Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:34:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004165.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_SRR6004165 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004165.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:34:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004165.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,597,543
Mapped reads	1,331,441 / 83.34%
Unmapped reads	266,102 / 16.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,222 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	42,040 / 2.63%
Duplication rate	2.41%
Clipped reads	741,749 / 46.43%

2.2. ACGT Content

Number/percentage of A's	23,898,236 / 28.04%
Number/percentage of C's	15,737,644 / 18.46%
Number/percentage of T's	26,216,596 / 30.76%
Number/percentage of G's	19,370,155 / 22.72%
Number/percentage of N's	16,434 / 0.02%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.264

2.4. Mapping Quality

Mean Mapping Quality	43.5

2.5. Mismatches and indels

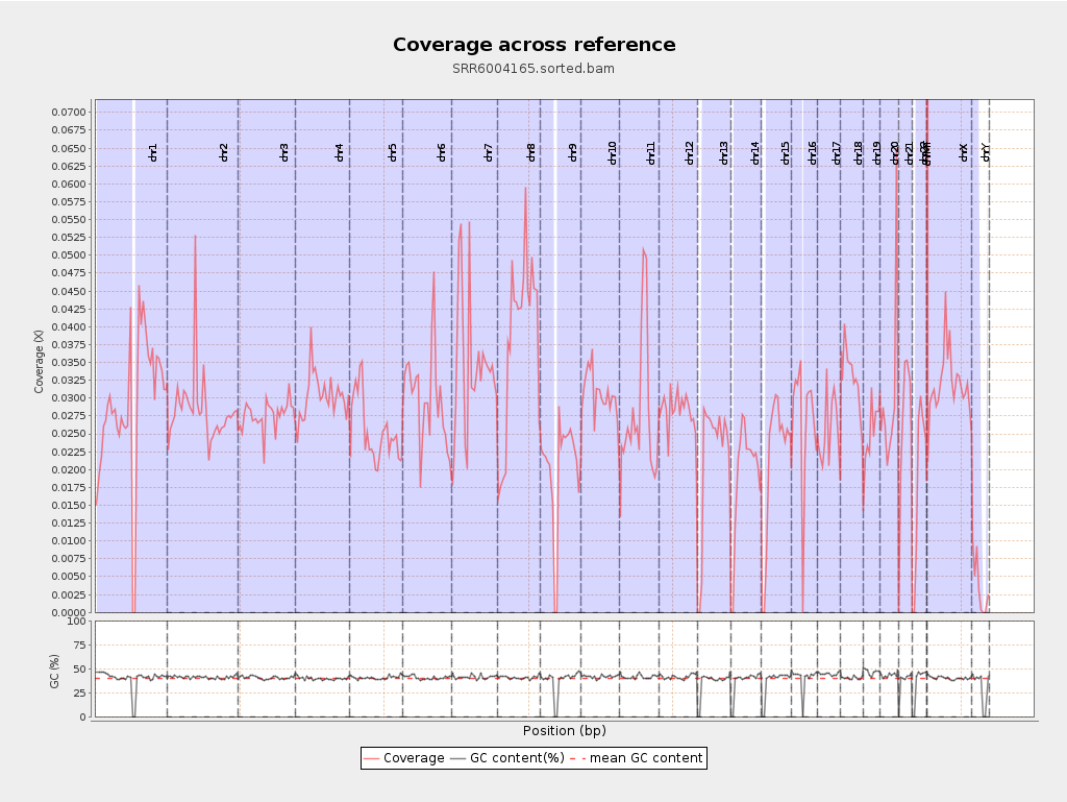
General error rate	1.03%
Mismatches	865,204
Insertions	7,508
Mapped reads with at least one insertion	0.56%
Deletions	33,326
Mapped reads with at least one deletion	2.46%
Homopolymer indels	47%

2.6. Chromosome stats

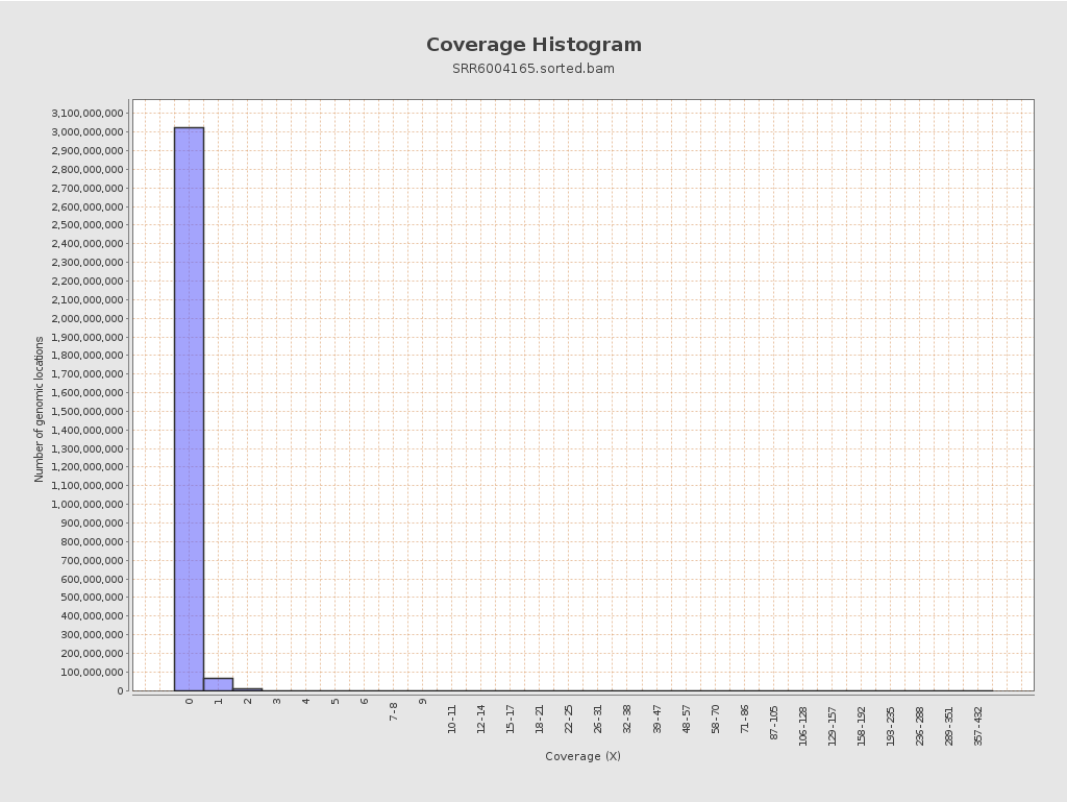
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7221257	0.029	0.3735
chr2	243199373	6897627	0.0284	0.3292
chr3	198022430	5470648	0.0276	0.1858
chr4	191154276	5782261	0.0302	0.1974
chr5	180915260	4612408	0.0255	0.1796
chr6	171115067	5092159	0.0298	0.2093
chr7	159138663	5460062	0.0343	0.4676

chr8	146364022	5626029	0.0384	0.2948
chr9	141213431	2840133	0.0201	0.2336
chr10	135534747	4117473	0.0304	0.2239
chr11	135006516	3706004	0.0275	0.2665
chr12	133851895	3768191	0.0282	0.1886
chr13	115169878	2481193	0.0215	0.1642
chr14	107349540	2048883	0.0191	0.1792
chr15	102531392	2204311	0.0215	0.1722
chr16	90354753	2382696	0.0264	0.1962
chr17	81195210	2069458	0.0255	0.1924
chr18	78077248	2581825	0.0331	0.4514
chr19	59128983	1497034	0.0253	0.2694
chr20	63025520	1934817	0.0307	0.206
chr21	48129895	1288863	0.0268	0.1908
chr22	51304566	951710	0.0186	0.1516
chrMT	16571	72974	4.4037	3.6564
chrX	155270560	4975570	0.032	0.2228
chrY	59373566	209175	0.0035	0.0778

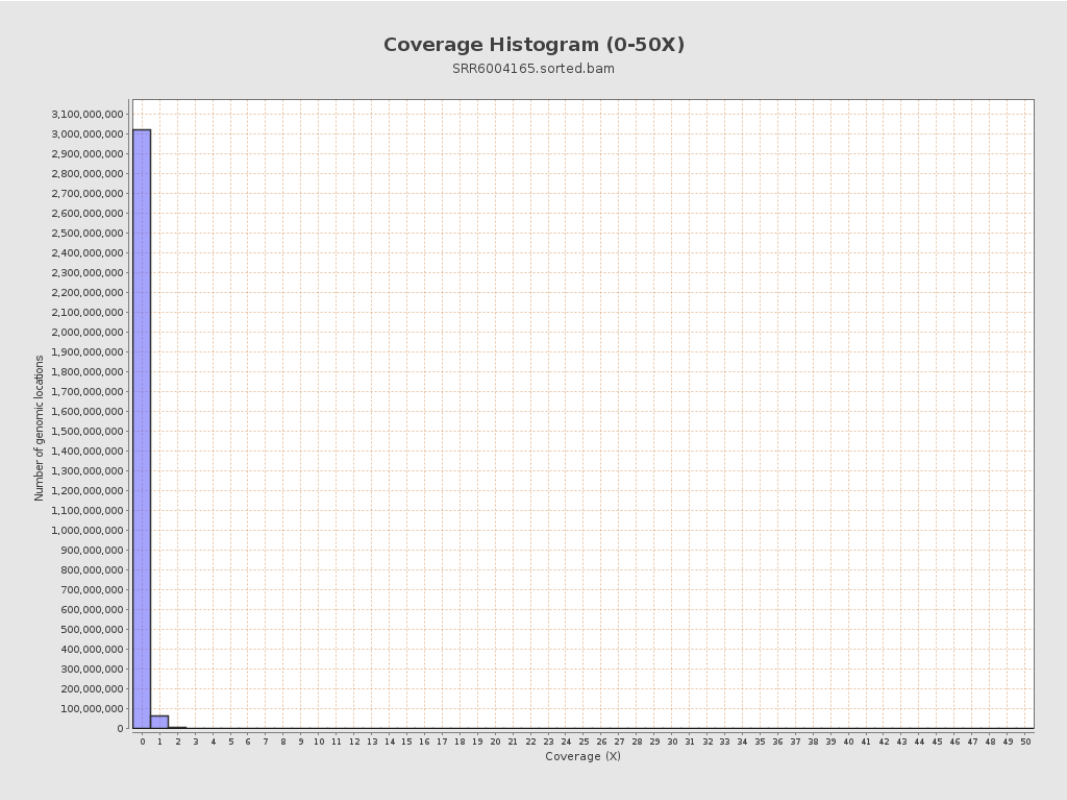
3. Results : Coverage across reference



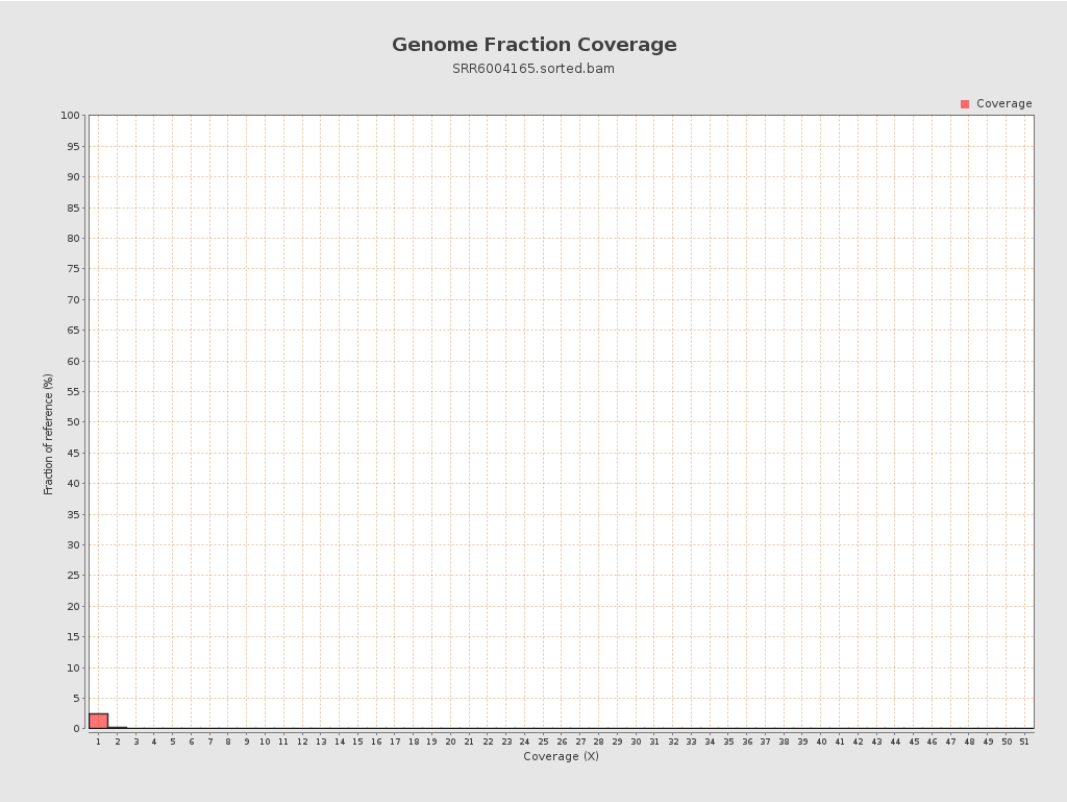
4. Results : Coverage Histogram



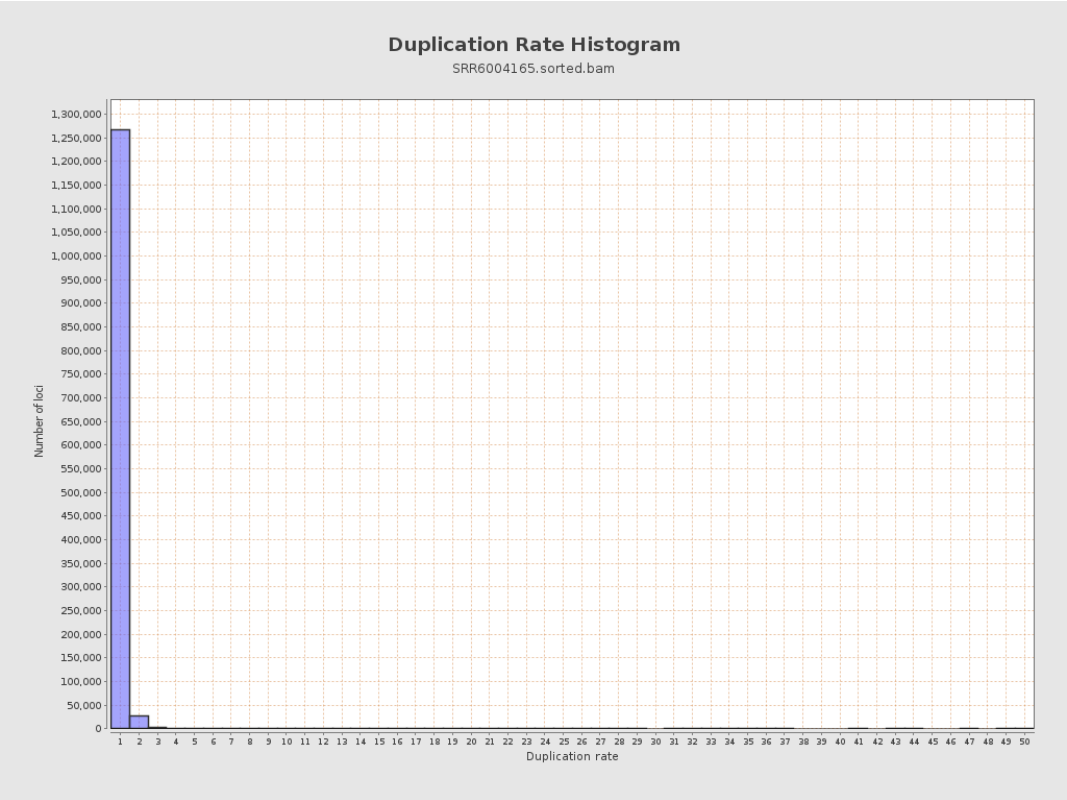
5. Results : Coverage Histogram (0-50X)



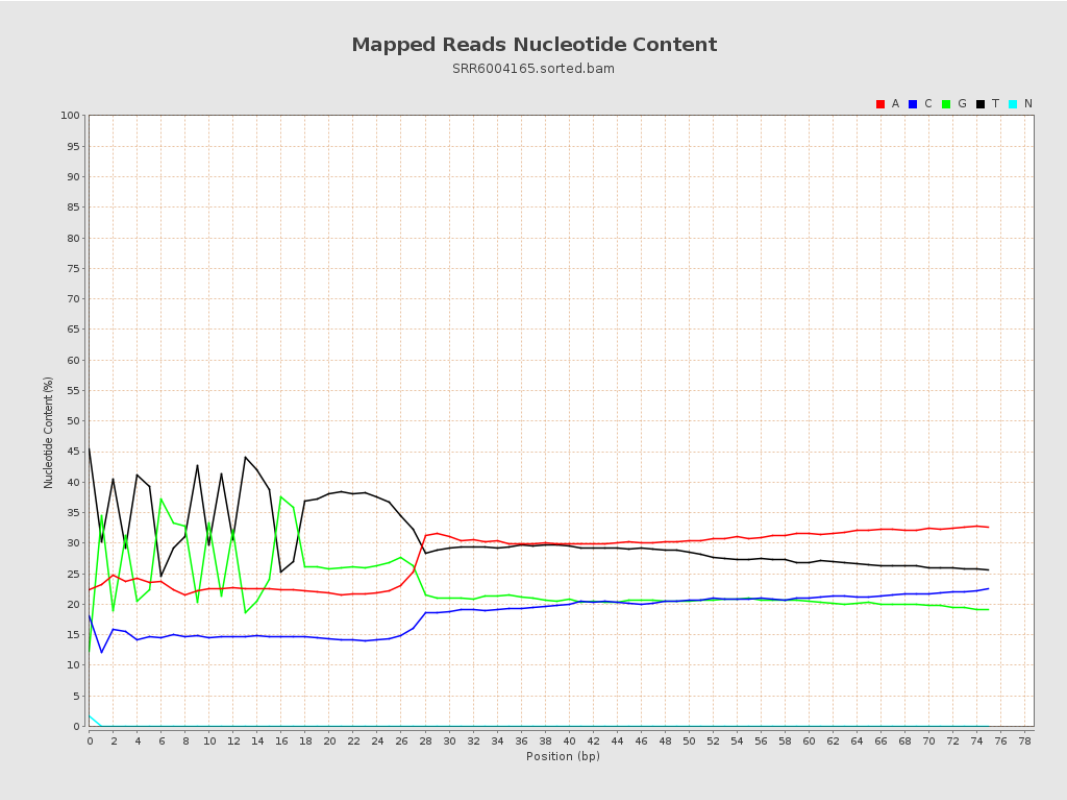
6. Results : Genome Fraction Coverage



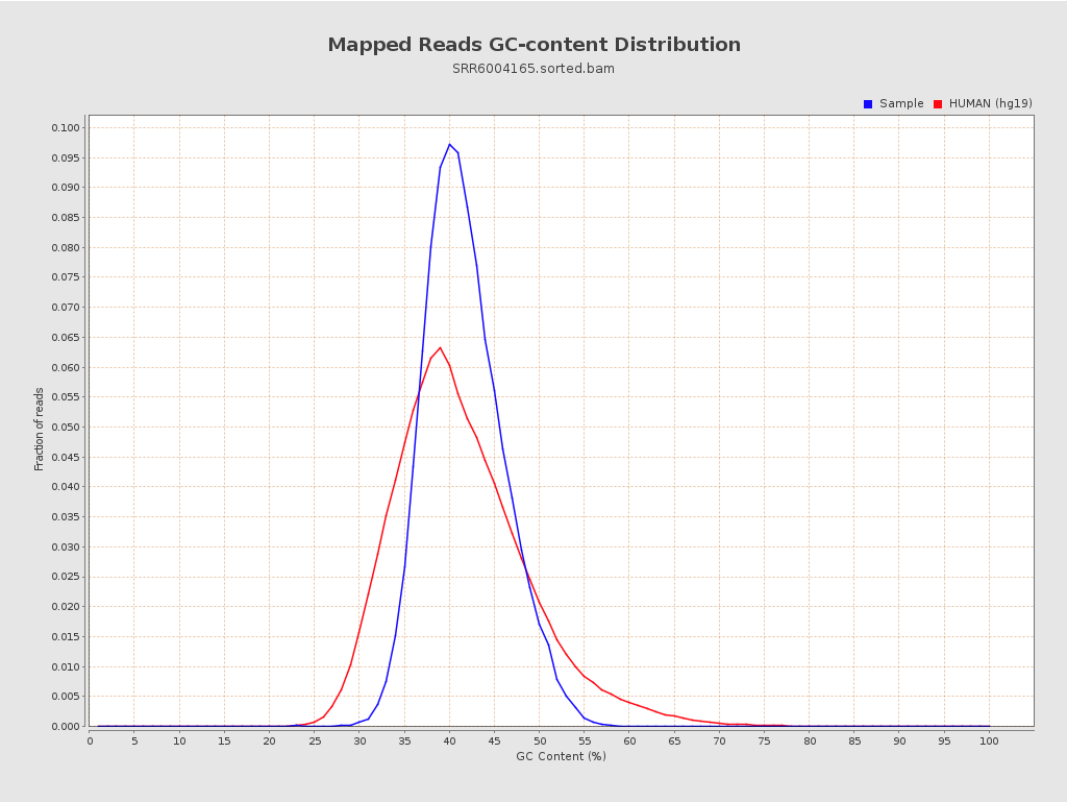
7. Results : Duplication Rate Histogram



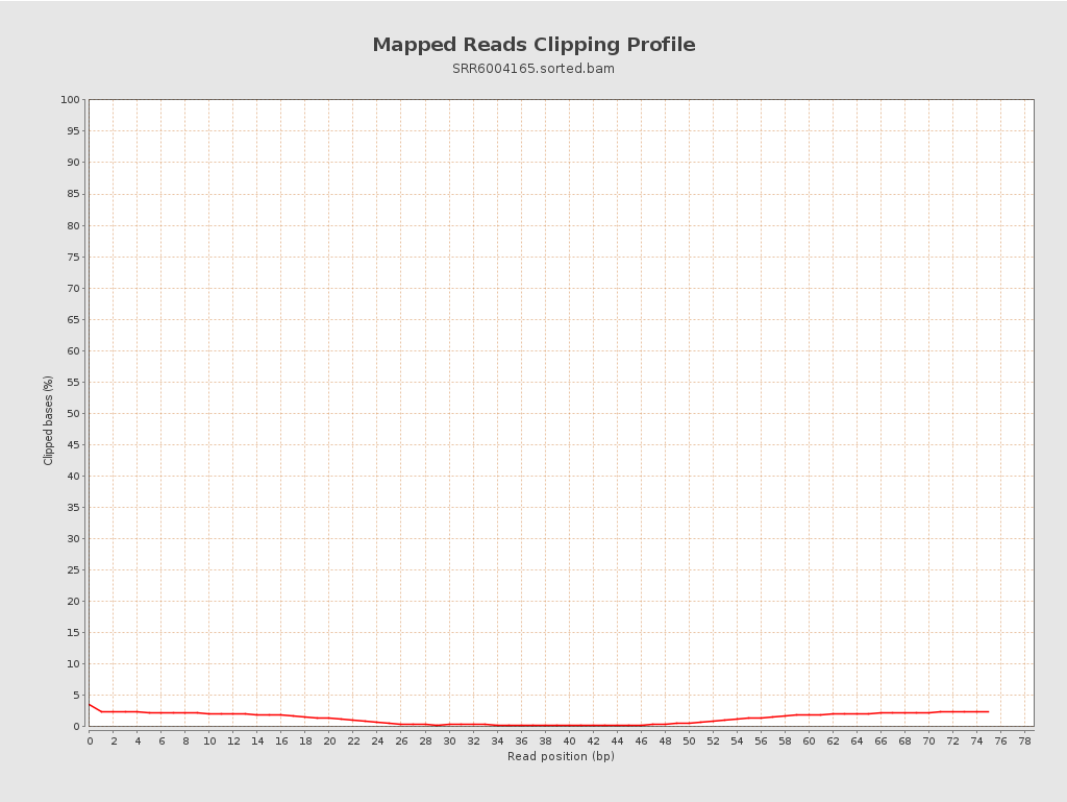
8. Results : Mapped Reads Nucleotide Content



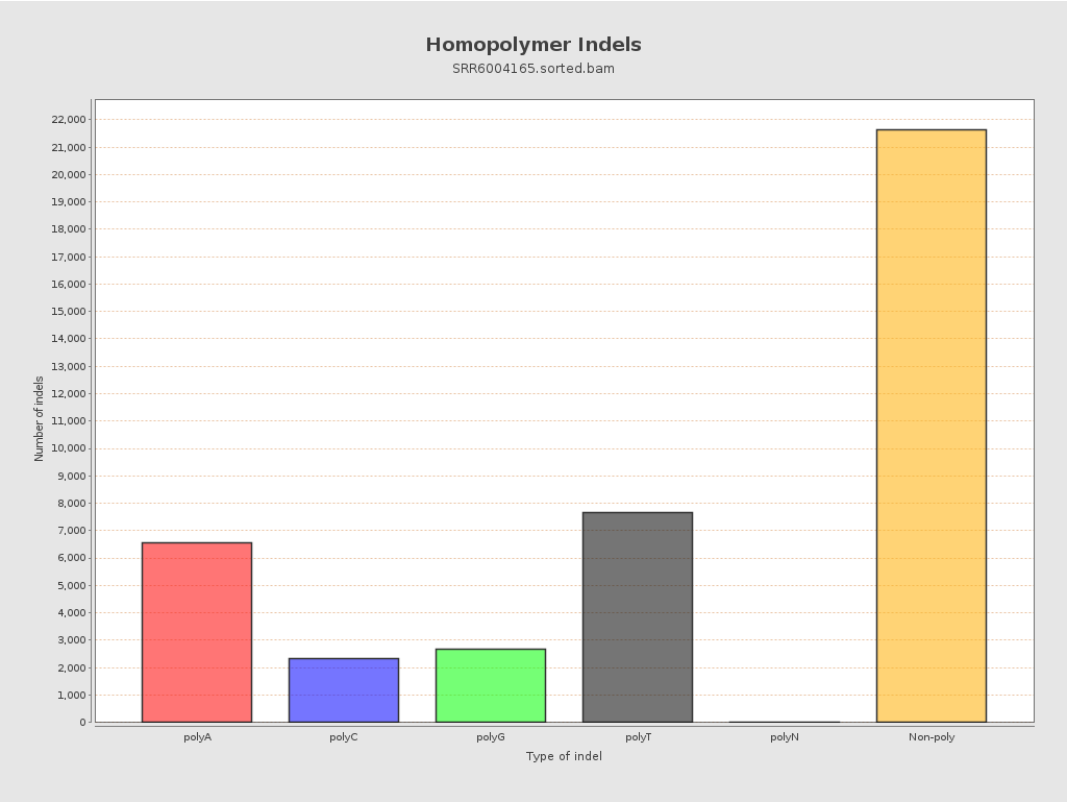
9. Results : Mapped Reads GC-content Distribution



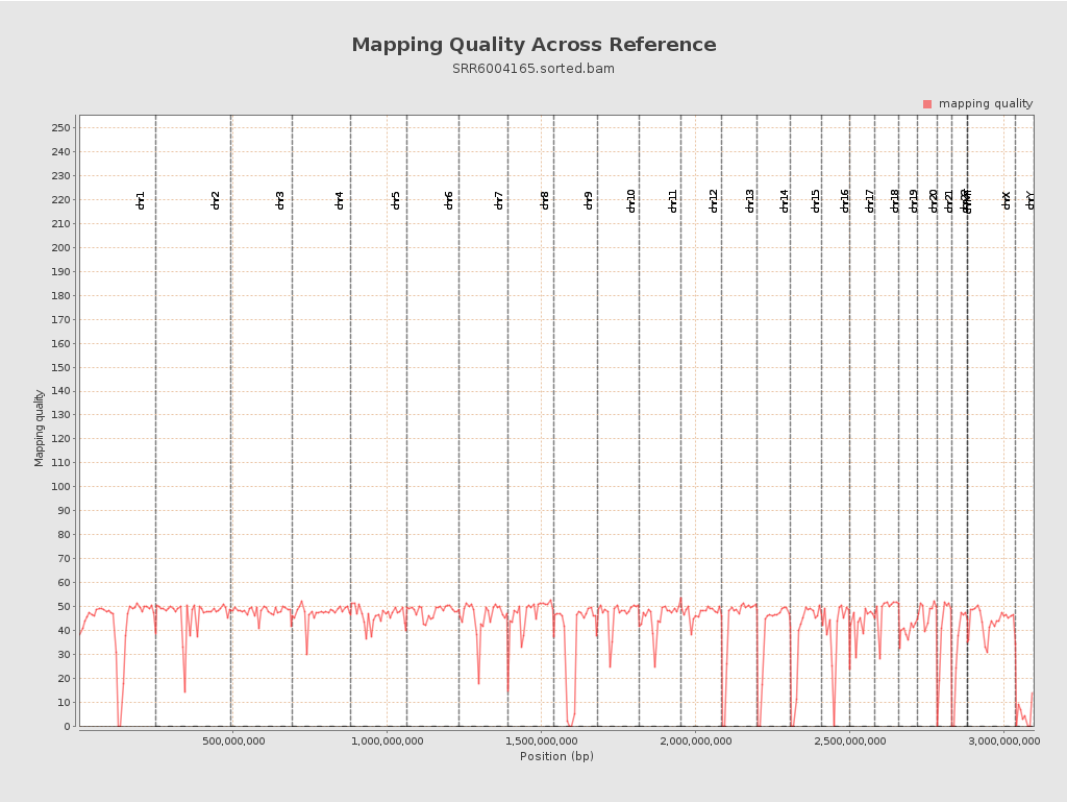
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram