Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:38:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716739.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_SRR9716739 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716739.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:38:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716739.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	874,990
Mapped reads	808,768 / 92.43%
Unmapped reads	66,222 / 7.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,338 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	19,927 / 2.28%
Duplication rate	1.77%
Clipped reads	811,225 / 92.71%

2.2. ACGT Content

Number/percentage of A's	11,759,165 / 24.84%
Number/percentage of C's	9,515,804 / 20.1%
Number/percentage of T's	14,565,416 / 30.77%
Number/percentage of G's	11,494,567 / 24.28%
Number/percentage of N's	637 / 0%
GC Percentage	44.39%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1725

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

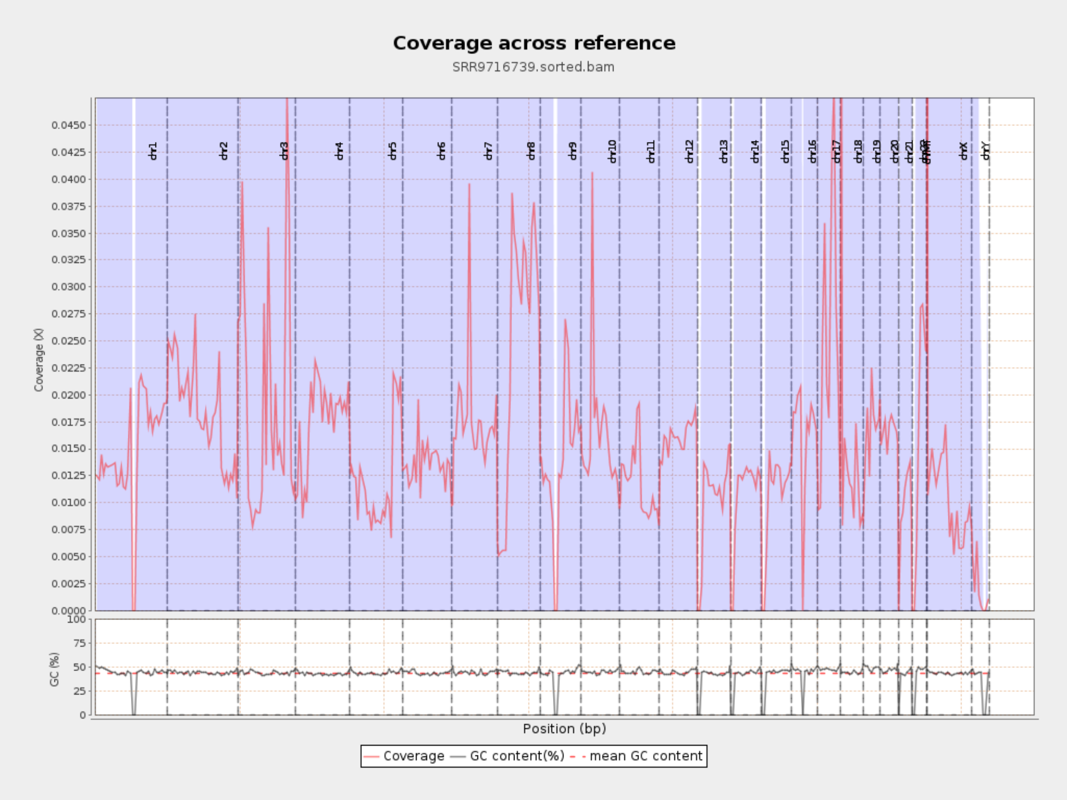
General error rate	0.5%
Mismatches	232,863
Insertions	3,168
Mapped reads with at least one insertion	0.39%
Deletions	8,629
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.37%

2.6. Chromosome stats

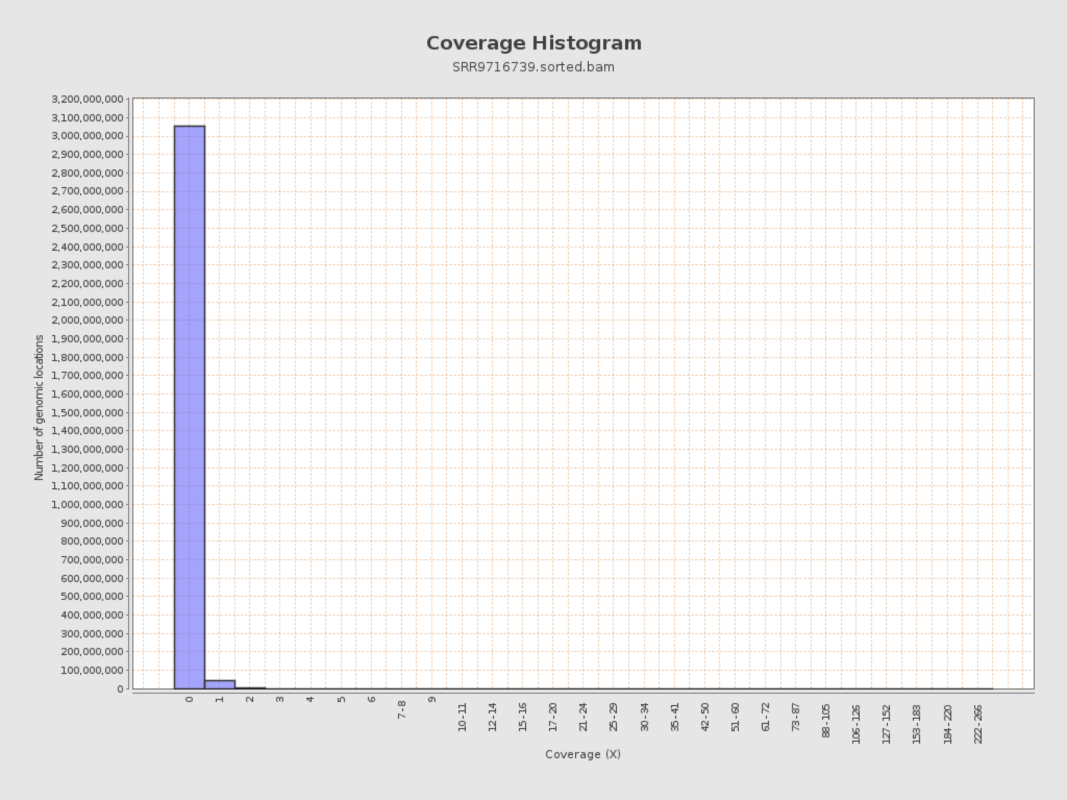
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3675928	0.0147	0.2236
chr2	243199373	4503370	0.0185	0.1904
chr3	198022430	3807751	0.0192	0.1501
chr4	191154276	3359997	0.0176	0.1463
chr5	180915260	2162603	0.012	0.1142
chr6	171115067	2336819	0.0137	0.1295
chr7	159138663	2841710	0.0179	0.3402

chr8	146364022	3684012	0.0252	0.2068
chr9	141213431	1927380	0.0136	0.1338
chr10	135534747	2217703	0.0164	0.2213
chr11	135006516	1624443	0.012	0.1303
chr12	133851895	2151621	0.0161	0.1426
chr13	115169878	1161684	0.0101	0.1057
chr14	107349540	1139804	0.0106	0.1096
chr15	102531392	1055608	0.0103	0.1065
chr16	90354753	1441961	0.016	0.1368
chr17	81195210	2045296	0.0252	0.1694
chr18	78077248	1093437	0.014	0.1783
chr19	59128983	999434	0.0169	0.2163
chr20	63025520	1048014	0.0166	0.1381
chr21	48129895	475714	0.0099	0.1098
chr22	51304566	837771	0.0163	0.1344
chrMT	16571	30184	1.8215	1.6986
chrX	155270560	1615378	0.0104	0.1147
chrY	59373566	111615	0.0019	0.0635

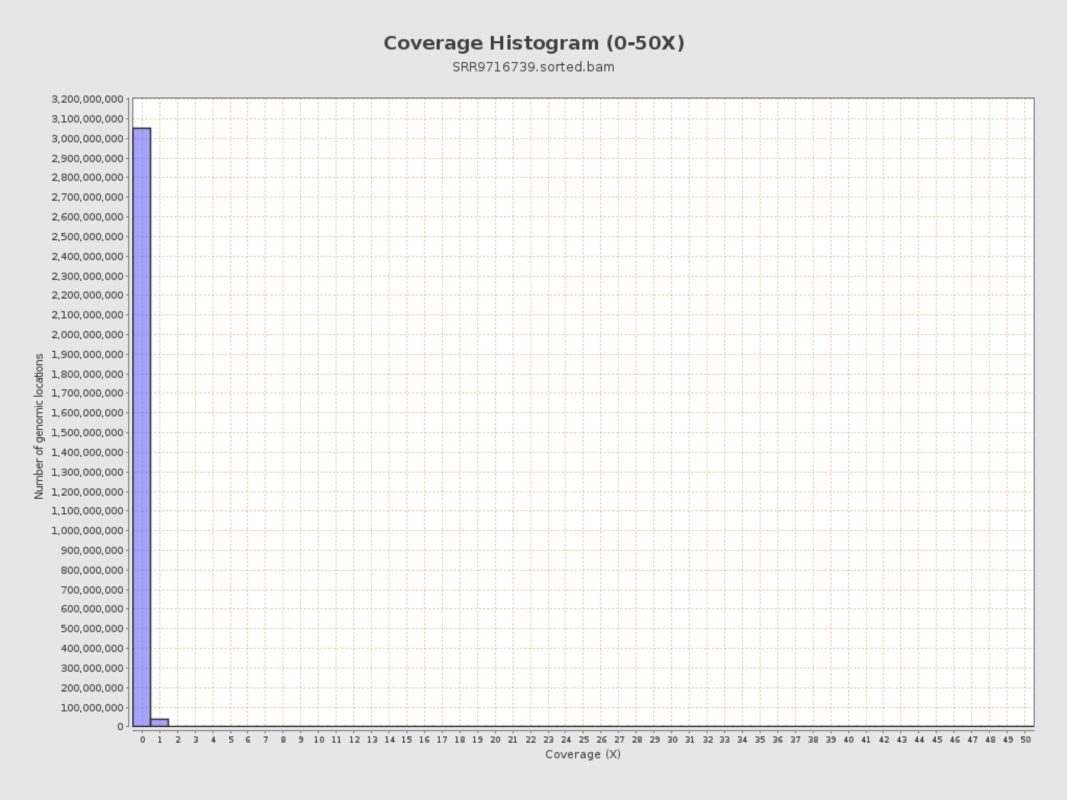
3. Results : Coverage across reference



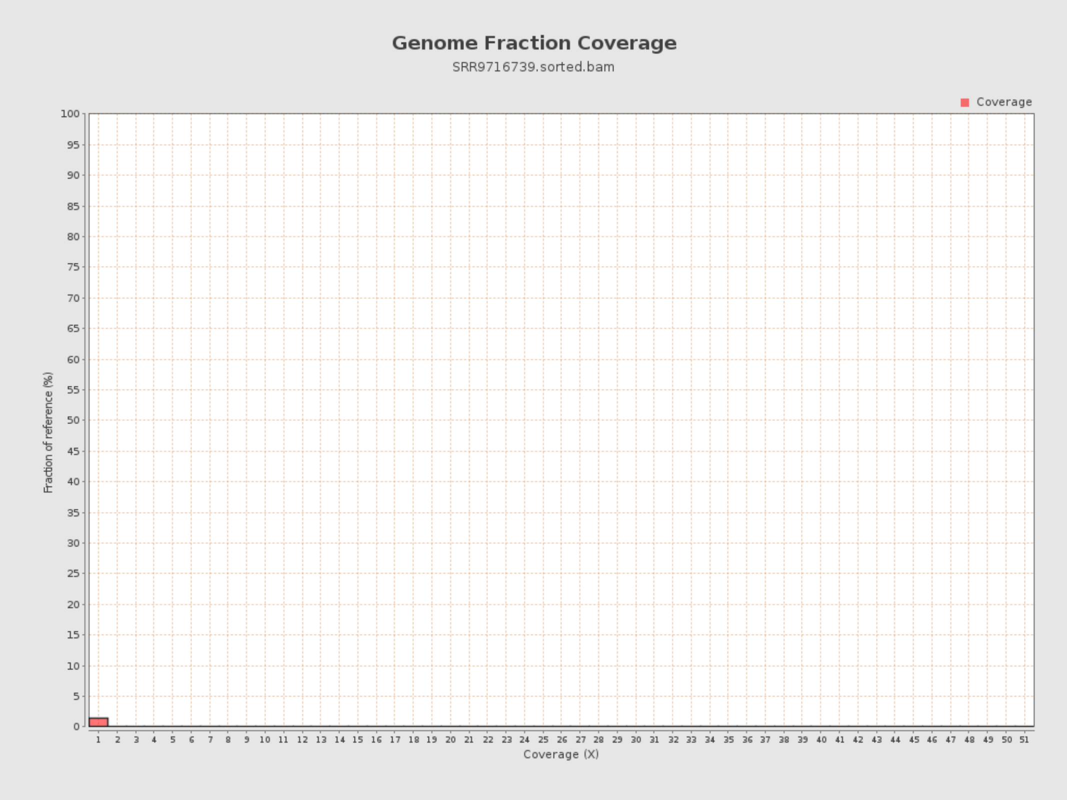
4. Results : Coverage Histogram



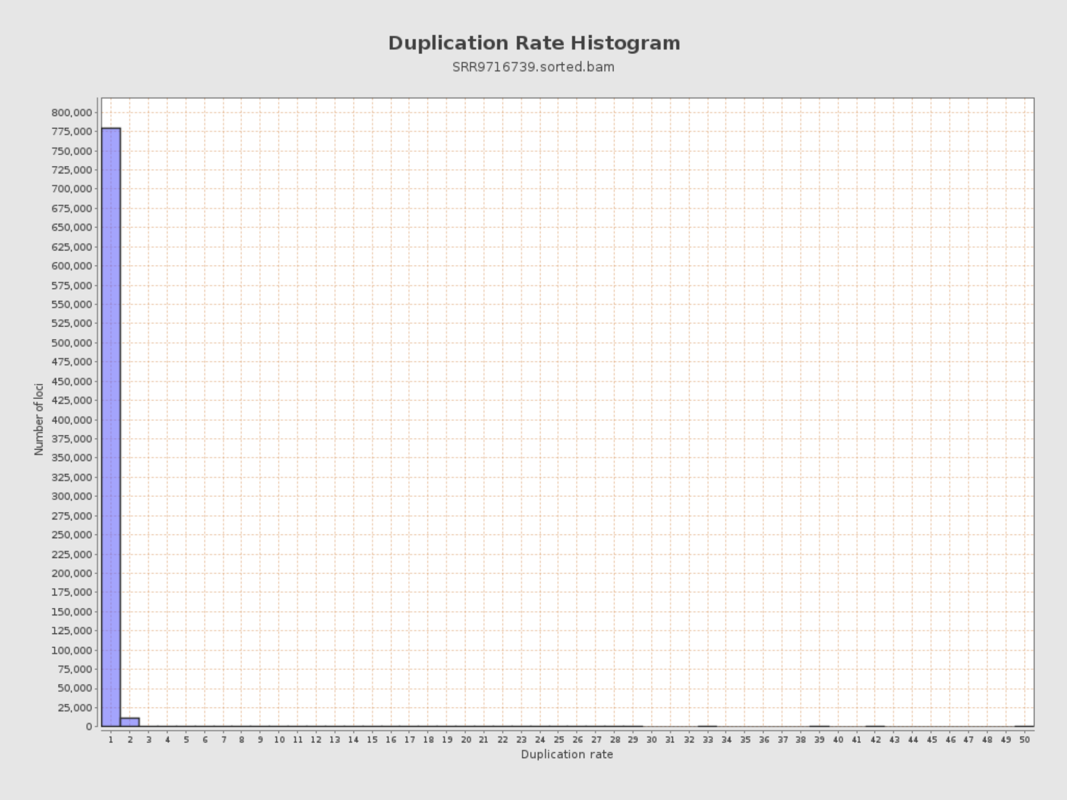
5. Results : Coverage Histogram (0-50X)



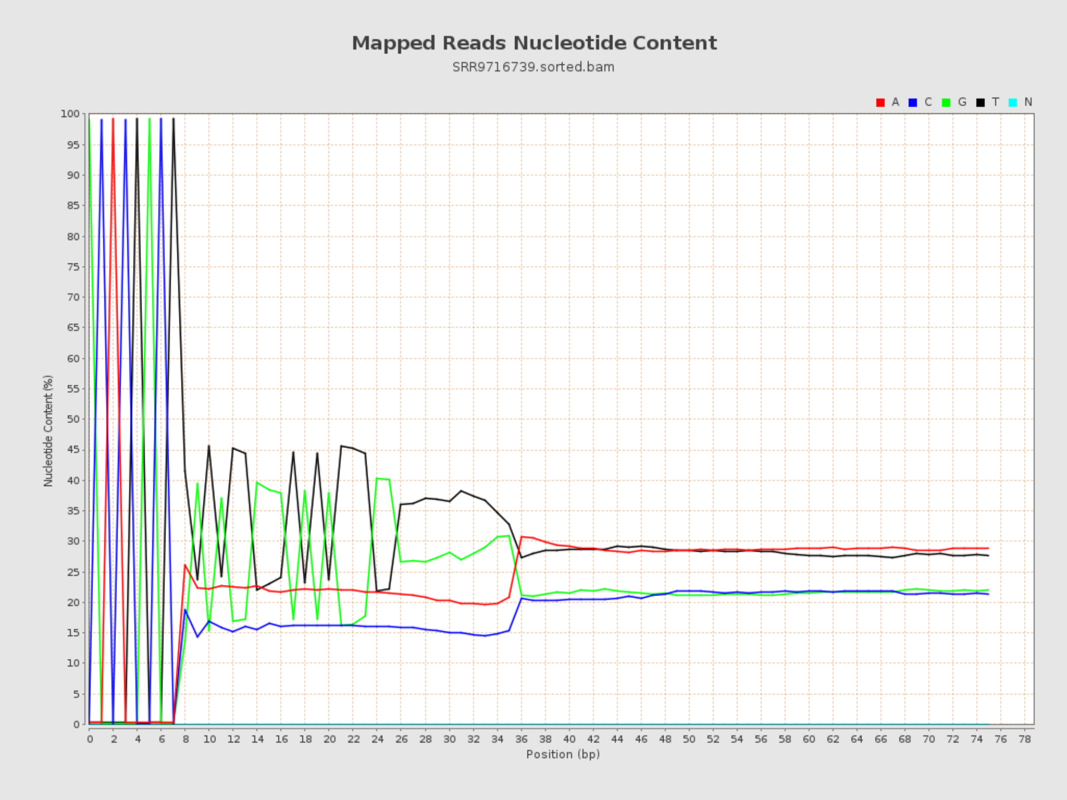
6. Results : Genome Fraction Coverage



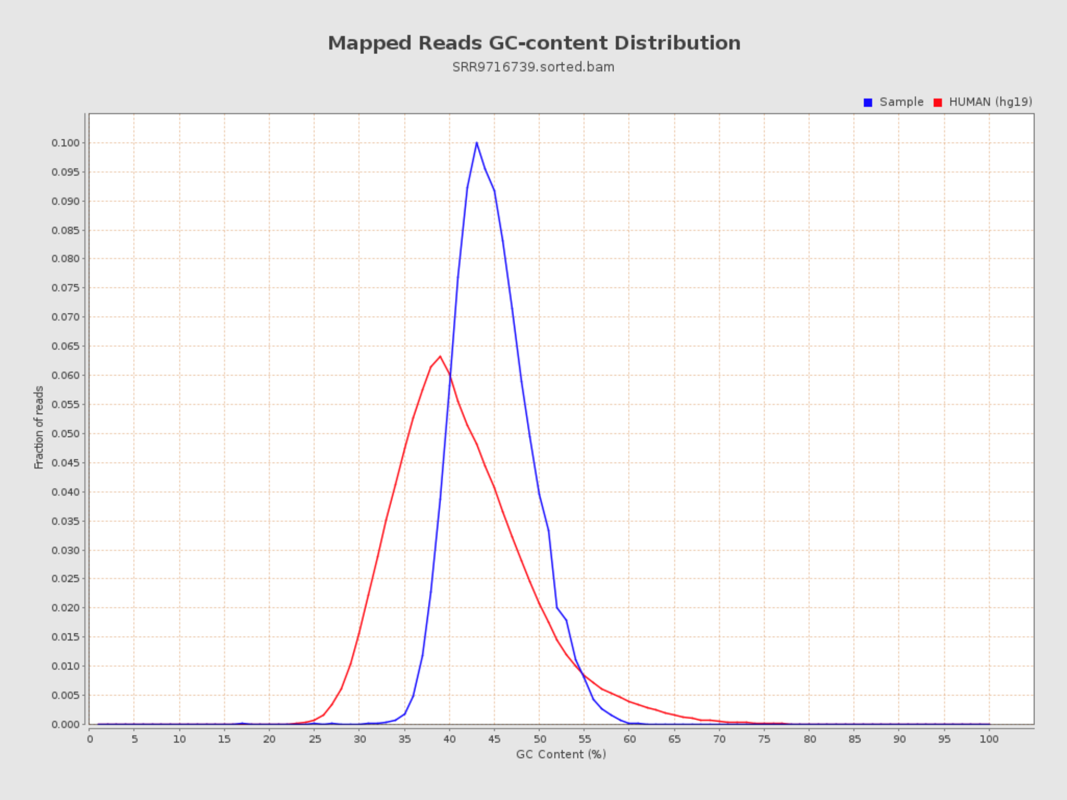
7. Results : Duplication Rate Histogram



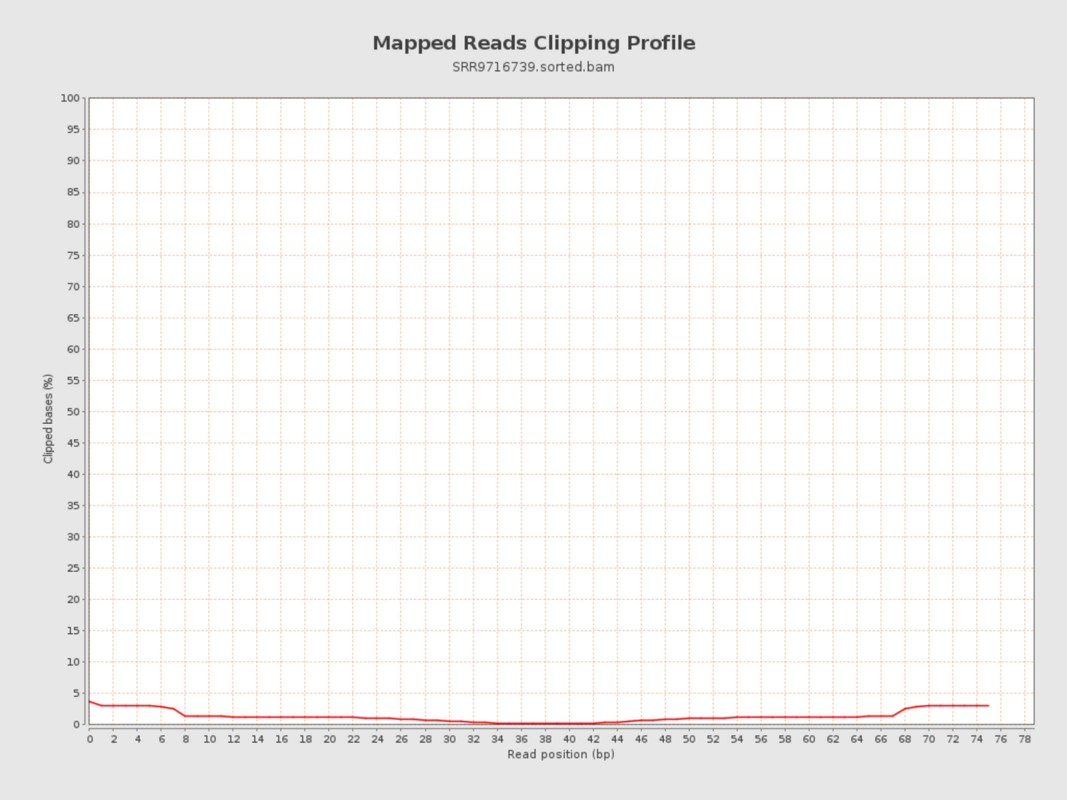
8. Results : Mapped Reads Nucleotide Content



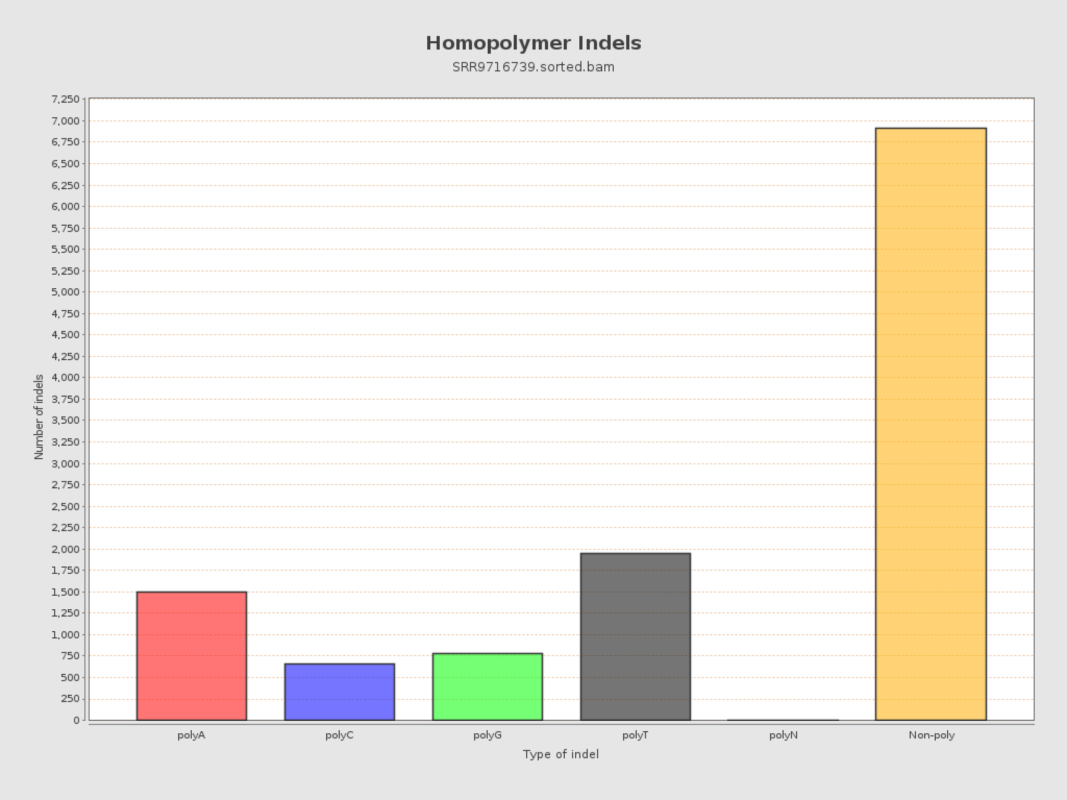
9. Results : Mapped Reads GC-content Distribution



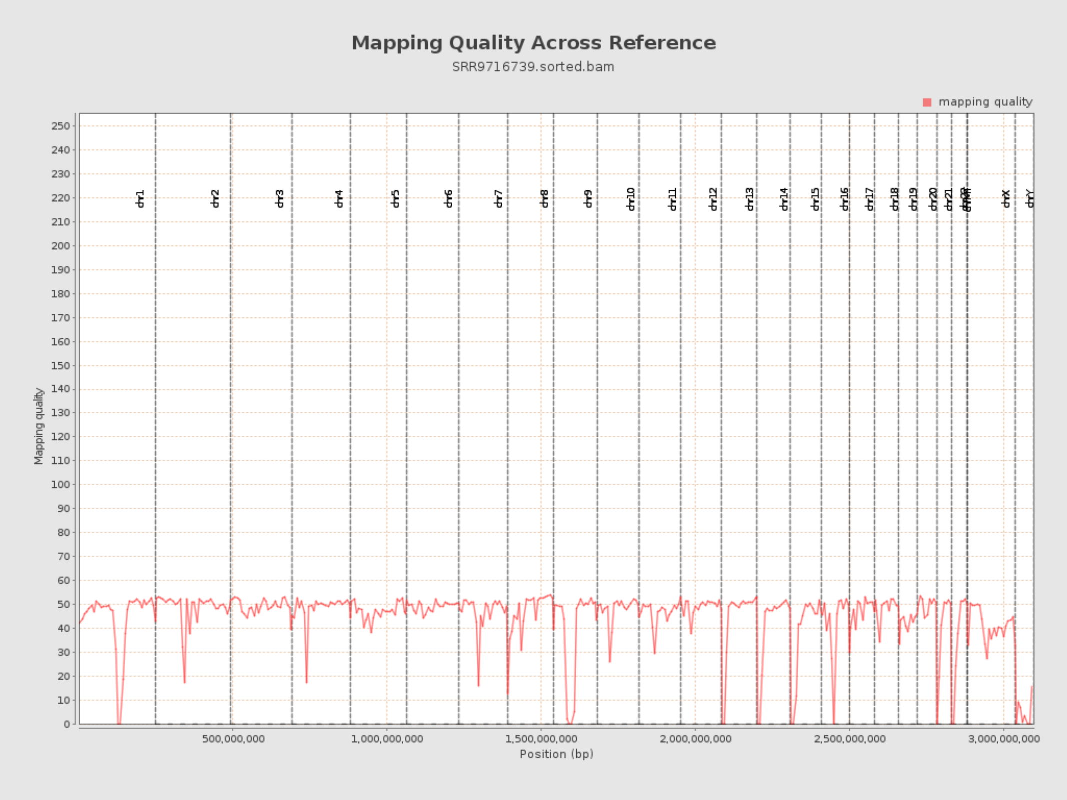
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram