

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:00:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716952.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_SRR9716952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716952.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:00:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,866,605
Mapped reads	1,706,615 / 91.43%
Unmapped reads	159,990 / 8.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,646 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	66,881 / 3.58%
Duplication rate	2.74%
Clipped reads	1,708,820 / 91.55%

2.2. ACGT Content

Number/percentage of A's	24,701,600 / 25.18%
Number/percentage of C's	17,877,006 / 18.23%
Number/percentage of T's	32,107,526 / 32.73%
Number/percentage of G's	23,400,856 / 23.86%
Number/percentage of N's	1,918 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0317

Standard Deviation	0.3032
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2.4. Mapping Quality

Mean Mapping Quality	44.01
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2.5. Mismatches and indels

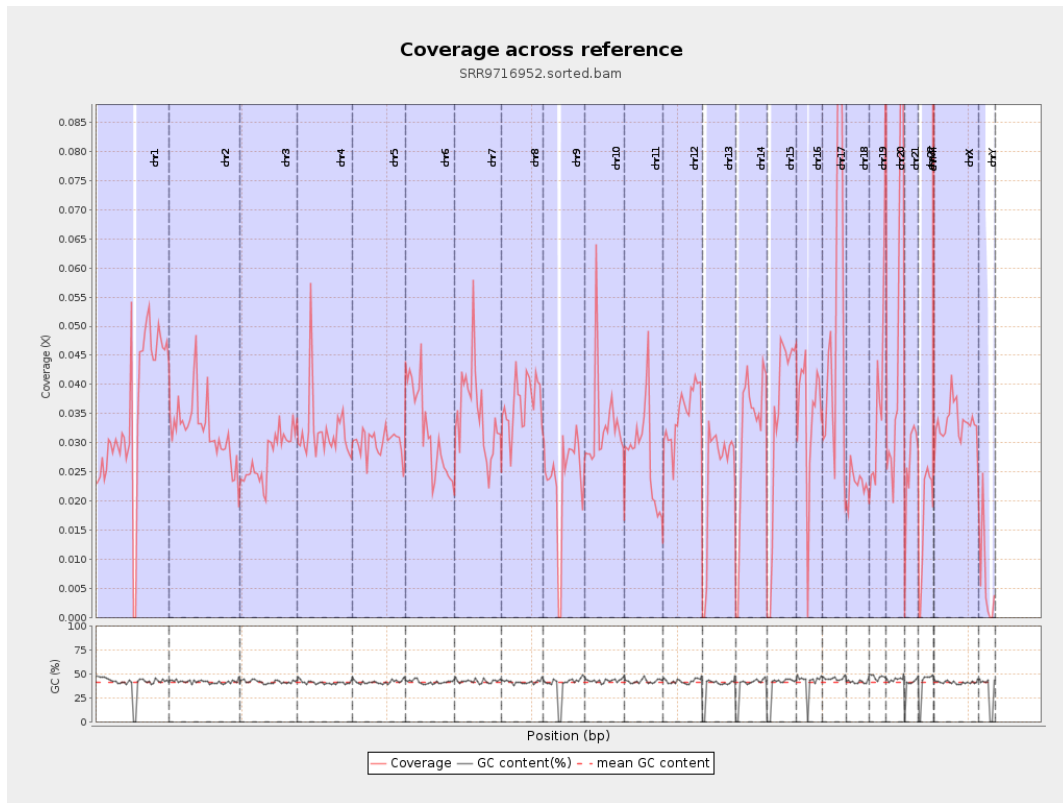
General error rate	0.53%
Mismatches	503,619
Insertions	7,445
Mapped reads with at least one insertion	0.43%
Deletions	19,218
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.35%

2.6. Chromosome stats

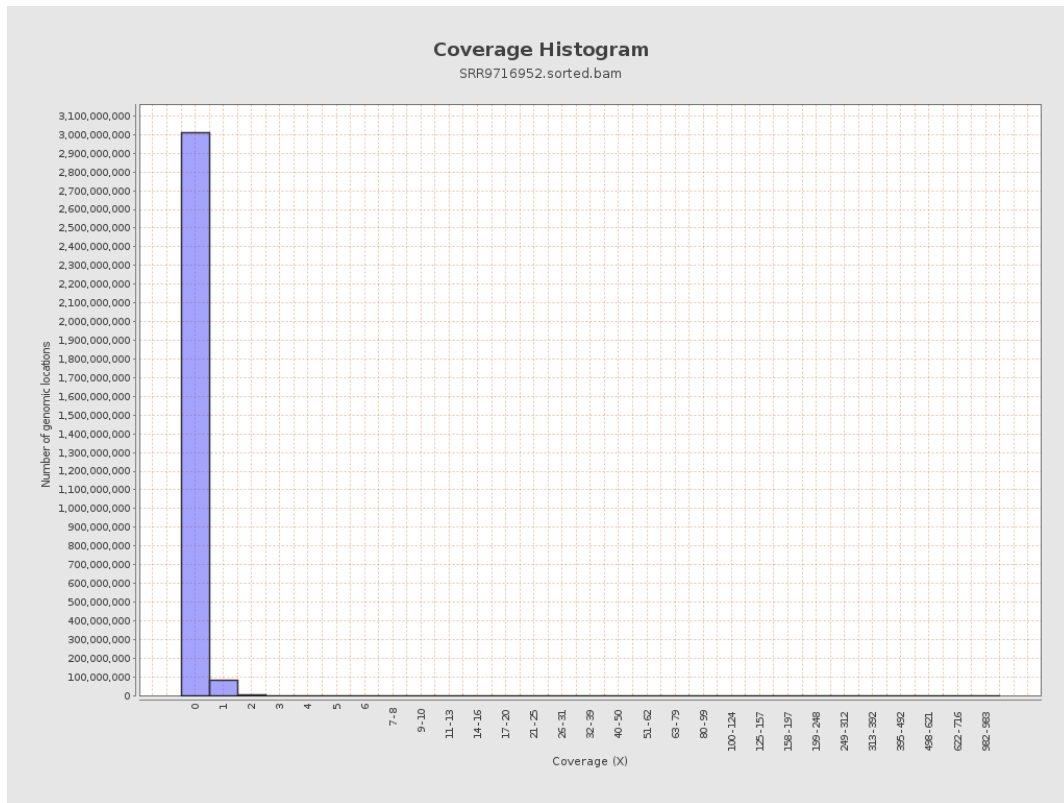
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8779614	0.0352	0.4899
chr2	243199373	7814623	0.0321	0.4506
chr3	198022430	5462842	0.0276	0.1866
chr4	191154276	6058488	0.0317	0.2384
chr5	180915260	5405929	0.0299	0.1898
chr6	171115067	5453889	0.0319	0.2384
chr7	159138663	5591152	0.0351	0.3779

chr8	146364022	5393615	0.0369	0.3843
chr9	141213431	3308722	0.0234	0.2218
chr10	135534747	4447444	0.0328	0.3227
chr11	135006516	3776200	0.028	0.2457
chr12	133851895	4677692	0.0349	0.2062
chr13	115169878	2839793	0.0247	0.1721
chr14	107349540	3418136	0.0318	0.201
chr15	102531392	3509821	0.0342	0.2073
chr16	90354753	3164125	0.035	0.2166
chr17	81195210	4053689	0.0499	0.258
chr18	78077248	1795391	0.023	0.3778
chr19	59128983	2329670	0.0394	0.4015
chr20	63025520	3092190	0.0491	0.2542
chr21	48129895	1257065	0.0261	0.2162
chr22	51304566	864609	0.0169	0.1415
chrMT	16571	88140	5.3189	3.7785
chrX	155270560	5175273	0.0333	0.2212
chrY	59373566	361658	0.0061	0.2542

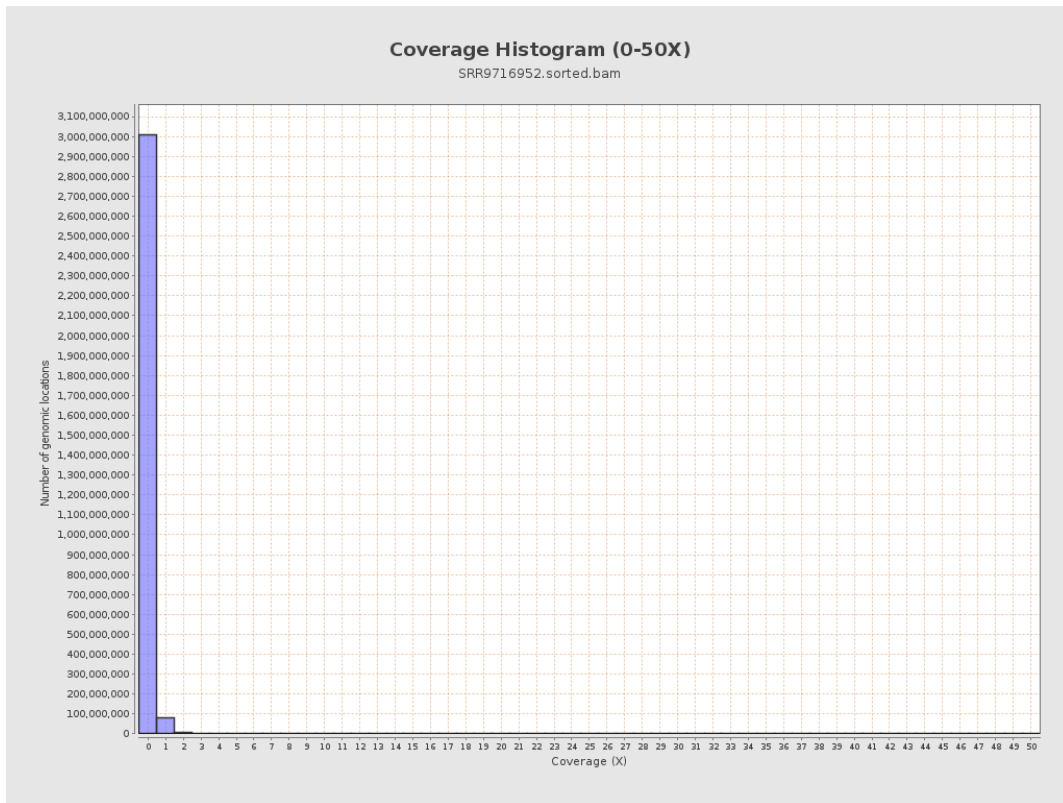
3. Results : Coverage across reference



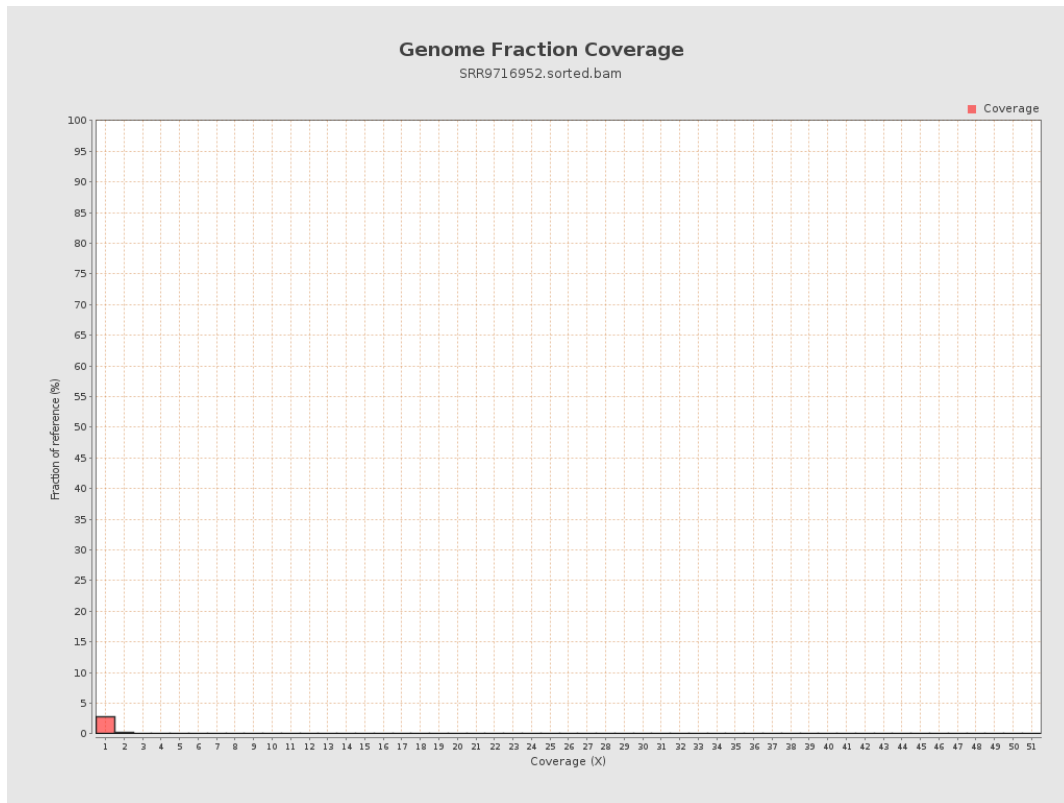
4. Results : Coverage Histogram



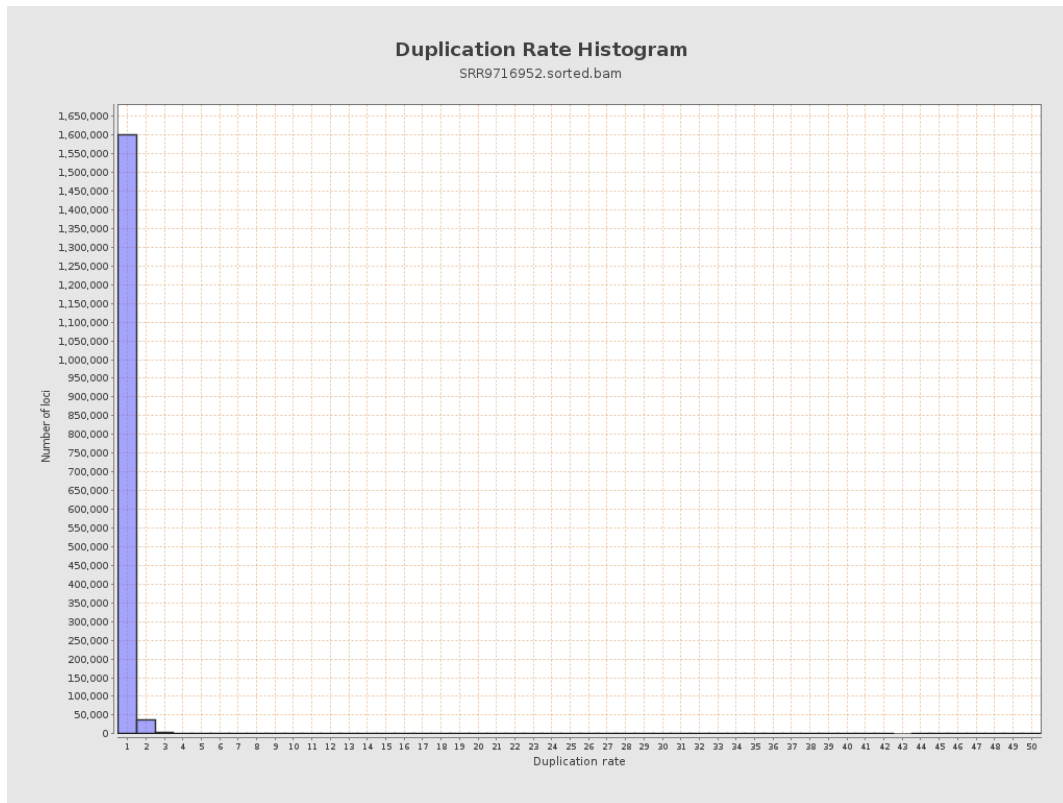
5. Results : Coverage Histogram (0-50X)



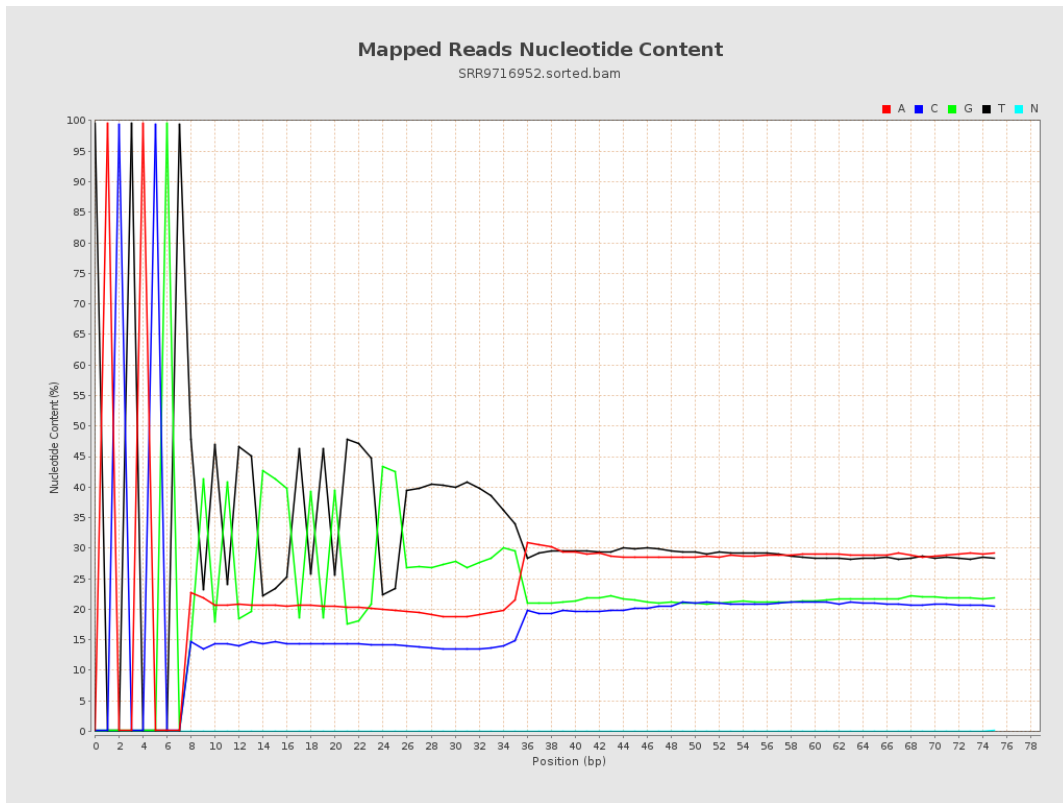
6. Results : Genome Fraction Coverage



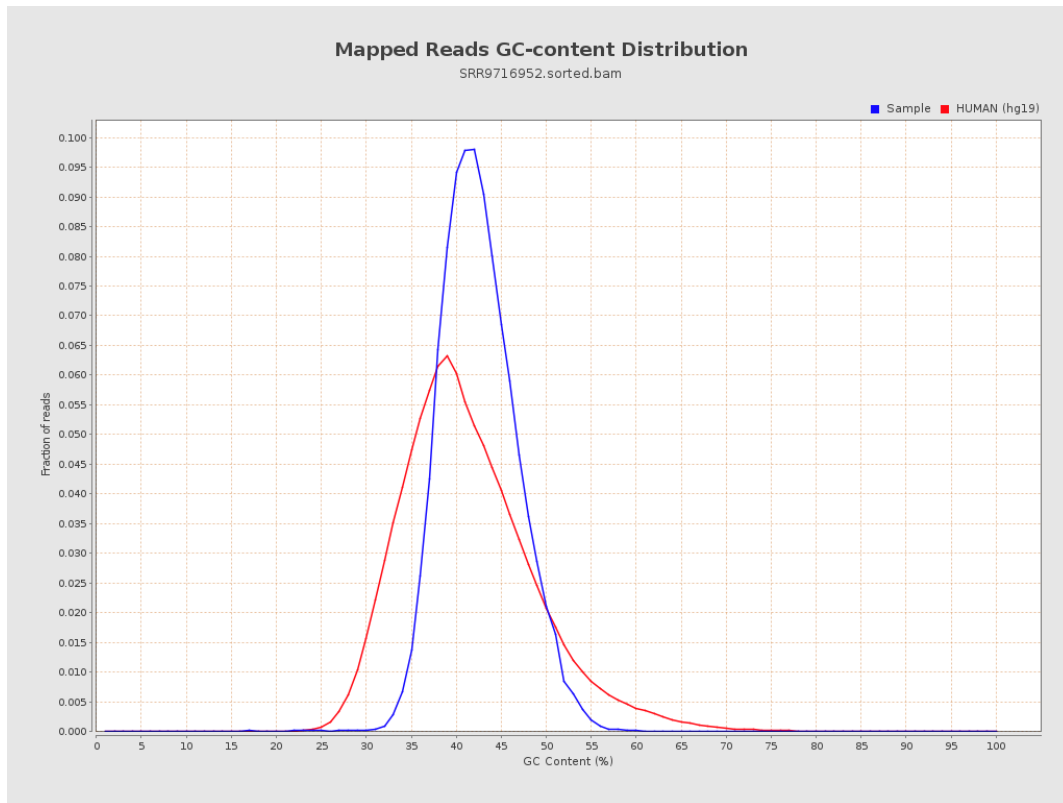
7. Results : Duplication Rate Histogram



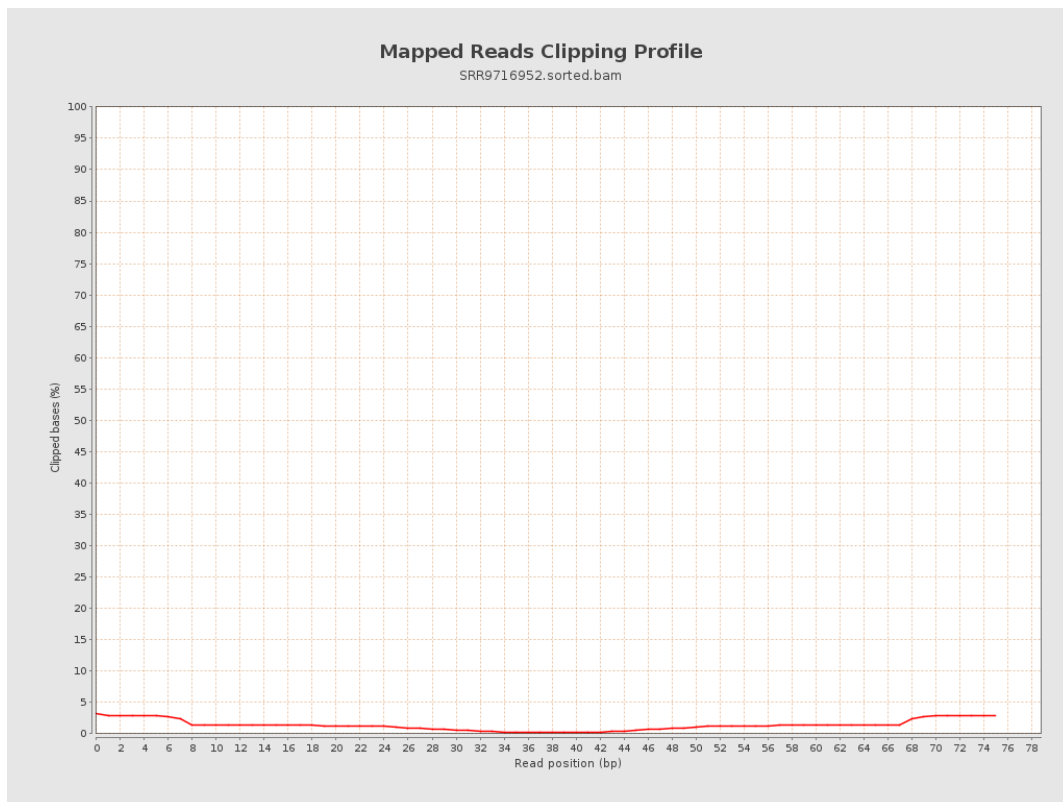
8. Results : Mapped Reads Nucleotide Content



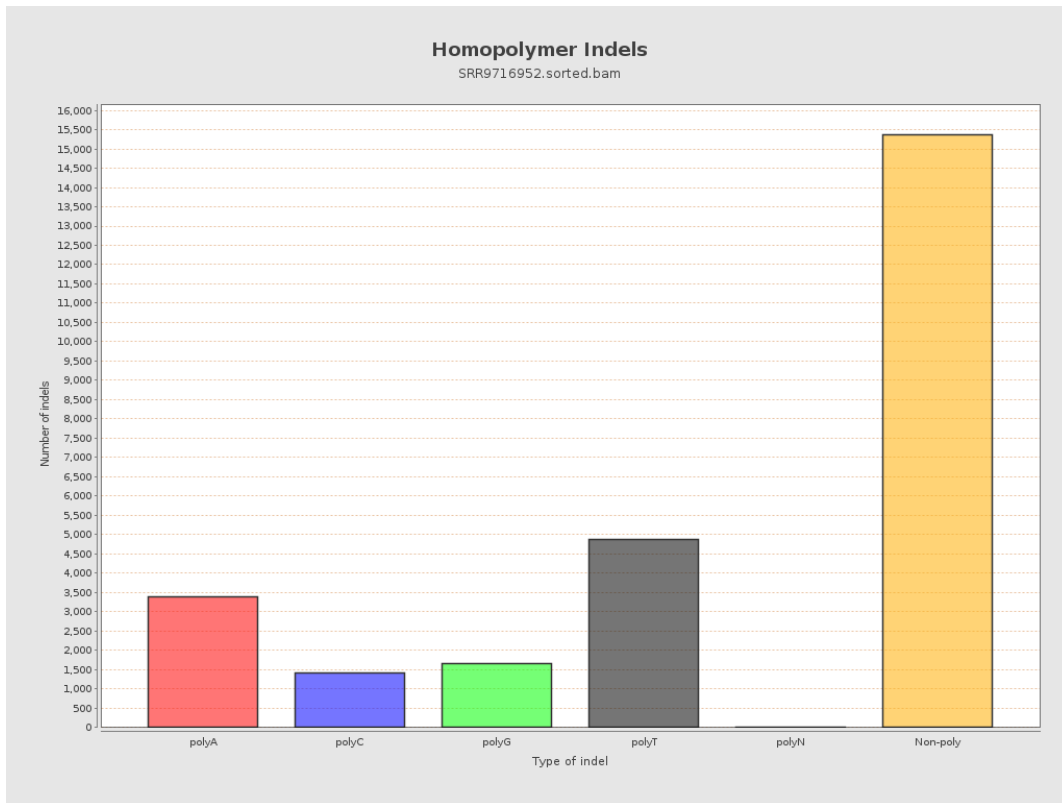
9. Results : Mapped Reads GC-content Distribution



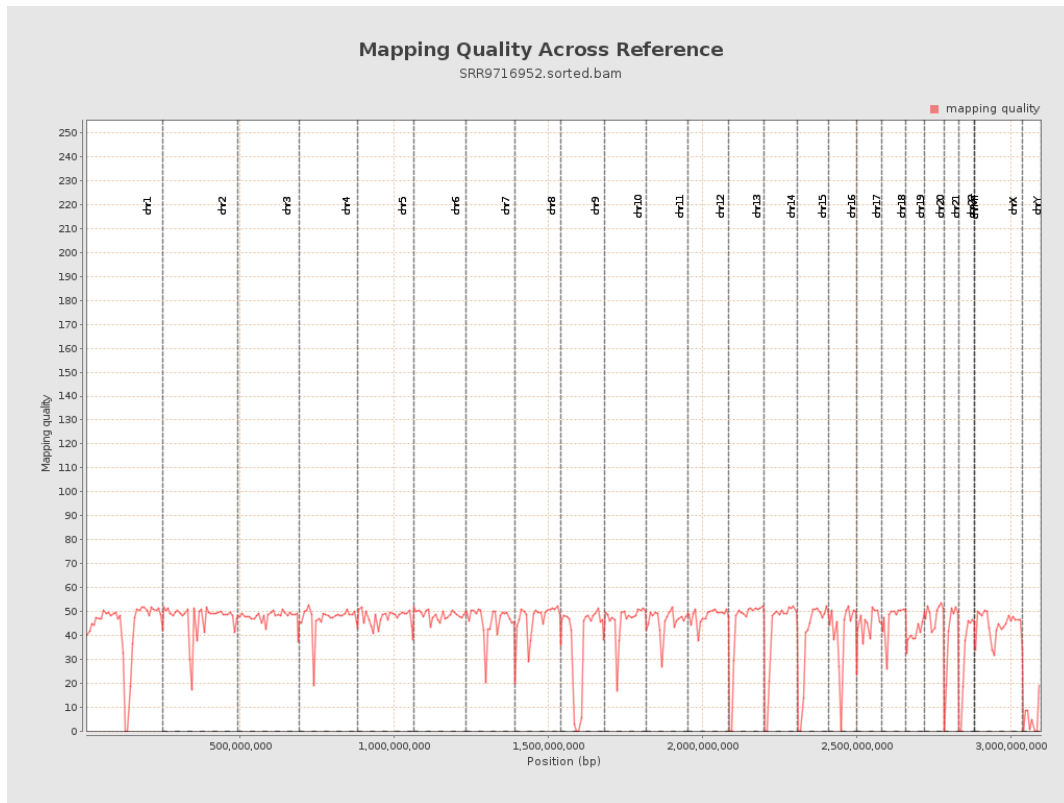
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

