Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:26:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004007.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_SRR6004007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004007.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:25:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,822,322
Mapped reads	1,644,648 / 90.25%
Unmapped reads	177,674 / 9.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,655 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	63,659 / 3.49%
Duplication rate	3.04%
Clipped reads	685,900 / 37.64%

2.2. ACGT Content

Number/percentage of A's	30,848,566 / 27.89%
Number/percentage of C's	20,272,196 / 18.33%
Number/percentage of T's	35,171,436 / 31.79%
Number/percentage of G's	24,306,671 / 21.97%
Number/percentage of N's	21,831 / 0.02%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0357

Standard Deviation	0.3309

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

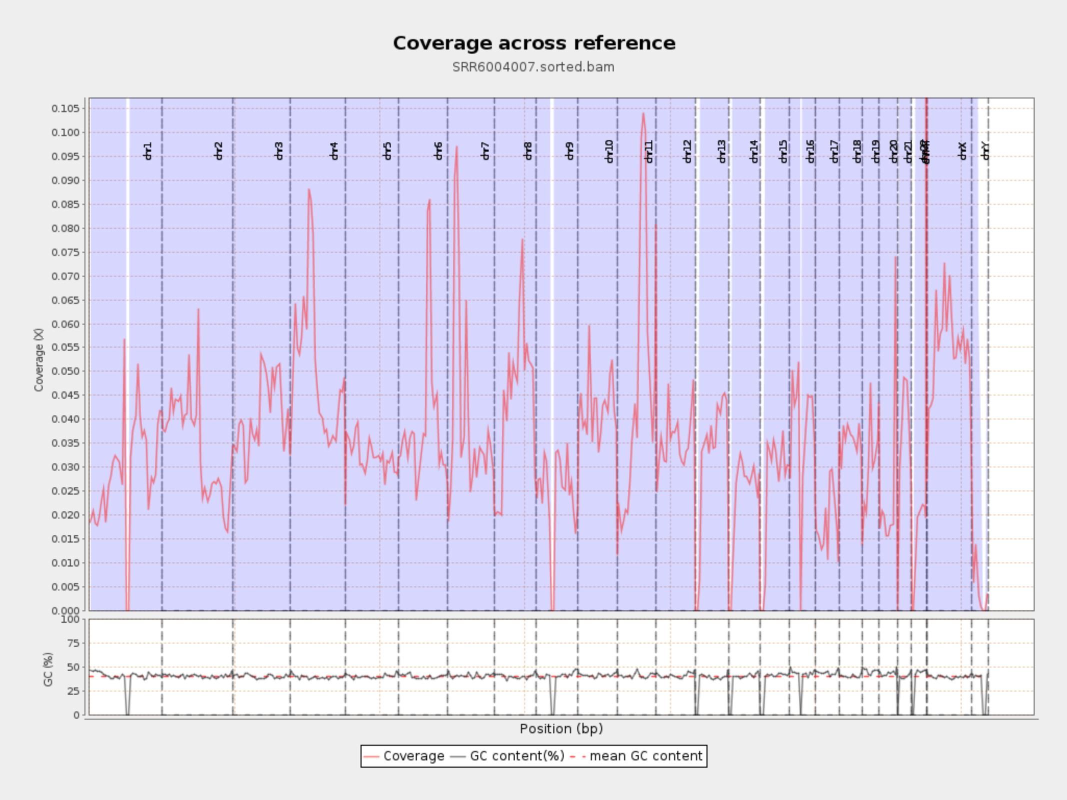
General error rate	0.88%
Mismatches	953,283
Insertions	7,813
Mapped reads with at least one insertion	0.47%
Deletions	28,402
Mapped reads with at least one deletion	1.71%
Homopolymer indels	46.12%

2.6. Chromosome stats

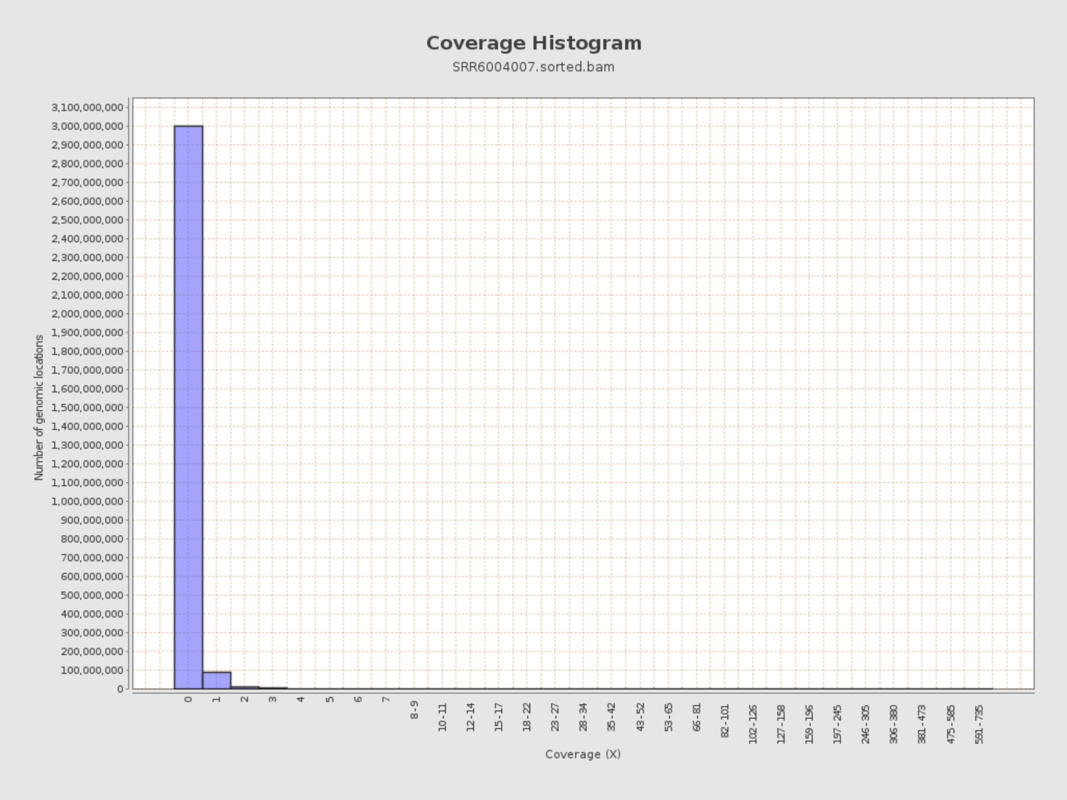
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7217231	0.029	0.6135
chr2	243199373	8377219	0.0344	0.3367
chr3	198022430	8075497	0.0408	0.2231
chr4	191154276	9776301	0.0511	0.2652
chr5	180915260	5878630	0.0325	0.2008
chr6	171115067	6718426	0.0393	0.2373
chr7	159138663	6595260	0.0414	0.4759

chr8	146364022	6523347	0.0446	0.4879
chr9	141213431	3394414	0.024	0.2535
chr10	135534747	5767399	0.0426	0.3123
chr11	135006516	6265542	0.0464	0.3134
chr12	133851895	4734057	0.0354	0.2134
chr13	115169878	3693738	0.0321	0.2032
chr14	107349540	2530145	0.0236	0.1799
chr15	102531392	2638736	0.0257	0.1805
chr16	90354753	3447118	0.0382	0.2327
chr17	81195210	1493392	0.0184	0.1657
chr18	78077248	2801498	0.0359	0.475
chr19	59128983	1811613	0.0306	0.4019
chr20	63025520	1630975	0.0259	0.1891
chr21	48129895	1703236	0.0354	0.2219
chr22	51304566	765426	0.0149	0.1326
chrMT	16571	29925	1.8059	1.9002
chrX	155270560	8518008	0.0549	0.2827
chrY	59373566	283219	0.0048	0.1046

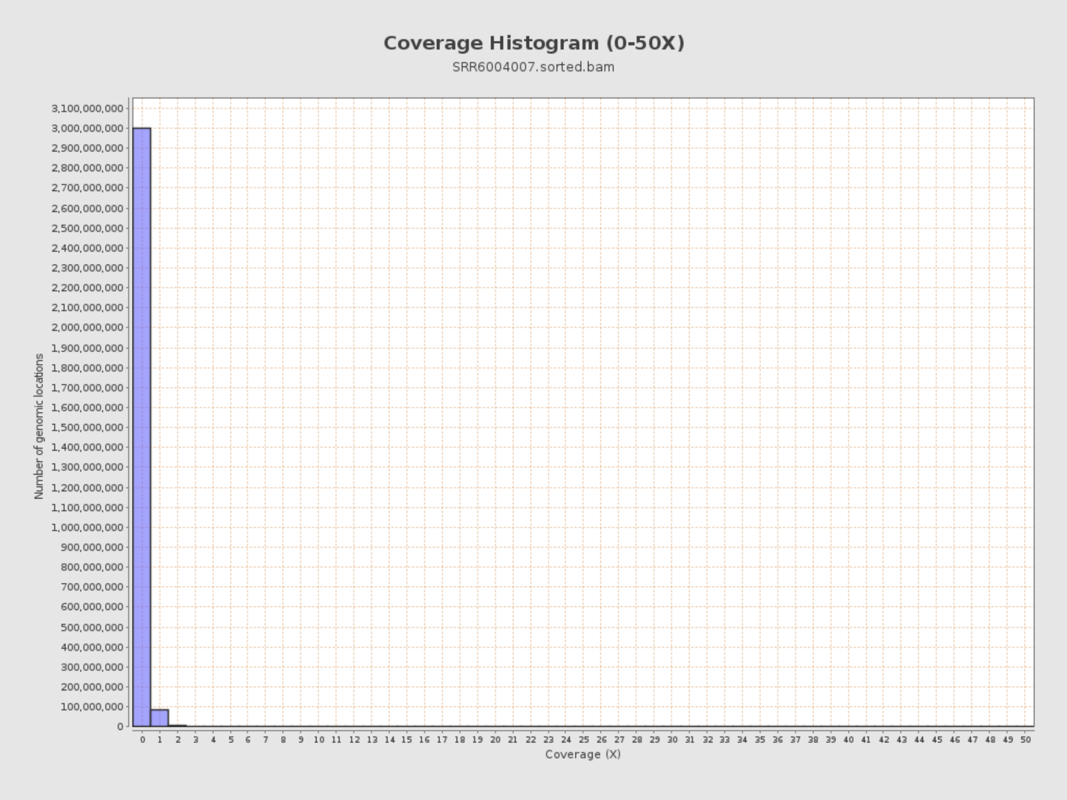
3. Results : Coverage across reference



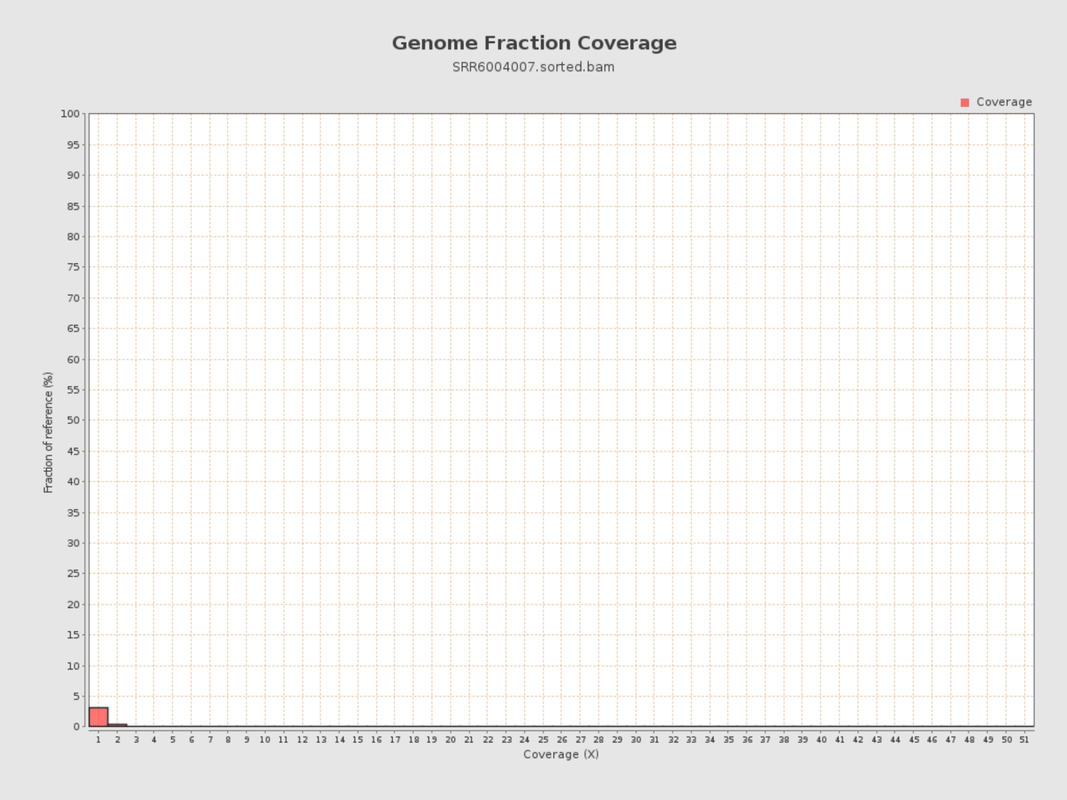
4. Results : Coverage Histogram



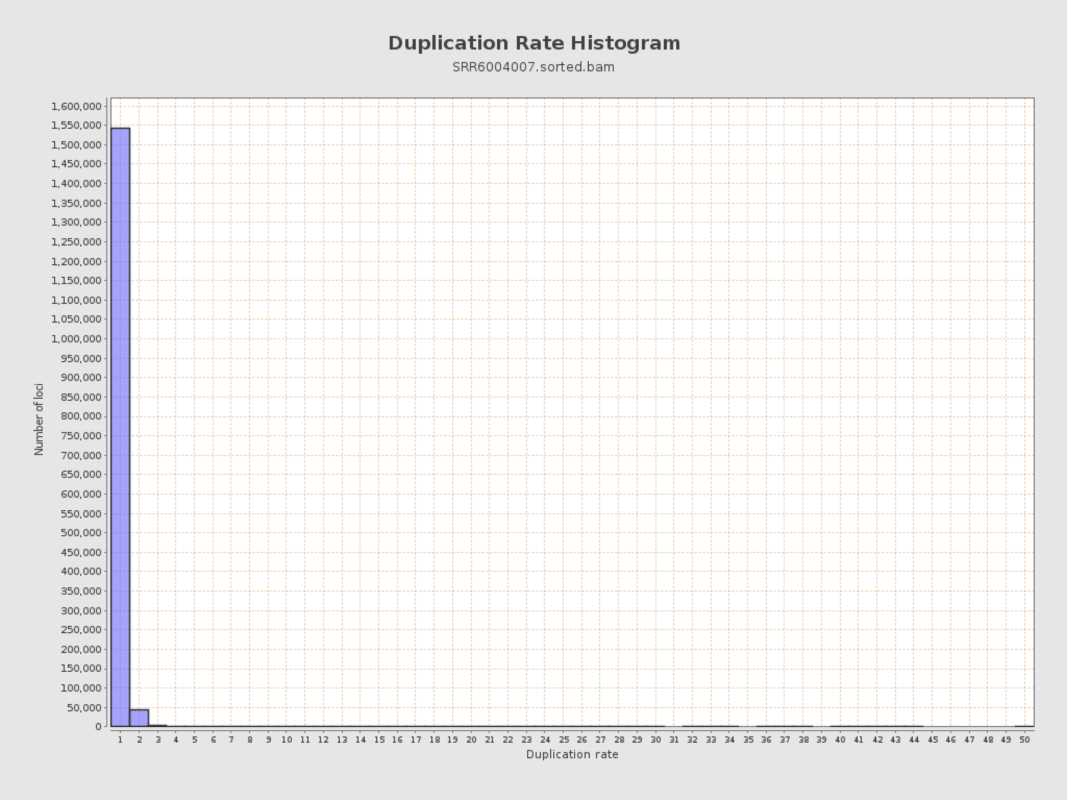
5. Results : Coverage Histogram (0-50X)



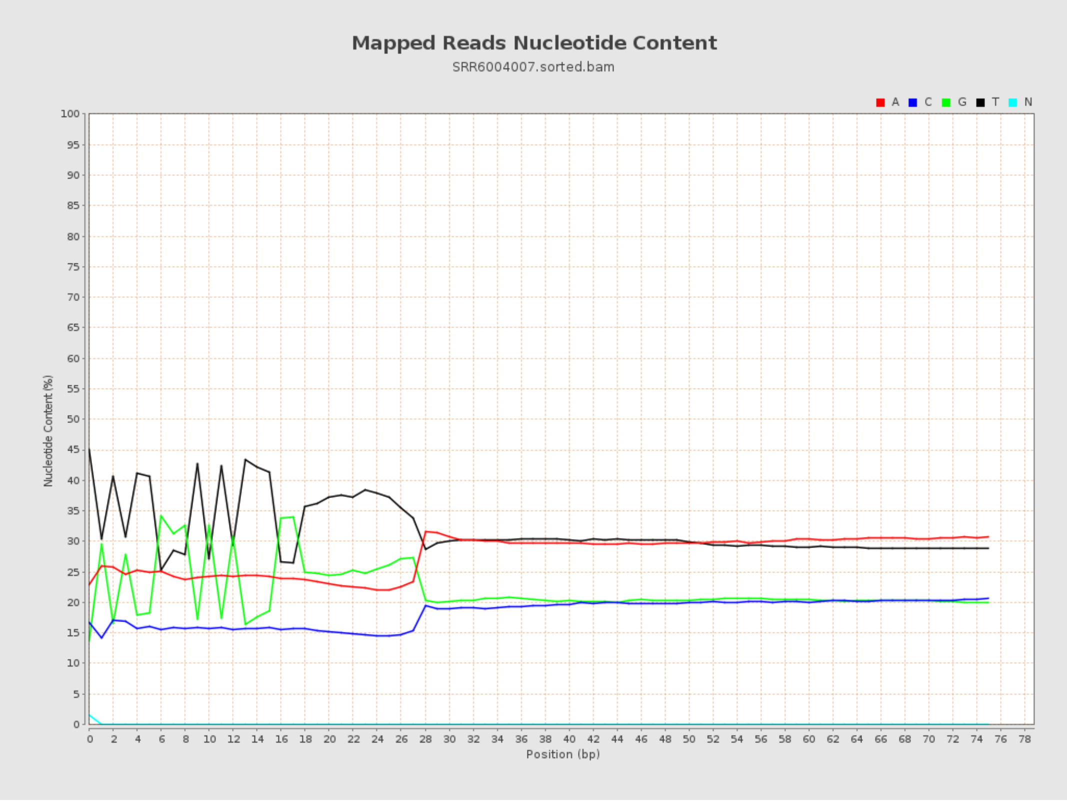
6. Results : Genome Fraction Coverage



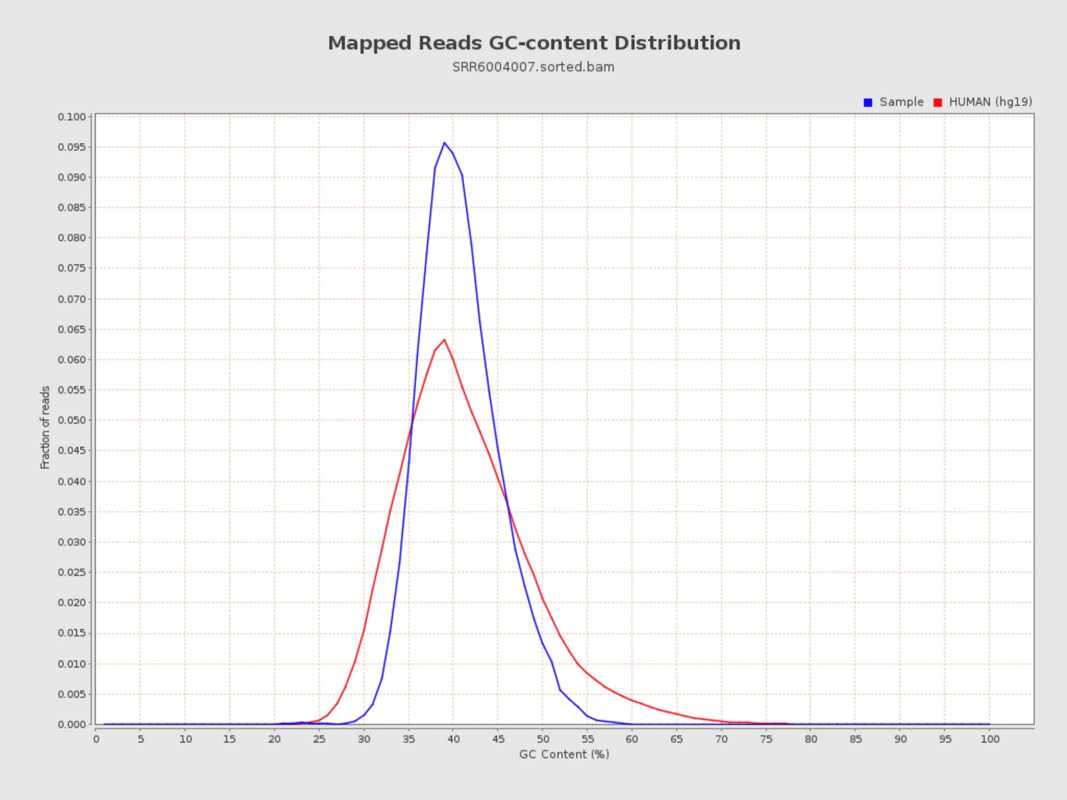
7. Results : Duplication Rate Histogram



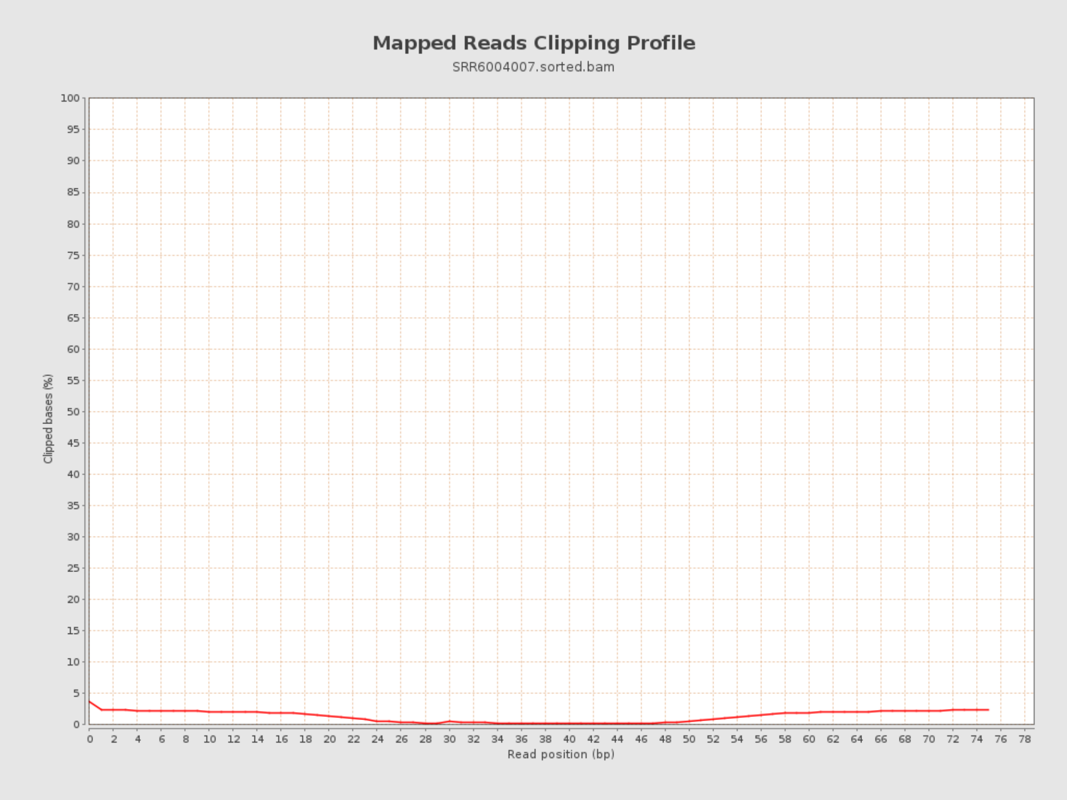
8. Results : Mapped Reads Nucleotide Content



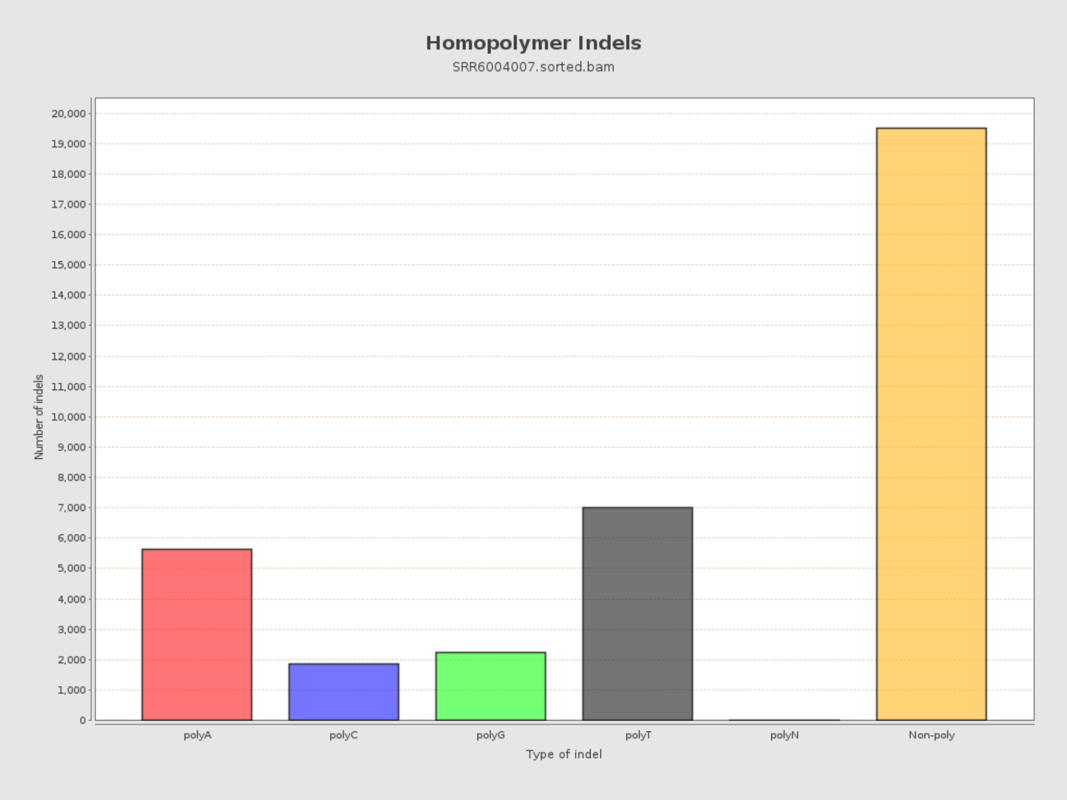
9. Results : Mapped Reads GC-content Distribution



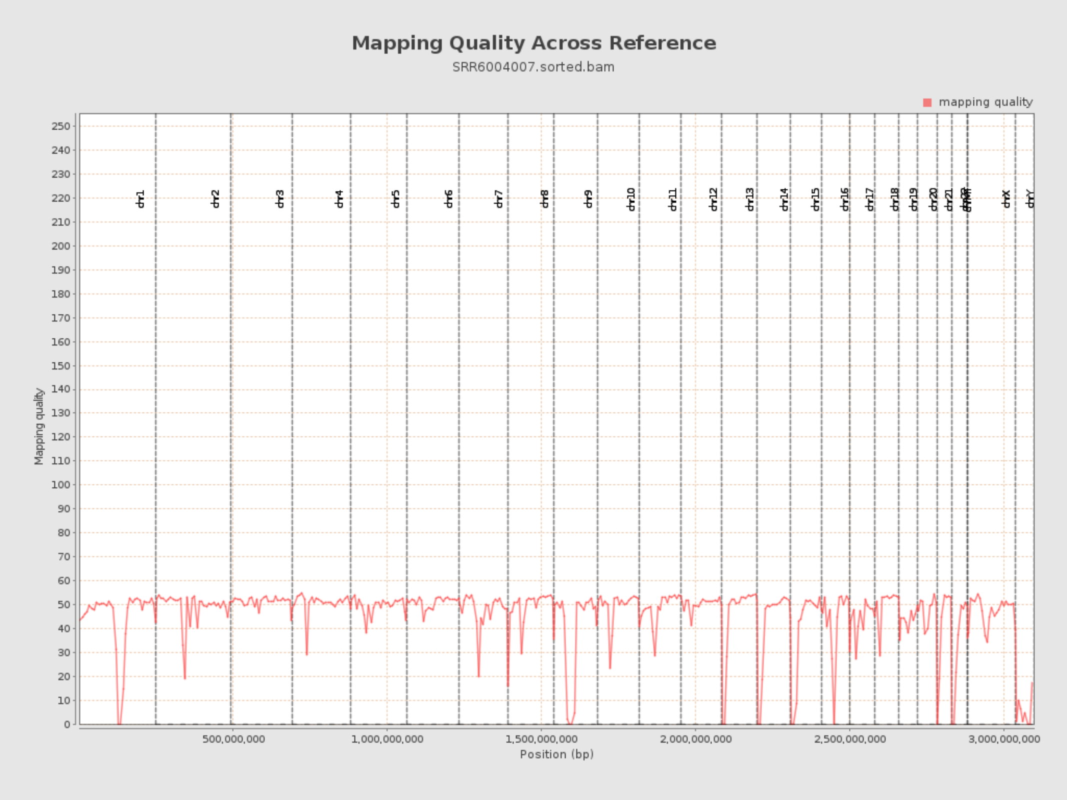
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram