Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:57:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716620.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_SRR9716620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716620.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:57:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,326,973
Mapped reads	1,230,448 / 92.73%
Unmapped reads	96,525 / 7.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,444 / 2.07%
Read min/max/mean length	30 / 101 / 101.75
Duplicated reads (estimated)	53,204 / 4.01%
Duplication rate	3.34%
Clipped reads	1,255,503 / 94.61%

2.2. ACGT Content

Number/percentage of A's	23,749,507 / 25.13%
Number/percentage of C's	18,617,164 / 19.7%
Number/percentage of T's	28,080,881 / 29.71%
Number/percentage of G's	24,056,924 / 25.45%
Number/percentage of N's	3,291 / 0%
GC Percentage	45.15%

2.3. Coverage

Mean	0.0305

Standard Deviation	0.2821

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

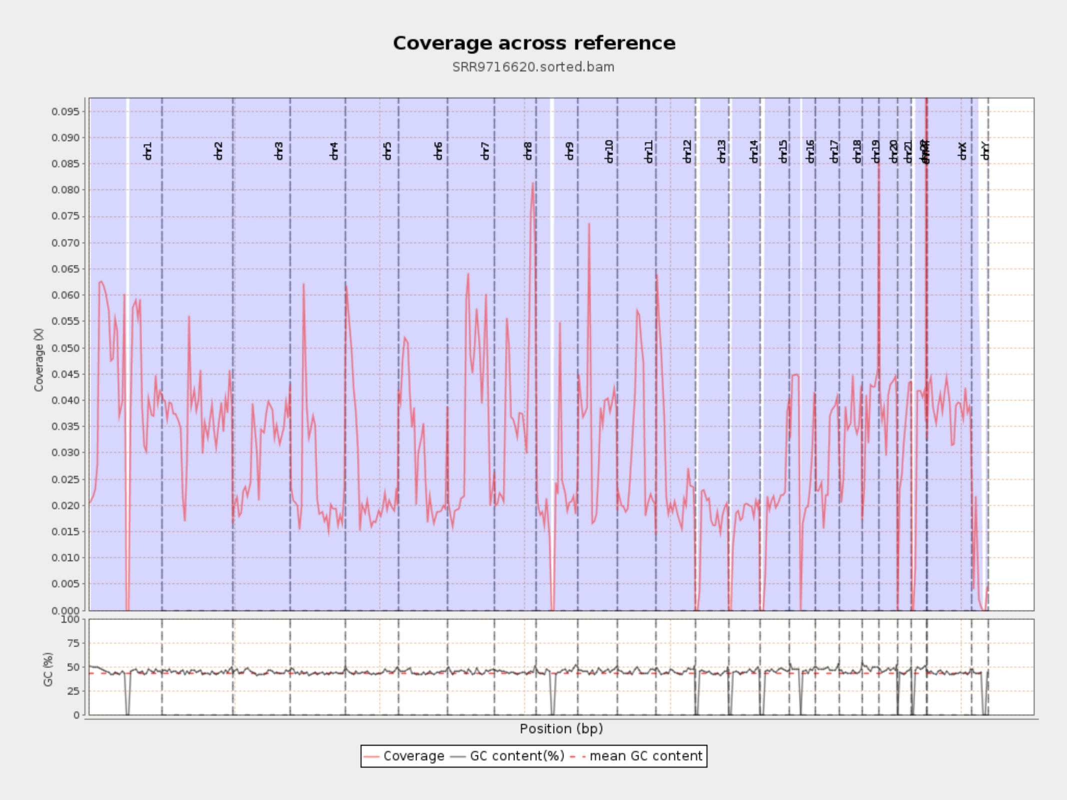
General error rate	0.7%
Mismatches	642,795
Insertions	8,103
Mapped reads with at least one insertion	0.65%
Deletions	19,132
Mapped reads with at least one deletion	1.53%
Homopolymer indels	39.09%

2.6. Chromosome stats

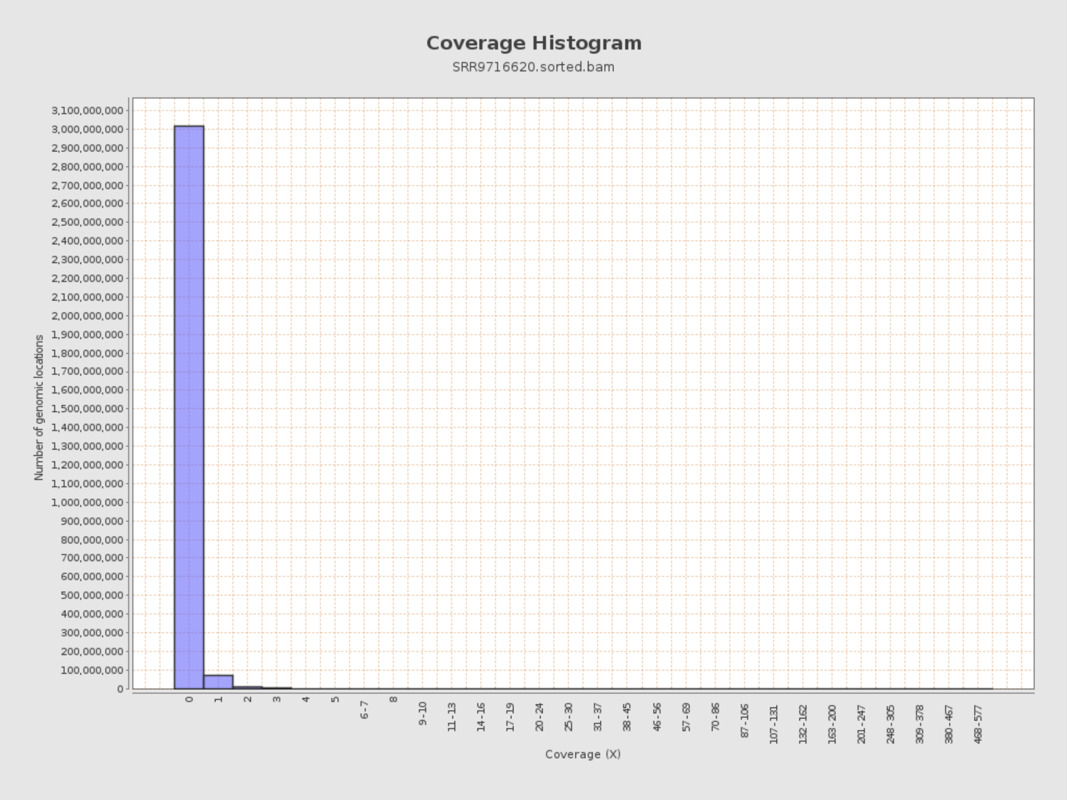
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10509947	0.0422	0.5317
chr2	243199373	8955734	0.0368	0.2987
chr3	198022430	6025517	0.0304	0.1982
chr4	191154276	4609565	0.0241	0.2447
chr5	180915260	4729771	0.0261	0.1834
chr6	171115067	5133063	0.03	0.2072
chr7	159138663	5839802	0.0367	0.368

chr8	146364022	5884689	0.0402	0.2935
chr9	141213431	2809021	0.0199	0.1946
chr10	135534747	4985245	0.0368	0.3801
chr11	135006516	4013637	0.0297	0.2518
chr12	133851895	3664650	0.0274	0.1869
chr13	115169878	1842222	0.016	0.1401
chr14	107349540	1751198	0.0163	0.1539
chr15	102531392	1936449	0.0189	0.1546
chr16	90354753	2730721	0.0302	0.2063
chr17	81195210	2340814	0.0288	0.207
chr18	78077248	2658268	0.034	0.2826
chr19	59128983	2325508	0.0393	0.3889
chr20	63025520	2509515	0.0398	0.2375
chr21	48129895	1475839	0.0307	0.2362
chr22	51304566	1421551	0.0277	0.1921
chrMT	16571	40845	2.4648	2.4736
chrX	155270560	6016382	0.0387	0.2293
chrY	59373566	337236	0.0057	0.2123

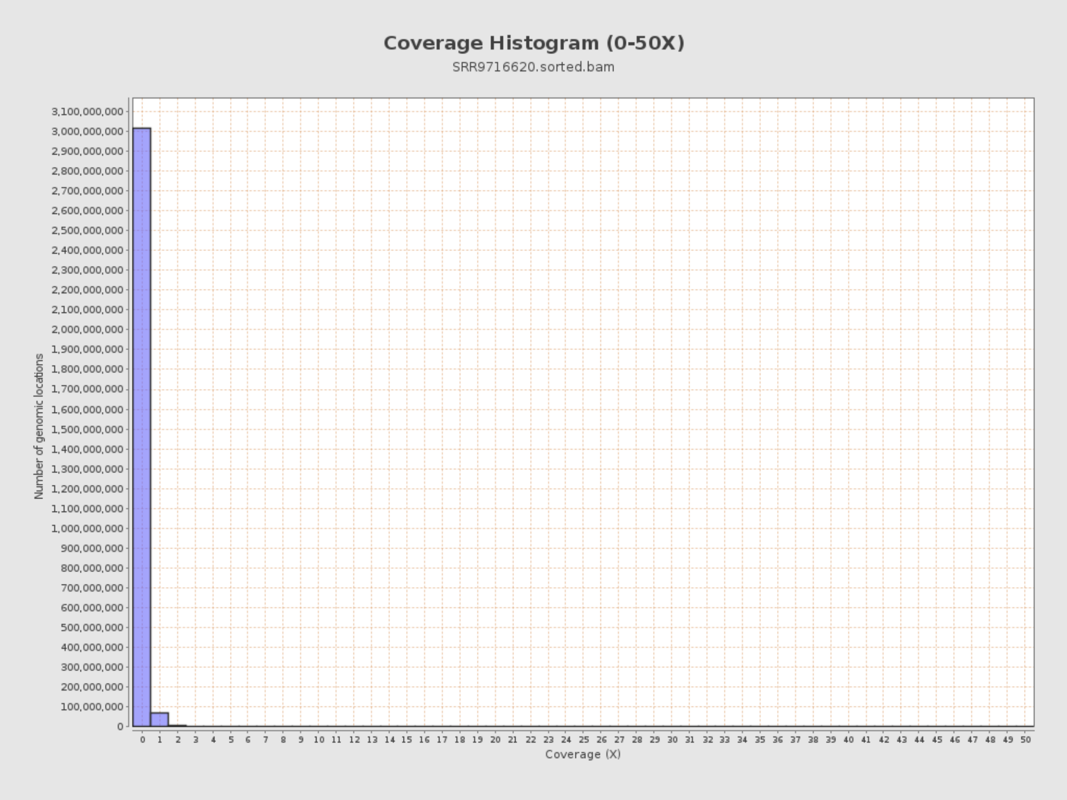
3. Results : Coverage across reference



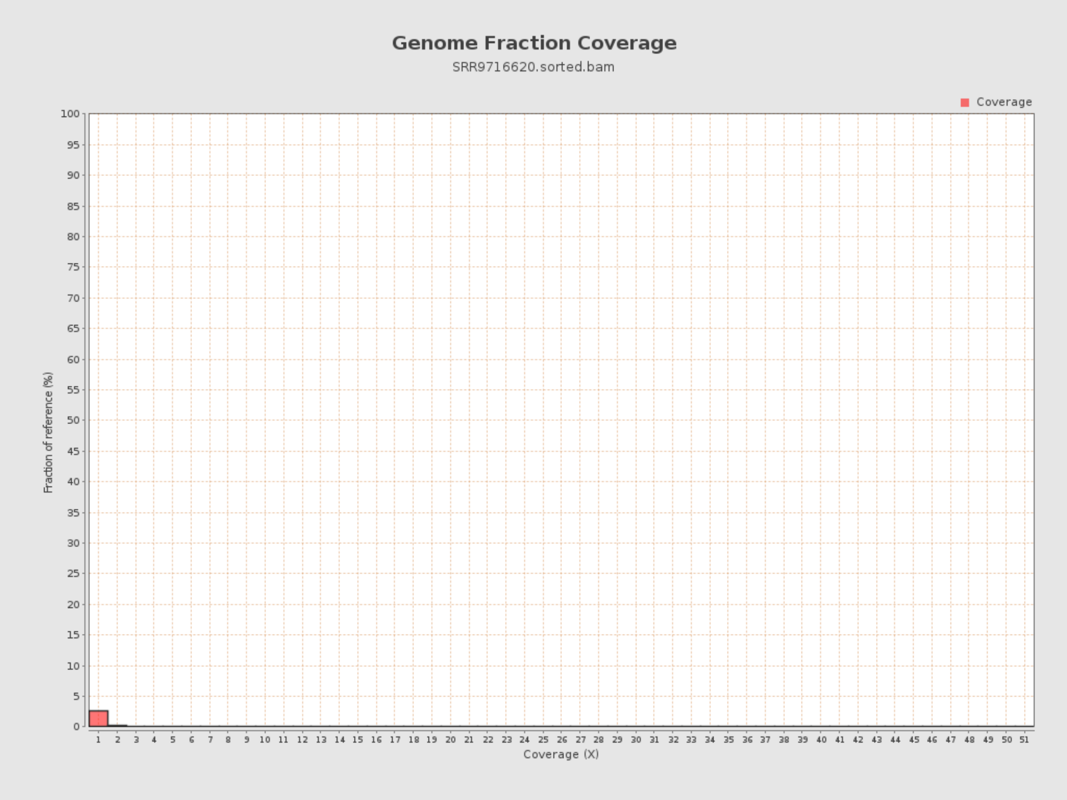
4. Results : Coverage Histogram



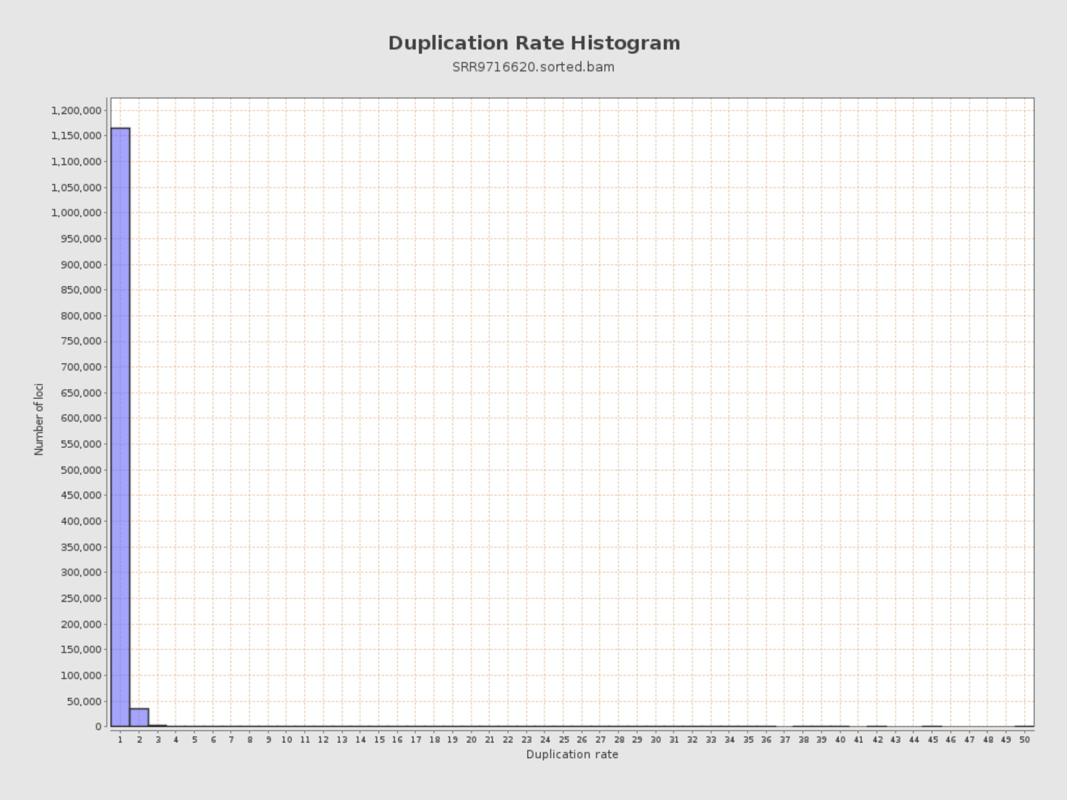
5. Results : Coverage Histogram (0-50X)



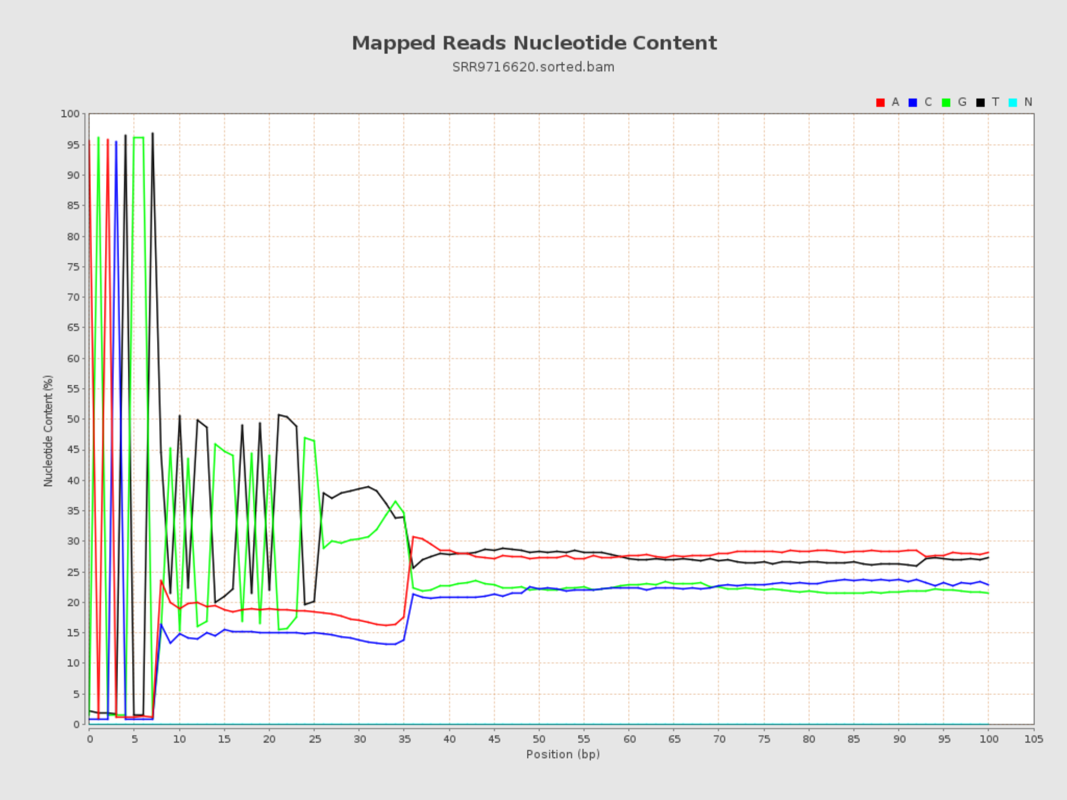
6. Results : Genome Fraction Coverage



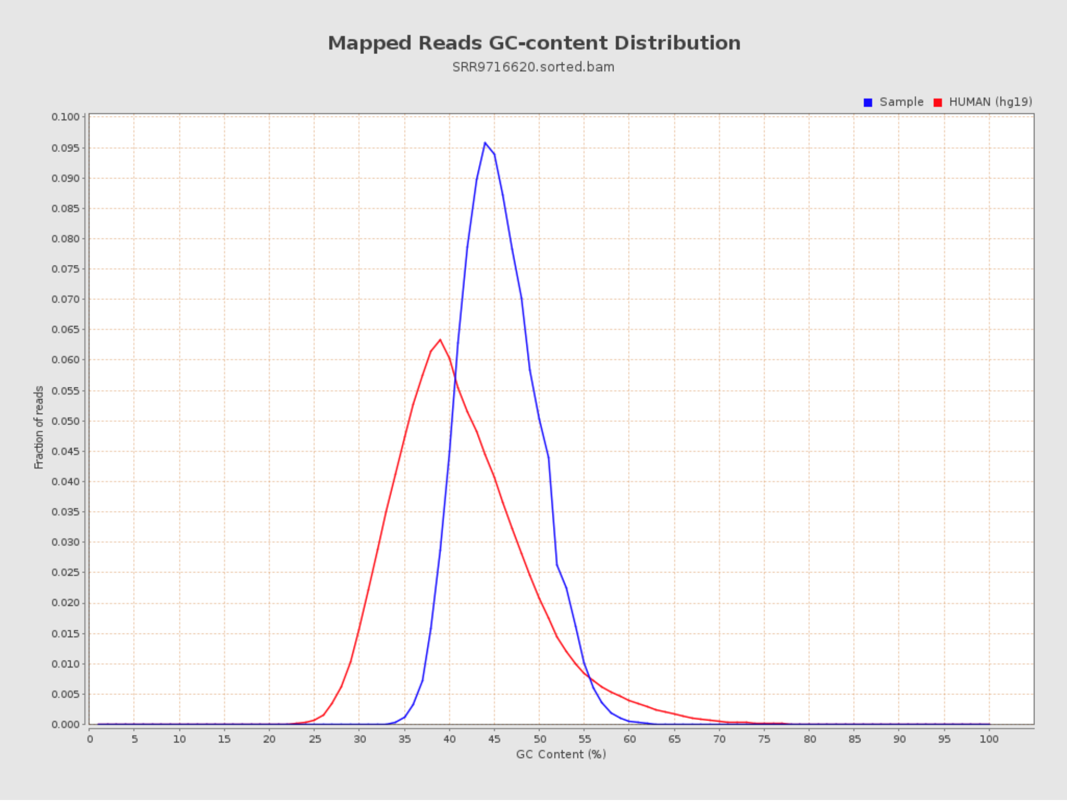
7. Results : Duplication Rate Histogram



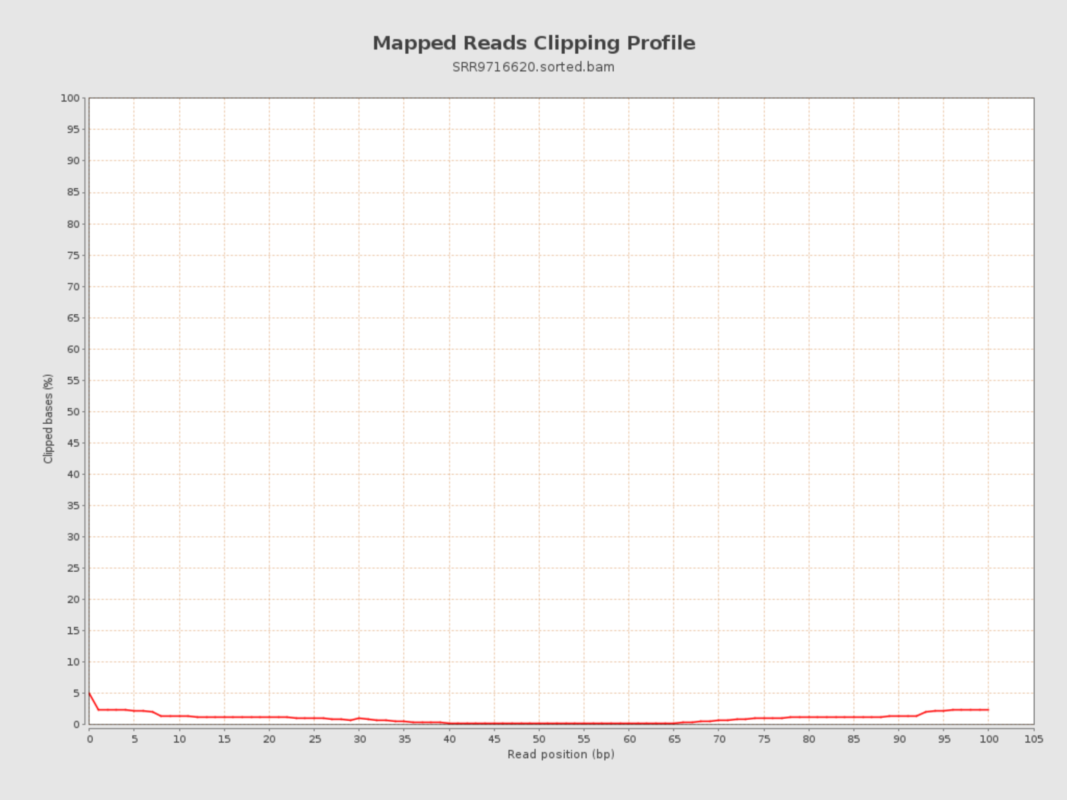
8. Results : Mapped Reads Nucleotide Content



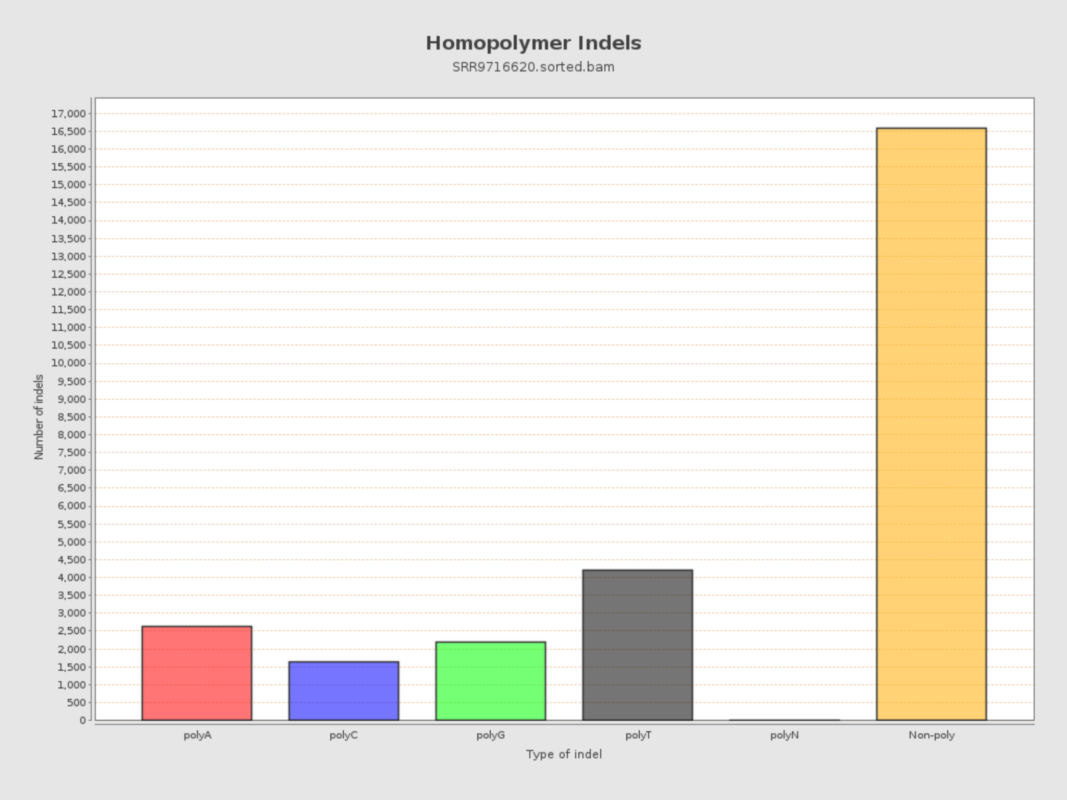
9. Results : Mapped Reads GC-content Distribution



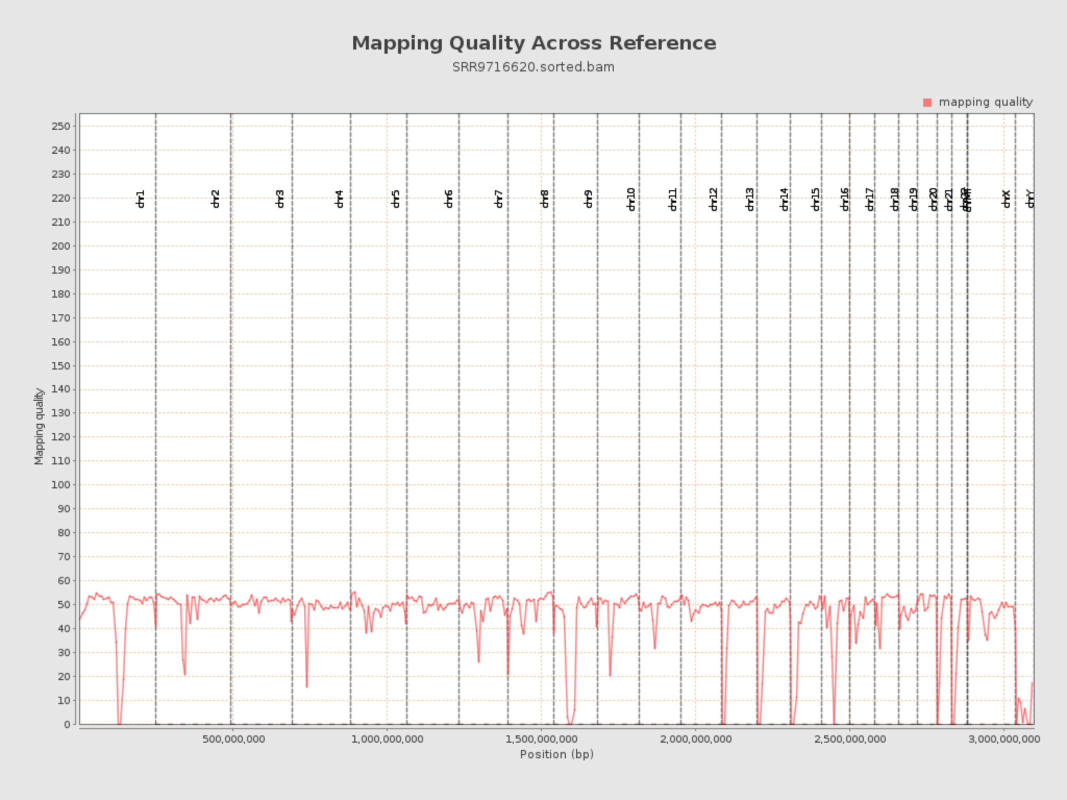
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram