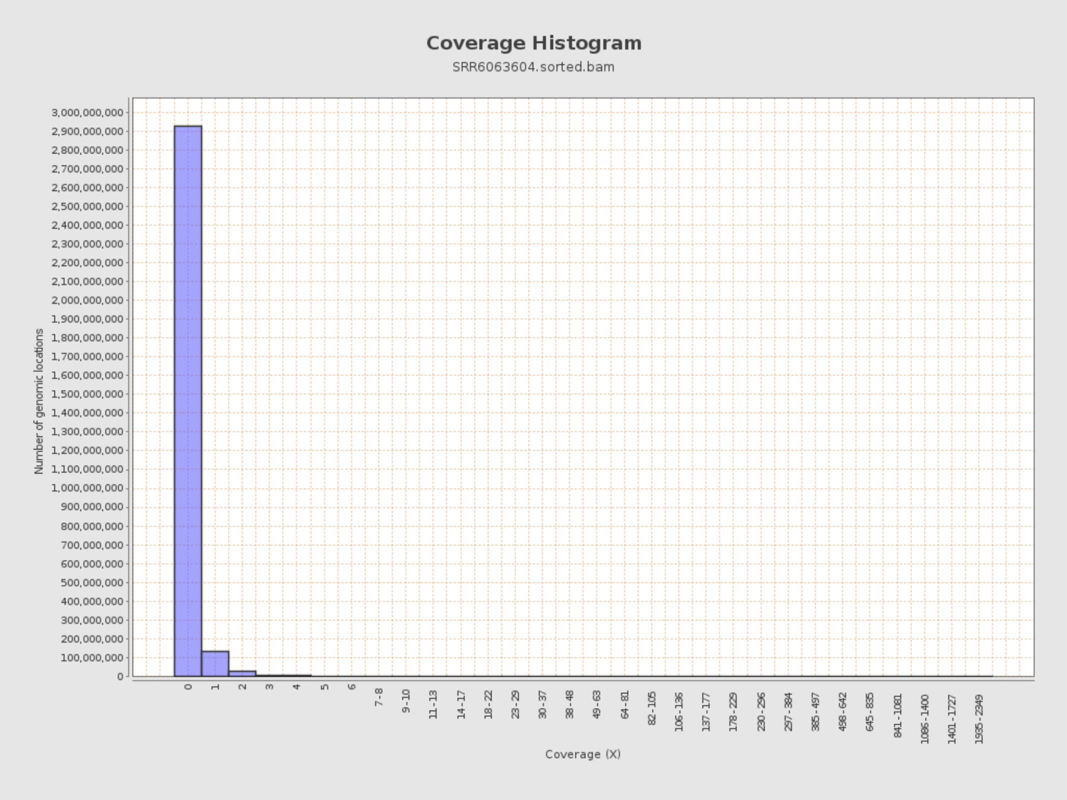
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20282843	0.0814	1.3747
chr2	243199373	22251365	0.0915	1.1468
chr3	198022430	13027641	0.0658	0.3201
chr4	191154276	12000899	0.0628	0.3211
chr5	180915260	8639366	0.0478	0.2781
chr6	171115067	17203358	0.1005	0.5416
chr7	159138663	17140915	0.1077	1.3871

chr8	146364022	9017043	0.0616	0.4965
chr9	141213431	6119661	0.0433	0.5229
chr10	135534747	9669055	0.0713	0.4216
chr11	135006516	9283959	0.0688	0.4247
chr12	133851895	11590718	0.0866	0.4185
chr13	115169878	5911361	0.0513	0.3238
chr14	107349540	4706389	0.0438	0.3555
chr15	102531392	3883606	0.0379	0.2824
chr16	90354753	3996660	0.0442	0.2962
chr17	81195210	6262918	0.0771	0.3724
chr18	78077248	5667134	0.0726	0.98
chr19	59128983	5049265	0.0854	0.8747
chr20	63025520	3419291	0.0543	0.3185
chr21	48129895	3963424	0.0823	0.3664
chr22	51304566	1608705	0.0314	0.2129
chrMT	16571	270119	16.3007	8.6452
chrX	155270560	13693897	0.0882	0.437
chrY	59373566	503875	0.0085	0.1992

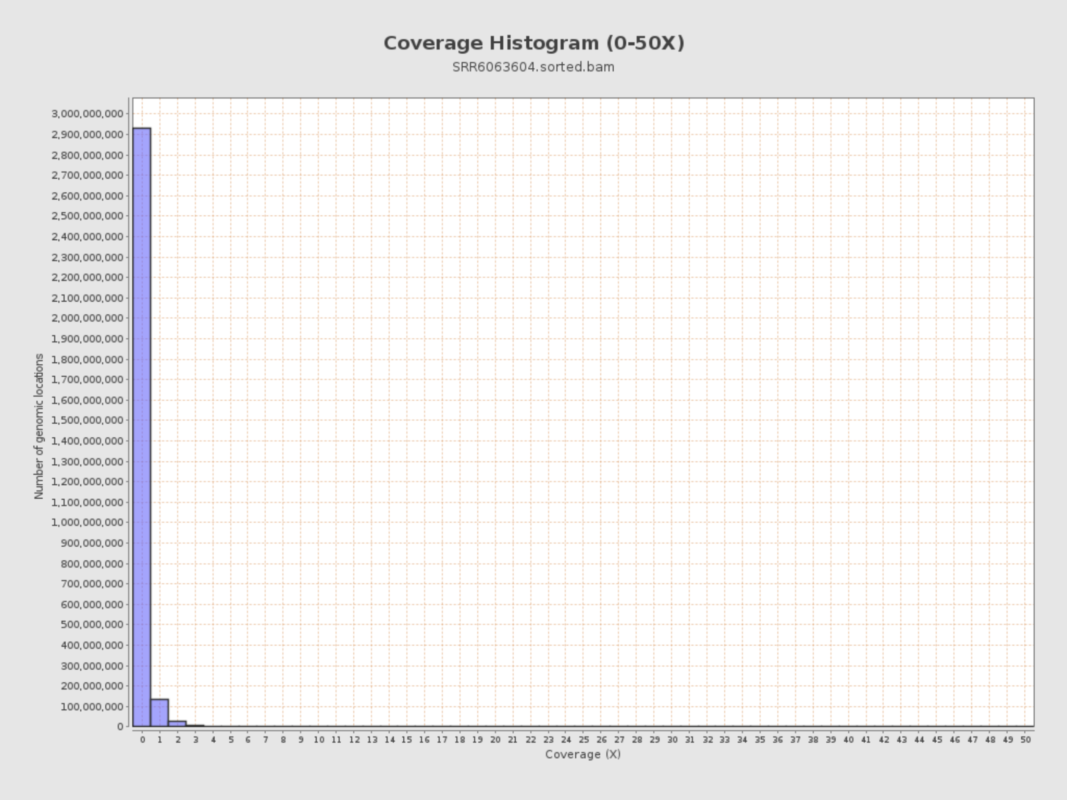
3. Results : Coverage across reference



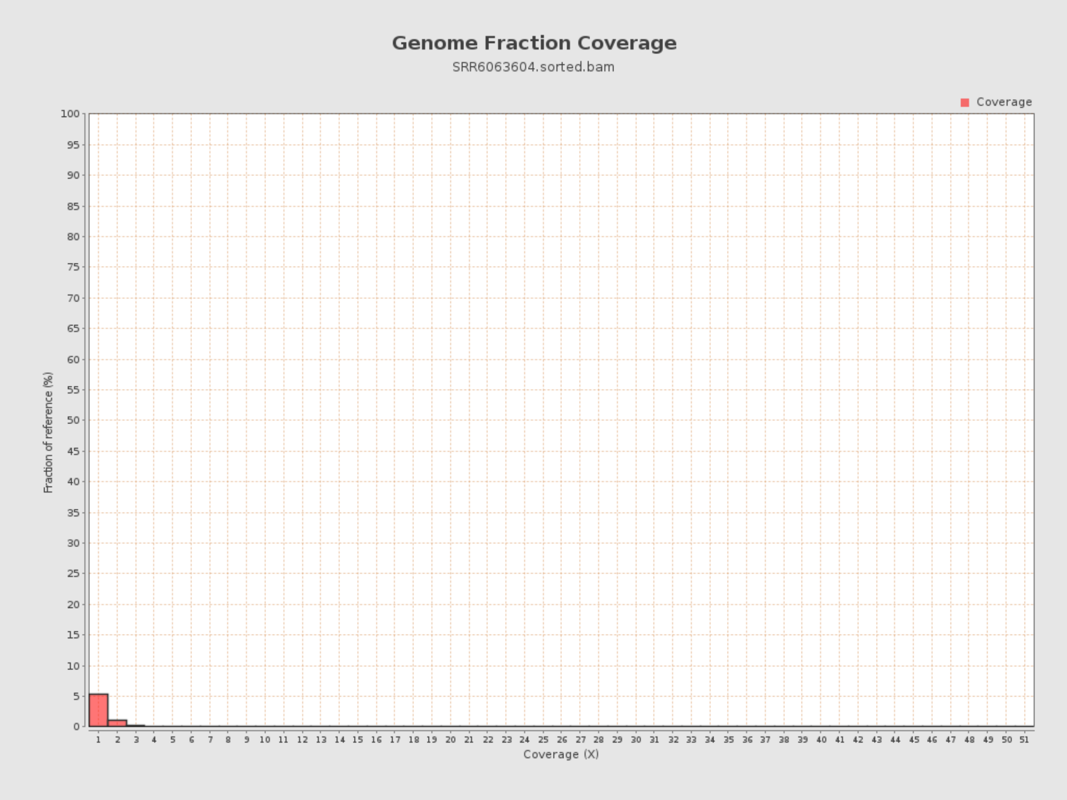
4. Results : Coverage Histogram



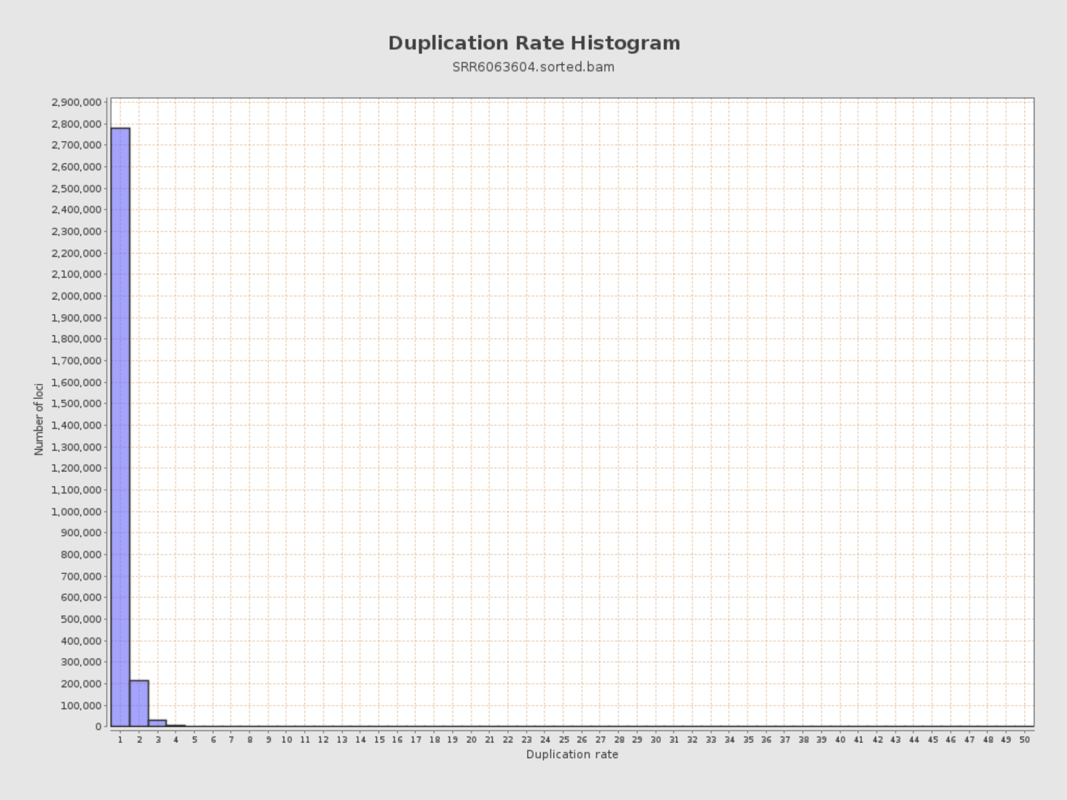
5. Results : Coverage Histogram (0-50X)



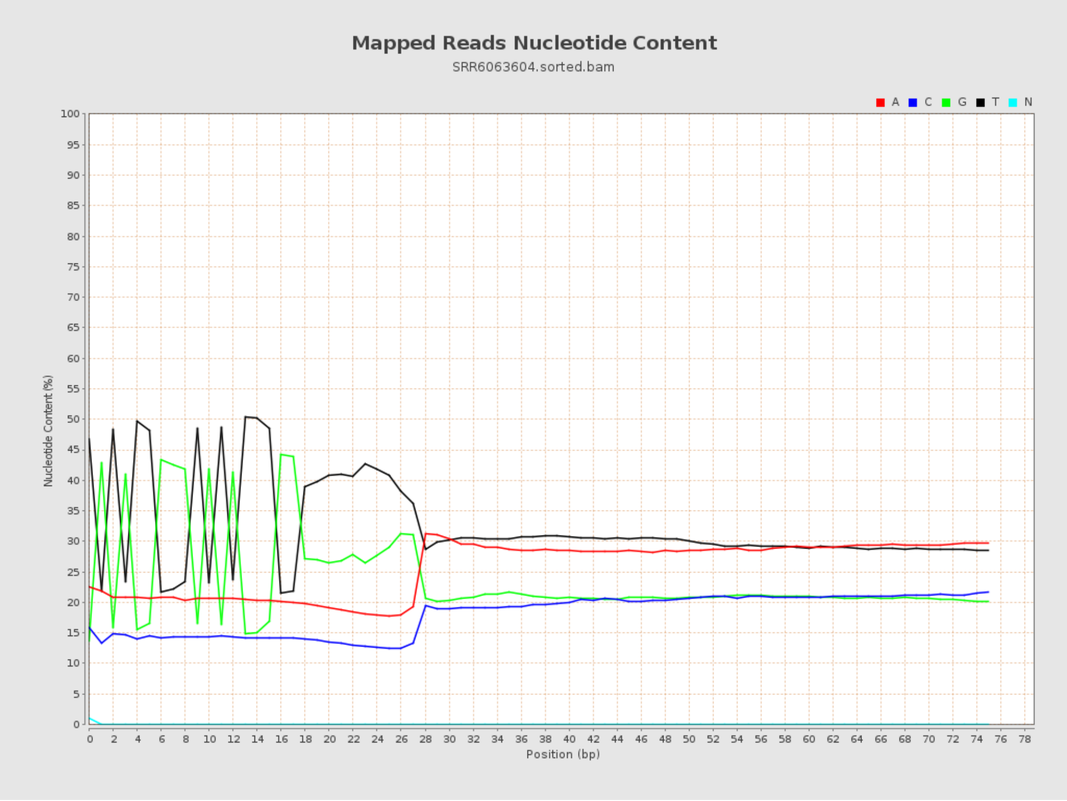
6. Results : Genome Fraction Coverage



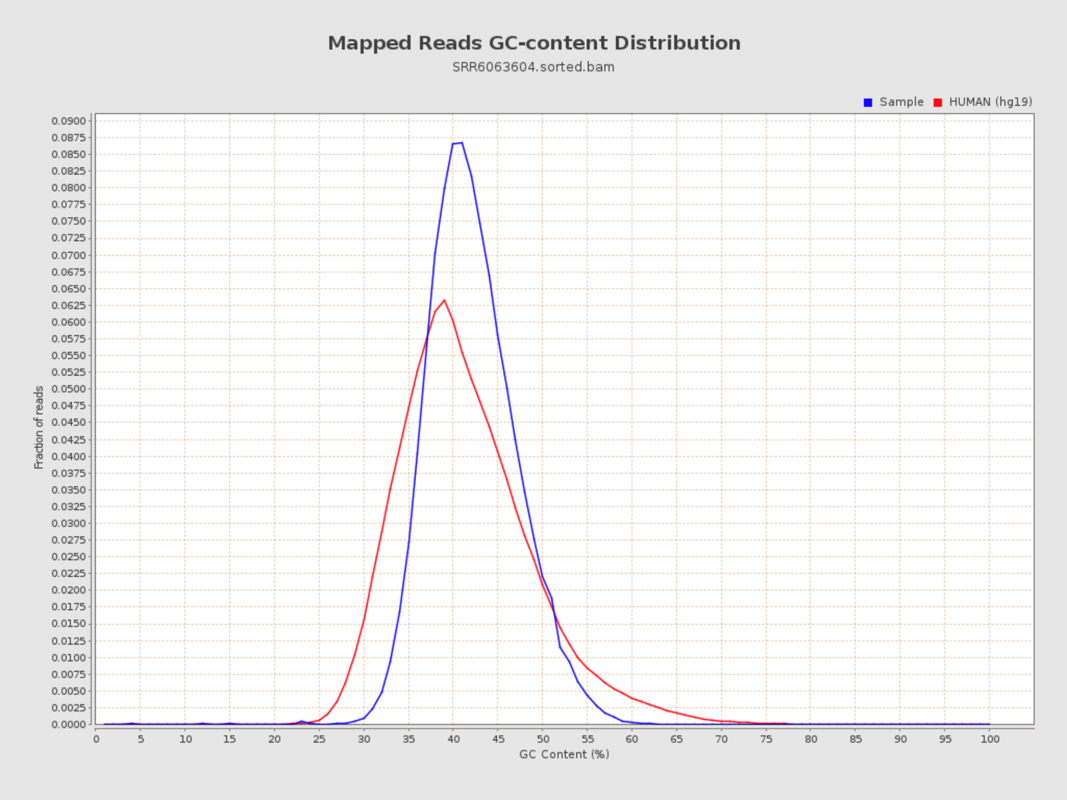
7. Results : Duplication Rate Histogram



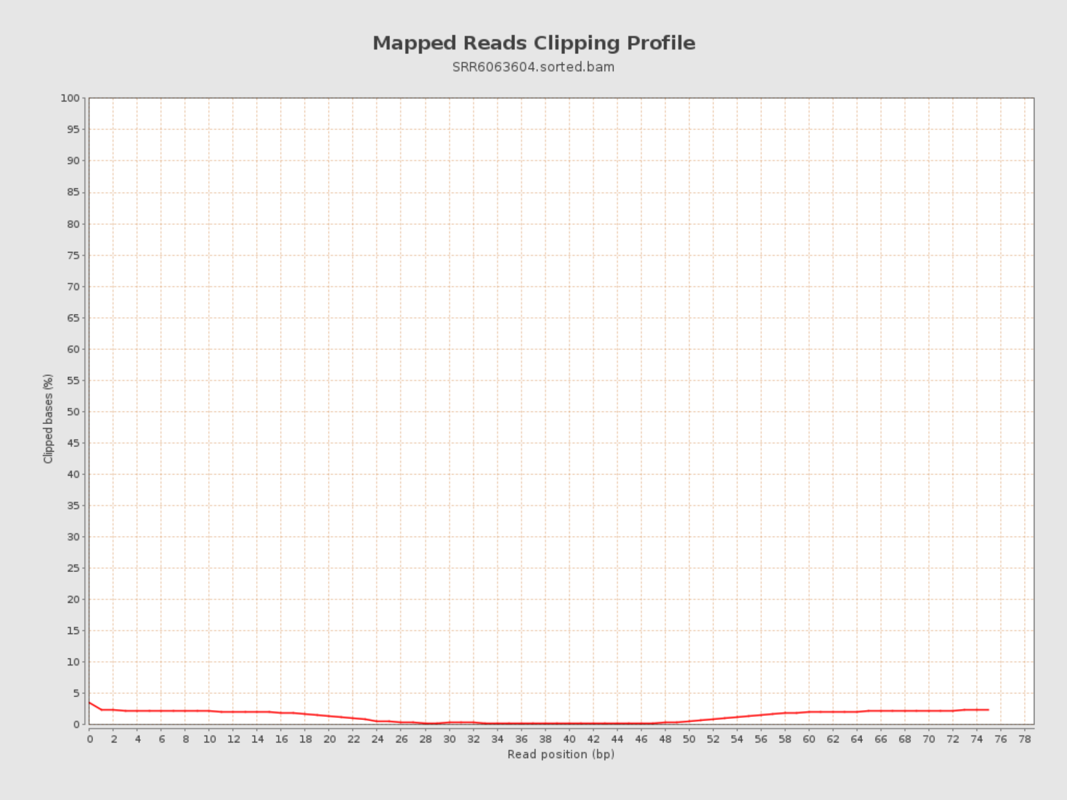
8. Results : Mapped Reads Nucleotide Content



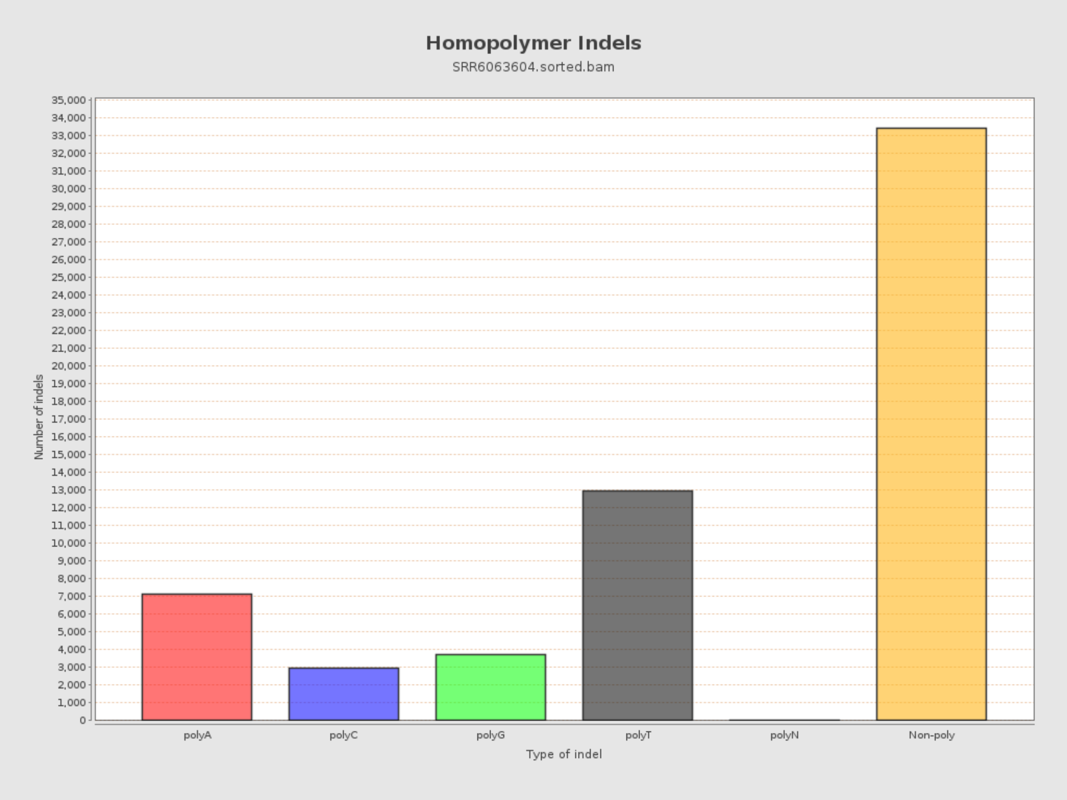
9. Results : Mapped Reads GC-content Distribution



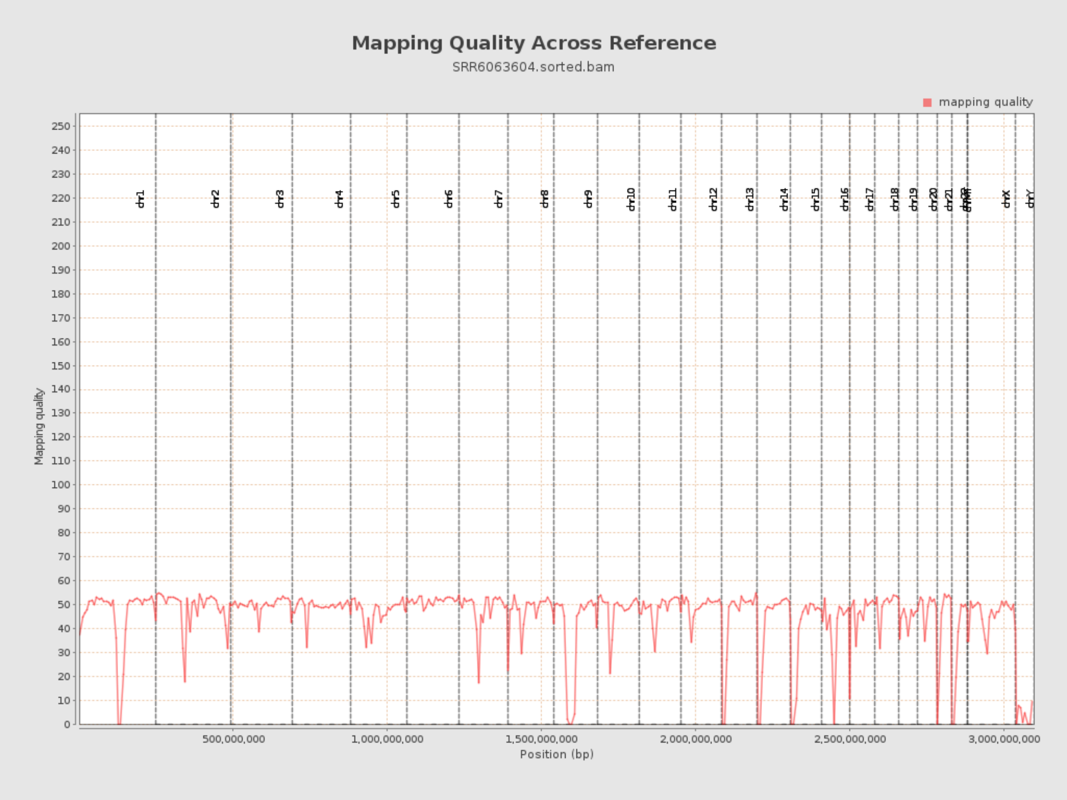
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram