Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:57:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063605.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_SRR6063605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063605.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:57:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,788,149
Mapped reads	5,437,434 / 93.94%
Unmapped reads	350,715 / 6.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	53,321 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	1,199,687 / 20.73%
Duplication rate	16.87%
Clipped reads	3,078,381 / 53.18%

2.2. ACGT Content

Number/percentage of A's	89,930,418 / 25.94%
Number/percentage of C's	63,274,408 / 18.25%
Number/percentage of T's	111,879,462 / 32.27%
Number/percentage of G's	81,602,246 / 23.54%
Number/percentage of N's	39,803 / 0.01%
GC Percentage	41.78%

2.3. Coverage

Mean	0.112

Standard Deviation	1.2438

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

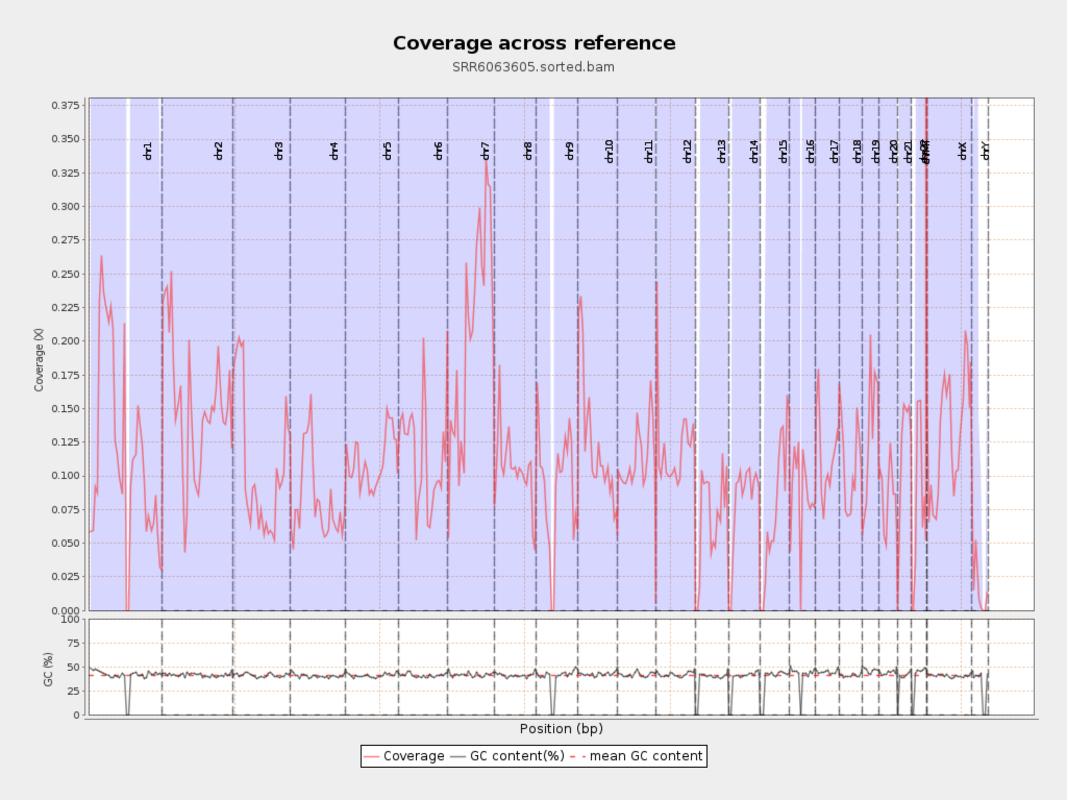
General error rate	0.54%
Mismatches	1,836,479
Insertions	22,120
Mapped reads with at least one insertion	0.4%
Deletions	75,078
Mapped reads with at least one deletion	1.37%
Homopolymer indels	44.12%

2.6. Chromosome stats

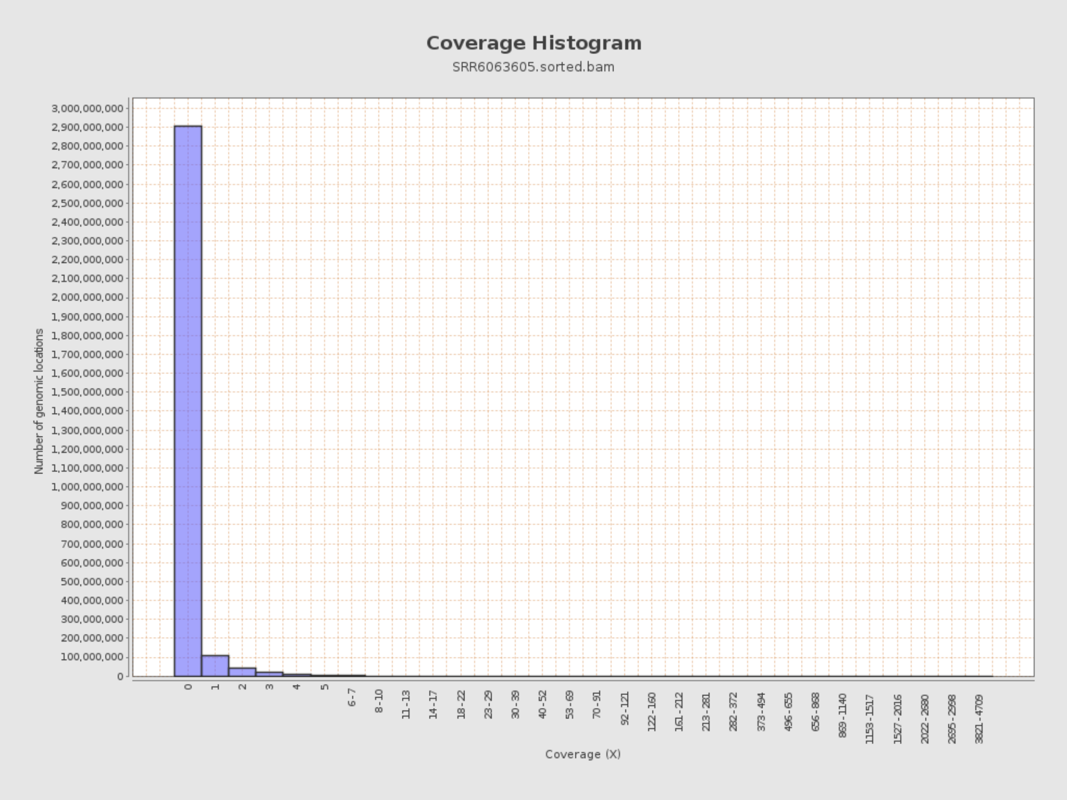
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29483732	0.1183	2.5249
chr2	243199373	36963333	0.152	2.2167
chr3	198022430	21151860	0.1068	0.5383
chr4	191154276	15539117	0.0813	0.5442
chr5	180915260	20039832	0.1108	0.5525
chr6	171115067	19699226	0.1151	0.8277
chr7	159138663	33131677	0.2082	1.846

chr8	146364022	15422623	0.1054	1.2546
chr9	141213431	12903431	0.0914	0.7516
chr10	135534747	17001067	0.1254	0.7847
chr11	135006516	15076743	0.1117	0.7854
chr12	133851895	16235367	0.1213	0.6
chr13	115169878	7738396	0.0672	0.5139
chr14	107349540	8585102	0.08	0.5185
chr15	102531392	7594281	0.0741	0.5153
chr16	90354753	7832817	0.0867	0.5158
chr17	81195210	9258729	0.114	0.6237
chr18	78077248	8518762	0.1091	1.5377
chr19	59128983	7723498	0.1306	1.6545
chr20	63025520	5380302	0.0854	0.505
chr21	48129895	5678781	0.118	0.5911
chr22	51304566	3924690	0.0765	0.4428
chrMT	16571	538139	32.4747	21.1925
chrX	155270560	20412737	0.1315	0.7055
chrY	59373566	1021284	0.0172	0.4881

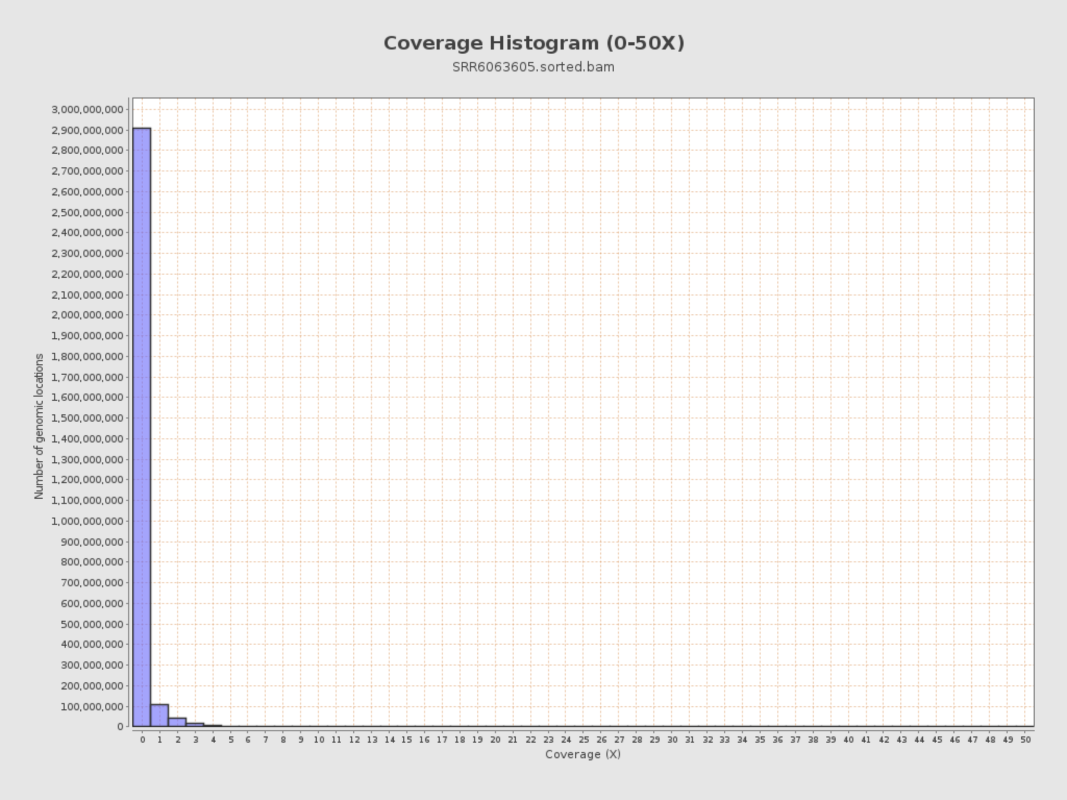
3. Results : Coverage across reference



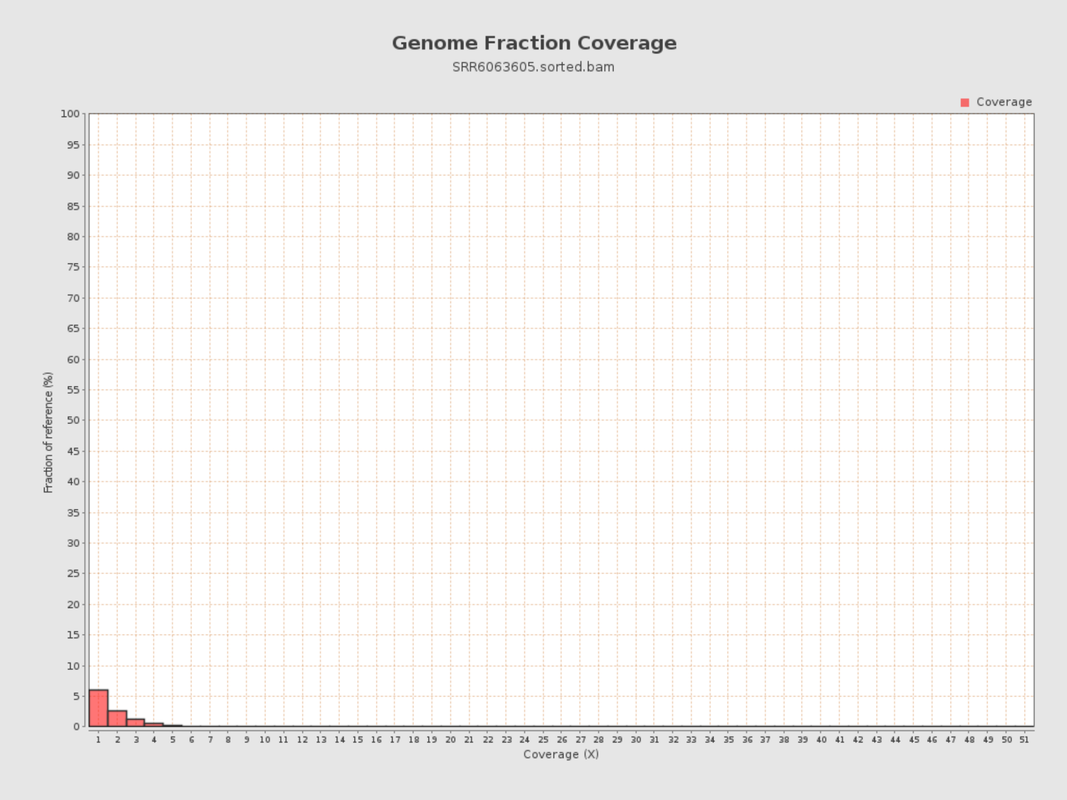
4. Results : Coverage Histogram



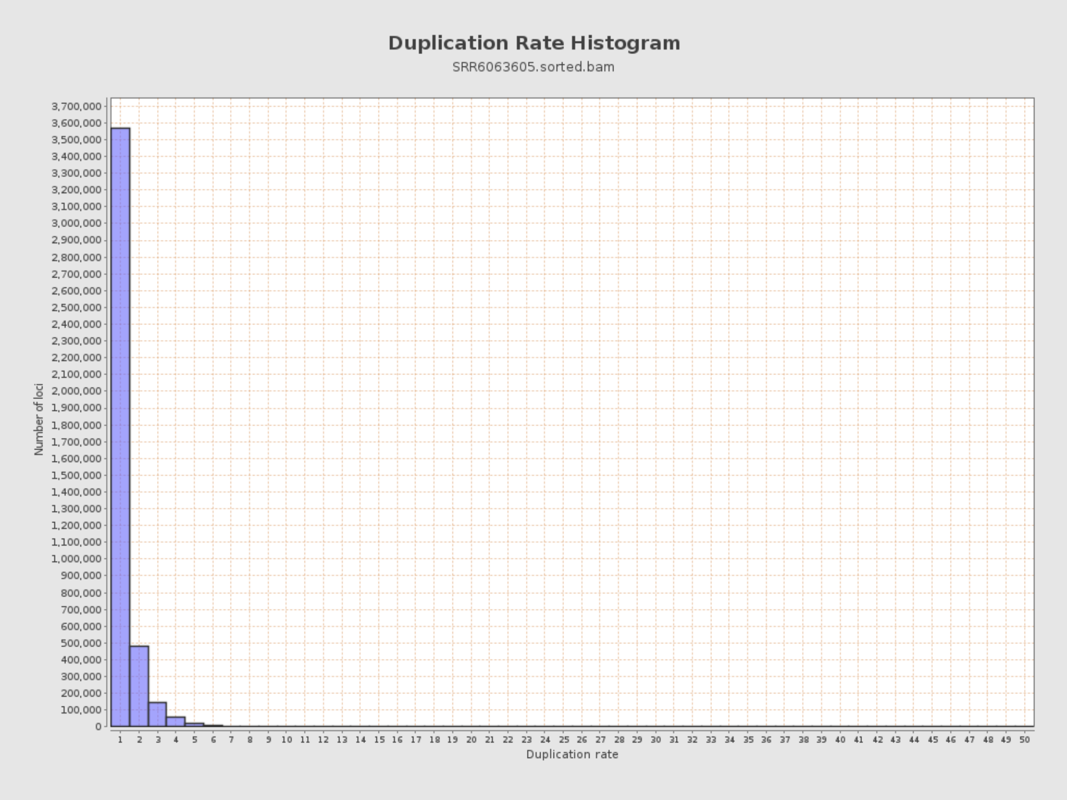
5. Results : Coverage Histogram (0-50X)



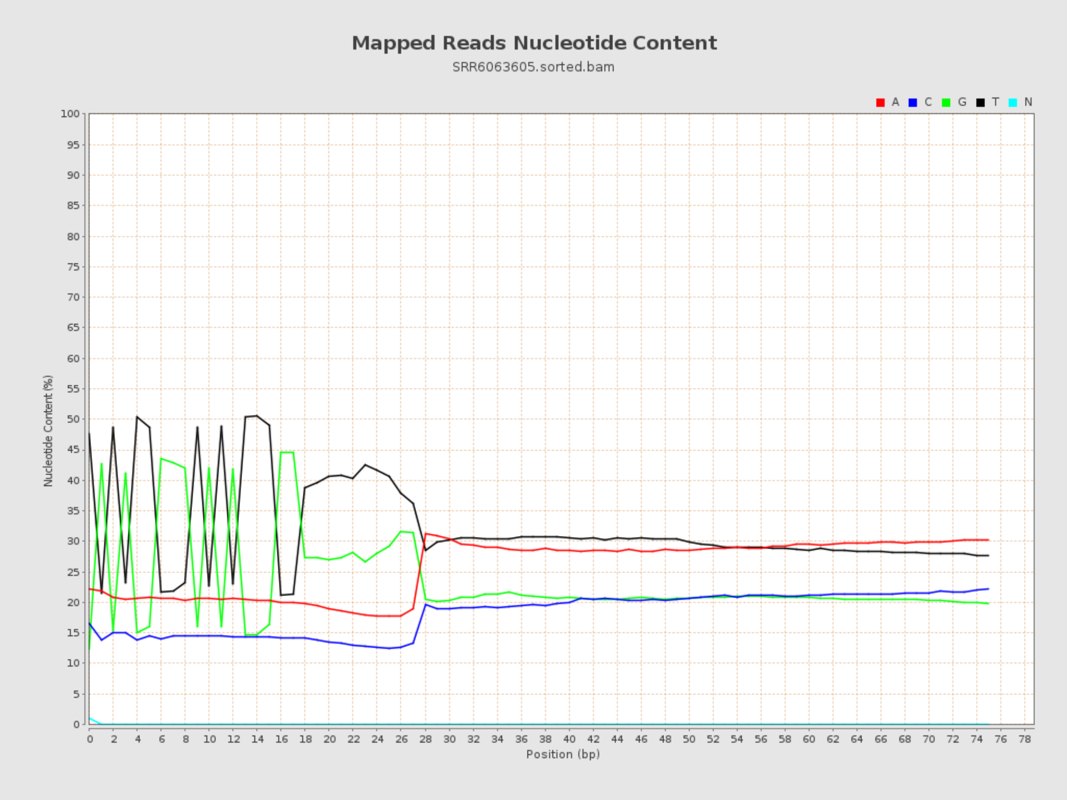
6. Results : Genome Fraction Coverage



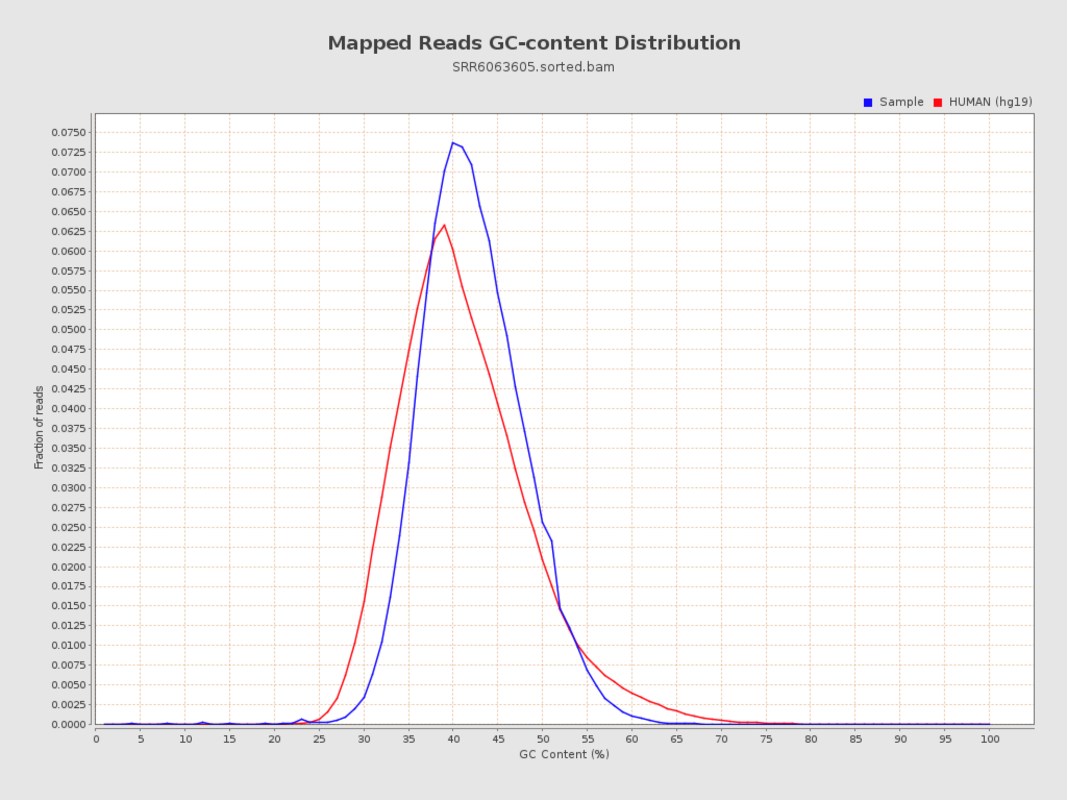
7. Results : Duplication Rate Histogram



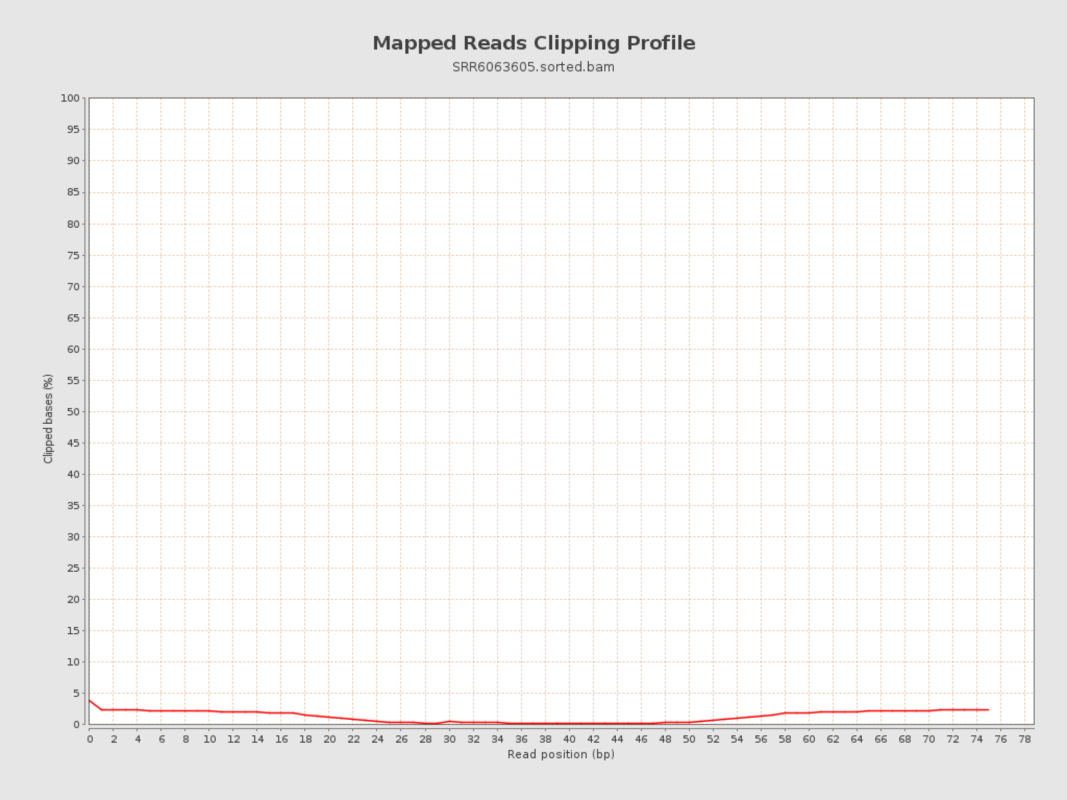
8. Results : Mapped Reads Nucleotide Content



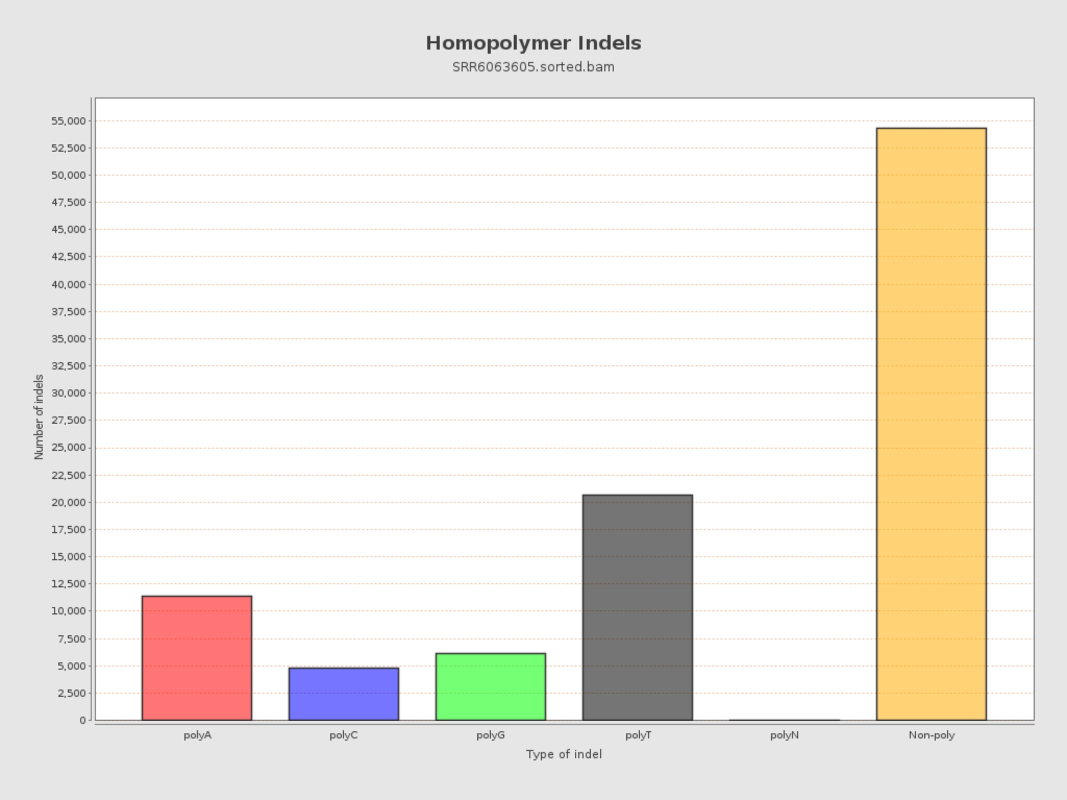
9. Results : Mapped Reads GC-content Distribution



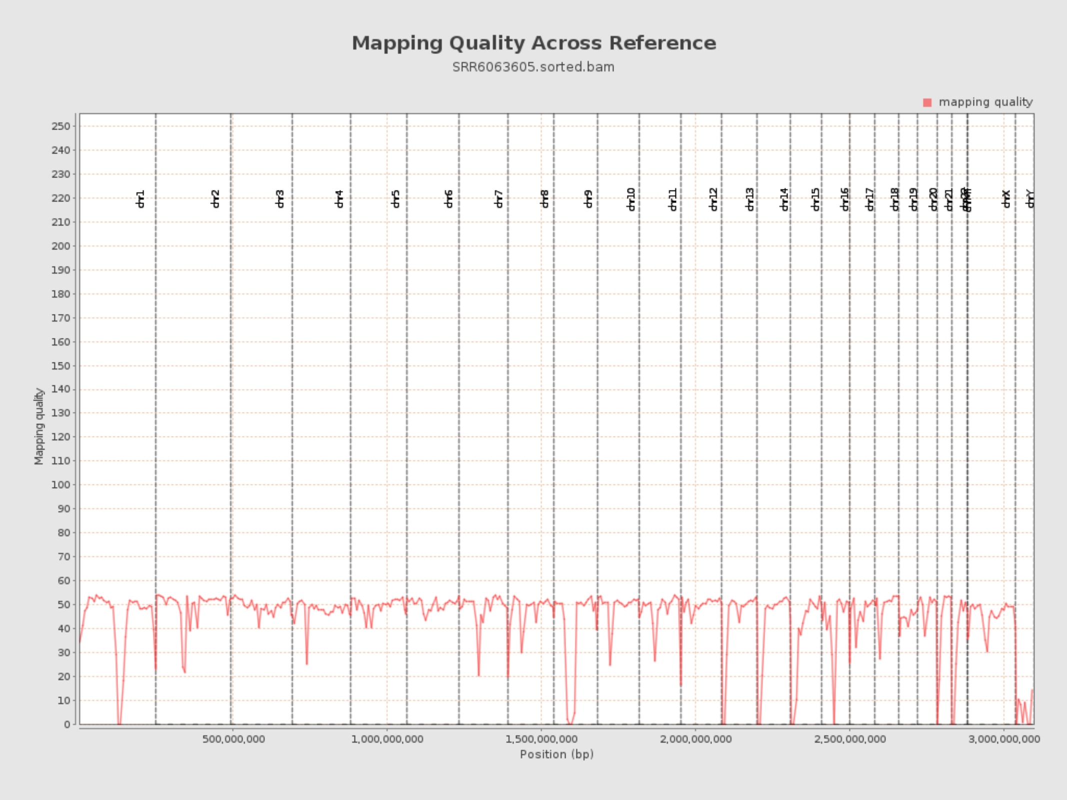
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram