Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:37:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716323.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_SRR9716323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716323.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:37:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,208,887
Mapped reads	2,024,009 / 91.63%
Unmapped reads	184,878 / 8.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,421 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	90,033 / 4.08%
Duplication rate	3.25%
Clipped reads	2,028,477 / 91.83%

2.2. ACGT Content

Number/percentage of A's	29,582,227 / 25.08%
Number/percentage of C's	21,075,316 / 17.87%
Number/percentage of T's	36,988,467 / 31.36%
Number/percentage of G's	30,310,243 / 25.7%
Number/percentage of N's	3,393 / 0%
GC Percentage	43.56%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.3859

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

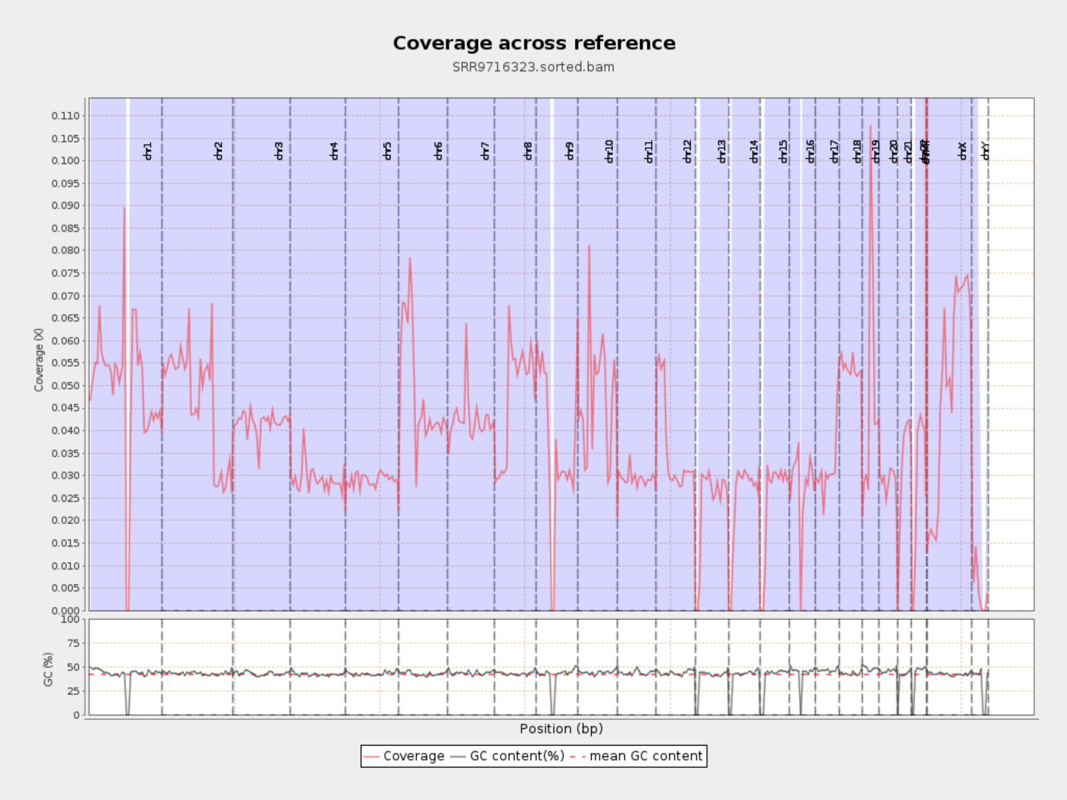
General error rate	0.5%
Mismatches	579,239
Insertions	7,807
Mapped reads with at least one insertion	0.38%
Deletions	20,262
Mapped reads with at least one deletion	0.99%
Homopolymer indels	42.35%

2.6. Chromosome stats

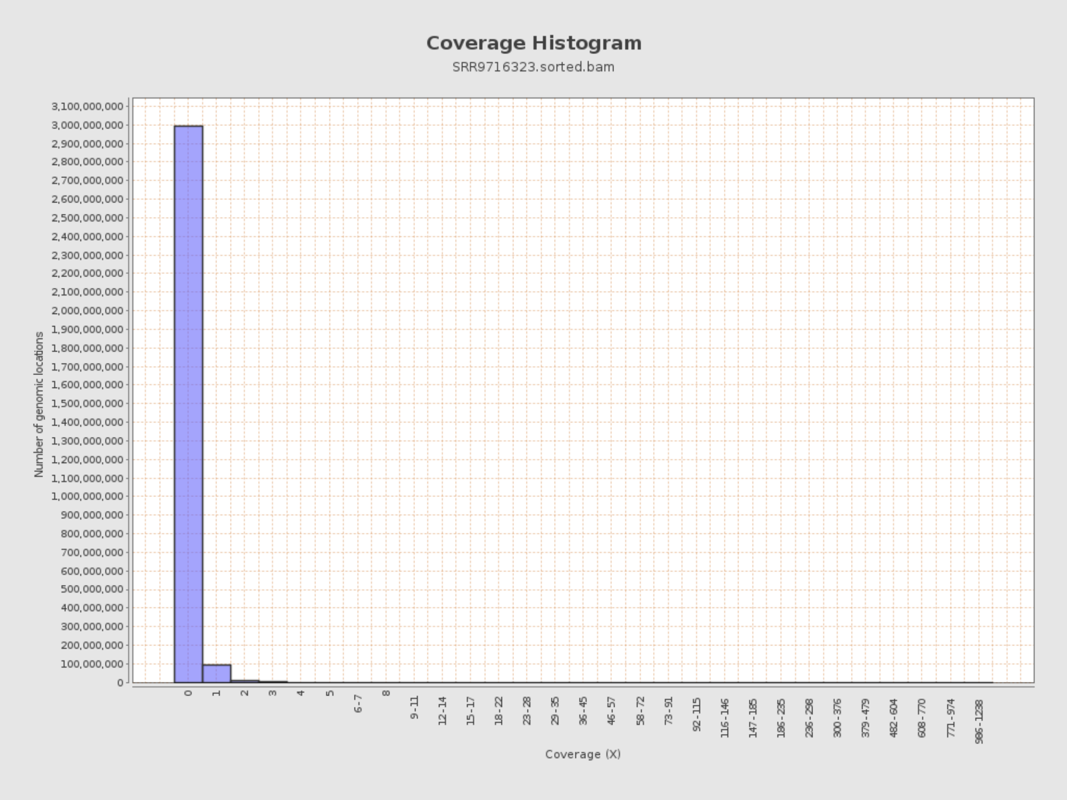
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12309842	0.0494	0.9039
chr2	243199373	11407006	0.0469	0.4503
chr3	198022430	8269321	0.0418	0.2324
chr4	191154276	5578148	0.0292	0.2025
chr5	180915260	5276801	0.0292	0.1953
chr6	171115067	8199468	0.0479	0.2898
chr7	159138663	6808750	0.0428	0.4336

chr8	146364022	6987000	0.0477	0.299
chr9	141213431	4933036	0.0349	0.2977
chr10	135534747	6457545	0.0476	0.3698
chr11	135006516	3952838	0.0293	0.2636
chr12	133851895	4799076	0.0359	0.2217
chr13	115169878	2697276	0.0234	0.1707
chr14	107349540	2613117	0.0243	0.1992
chr15	102531392	2493248	0.0243	0.176
chr16	90354753	2498784	0.0277	0.2084
chr17	81195210	2596963	0.032	0.2086
chr18	78077248	4223380	0.0541	0.516
chr19	59128983	2923674	0.0494	0.51
chr20	63025520	1813393	0.0288	0.1918
chr21	48129895	1510612	0.0314	0.2159
chr22	51304566	1420031	0.0277	0.1851
chrMT	16571	173051	10.443	6.2322
chrX	155270560	7772666	0.0501	0.3009
chrY	59373566	276574	0.0047	0.1075

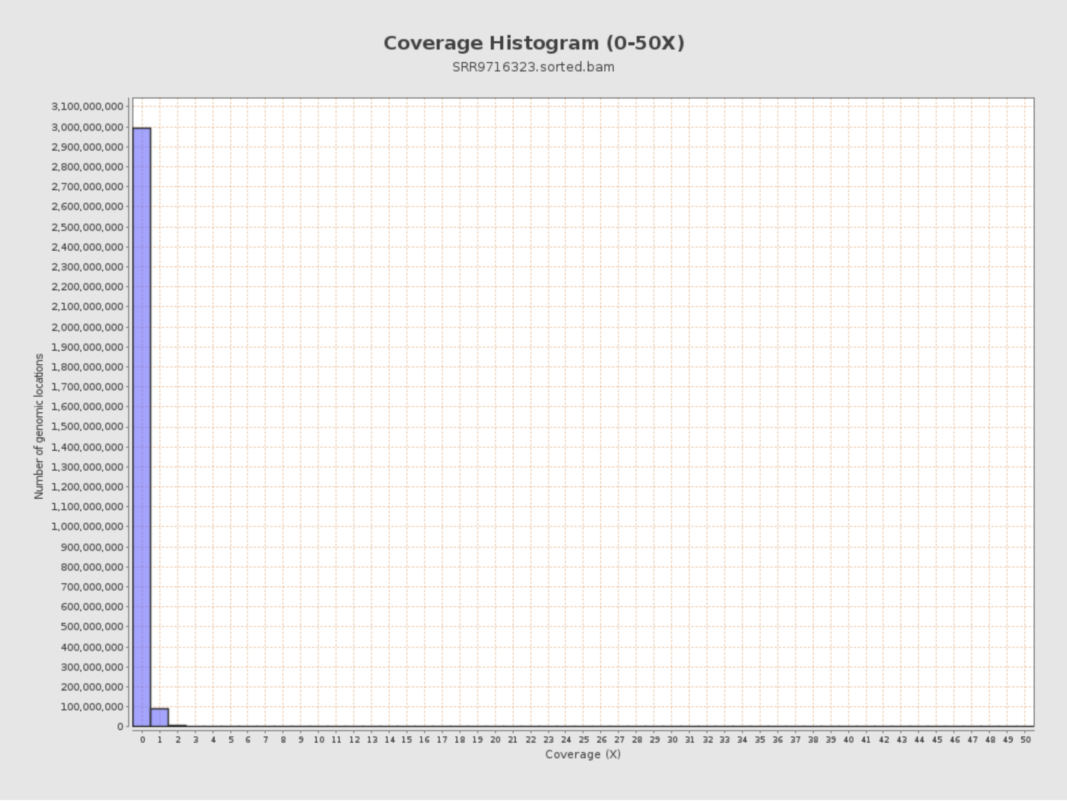
3. Results : Coverage across reference



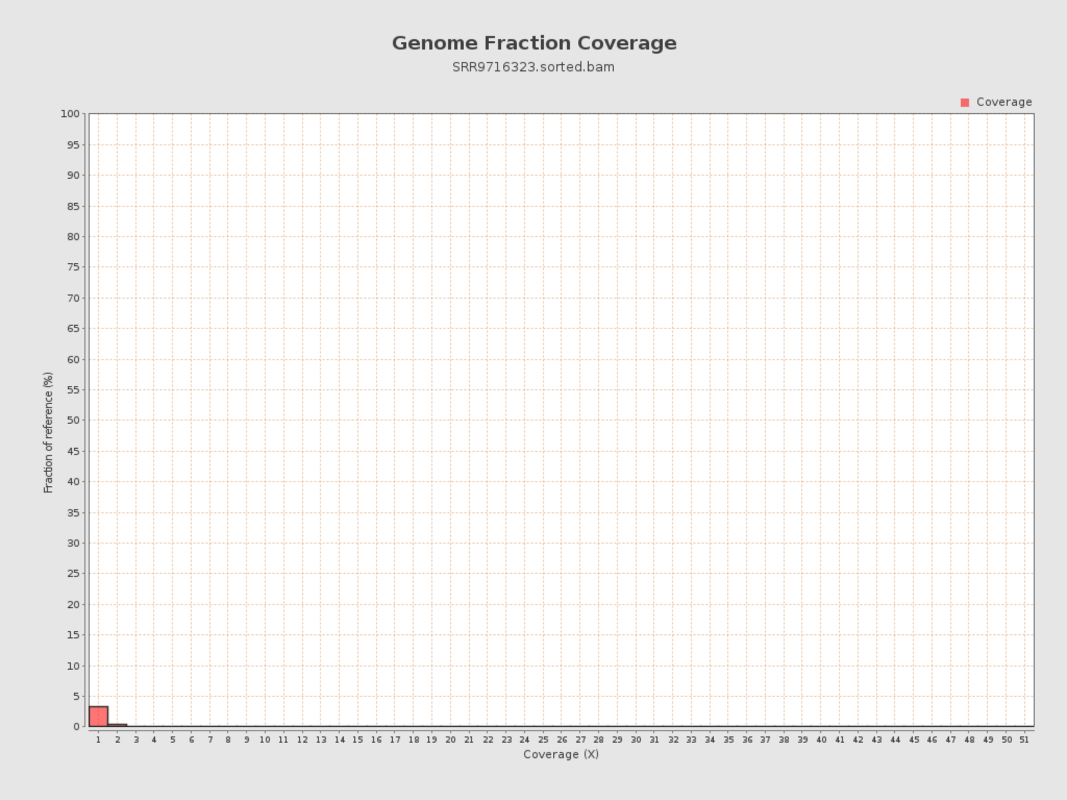
4. Results : Coverage Histogram



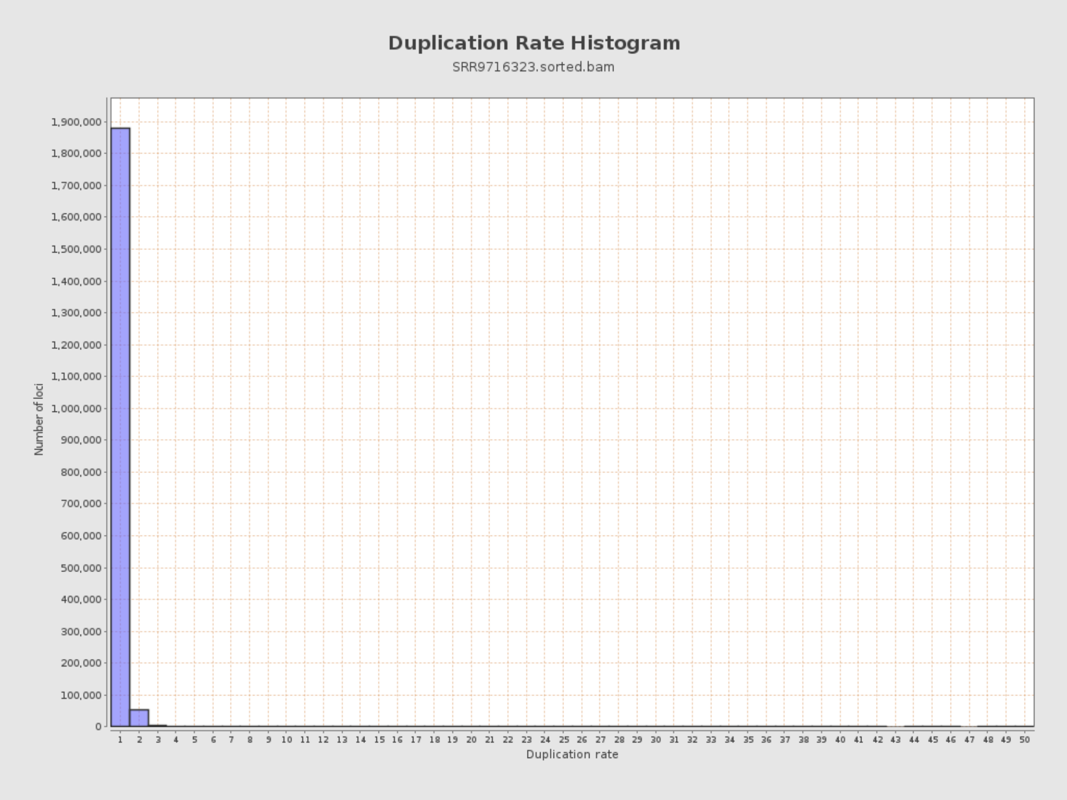
5. Results : Coverage Histogram (0-50X)



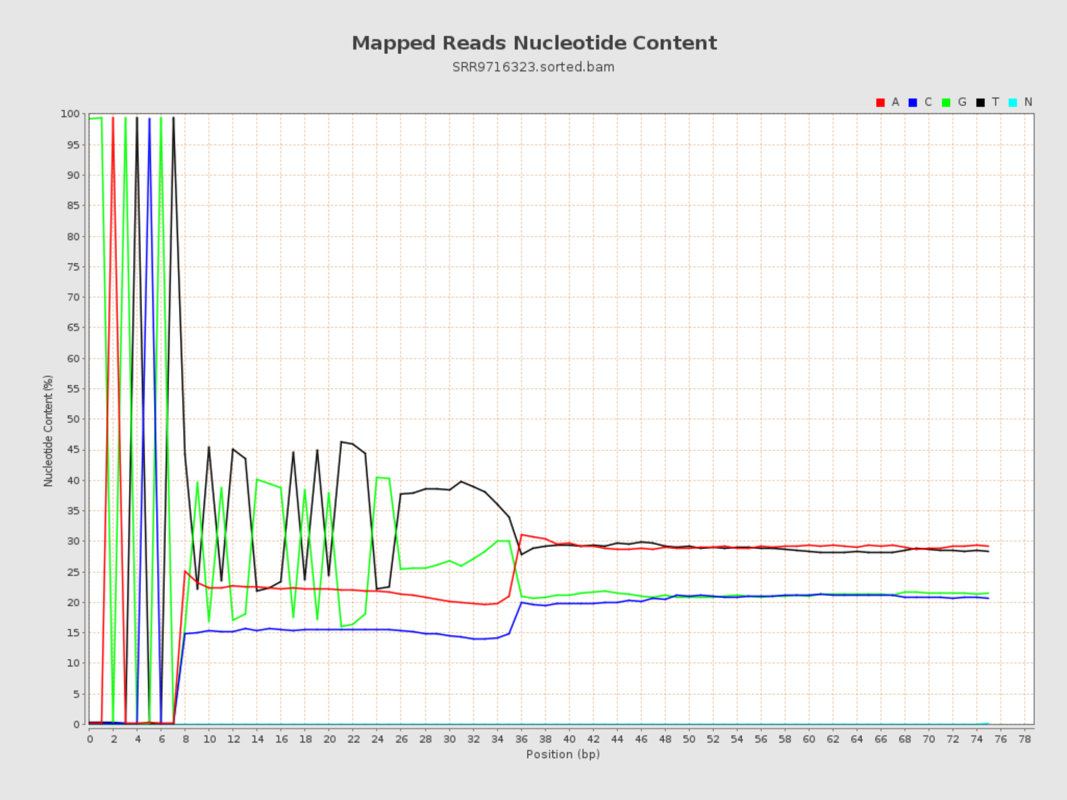
6. Results : Genome Fraction Coverage



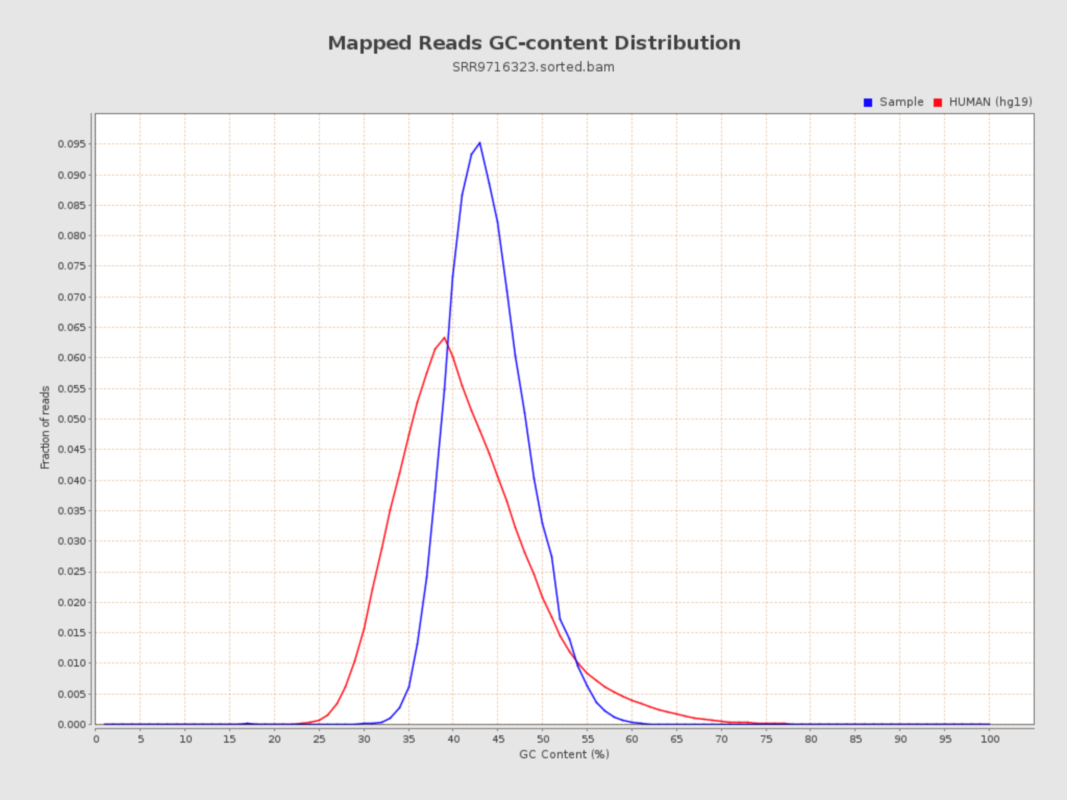
7. Results : Duplication Rate Histogram



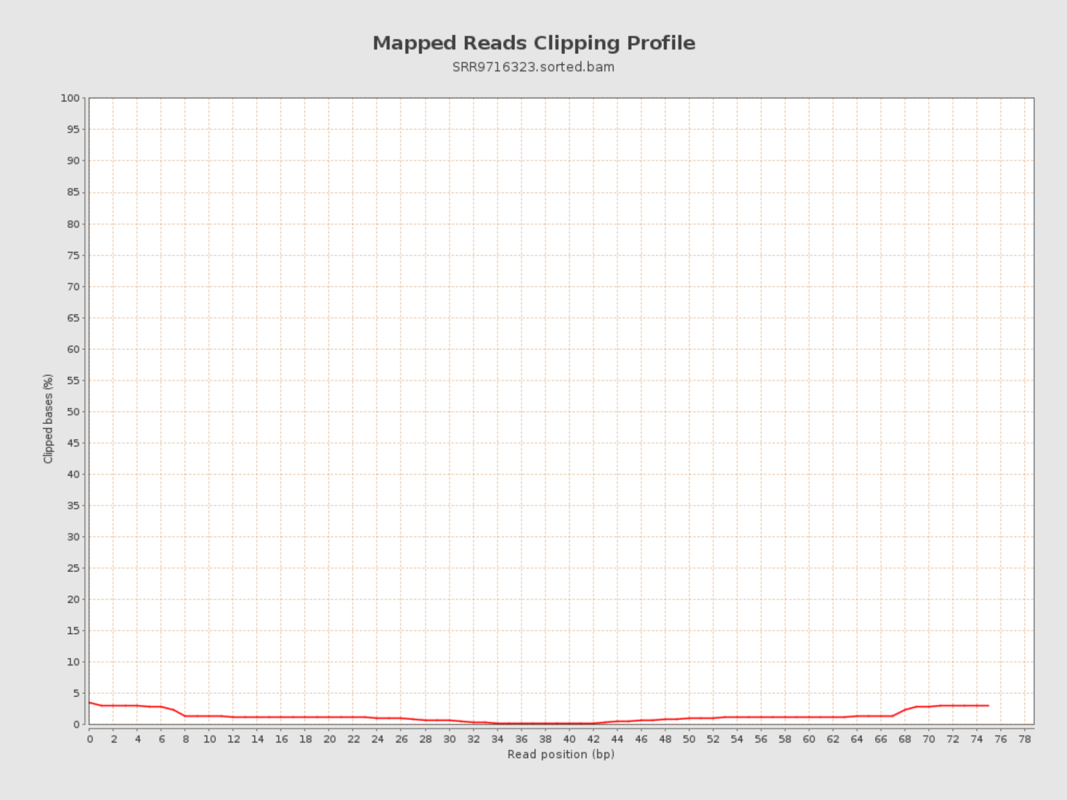
8. Results : Mapped Reads Nucleotide Content



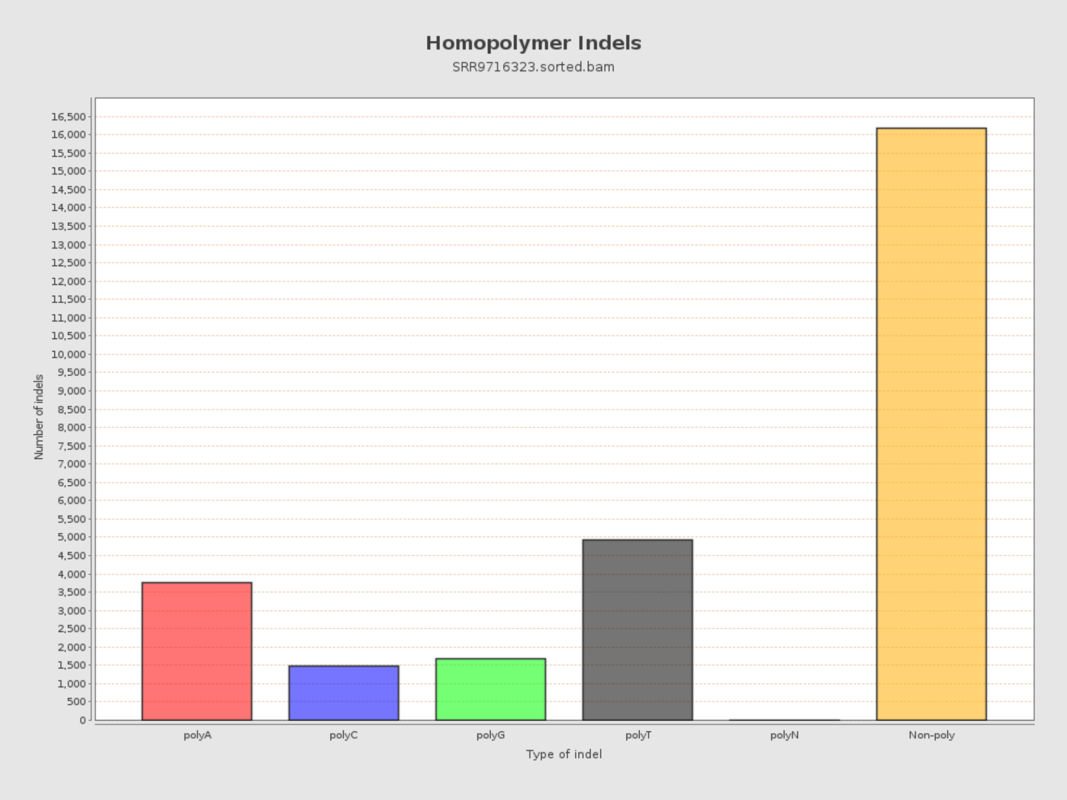
9. Results : Mapped Reads GC-content Distribution



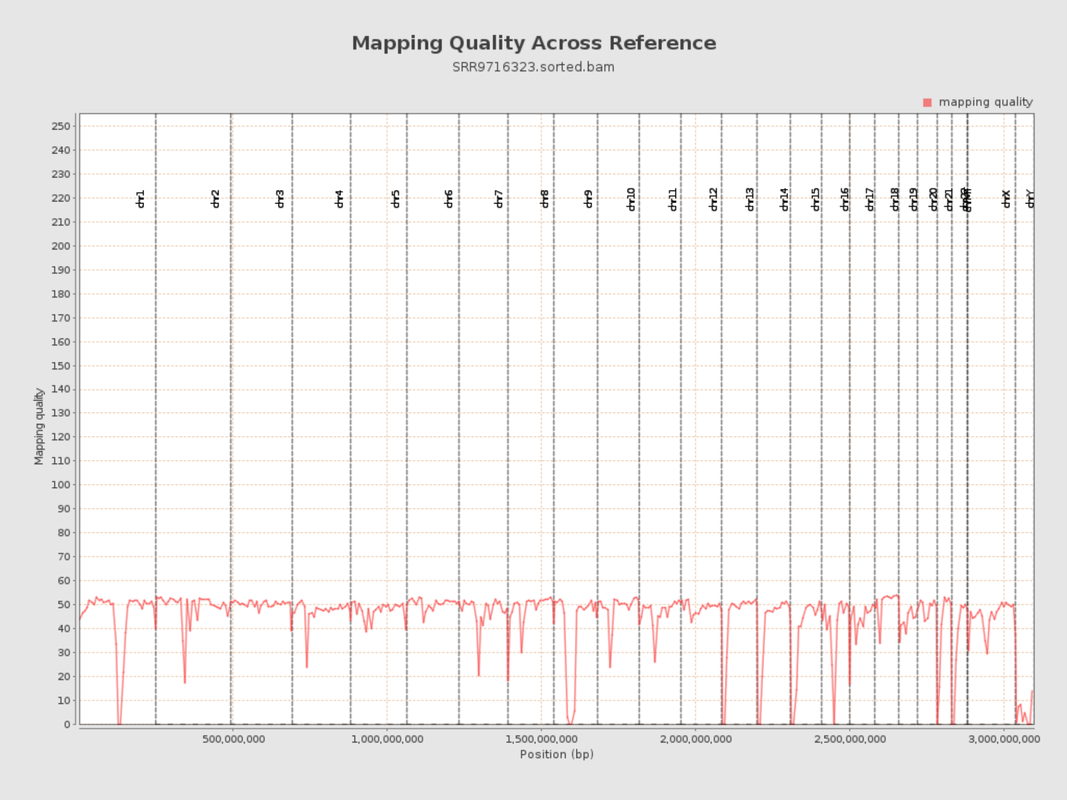
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram