Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:18:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716812.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_SRR9716812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716812.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:18:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716812.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,654,233
Mapped reads	1,527,205 / 92.32%
Unmapped reads	127,028 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,555 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	51,637 / 3.12%
Duplication rate	2.52%
Clipped reads	1,532,987 / 92.67%

2.2. ACGT Content

Number/percentage of A's	21,517,093 / 24.19%
Number/percentage of C's	18,059,238 / 20.3%
Number/percentage of T's	28,618,945 / 32.18%
Number/percentage of G's	20,742,221 / 23.32%
Number/percentage of N's	2,440 / 0%
GC Percentage	43.63%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2624

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

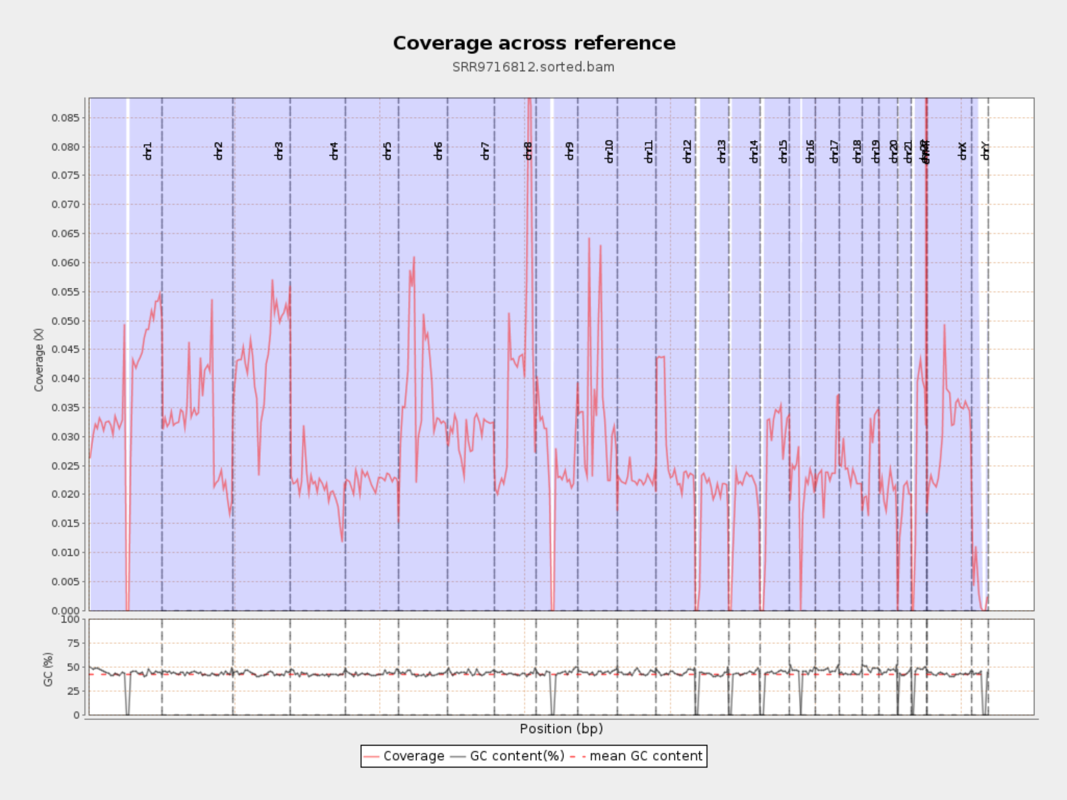
General error rate	0.5%
Mismatches	439,717
Insertions	5,170
Mapped reads with at least one insertion	0.34%
Deletions	16,471
Mapped reads with at least one deletion	1.07%
Homopolymer indels	45.28%

2.6. Chromosome stats

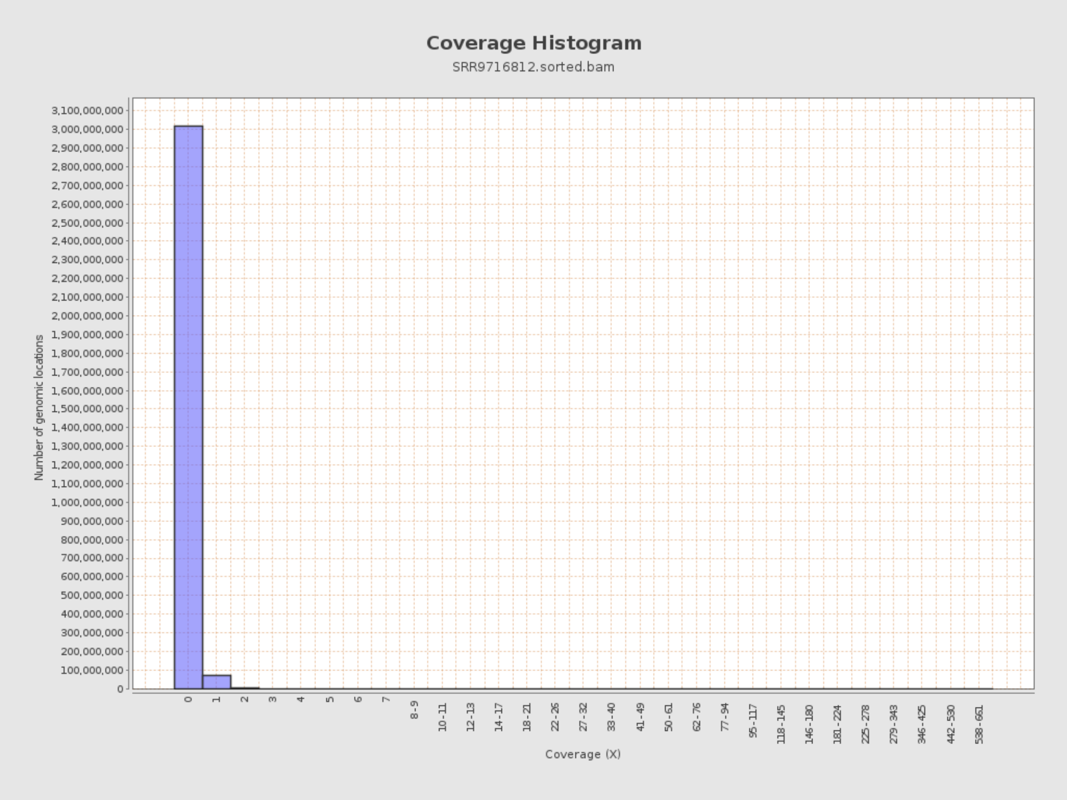
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9168677	0.0368	0.4673
chr2	243199373	7831910	0.0322	0.3417
chr3	198022430	8742098	0.0441	0.2305
chr4	191154276	4034693	0.0211	0.1674
chr5	180915260	4058912	0.0224	0.1643
chr6	171115067	6552968	0.0383	0.2999
chr7	159138663	4886165	0.0307	0.2464

chr8	146364022	6101800	0.0417	0.2517
chr9	141213431	3384163	0.024	0.2274
chr10	135534747	4744281	0.035	0.2942
chr11	135006516	3048436	0.0226	0.2201
chr12	133851895	3740546	0.0279	0.1869
chr13	115169878	2072363	0.018	0.1463
chr14	107349540	1994676	0.0186	0.1637
chr15	102531392	2651076	0.0259	0.1773
chr16	90354753	1900455	0.021	0.1776
chr17	81195210	2003808	0.0247	0.177
chr18	78077248	1874897	0.024	0.3986
chr19	59128983	1560426	0.0264	0.3177
chr20	63025520	1301626	0.0207	0.1587
chr21	48129895	818502	0.017	0.1574
chr22	51304566	1393950	0.0272	0.1796
chrMT	16571	28432	1.7158	1.572
chrX	155270560	4852217	0.0313	0.2202
chrY	59373566	218869	0.0037	0.087

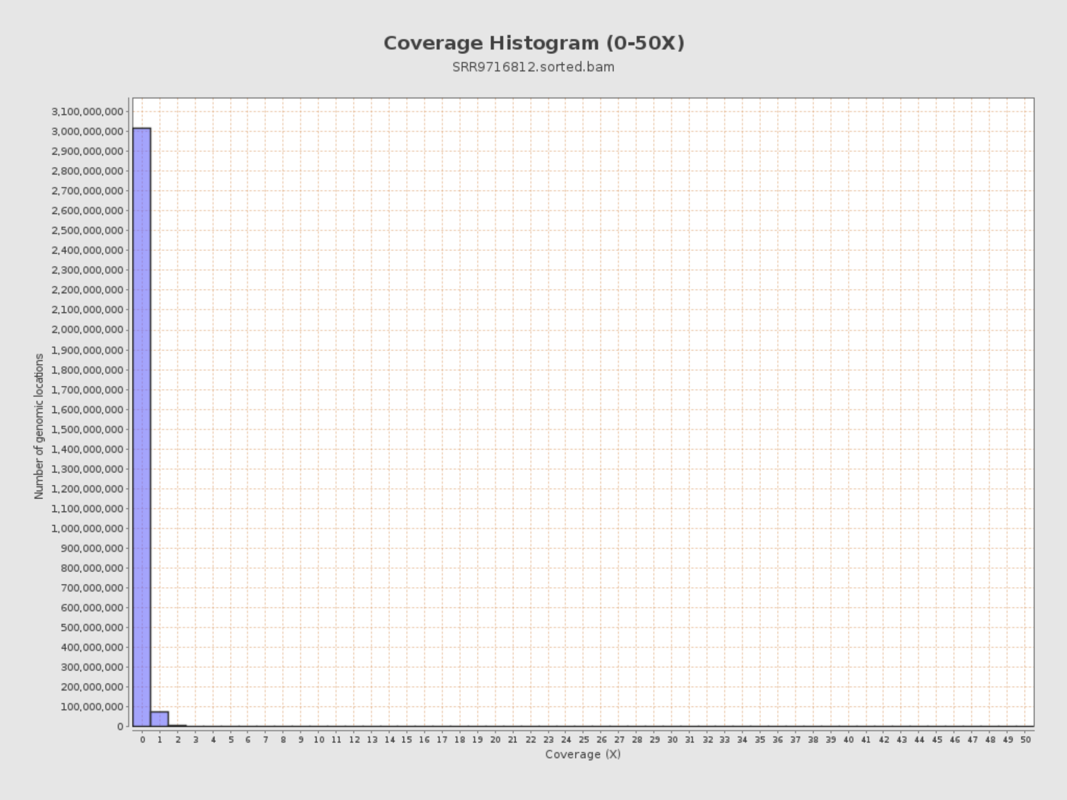
3. Results : Coverage across reference



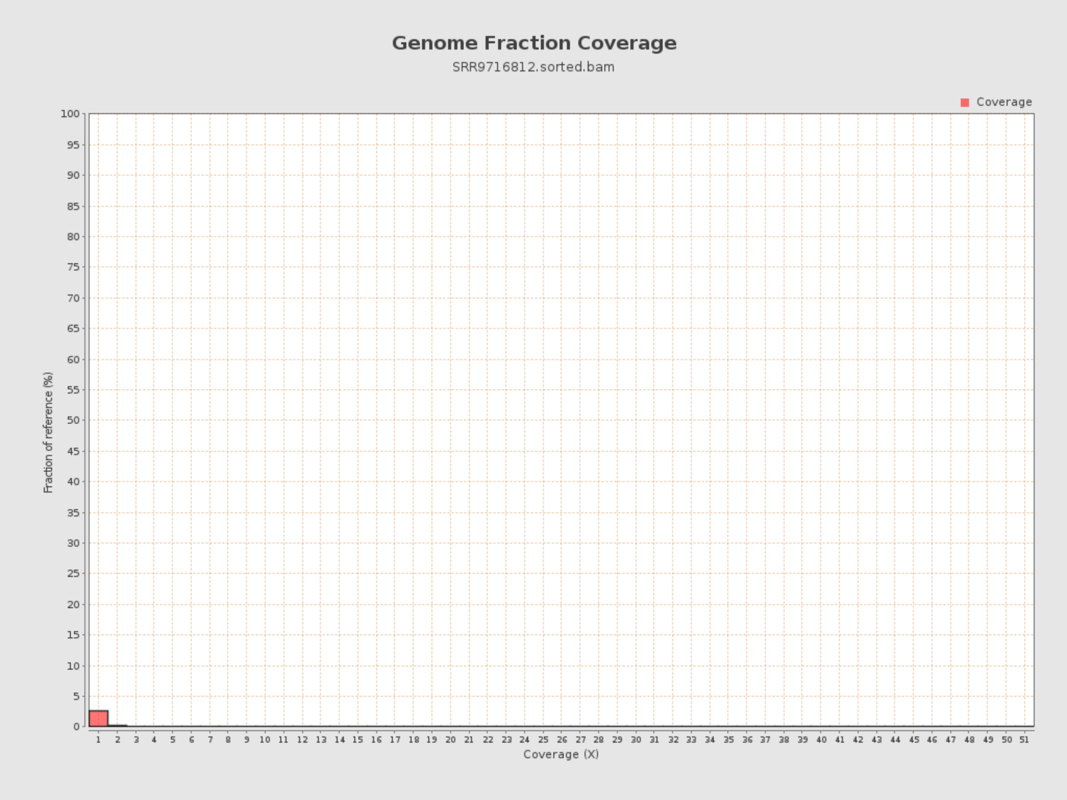
4. Results : Coverage Histogram



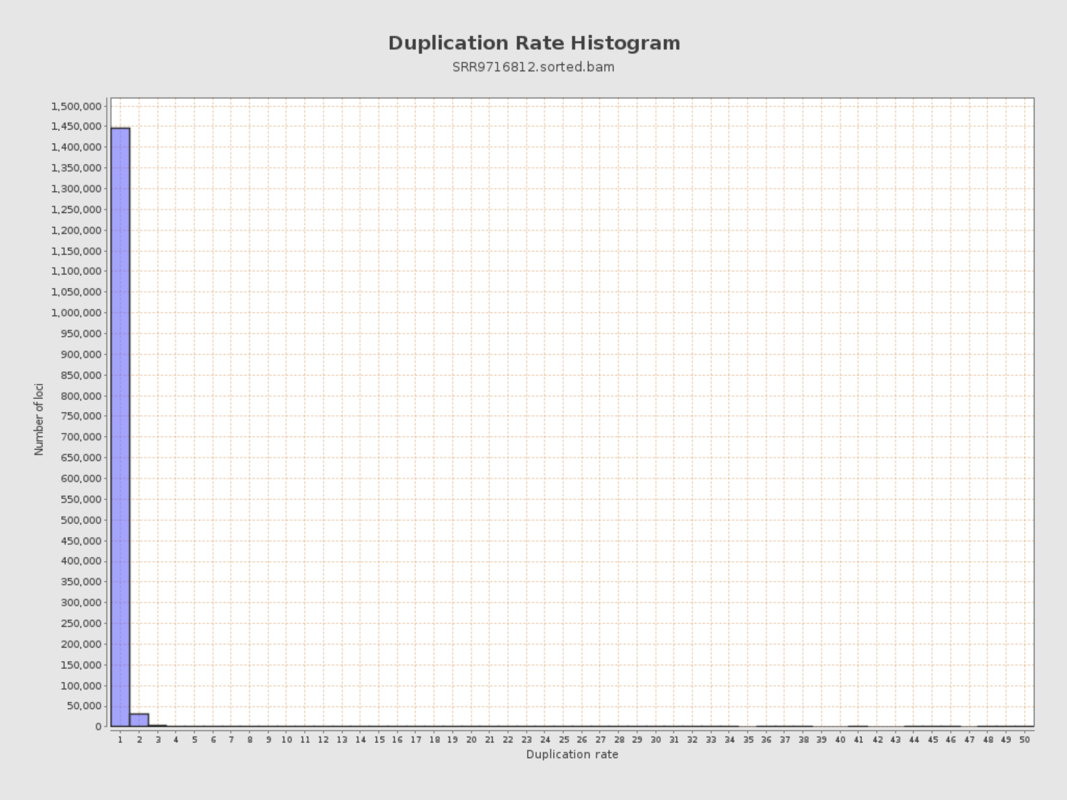
5. Results : Coverage Histogram (0-50X)



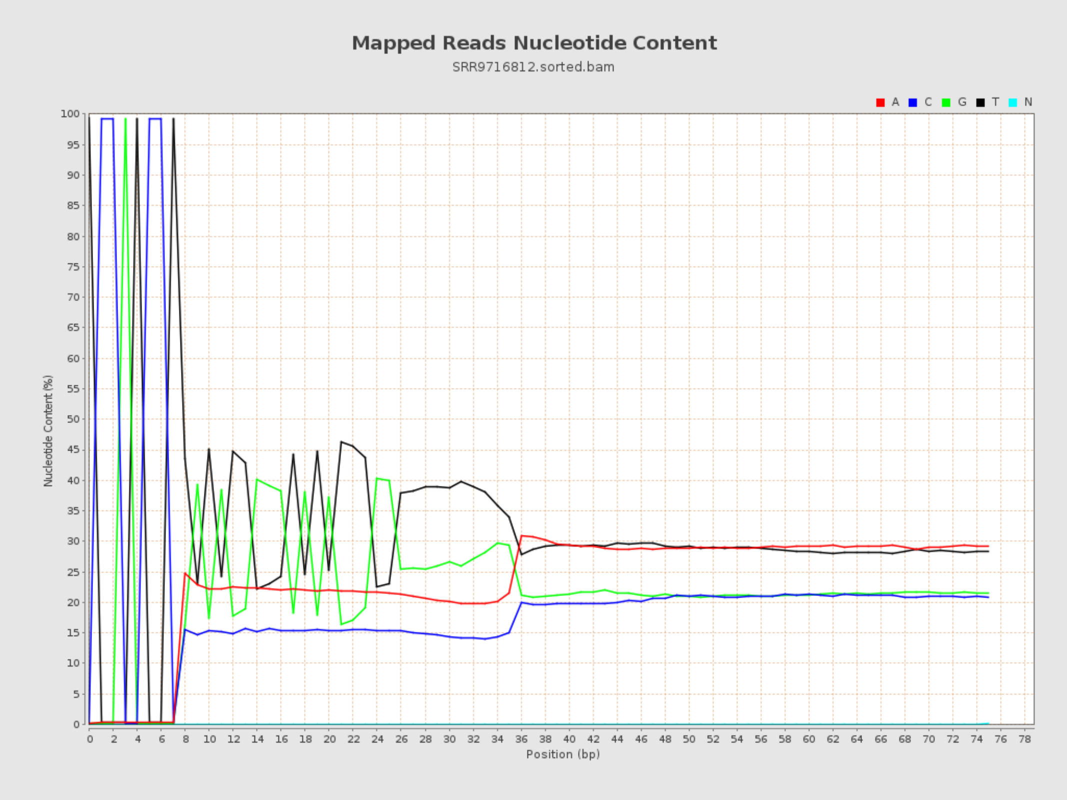
6. Results : Genome Fraction Coverage



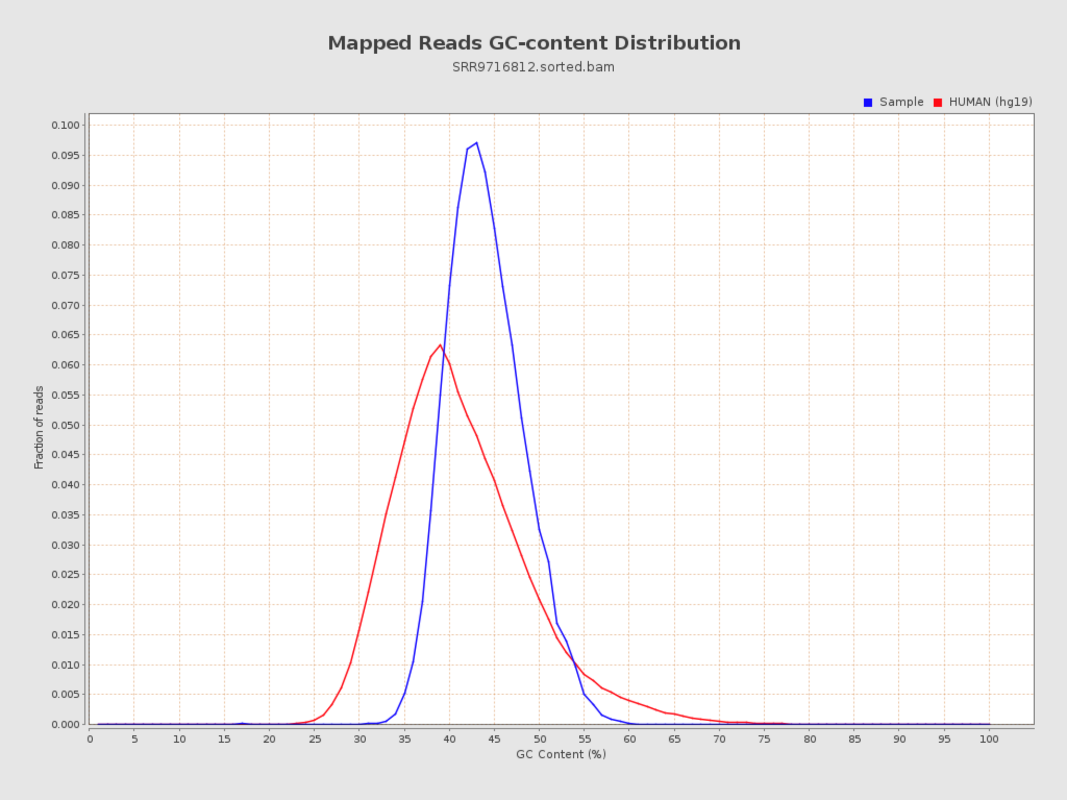
7. Results : Duplication Rate Histogram



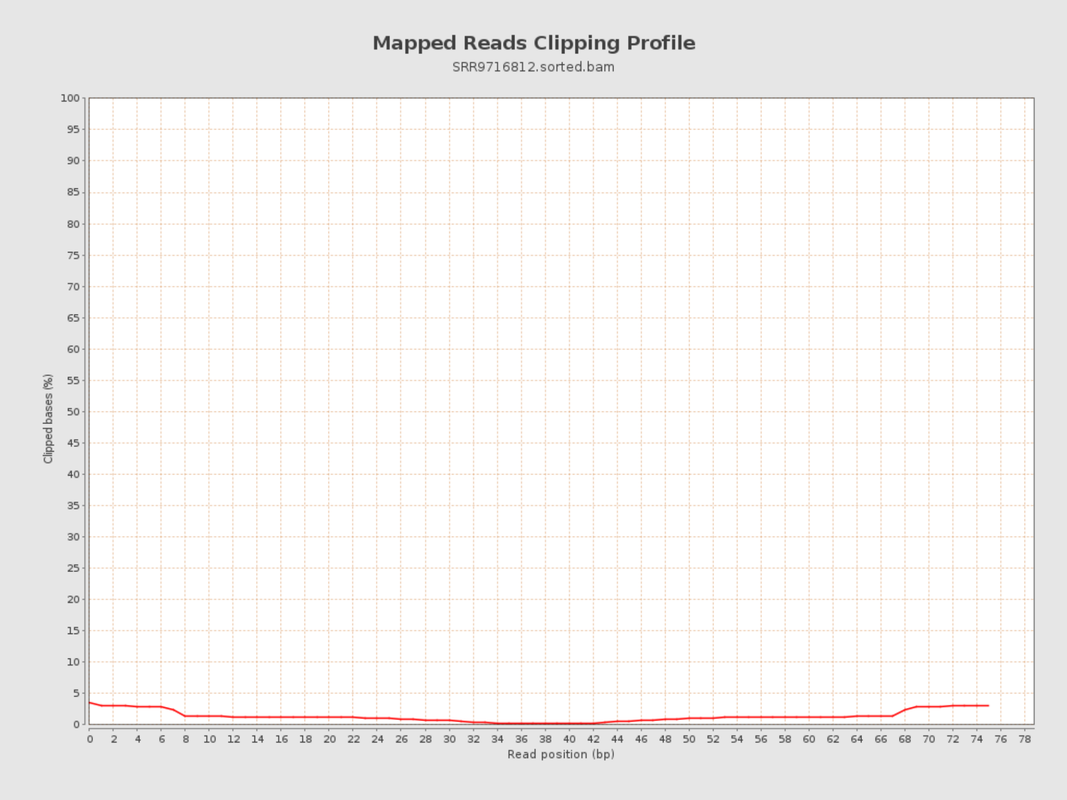
8. Results : Mapped Reads Nucleotide Content



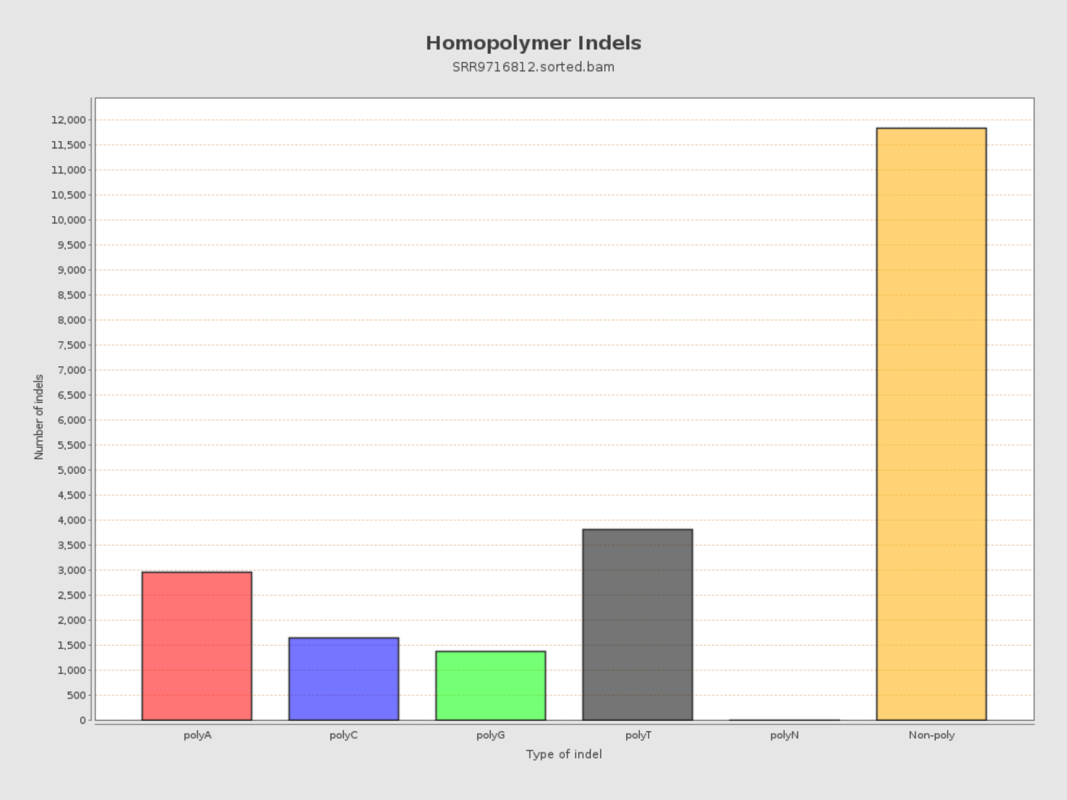
9. Results : Mapped Reads GC-content Distribution



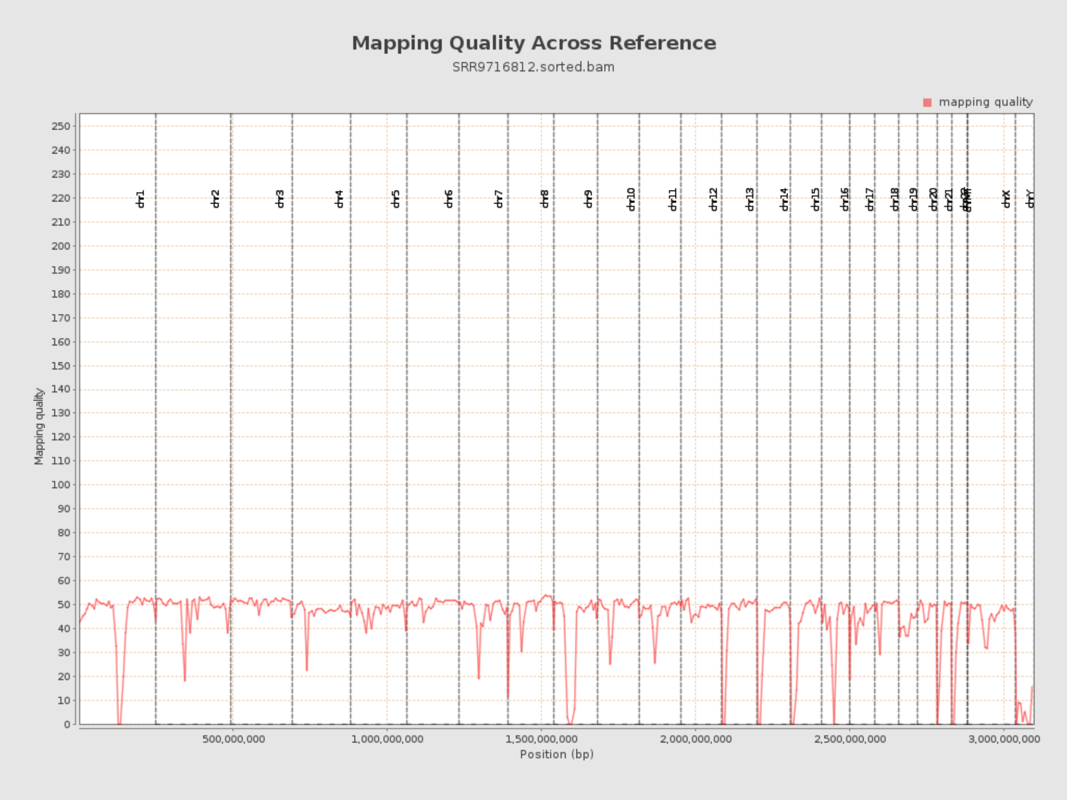
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram