Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:22:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716302.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_SRR9716302 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716302.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:22:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716302.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,299,787
Mapped reads	1,157,440 / 89.05%
Unmapped reads	142,347 / 10.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,547 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	37,625 / 2.89%
Duplication rate	2.52%
Clipped reads	1,158,736 / 89.15%

2.2. ACGT Content

Number/percentage of A's	16,624,134 / 24.86%
Number/percentage of C's	11,969,201 / 17.9%
Number/percentage of T's	21,993,785 / 32.89%
Number/percentage of G's	16,282,342 / 24.35%
Number/percentage of N's	1,891 / 0%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.209

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

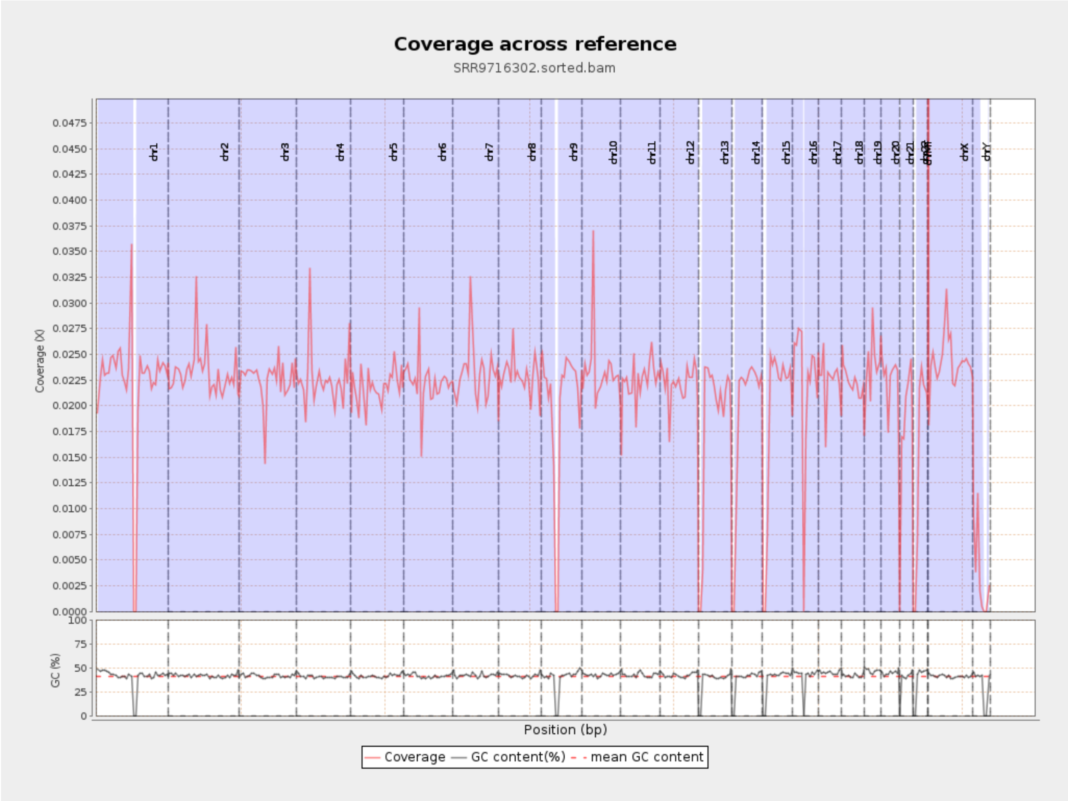
General error rate	0.52%
Mismatches	333,875
Insertions	5,365
Mapped reads with at least one insertion	0.46%
Deletions	11,820
Mapped reads with at least one deletion	1.01%
Homopolymer indels	41.23%

2.6. Chromosome stats

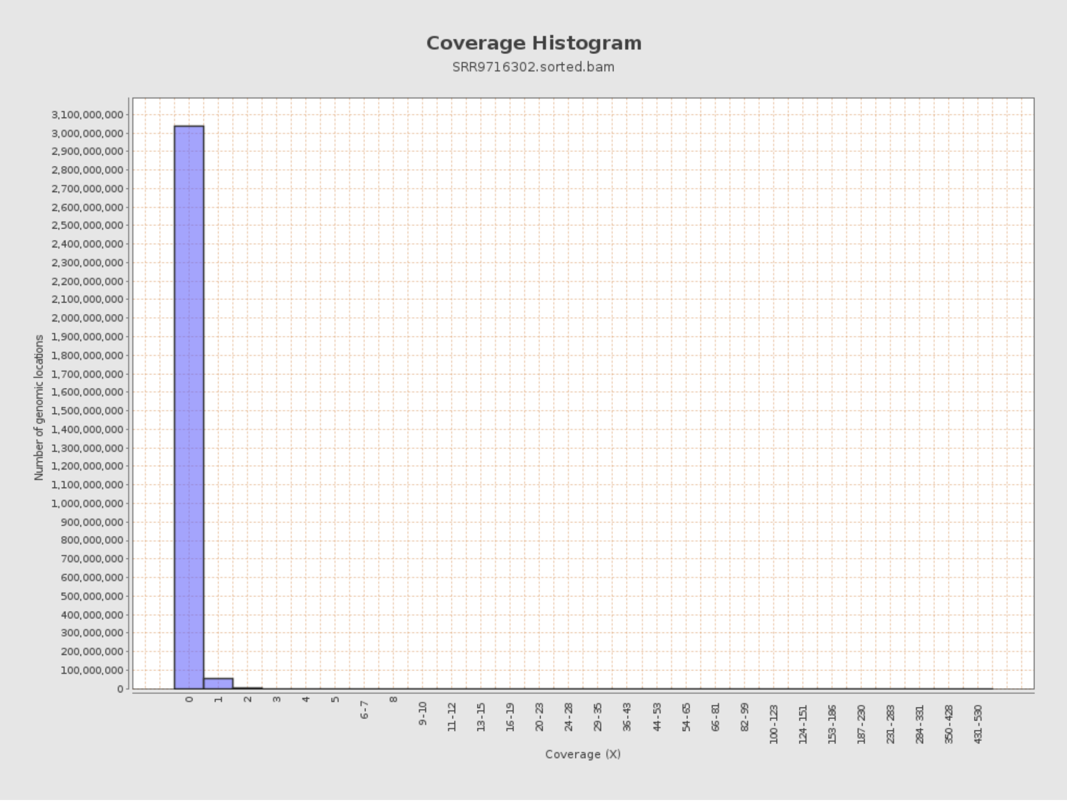
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5530813	0.0222	0.3522
chr2	243199373	5654783	0.0233	0.2768
chr3	198022430	4457722	0.0225	0.1626
chr4	191154276	4336118	0.0227	0.1732
chr5	180915260	3961654	0.0219	0.1606
chr6	171115067	3810042	0.0223	0.1857
chr7	159138663	3708548	0.0233	0.23

chr8	146364022	3345408	0.0229	0.1962
chr9	141213431	2782836	0.0197	0.1822
chr10	135534747	3186236	0.0235	0.207
chr11	135006516	3041376	0.0225	0.1857
chr12	133851895	2977485	0.0222	0.1619
chr13	115169878	2097936	0.0182	0.1451
chr14	107349540	2030447	0.0189	0.1524
chr15	102531392	1944582	0.019	0.1492
chr16	90354753	1956066	0.0216	0.166
chr17	81195210	1818233	0.0224	0.1657
chr18	78077248	1742520	0.0223	0.2768
chr19	59128983	1422637	0.0241	0.2623
chr20	63025520	1415938	0.0225	0.1635
chr21	48129895	880510	0.0183	0.1568
chr22	51304566	779313	0.0152	0.1324
chrMT	16571	11792	0.7116	0.96
chrX	155270560	3792945	0.0244	0.1815
chrY	59373566	204239	0.0034	0.094

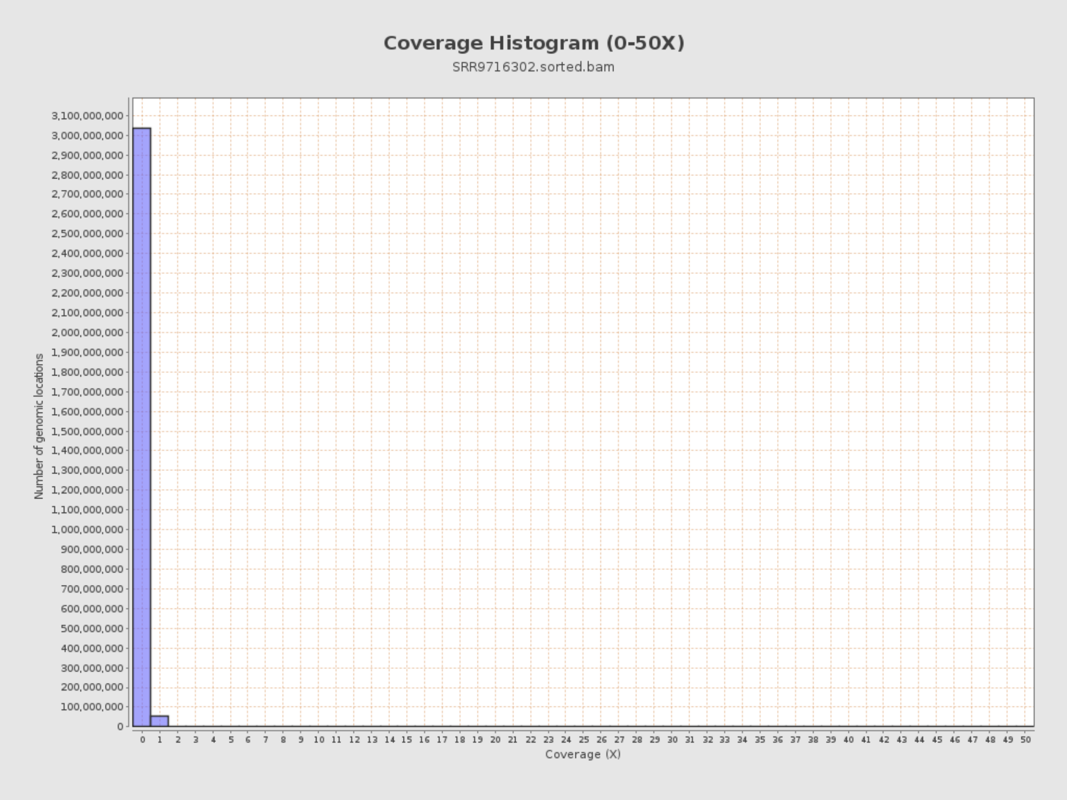
3. Results : Coverage across reference



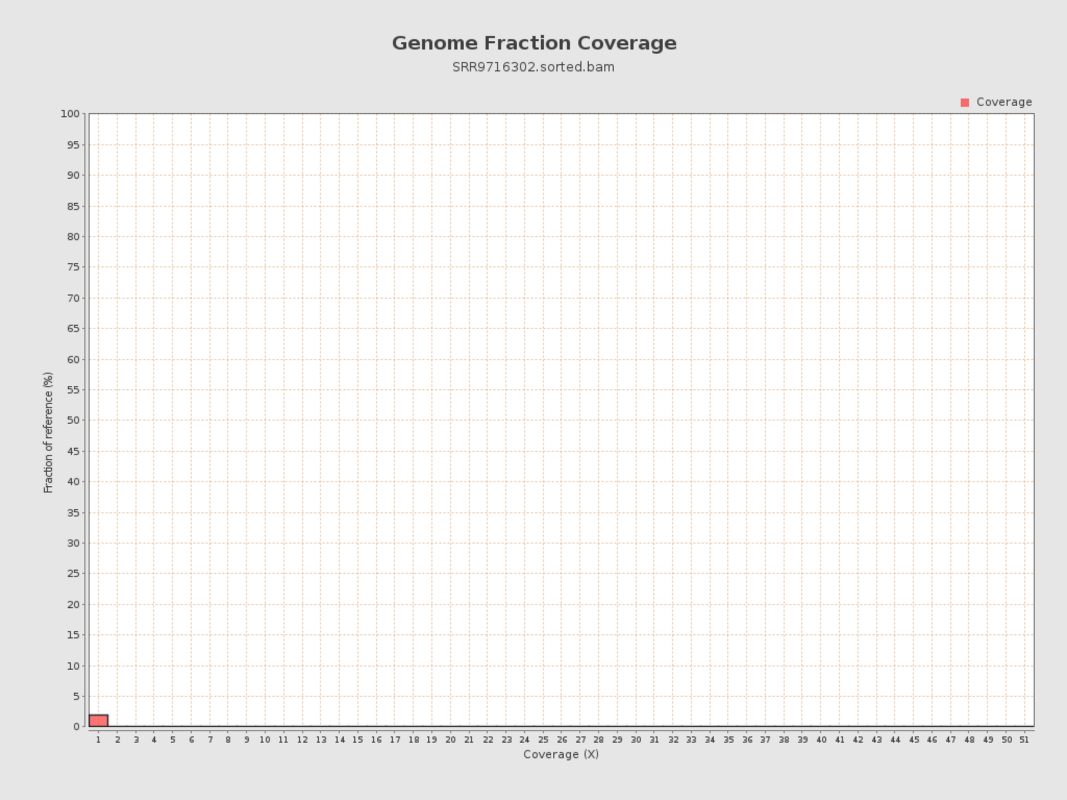
4. Results : Coverage Histogram



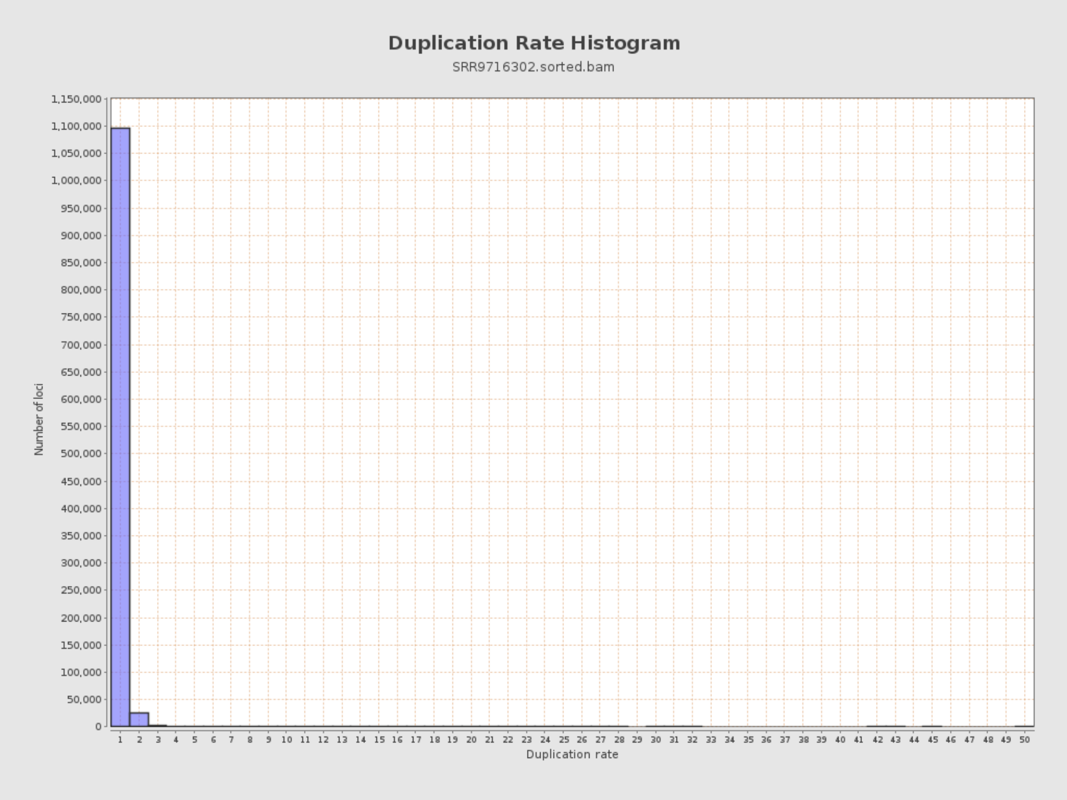
5. Results : Coverage Histogram (0-50X)



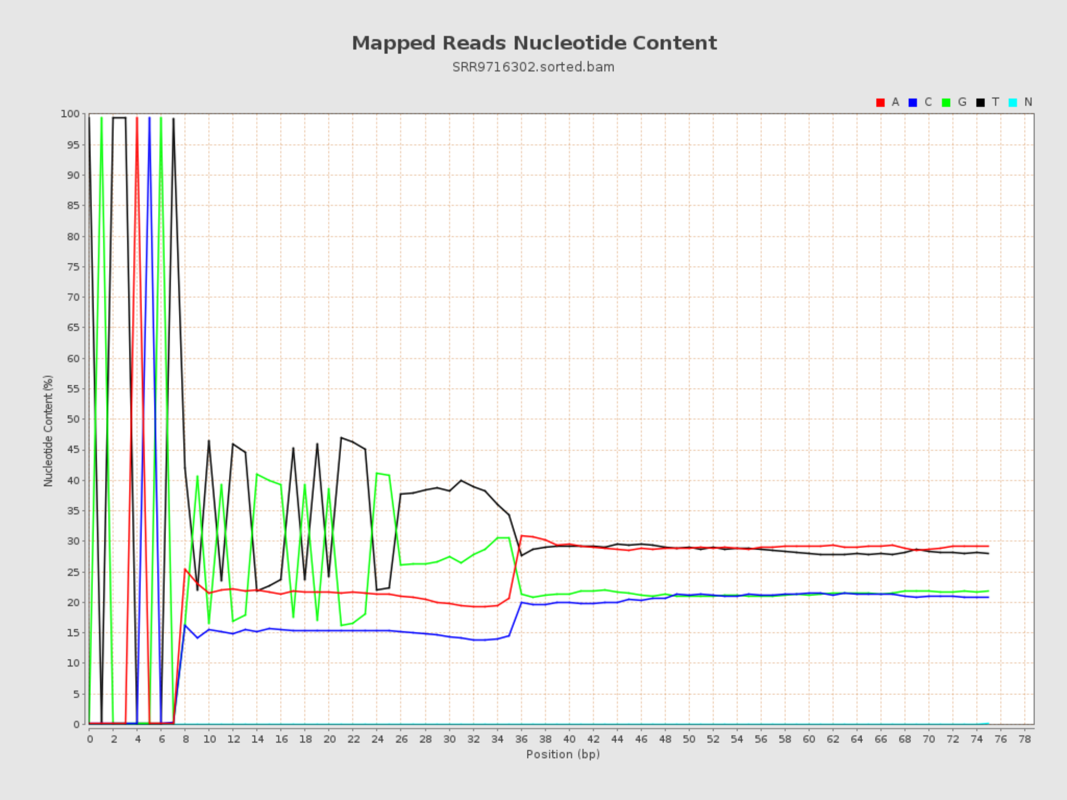
6. Results : Genome Fraction Coverage



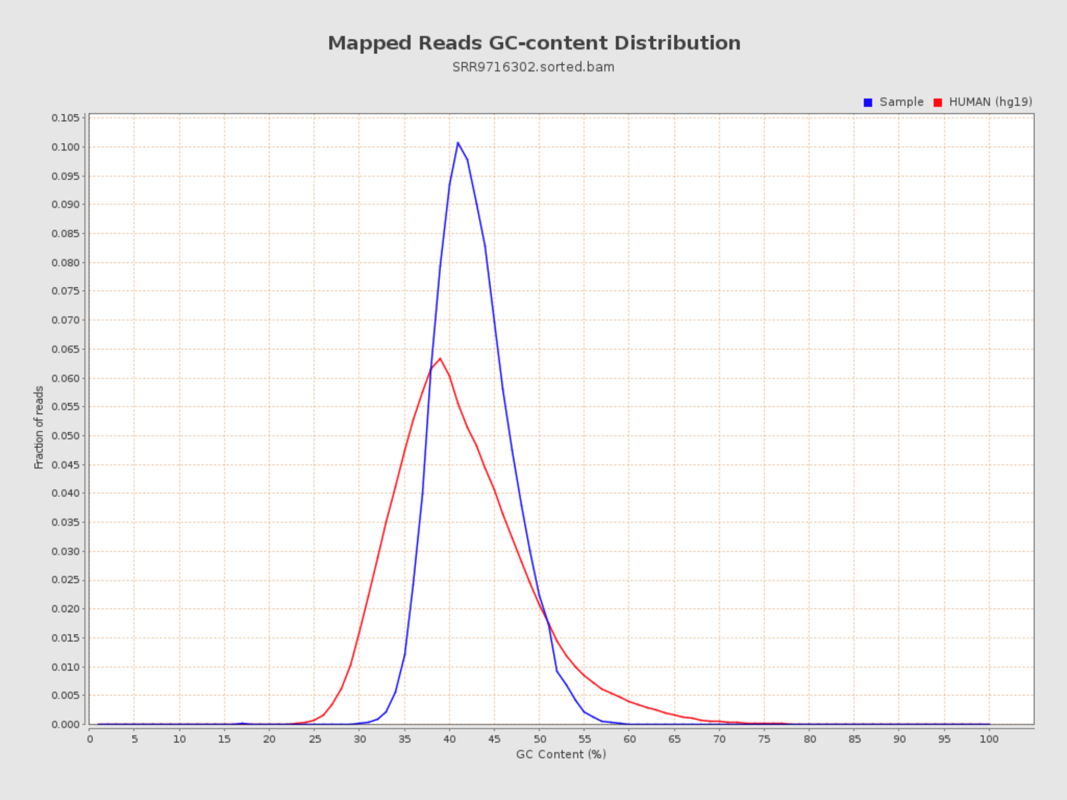
7. Results : Duplication Rate Histogram



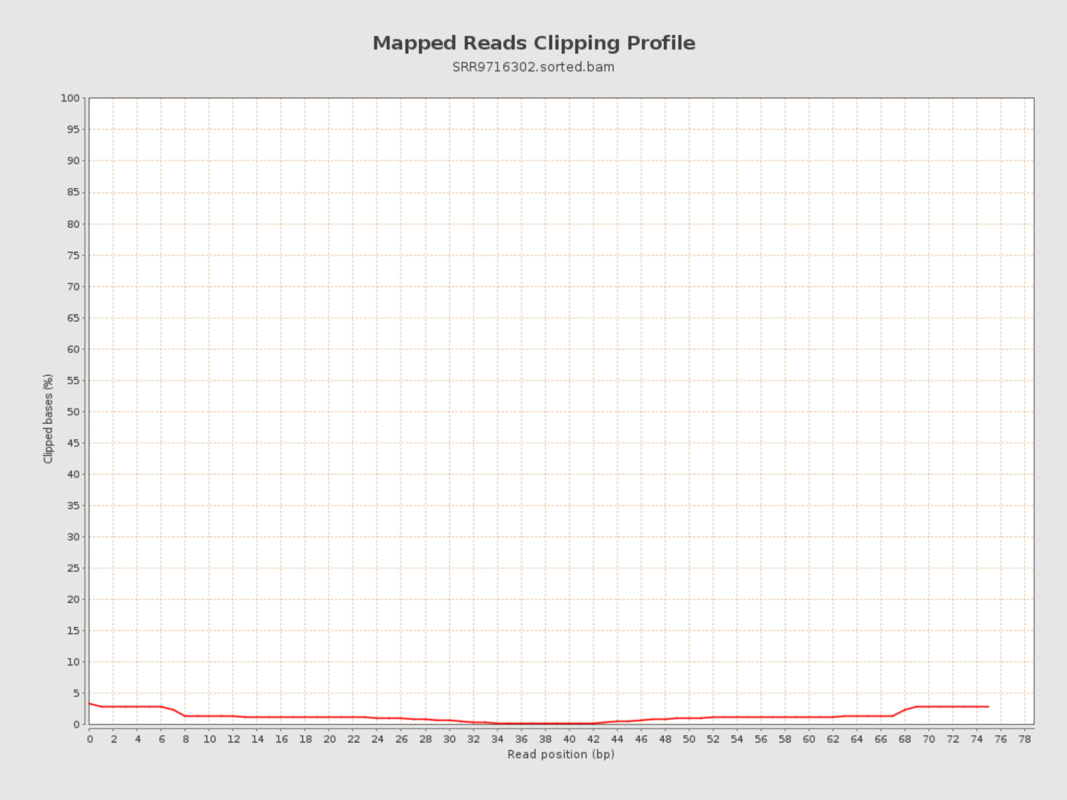
8. Results : Mapped Reads Nucleotide Content



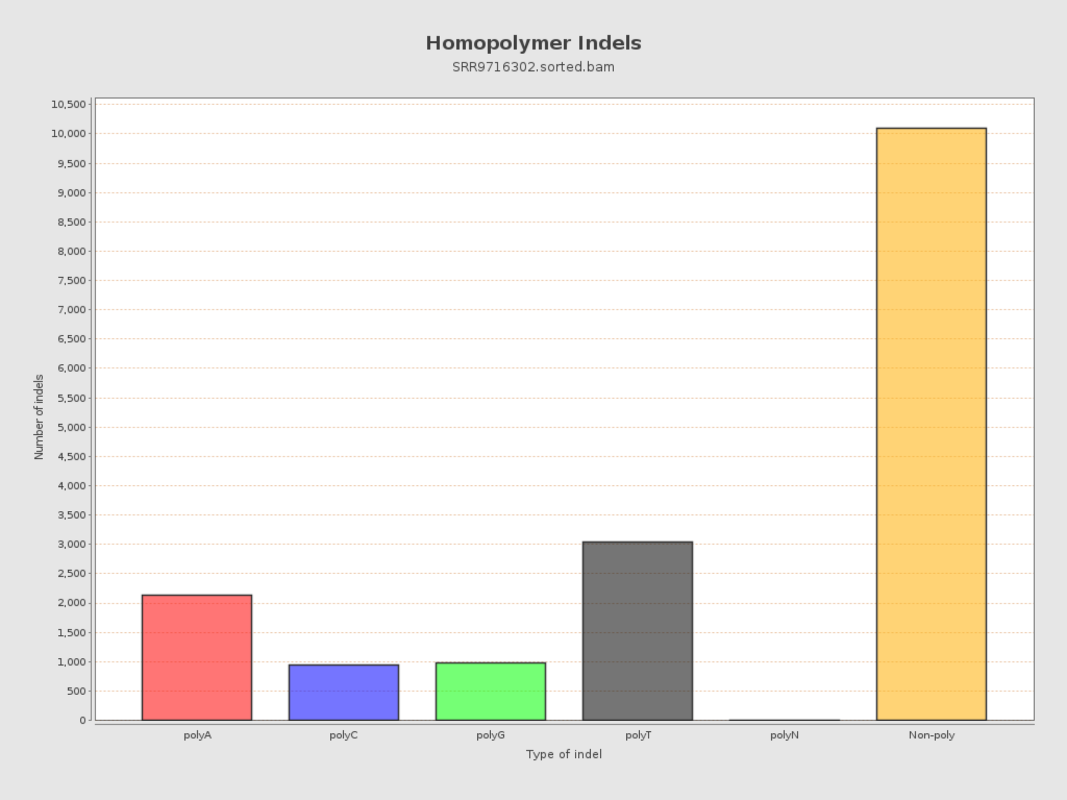
9. Results : Mapped Reads GC-content Distribution



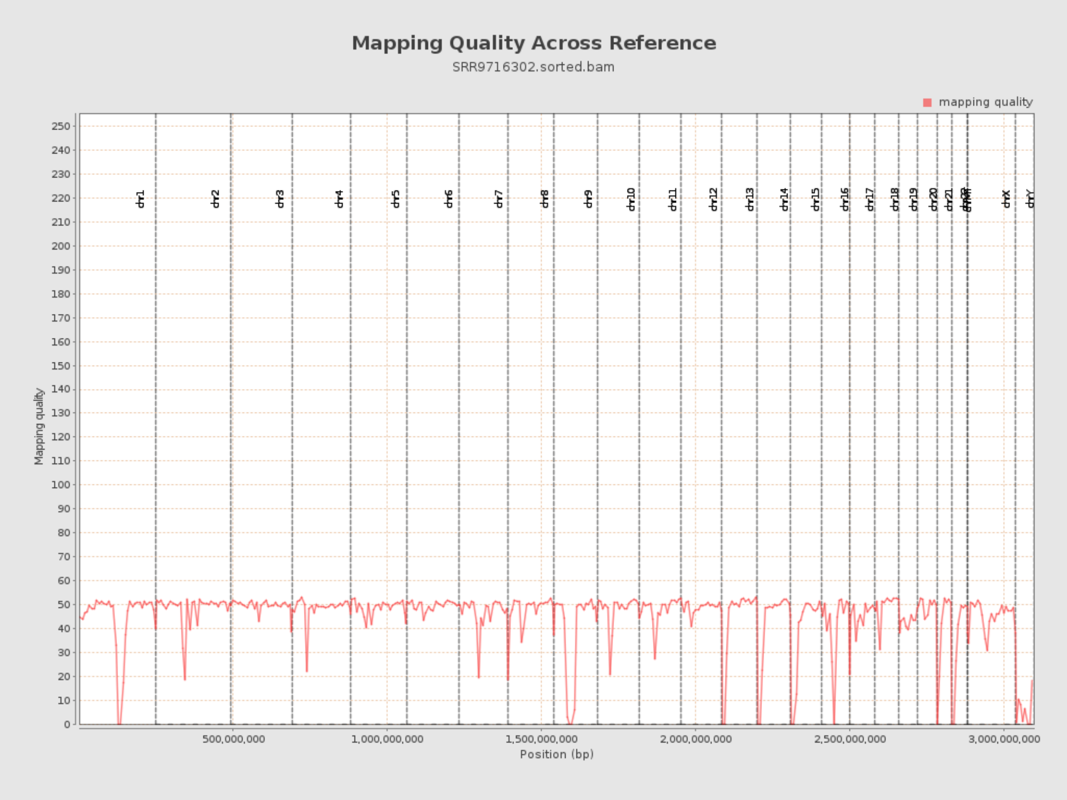
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram