Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:08:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716605.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_SRR9716605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716605.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:08:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,057,824
Mapped reads	1,933,723 / 93.97%
Unmapped reads	124,101 / 6.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,765 / 2.27%
Read min/max/mean length	30 / 101 / 101.82
Duplicated reads (estimated)	66,864 / 3.25%
Duplication rate	2.37%
Clipped reads	1,979,181 / 96.18%

2.2. ACGT Content

Number/percentage of A's	38,608,747 / 25.9%
Number/percentage of C's	31,384,744 / 21.05%
Number/percentage of T's	44,140,153 / 29.61%
Number/percentage of G's	34,929,729 / 23.43%
Number/percentage of N's	18,356 / 0.01%
GC Percentage	44.48%

2.3. Coverage

Mean	0.0482

Standard Deviation	0.4031

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

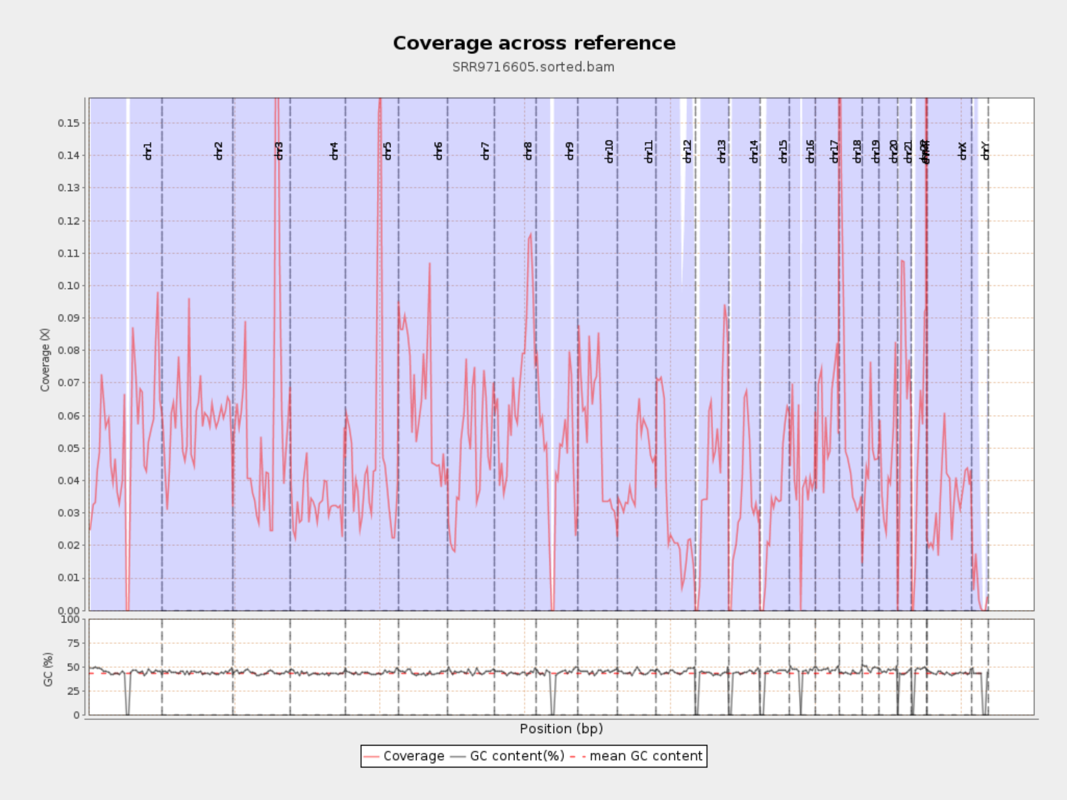
General error rate	0.77%
Mismatches	1,127,241
Insertions	11,430
Mapped reads with at least one insertion	0.58%
Deletions	32,845
Mapped reads with at least one deletion	1.68%
Homopolymer indels	42.67%

2.6. Chromosome stats

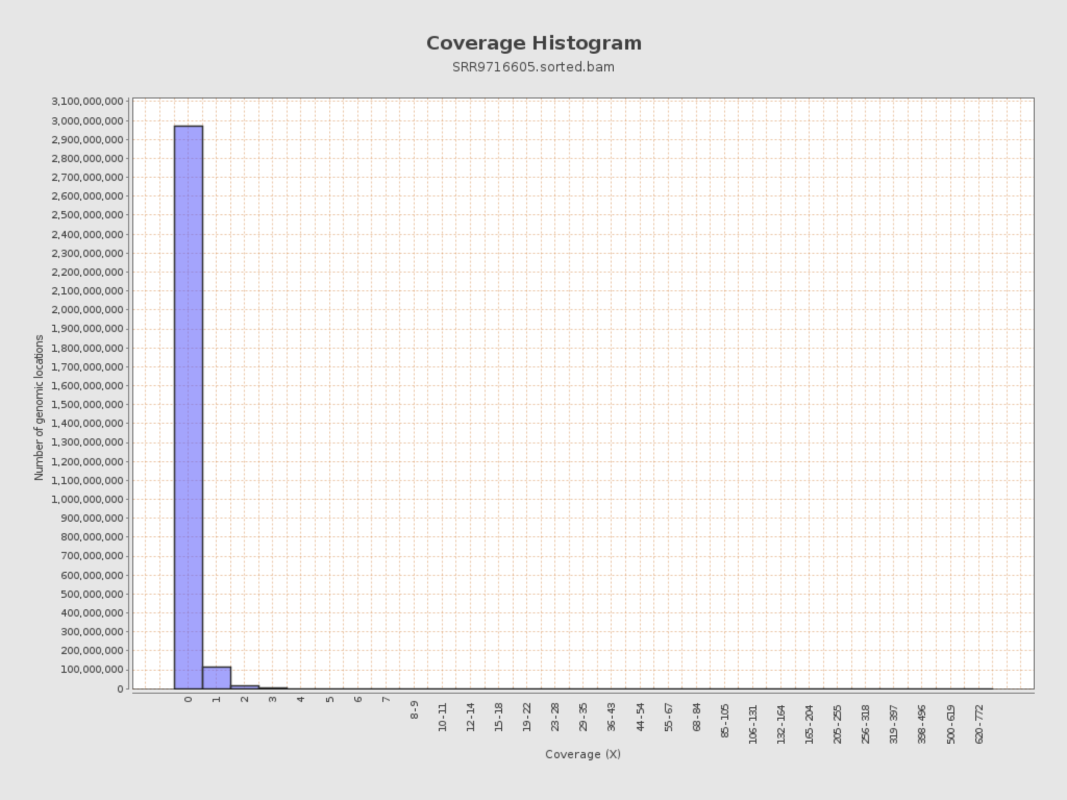
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12779601	0.0513	0.6109
chr2	243199373	14177747	0.0583	0.6222
chr3	198022430	11487061	0.058	0.2802
chr4	191154276	6334803	0.0331	0.2257
chr5	180915260	8770548	0.0485	0.253
chr6	171115067	11245927	0.0657	0.3404
chr7	159138663	7798991	0.049	0.5704

chr8	146364022	10152728	0.0694	0.4859
chr9	141213431	6442129	0.0456	0.3598
chr10	135534747	7579012	0.0559	0.3853
chr11	135006516	5953532	0.0441	0.3306
chr12	133851895	4090544	0.0306	0.2027
chr13	115169878	5476420	0.0476	0.2492
chr14	107349540	3455832	0.0322	0.245
chr15	102531392	3191086	0.0311	0.1998
chr16	90354753	3629459	0.0402	0.2622
chr17	81195210	4859036	0.0598	0.3037
chr18	78077248	4760695	0.061	0.7381
chr19	59128983	2745127	0.0464	0.5008
chr20	63025520	2868108	0.0455	0.2749
chr21	48129895	3319991	0.069	0.3146
chr22	51304566	2310906	0.045	0.245
chrMT	16571	43558	2.6286	2.4697
chrX	155270560	5339002	0.0344	0.2608
chrY	59373566	326891	0.0055	0.1572

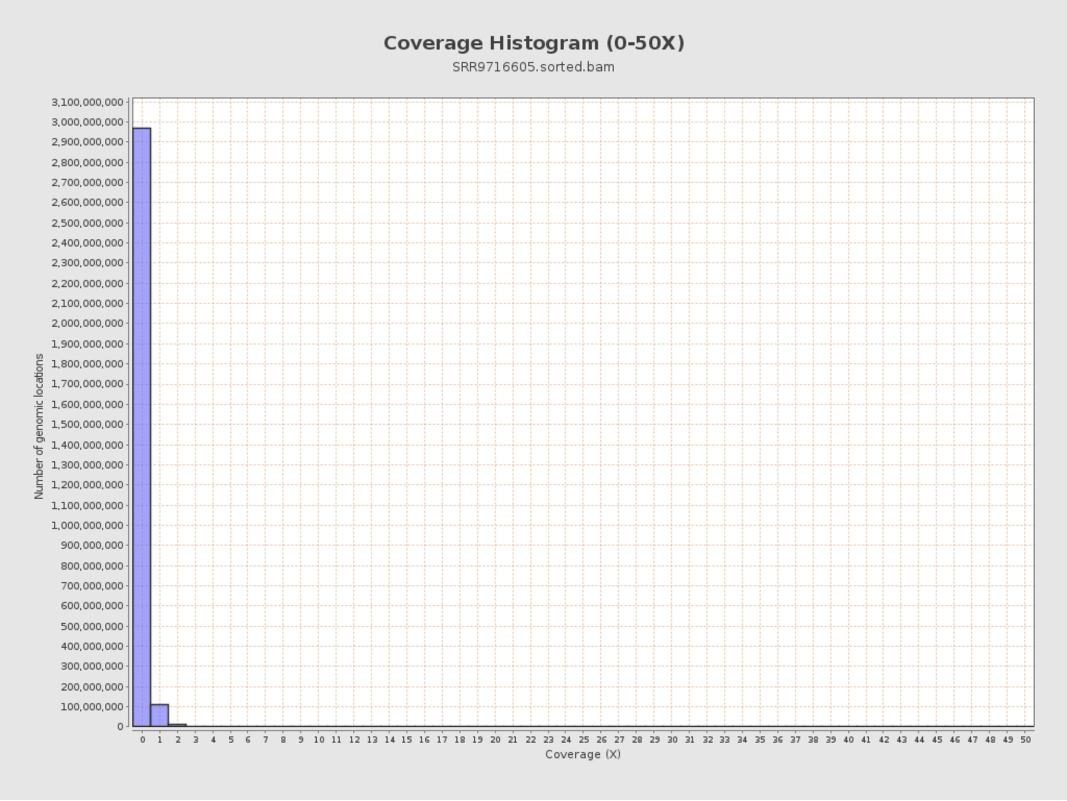
3. Results : Coverage across reference



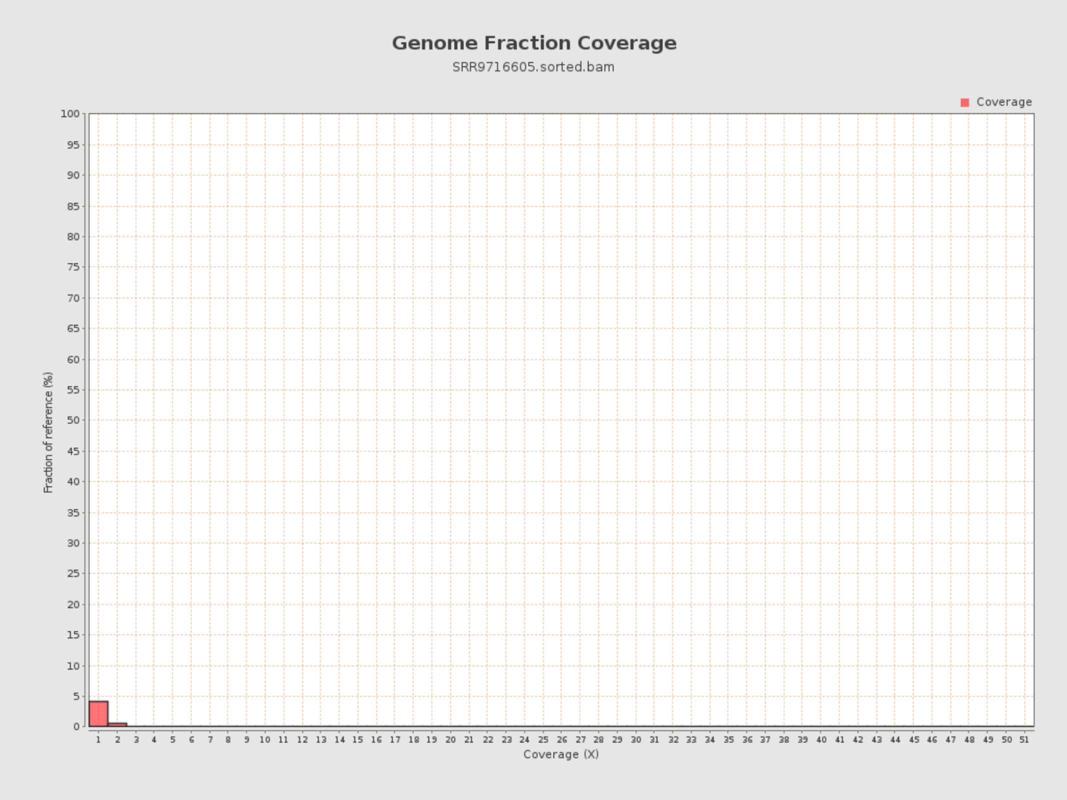
4. Results : Coverage Histogram



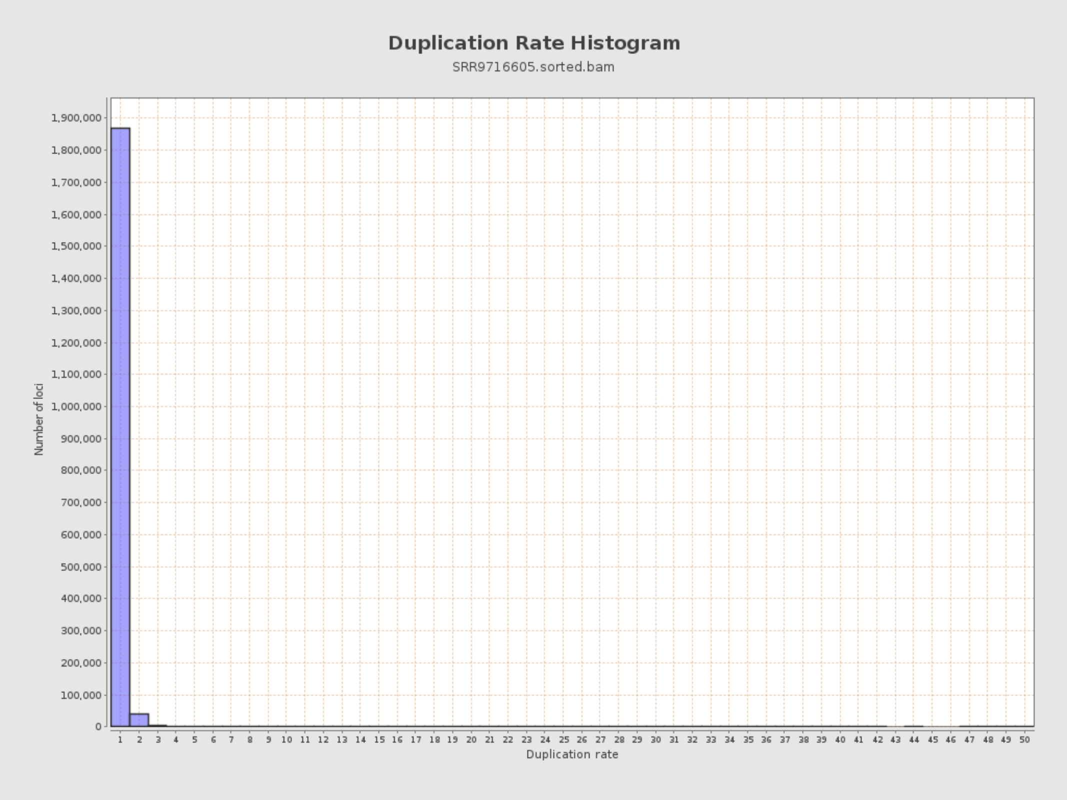
5. Results : Coverage Histogram (0-50X)



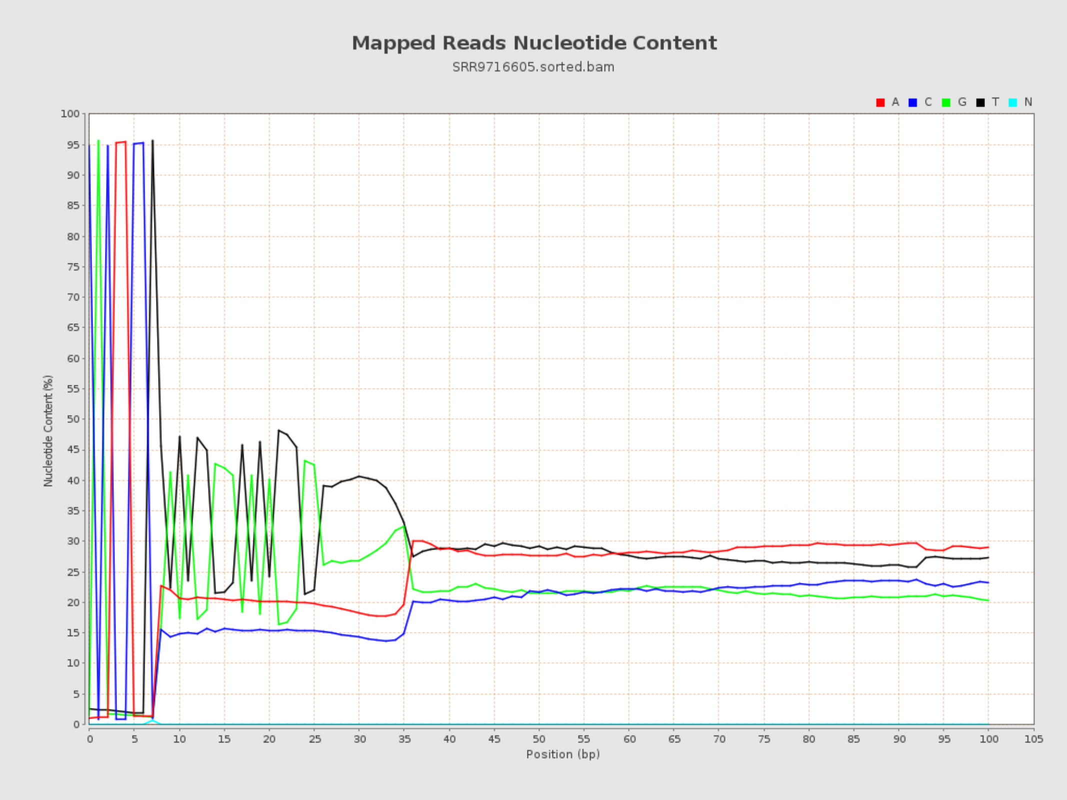
6. Results : Genome Fraction Coverage



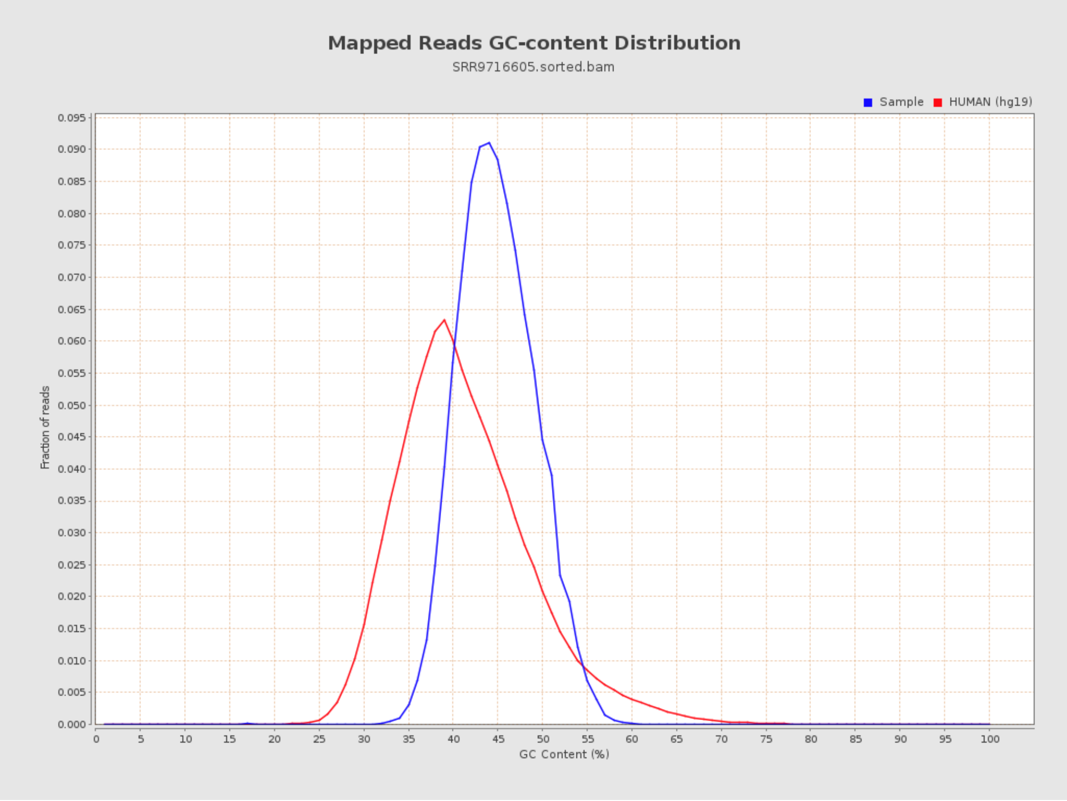
7. Results : Duplication Rate Histogram



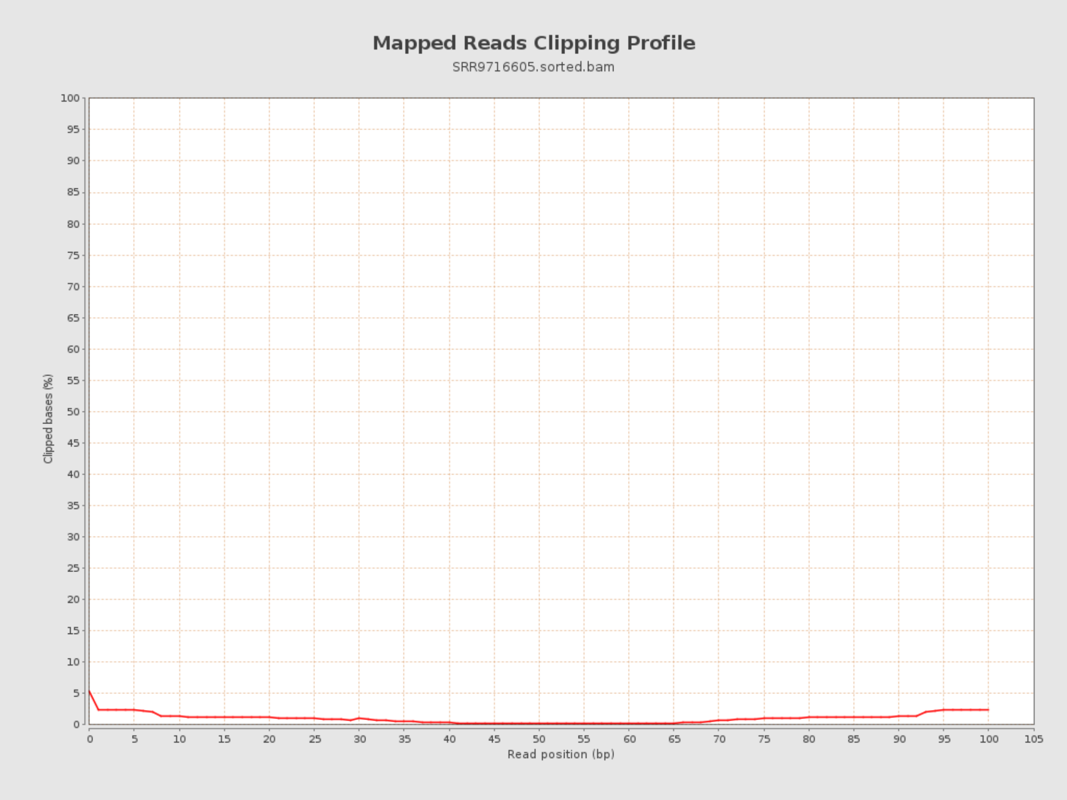
8. Results : Mapped Reads Nucleotide Content



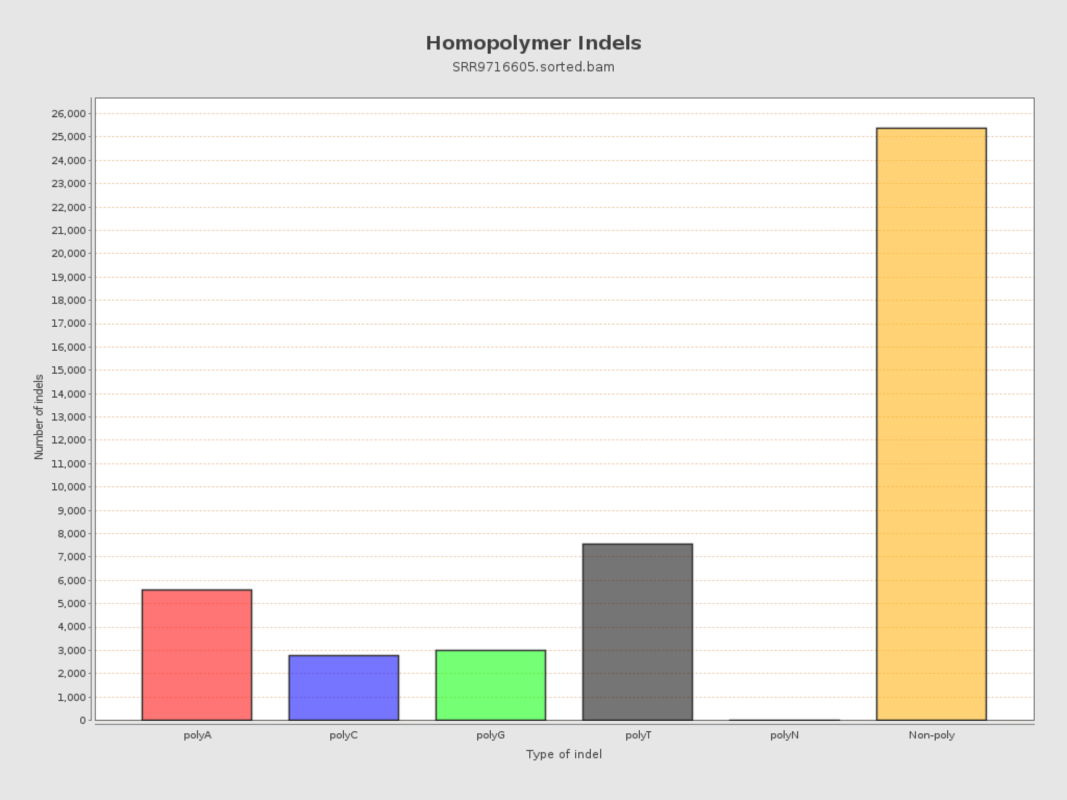
9. Results : Mapped Reads GC-content Distribution



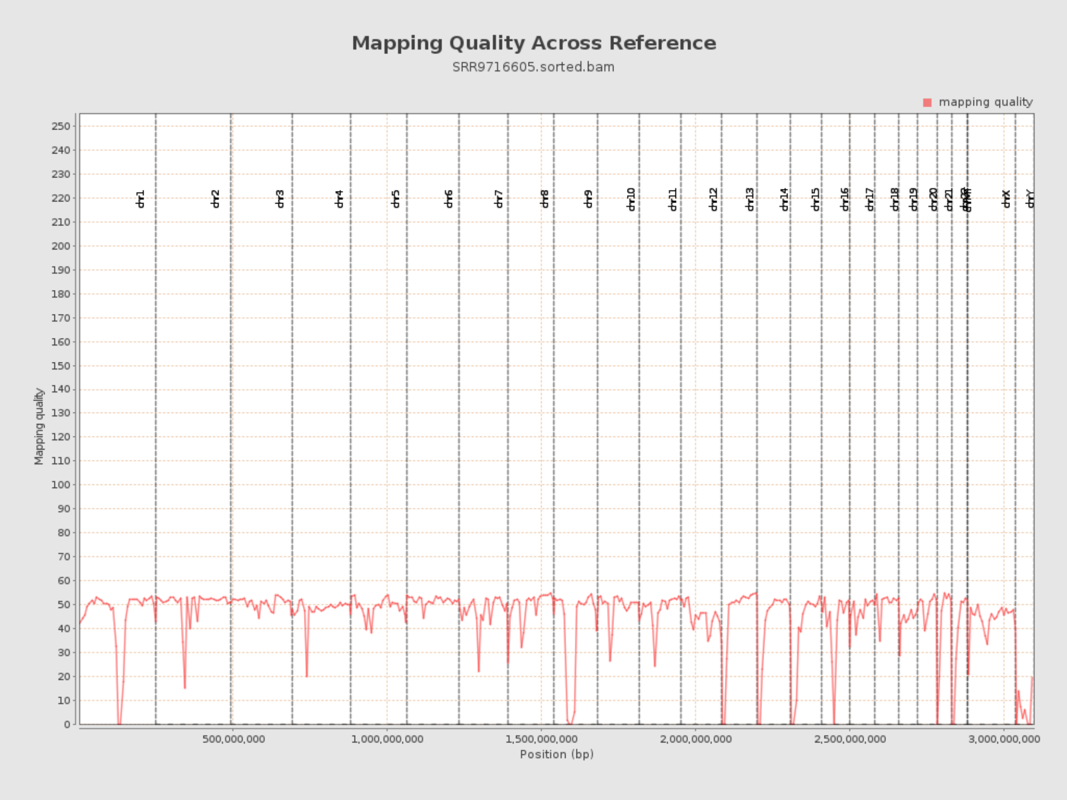
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram