Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:27:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004163.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_SRR6004163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004163.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:27:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,094,207
Mapped reads	1,757,579 / 83.93%
Unmapped reads	336,628 / 16.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,943 / 1.14%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	85,763 / 4.1%
Duplication rate	3.87%
Clipped reads	962,274 / 45.95%

2.2. ACGT Content

Number/percentage of A's	31,992,537 / 28.18%
Number/percentage of C's	20,849,281 / 18.36%
Number/percentage of T's	36,014,298 / 31.72%
Number/percentage of G's	24,657,403 / 21.72%
Number/percentage of N's	17,052 / 0.02%
GC Percentage	40.08%

2.3. Coverage

Mean	0.0367

Standard Deviation	0.3476

2.4. Mapping Quality

Mean Mapping Quality	45.55

2.5. Mismatches and indels

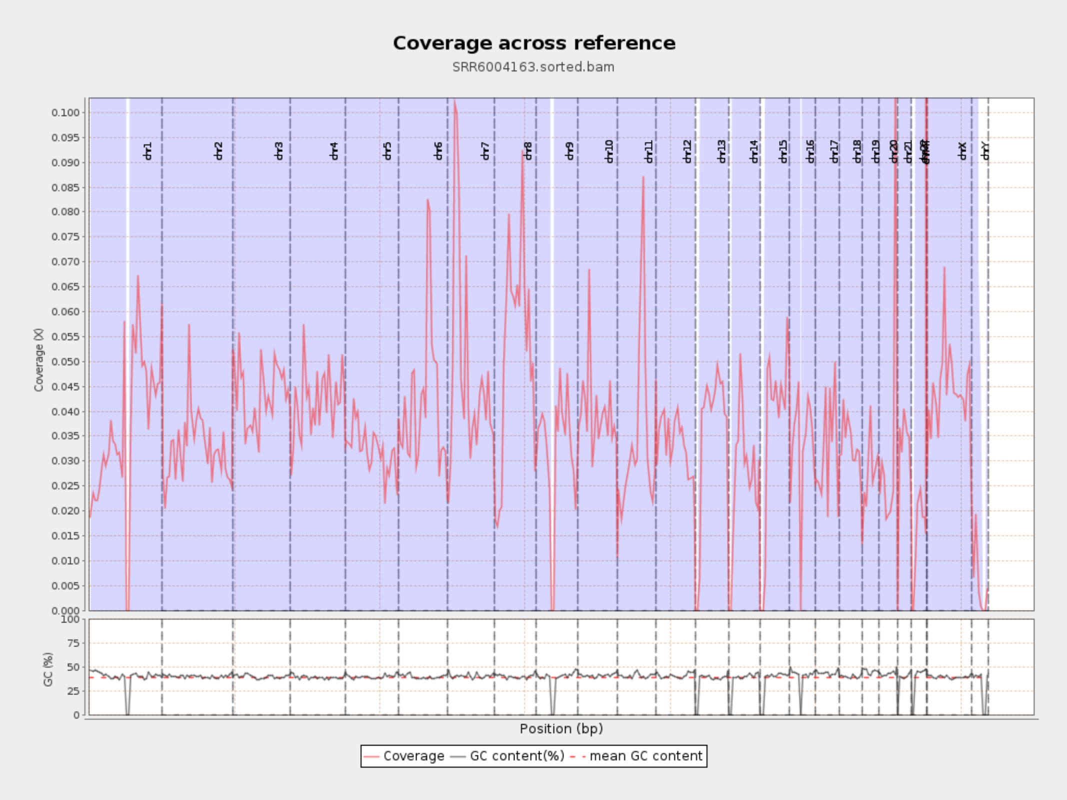
General error rate	1.01%
Mismatches	1,127,952
Insertions	8,462
Mapped reads with at least one insertion	0.48%
Deletions	42,689
Mapped reads with at least one deletion	2.39%
Homopolymer indels	43.39%

2.6. Chromosome stats

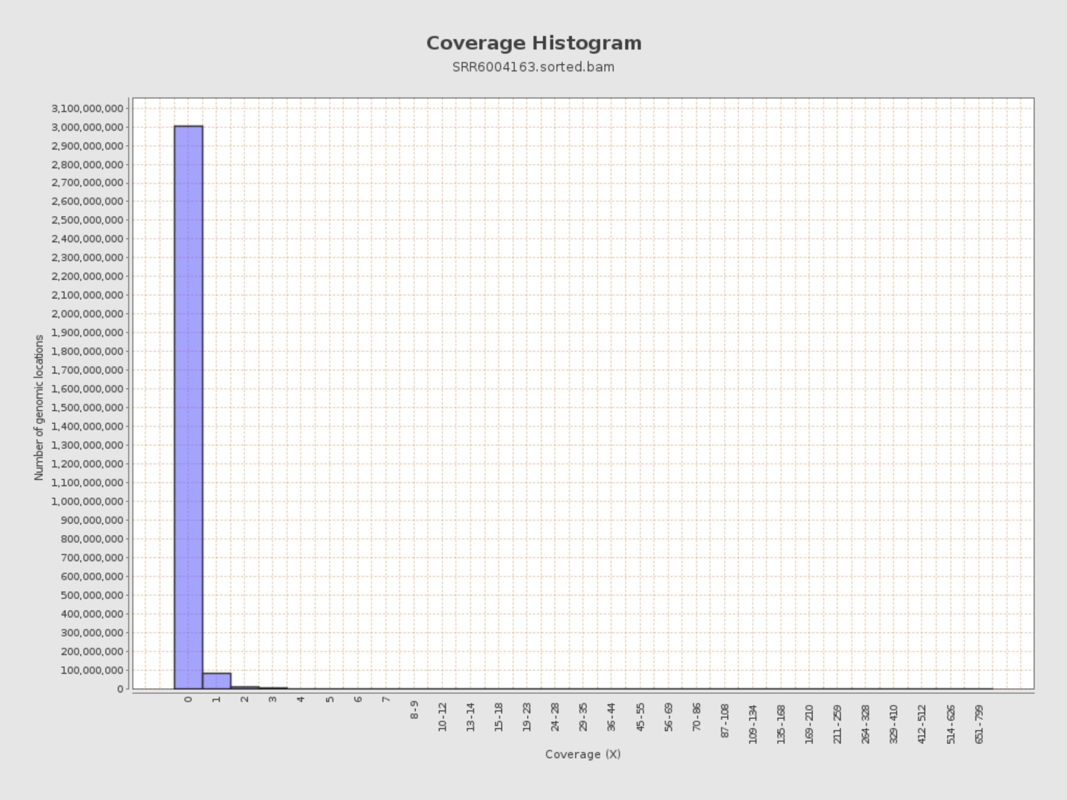
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9142709	0.0367	0.6358
chr2	243199373	7932711	0.0326	0.3409
chr3	198022430	8618844	0.0435	0.241
chr4	191154276	8023757	0.042	0.2586
chr5	180915260	5839333	0.0323	0.2109
chr6	171115067	7205440	0.0421	0.2604
chr7	159138663	7788355	0.0489	0.4771

chr8	146364022	7593450	0.0519	0.5542
chr9	141213431	4511521	0.0319	0.3009
chr10	135534747	5414184	0.0399	0.3487
chr11	135006516	4755644	0.0352	0.266
chr12	133851895	4471841	0.0334	0.2188
chr13	115169878	4080665	0.0354	0.2199
chr14	107349540	2844515	0.0265	0.2121
chr15	102531392	3734649	0.0364	0.2212
chr16	90354753	3002272	0.0332	0.2398
chr17	81195210	2608269	0.0321	0.2314
chr18	78077248	2612111	0.0335	0.4879
chr19	59128983	1658261	0.028	0.4401
chr20	63025520	2277199	0.0361	0.2318
chr21	48129895	1506487	0.0313	0.2306
chr22	51304566	748584	0.0146	0.1372
chrMT	16571	14737	0.8893	1.1498
chrX	155270560	6880226	0.0443	0.2707
chrY	59373566	336952	0.0057	0.1445

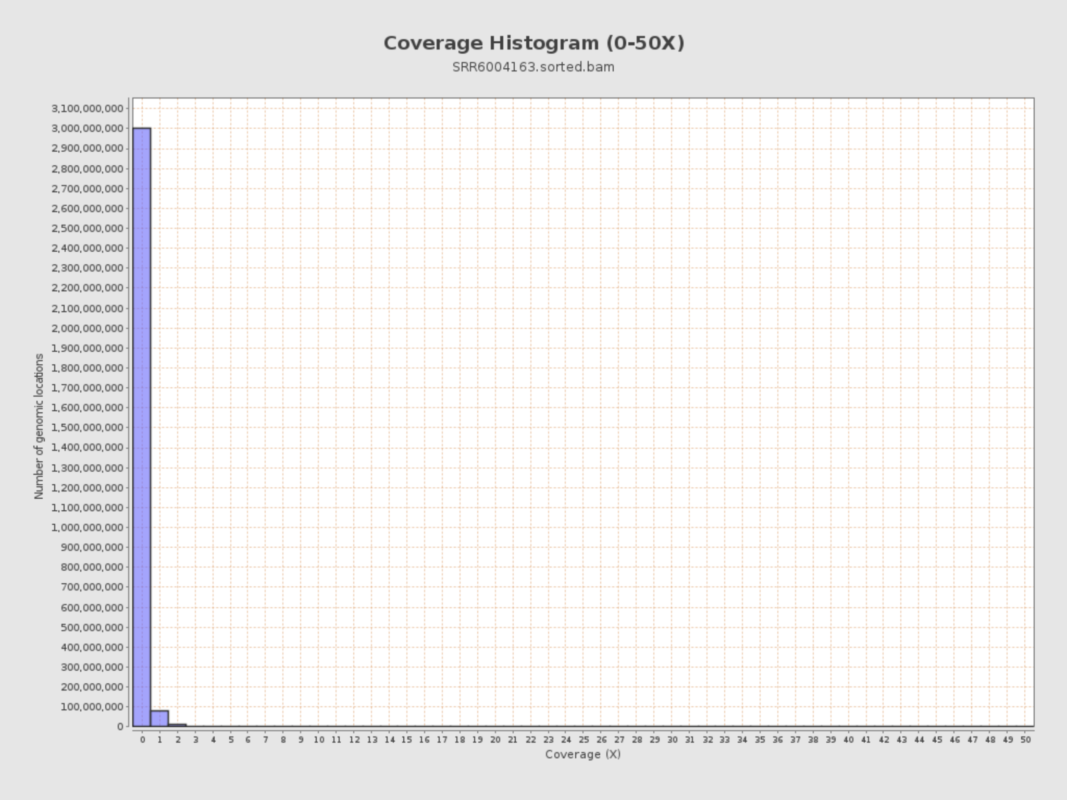
3. Results : Coverage across reference



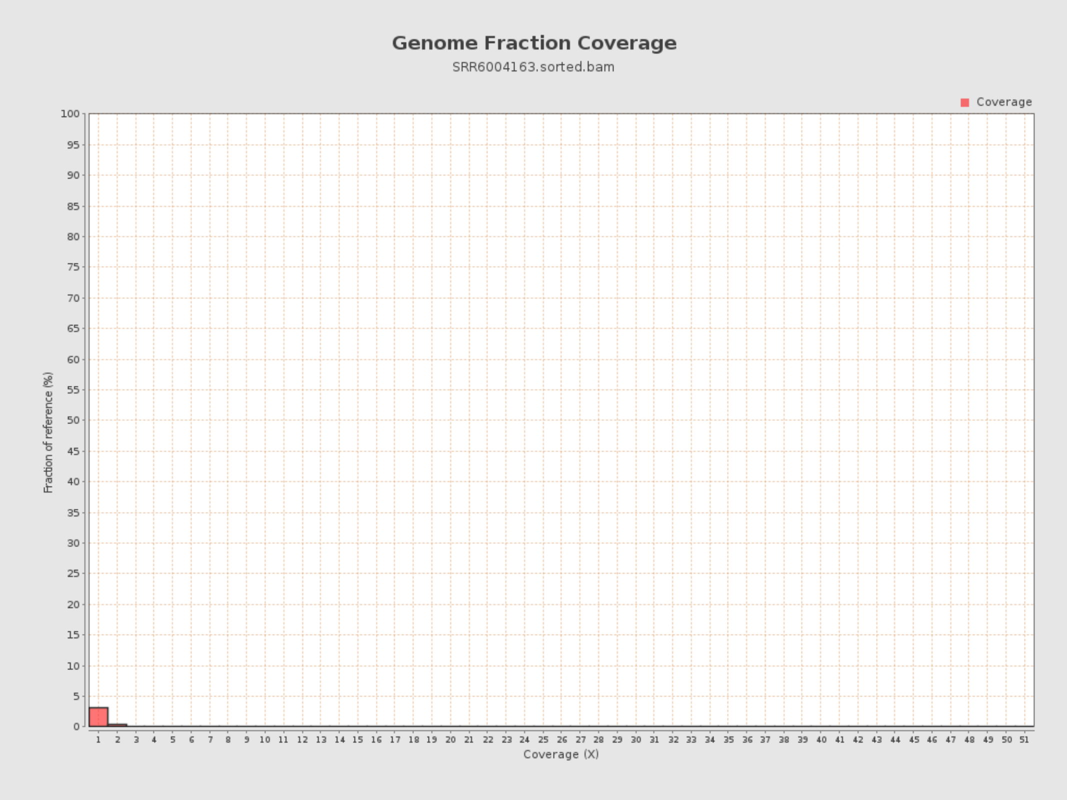
4. Results : Coverage Histogram



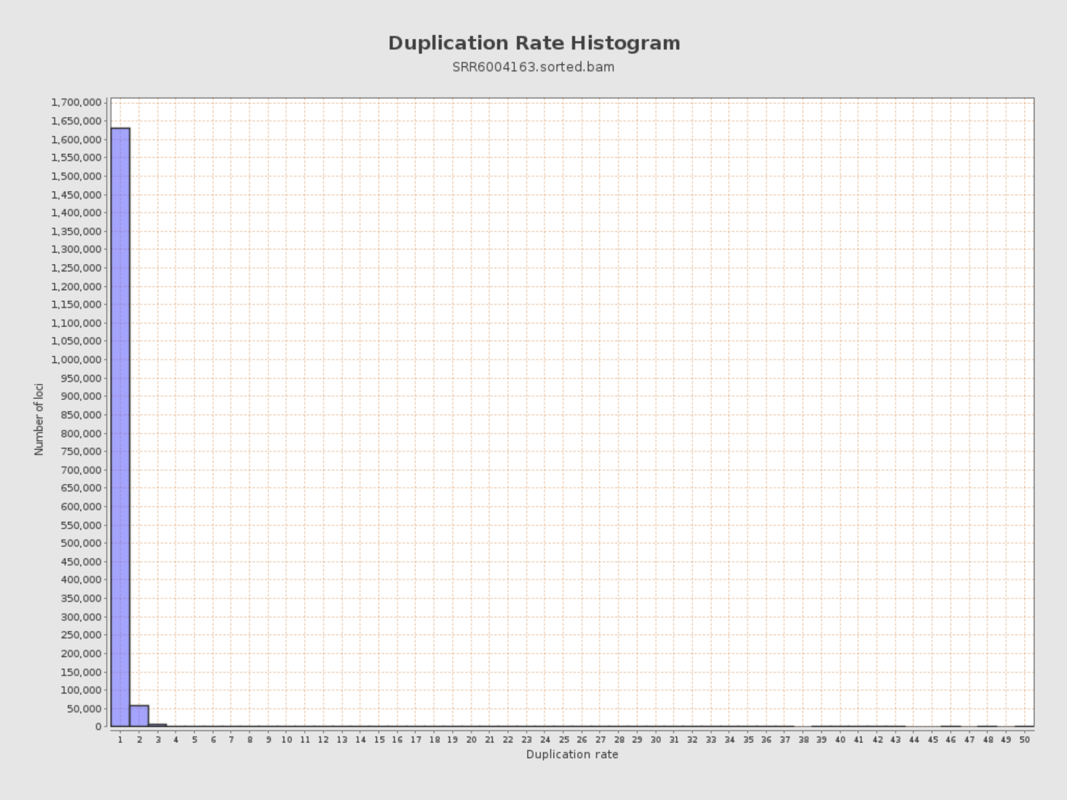
5. Results : Coverage Histogram (0-50X)



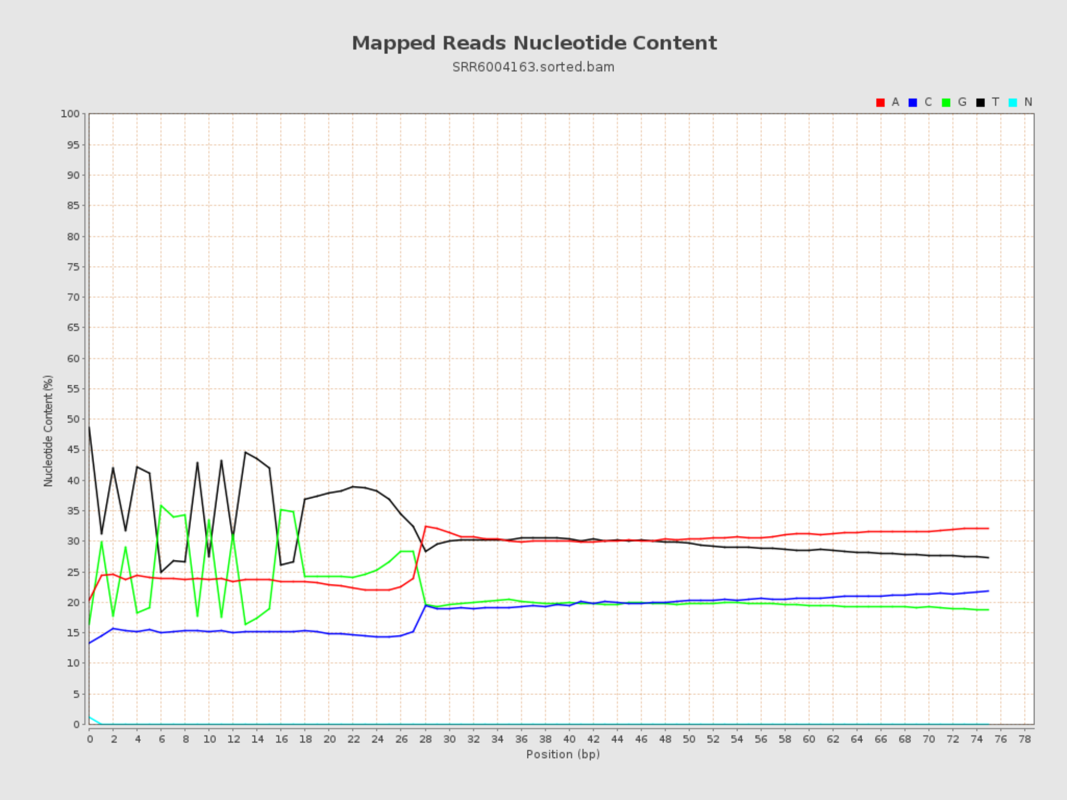
6. Results : Genome Fraction Coverage



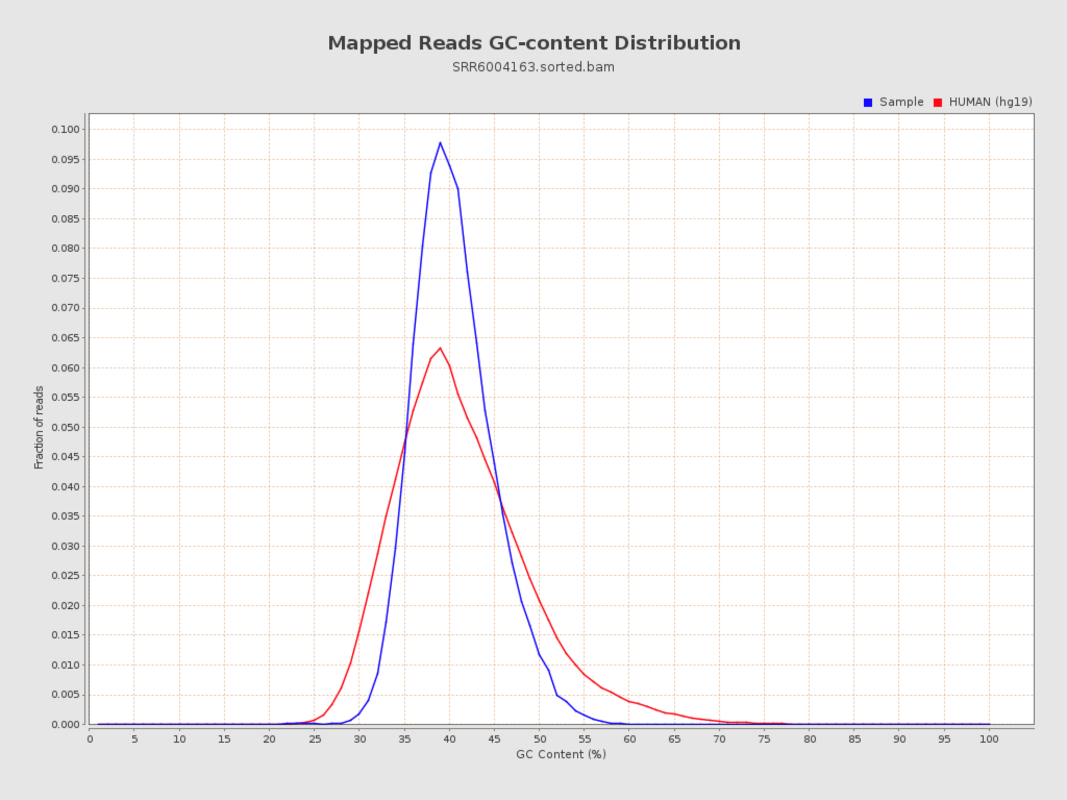
7. Results : Duplication Rate Histogram



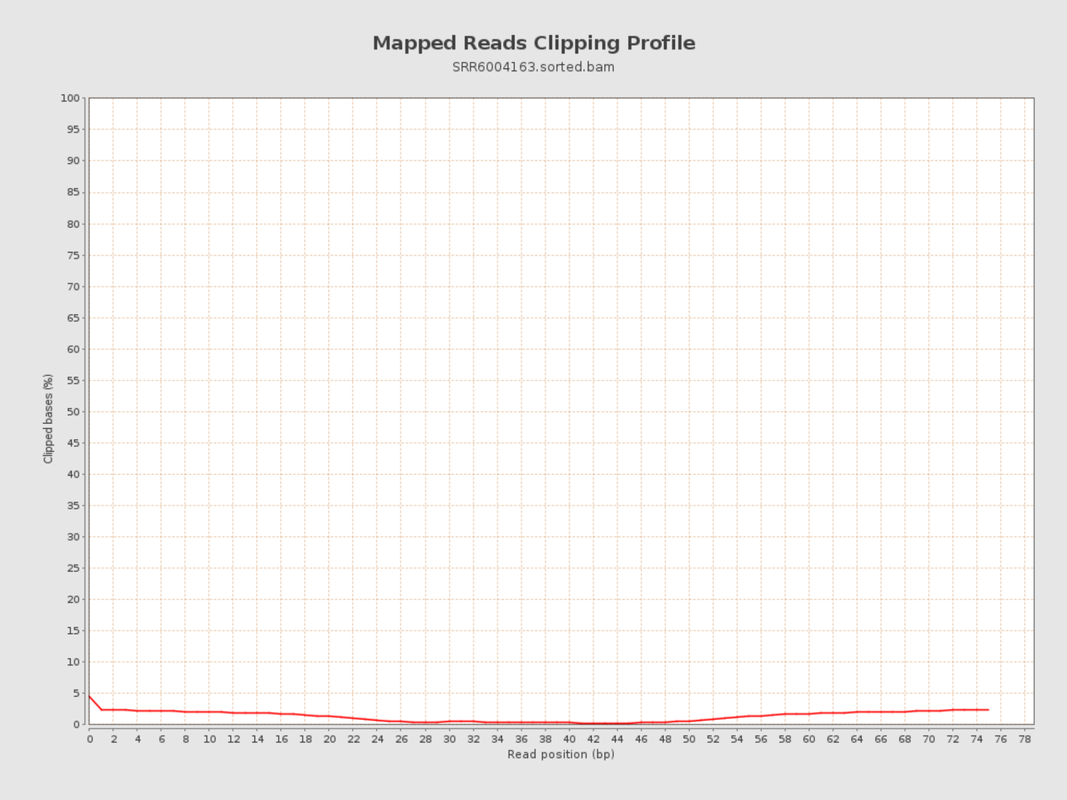
8. Results : Mapped Reads Nucleotide Content



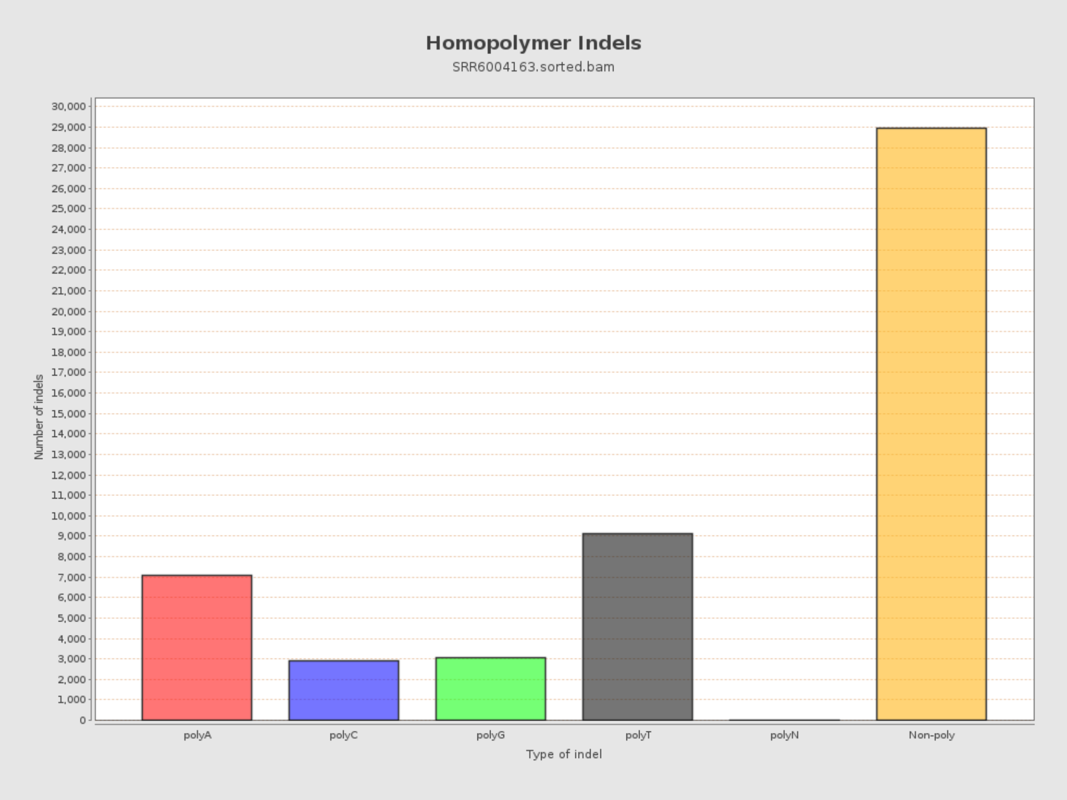
9. Results : Mapped Reads GC-content Distribution



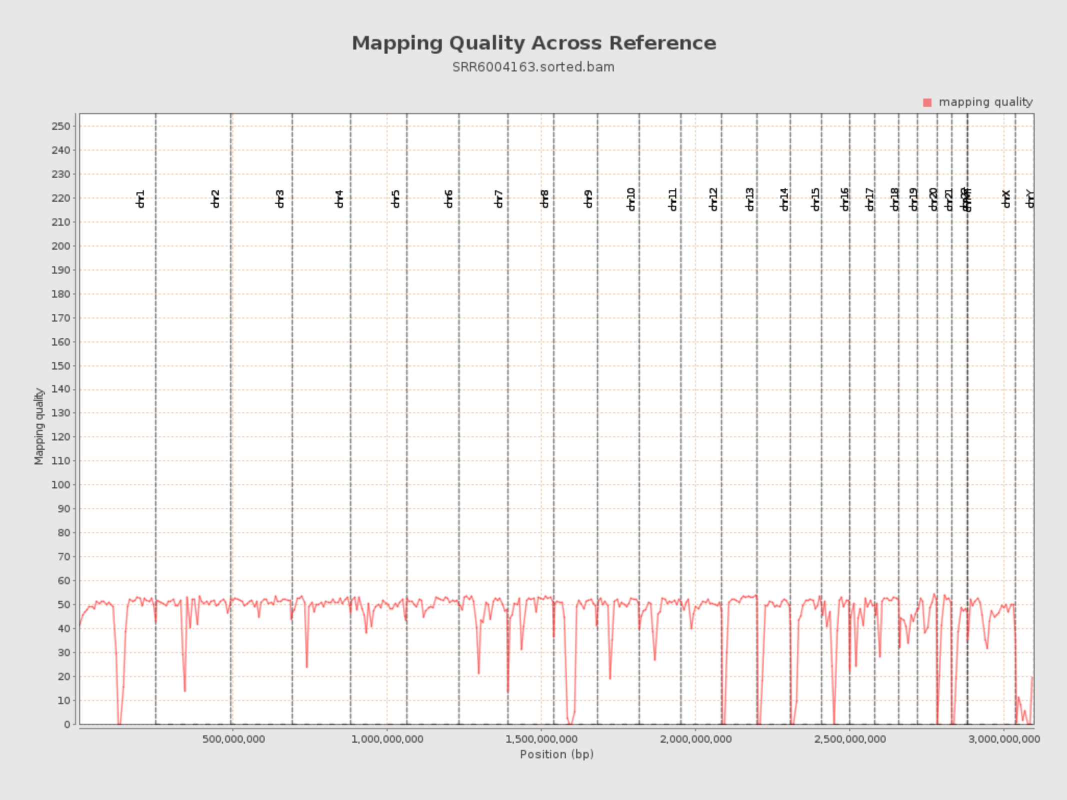
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram