Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:31:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004147.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_SRR6004147 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004147.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:31:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004147.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,674,892
Mapped reads	2,005,516 / 74.98%
Unmapped reads	669,376 / 25.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,960 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	323,538 / 12.1%
Duplication rate	12.6%
Clipped reads	1,136,855 / 42.5%

2.2. ACGT Content

Number/percentage of A's	33,938,689 / 26.53%
Number/percentage of C's	22,094,451 / 17.27%
Number/percentage of T's	42,943,581 / 33.57%
Number/percentage of G's	28,936,519 / 22.62%
Number/percentage of N's	12,355 / 0.01%
GC Percentage	39.89%

2.3. Coverage

Mean	0.0413

Standard Deviation	0.4202

2.4. Mapping Quality

Mean Mapping Quality	46.47

2.5. Mismatches and indels

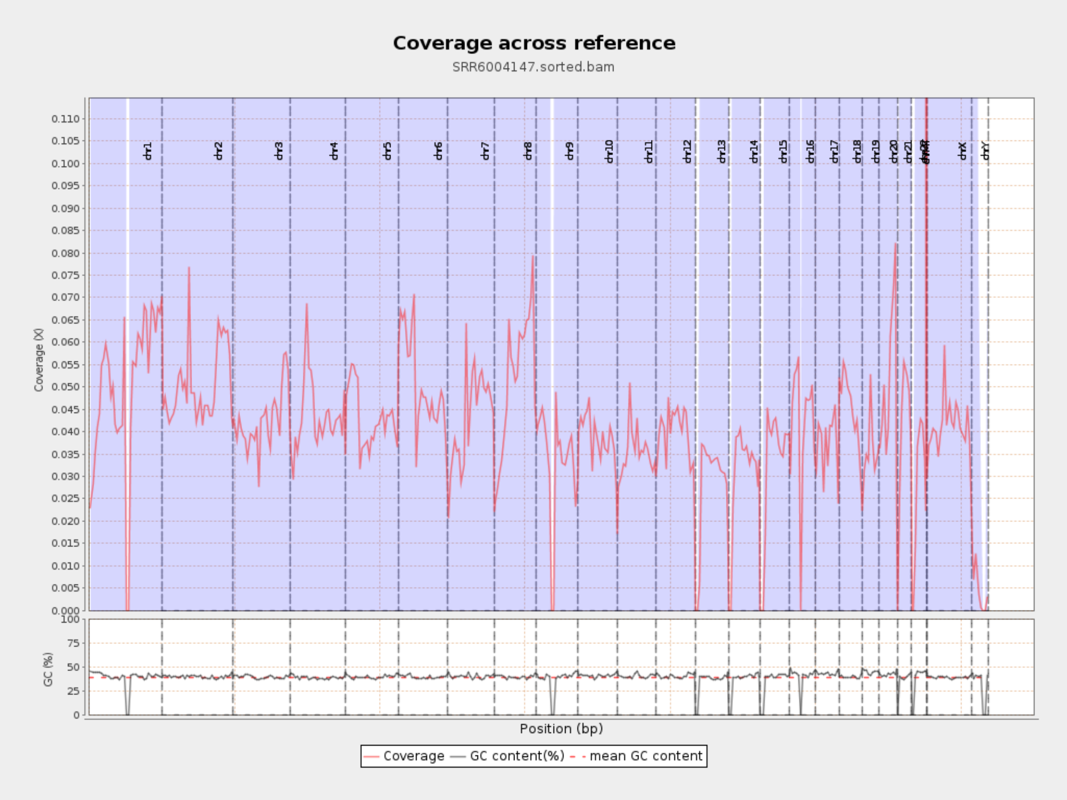
General error rate	1.02%
Mismatches	1,287,722
Insertions	10,707
Mapped reads with at least one insertion	0.53%
Deletions	39,388
Mapped reads with at least one deletion	1.94%
Homopolymer indels	49.65%

2.6. Chromosome stats

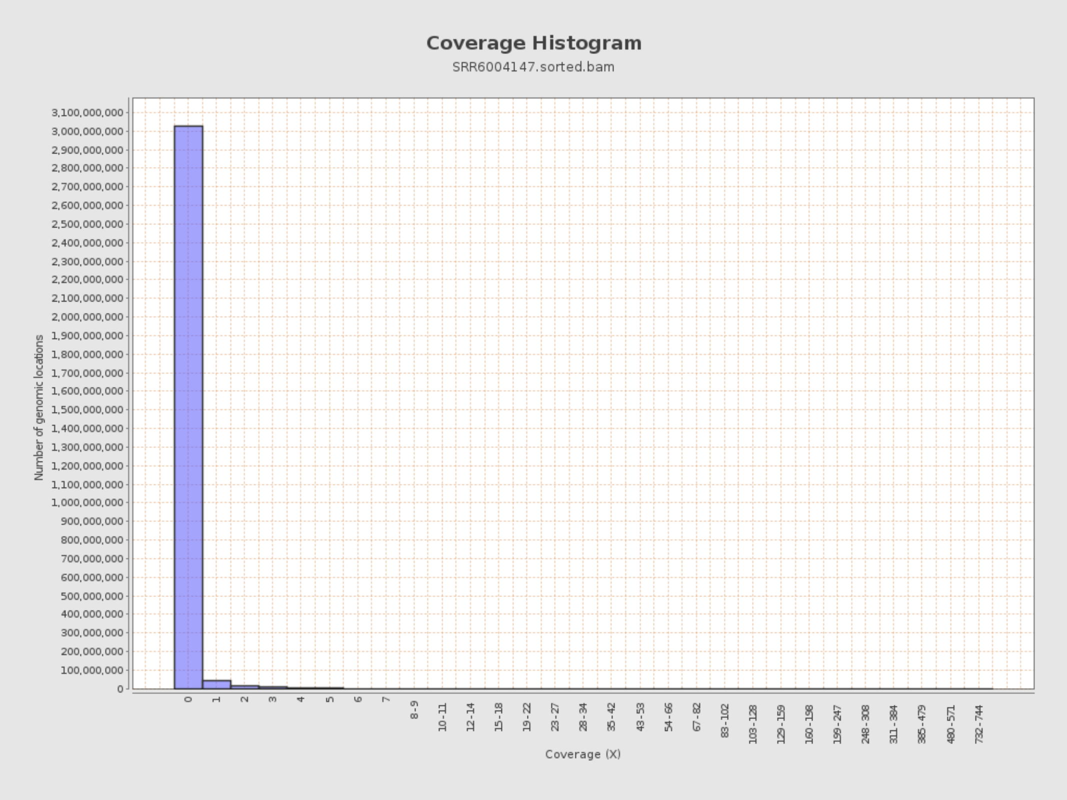
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12334498	0.0495	0.5875
chr2	243199373	12270058	0.0505	0.5439
chr3	198022430	8436243	0.0426	0.3358
chr4	191154276	8282167	0.0433	0.3411
chr5	180915260	7786200	0.043	0.3347
chr6	171115067	8705177	0.0509	0.4162
chr7	159138663	6946282	0.0436	0.5567

chr8	146364022	7615635	0.052	0.5094
chr9	141213431	4694192	0.0332	0.3911
chr10	135534747	5310154	0.0392	0.3508
chr11	135006516	4750904	0.0352	0.3969
chr12	133851895	5321596	0.0398	0.3206
chr13	115169878	3170914	0.0275	0.2687
chr14	107349540	3235918	0.0301	0.3013
chr15	102531392	3316012	0.0323	0.2866
chr16	90354753	3818218	0.0423	0.3343
chr17	81195210	2988633	0.0368	0.3256
chr18	78077248	3555757	0.0455	0.7025
chr19	59128983	2132020	0.0361	0.4405
chr20	63025520	3255882	0.0517	0.3703
chr21	48129895	1951894	0.0406	0.3366
chr22	51304566	1354162	0.0264	0.2503
chrMT	16571	82797	4.9965	5.7254
chrX	155270560	6405754	0.0413	0.3513
chrY	59373566	269593	0.0045	0.1059

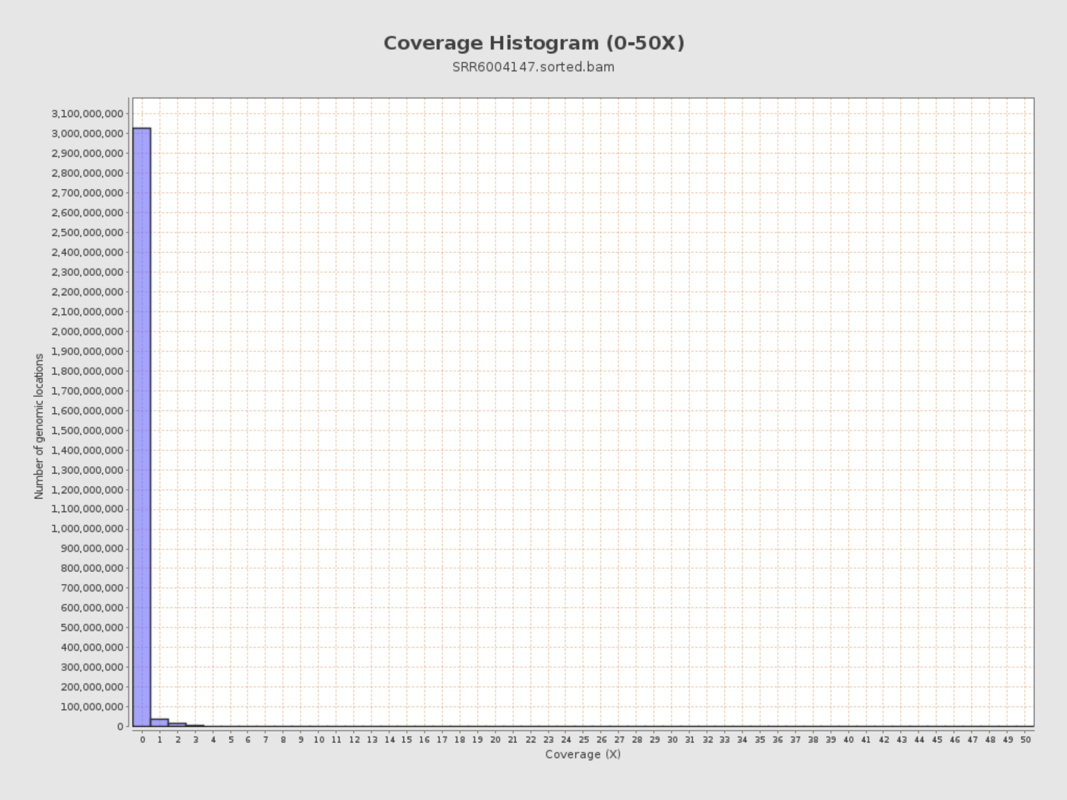
3. Results : Coverage across reference



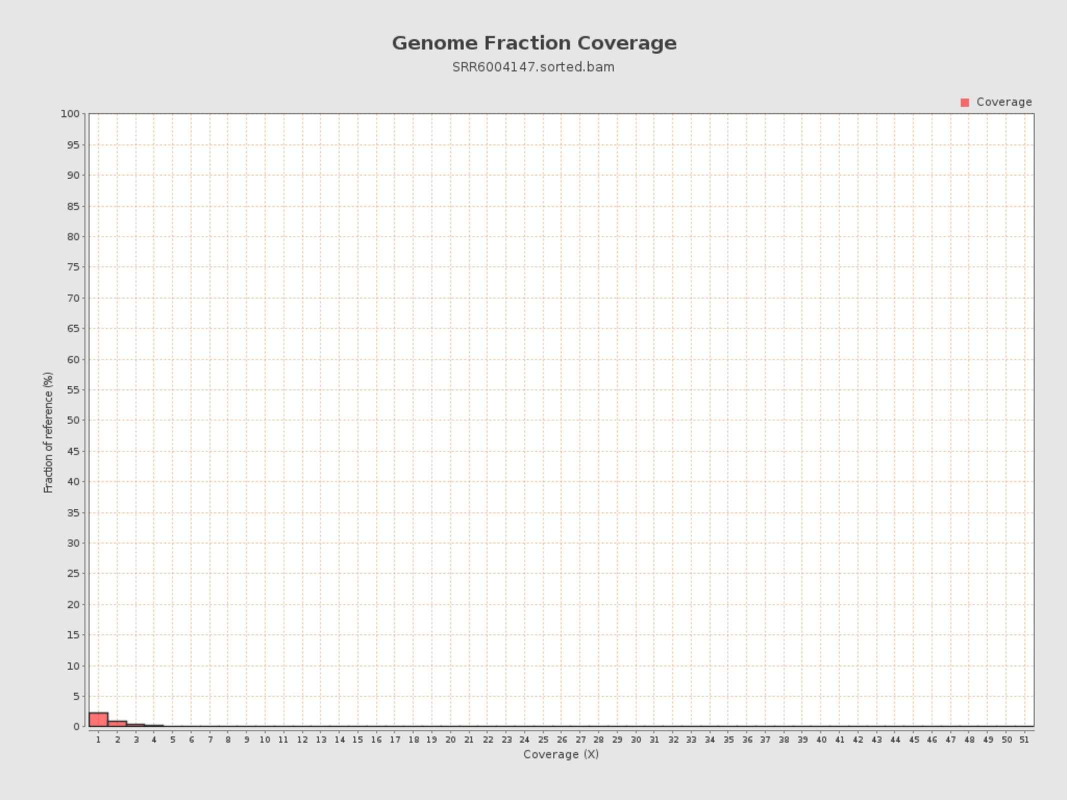
4. Results : Coverage Histogram



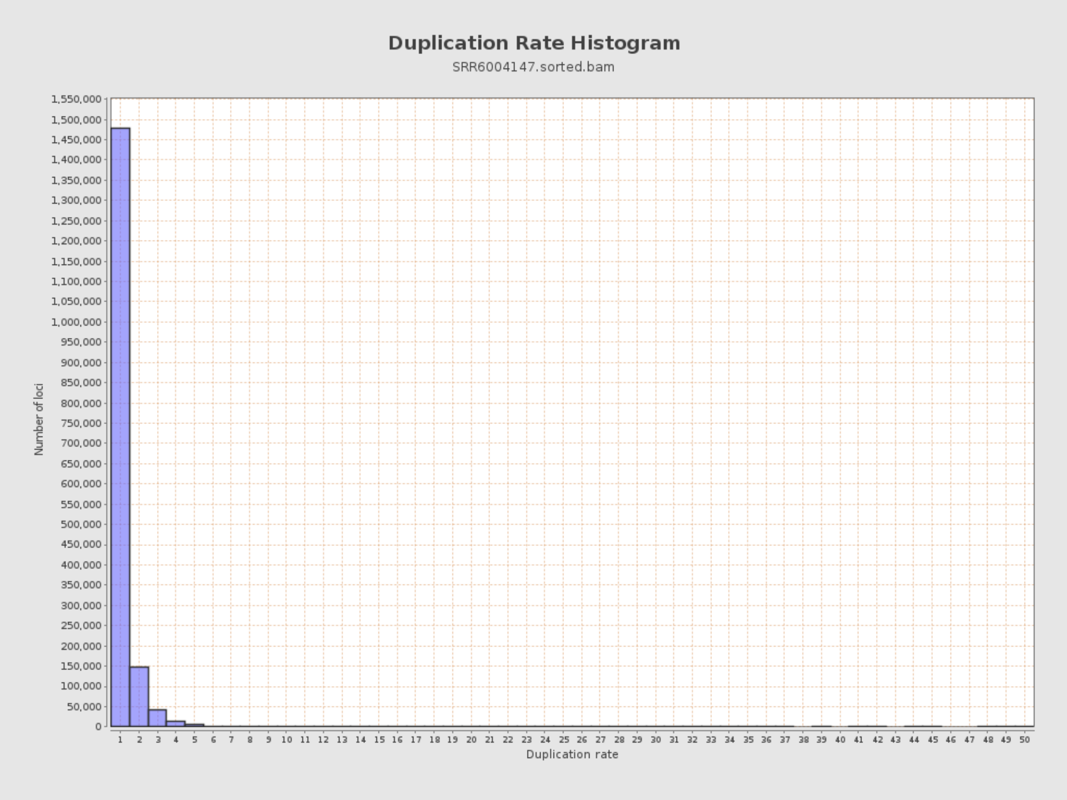
5. Results : Coverage Histogram (0-50X)



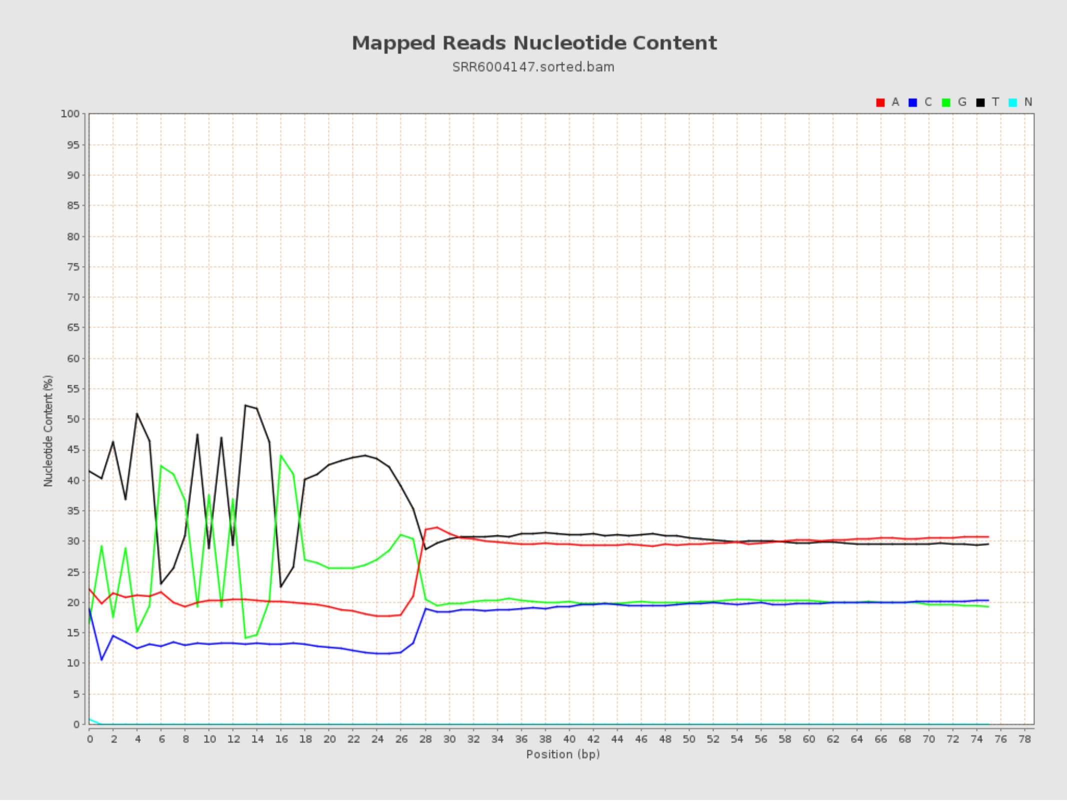
6. Results : Genome Fraction Coverage



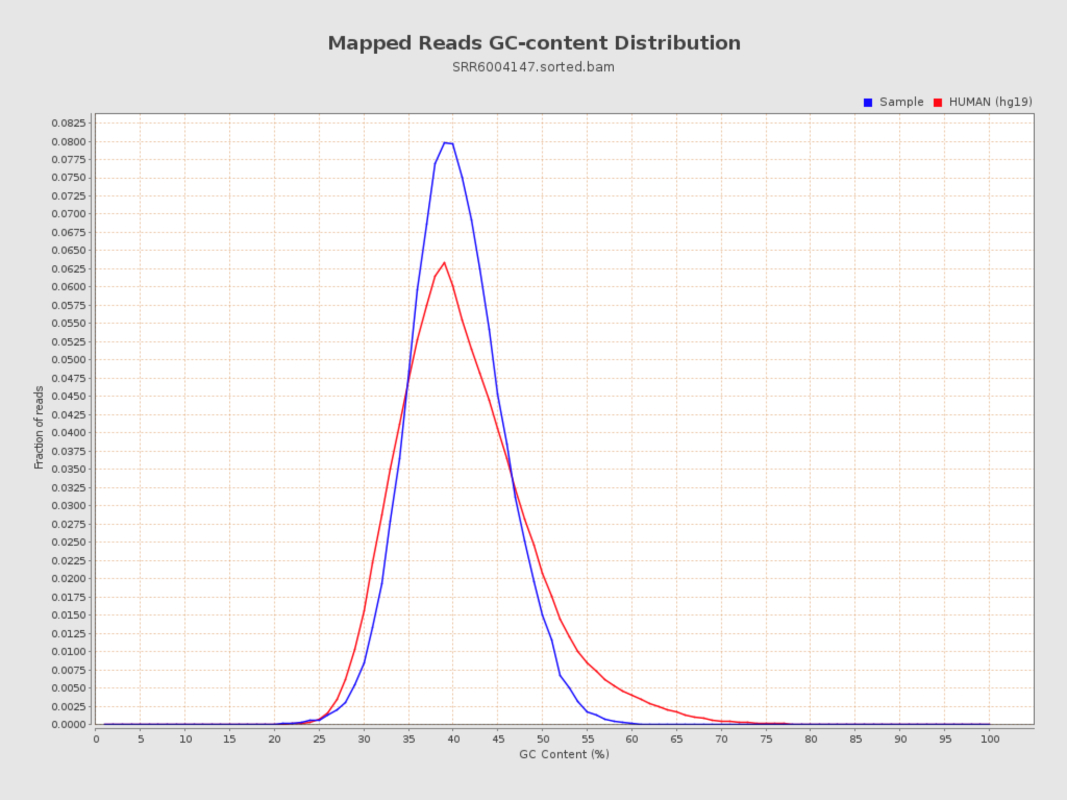
7. Results : Duplication Rate Histogram



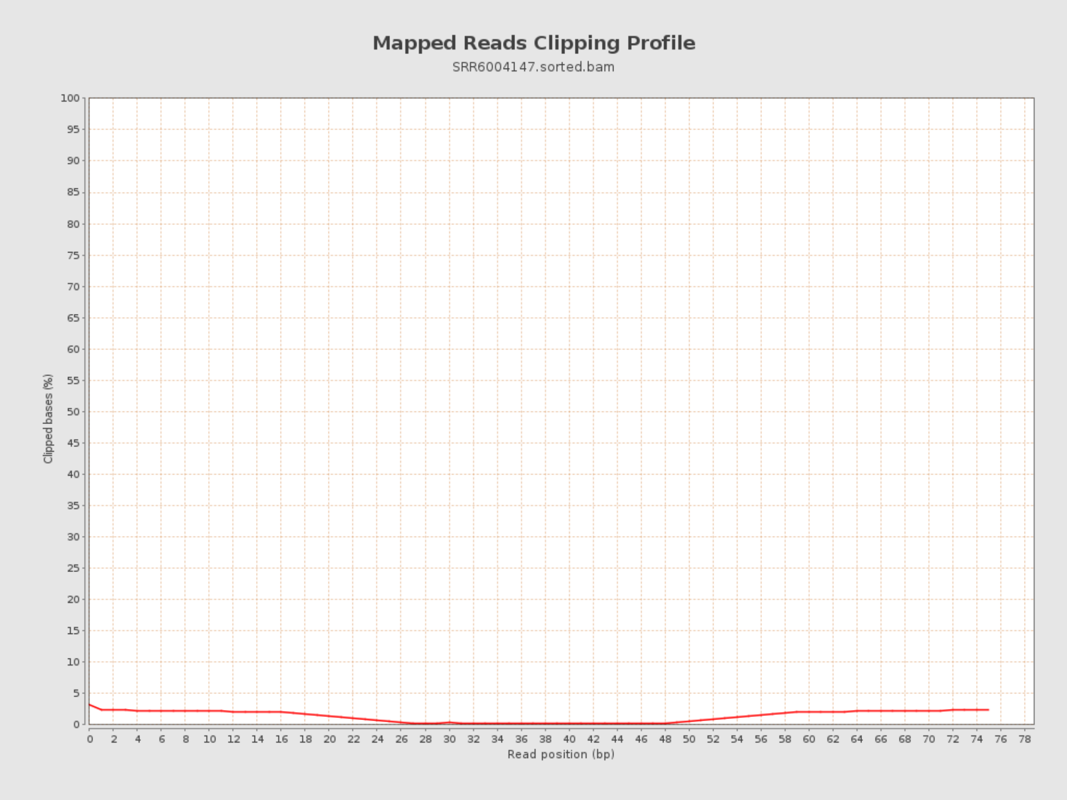
8. Results : Mapped Reads Nucleotide Content



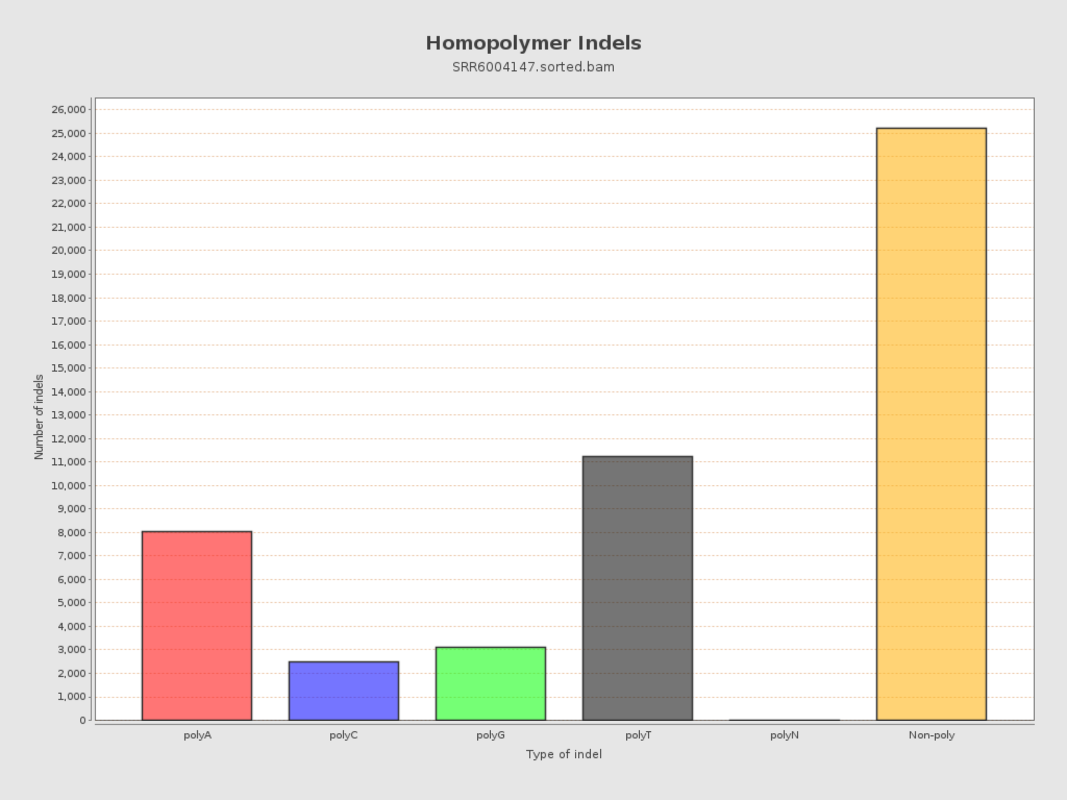
9. Results : Mapped Reads GC-content Distribution



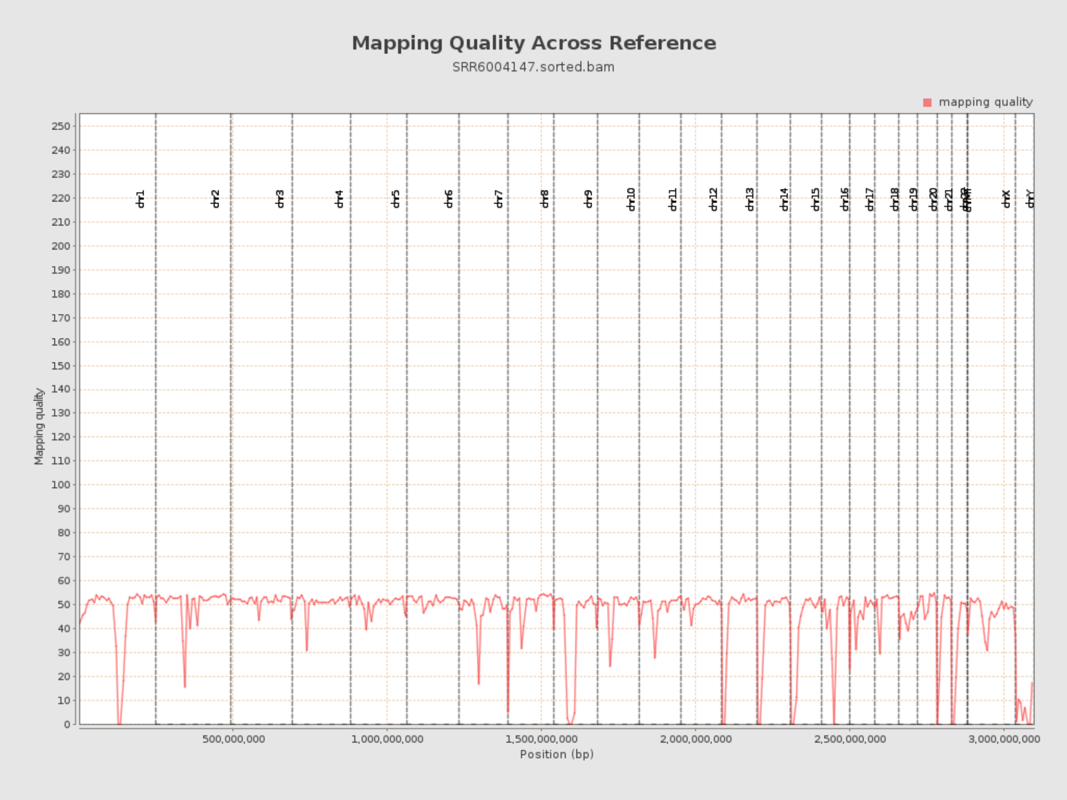
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram