Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:14:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716607.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_SRR9716607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716607.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:14:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,005,673
Mapped reads	851,941 / 84.71%
Unmapped reads	153,732 / 15.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,452 / 2.73%
Read min/max/mean length	30 / 101 / 101.98
Duplicated reads (estimated)	15,071 / 1.5%
Duplication rate	1.04%
Clipped reads	878,301 / 87.33%

2.2. ACGT Content

Number/percentage of A's	16,266,910 / 25.33%
Number/percentage of C's	13,169,370 / 20.51%
Number/percentage of T's	19,290,227 / 30.04%
Number/percentage of G's	15,475,421 / 24.1%
Number/percentage of N's	8,117 / 0.01%
GC Percentage	44.61%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2084

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

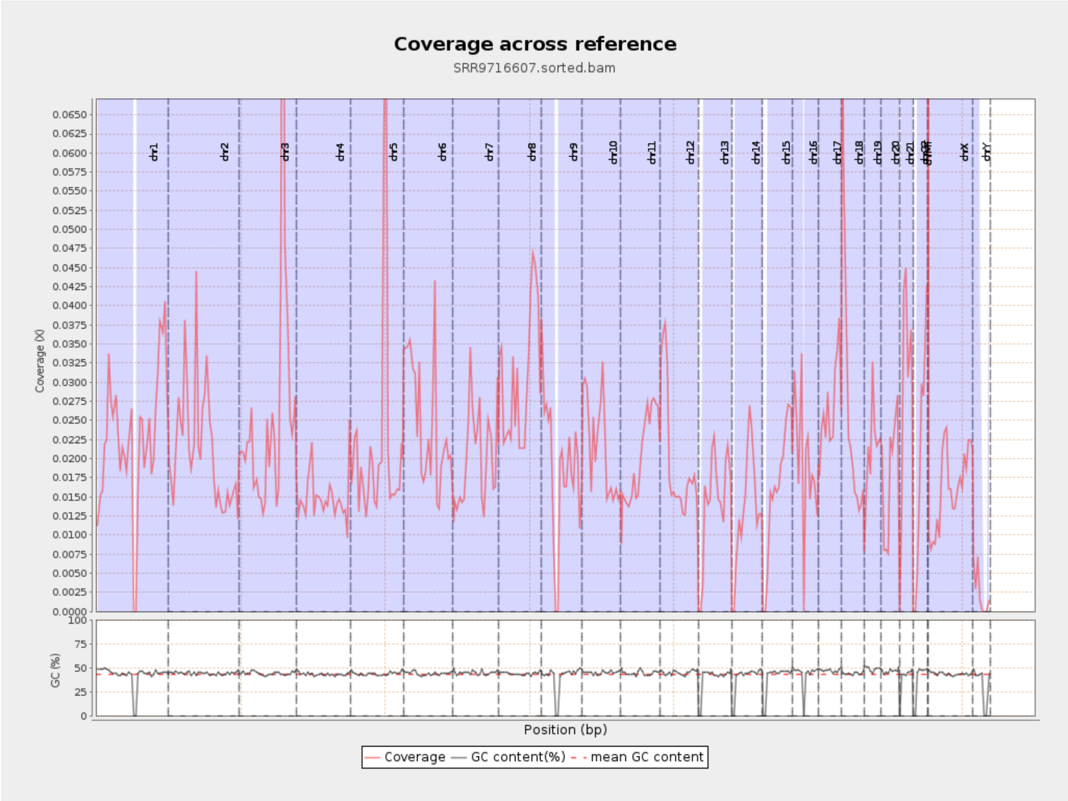
General error rate	0.79%
Mismatches	498,544
Insertions	5,332
Mapped reads with at least one insertion	0.62%
Deletions	13,441
Mapped reads with at least one deletion	1.56%
Homopolymer indels	40.45%

2.6. Chromosome stats

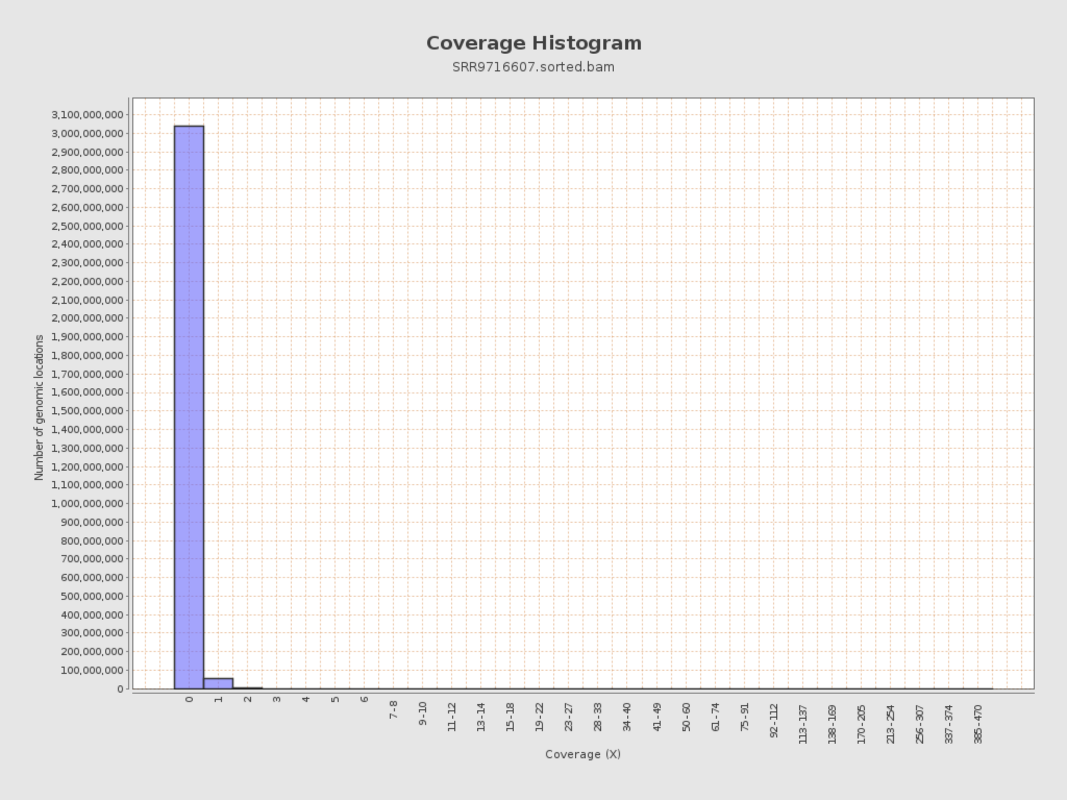
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5640907	0.0226	0.2325
chr2	243199373	5161404	0.0212	0.3374
chr3	198022430	5249766	0.0265	0.1752
chr4	191154276	2876817	0.015	0.1323
chr5	180915260	4050005	0.0224	0.1603
chr6	171115067	4258781	0.0249	0.1855
chr7	159138663	3205097	0.0201	0.2673

chr8	146364022	4464486	0.0305	0.2787
chr9	141213431	2638001	0.0187	0.1963
chr10	135534747	2939137	0.0217	0.1803
chr11	135006516	2734975	0.0203	0.175
chr12	133851895	2663122	0.0199	0.1514
chr13	115169878	1672813	0.0145	0.1262
chr14	107349540	1431269	0.0133	0.1382
chr15	102531392	1637911	0.016	0.133
chr16	90354753	1764810	0.0195	0.1579
chr17	81195210	2179393	0.0268	0.197
chr18	78077248	2162858	0.0277	0.3671
chr19	59128983	1271897	0.0215	0.2336
chr20	63025520	1108172	0.0176	0.1544
chr21	48129895	1446377	0.0301	0.189
chr22	51304566	1022917	0.0199	0.1524
chrMT	16571	2796	0.1687	0.5416
chrX	155270560	2511766	0.0162	0.1574
chrY	59373566	138087	0.0023	0.0766

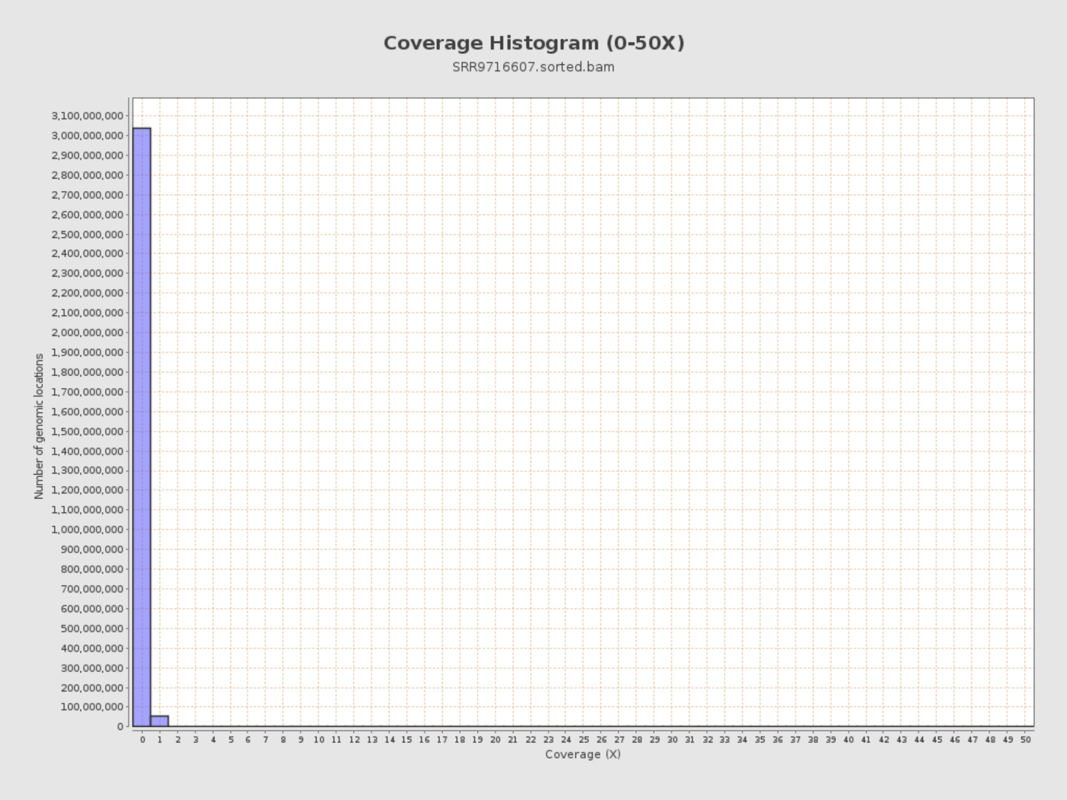
3. Results : Coverage across reference



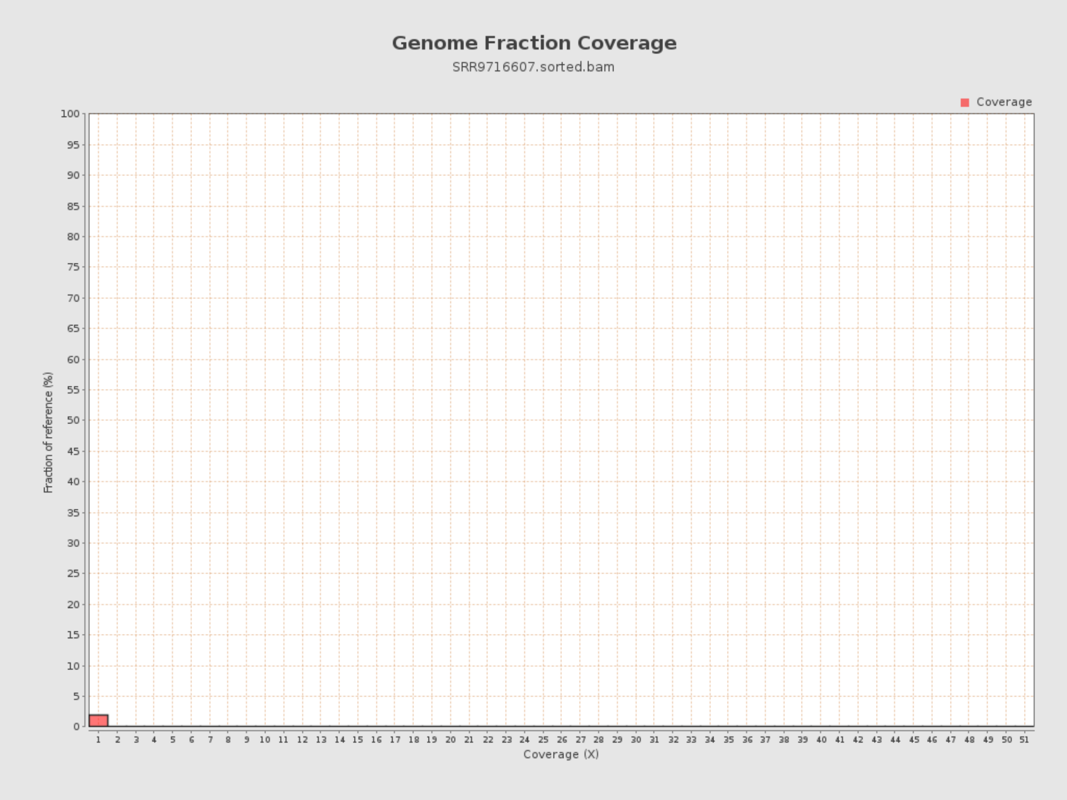
4. Results : Coverage Histogram



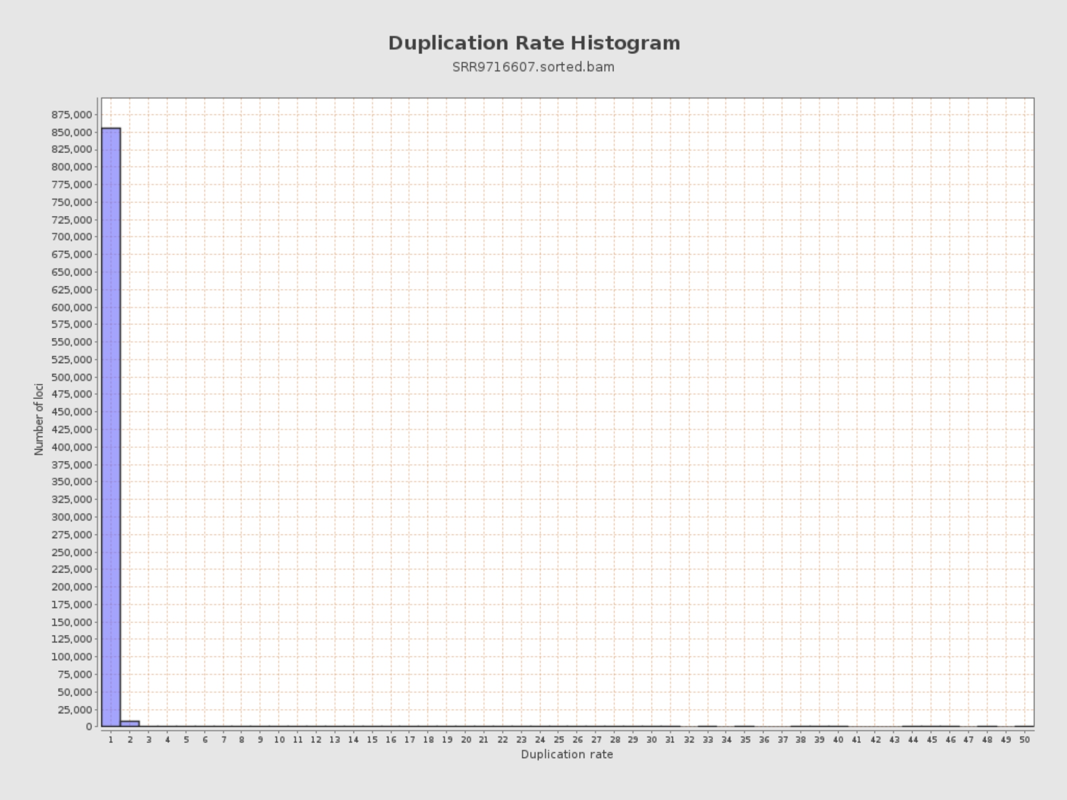
5. Results : Coverage Histogram (0-50X)



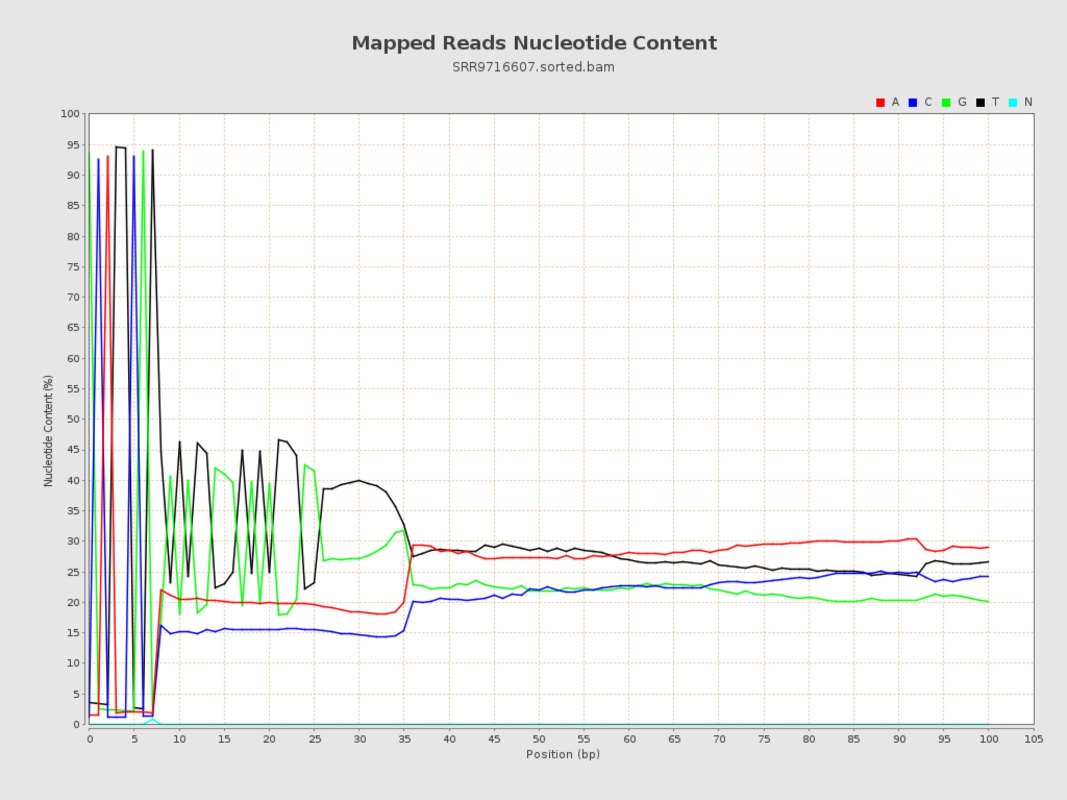
6. Results : Genome Fraction Coverage



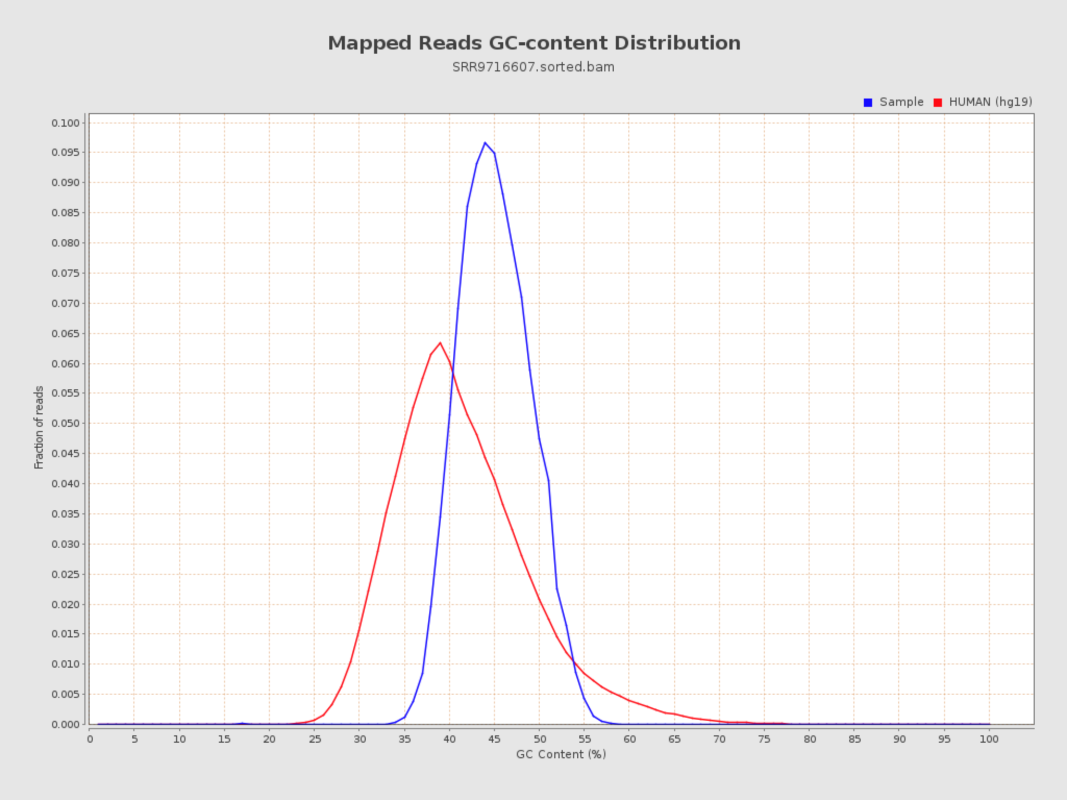
7. Results : Duplication Rate Histogram



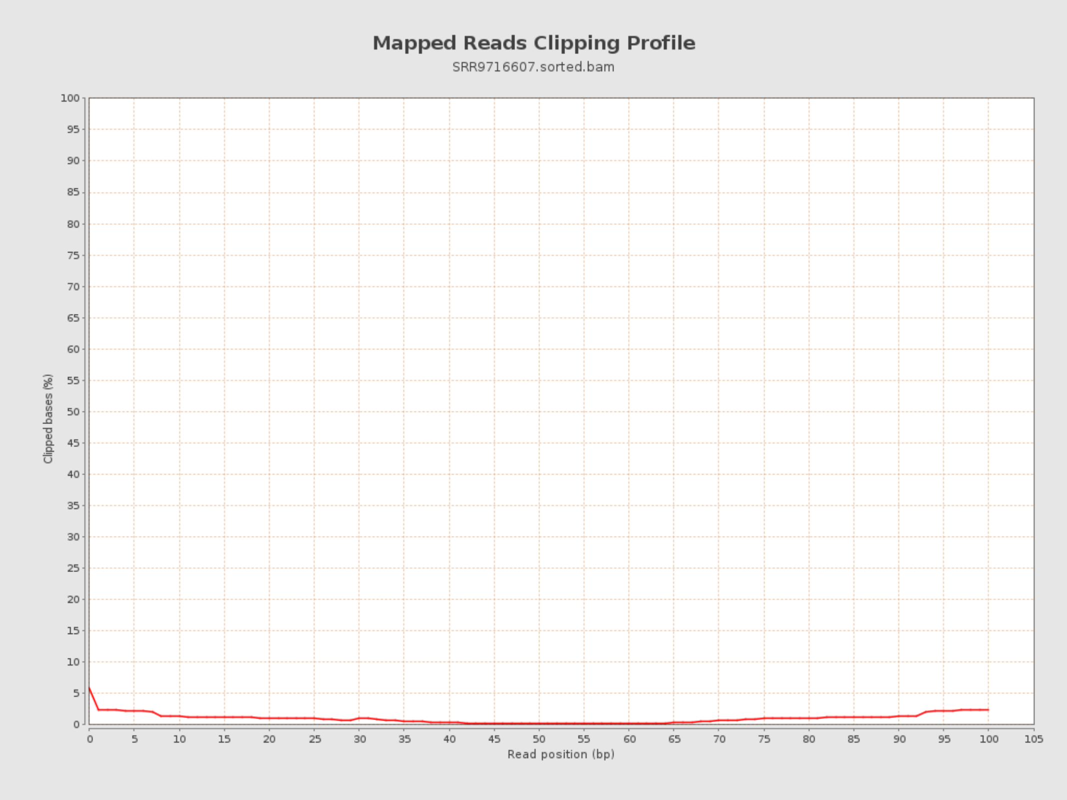
8. Results : Mapped Reads Nucleotide Content



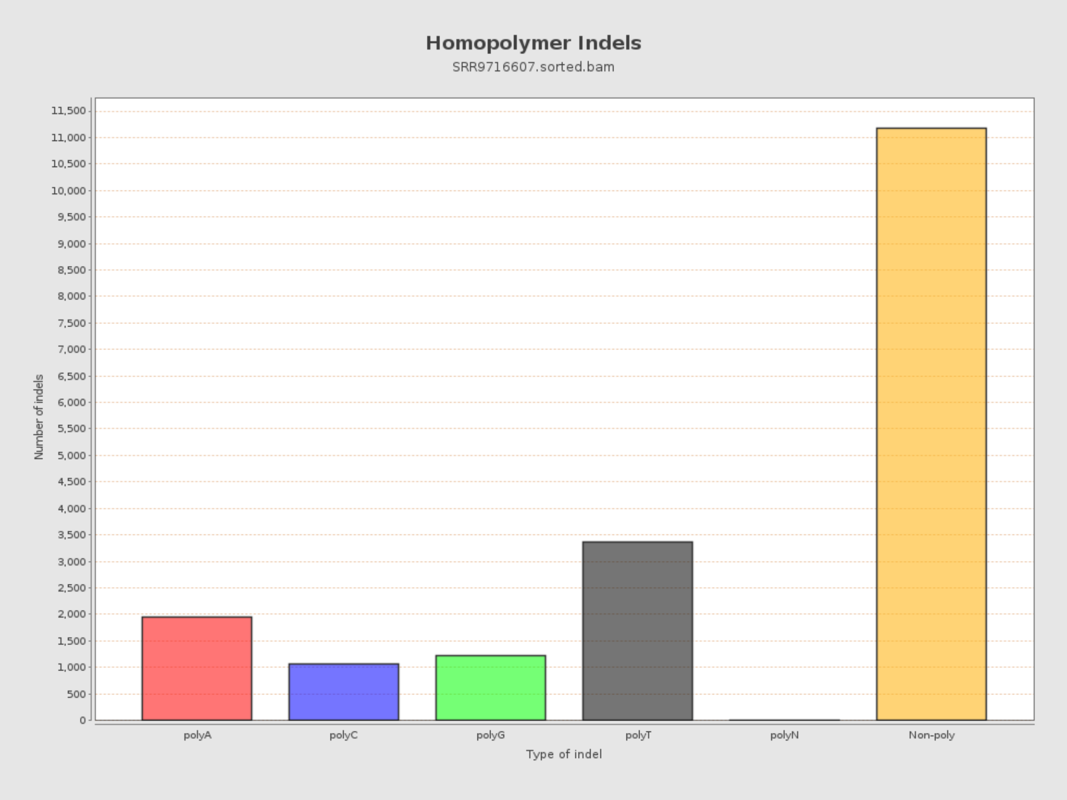
9. Results : Mapped Reads GC-content Distribution



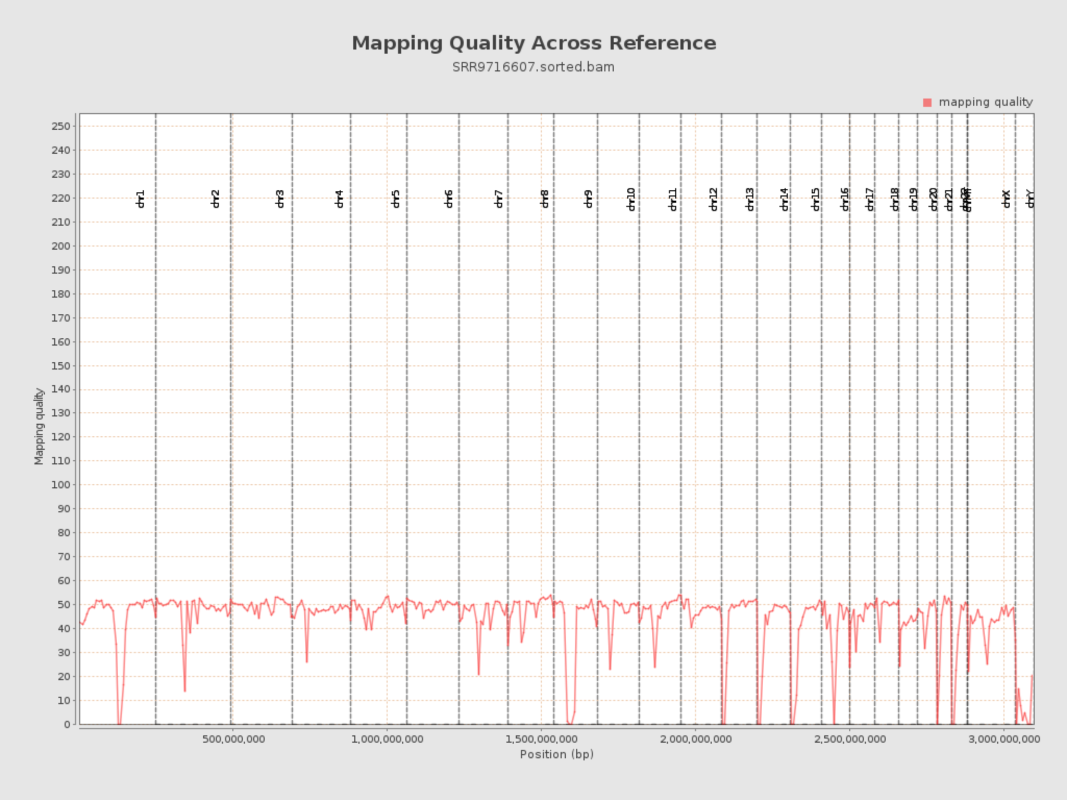
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram