Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:35:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717044.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_SRR9717044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717044.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:35:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,867,859
Mapped reads	1,710,095 / 91.55%
Unmapped reads	157,764 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,250 / 2.53%
Read min/max/mean length	30 / 101 / 101.91
Duplicated reads (estimated)	50,207 / 2.69%
Duplication rate	1.9%
Clipped reads	1,756,770 / 94.05%

2.2. ACGT Content

Number/percentage of A's	33,742,257 / 25.92%
Number/percentage of C's	26,936,923 / 20.69%
Number/percentage of T's	38,924,719 / 29.9%
Number/percentage of G's	30,583,752 / 23.49%
Number/percentage of N's	15,001 / 0.01%
GC Percentage	44.18%

2.3. Coverage

Mean	0.0421

Standard Deviation	0.3631

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

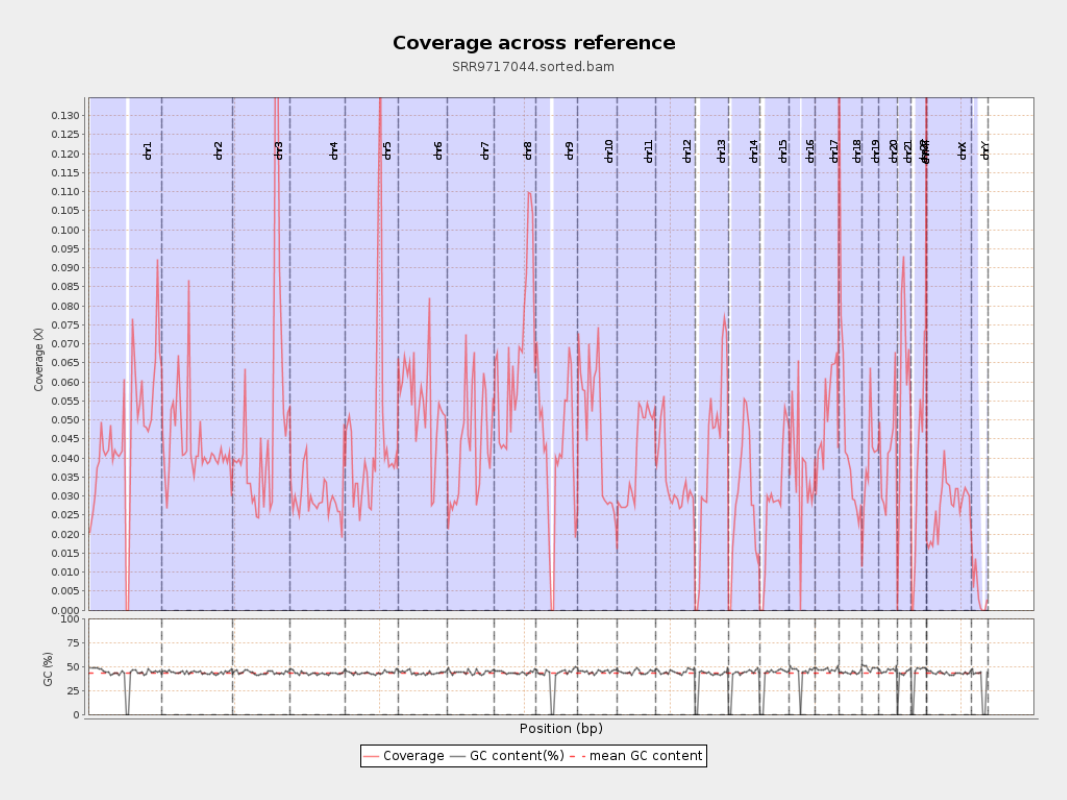
General error rate	0.77%
Mismatches	980,555
Insertions	9,450
Mapped reads with at least one insertion	0.54%
Deletions	27,731
Mapped reads with at least one deletion	1.6%
Homopolymer indels	40.91%

2.6. Chromosome stats

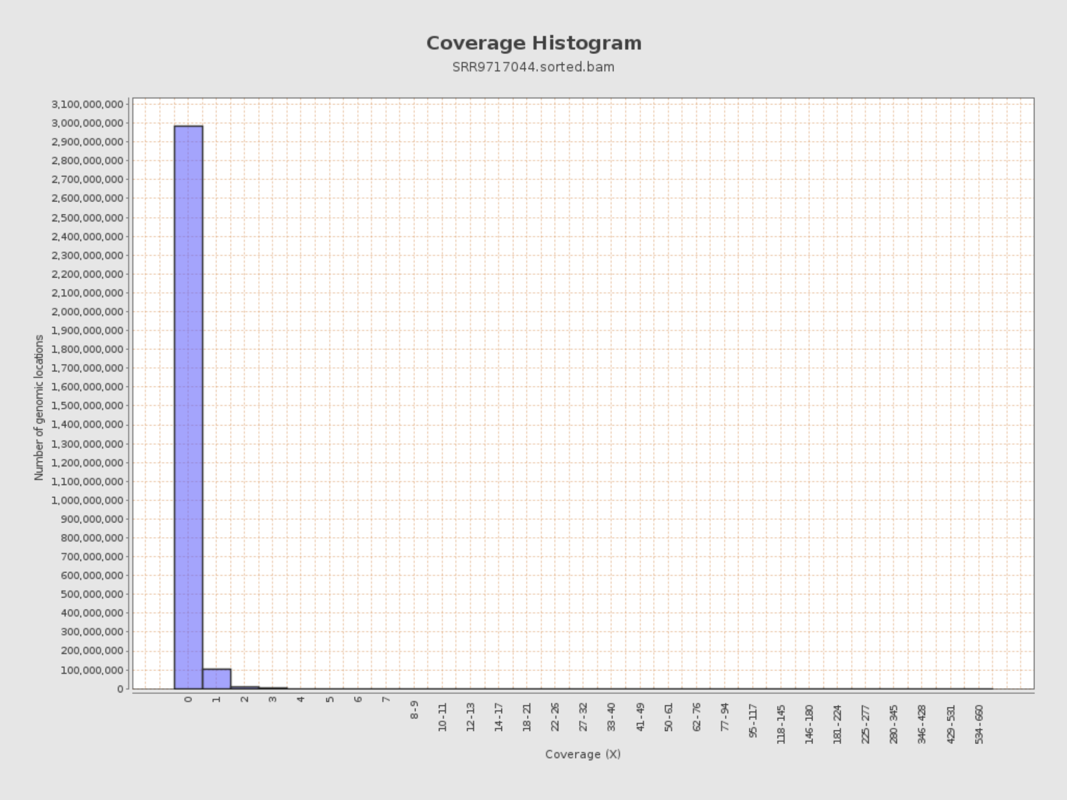
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11404580	0.0458	0.5071
chr2	243199373	10588955	0.0435	0.5406
chr3	198022430	9806701	0.0495	0.2522
chr4	191154276	5700490	0.0298	0.201
chr5	180915260	8207279	0.0454	0.2397
chr6	171115067	9361171	0.0547	0.3109
chr7	159138663	6962686	0.0438	0.544

chr8	146364022	9908758	0.0677	0.4907
chr9	141213431	5760913	0.0408	0.3357
chr10	135534747	6531355	0.0482	0.3471
chr11	135006516	5423510	0.0402	0.3232
chr12	133851895	4517010	0.0337	0.2051
chr13	115169878	4849042	0.0421	0.2282
chr14	107349540	3089740	0.0288	0.2136
chr15	102531392	2924489	0.0285	0.1881
chr16	90354753	3266361	0.0362	0.2406
chr17	81195210	4175717	0.0514	0.2865
chr18	78077248	3566185	0.0457	0.6469
chr19	59128983	2355224	0.0398	0.4612
chr20	63025520	2573137	0.0408	0.2535
chr21	48129895	2835880	0.0589	0.2813
chr22	51304566	1885674	0.0368	0.2158
chrMT	16571	2946	0.1778	0.7393
chrX	155270560	4279839	0.0276	0.23
chrY	59373566	272511	0.0046	0.1298

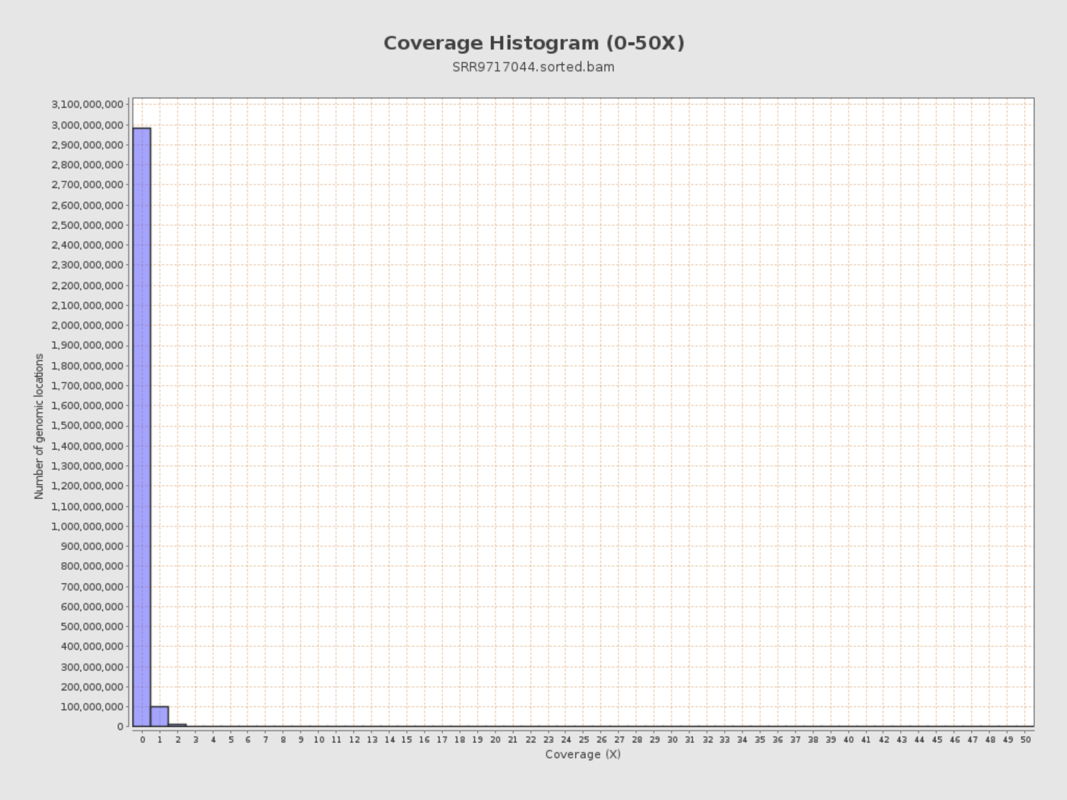
3. Results : Coverage across reference



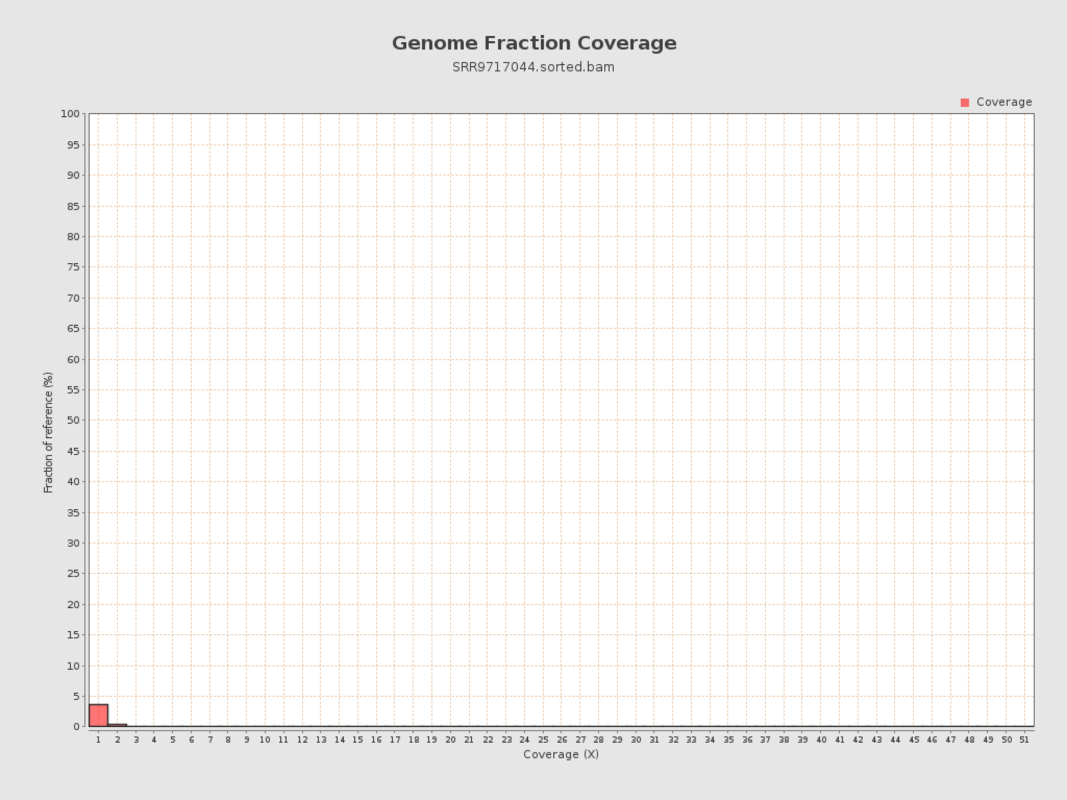
4. Results : Coverage Histogram



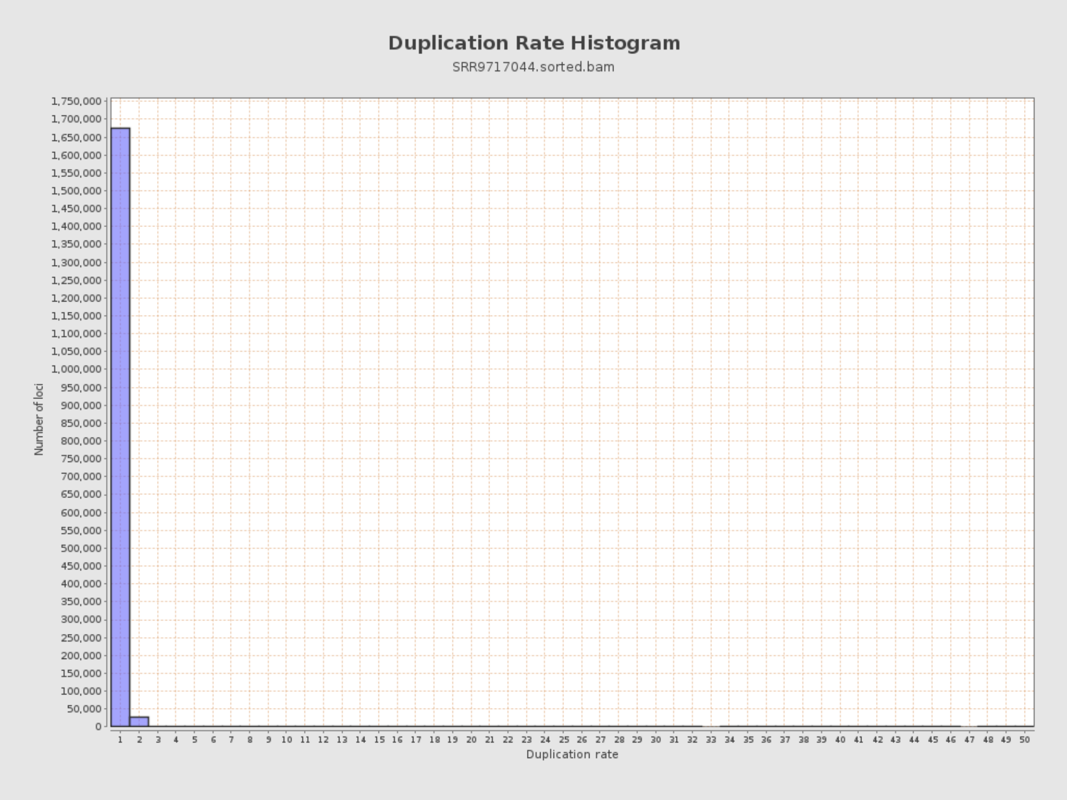
5. Results : Coverage Histogram (0-50X)



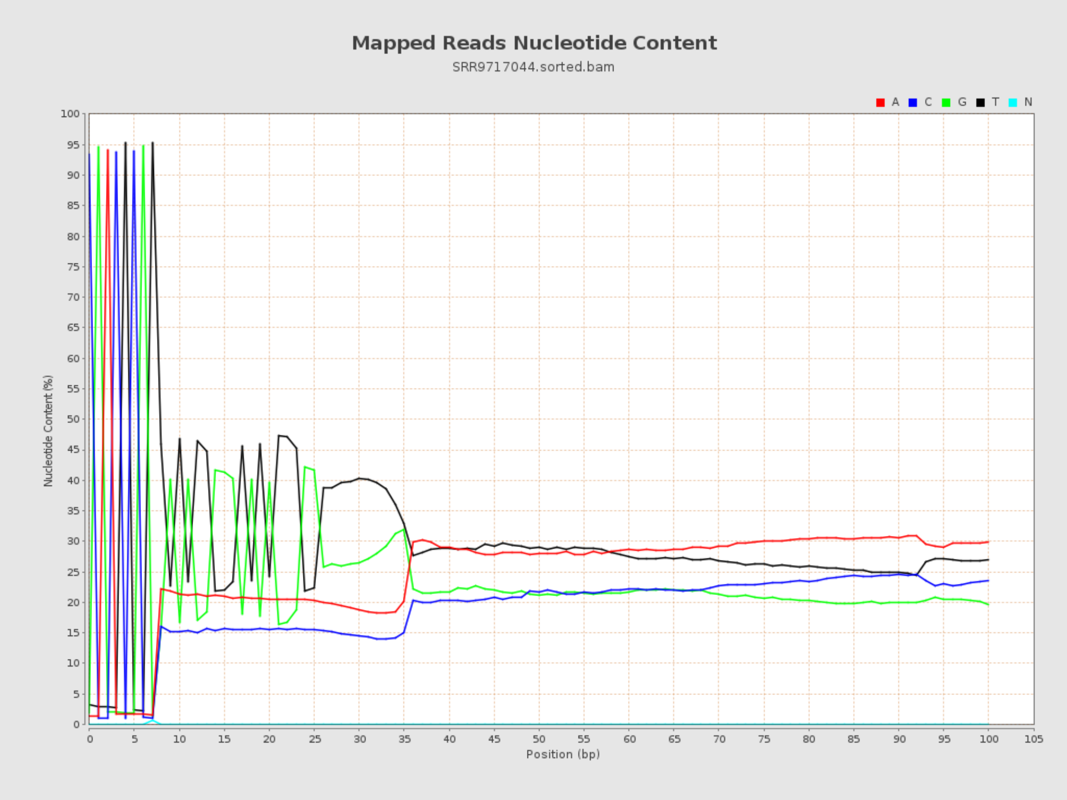
6. Results : Genome Fraction Coverage



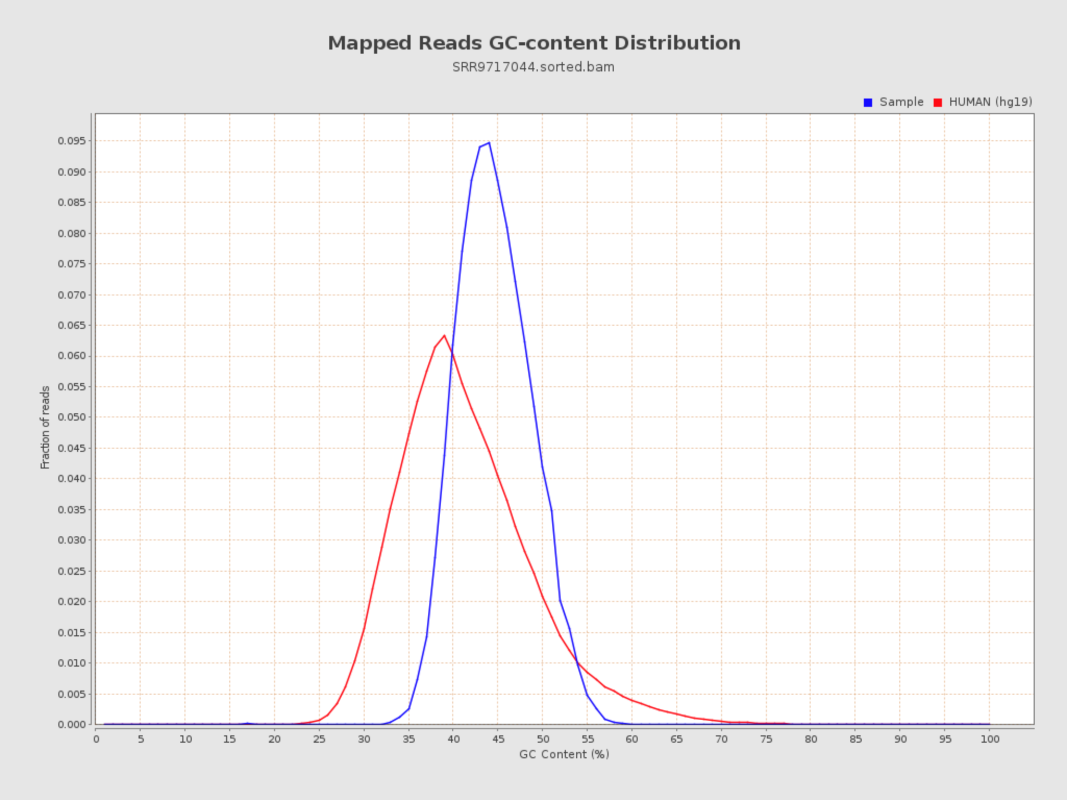
7. Results : Duplication Rate Histogram



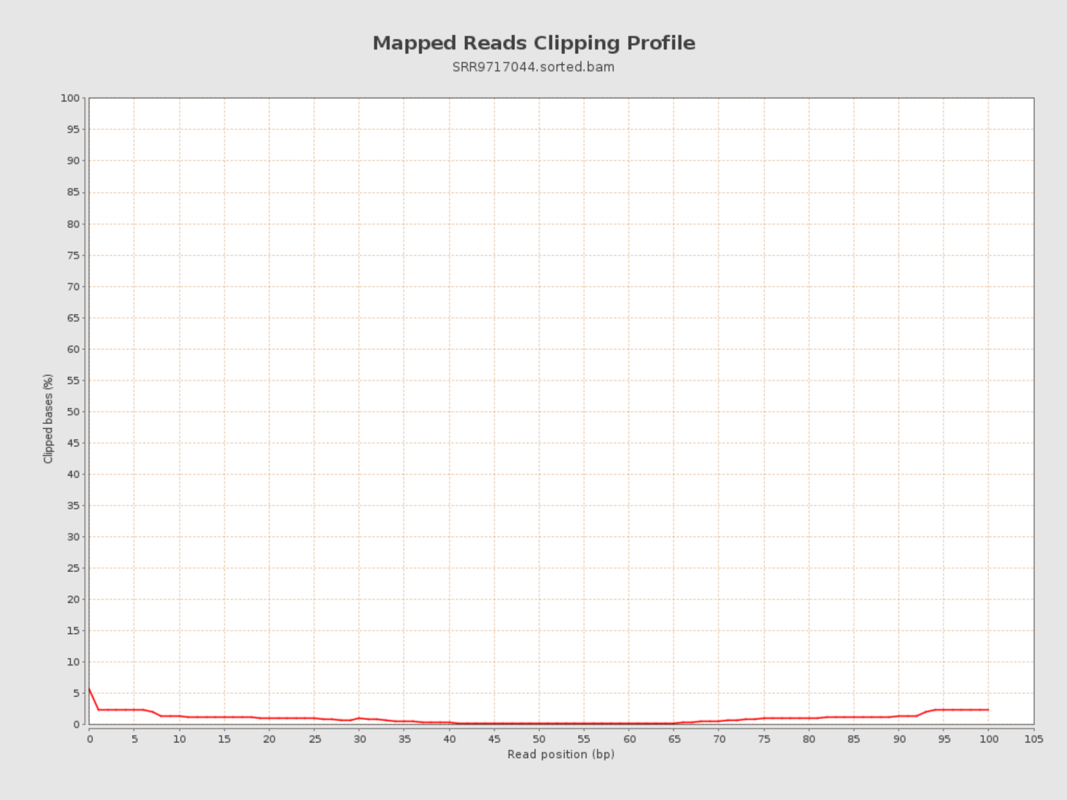
8. Results : Mapped Reads Nucleotide Content



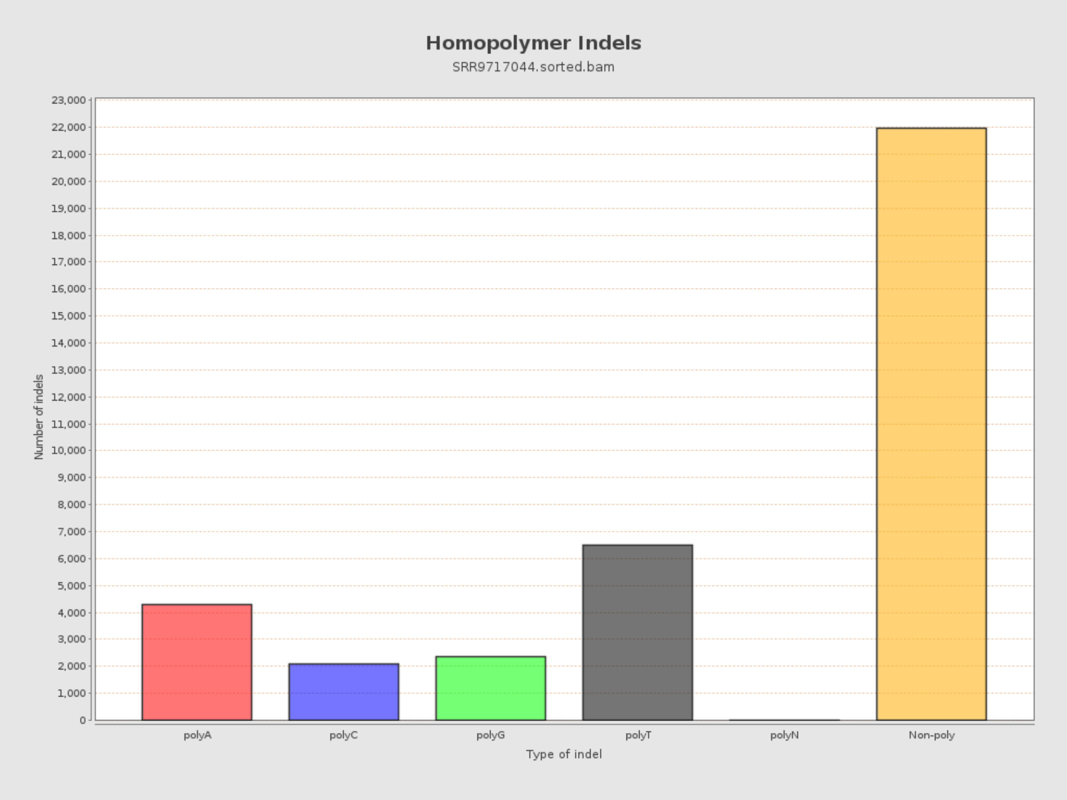
9. Results : Mapped Reads GC-content Distribution



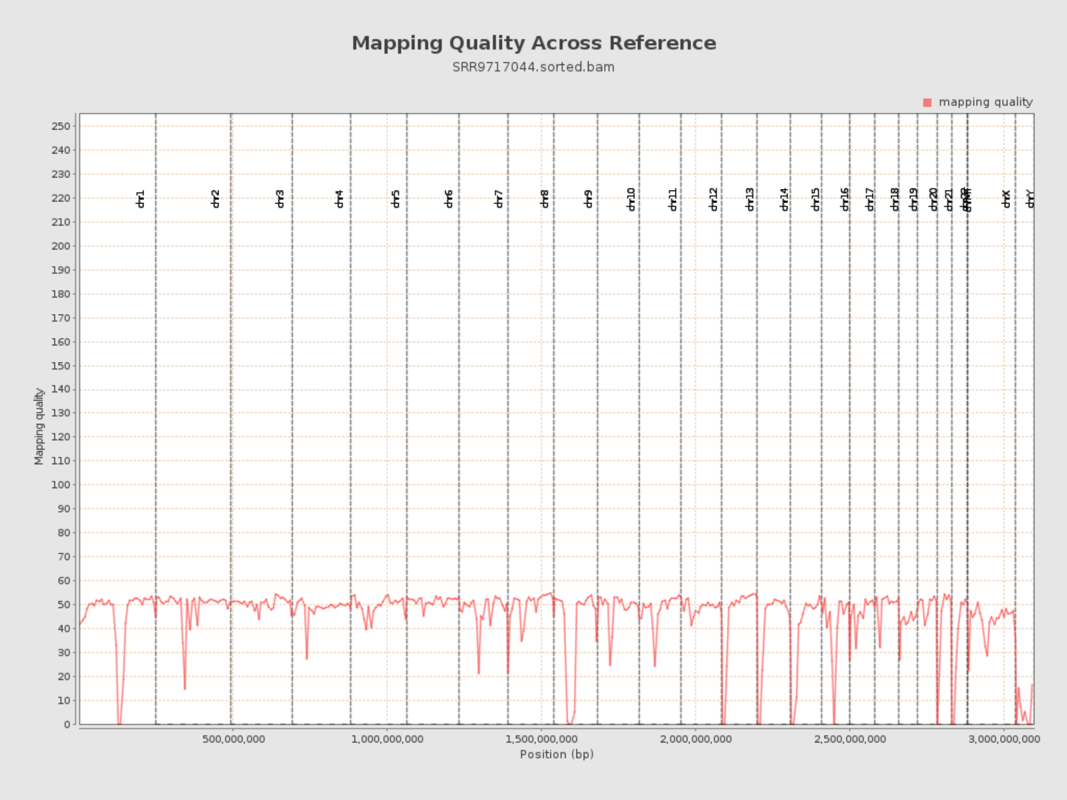
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram