Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:13:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717065.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_SRR9717065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:13:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,180,355
Mapped reads	1,071,505 / 90.78%
Unmapped reads	108,850 / 9.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,710 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	26,619 / 2.26%
Duplication rate	1.75%
Clipped reads	1,073,601 / 90.96%

2.2. ACGT Content

Number/percentage of A's	16,063,725 / 25.69%
Number/percentage of C's	11,545,027 / 18.46%
Number/percentage of T's	19,264,966 / 30.8%
Number/percentage of G's	15,664,412 / 25.05%
Number/percentage of N's	748 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.2049

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Mismatches and indels

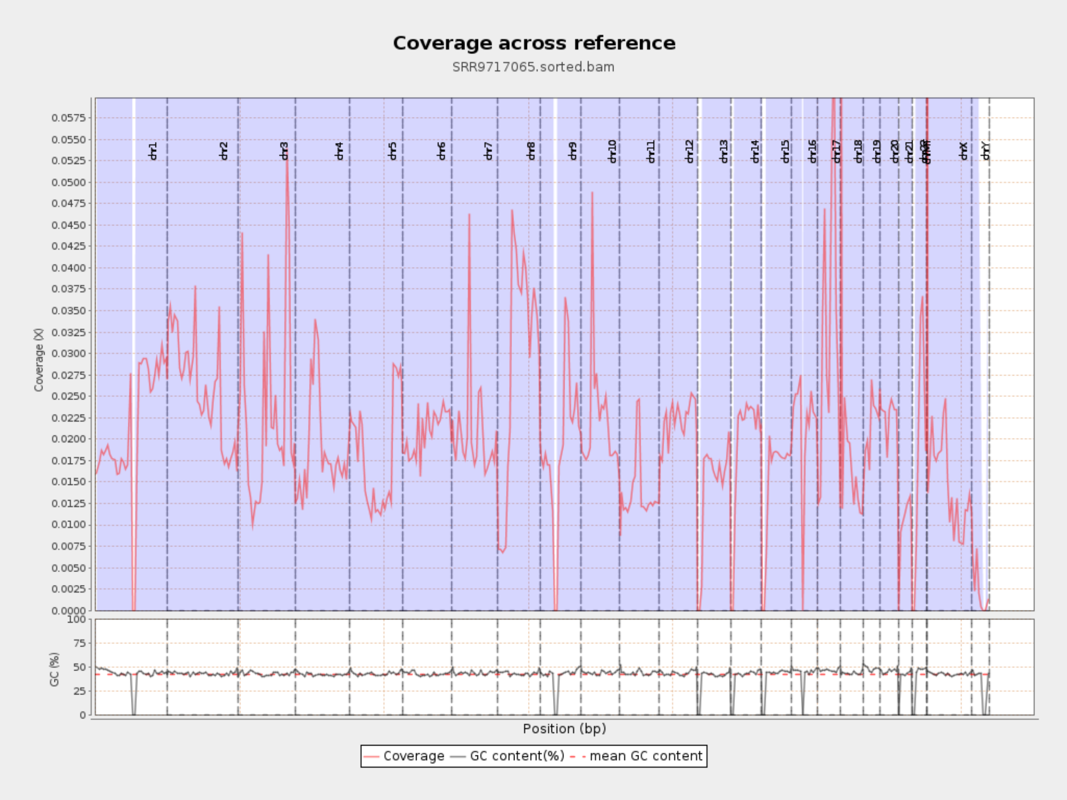
General error rate	0.5%
Mismatches	305,193
Insertions	5,078
Mapped reads with at least one insertion	0.47%
Deletions	11,533
Mapped reads with at least one deletion	1.07%
Homopolymer indels	39.09%

2.6. Chromosome stats

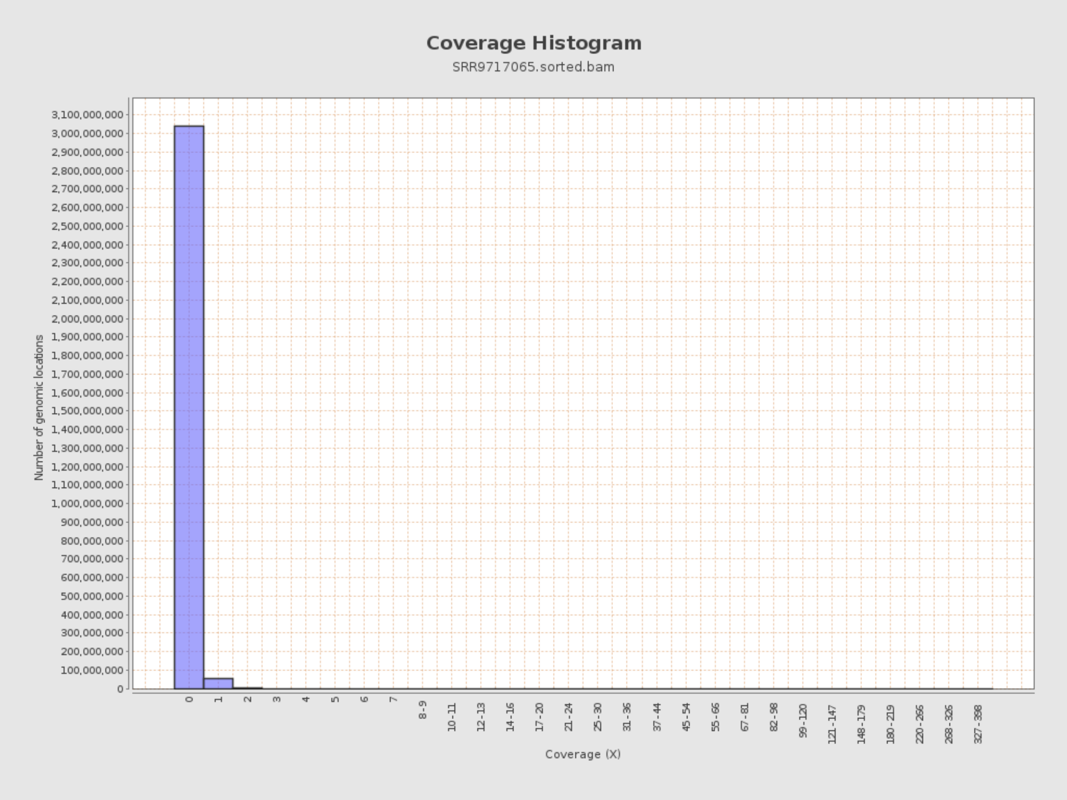
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5279473	0.0212	0.2864
chr2	243199373	6322513	0.026	0.2458
chr3	198022430	4567580	0.0231	0.1653
chr4	191154276	3570267	0.0187	0.1522
chr5	180915260	3190210	0.0176	0.1404
chr6	171115067	3573024	0.0209	0.161
chr7	159138663	3327900	0.0209	0.3828

chr8	146364022	4302152	0.0294	0.2236
chr9	141213431	2665460	0.0189	0.1625
chr10	135534747	3024209	0.0223	0.2563
chr11	135006516	1891398	0.014	0.1462
chr12	133851895	2973286	0.0222	0.1659
chr13	115169878	1647092	0.0143	0.1258
chr14	107349540	2063254	0.0192	0.148
chr15	102531392	1524086	0.0149	0.1307
chr16	90354753	1925441	0.0213	0.1603
chr17	81195210	2678774	0.033	0.1974
chr18	78077248	1419055	0.0182	0.2446
chr19	59128983	1268883	0.0215	0.2551
chr20	63025520	1422930	0.0226	0.163
chr21	48129895	488782	0.0102	0.1128
chr22	51304566	955303	0.0186	0.1445
chrMT	16571	57278	3.4565	2.6588
chrX	155270560	2282960	0.0147	0.1439
chrY	59373566	135615	0.0023	0.0657

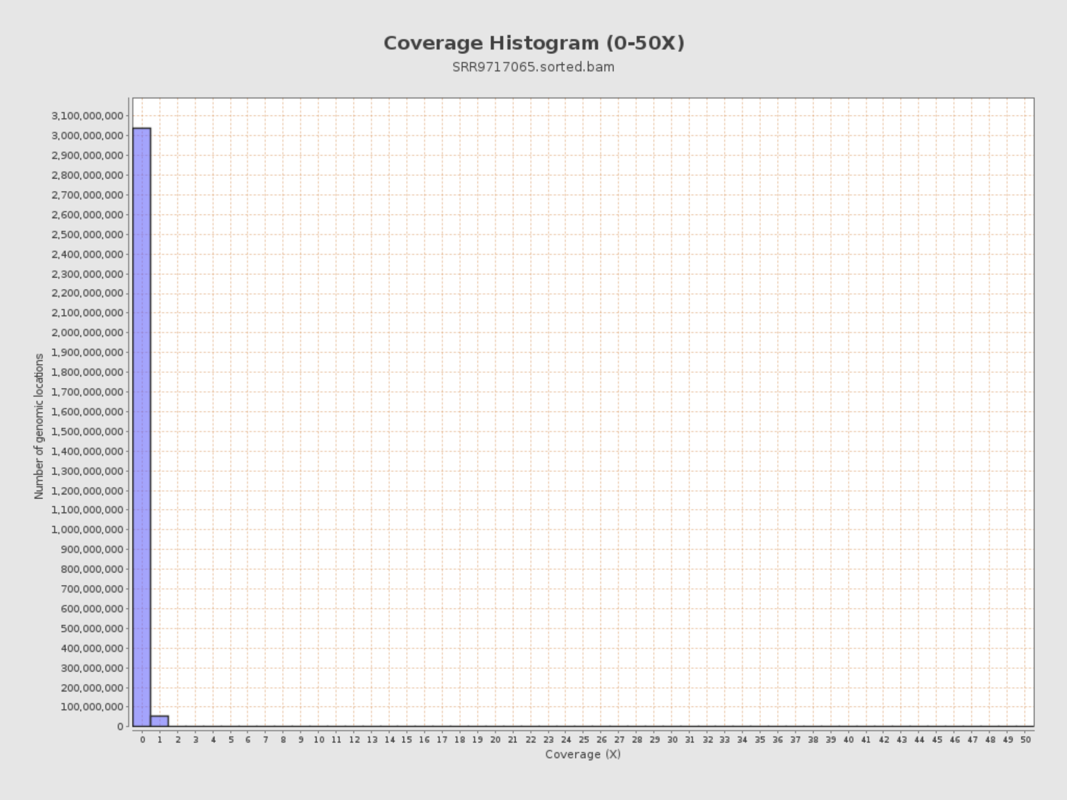
3. Results : Coverage across reference



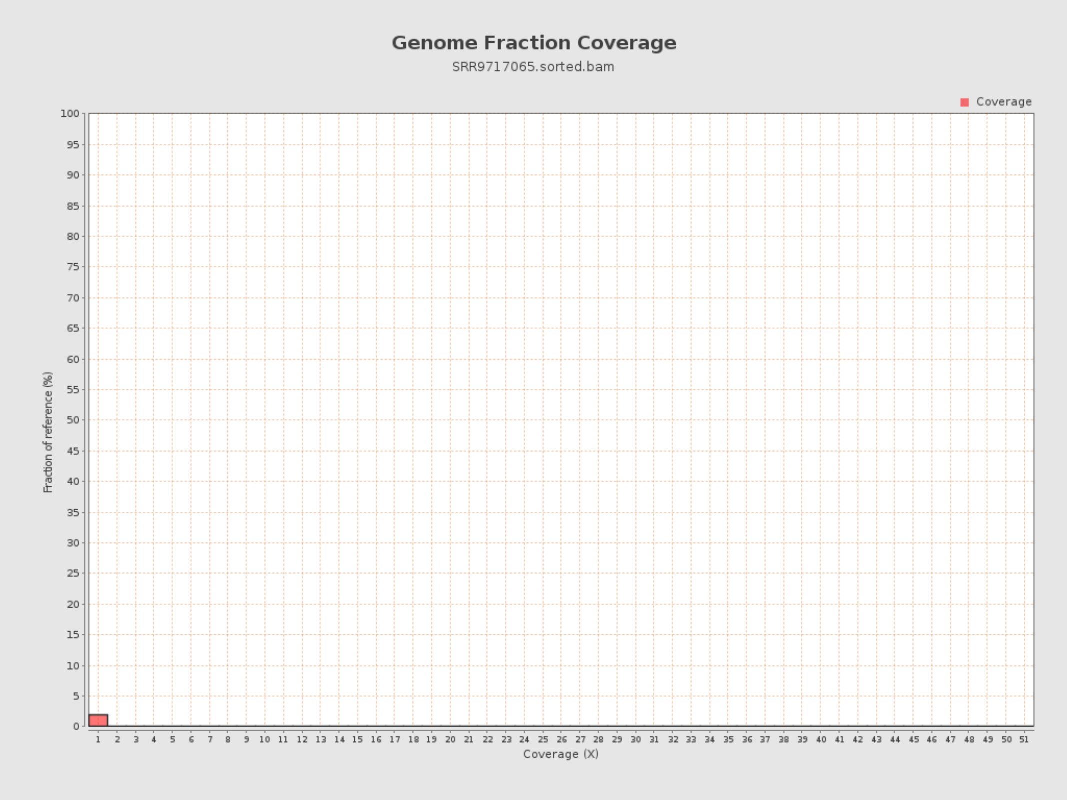
4. Results : Coverage Histogram



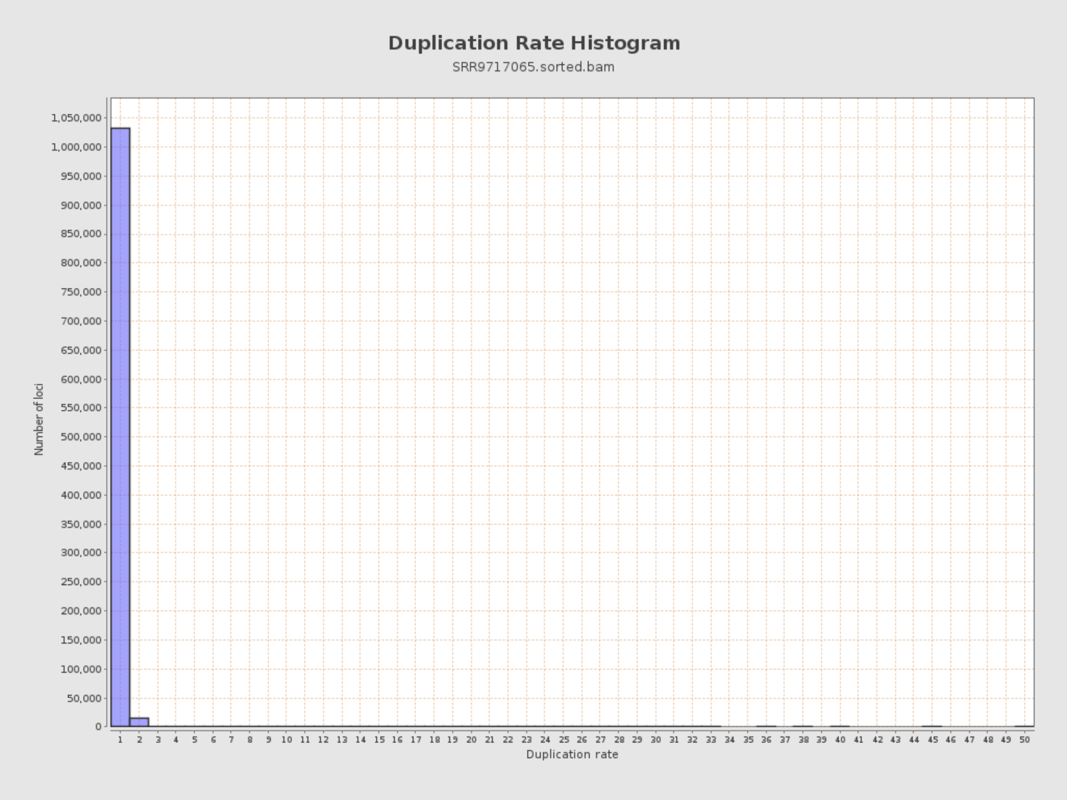
5. Results : Coverage Histogram (0-50X)



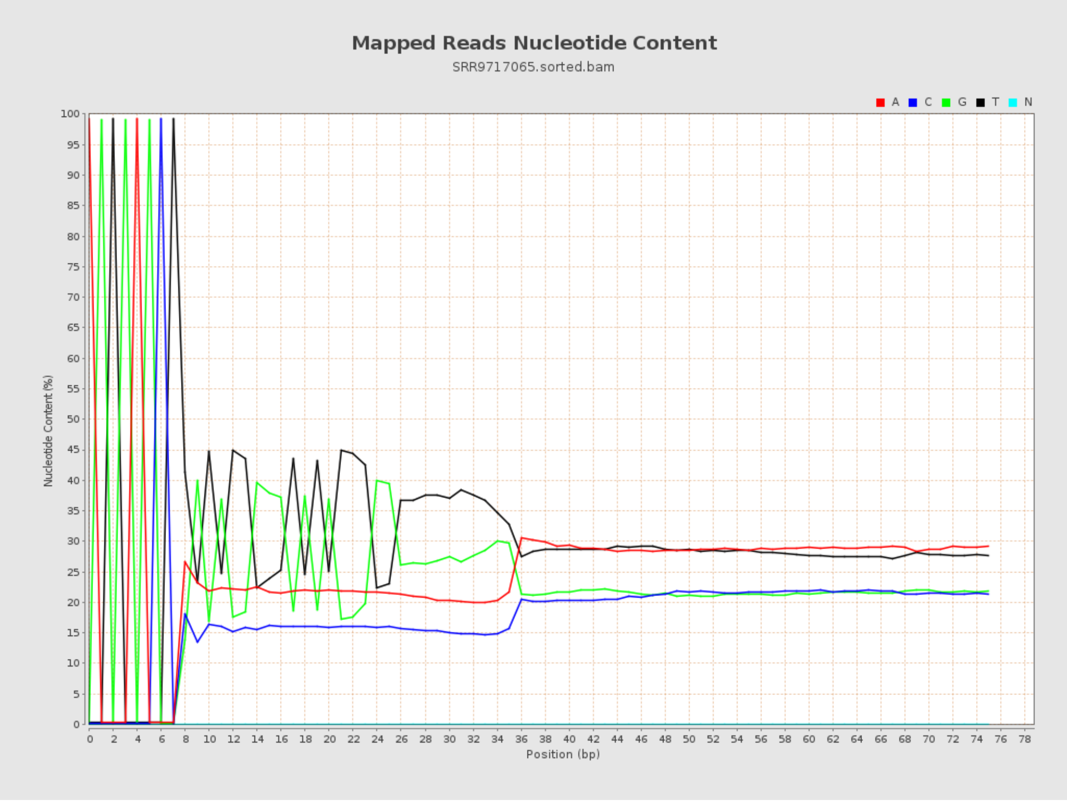
6. Results : Genome Fraction Coverage



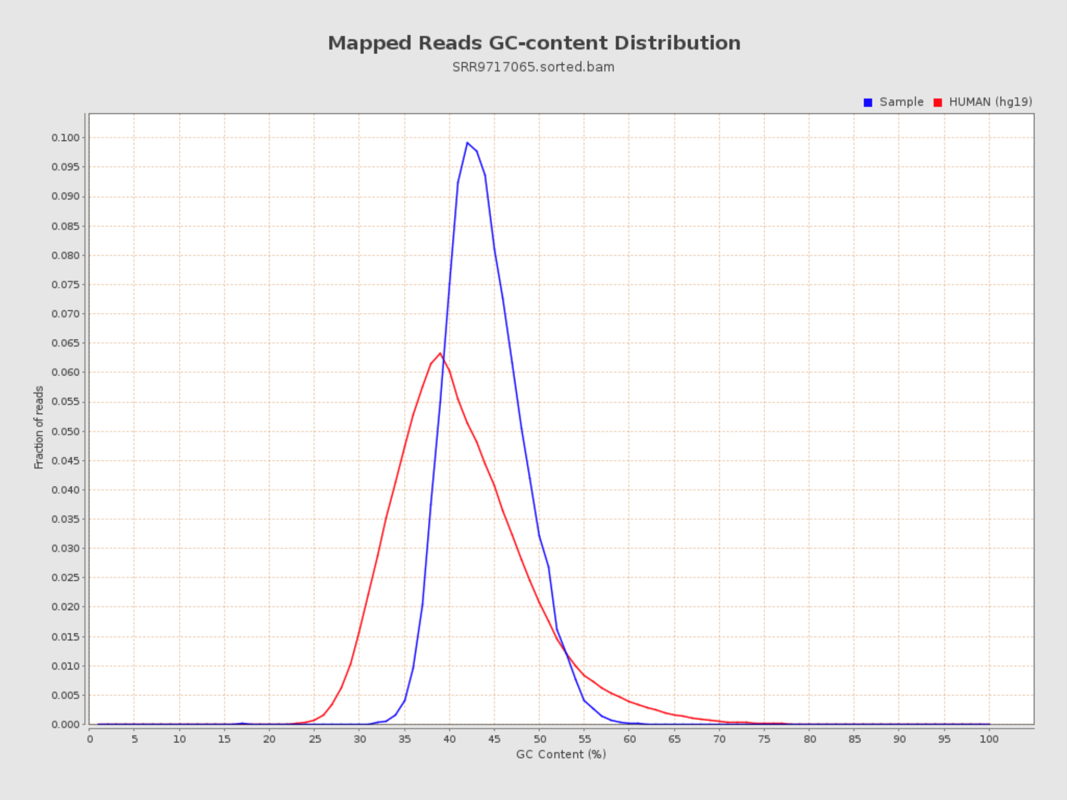
7. Results : Duplication Rate Histogram



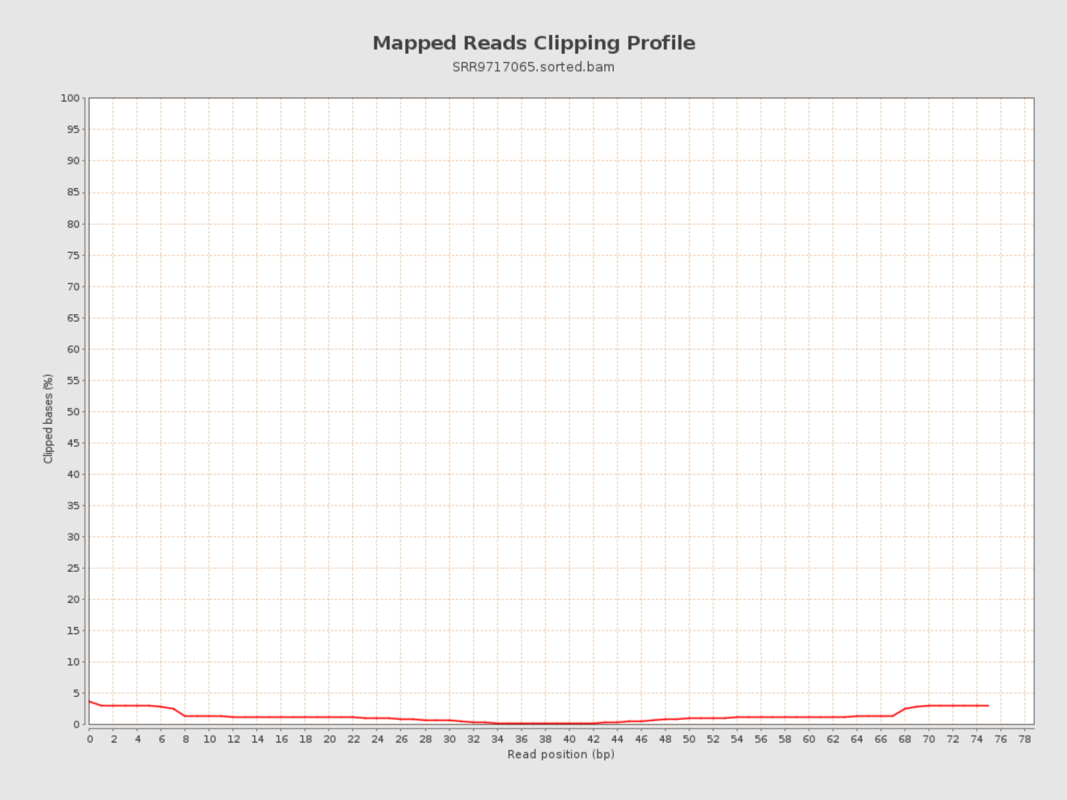
8. Results : Mapped Reads Nucleotide Content



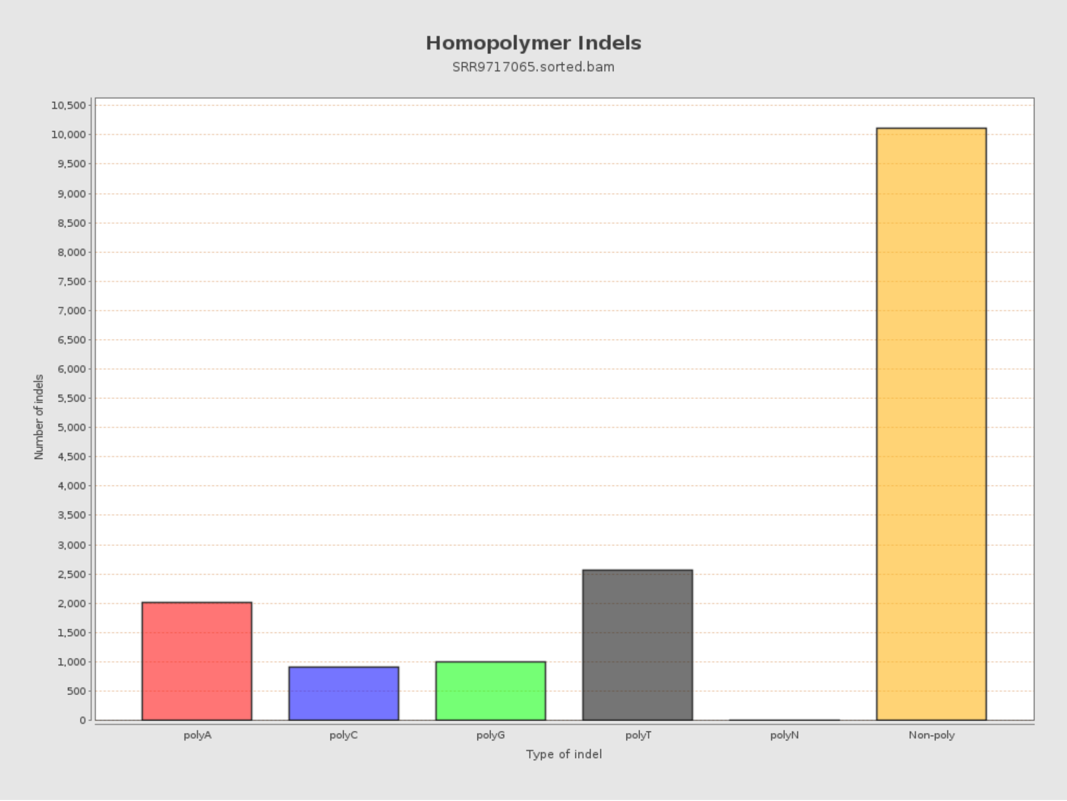
9. Results : Mapped Reads GC-content Distribution



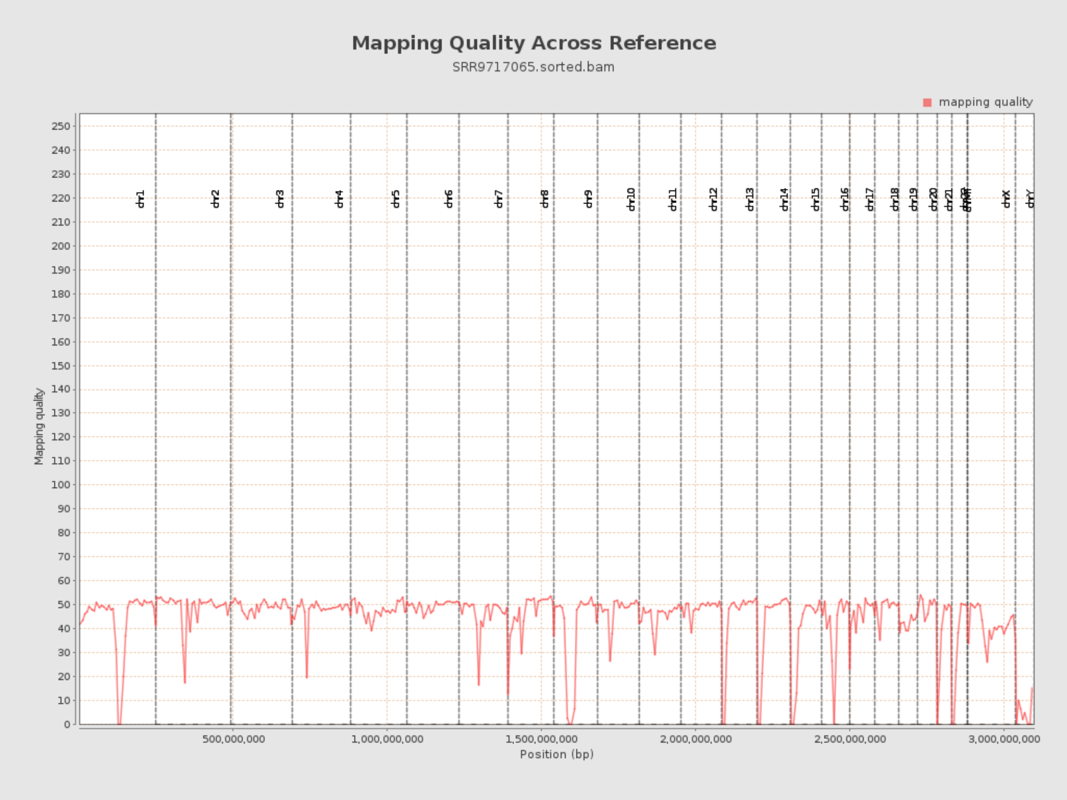
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram