Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:03:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716604.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_SRR9716604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716604.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:03:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,713,518
Mapped reads	2,515,113 / 92.69%
Unmapped reads	198,405 / 7.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	65,879 / 2.43%
Read min/max/mean length	30 / 101 / 101.87
Duplicated reads (estimated)	98,579 / 3.63%
Duplication rate	2.72%
Clipped reads	2,576,177 / 94.94%

2.2. ACGT Content

Number/percentage of A's	49,957,941 / 26.42%
Number/percentage of C's	38,550,369 / 20.39%
Number/percentage of T's	57,137,178 / 30.22%
Number/percentage of G's	43,390,269 / 22.95%
Number/percentage of N's	22,962 / 0.01%
GC Percentage	43.34%

2.3. Coverage

Mean	0.0611

Standard Deviation	0.4787

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

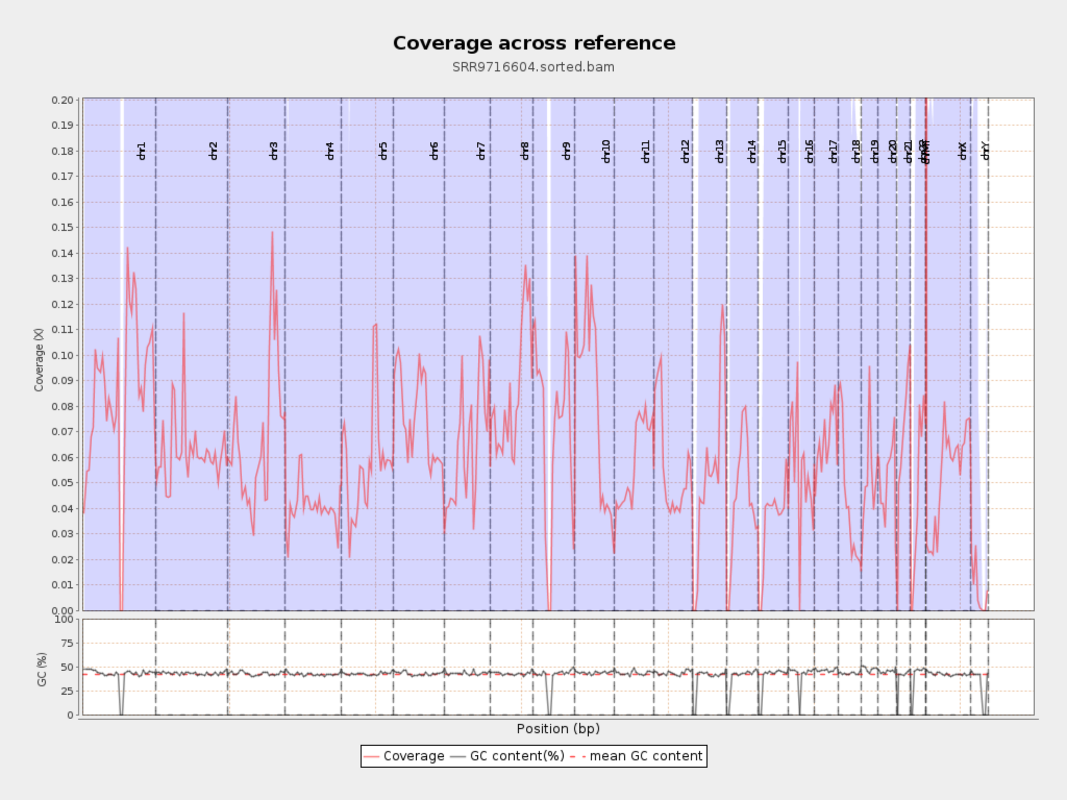
General error rate	0.77%
Mismatches	1,416,958
Insertions	17,313
Mapped reads with at least one insertion	0.68%
Deletions	40,693
Mapped reads with at least one deletion	1.6%
Homopolymer indels	39.72%

2.6. Chromosome stats

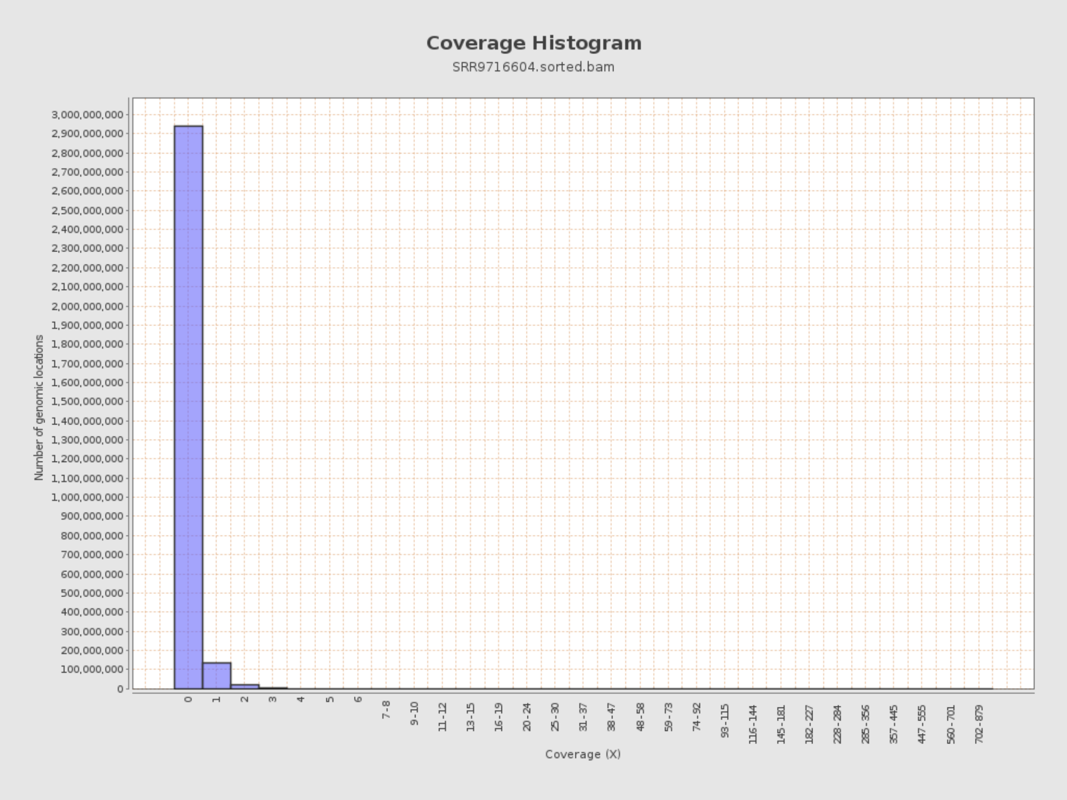
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20945506	0.084	0.8098
chr2	243199373	15191182	0.0625	0.6678
chr3	198022430	13444126	0.0679	0.3067
chr4	191154276	7753152	0.0406	0.2619
chr5	180915260	10356519	0.0572	0.2759
chr6	171115067	12883721	0.0753	0.3578
chr7	159138663	10276842	0.0646	0.7042

chr8	146364022	12542641	0.0857	0.5684
chr9	141213431	9880320	0.07	0.4529
chr10	135534747	11343730	0.0837	0.5776
chr11	135006516	7799577	0.0578	0.4173
chr12	133851895	7570250	0.0566	0.2772
chr13	115169878	6379963	0.0554	0.272
chr14	107349540	4711952	0.0439	0.2713
chr15	102531392	3547488	0.0346	0.2169
chr16	90354753	4820141	0.0533	0.3083
chr17	81195210	5401379	0.0665	0.3536
chr18	78077248	3407358	0.0436	0.7069
chr19	59128983	3106667	0.0525	0.6211
chr20	63025520	3308283	0.0525	0.2821
chr21	48129895	3277148	0.0681	0.3233
chr22	51304566	2362573	0.046	0.2528
chrMT	16571	83429	5.0346	4.2788
chrX	155270560	8247151	0.0531	0.3234
chrY	59373566	487615	0.0082	0.2256

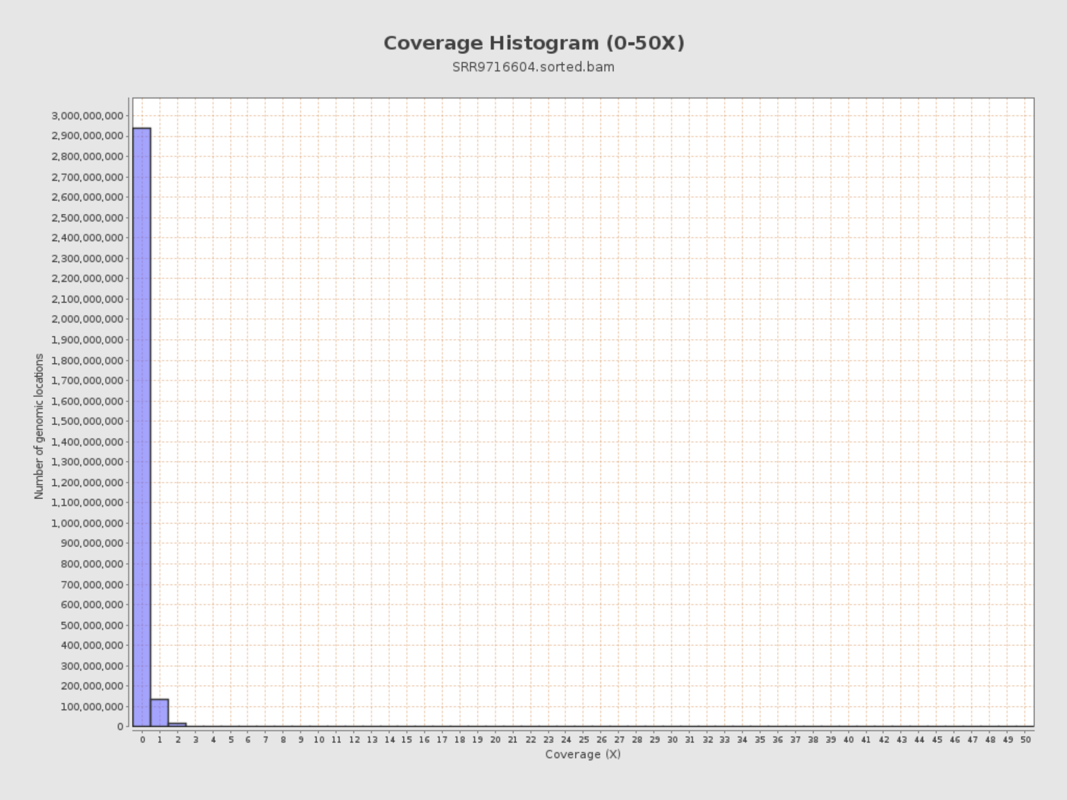
3. Results : Coverage across reference



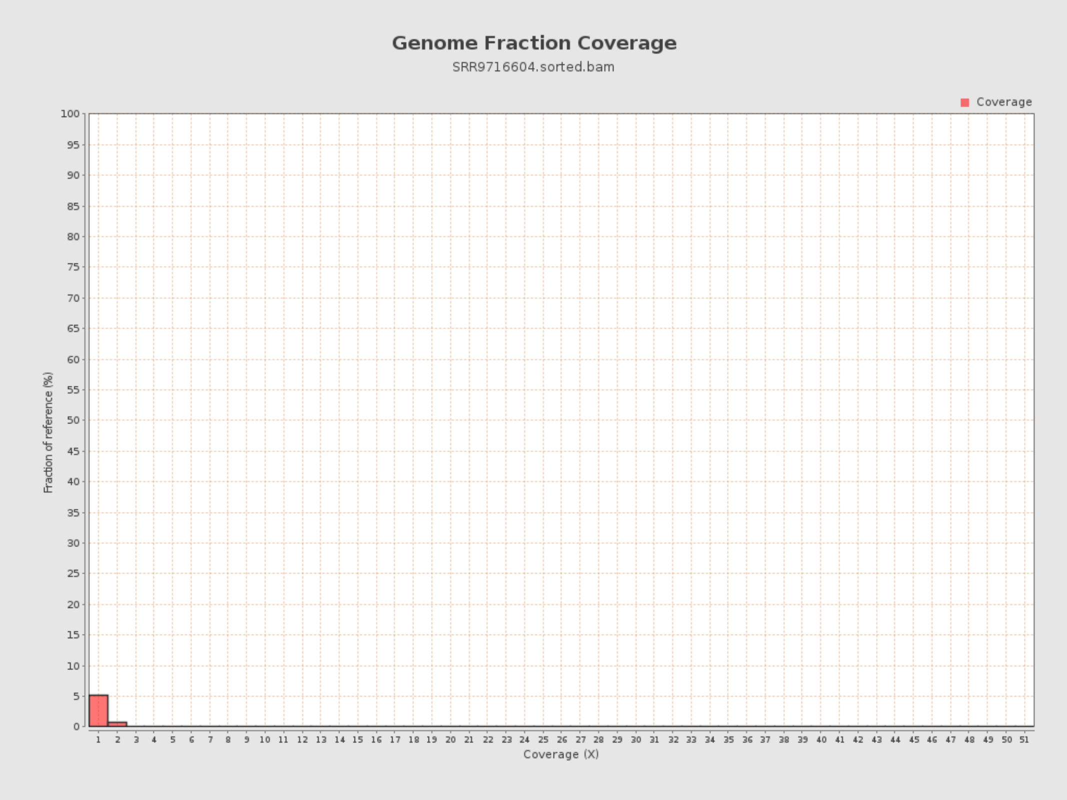
4. Results : Coverage Histogram



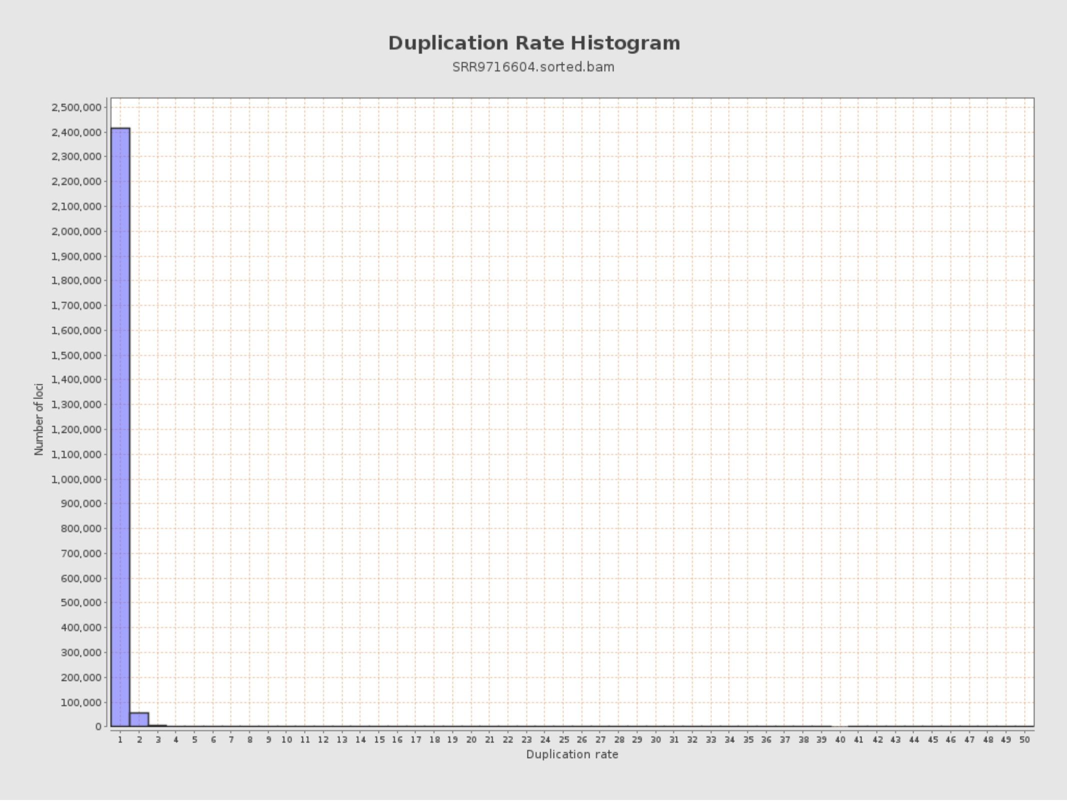
5. Results : Coverage Histogram (0-50X)



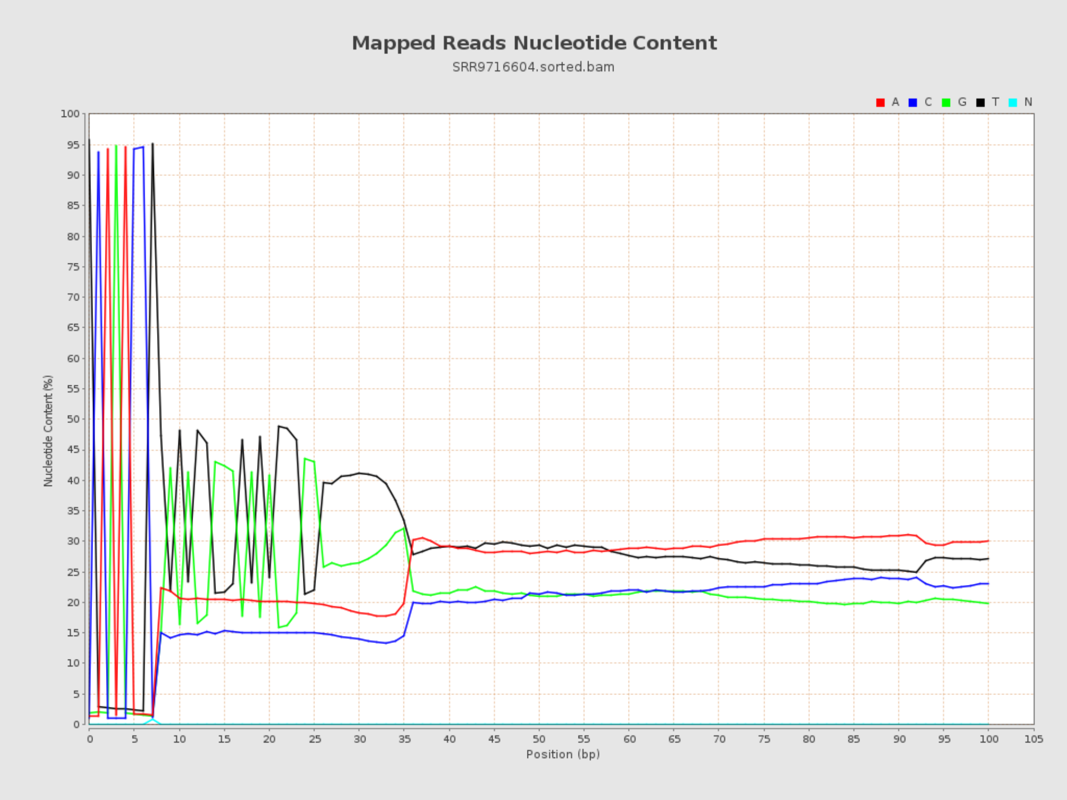
6. Results : Genome Fraction Coverage



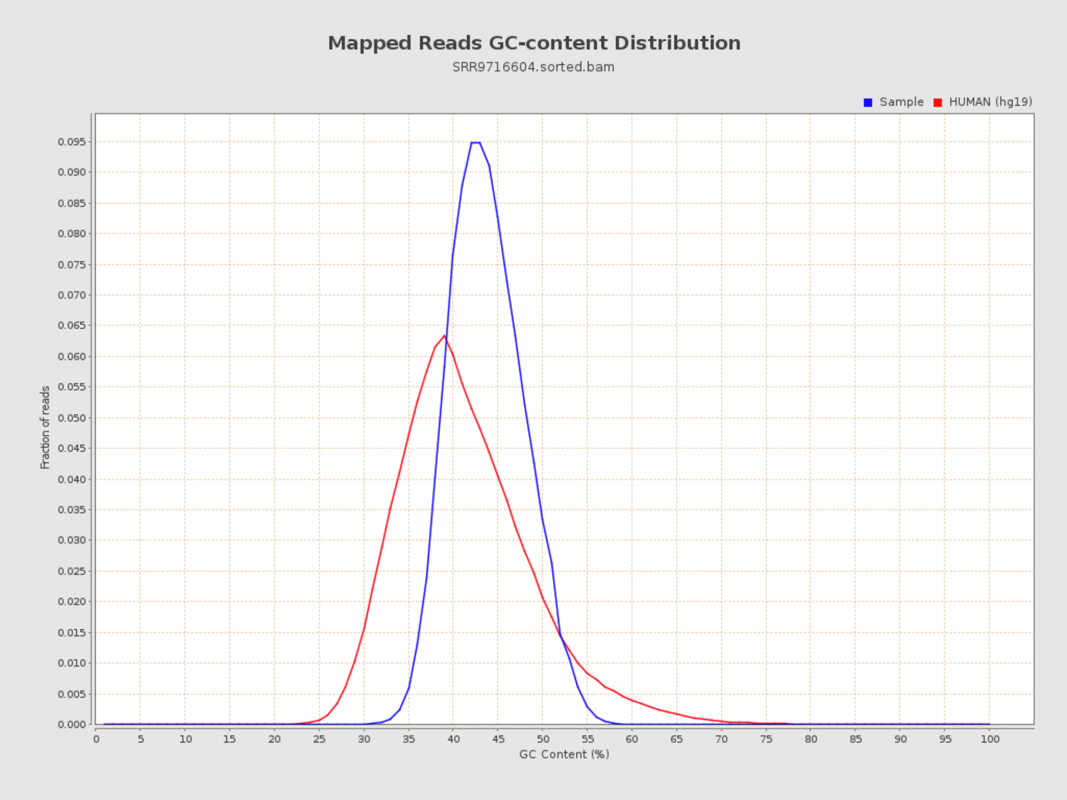
7. Results : Duplication Rate Histogram



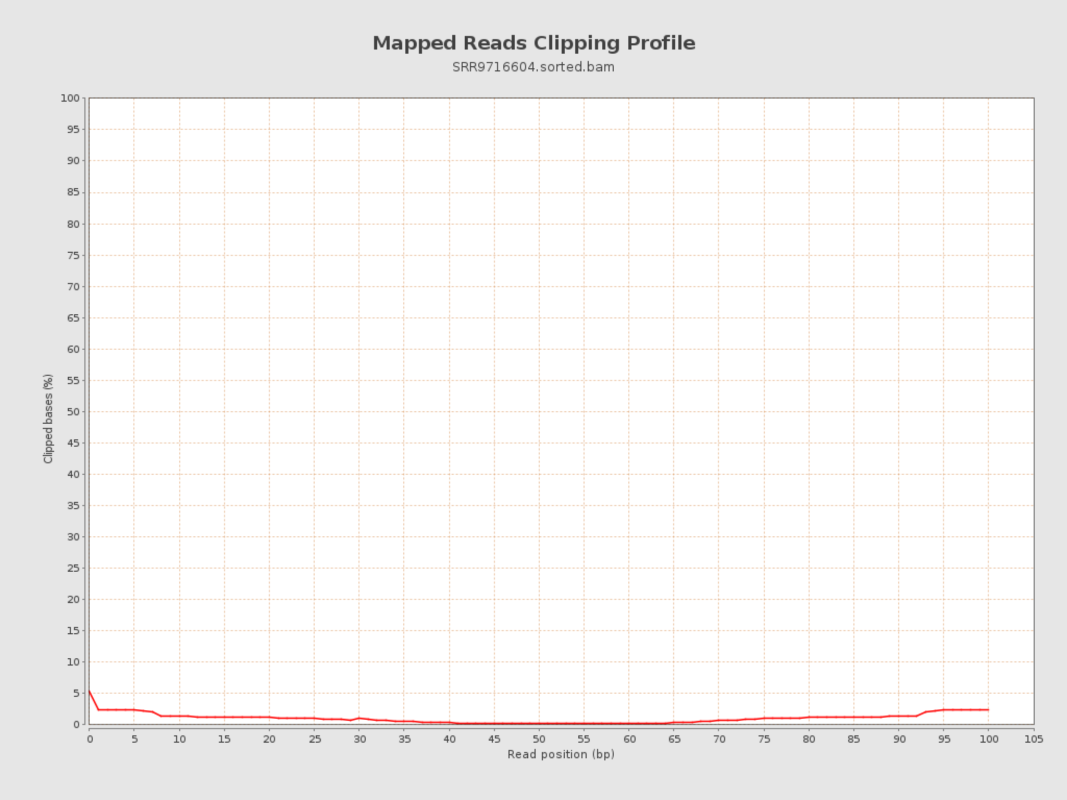
8. Results : Mapped Reads Nucleotide Content



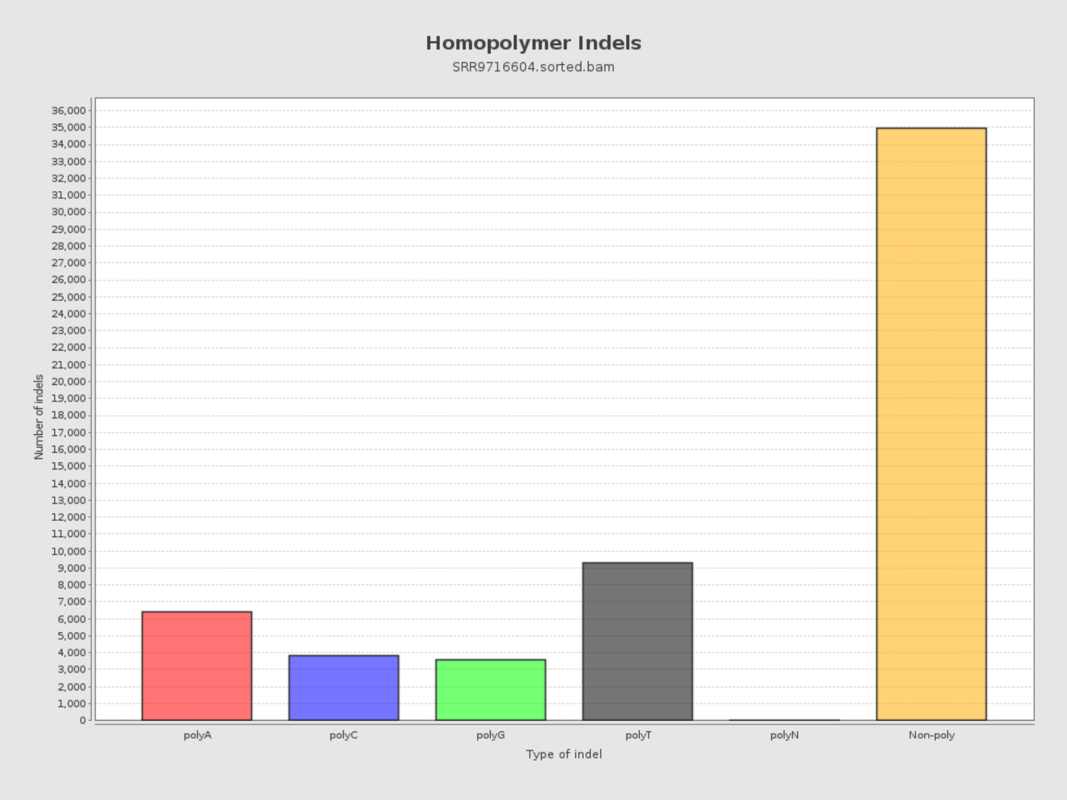
9. Results : Mapped Reads GC-content Distribution



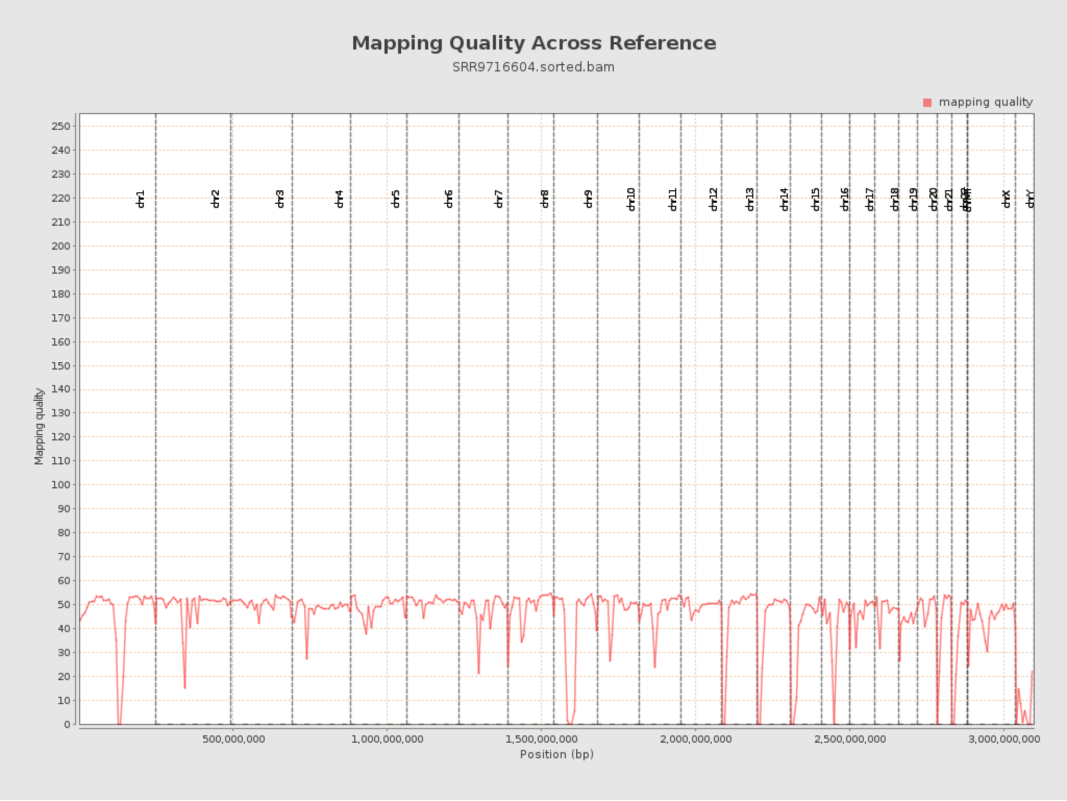
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram