Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:26:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716776.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_SRR9716776 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716776.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:26:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716776.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,626,523
Mapped reads	3,353,010 / 92.46%
Unmapped reads	273,513 / 7.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	68,079 / 1.88%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	271,895 / 7.5%
Duplication rate	6.22%
Clipped reads	3,414,519 / 94.15%

2.2. ACGT Content

Number/percentage of A's	63,160,260 / 24.45%
Number/percentage of C's	54,957,537 / 21.27%
Number/percentage of T's	77,903,801 / 30.16%
Number/percentage of G's	62,303,782 / 24.12%
Number/percentage of N's	9,489 / 0%
GC Percentage	45.39%

2.3. Coverage

Mean	0.0835

Standard Deviation	0.6318

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

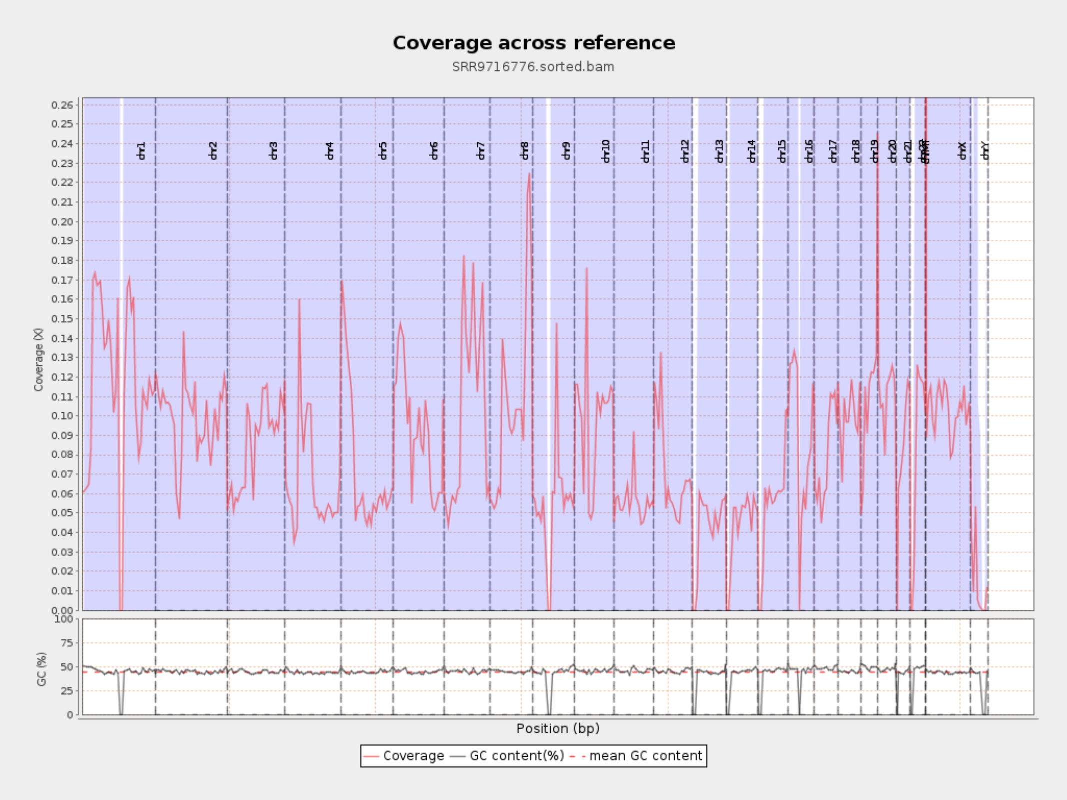
General error rate	0.7%
Mismatches	1,753,308
Insertions	21,466
Mapped reads with at least one insertion	0.63%
Deletions	47,378
Mapped reads with at least one deletion	1.39%
Homopolymer indels	39.86%

2.6. Chromosome stats

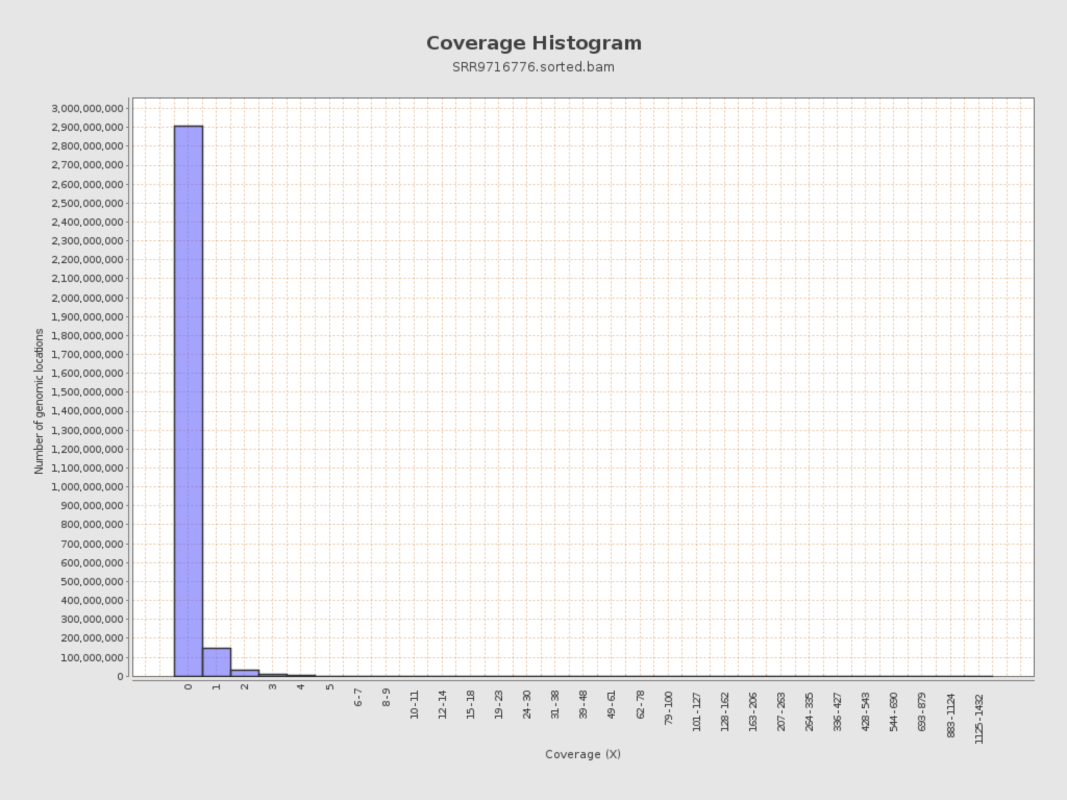
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29153255	0.117	1.2861
chr2	243199373	24148849	0.0993	0.6681
chr3	198022430	16867103	0.0852	0.3888
chr4	191154276	12684677	0.0664	0.5321
chr5	180915260	13409264	0.0741	0.3636
chr6	171115067	15789744	0.0923	0.4409
chr7	159138663	16505209	0.1037	0.8212

chr8	146364022	16006425	0.1094	0.6078
chr9	141213431	7738236	0.0548	0.4332
chr10	135534747	13291008	0.0981	0.8915
chr11	135006516	7577959	0.0561	0.4542
chr12	133851895	9663004	0.0722	0.3553
chr13	115169878	4873594	0.0423	0.2656
chr14	107349540	4657146	0.0434	0.3088
chr15	102531392	5395678	0.0526	0.3027
chr16	90354753	7844098	0.0868	0.435
chr17	81195210	6454364	0.0795	0.4284
chr18	78077248	7756640	0.0993	0.6606
chr19	59128983	6534363	0.1105	0.9623
chr20	63025520	7001070	0.1111	0.481
chr21	48129895	3971374	0.0825	0.5074
chr22	51304566	4110818	0.0801	0.3894
chrMT	16571	162578	9.811	6.9723
chrX	155270560	16002804	0.1031	0.4581
chrY	59373566	833053	0.014	0.4745

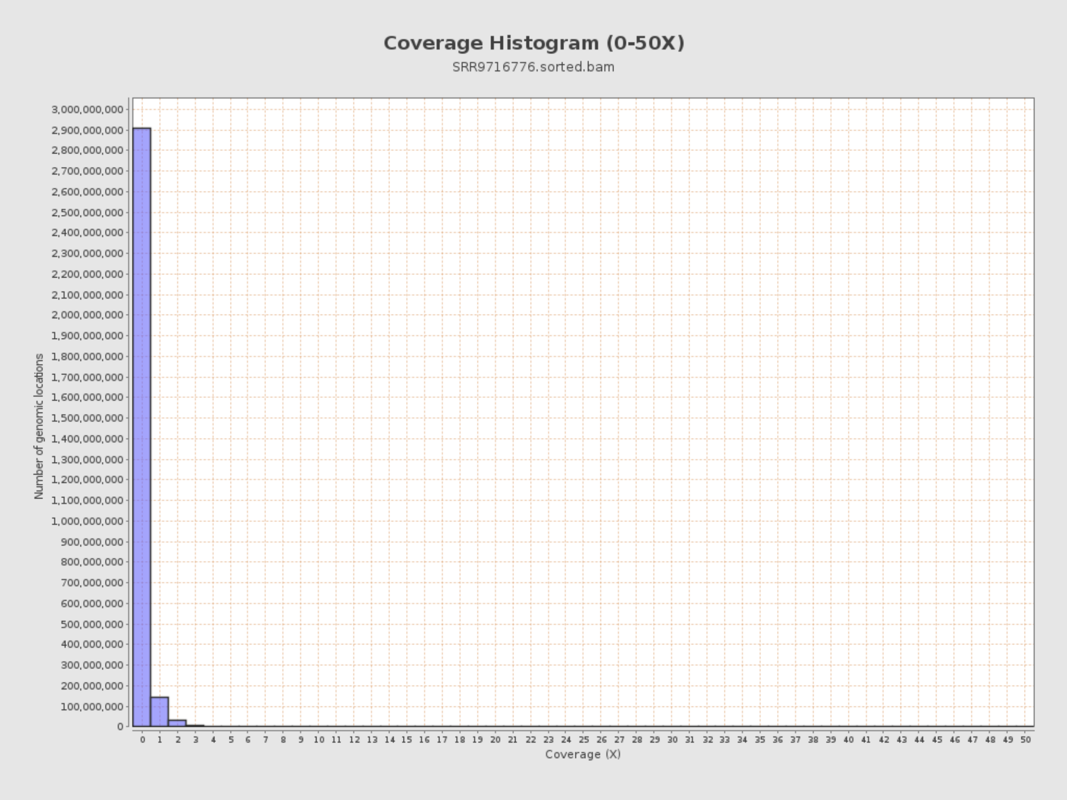
3. Results : Coverage across reference



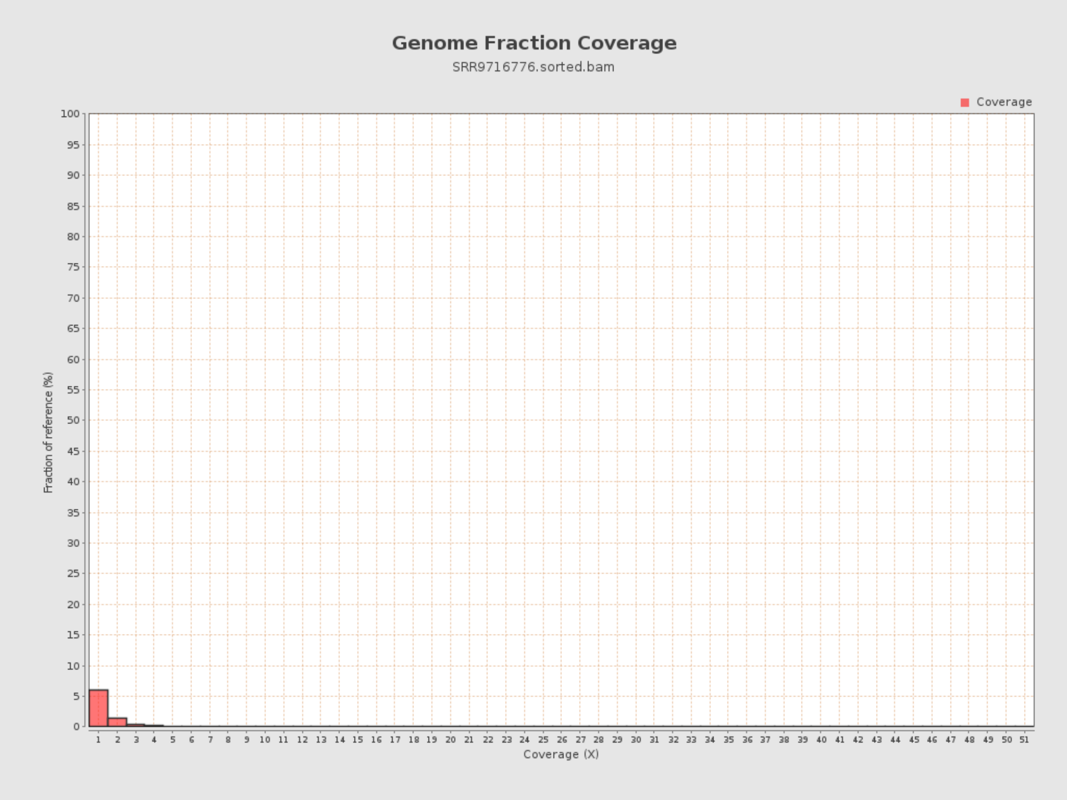
4. Results : Coverage Histogram



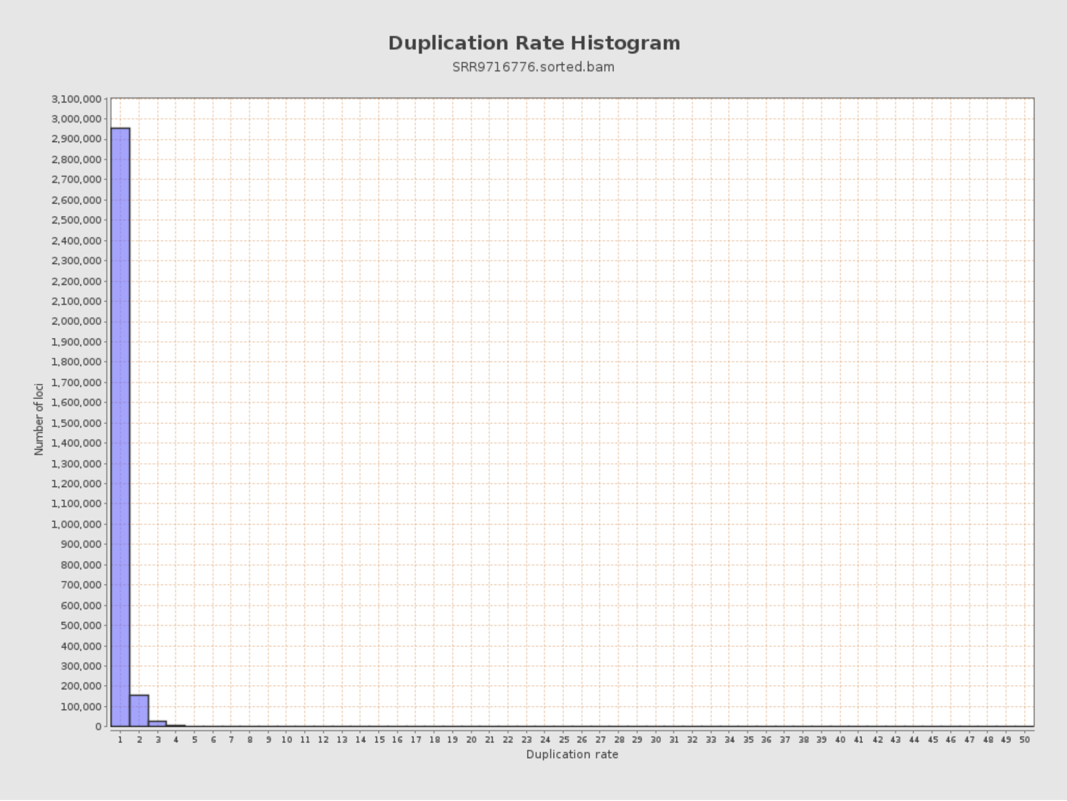
5. Results : Coverage Histogram (0-50X)



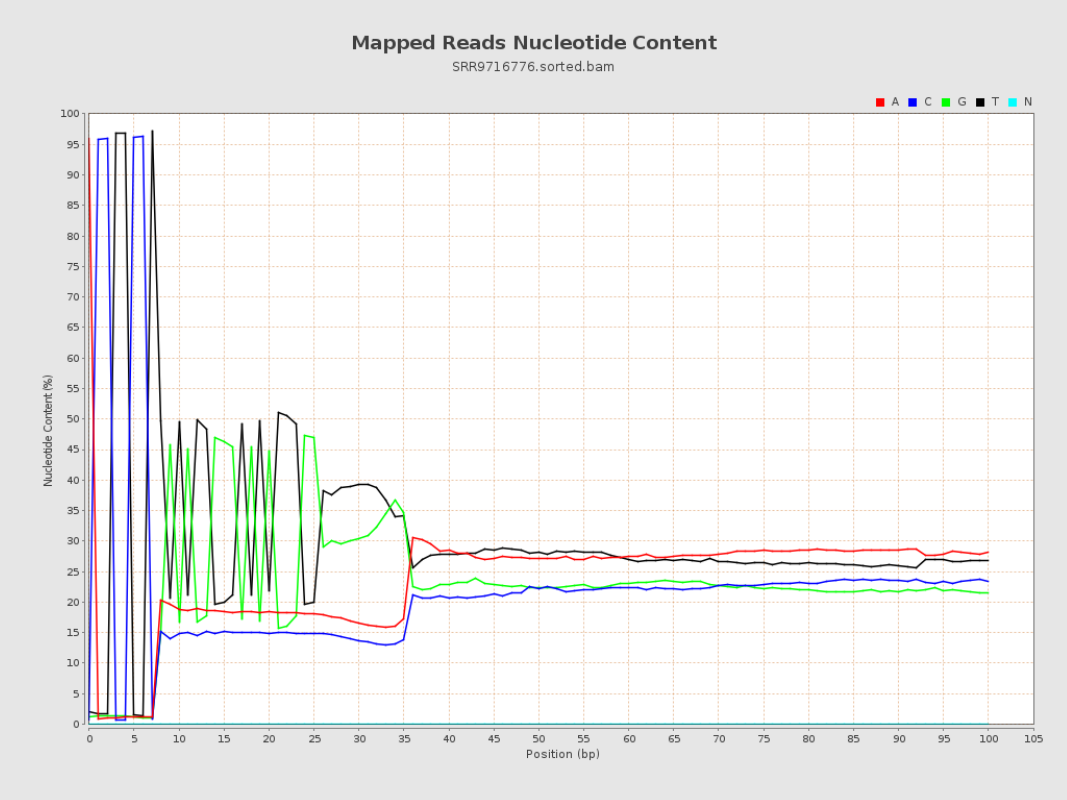
6. Results : Genome Fraction Coverage



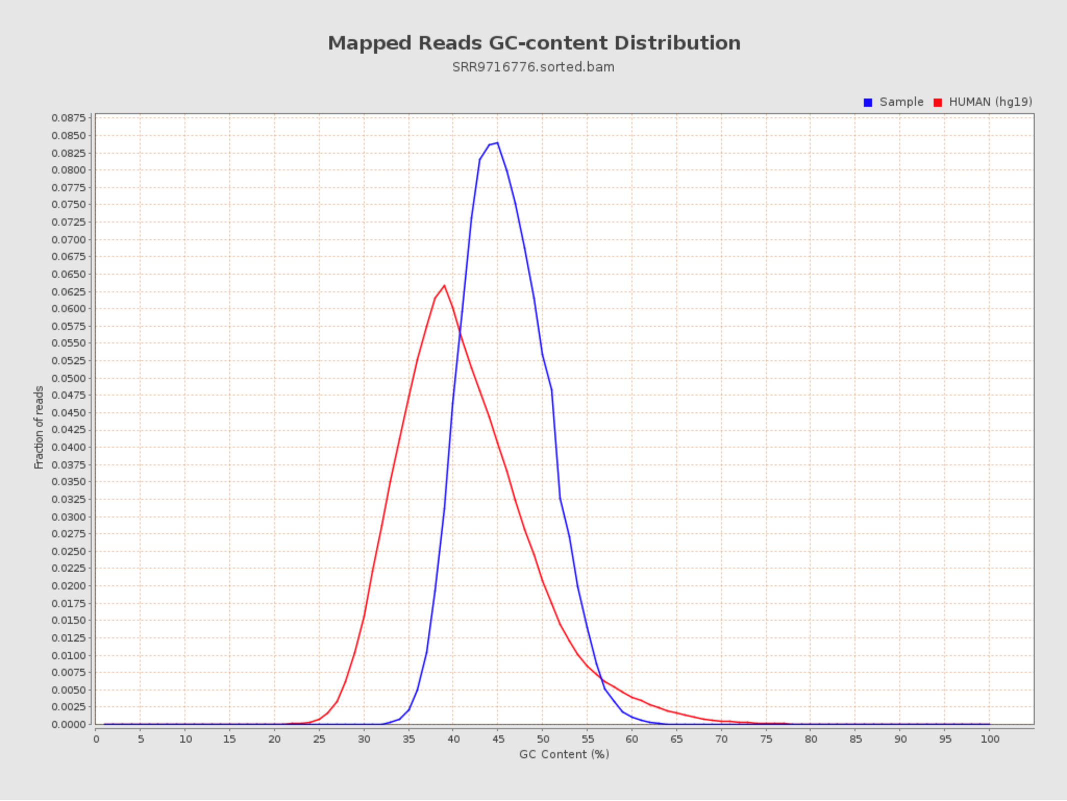
7. Results : Duplication Rate Histogram



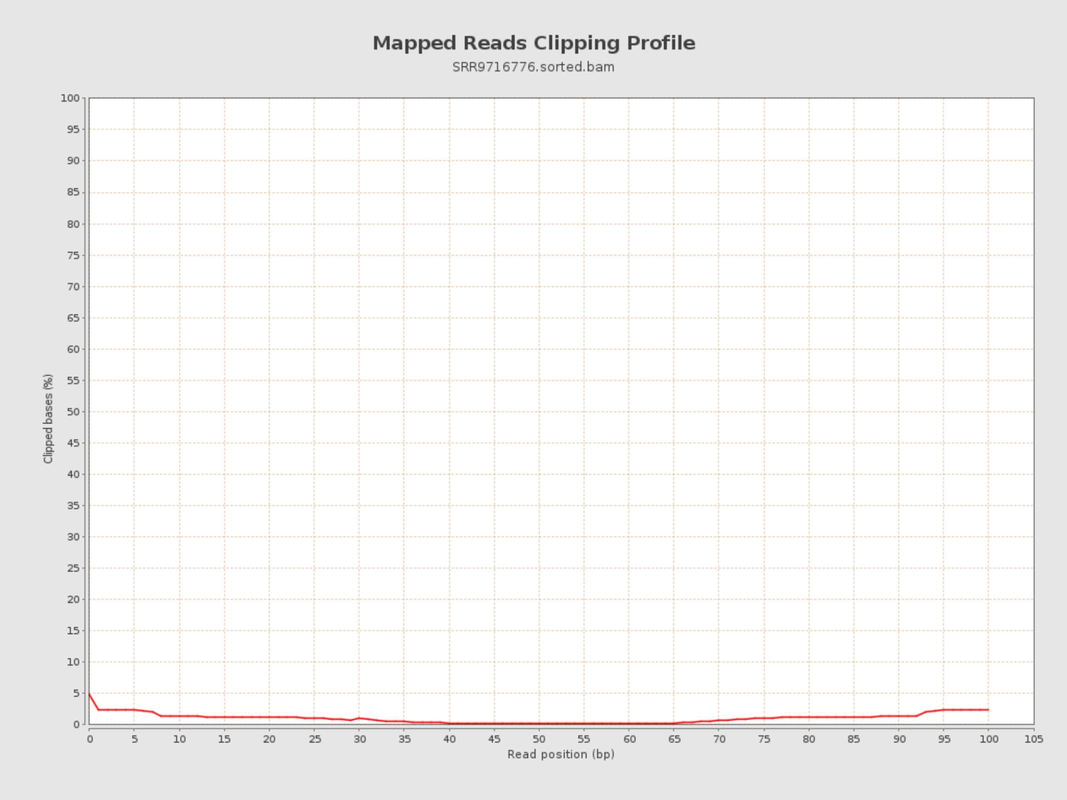
8. Results : Mapped Reads Nucleotide Content



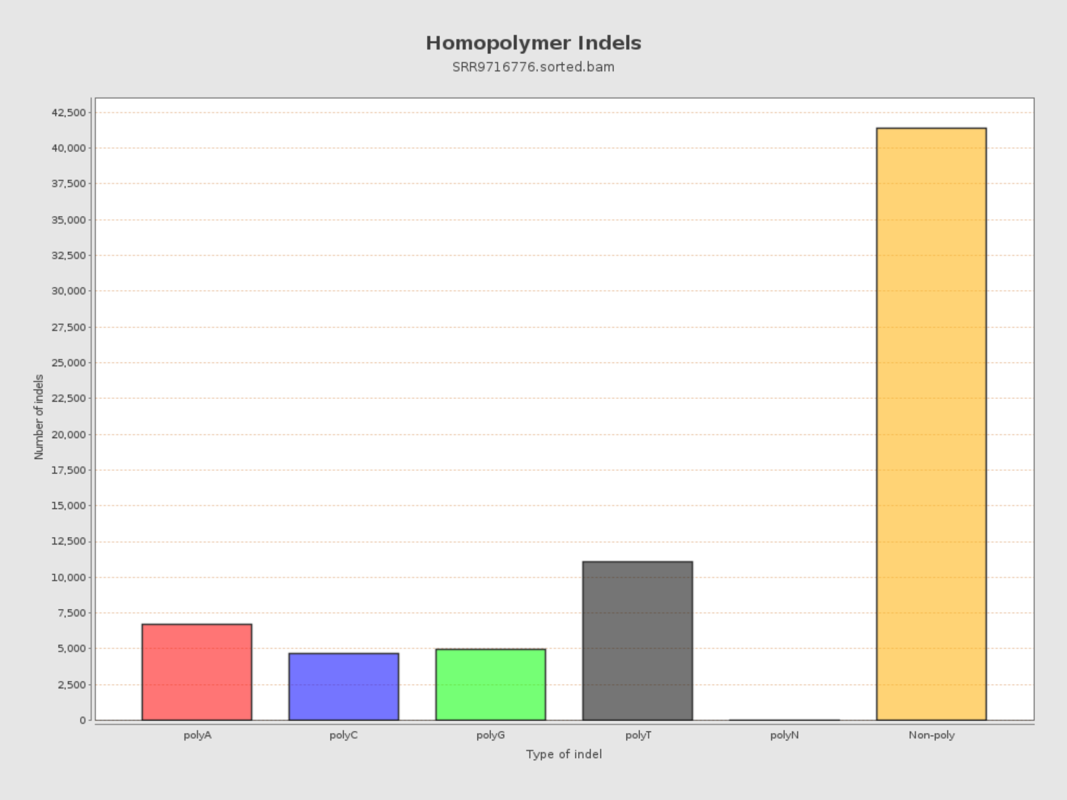
9. Results : Mapped Reads GC-content Distribution



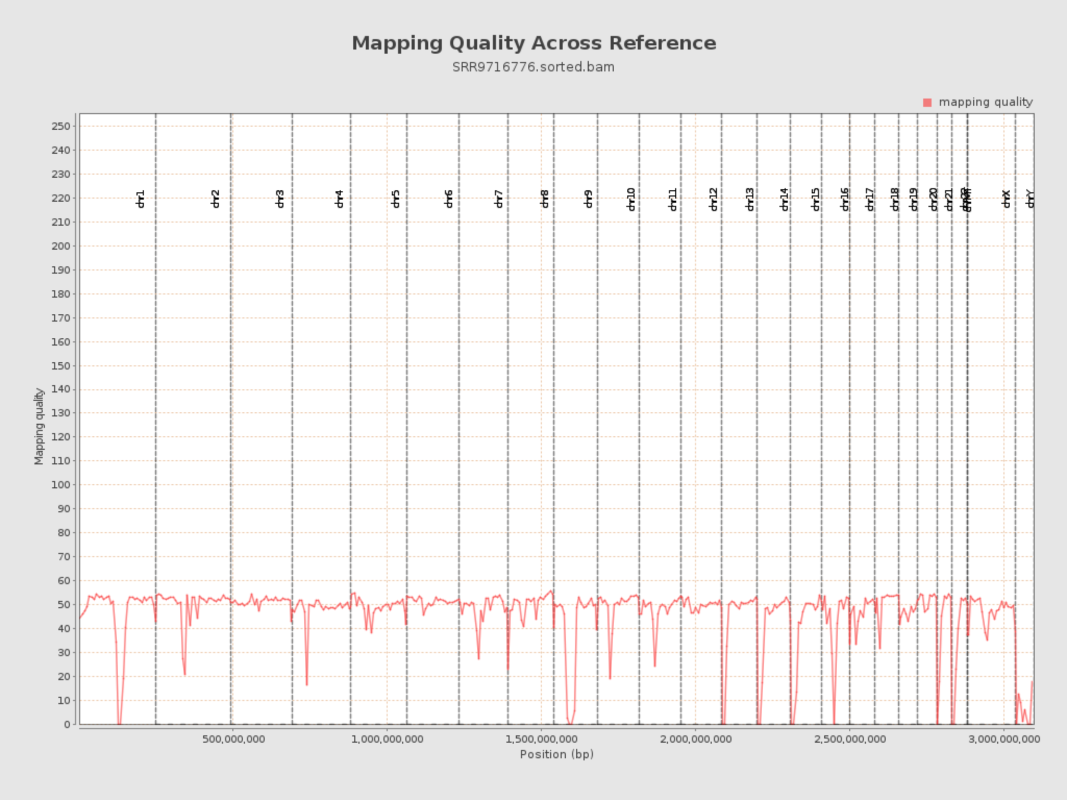
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram