Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:49:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717075.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_SRR9717075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:49:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	463,757
Mapped reads	423,693 / 91.36%
Unmapped reads	40,064 / 8.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,602 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	9,354 / 2.02%
Duplication rate	1.82%
Clipped reads	425,833 / 91.82%

2.2. ACGT Content

Number/percentage of A's	6,289,287 / 25.19%
Number/percentage of C's	4,658,188 / 18.66%
Number/percentage of T's	7,610,115 / 30.49%
Number/percentage of G's	6,405,284 / 25.66%
Number/percentage of N's	143 / 0%
GC Percentage	44.32%

2.3. Coverage

Mean	0.0081

Standard Deviation	0.105

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

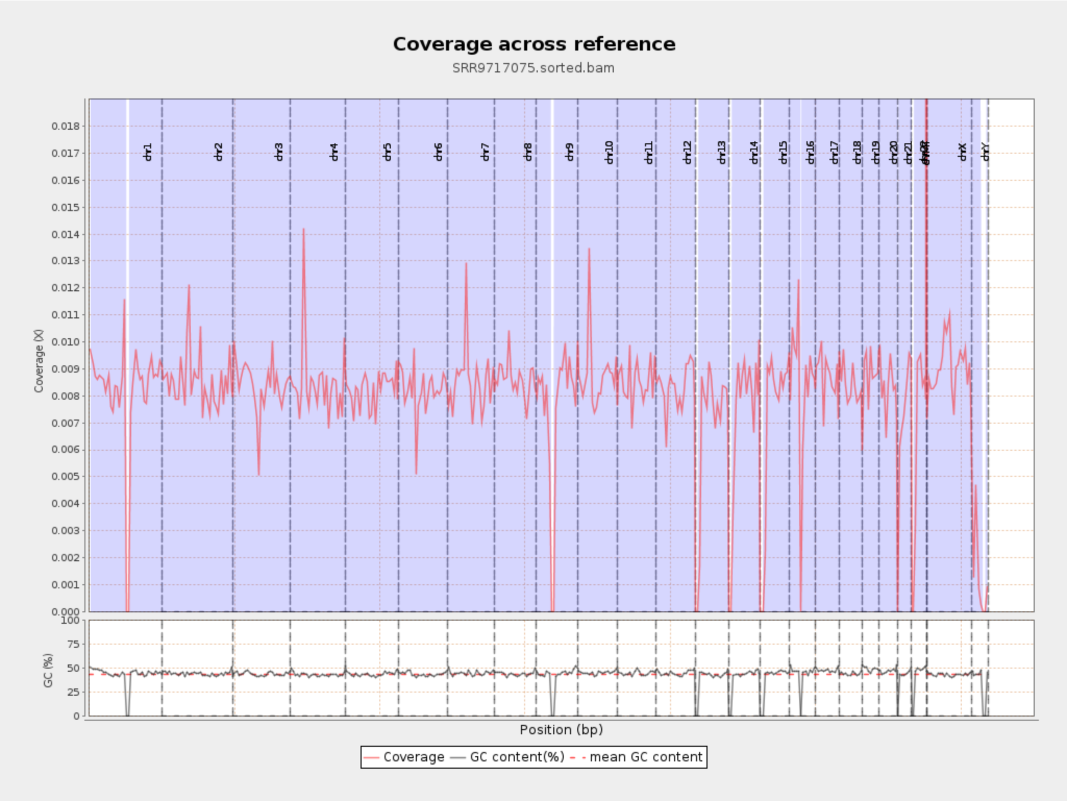
General error rate	0.51%
Mismatches	123,201
Insertions	1,497
Mapped reads with at least one insertion	0.35%
Deletions	4,328
Mapped reads with at least one deletion	1.01%
Homopolymer indels	43.24%

2.6. Chromosome stats

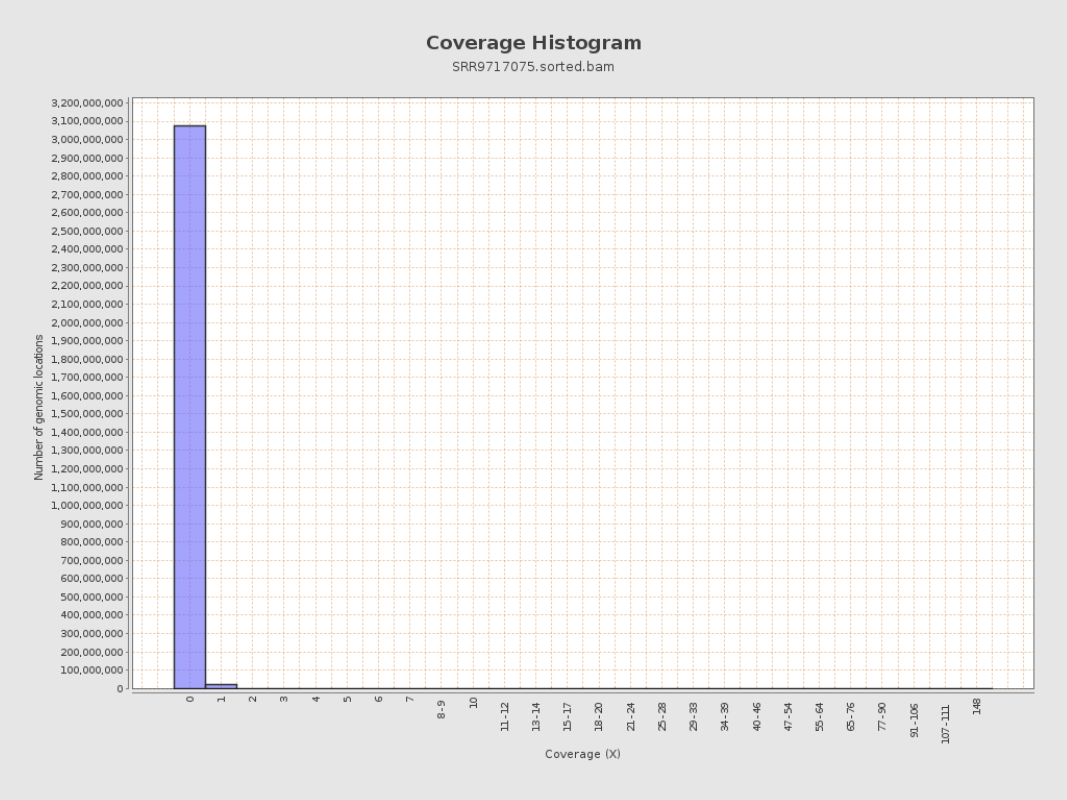
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2027204	0.0081	0.1291
chr2	243199373	2083279	0.0086	0.1201
chr3	198022430	1661554	0.0084	0.0957
chr4	191154276	1608110	0.0084	0.1012
chr5	180915260	1487568	0.0082	0.0947
chr6	171115067	1410227	0.0082	0.0991
chr7	159138663	1358591	0.0085	0.1219

chr8	146364022	1260502	0.0086	0.1172
chr9	141213431	1048652	0.0074	0.0947
chr10	135534747	1181237	0.0087	0.1113
chr11	135006516	1149488	0.0085	0.103
chr12	133851895	1114927	0.0083	0.0958
chr13	115169878	775813	0.0067	0.0857
chr14	107349540	753472	0.007	0.0882
chr15	102531392	717470	0.007	0.0882
chr16	90354753	755665	0.0084	0.0969
chr17	81195210	708974	0.0087	0.1009
chr18	78077248	659836	0.0085	0.1272
chr19	59128983	521568	0.0088	0.118
chr20	63025520	523636	0.0083	0.0964
chr21	48129895	342493	0.0071	0.0925
chr22	51304566	316851	0.0062	0.0826
chrMT	16571	20484	1.2361	1.334
chrX	155270560	1403416	0.009	0.1013
chrY	59373566	79032	0.0013	0.052

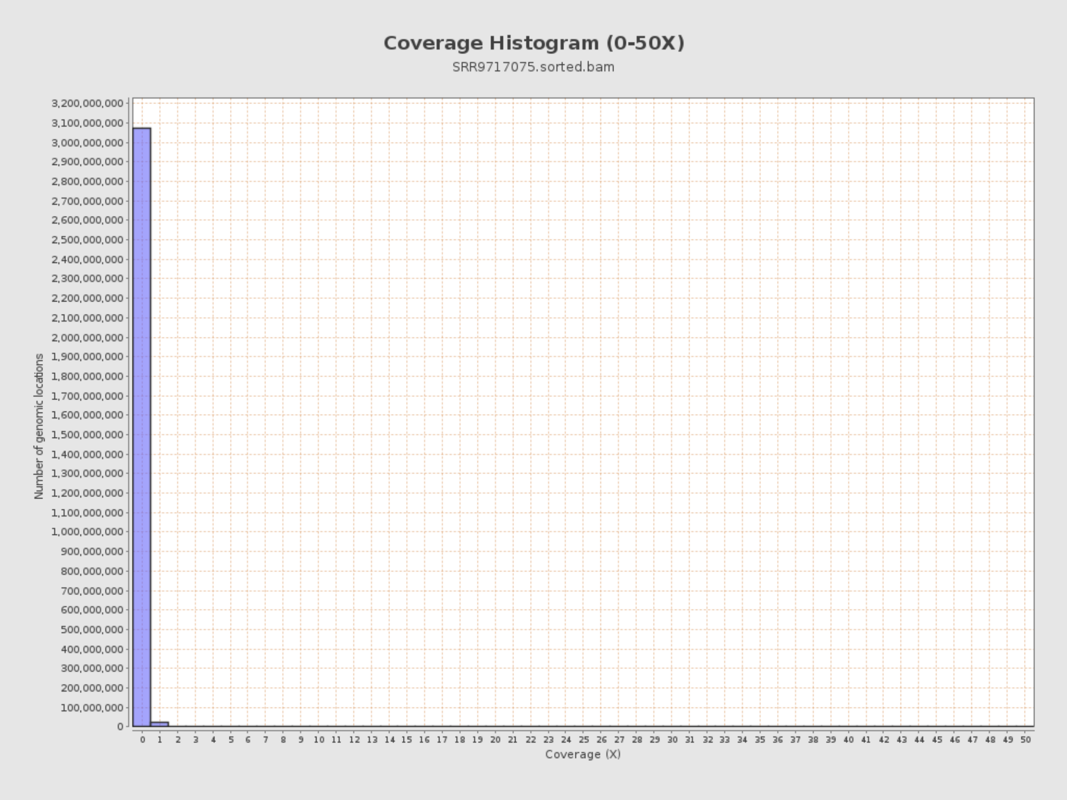
3. Results : Coverage across reference



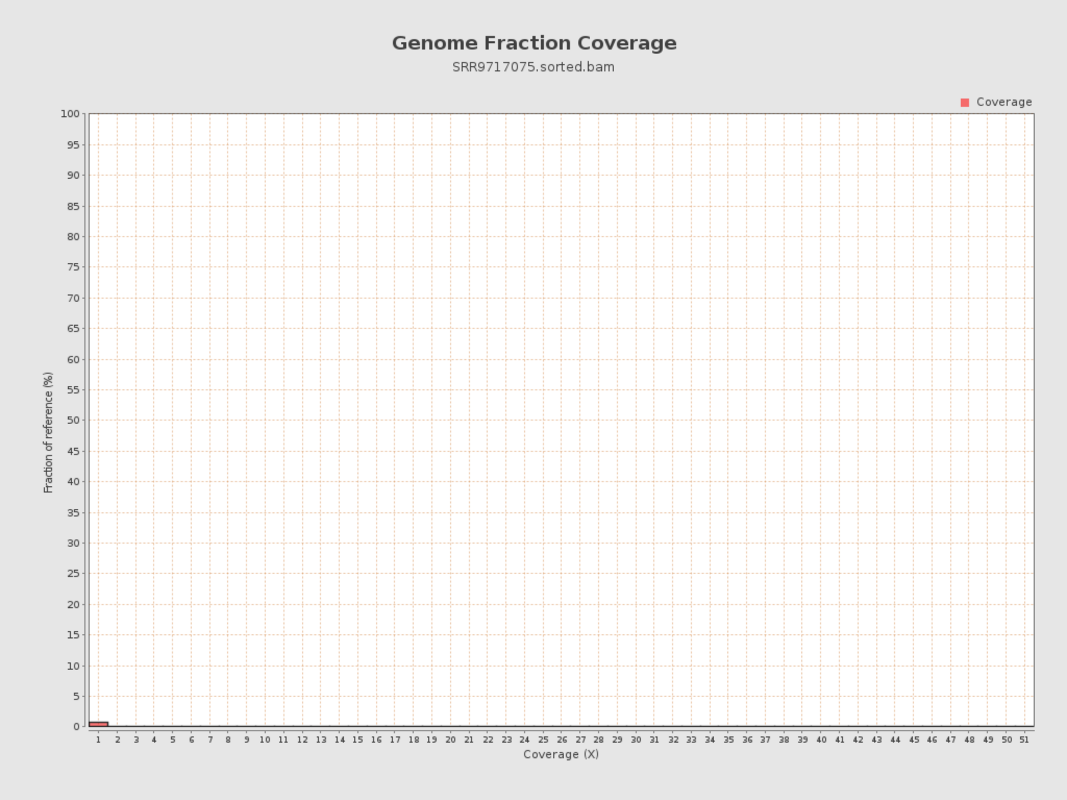
4. Results : Coverage Histogram



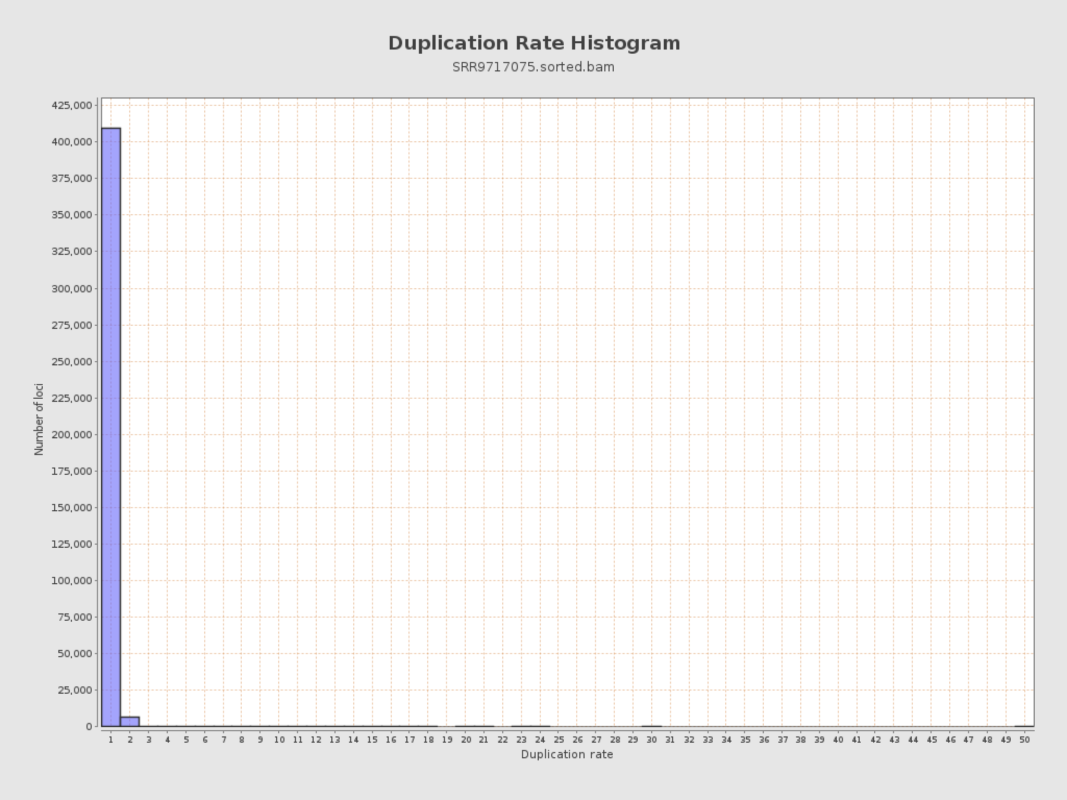
5. Results : Coverage Histogram (0-50X)



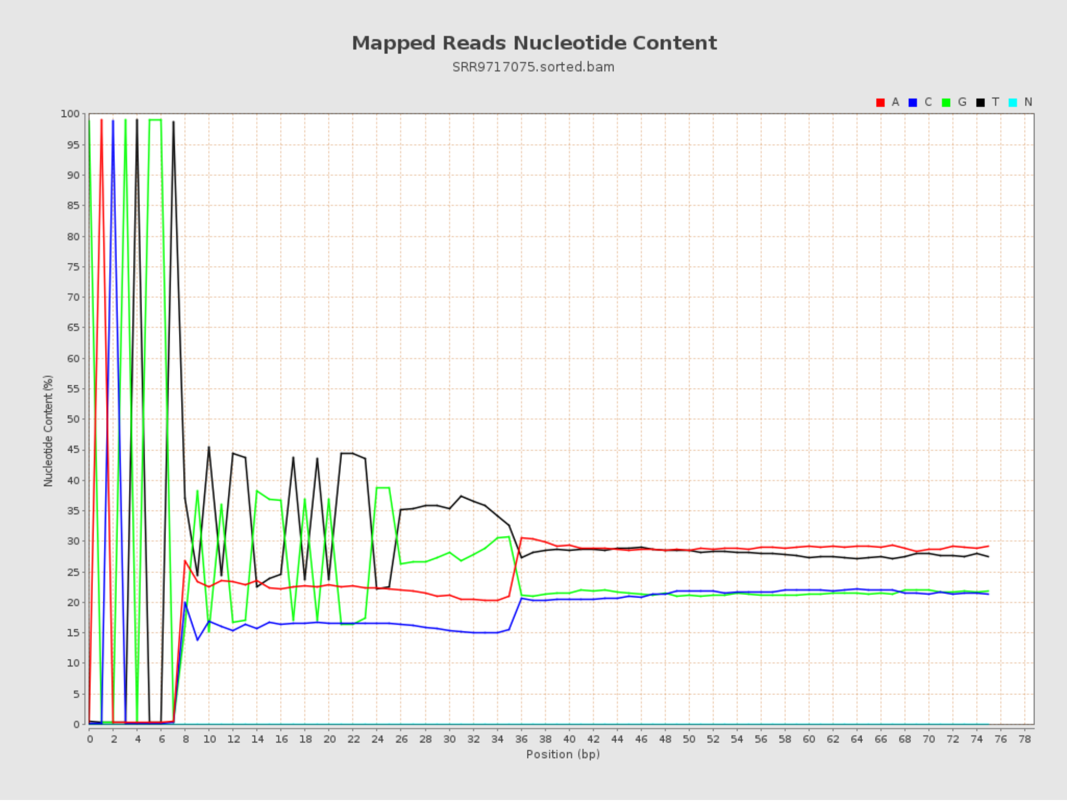
6. Results : Genome Fraction Coverage



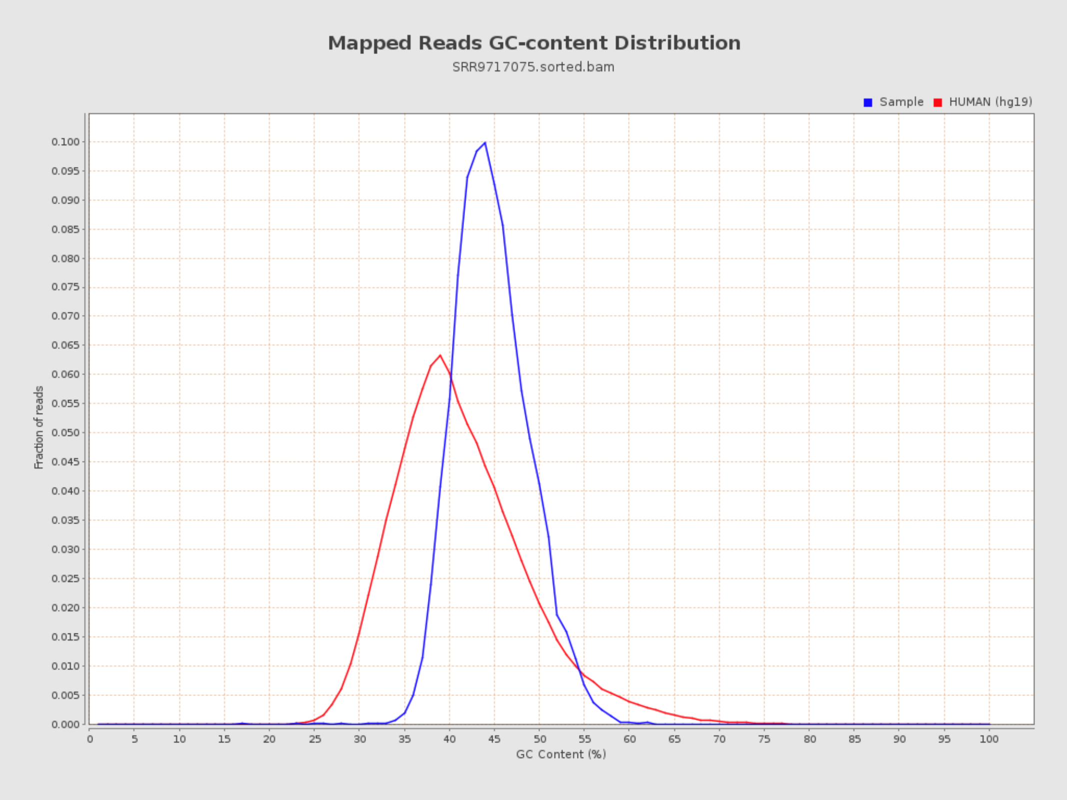
7. Results : Duplication Rate Histogram



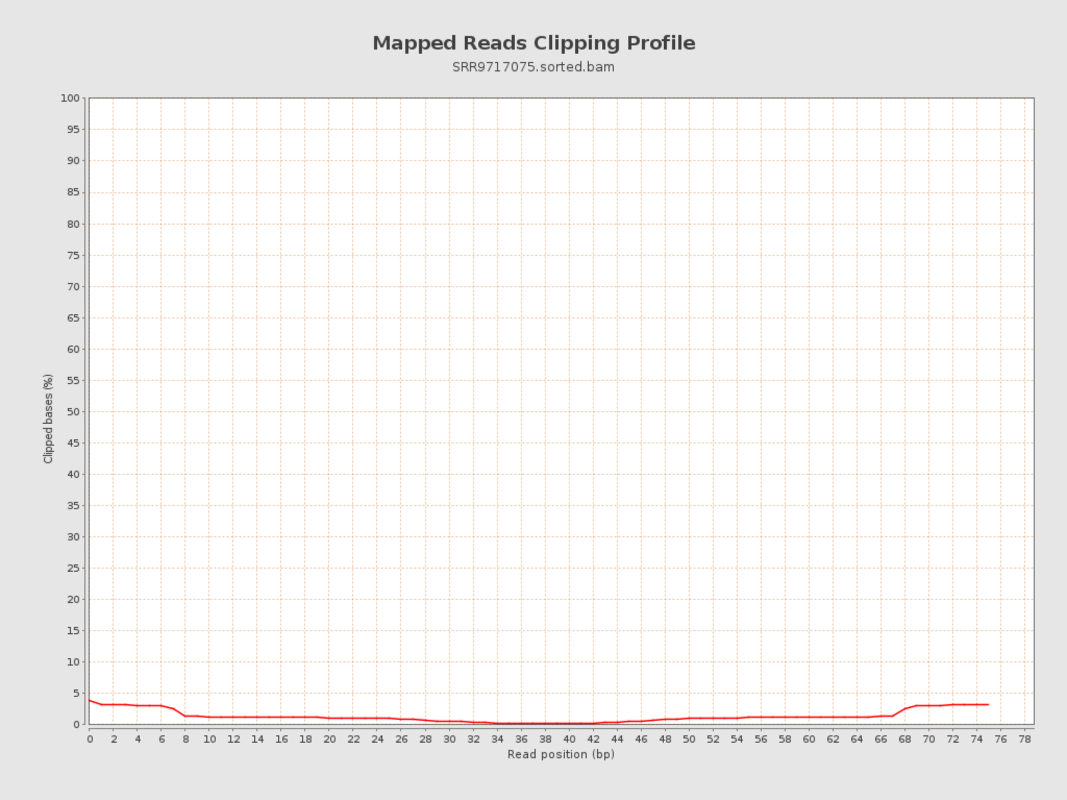
8. Results : Mapped Reads Nucleotide Content



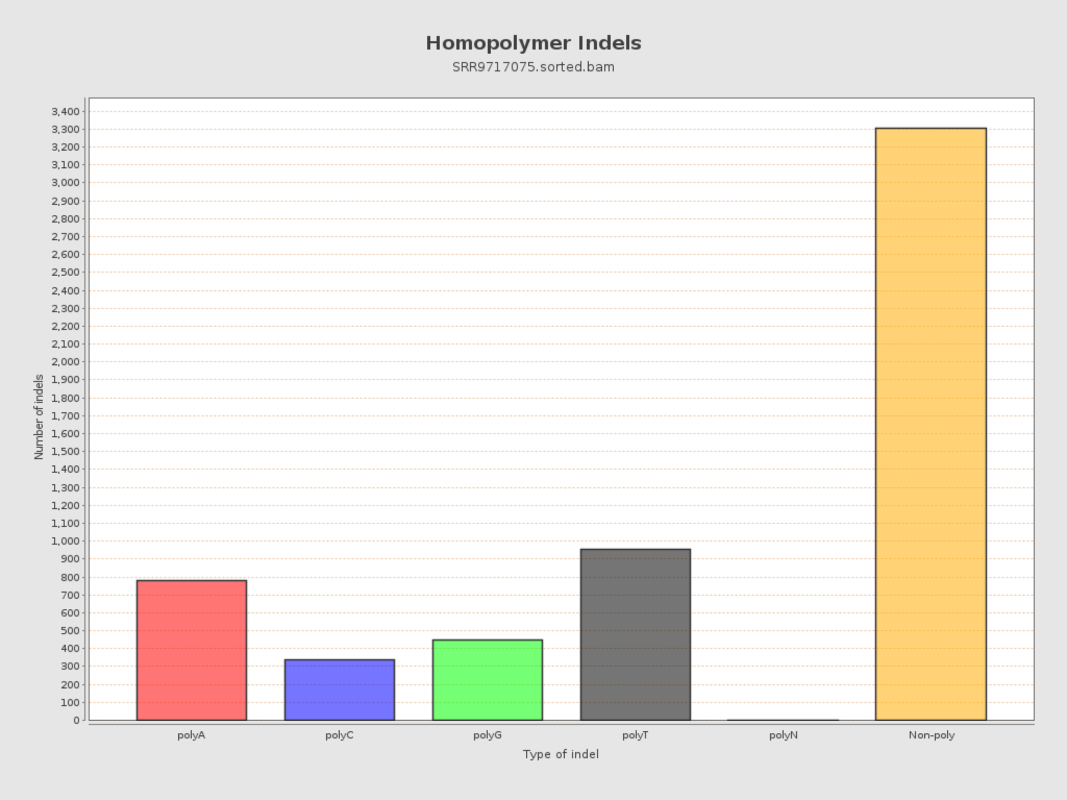
9. Results : Mapped Reads GC-content Distribution



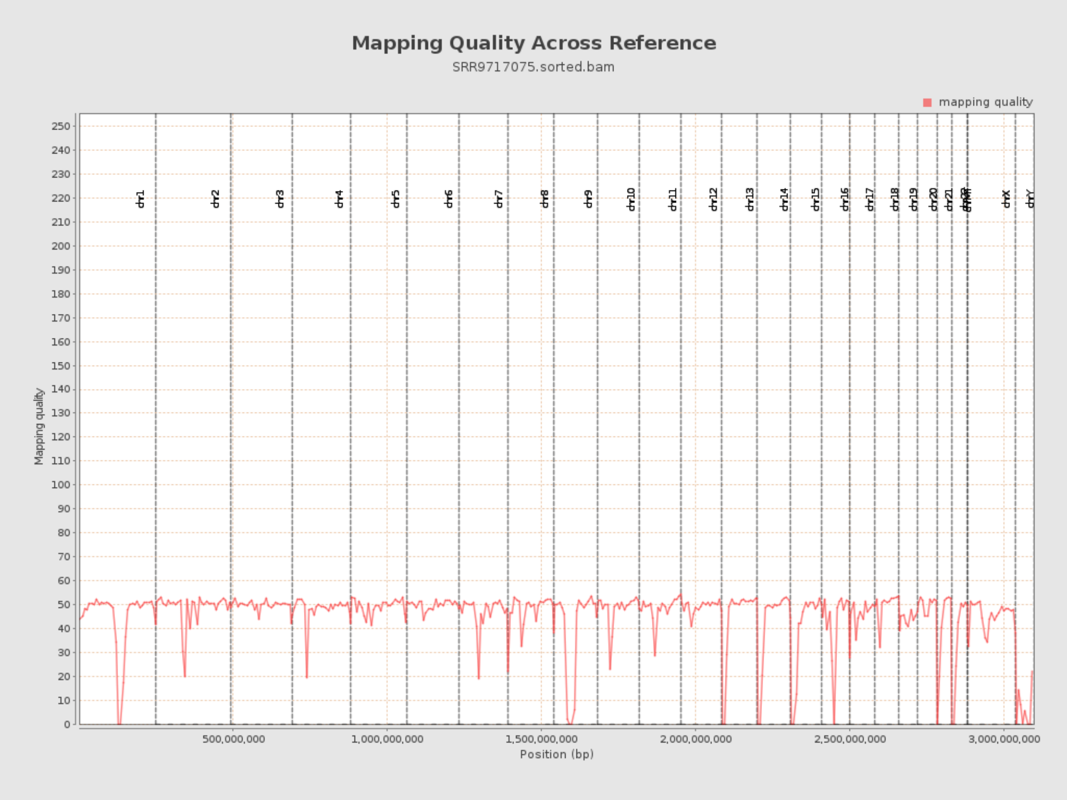
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram