Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:51:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004104.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_SRR6004104 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:51:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,424,497
Mapped reads	1,647,986 / 67.97%
Unmapped reads	776,511 / 32.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,584 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	146,749 / 6.05%
Duplication rate	7.03%
Clipped reads	899,923 / 37.12%

2.2. ACGT Content

Number/percentage of A's	28,140,414 / 26.44%
Number/percentage of C's	19,377,339 / 18.21%
Number/percentage of T's	34,727,780 / 32.63%
Number/percentage of G's	24,157,735 / 22.7%
Number/percentage of N's	13,382 / 0.01%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0344

Standard Deviation	0.3624

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

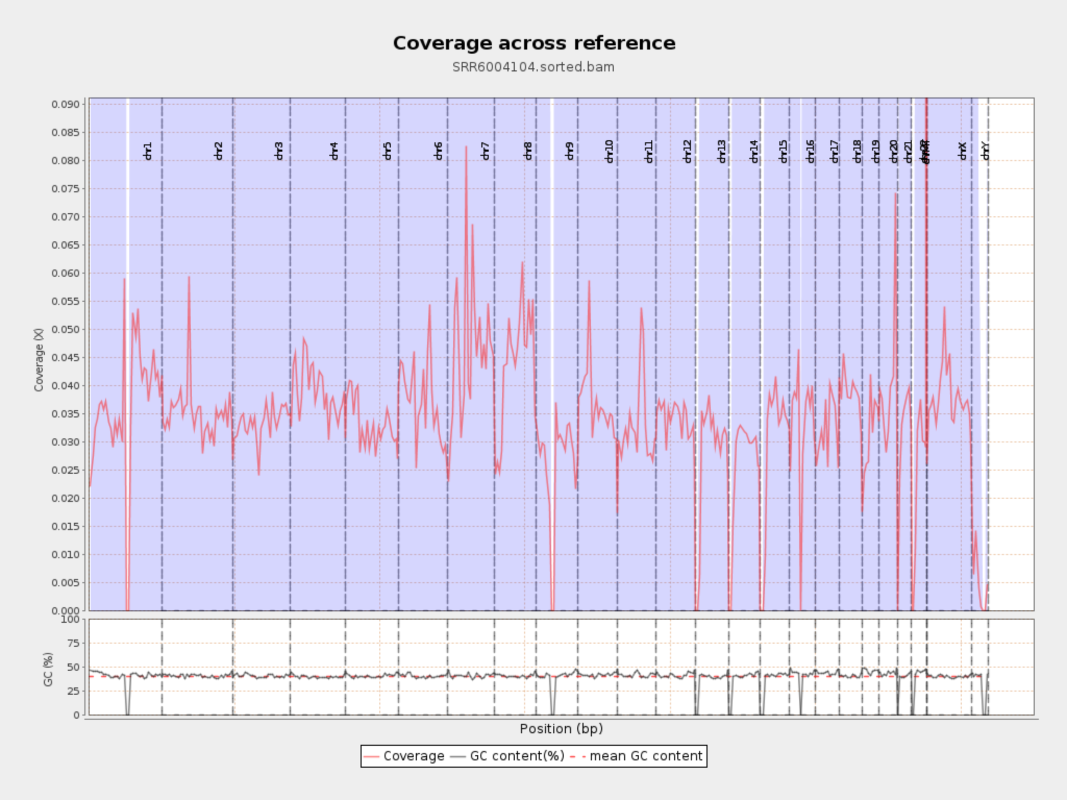
General error rate	1.13%
Mismatches	1,188,425
Insertions	9,354
Mapped reads with at least one insertion	0.56%
Deletions	36,142
Mapped reads with at least one deletion	2.16%
Homopolymer indels	46.76%

2.6. Chromosome stats

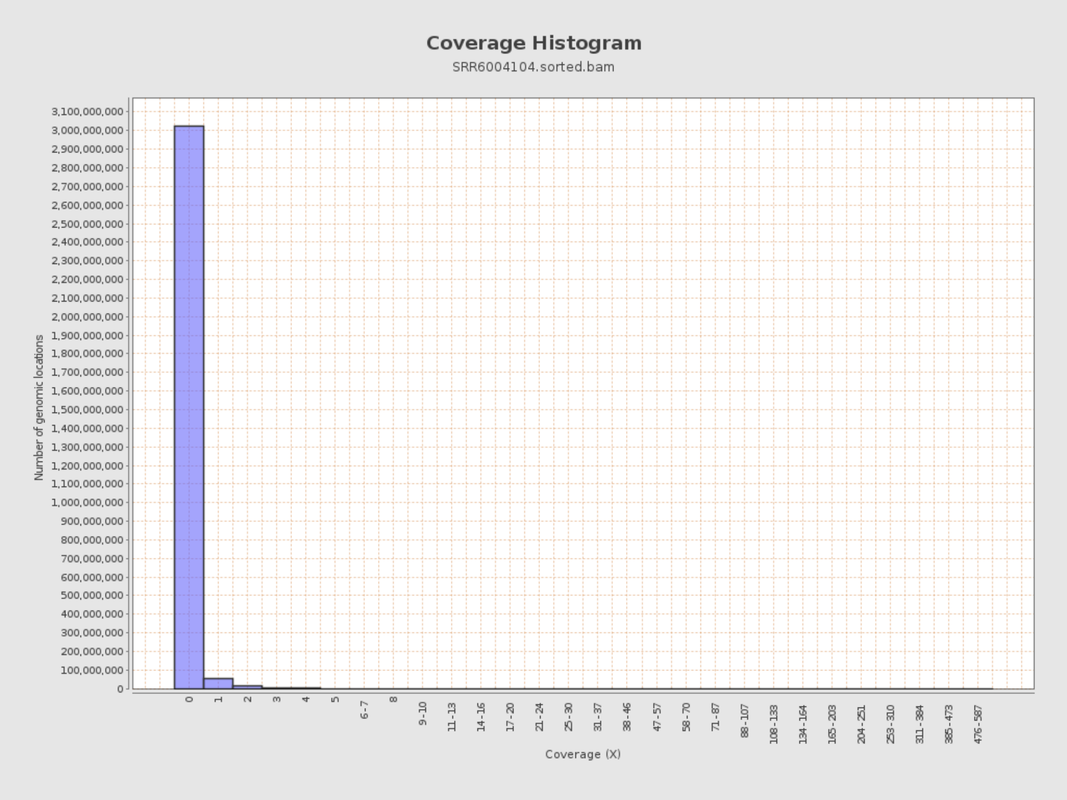
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8996123	0.0361	0.5611
chr2	243199373	8577791	0.0353	0.4003
chr3	198022430	6608748	0.0334	0.2548
chr4	191154276	7448857	0.039	0.2858
chr5	180915260	6009460	0.0332	0.2543
chr6	171115067	6403049	0.0374	0.2936
chr7	159138663	7478888	0.047	0.6845

chr8	146364022	6378811	0.0436	0.3642
chr9	141213431	3647977	0.0258	0.3032
chr10	135534747	5042431	0.0372	0.3414
chr11	135006516	4454953	0.033	0.3305
chr12	133851895	4568252	0.0341	0.2627
chr13	115169878	3136433	0.0272	0.2341
chr14	107349540	2752838	0.0256	0.2342
chr15	102531392	2968492	0.029	0.24
chr16	90354753	3006746	0.0333	0.2639
chr17	81195210	2599813	0.032	0.2702
chr18	78077248	3065032	0.0393	0.5507
chr19	59128983	1853232	0.0313	0.3677
chr20	63025520	2573992	0.0408	0.2935
chr21	48129895	1475322	0.0307	0.2544
chr22	51304566	1146220	0.0223	0.2031
chrMT	16571	88205	5.3229	4.8616
chrX	155270560	5903133	0.038	0.2906
chrY	59373566	291385	0.0049	0.1109

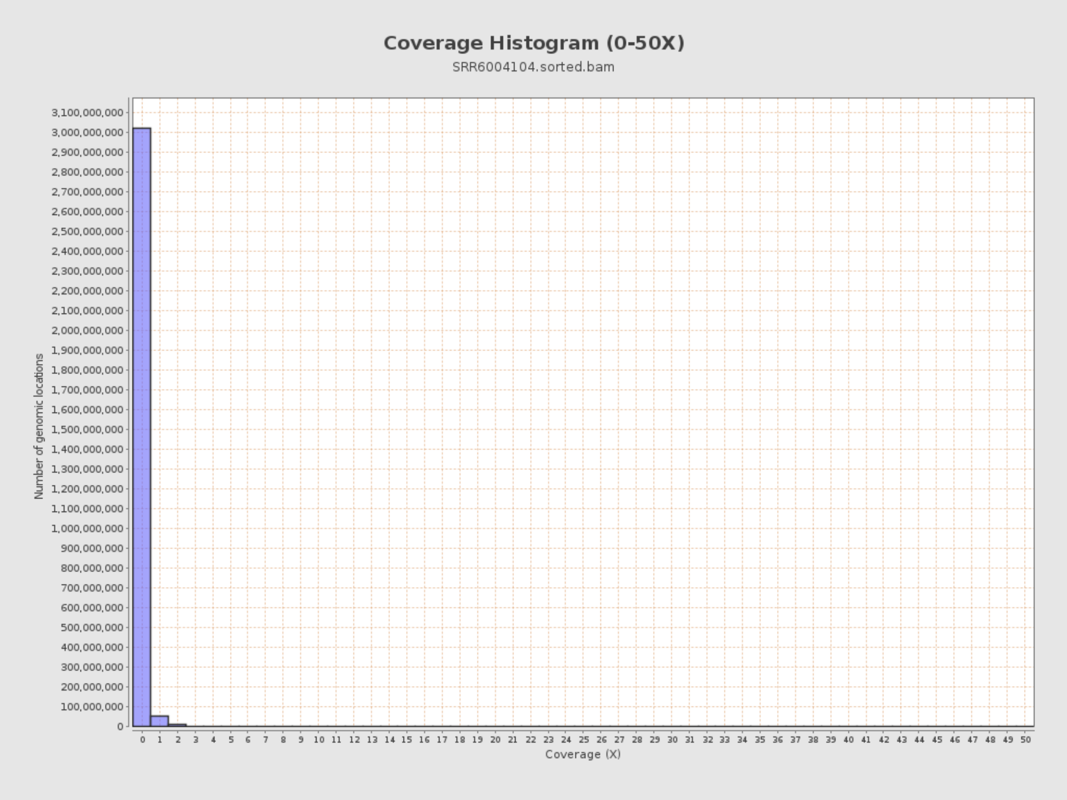
3. Results : Coverage across reference



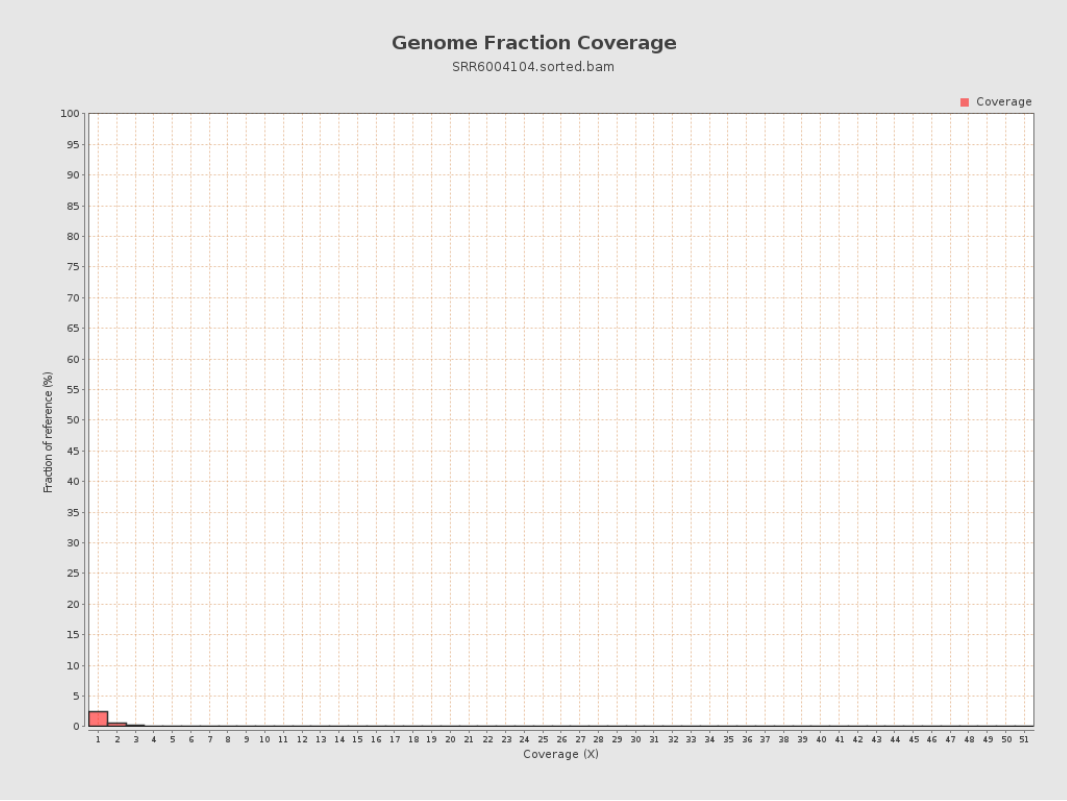
4. Results : Coverage Histogram



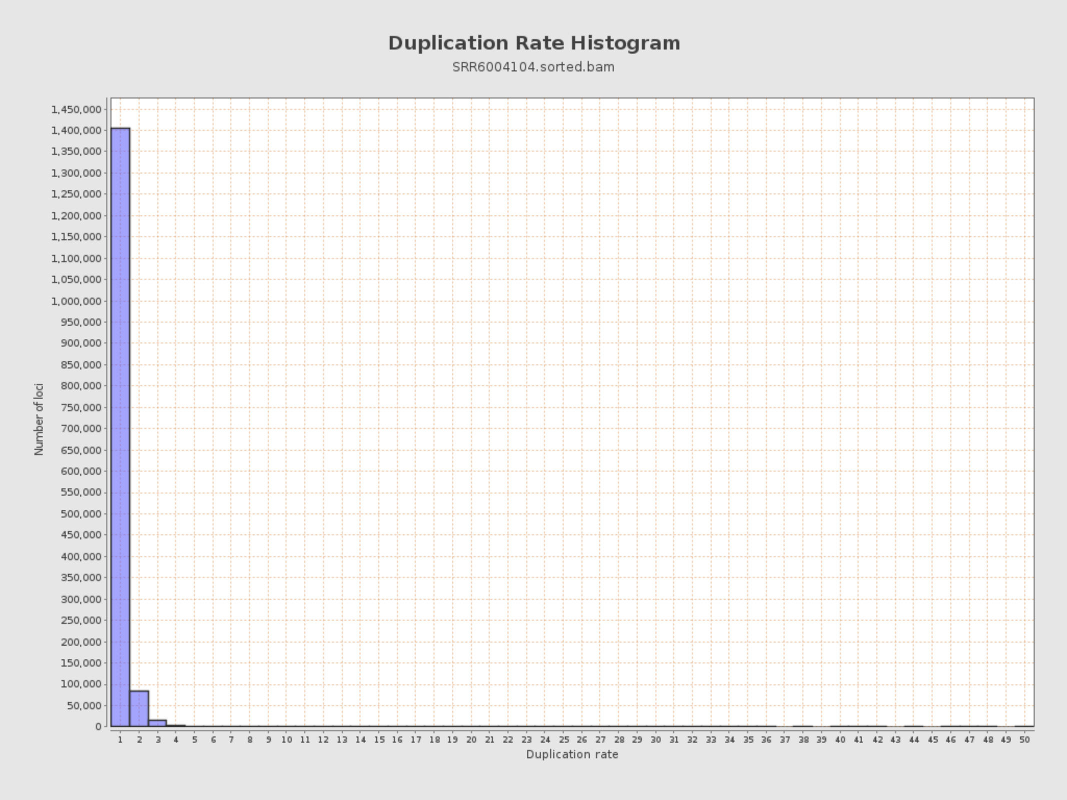
5. Results : Coverage Histogram (0-50X)



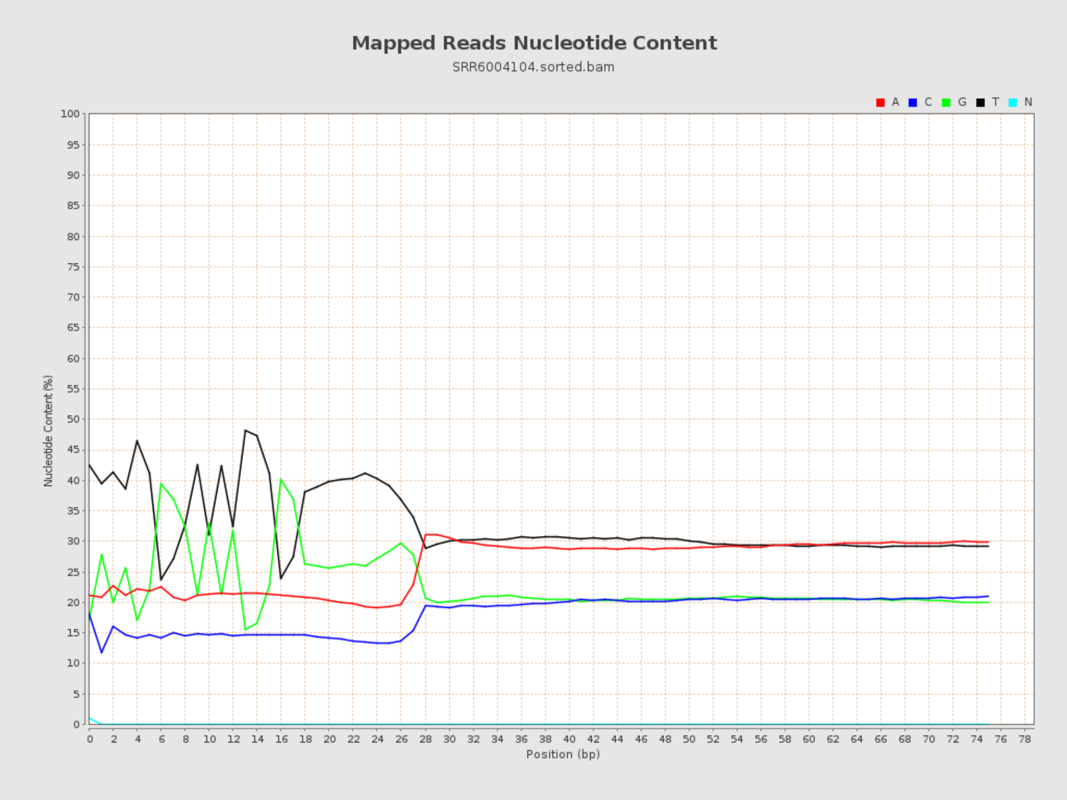
6. Results : Genome Fraction Coverage



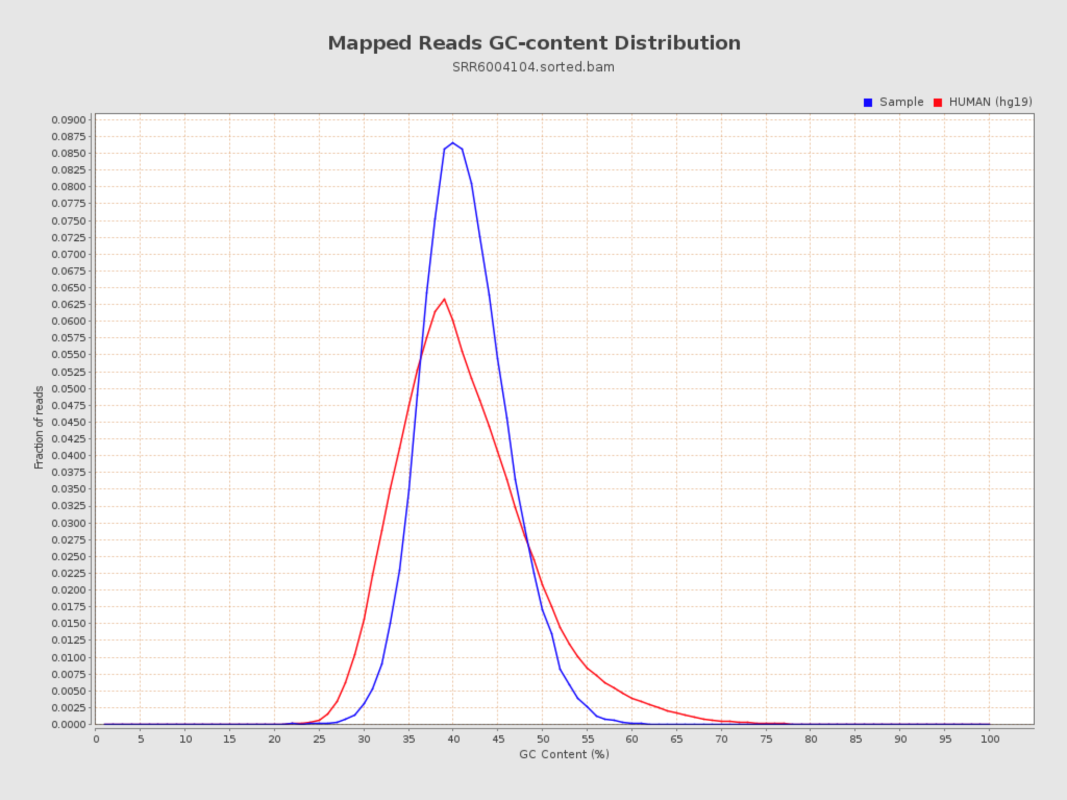
7. Results : Duplication Rate Histogram



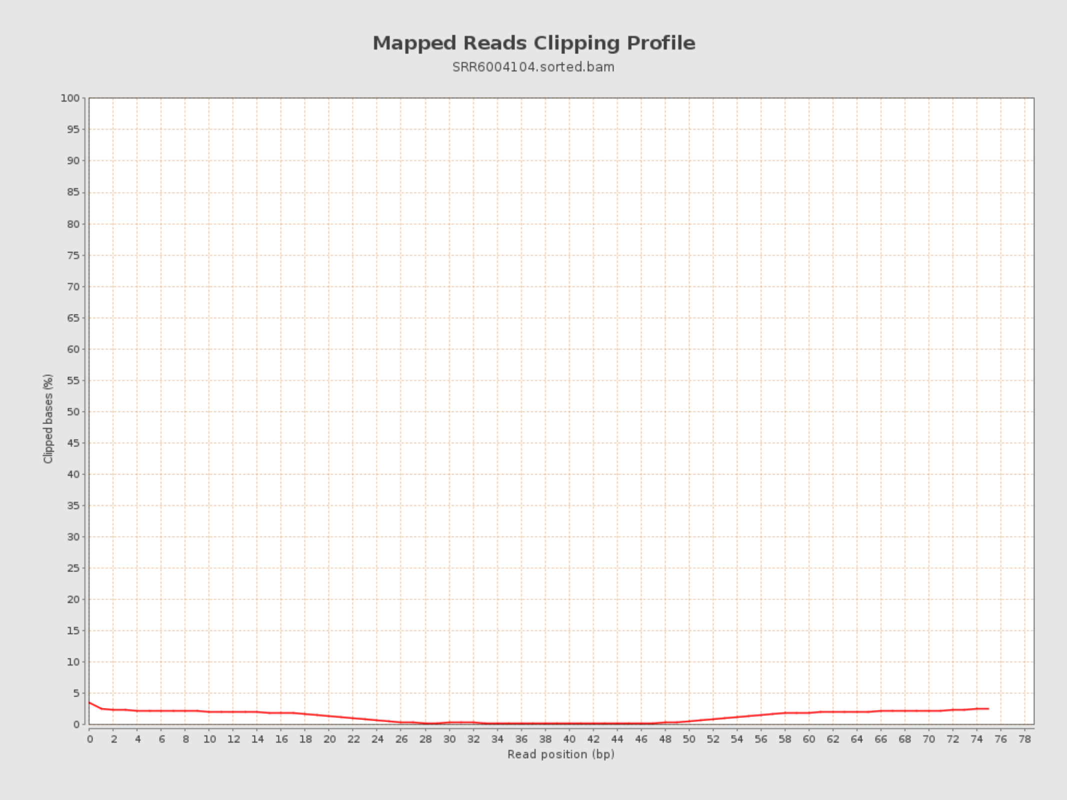
8. Results : Mapped Reads Nucleotide Content



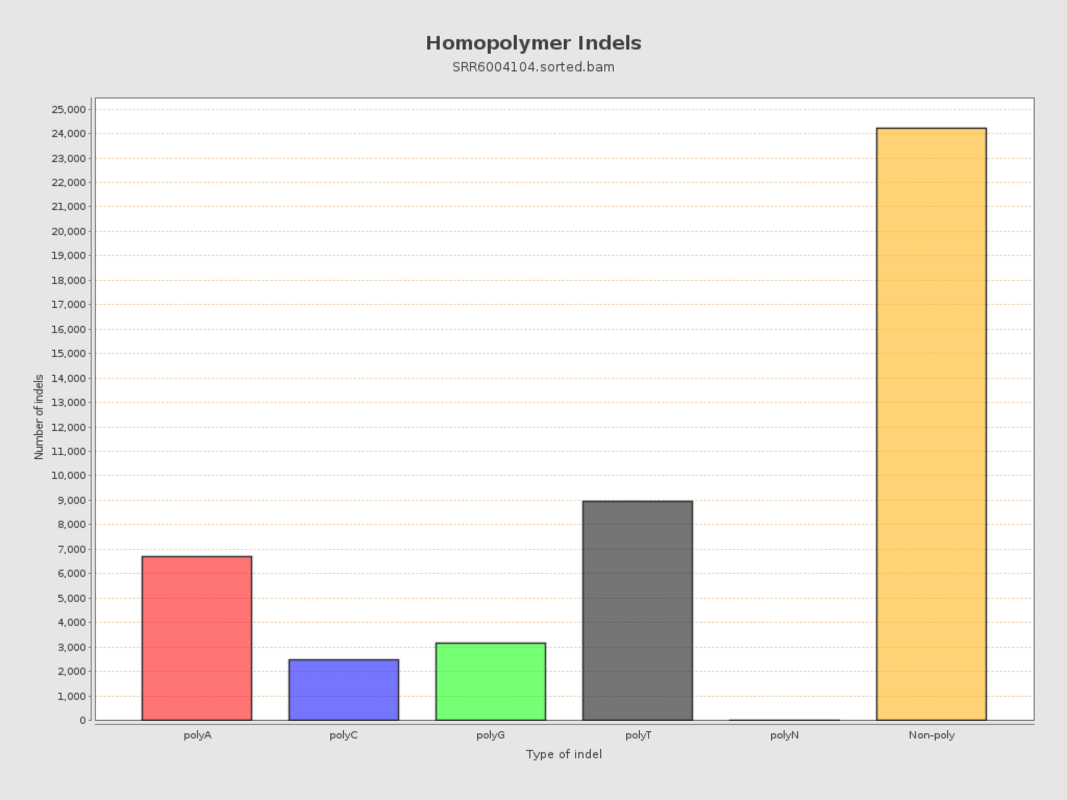
9. Results : Mapped Reads GC-content Distribution



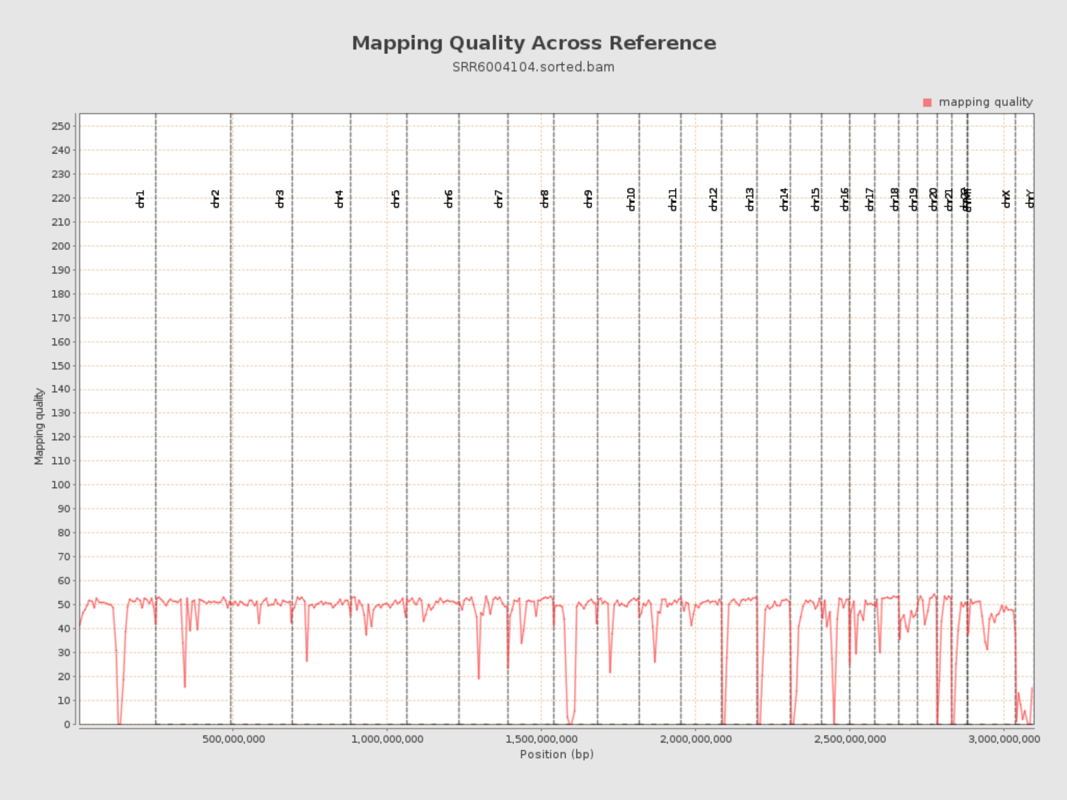
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram