Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:38:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013265.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_SRR6013265 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013265.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:38:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,697,623
Mapped reads	1,539,224 / 90.67%
Unmapped reads	158,399 / 9.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,050 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	58,274 / 3.43%
Duplication rate	2.94%
Clipped reads	669,800 / 39.46%

2.2. ACGT Content

Number/percentage of A's	28,576,809 / 27.76%
Number/percentage of C's	18,713,975 / 18.18%
Number/percentage of T's	32,987,510 / 32.04%
Number/percentage of G's	22,655,857 / 22.01%
Number/percentage of N's	22,385 / 0.02%
GC Percentage	40.18%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.319

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

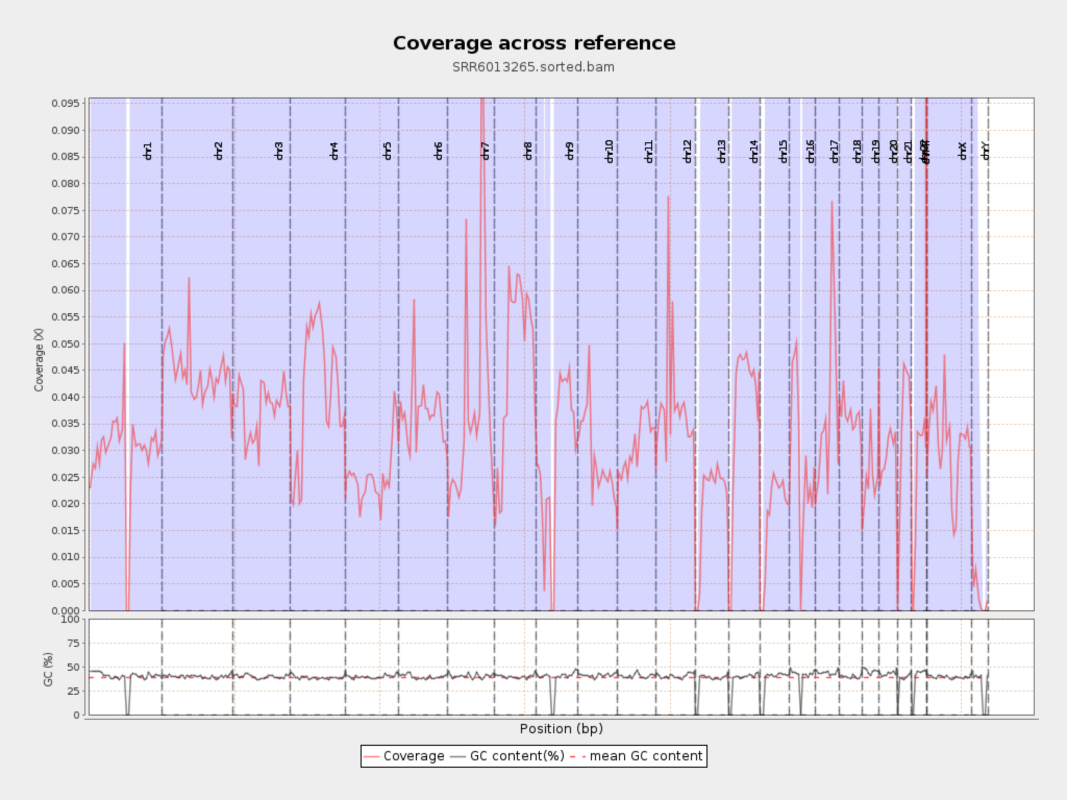
General error rate	0.8%
Mismatches	811,529
Insertions	7,485
Mapped reads with at least one insertion	0.48%
Deletions	25,498
Mapped reads with at least one deletion	1.64%
Homopolymer indels	46.79%

2.6. Chromosome stats

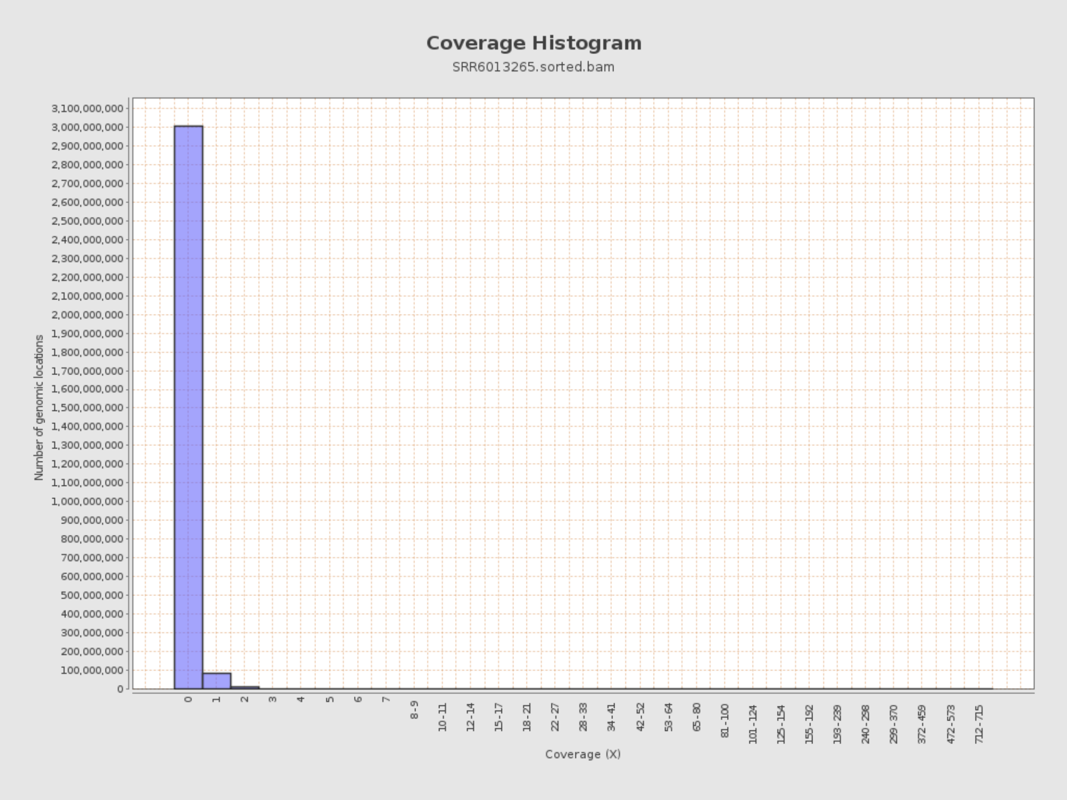
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7353228	0.0295	0.4406
chr2	243199373	10935827	0.045	0.4171
chr3	198022430	7494405	0.0378	0.2131
chr4	191154276	7817363	0.0409	0.2269
chr5	180915260	4587287	0.0254	0.175
chr6	171115067	6347990	0.0371	0.2712
chr7	159138663	6377430	0.0401	0.6541

chr8	146364022	6848602	0.0468	0.389
chr9	141213431	4047263	0.0287	0.2676
chr10	135534747	3929937	0.029	0.3016
chr11	135006516	4197575	0.0311	0.2336
chr12	133851895	5206918	0.0389	0.2201
chr13	115169878	2305317	0.02	0.1571
chr14	107349540	4032952	0.0376	0.2282
chr15	102531392	1820976	0.0178	0.1475
chr16	90354753	2577039	0.0285	0.2042
chr17	81195210	3026409	0.0373	0.2211
chr18	78077248	2859378	0.0366	0.5206
chr19	59128983	1517021	0.0257	0.3587
chr20	63025520	1831700	0.0291	0.19
chr21	48129895	1615453	0.0336	0.208
chr22	51304566	1202319	0.0234	0.1677
chrMT	16571	66991	4.0427	3.122
chrX	155270560	4824913	0.0311	0.21
chrY	59373566	175663	0.003	0.0776

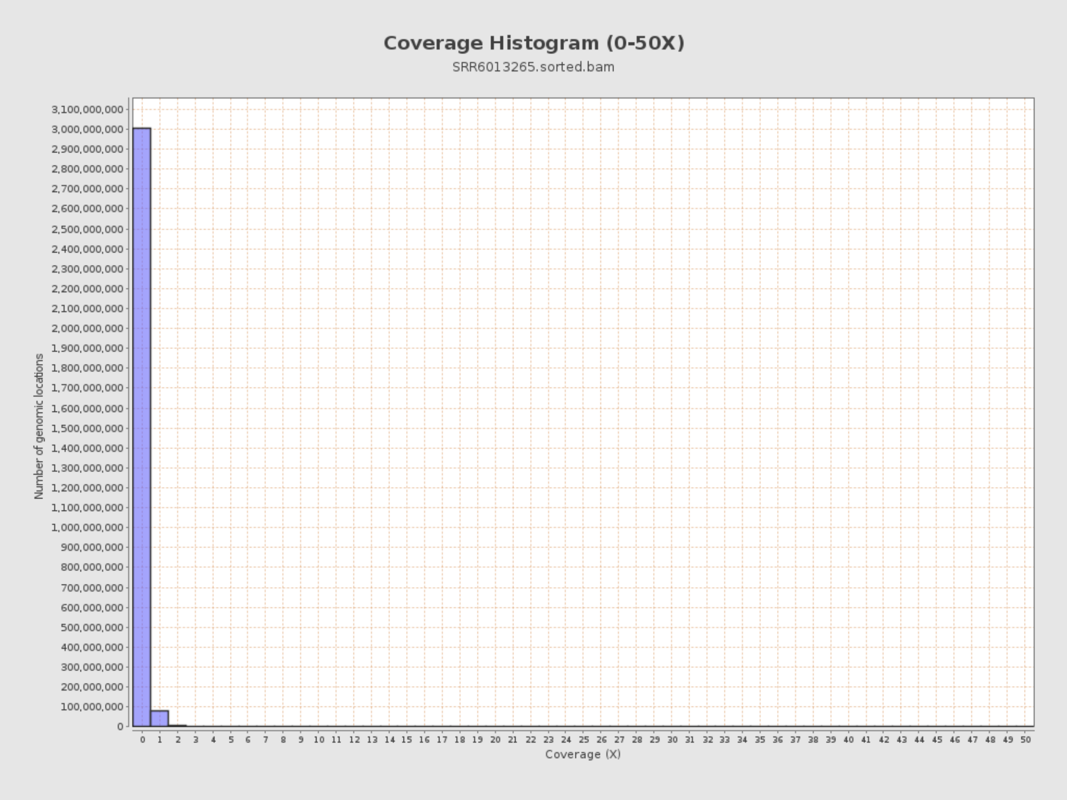
3. Results : Coverage across reference



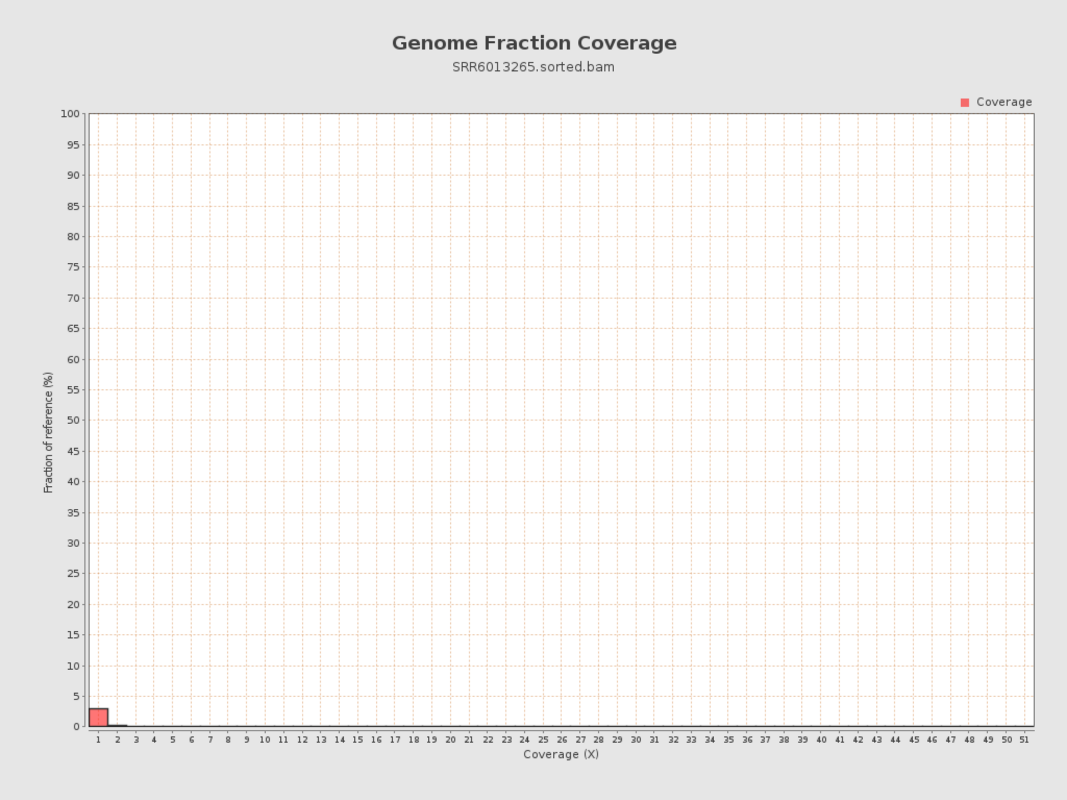
4. Results : Coverage Histogram



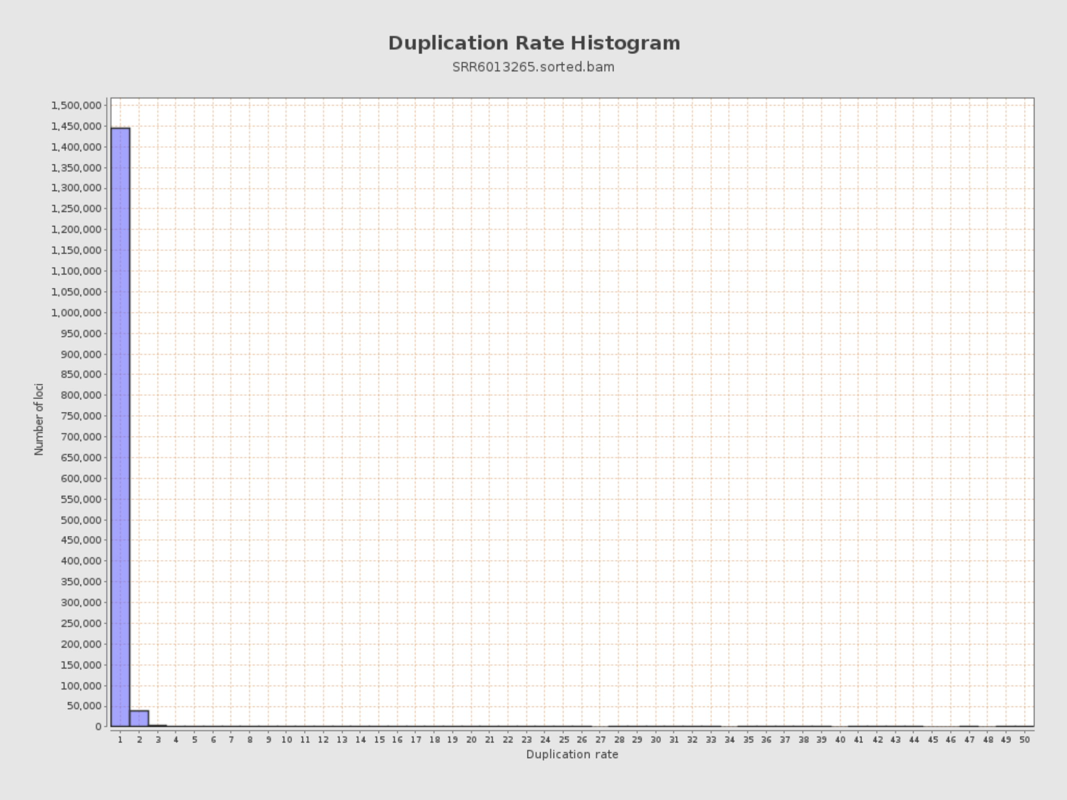
5. Results : Coverage Histogram (0-50X)



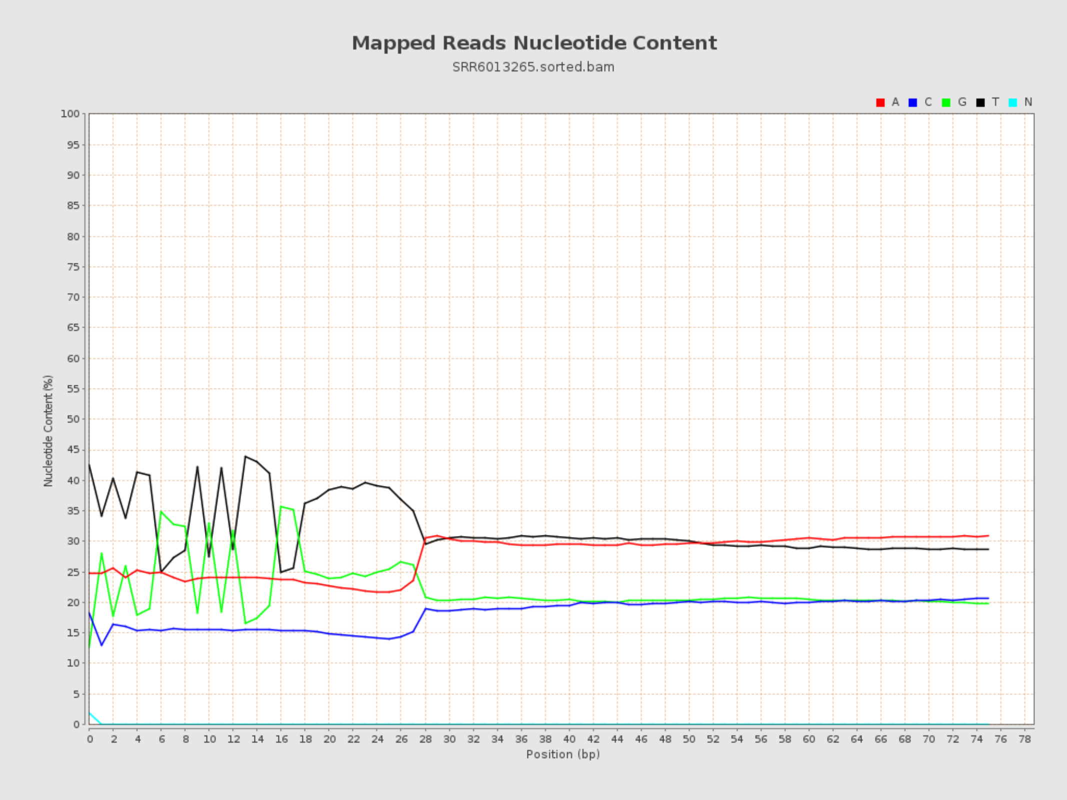
6. Results : Genome Fraction Coverage



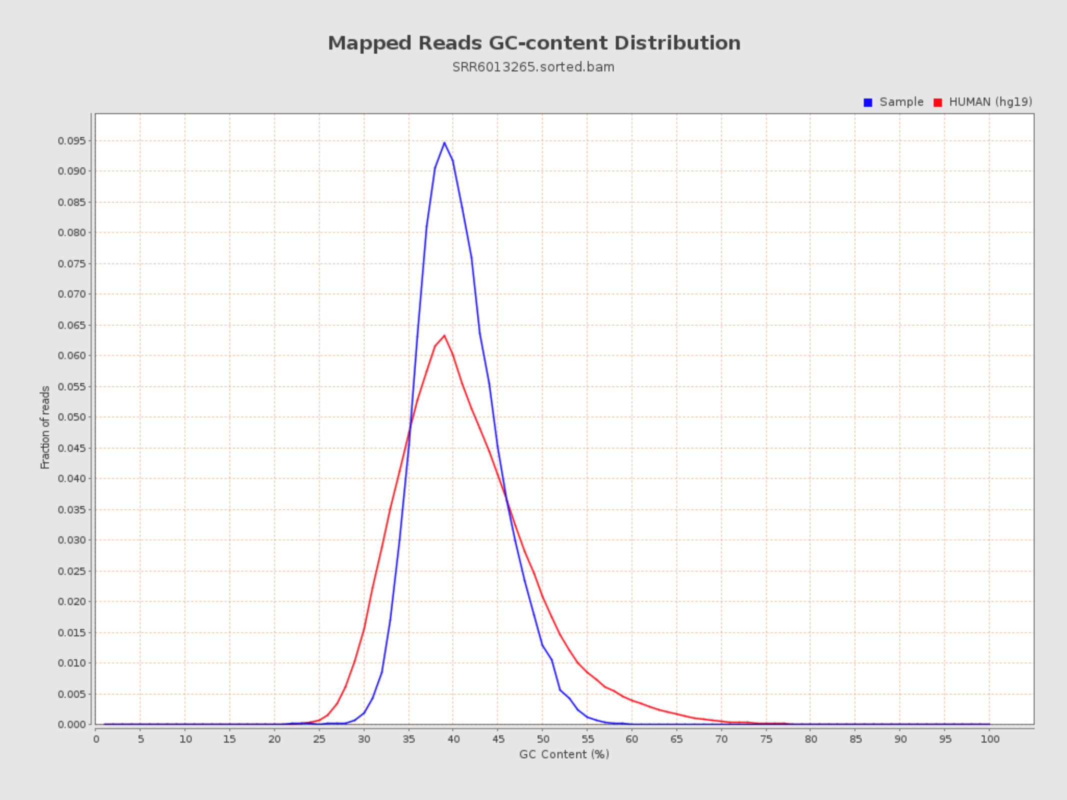
7. Results : Duplication Rate Histogram



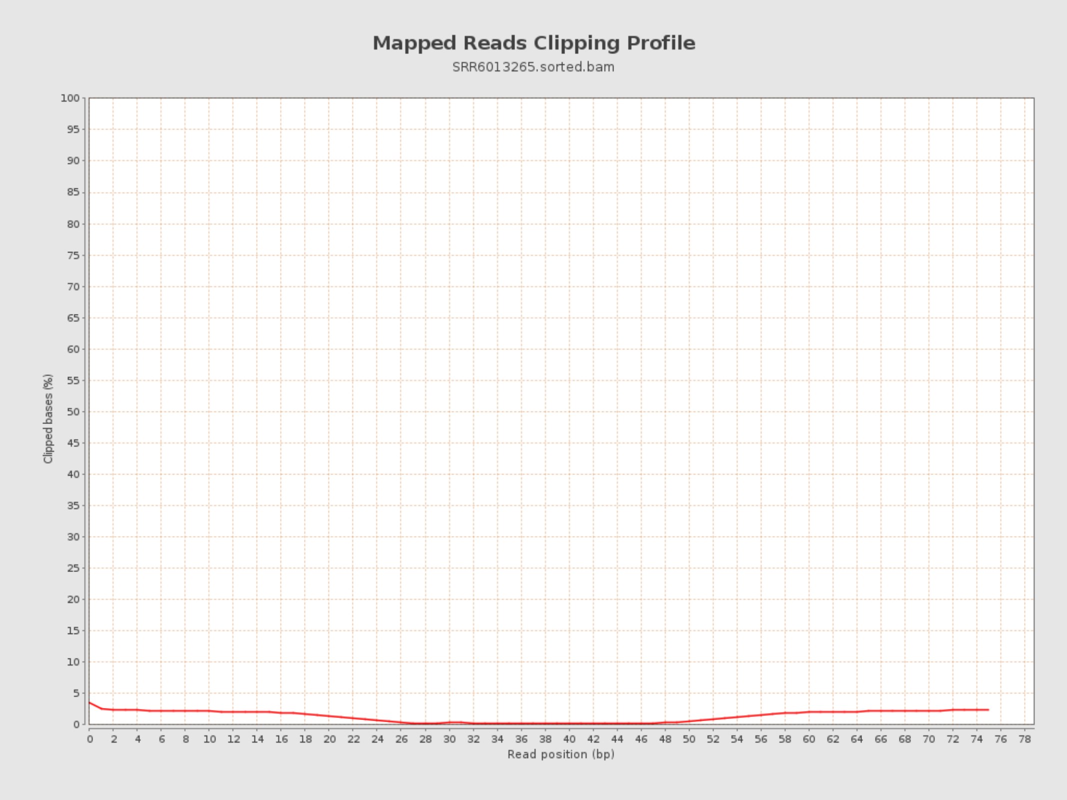
8. Results : Mapped Reads Nucleotide Content



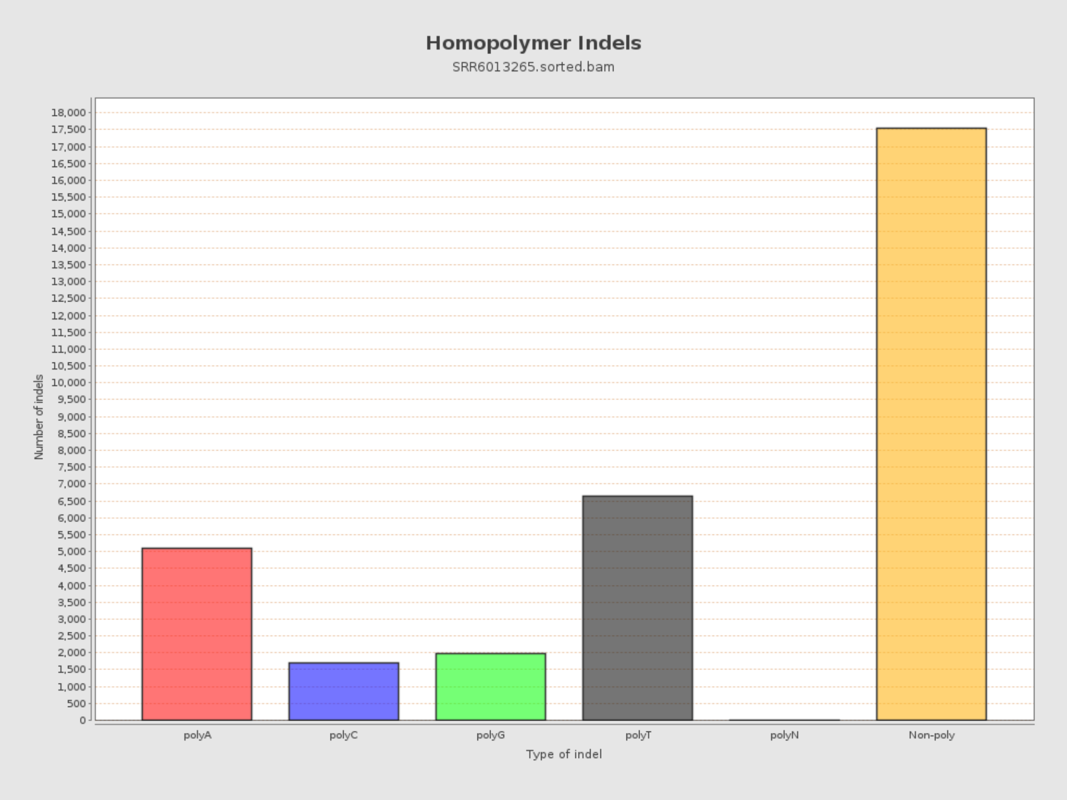
9. Results : Mapped Reads GC-content Distribution



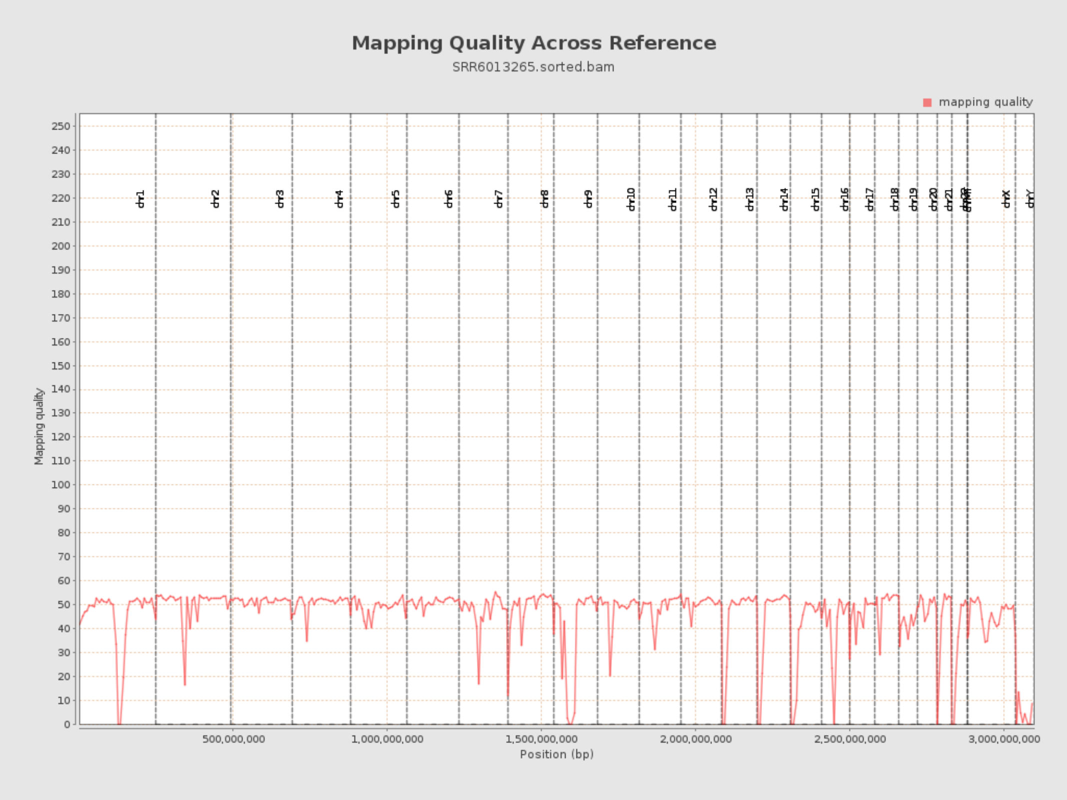
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram