Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:40:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716117.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_SRR9716117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:40:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	826,281
Mapped reads	649,227 / 78.57%
Unmapped reads	177,054 / 21.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,097 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	12,168 / 1.47%
Duplication rate	1.42%
Clipped reads	649,860 / 78.65%

2.2. ACGT Content

Number/percentage of A's	9,227,556 / 25.12%
Number/percentage of C's	6,951,834 / 18.93%
Number/percentage of T's	11,749,551 / 31.99%
Number/percentage of G's	8,800,879 / 23.96%
Number/percentage of N's	618 / 0%
GC Percentage	42.89%

2.3. Coverage

Mean	0.0119

Standard Deviation	0.132

2.4. Mapping Quality

Mean Mapping Quality	43.39

2.5. Mismatches and indels

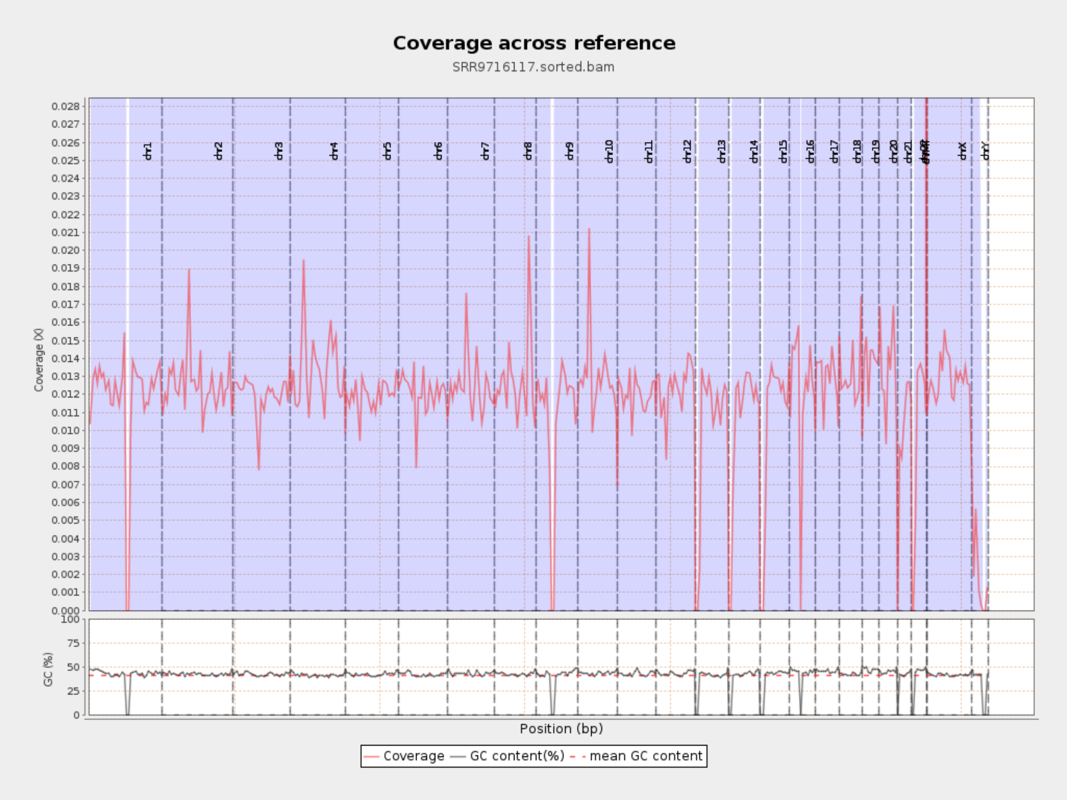
General error rate	0.54%
Mismatches	191,538
Insertions	2,772
Mapped reads with at least one insertion	0.42%
Deletions	7,155
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.14%

2.6. Chromosome stats

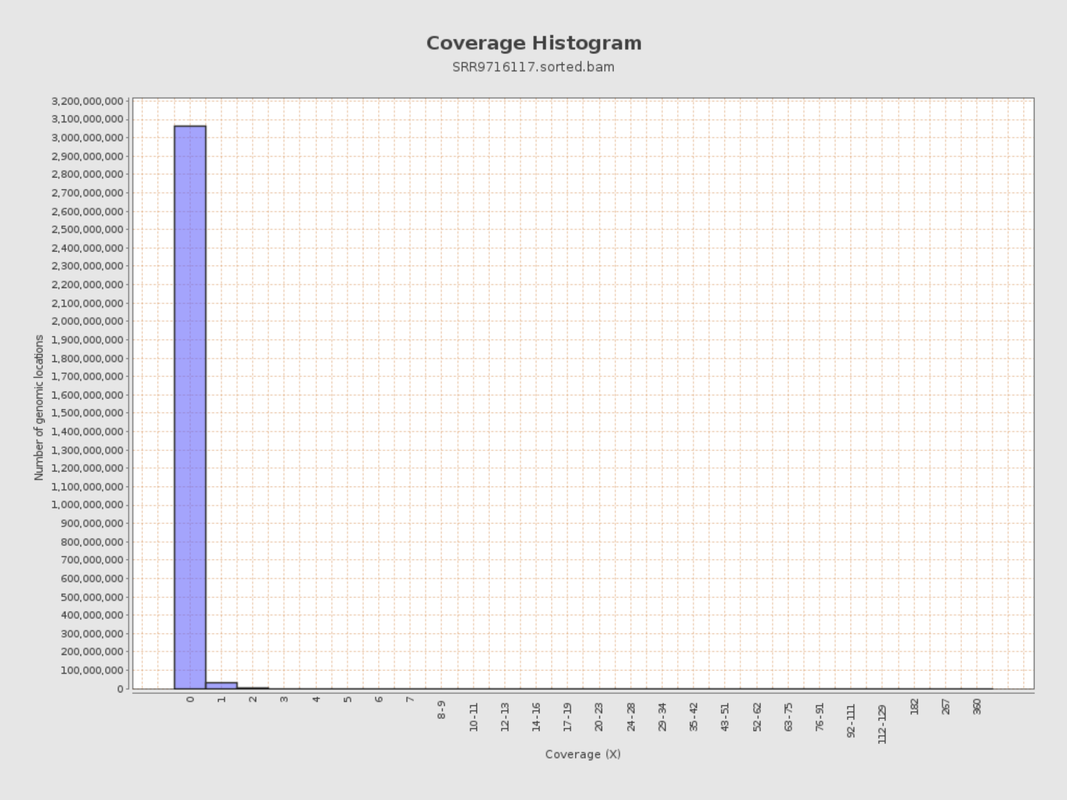
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2935702	0.0118	0.1548
chr2	243199373	3072889	0.0126	0.1899
chr3	198022430	2370371	0.012	0.1137
chr4	191154276	2551776	0.0133	0.126
chr5	180915260	2162014	0.012	0.1141
chr6	171115067	2069843	0.0121	0.1214
chr7	159138663	1986501	0.0125	0.1558

chr8	146364022	1875698	0.0128	0.128
chr9	141213431	1492465	0.0106	0.1154
chr10	135534747	1759480	0.013	0.1389
chr11	135006516	1610329	0.0119	0.1259
chr12	133851895	1654652	0.0124	0.116
chr13	115169878	1144507	0.0099	0.1045
chr14	107349540	1104203	0.0103	0.1067
chr15	102531392	1048385	0.0102	0.1065
chr16	90354753	1103602	0.0122	0.12
chr17	81195210	1048709	0.0129	0.1211
chr18	78077248	1014185	0.013	0.1509
chr19	59128983	811034	0.0137	0.1496
chr20	63025520	836235	0.0133	0.1211
chr21	48129895	470302	0.0098	0.1073
chr22	51304566	466499	0.0091	0.0998
chrMT	16571	44366	2.6773	2.2102
chrX	155270560	1998861	0.0129	0.1231
chrY	59373566	109094	0.0018	0.0581

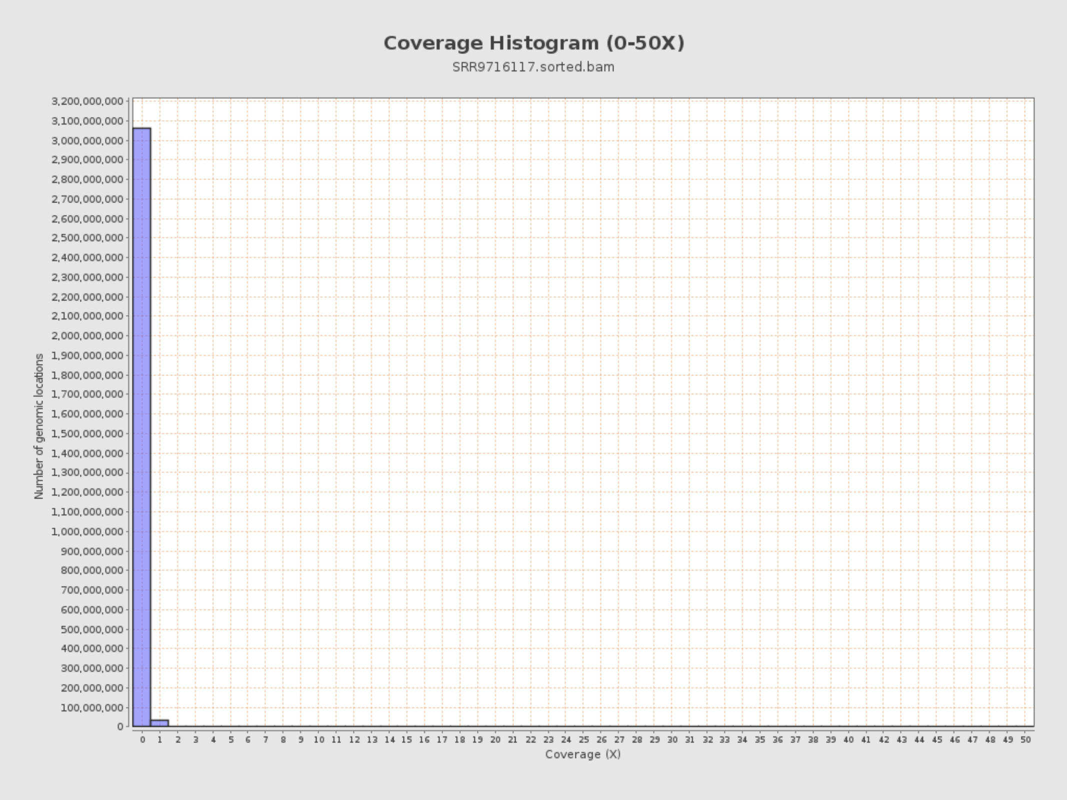
3. Results : Coverage across reference



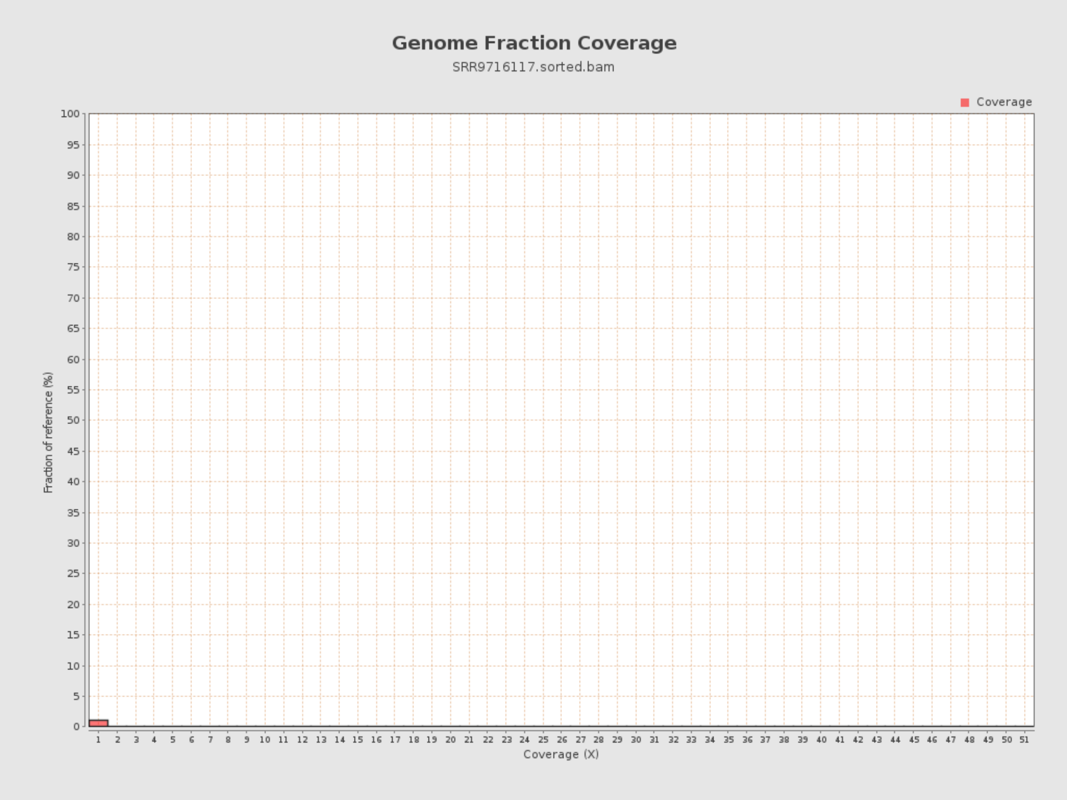
4. Results : Coverage Histogram



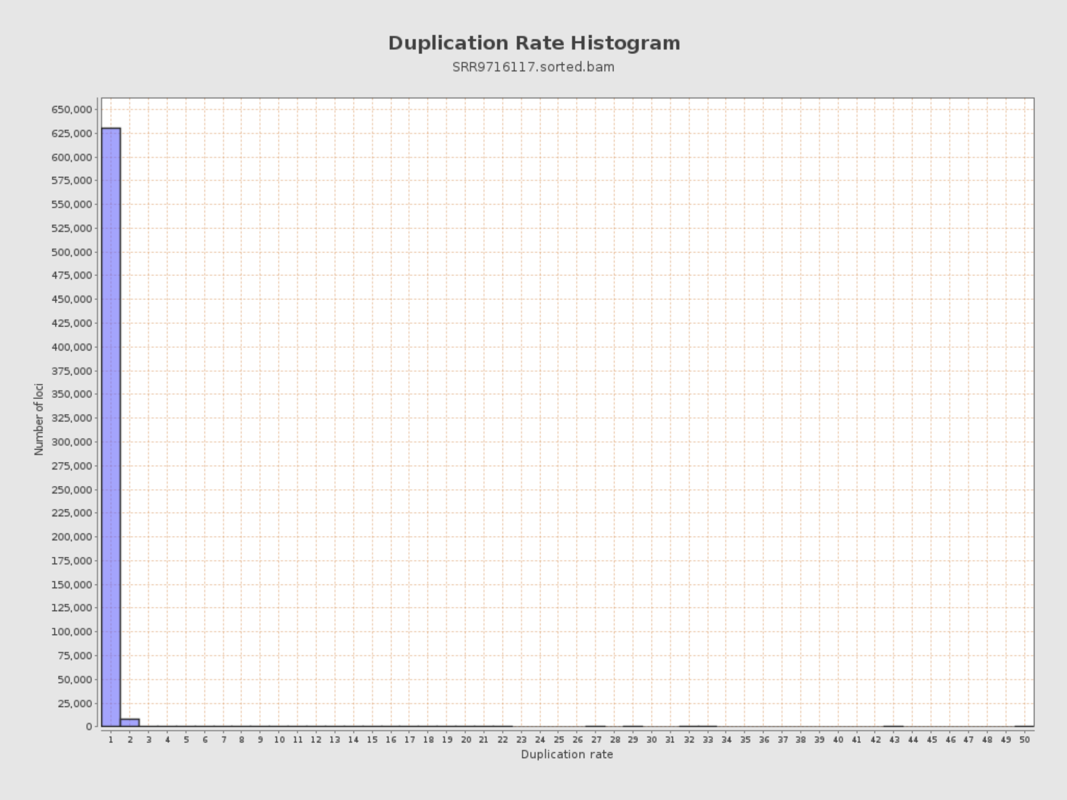
5. Results : Coverage Histogram (0-50X)



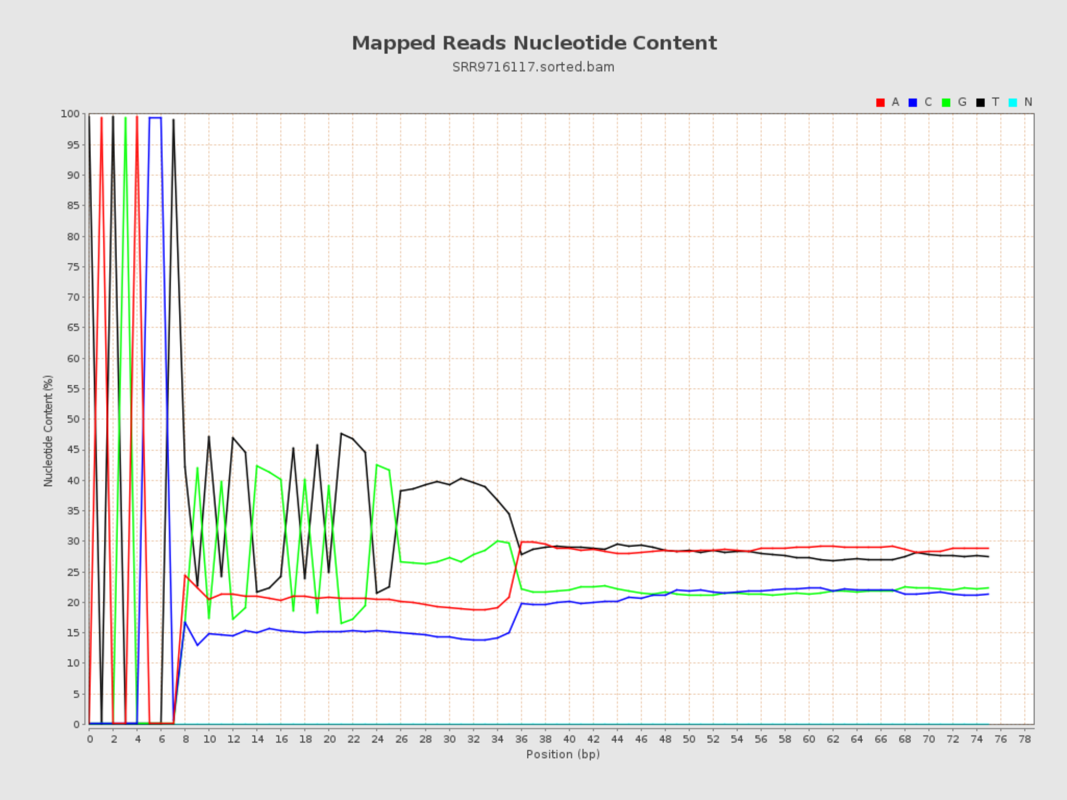
6. Results : Genome Fraction Coverage



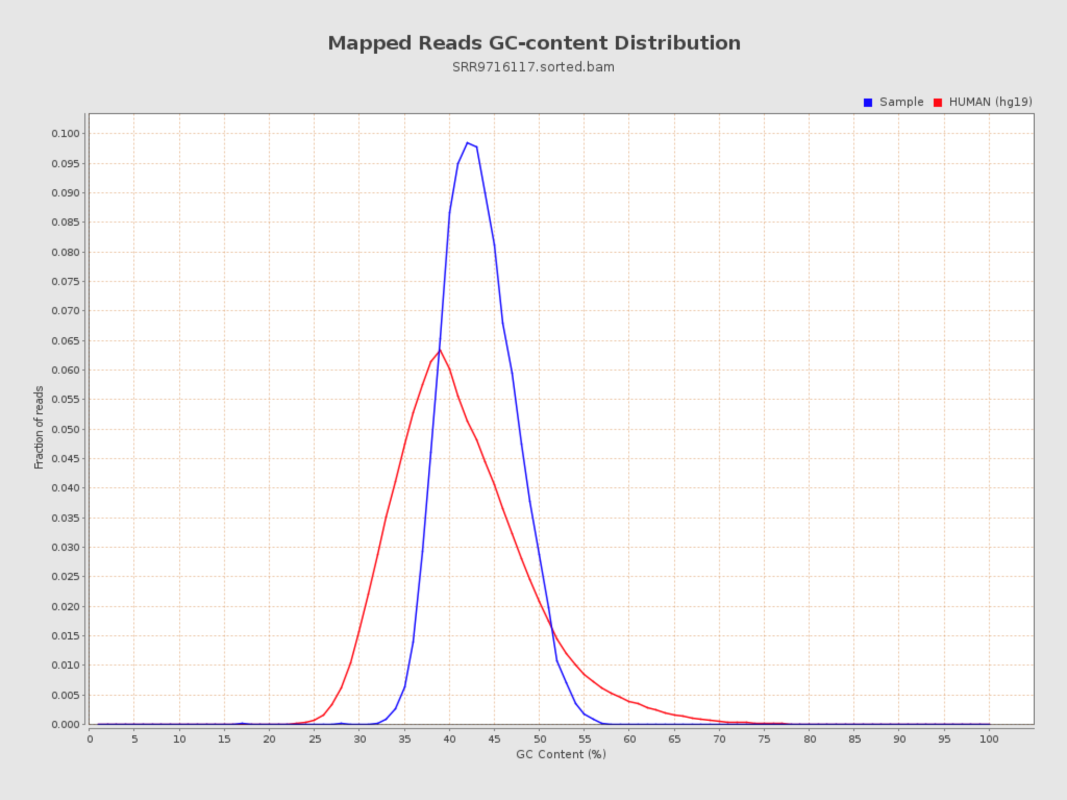
7. Results : Duplication Rate Histogram



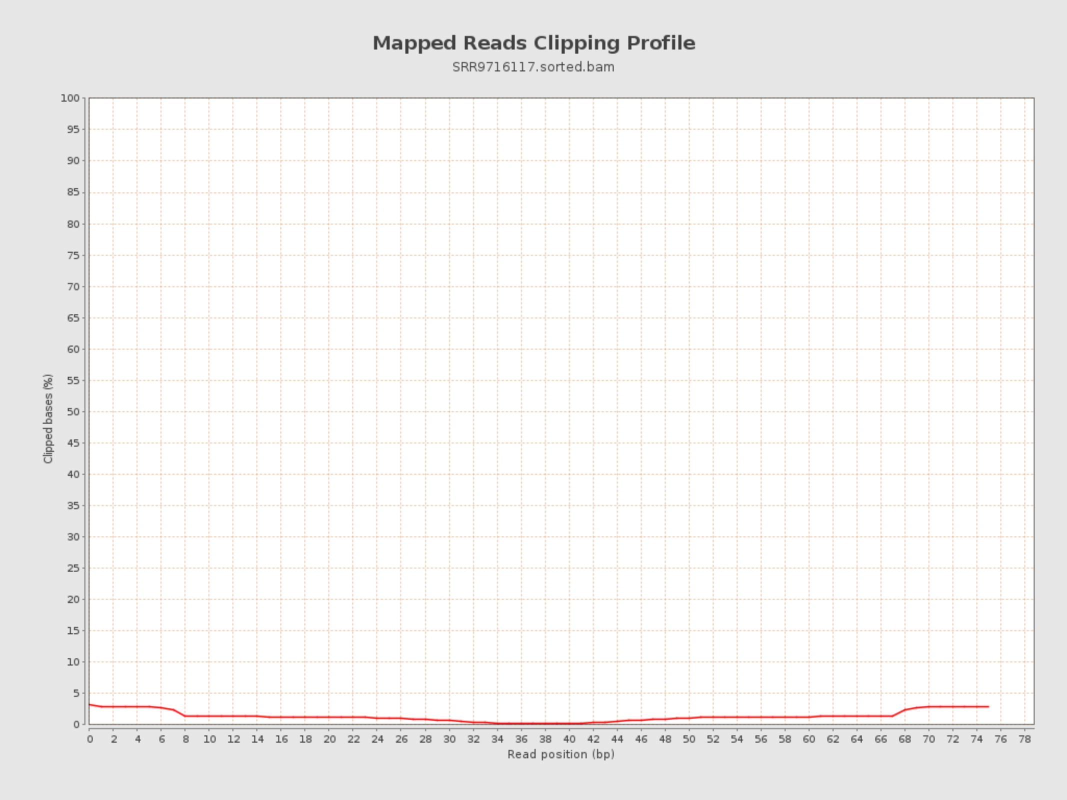
8. Results : Mapped Reads Nucleotide Content



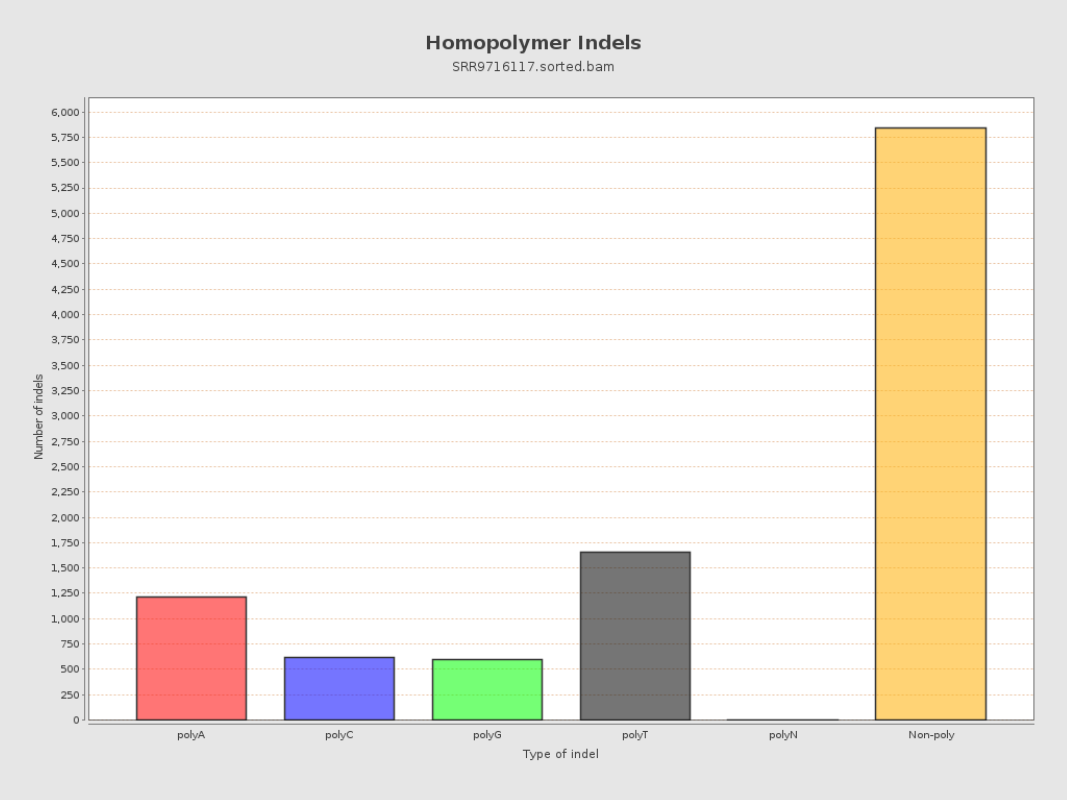
9. Results : Mapped Reads GC-content Distribution



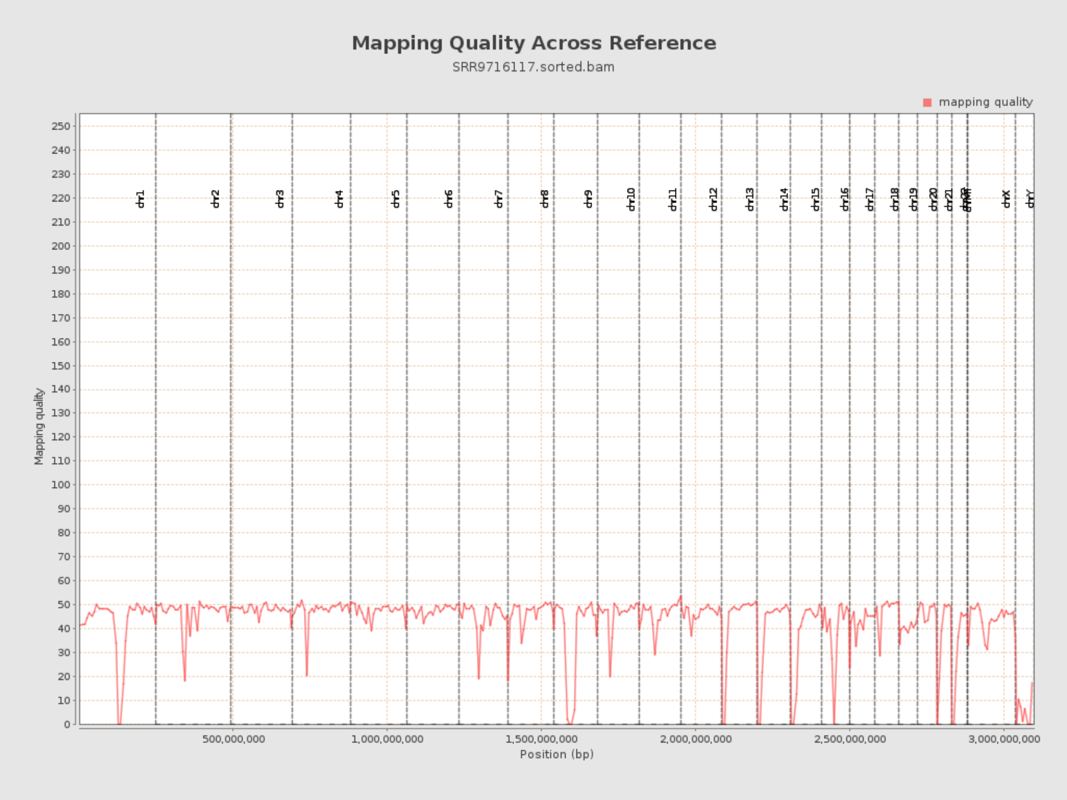
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram