Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:31:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717027.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_SRR9717027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717027.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:31:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,579,635
Mapped reads	2,390,685 / 92.68%
Unmapped reads	188,950 / 7.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,253 / 1.79%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	154,738 / 6%
Duplication rate	5.05%
Clipped reads	2,434,291 / 94.37%

2.2. ACGT Content

Number/percentage of A's	46,662,099 / 25.21%
Number/percentage of C's	37,903,995 / 20.48%
Number/percentage of T's	55,272,839 / 29.87%
Number/percentage of G's	45,210,941 / 24.43%
Number/percentage of N's	7,178 / 0%
GC Percentage	44.91%

2.3. Coverage

Mean	0.0598

Standard Deviation	0.4696

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

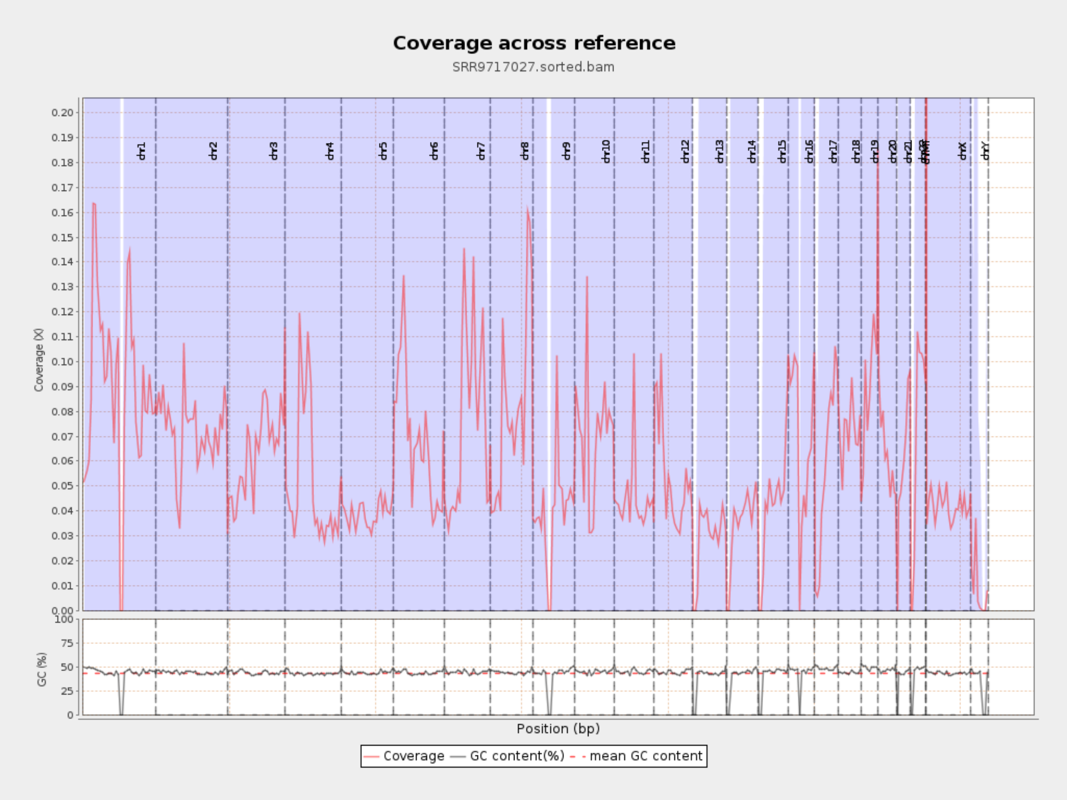
General error rate	0.68%
Mismatches	1,213,729
Insertions	15,068
Mapped reads with at least one insertion	0.62%
Deletions	33,311
Mapped reads with at least one deletion	1.37%
Homopolymer indels	38.95%

2.6. Chromosome stats

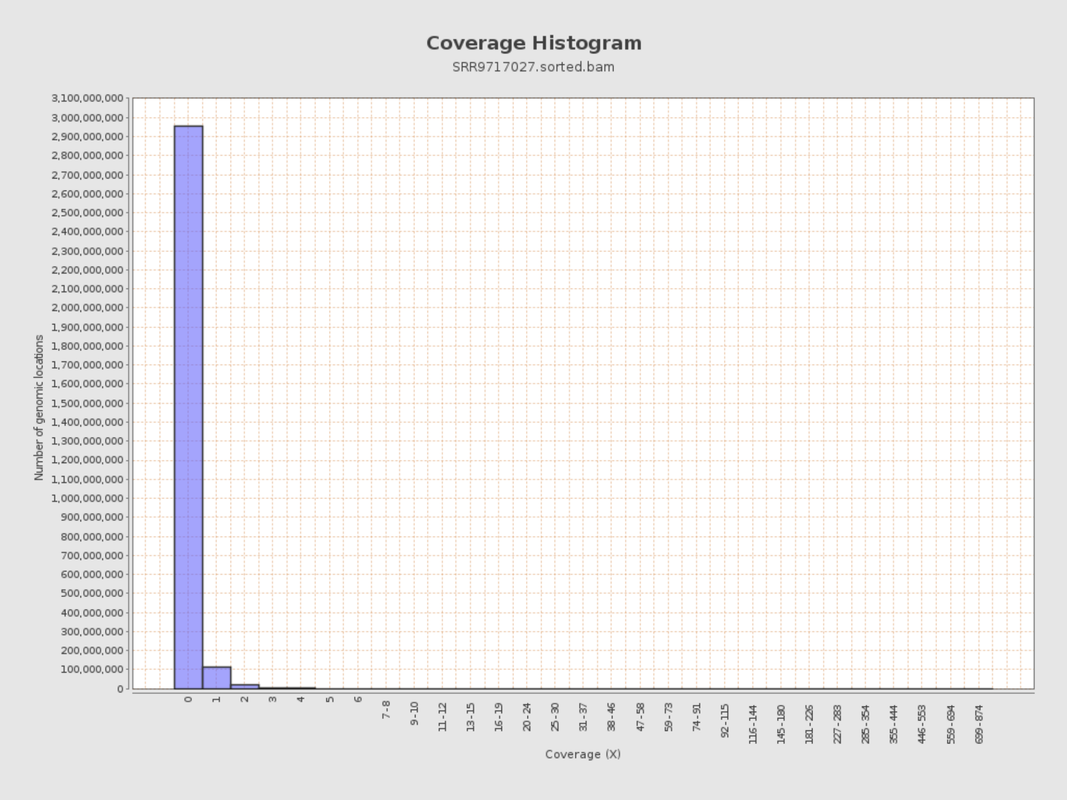
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22641997	0.0908	0.8697
chr2	243199373	17637726	0.0725	0.5168
chr3	198022430	12474494	0.063	0.3221
chr4	191154276	9906583	0.0518	0.4164
chr5	180915260	7085867	0.0392	0.2427
chr6	171115067	11736103	0.0686	0.3543
chr7	159138663	12039402	0.0757	0.6161

chr8	146364022	11974907	0.0818	0.5209
chr9	141213431	5659900	0.0401	0.3224
chr10	135534747	9569502	0.0706	0.6961
chr11	135006516	6124979	0.0454	0.3767
chr12	133851895	7332456	0.0548	0.2934
chr13	115169878	3388645	0.0294	0.2067
chr14	107349540	3763756	0.0351	0.2525
chr15	102531392	4167002	0.0406	0.2473
chr16	90354753	6141368	0.068	0.3511
chr17	81195210	4584146	0.0565	0.3219
chr18	78077248	5605318	0.0718	0.5099
chr19	59128983	5457271	0.0923	0.6701
chr20	63025520	3997715	0.0634	0.3321
chr21	48129895	2915296	0.0606	0.378
chr22	51304566	3587727	0.0699	0.3558
chrMT	16571	285350	17.2198	12.6364
chrX	155270560	6523601	0.042	0.2712
chrY	59373566	526034	0.0089	0.3518

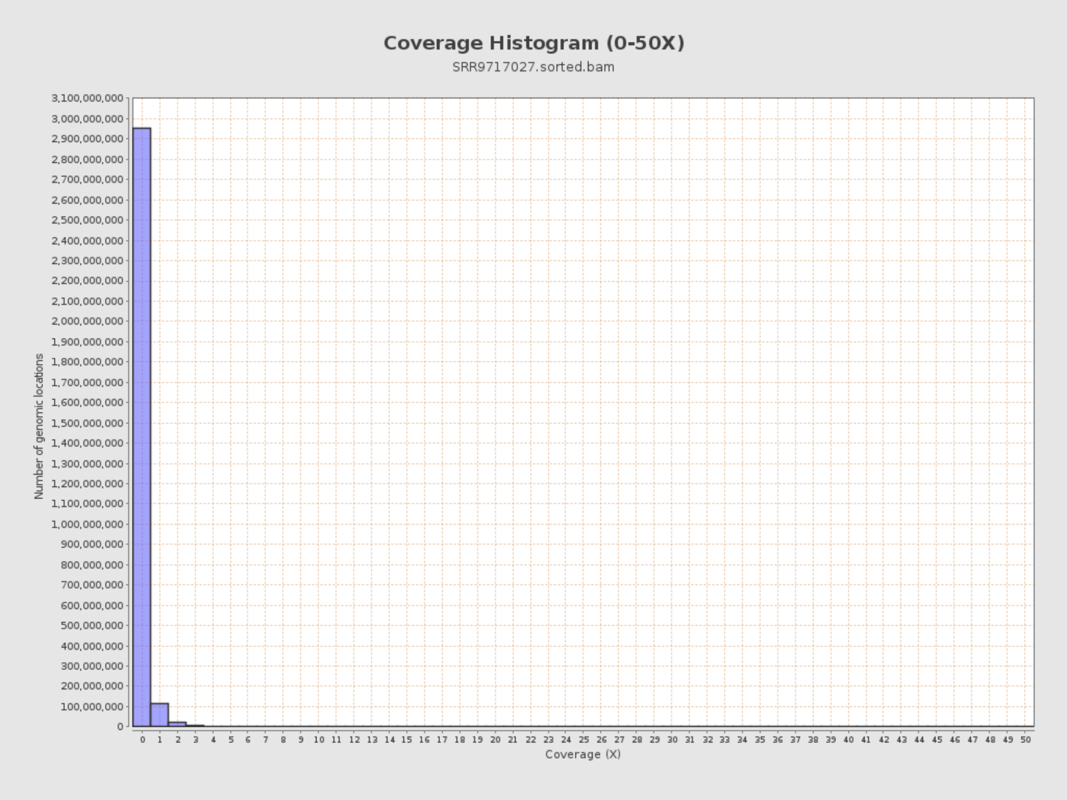
3. Results : Coverage across reference



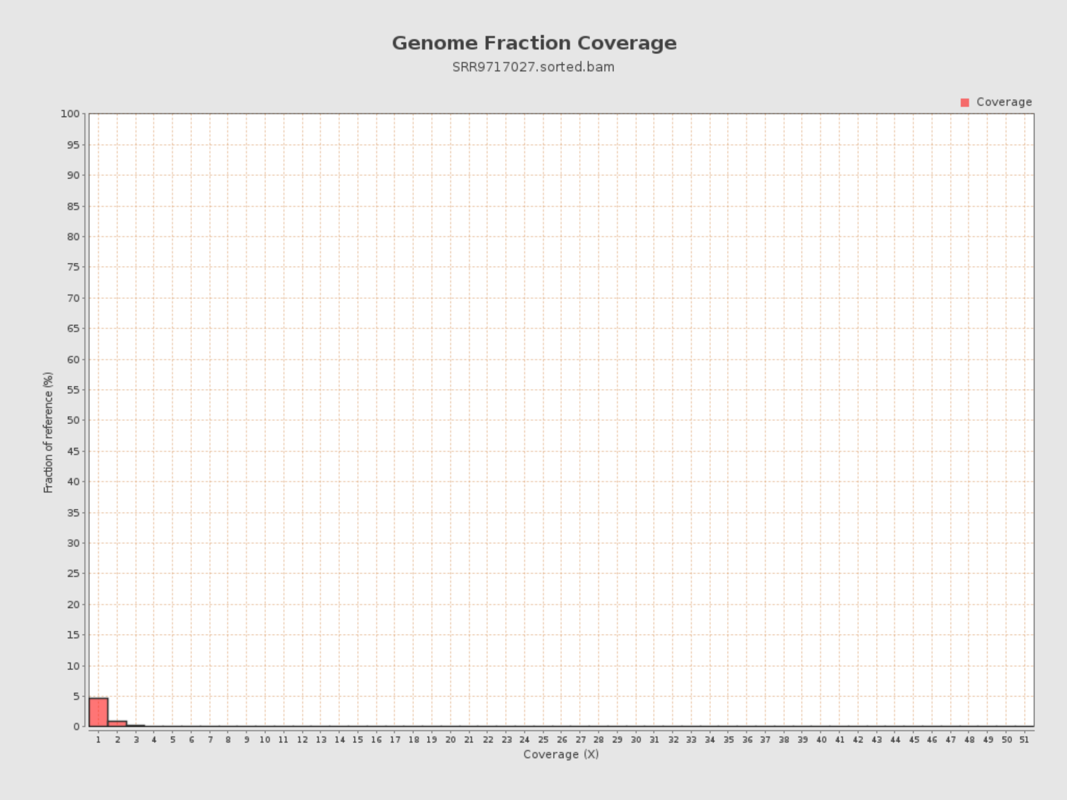
4. Results : Coverage Histogram



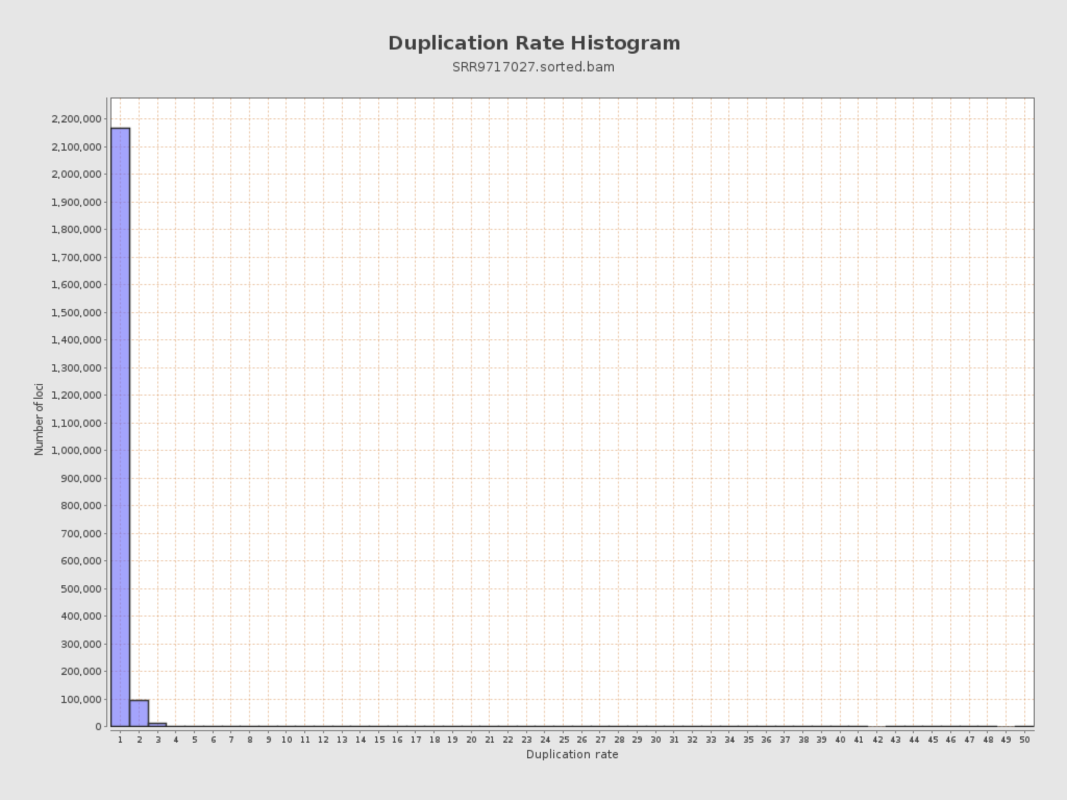
5. Results : Coverage Histogram (0-50X)



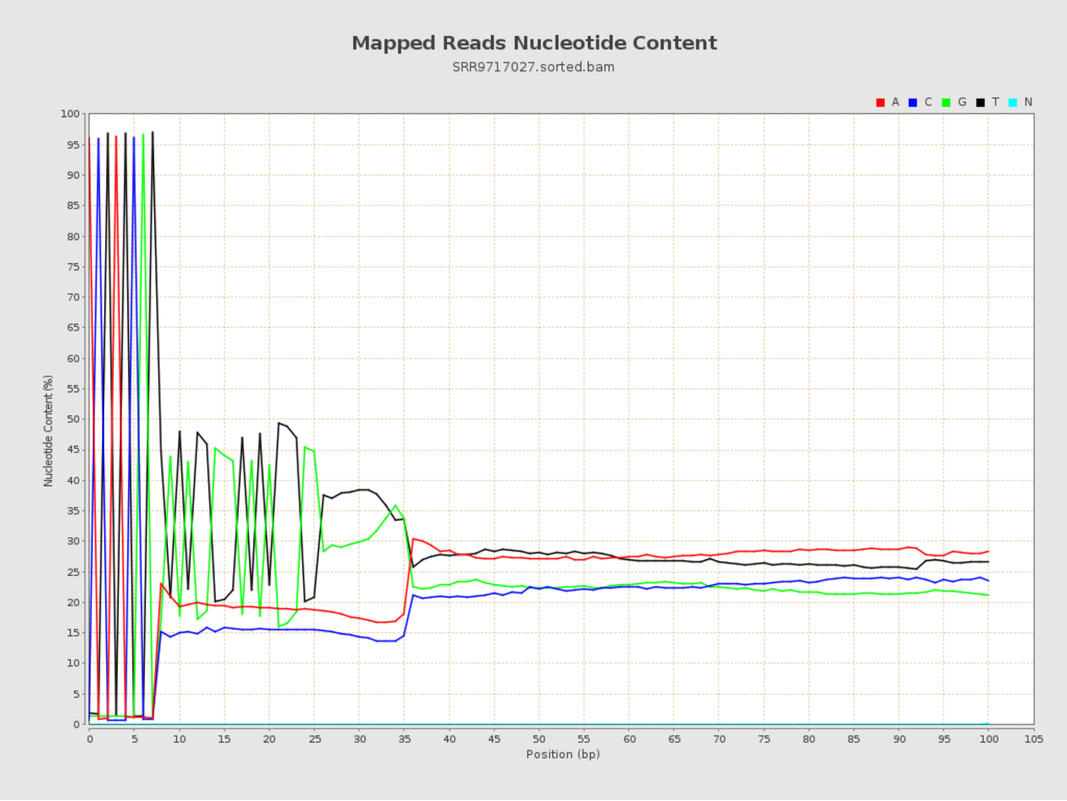
6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



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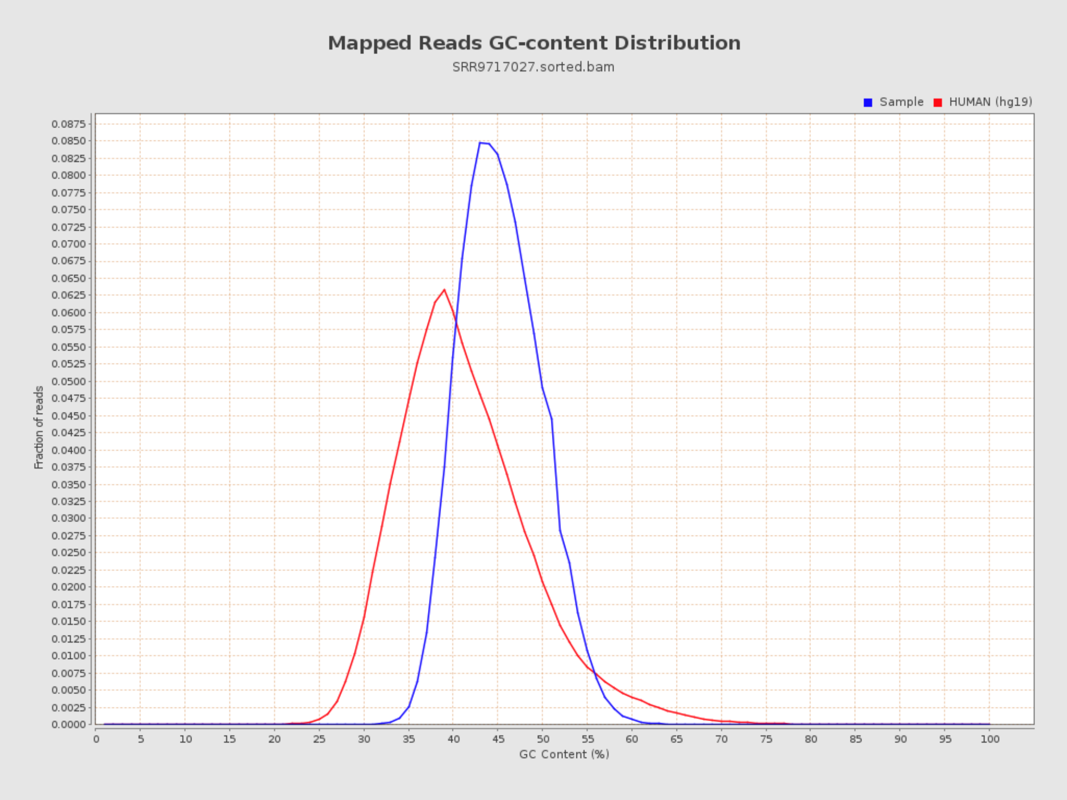
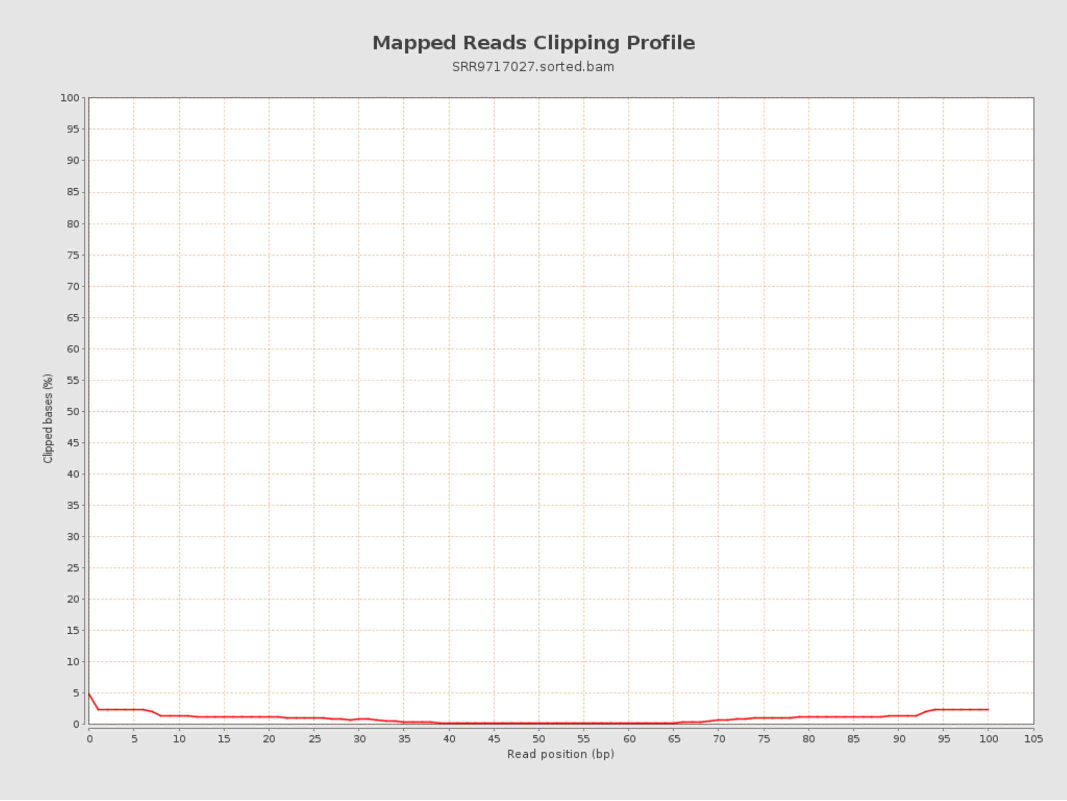
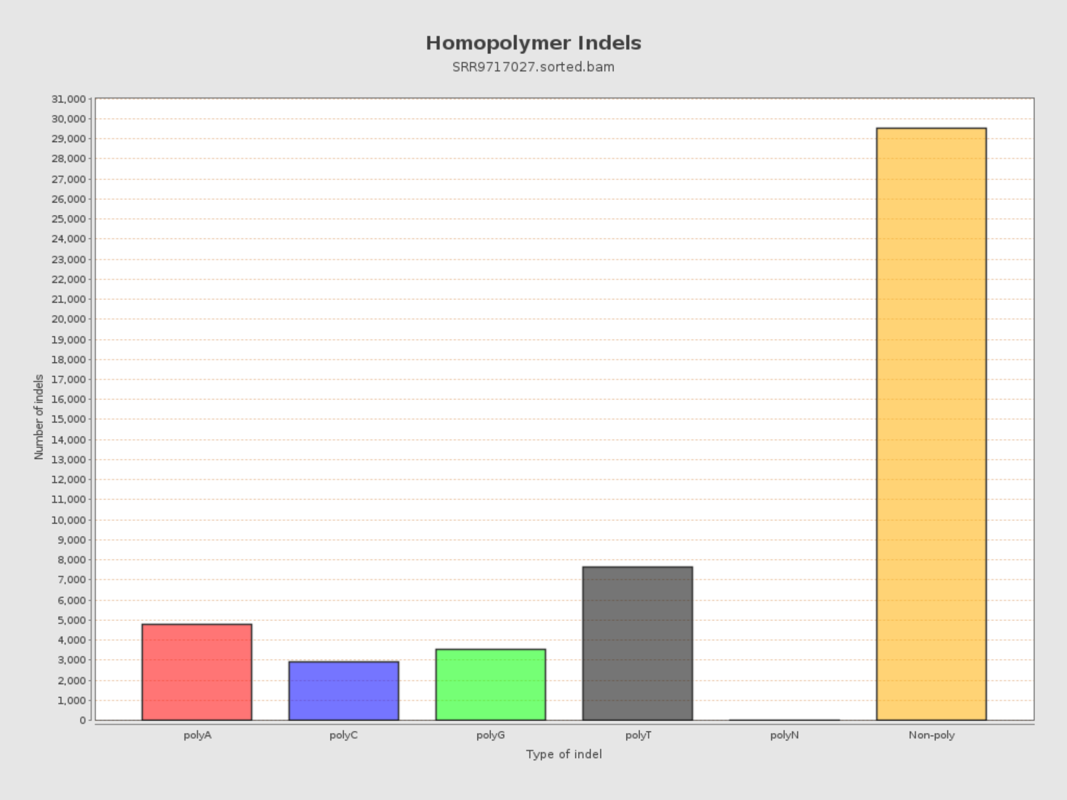
9. Results : Mapped Reads GC-content Distribution



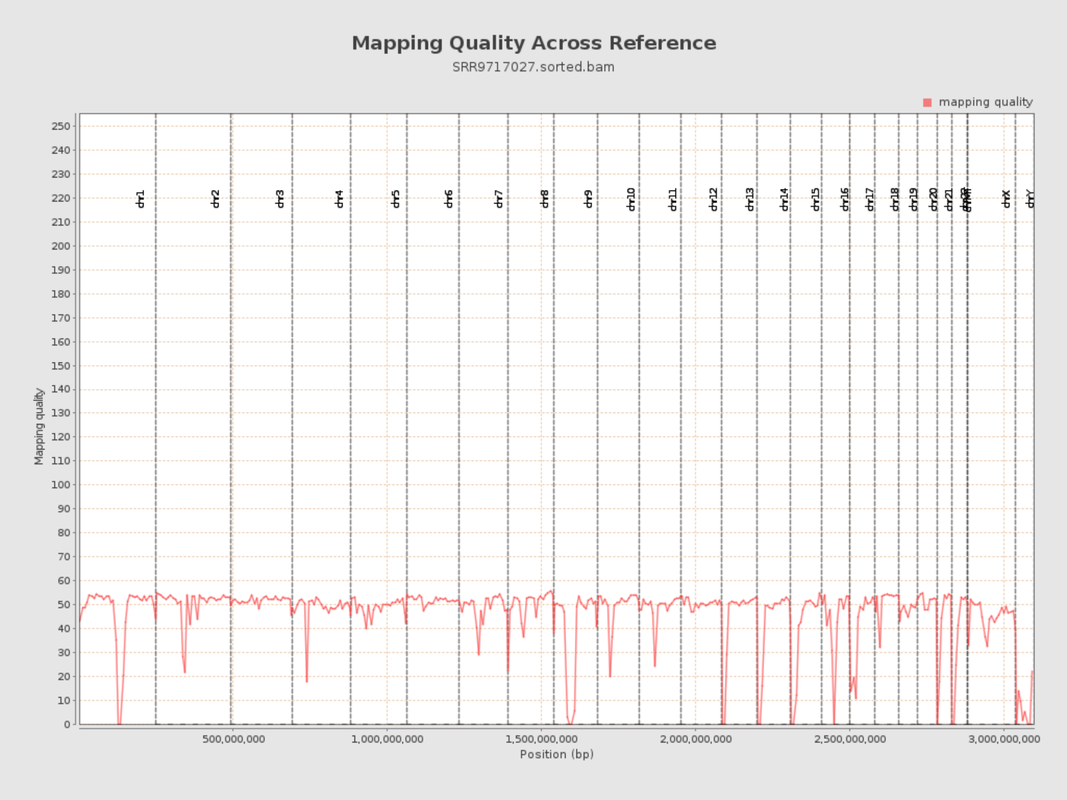
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram