

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:44:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004150.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_SRR6004150 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004150.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:44:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004150.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,991,548
Mapped reads	3,247,131 / 81.35%
Unmapped reads	744,417 / 18.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,884 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	203,683 / 5.1%
Duplication rate	4.31%
Clipped reads	1,846,038 / 46.25%

2.2. ACGT Content

Number/percentage of A's	55,098,006 / 26.48%
Number/percentage of C's	38,382,392 / 18.45%
Number/percentage of T's	65,165,526 / 31.32%
Number/percentage of G's	49,400,462 / 23.74%
Number/percentage of N's	20,651 / 0.01%
GC Percentage	42.19%

2.3. Coverage

Mean	0.0672

Standard Deviation	0.7301
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2.4. Mapping Quality

Mean Mapping Quality	41.28
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2.5. Mismatches and indels

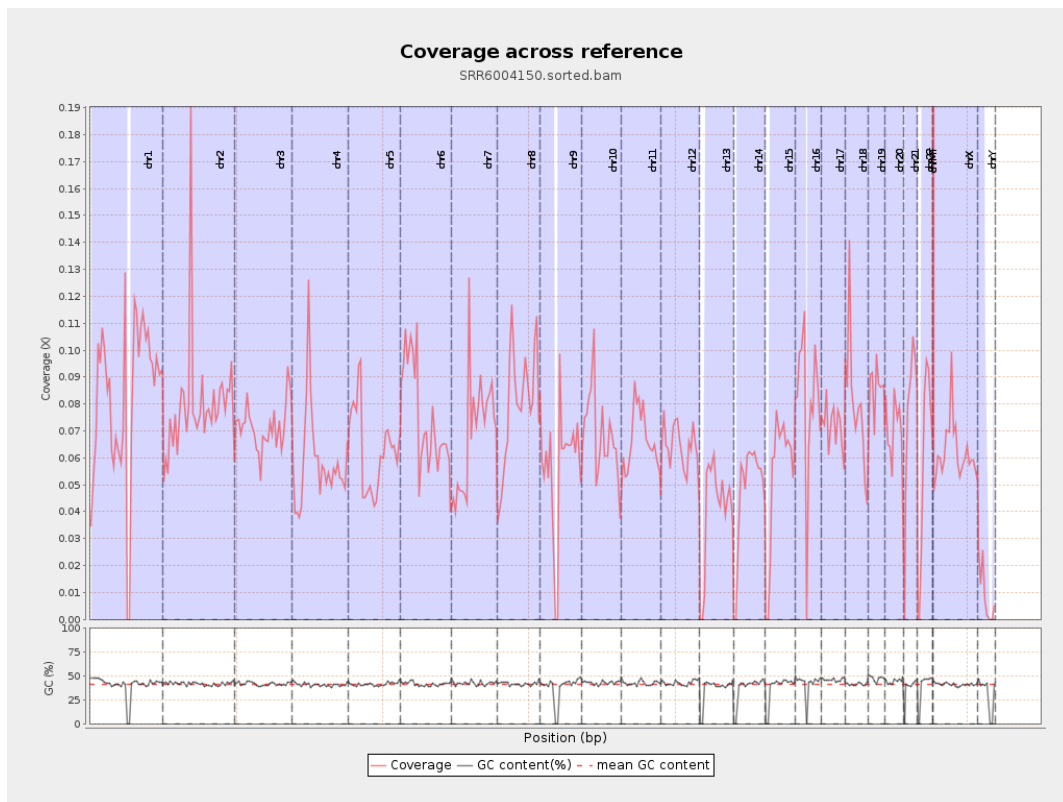
General error rate	1.05%
Mismatches	2,152,732
Insertions	21,293
Mapped reads with at least one insertion	0.65%
Deletions	62,325
Mapped reads with at least one deletion	1.9%
Homopolymer indels	47.29%

2.6. Chromosome stats

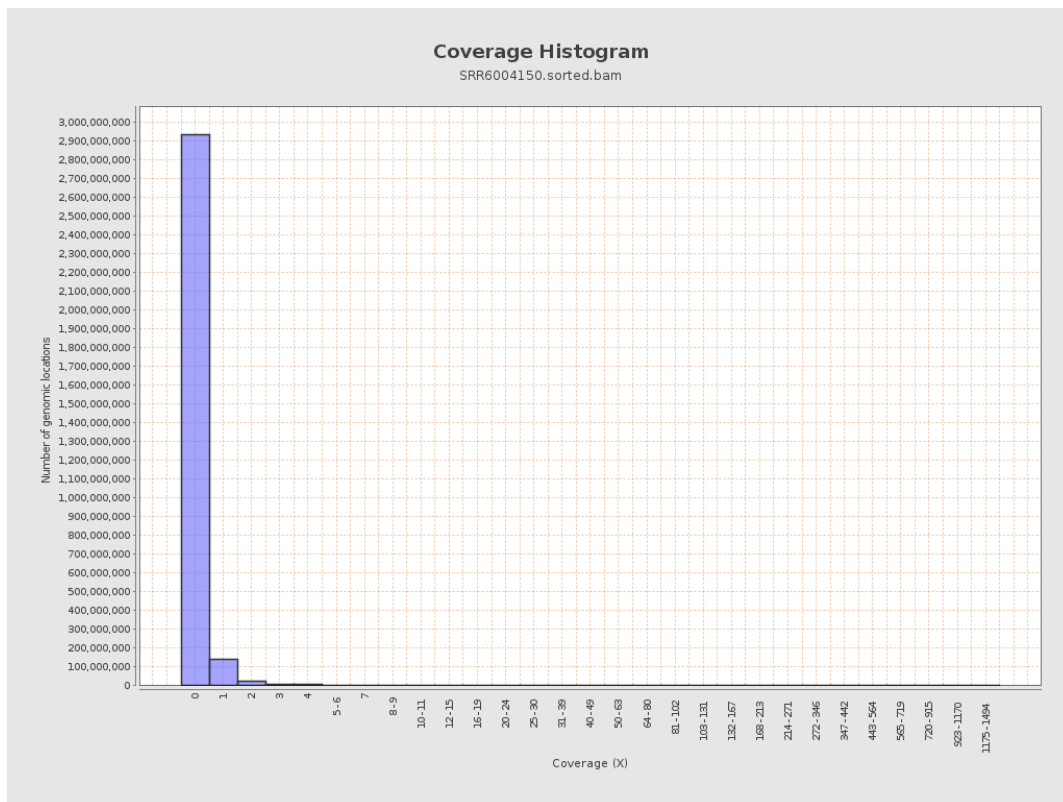
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20587017	0.0826	1.2094
chr2	243199373	19358205	0.0796	1.1359
chr3	198022430	14119622	0.0713	0.3328
chr4	191154276	11250062	0.0589	0.3294
chr5	180915260	11416987	0.0631	0.3235
chr6	171115067	12833637	0.075	0.4931
chr7	159138663	10939146	0.0687	0.9384

chr8	146364022	11705268	0.08	0.7536
chr9	141213431	7960770	0.0564	0.8229
chr10	135534747	9286365	0.0685	0.5426
chr11	135006516	8948355	0.0663	0.6754
chr12	133851895	8680605	0.0649	0.3426
chr13	115169878	4725529	0.041	0.2439
chr14	107349540	5189031	0.0483	0.4251
chr15	102531392	5401252	0.0527	0.3114
chr16	90354753	7195286	0.0796	0.4731
chr17	81195210	5847811	0.072	0.4263
chr18	78077248	6275450	0.0804	1.7759
chr19	59128983	5043805	0.0853	0.9214
chr20	63025520	4411793	0.07	0.3964
chr21	48129895	3670941	0.0763	0.4069
chr22	51304566	3045152	0.0594	0.3041
chrMT	16571	111127	6.7061	6.335
chrX	155270560	9626332	0.062	0.4949
chrY	59373566	543107	0.0091	0.1876

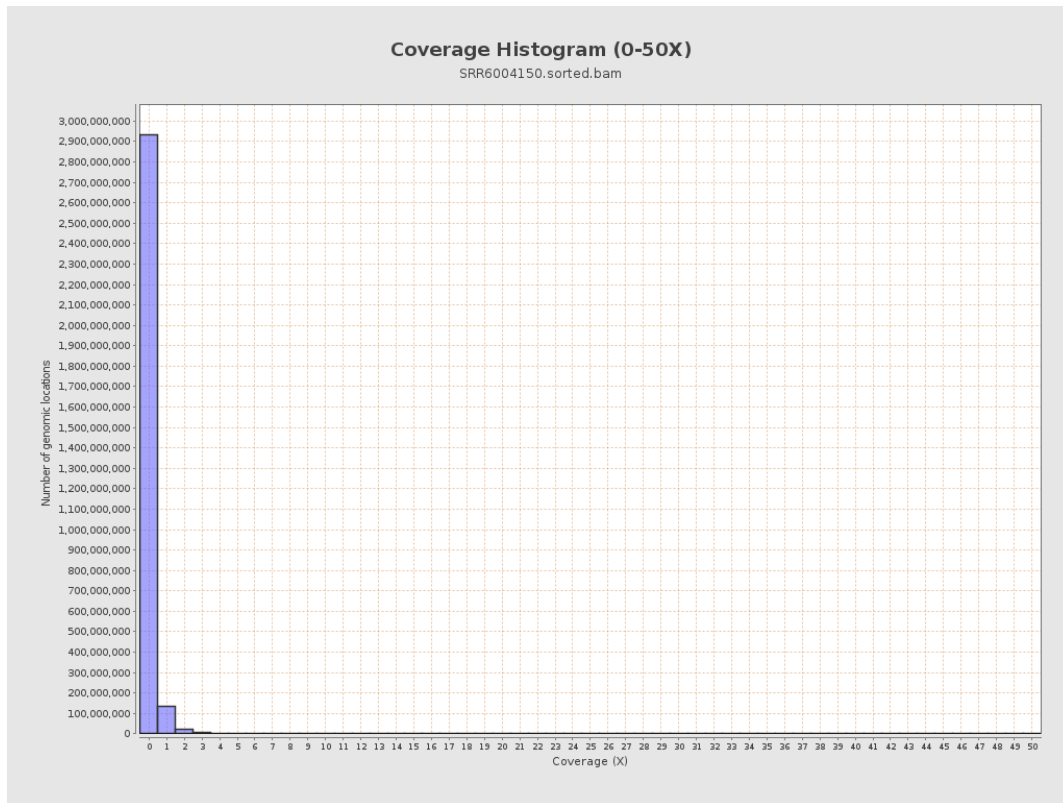
3. Results : Coverage across reference



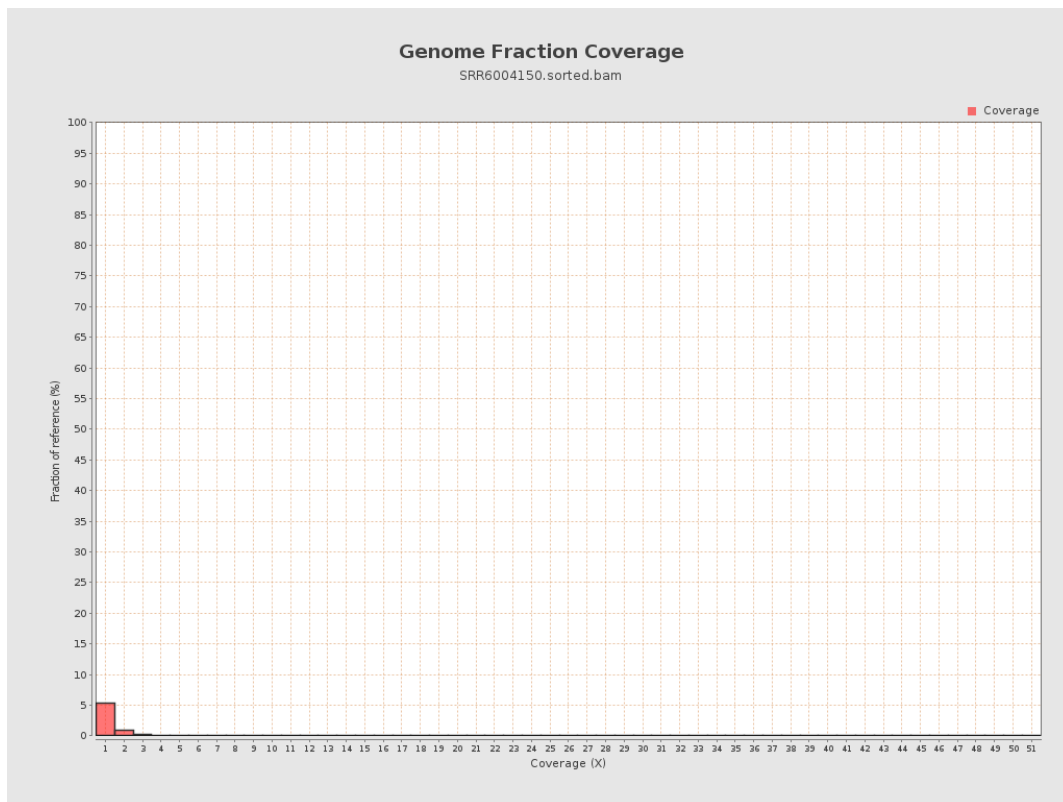
4. Results : Coverage Histogram



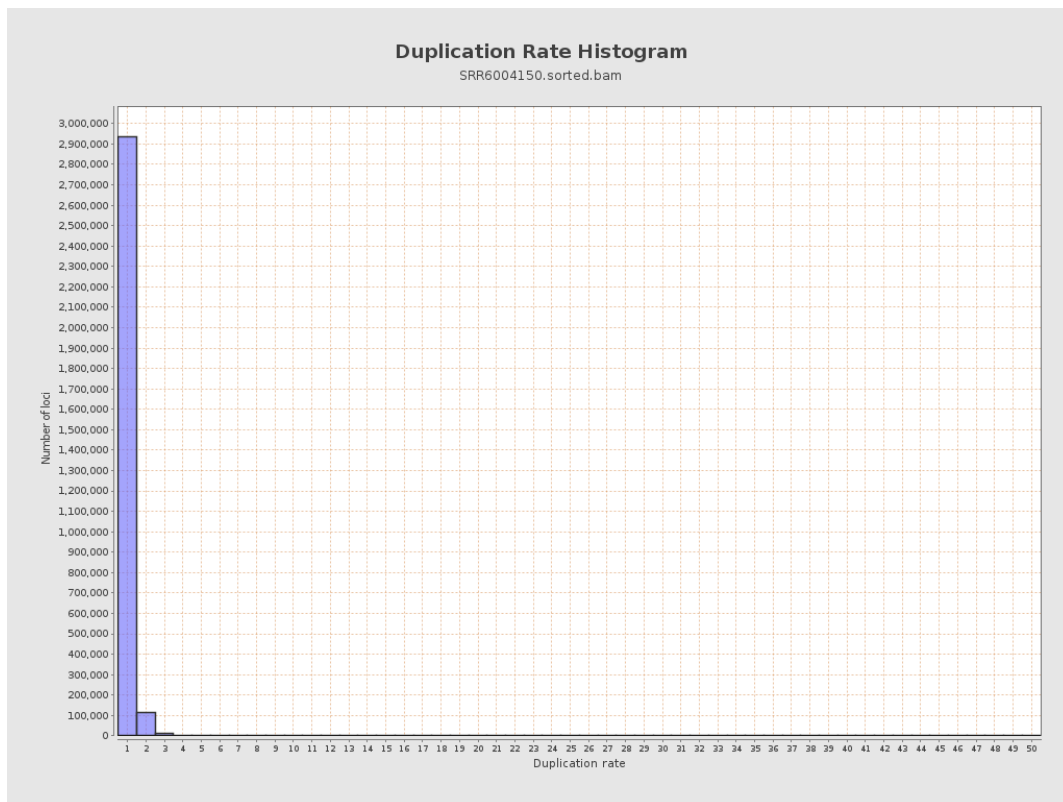
5. Results : Coverage Histogram (0-50X)



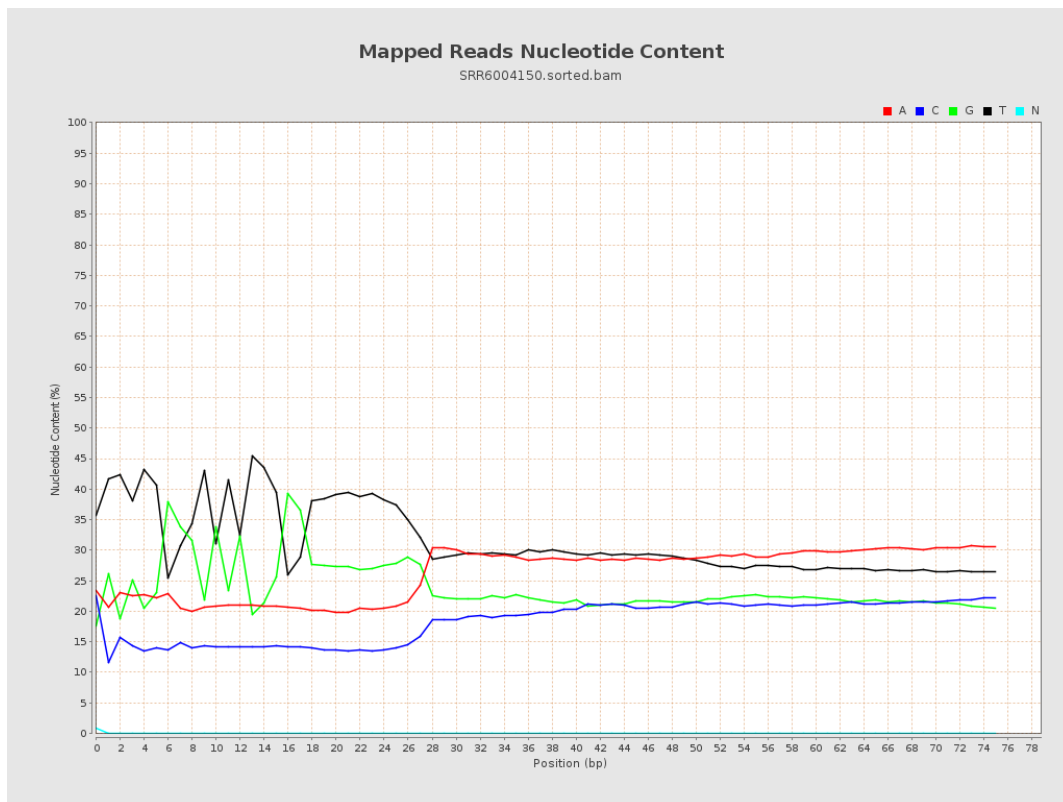
6. Results : Genome Fraction Coverage



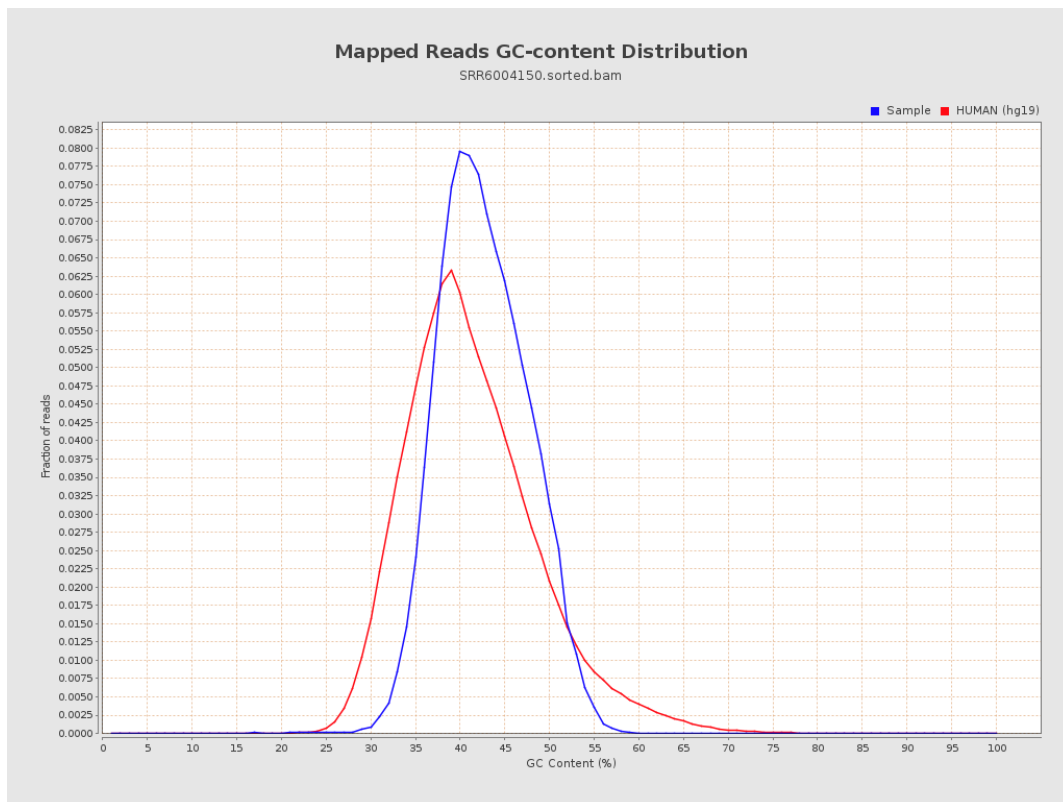
7. Results : Duplication Rate Histogram



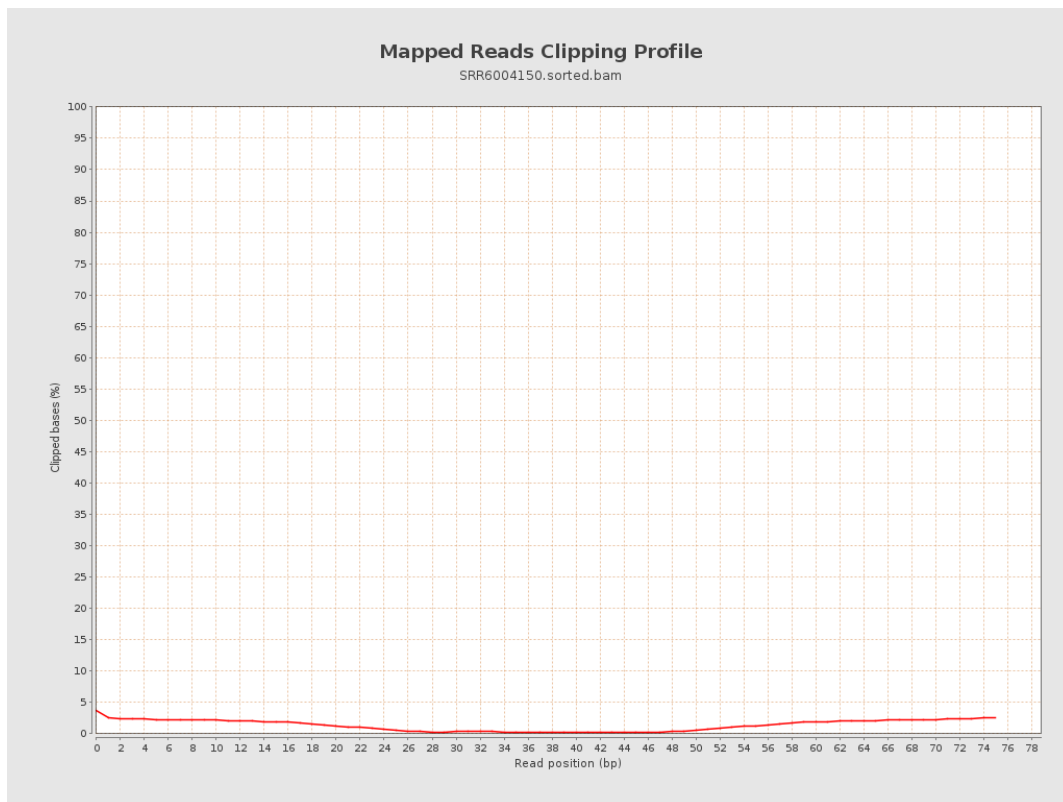
8. Results : Mapped Reads Nucleotide Content



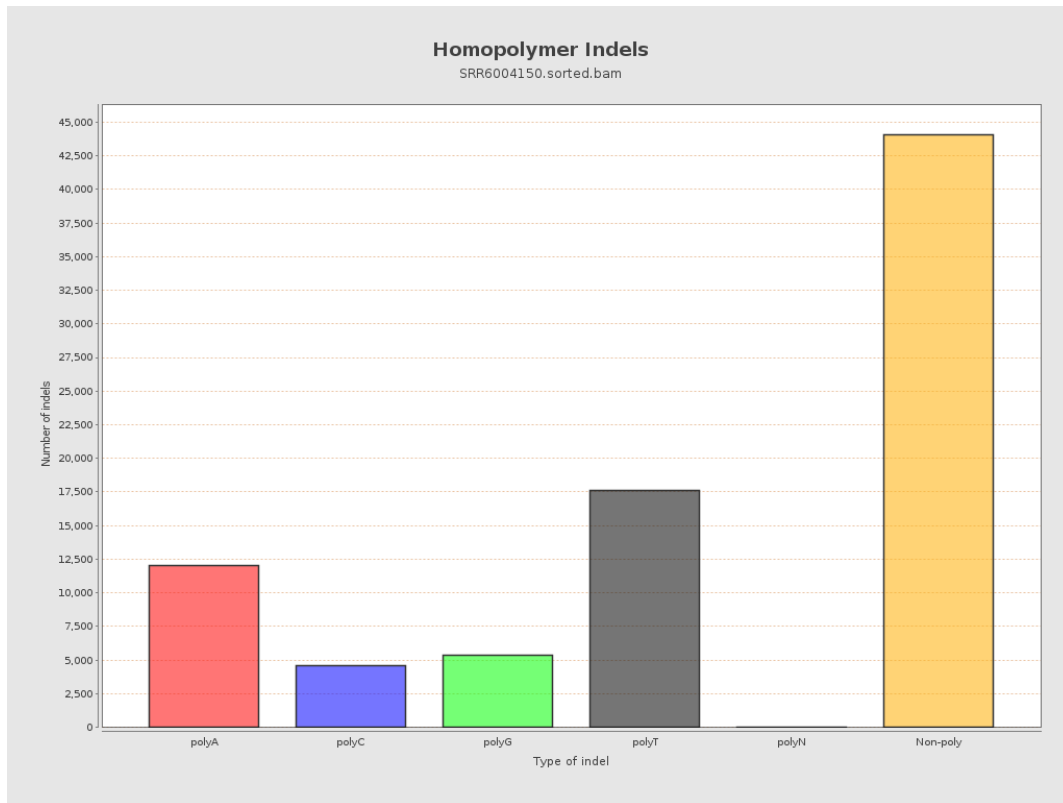
9. Results : Mapped Reads GC-content Distribution



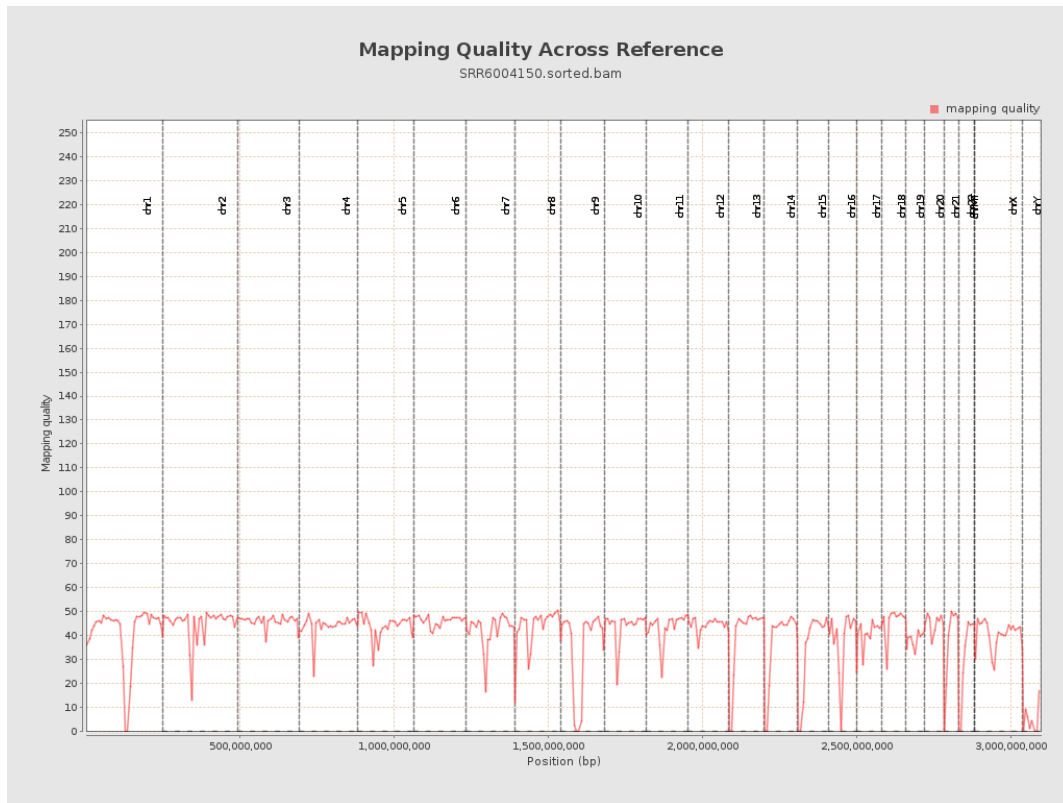
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

