Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:44:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004050.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_SRR6004050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004050.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:44:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,434,743
Mapped reads	2,073,839 / 85.18%
Unmapped reads	360,904 / 14.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,676 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	309,879 / 12.73%
Duplication rate	10.66%
Clipped reads	1,054,468 / 43.31%

2.2. ACGT Content

Number/percentage of A's	37,392,322 / 27.59%
Number/percentage of C's	25,481,741 / 18.8%
Number/percentage of T's	42,319,719 / 31.23%
Number/percentage of G's	30,303,585 / 22.36%
Number/percentage of N's	15,945 / 0.01%
GC Percentage	41.17%

2.3. Coverage

Mean	0.0438

Standard Deviation	0.575

2.4. Mapping Quality

Mean Mapping Quality	42.1

2.5. Mismatches and indels

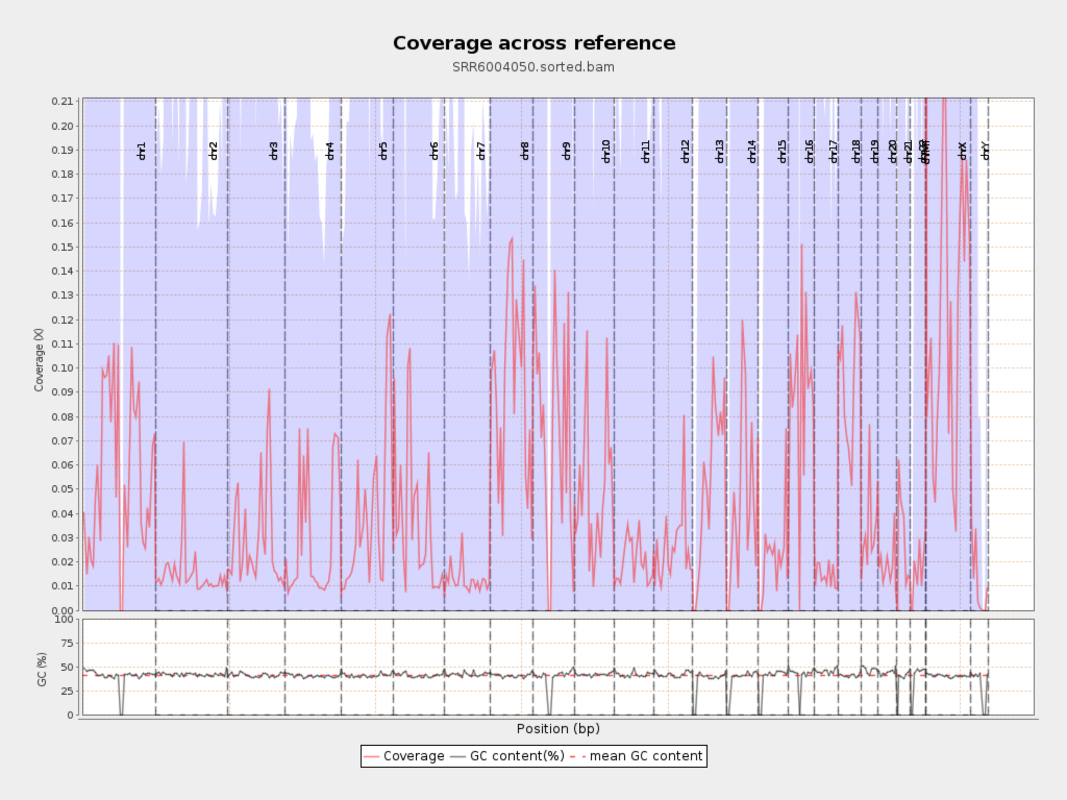
General error rate	0.81%
Mismatches	1,081,347
Insertions	10,703
Mapped reads with at least one insertion	0.51%
Deletions	31,669
Mapped reads with at least one deletion	1.51%
Homopolymer indels	44.72%

2.6. Chromosome stats

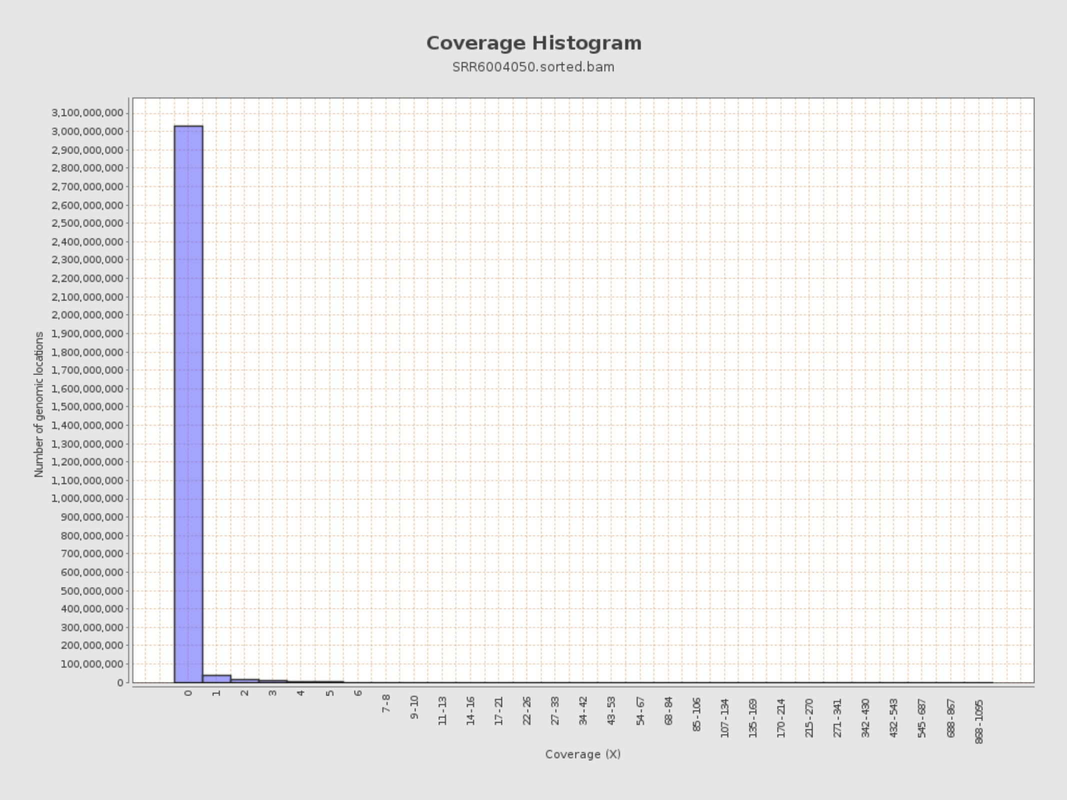
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14097228	0.0566	1.0776
chr2	243199373	3722067	0.0153	0.6108
chr3	198022430	5717310	0.0289	0.2977
chr4	191154276	5543973	0.029	0.3705
chr5	180915260	6863409	0.0379	0.3446
chr6	171115067	6121109	0.0358	0.5042
chr7	159138663	2037630	0.0128	0.2878

chr8	146364022	13601202	0.0929	0.6188
chr9	141213431	10467967	0.0741	0.66
chr10	135534747	6583453	0.0486	0.5833
chr11	135006516	2710641	0.0201	0.362
chr12	133851895	3515126	0.0263	0.3051
chr13	115169878	6112060	0.0531	0.4055
chr14	107349540	4631329	0.0431	0.409
chr15	102531392	2306932	0.0225	0.2783
chr16	90354753	7897391	0.0874	0.5933
chr17	81195210	1161826	0.0143	0.2198
chr18	78077248	7458930	0.0955	1.1291
chr19	59128983	2036866	0.0344	0.8748
chr20	63025520	1228493	0.0195	0.2552
chr21	48129895	1387913	0.0288	0.3614
chr22	51304566	796048	0.0155	0.2117
chrMT	16571	18993	1.1462	1.6635
chrX	155270560	18882952	0.1216	0.727
chrY	59373566	668759	0.0113	0.2818

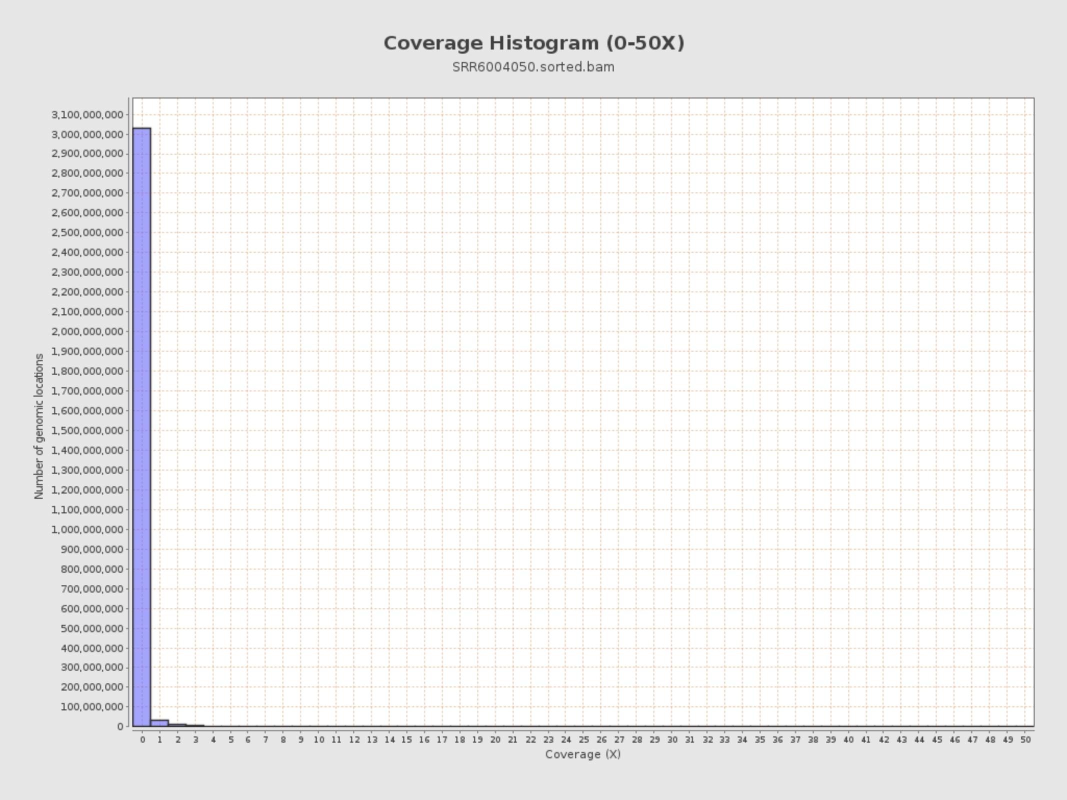
3. Results : Coverage across reference



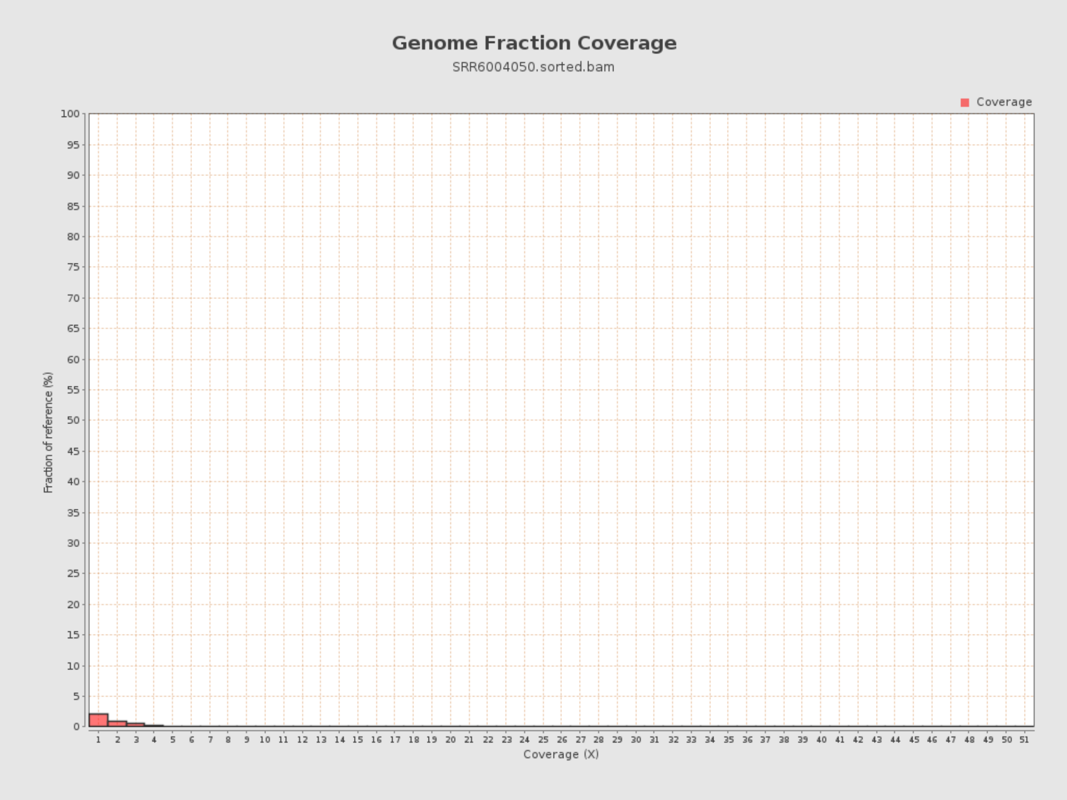
4. Results : Coverage Histogram



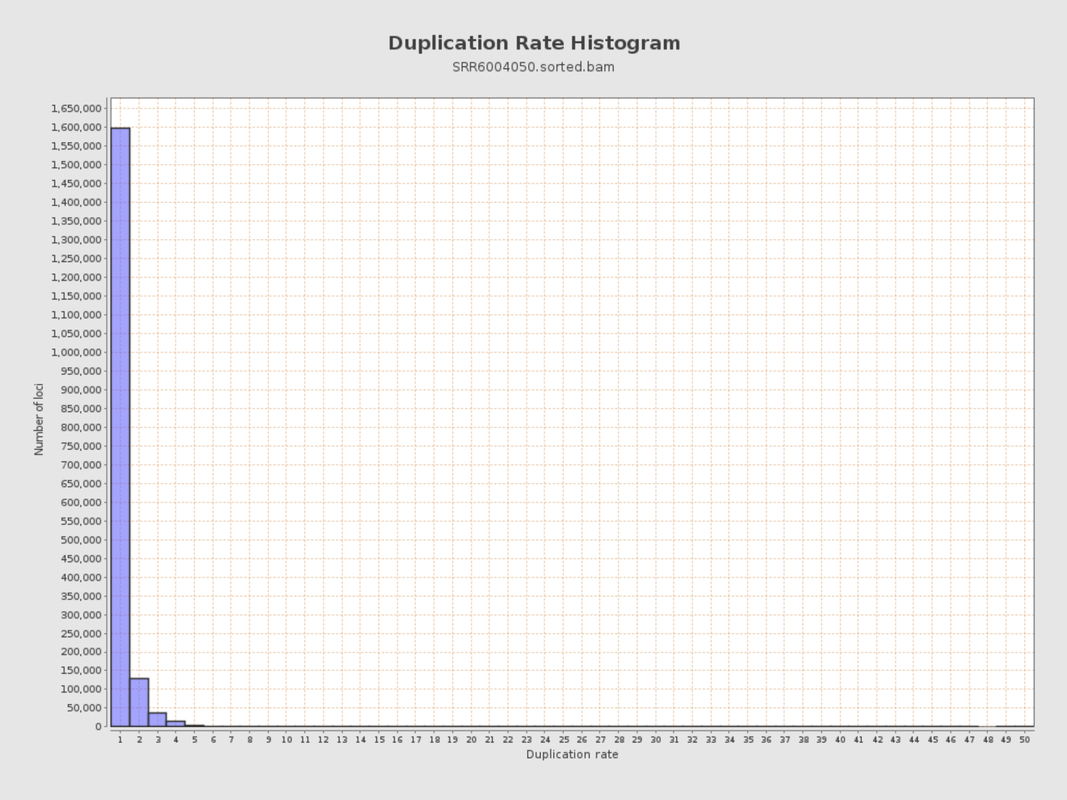
5. Results : Coverage Histogram (0-50X)



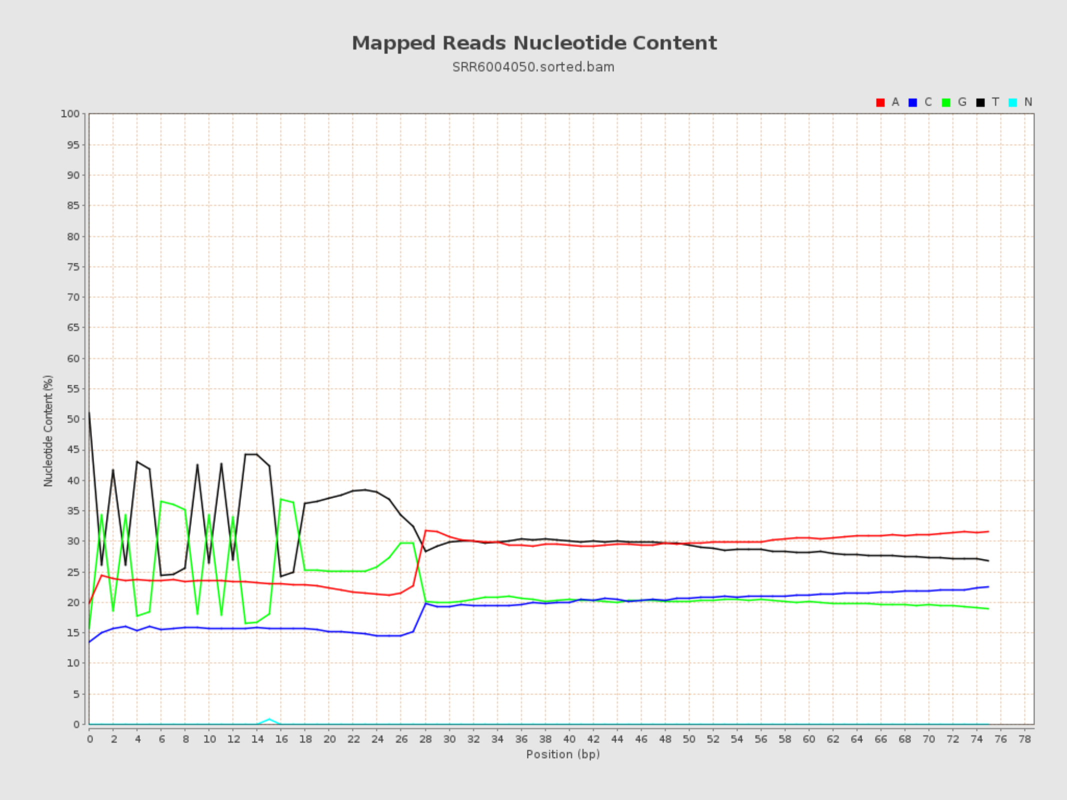
6. Results : Genome Fraction Coverage



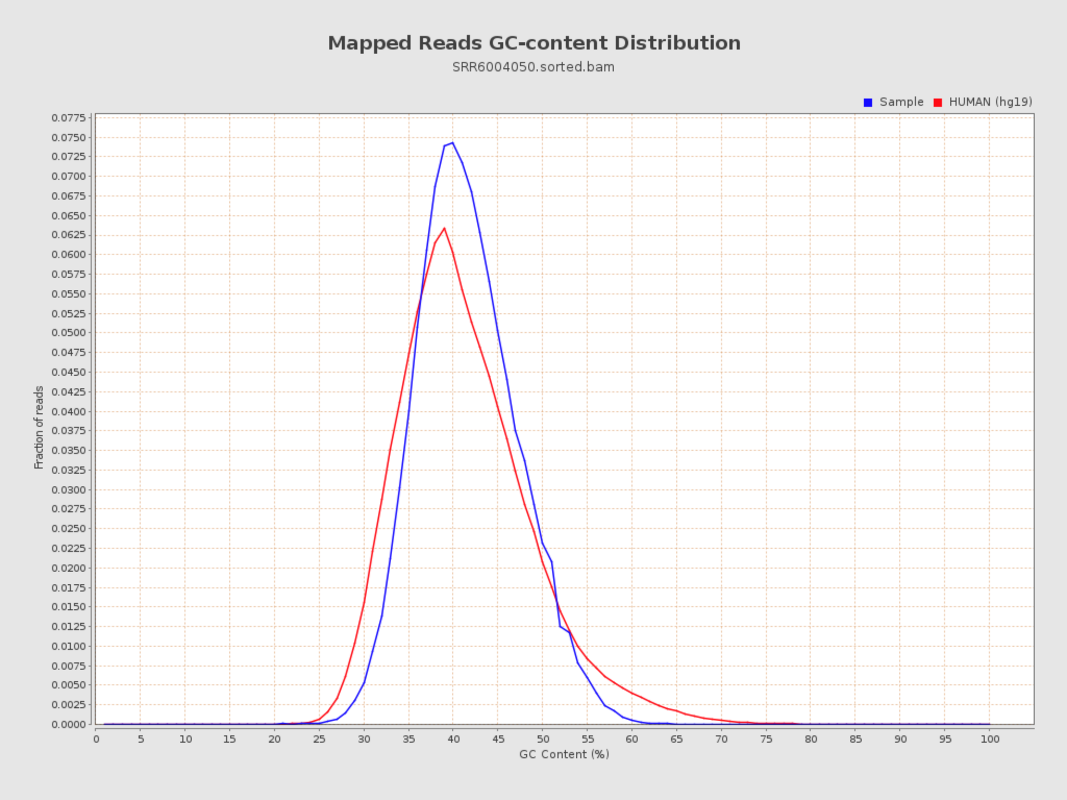
7. Results : Duplication Rate Histogram



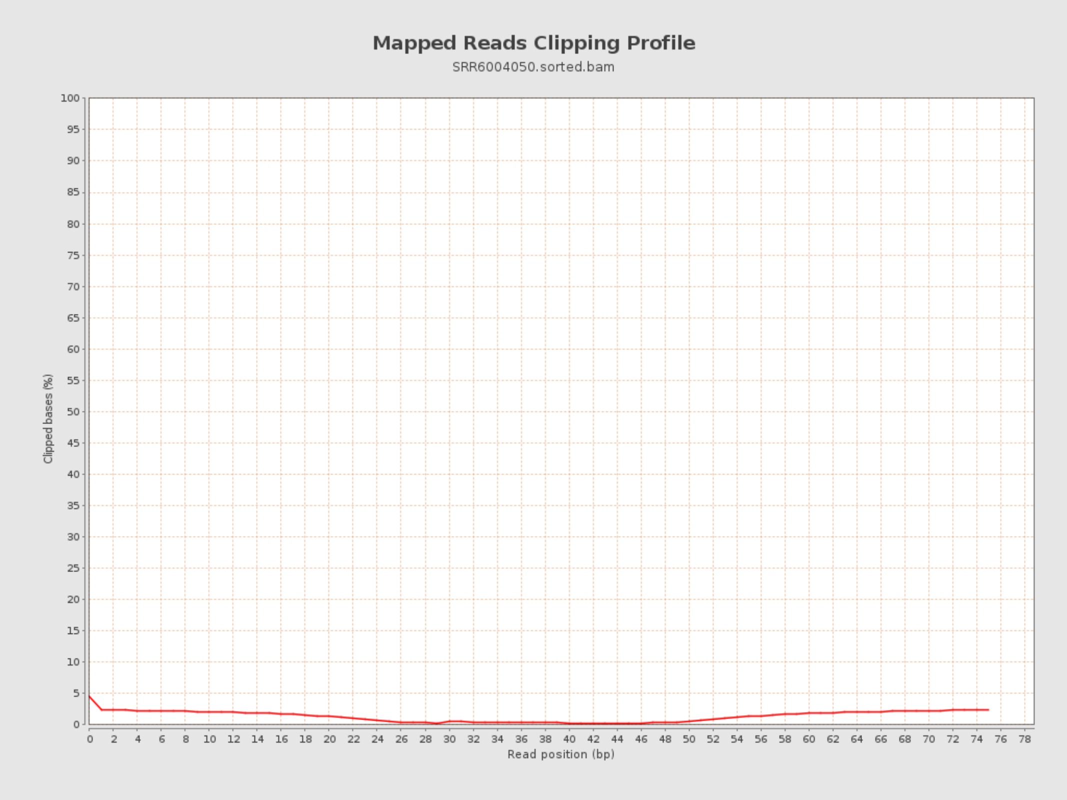
8. Results : Mapped Reads Nucleotide Content



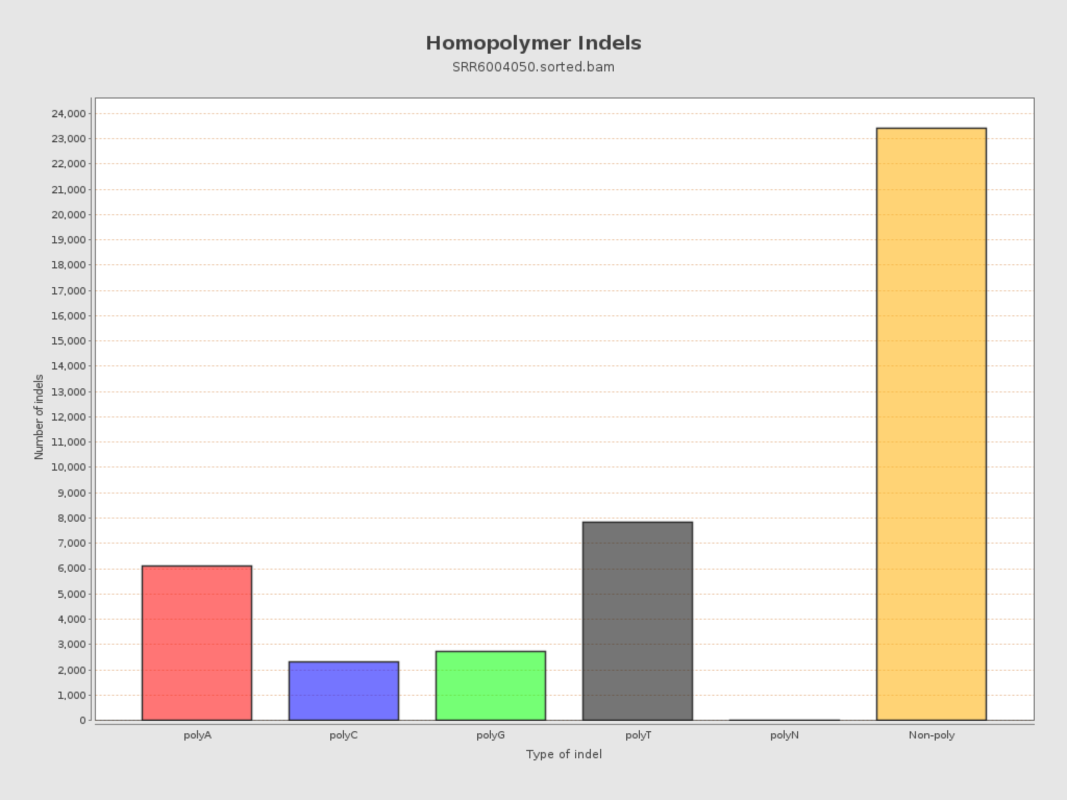
9. Results : Mapped Reads GC-content Distribution



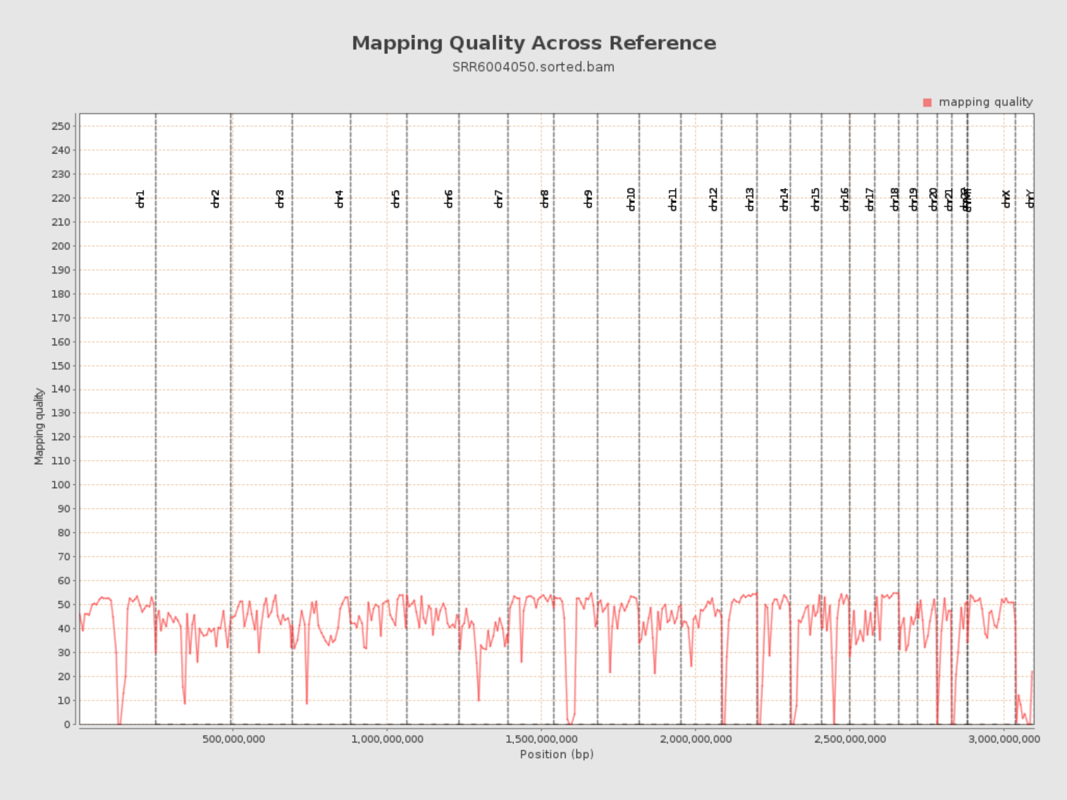
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram