Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:07:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717009.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_SRR9717009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717009.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:07:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,623,846
Mapped reads	2,346,497 / 89.43%
Unmapped reads	277,349 / 10.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,001 / 1.33%
Read min/max/mean length	30 / 101 / 101.49
Duplicated reads (estimated)	119,099 / 4.54%
Duplication rate	2.99%
Clipped reads	2,376,358 / 90.57%

2.2. ACGT Content

Number/percentage of A's	46,239,245 / 25.03%
Number/percentage of C's	33,665,152 / 18.22%
Number/percentage of T's	57,427,111 / 31.08%
Number/percentage of G's	47,420,405 / 25.67%
Number/percentage of N's	10,191 / 0.01%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0597

Standard Deviation	0.7421

2.4. Mapping Quality

Mean Mapping Quality	42.82

2.5. Mismatches and indels

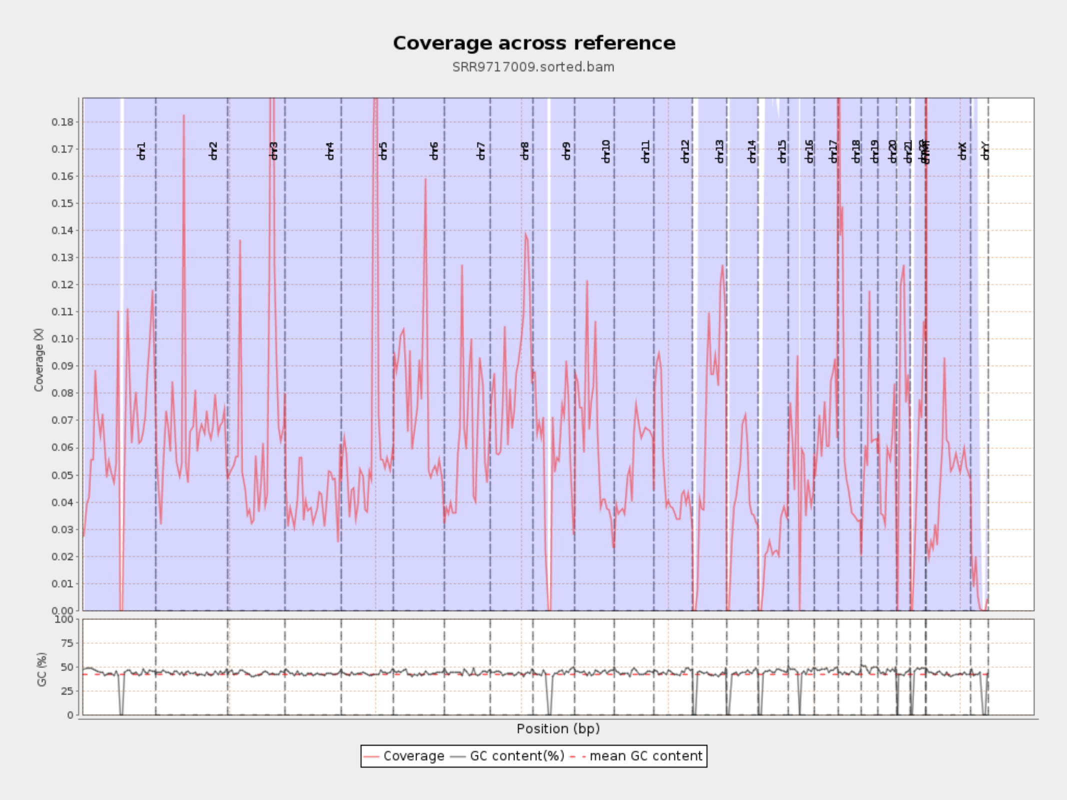
General error rate	0.85%
Mismatches	1,541,986
Insertions	17,186
Mapped reads with at least one insertion	0.72%
Deletions	44,821
Mapped reads with at least one deletion	1.88%
Homopolymer indels	43.7%

2.6. Chromosome stats

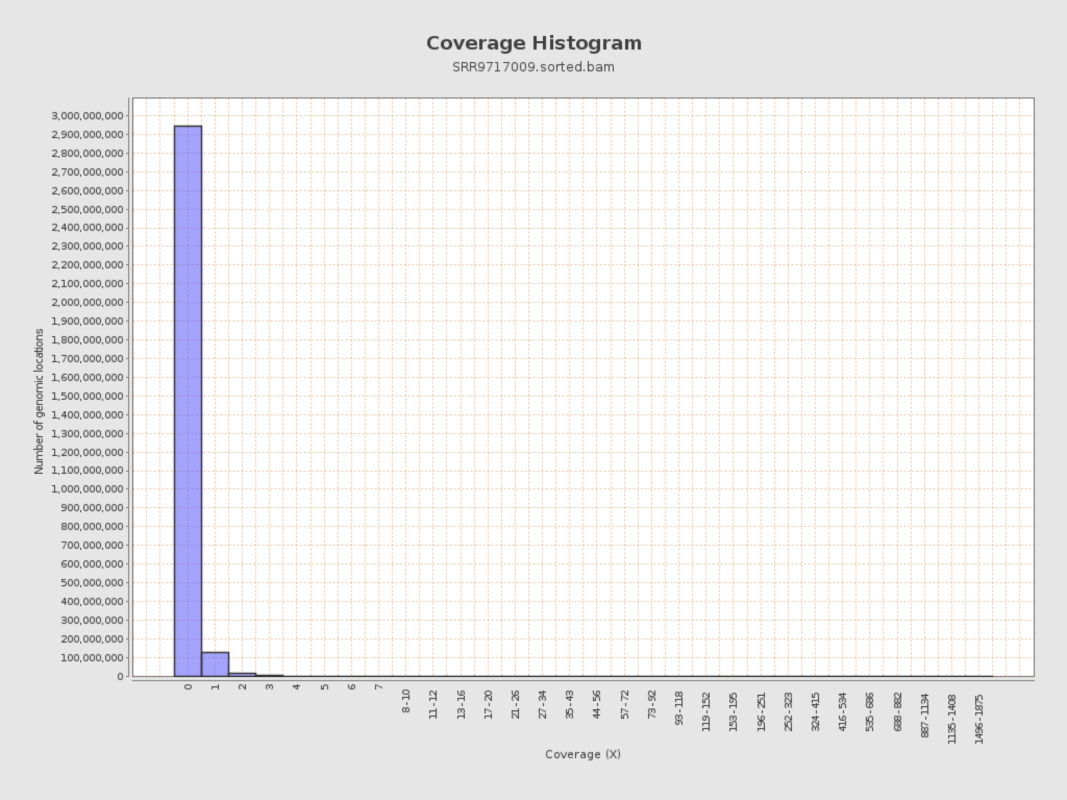
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16079714	0.0645	1.2103
chr2	243199373	16262126	0.0669	1.3268
chr3	198022430	14079627	0.0711	0.3342
chr4	191154276	7848523	0.0411	0.2676
chr5	180915260	11412637	0.0631	0.3058
chr6	171115067	13341240	0.078	0.4543
chr7	159138663	9764560	0.0614	1.0218

chr8	146364022	12844462	0.0878	0.9623
chr9	141213431	7971160	0.0564	0.6762
chr10	135534747	8762781	0.0647	0.631
chr11	135006516	7291481	0.054	0.5012
chr12	133851895	6856339	0.0512	0.2805
chr13	115169878	8233233	0.0715	0.3204
chr14	107349540	4302171	0.0401	0.3333
chr15	102531392	2184610	0.0213	0.1839
chr16	90354753	4650307	0.0515	0.3645
chr17	81195210	5674971	0.0699	0.3979
chr18	78077248	5604715	0.0718	1.6065
chr19	59128983	3763015	0.0636	0.9542
chr20	63025520	3359118	0.0533	0.3978
chr21	48129895	3824604	0.0795	0.3578
chr22	51304566	2728570	0.0532	0.2782
chrMT	16571	135500	8.1769	6.0593
chrX	155270560	7457331	0.048	0.4173
chrY	59373566	407737	0.0069	0.172

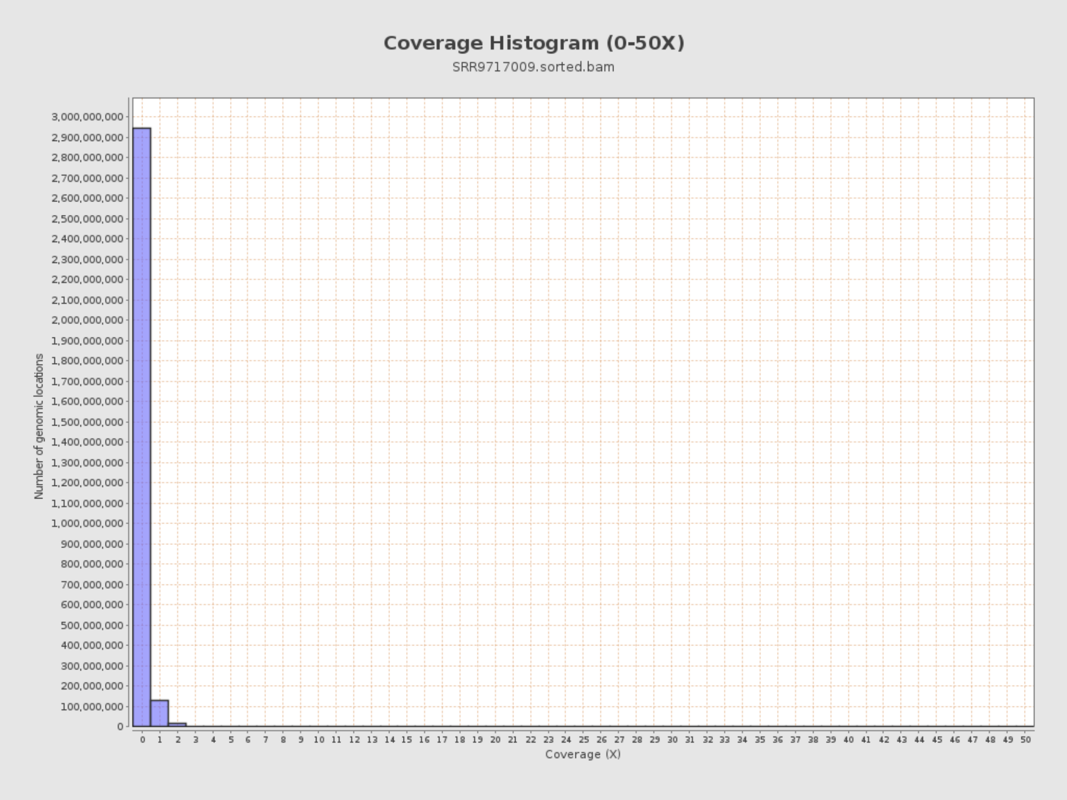
3. Results : Coverage across reference



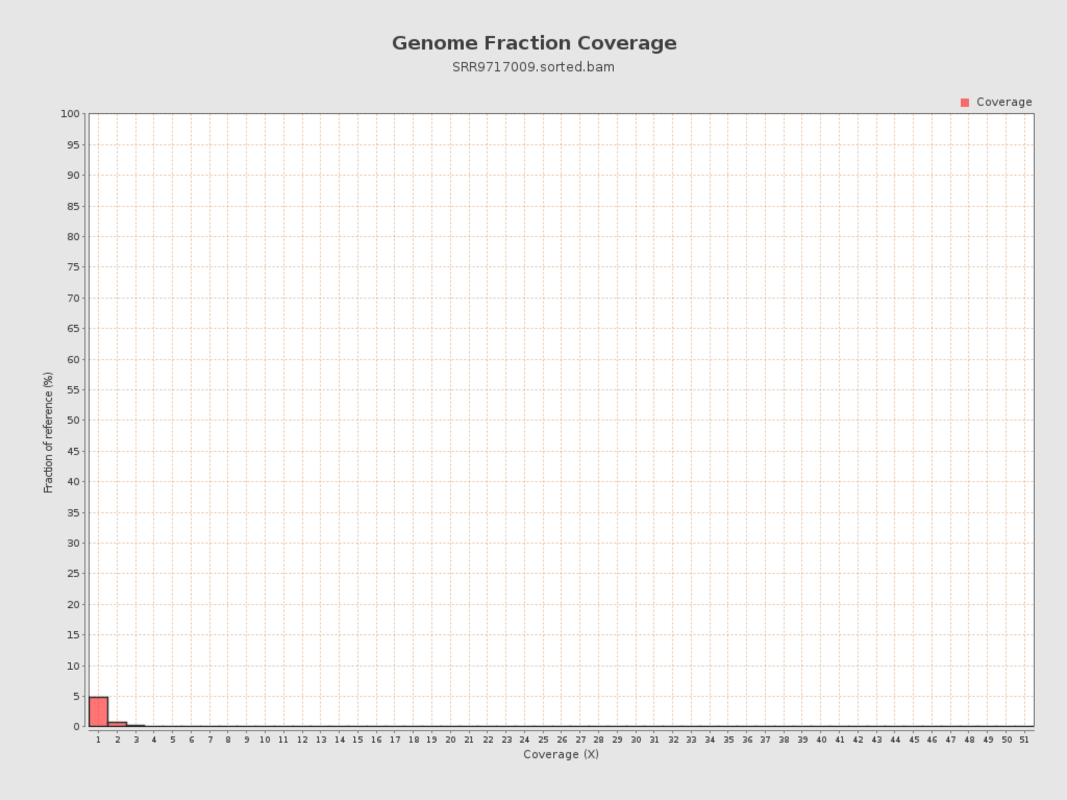
4. Results : Coverage Histogram



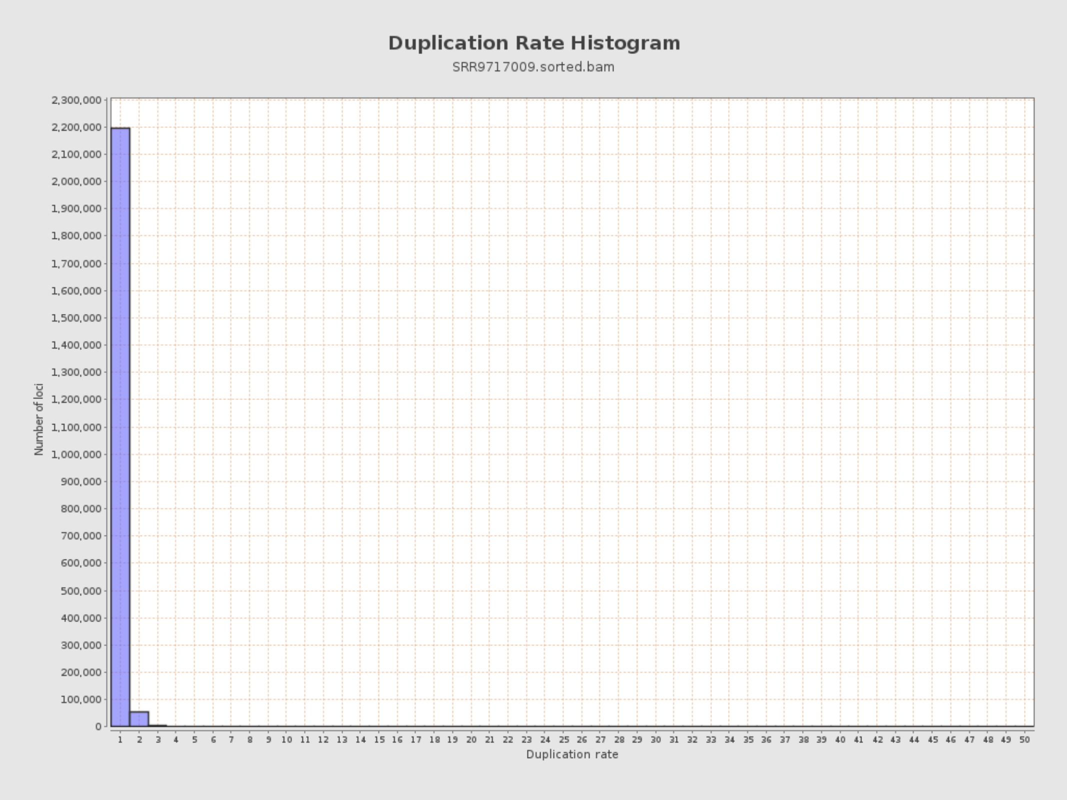
5. Results : Coverage Histogram (0-50X)



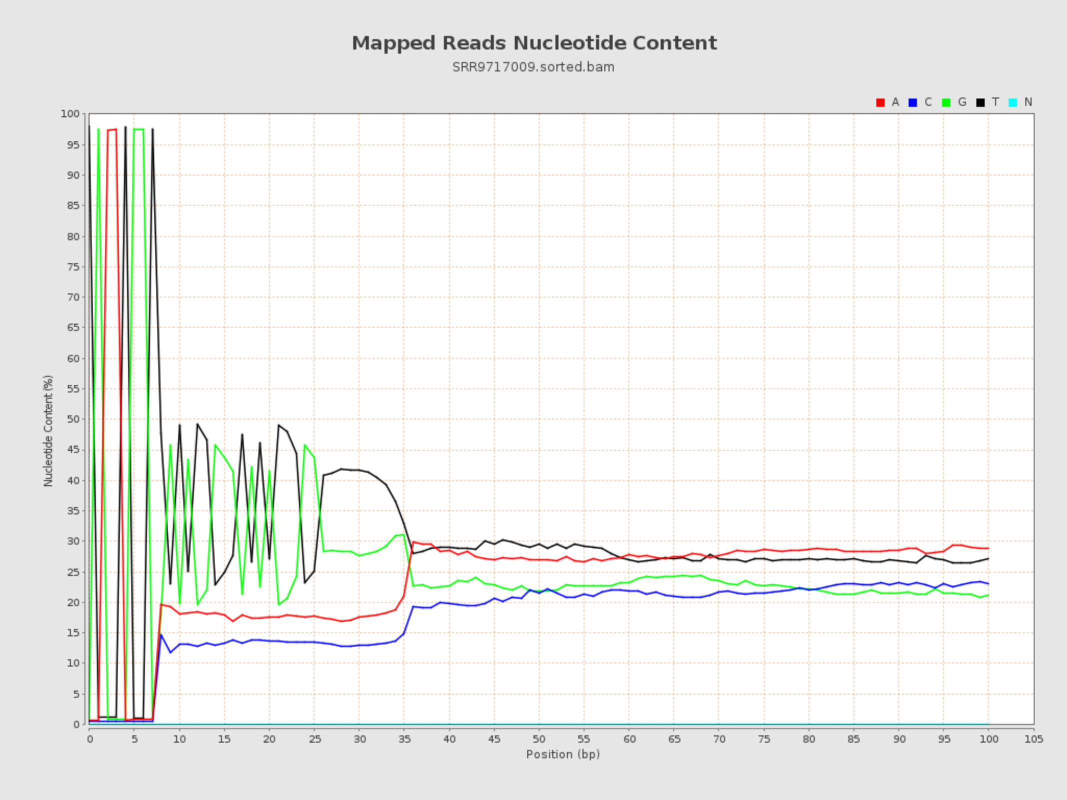
6. Results : Genome Fraction Coverage



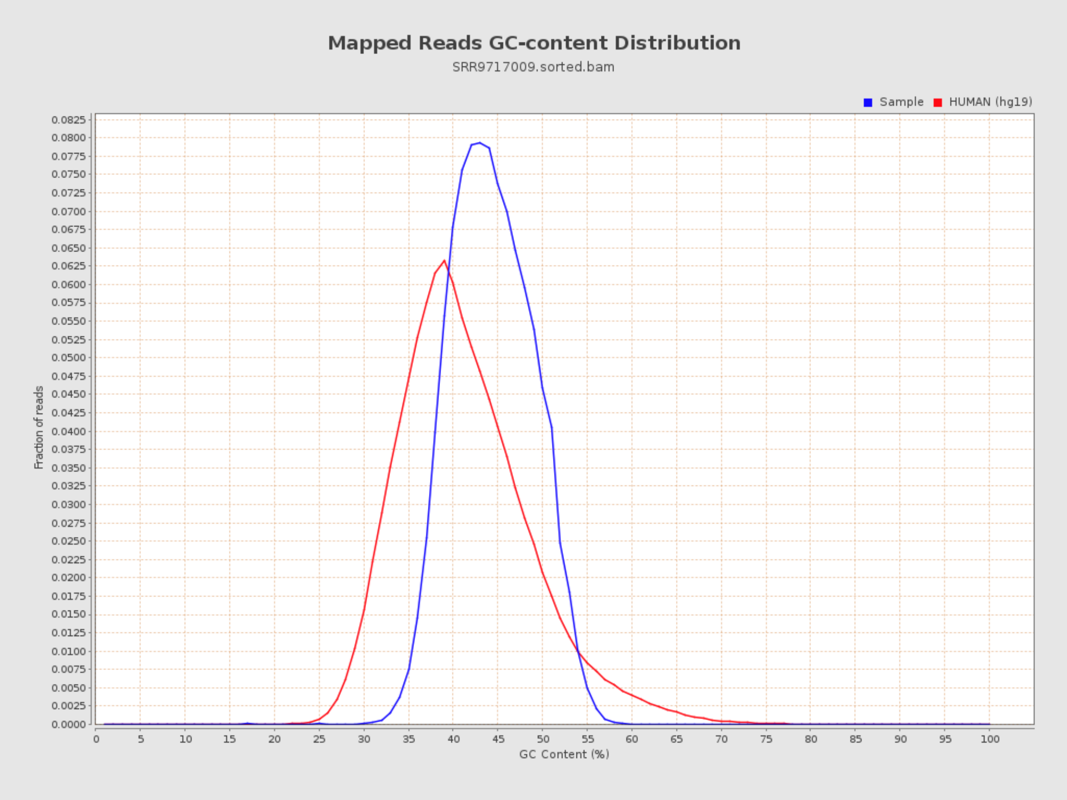
7. Results : Duplication Rate Histogram



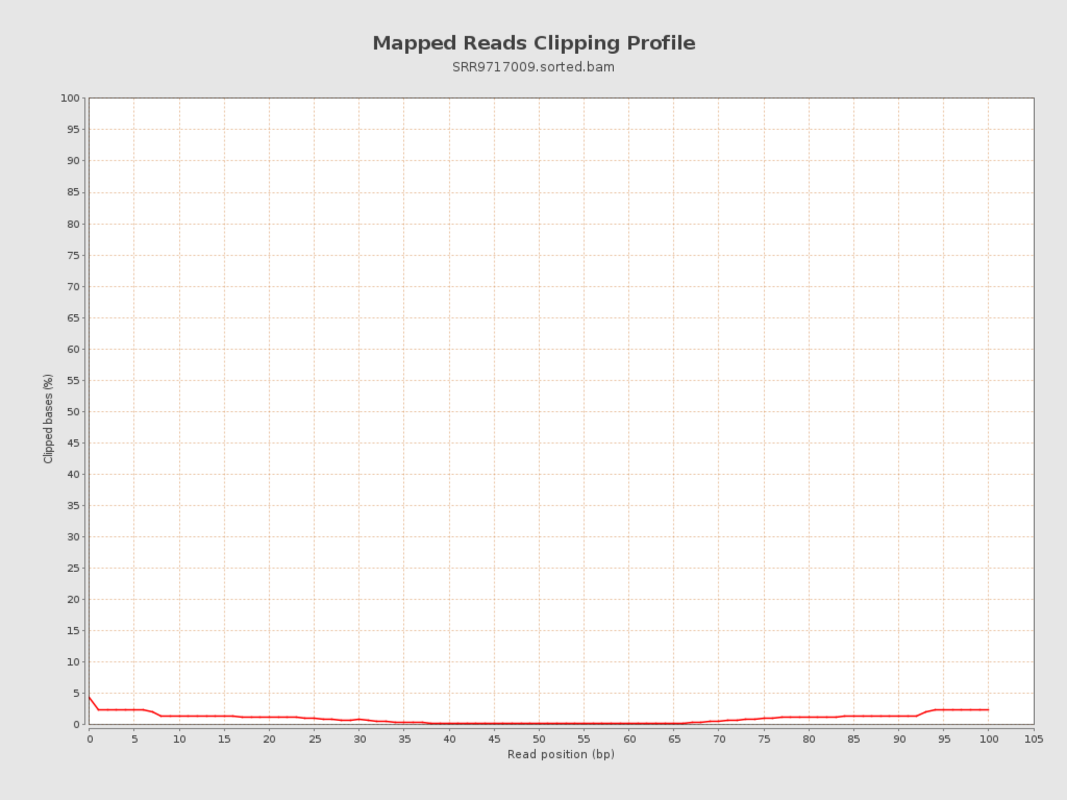
8. Results : Mapped Reads Nucleotide Content



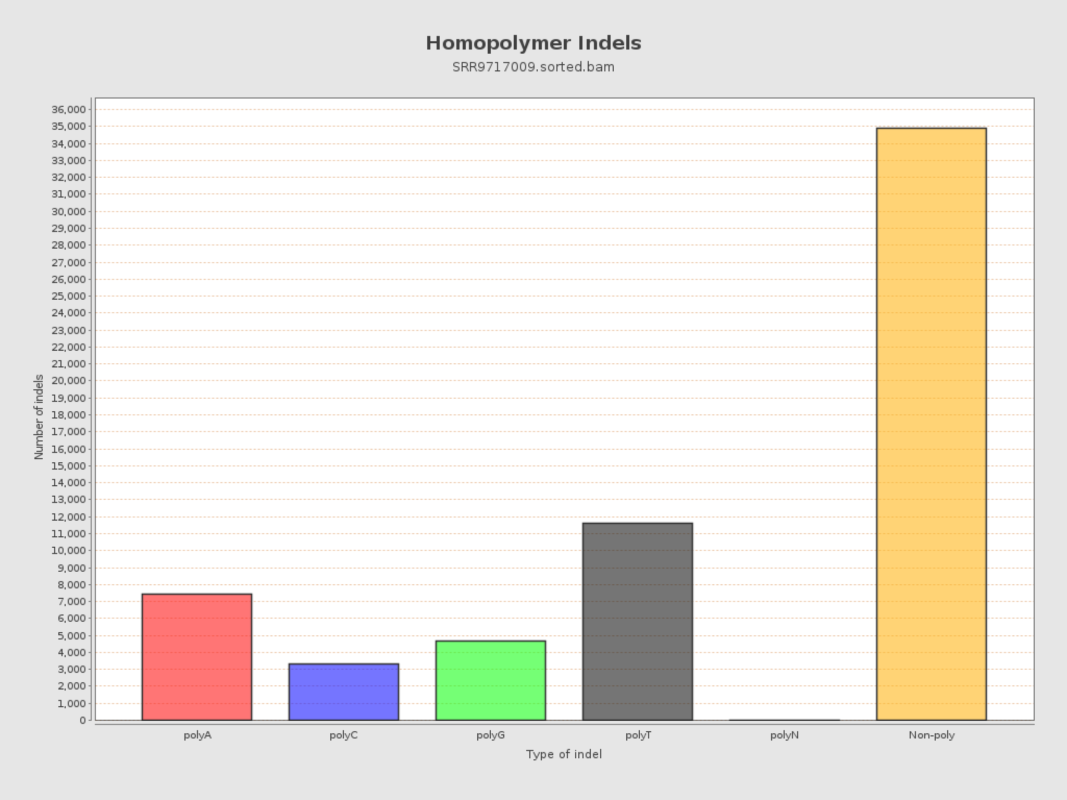
9. Results : Mapped Reads GC-content Distribution



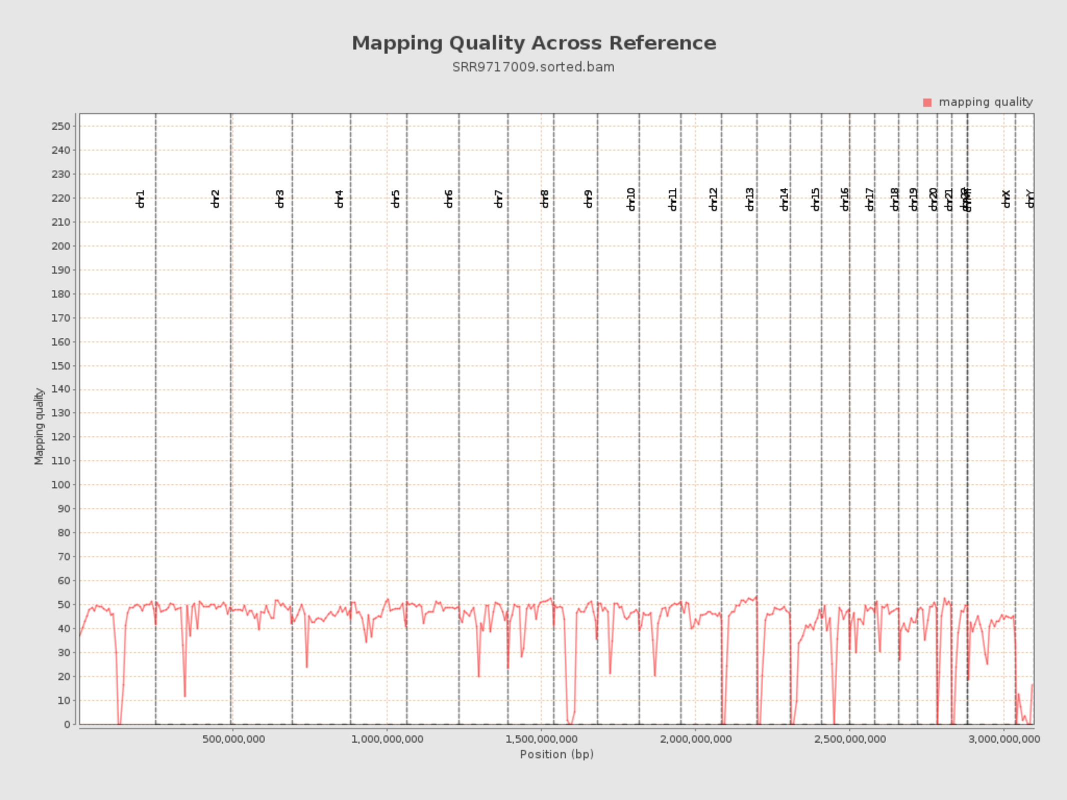
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram