Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 03:27:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716663.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_SRR9716663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716663.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 03:27:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,900,185
Mapped reads	2,669,669 / 92.05%
Unmapped reads	230,516 / 7.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	53,732 / 1.85%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	143,783 / 4.96%
Duplication rate	4%
Clipped reads	2,717,956 / 93.72%

2.2. ACGT Content

Number/percentage of A's	53,553,004 / 25.7%
Number/percentage of C's	43,152,806 / 20.71%
Number/percentage of T's	63,634,041 / 30.54%
Number/percentage of G's	48,024,010 / 23.05%
Number/percentage of N's	15,192 / 0.01%
GC Percentage	43.76%

2.3. Coverage

Mean	0.0673

Standard Deviation	0.5393

2.4. Mapping Quality

Mean Mapping Quality	47.27

2.5. Mismatches and indels

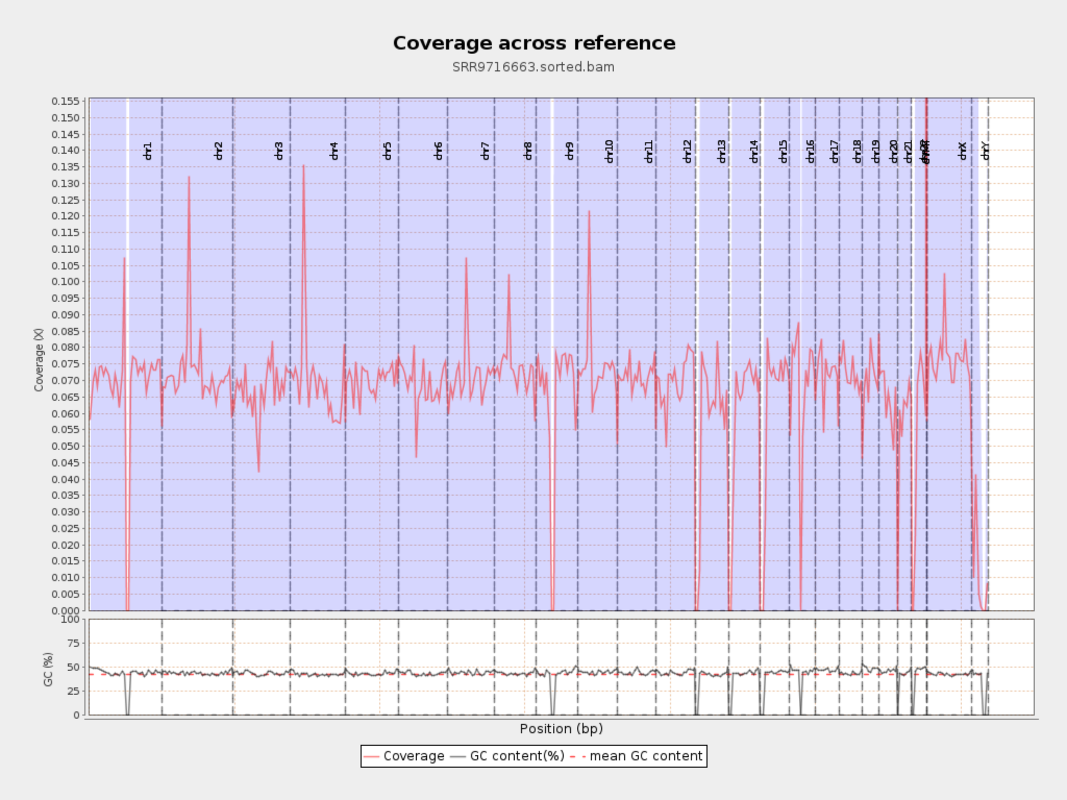
General error rate	0.7%
Mismatches	1,412,588
Insertions	16,963
Mapped reads with at least one insertion	0.63%
Deletions	48,720
Mapped reads with at least one deletion	1.79%
Homopolymer indels	42.98%

2.6. Chromosome stats

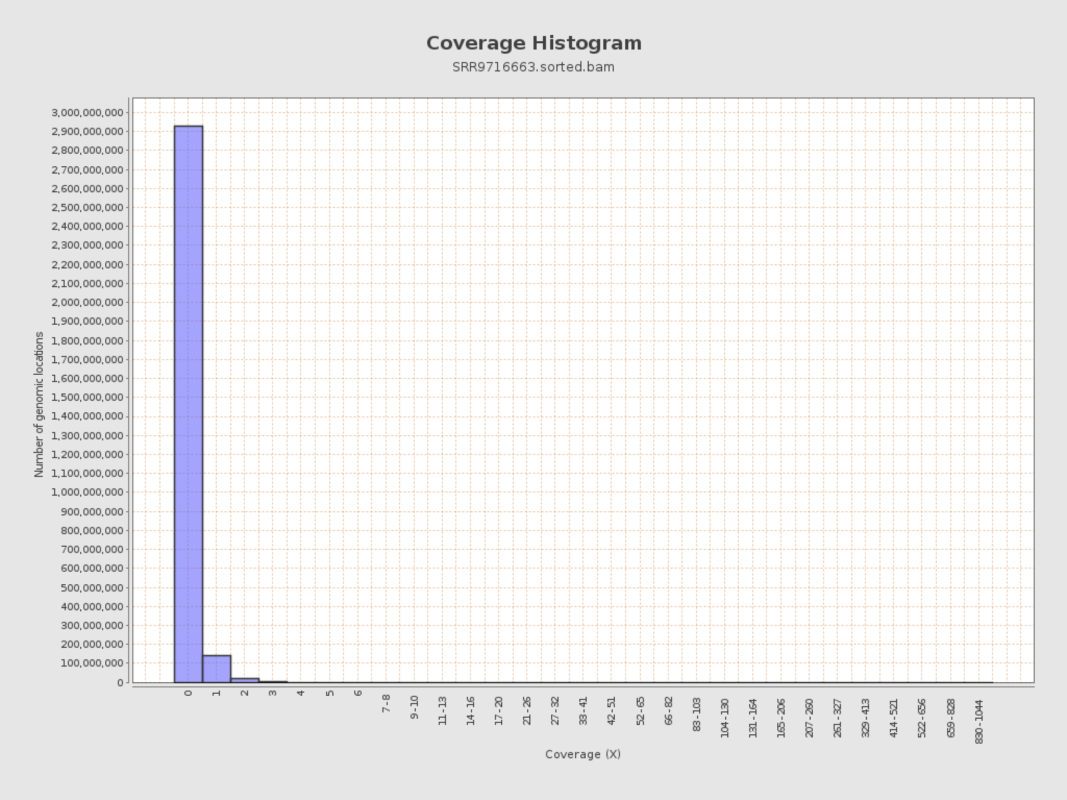
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16963983	0.0681	0.9417
chr2	243199373	17696508	0.0728	0.6734
chr3	198022430	13259017	0.067	0.3043
chr4	191154276	13384236	0.07	0.4332
chr5	180915260	12690359	0.0701	0.3185
chr6	171115067	11807443	0.069	0.354
chr7	159138663	11426042	0.0718	0.7623

chr8	146364022	10778201	0.0736	0.6969
chr9	141213431	8995335	0.0637	0.5048
chr10	135534747	10075593	0.0743	0.576
chr11	135006516	9598331	0.0711	0.5072
chr12	133851895	9369787	0.07	0.3177
chr13	115169878	6373878	0.0553	0.2769
chr14	107349540	6296461	0.0587	0.3213
chr15	102531392	6140831	0.0599	0.2924
chr16	90354753	6126964	0.0678	0.3444
chr17	81195210	5791570	0.0713	0.3776
chr18	78077248	5676284	0.0727	0.8489
chr19	59128983	4195524	0.071	0.6556
chr20	63025520	4060928	0.0644	0.3281
chr21	48129895	2711036	0.0563	0.3551
chr22	51304566	2508924	0.0489	0.264
chrMT	16571	29862	1.8021	1.8302
chrX	155270560	11868494	0.0764	0.4002
chrY	59373566	646753	0.0109	0.3644

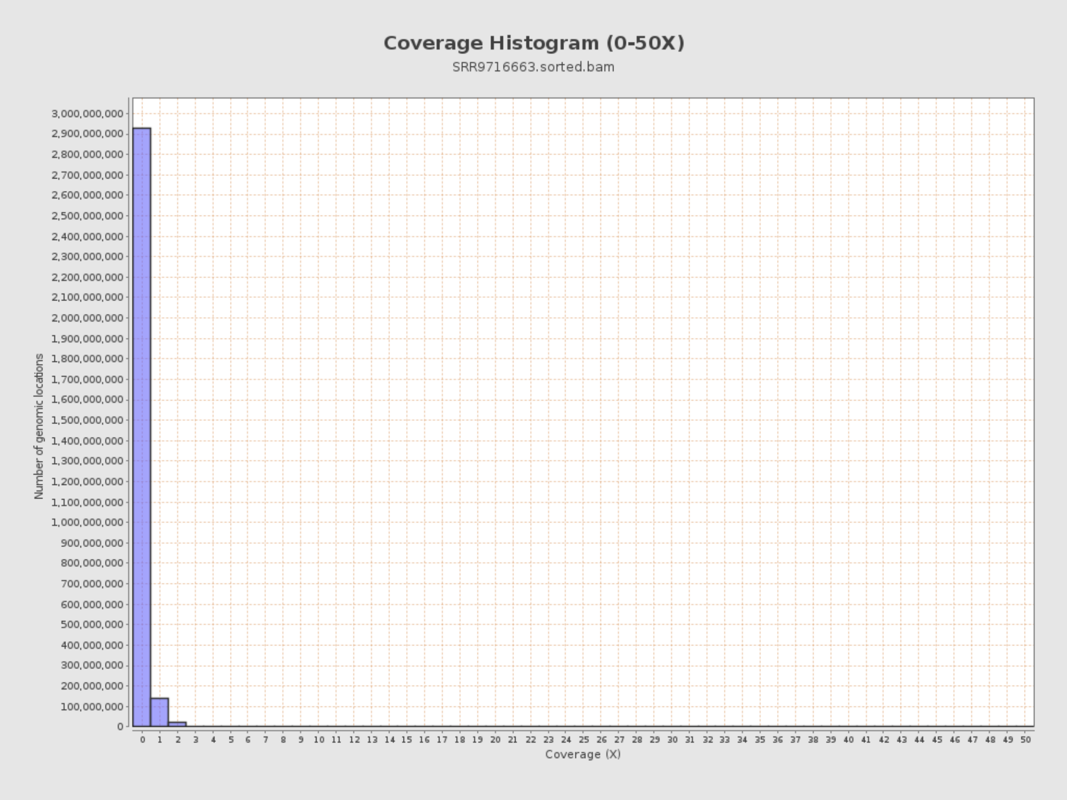
3. Results : Coverage across reference



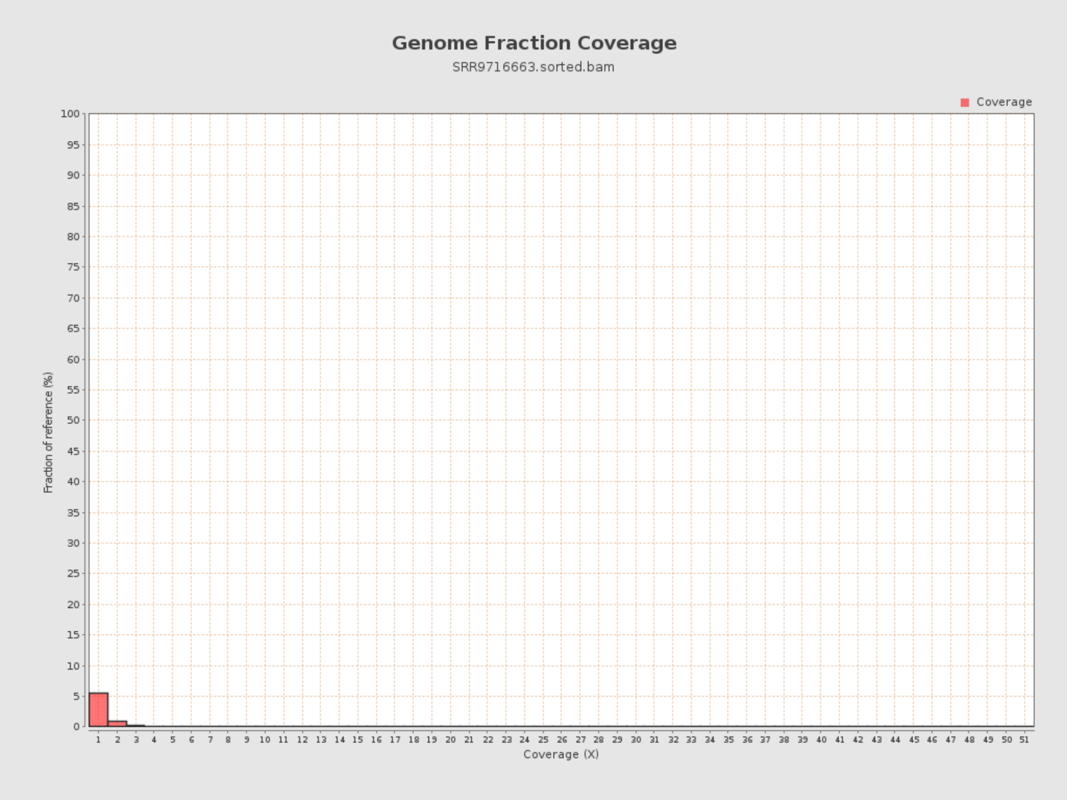
4. Results : Coverage Histogram



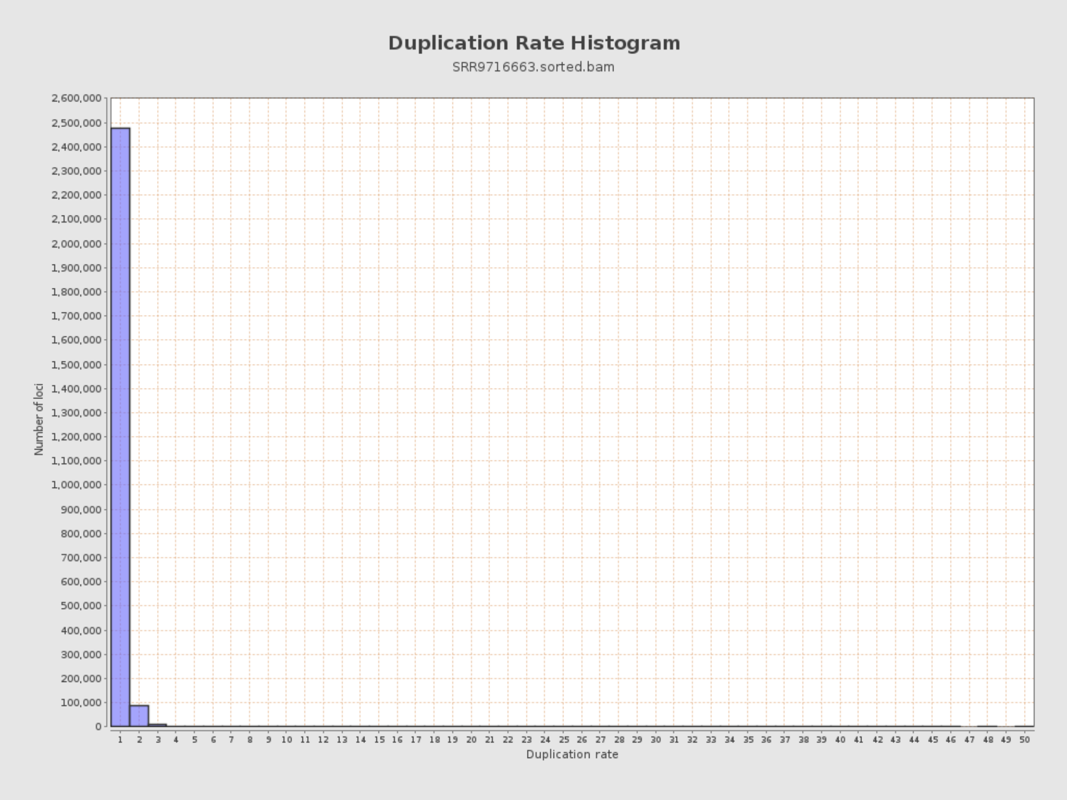
5. Results : Coverage Histogram (0-50X)



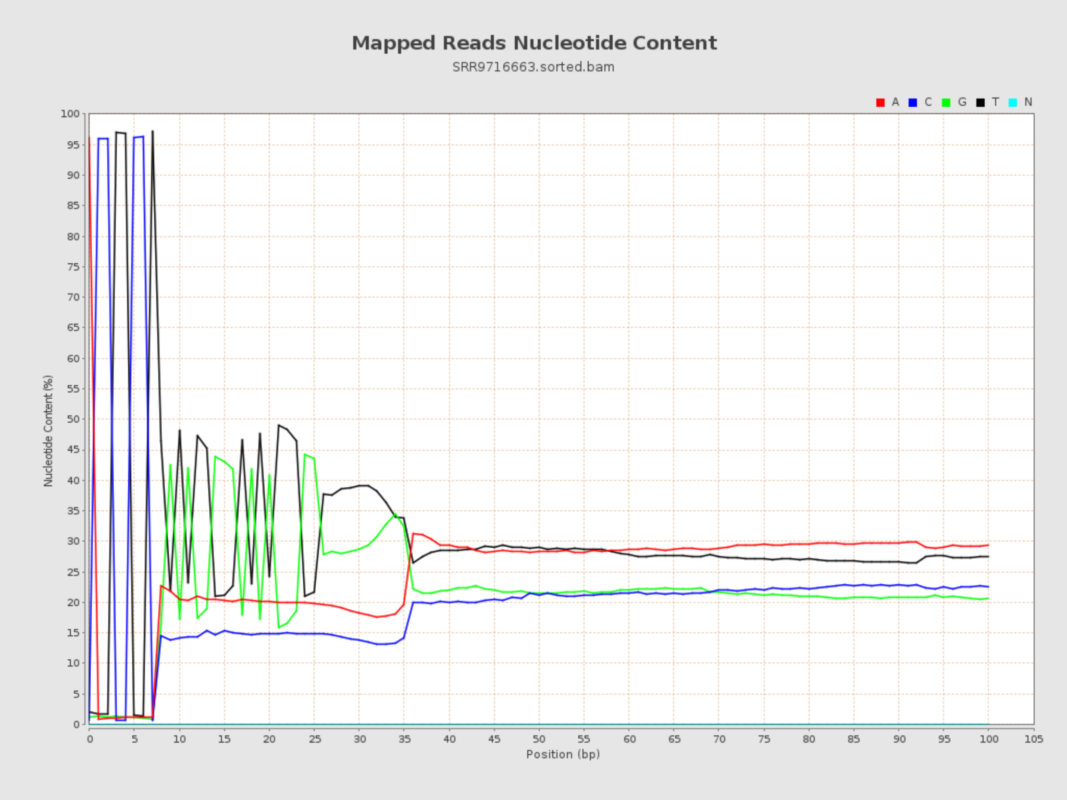
6. Results : Genome Fraction Coverage



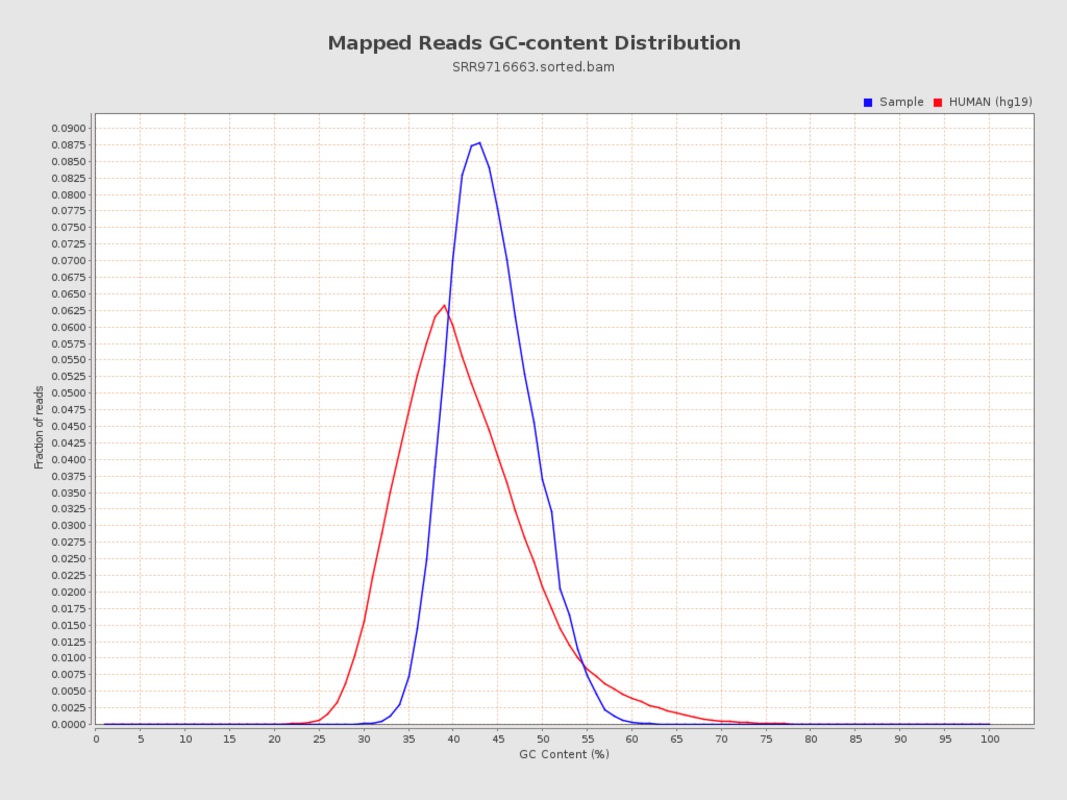
7. Results : Duplication Rate Histogram



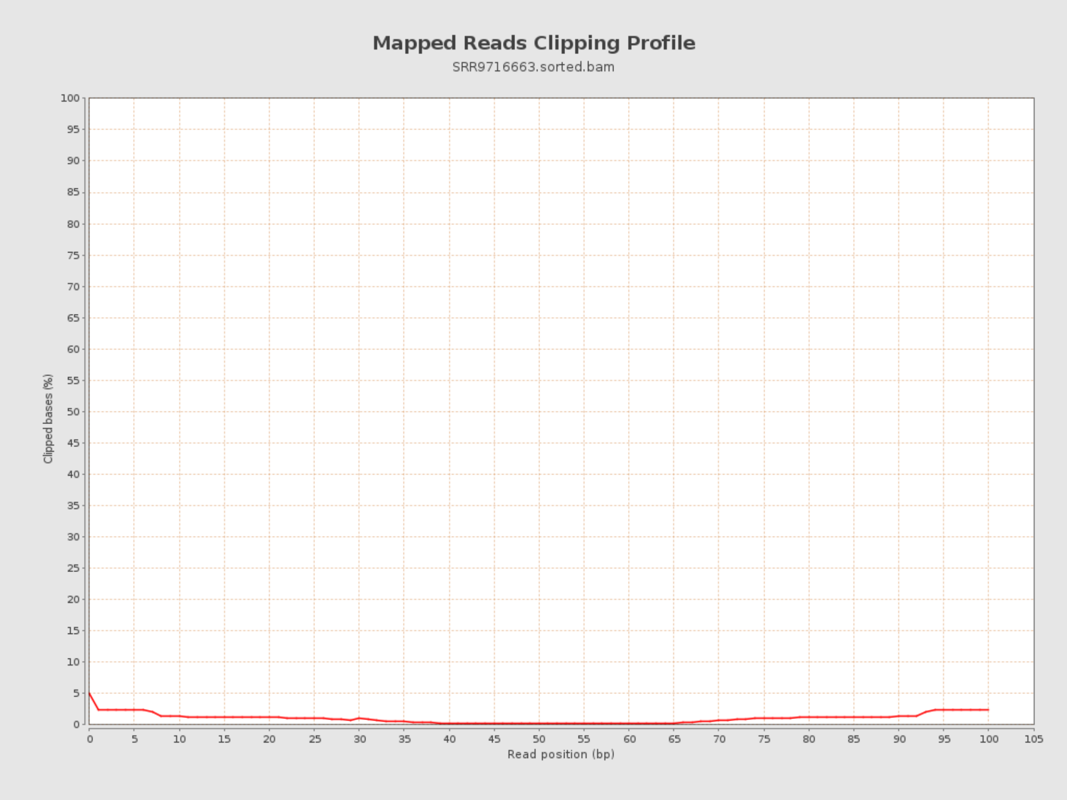
8. Results : Mapped Reads Nucleotide Content



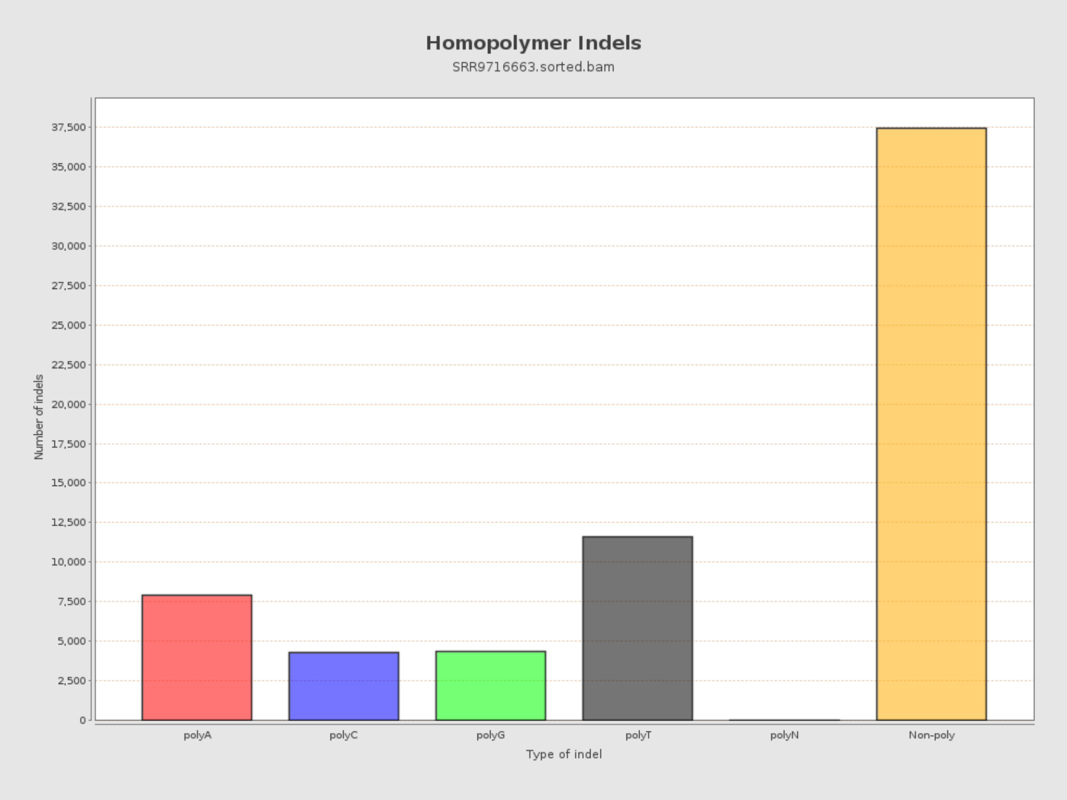
9. Results : Mapped Reads GC-content Distribution



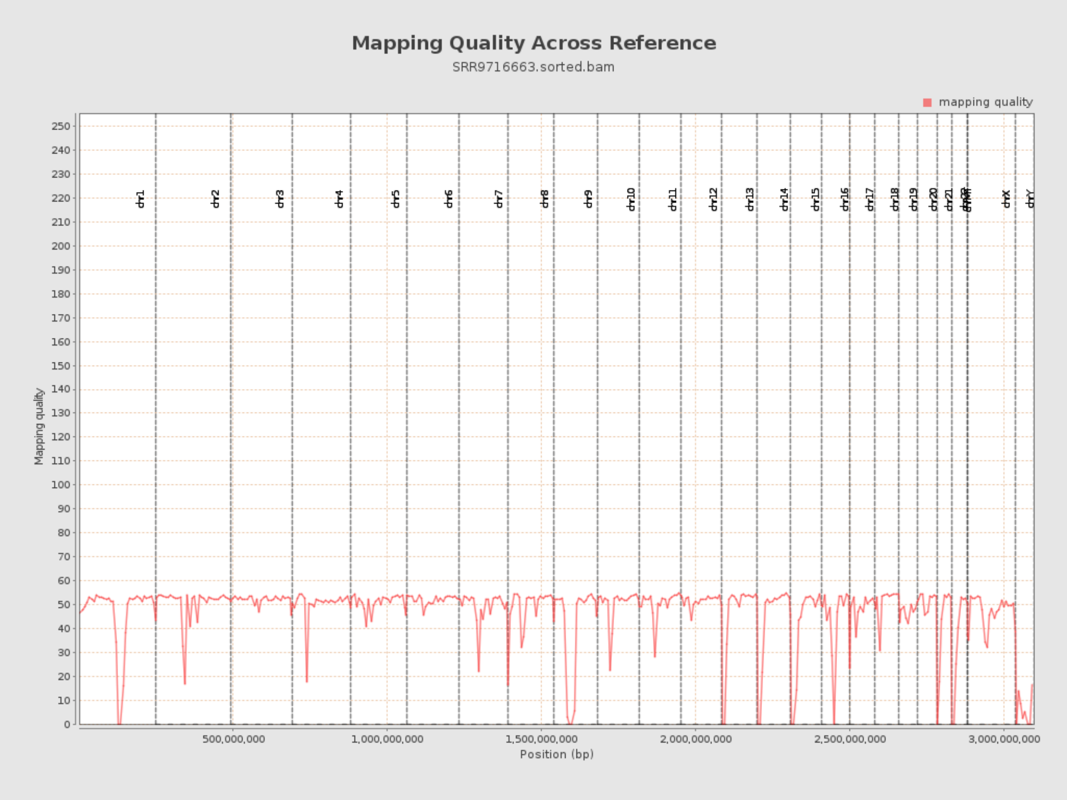
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram