Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 03:59:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716666.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_SRR9716666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716666.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 03:59:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,413,843
Mapped reads	2,242,224 / 92.89%
Unmapped reads	171,619 / 7.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,958 / 1.78%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	106,218 / 4.4%
Duplication rate	3.4%
Clipped reads	2,280,218 / 94.46%

2.2. ACGT Content

Number/percentage of A's	46,543,688 / 26.17%
Number/percentage of C's	33,592,174 / 18.88%
Number/percentage of T's	53,909,067 / 30.31%
Number/percentage of G's	43,820,440 / 24.64%
Number/percentage of N's	12,957 / 0.01%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0575

Standard Deviation	0.5123

2.4. Mapping Quality

Mean Mapping Quality	47.49

2.5. Mismatches and indels

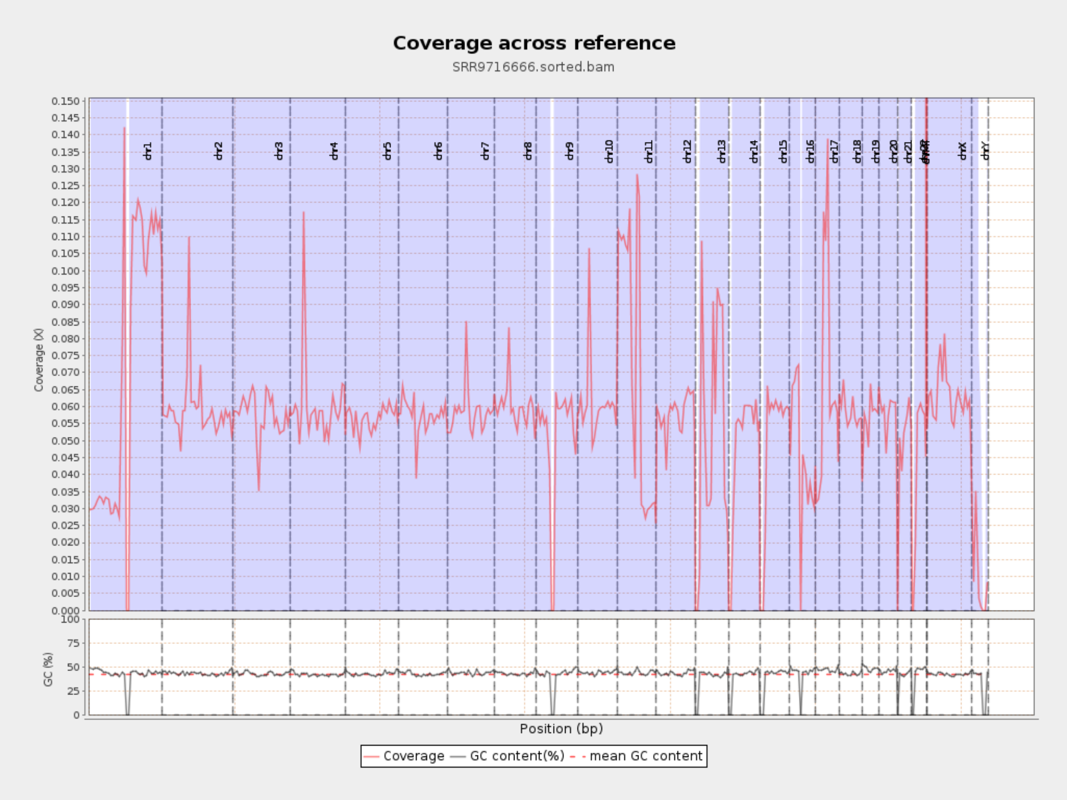
General error rate	0.66%
Mismatches	1,145,741
Insertions	15,136
Mapped reads with at least one insertion	0.66%
Deletions	42,904
Mapped reads with at least one deletion	1.88%
Homopolymer indels	42.76%

2.6. Chromosome stats

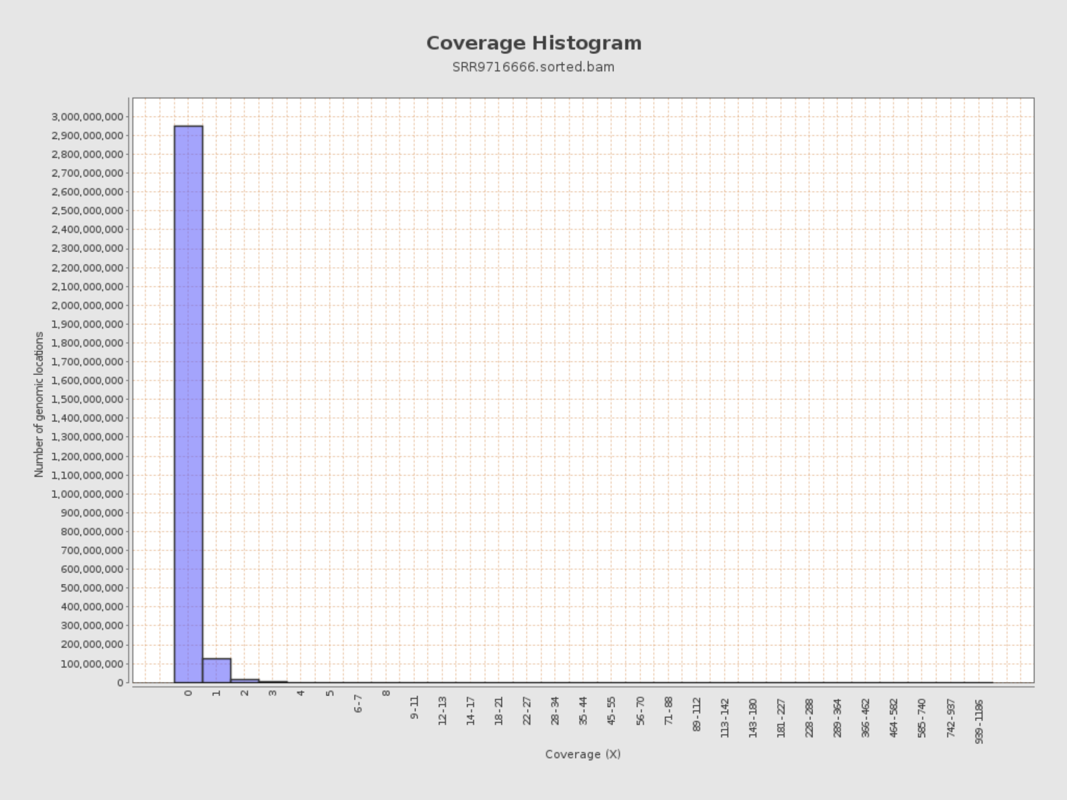
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17287500	0.0694	1.0675
chr2	243199373	14462453	0.0595	0.5729
chr3	198022430	11402906	0.0576	0.2762
chr4	191154276	11459960	0.06	0.3824
chr5	180915260	10246811	0.0566	0.2771
chr6	171115067	9815112	0.0574	0.3018
chr7	159138663	9311277	0.0585	0.6136

chr8	146364022	8785492	0.06	0.5899
chr9	141213431	7156610	0.0507	0.4318
chr10	135534747	8230277	0.0607	0.5035
chr11	135006516	9770328	0.0724	0.568
chr12	133851895	7773222	0.0581	0.2802
chr13	115169878	5962727	0.0518	0.2654
chr14	107349540	5138874	0.0479	0.278
chr15	102531392	5015295	0.0489	0.2544
chr16	90354753	4070524	0.0451	0.2789
chr17	81195210	5637898	0.0694	0.3783
chr18	78077248	4590421	0.0588	0.7323
chr19	59128983	3377111	0.0571	0.6932
chr20	63025520	3642230	0.0578	0.2999
chr21	48129895	2311498	0.048	0.3135
chr22	51304566	2063057	0.0402	0.2344
chrMT	16571	54273	3.2752	2.536
chrX	155270560	9838093	0.0634	0.3509
chrY	59373566	556541	0.0094	0.309

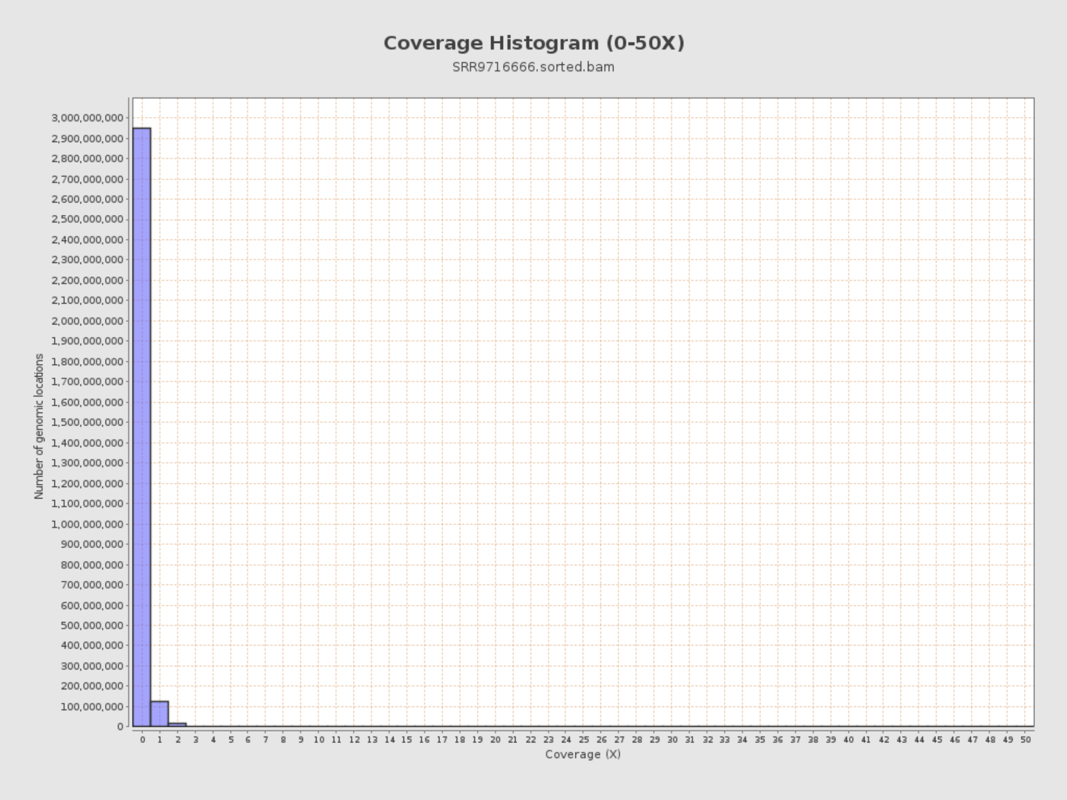
3. Results : Coverage across reference



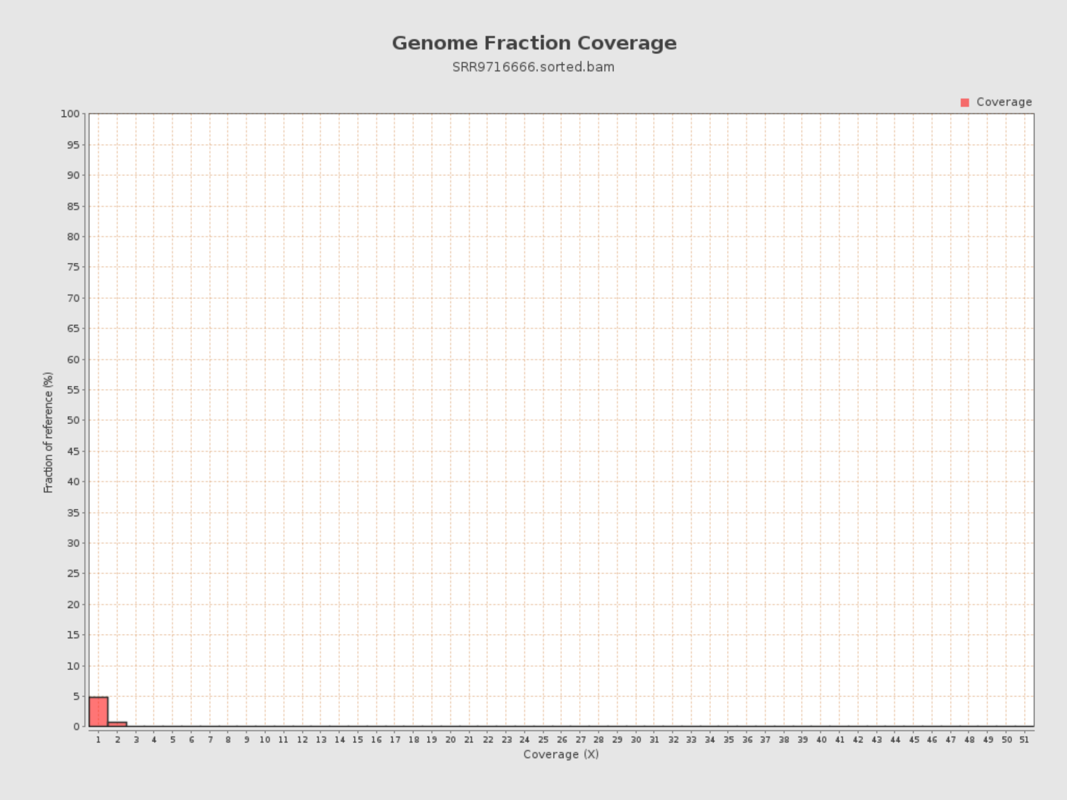
4. Results : Coverage Histogram



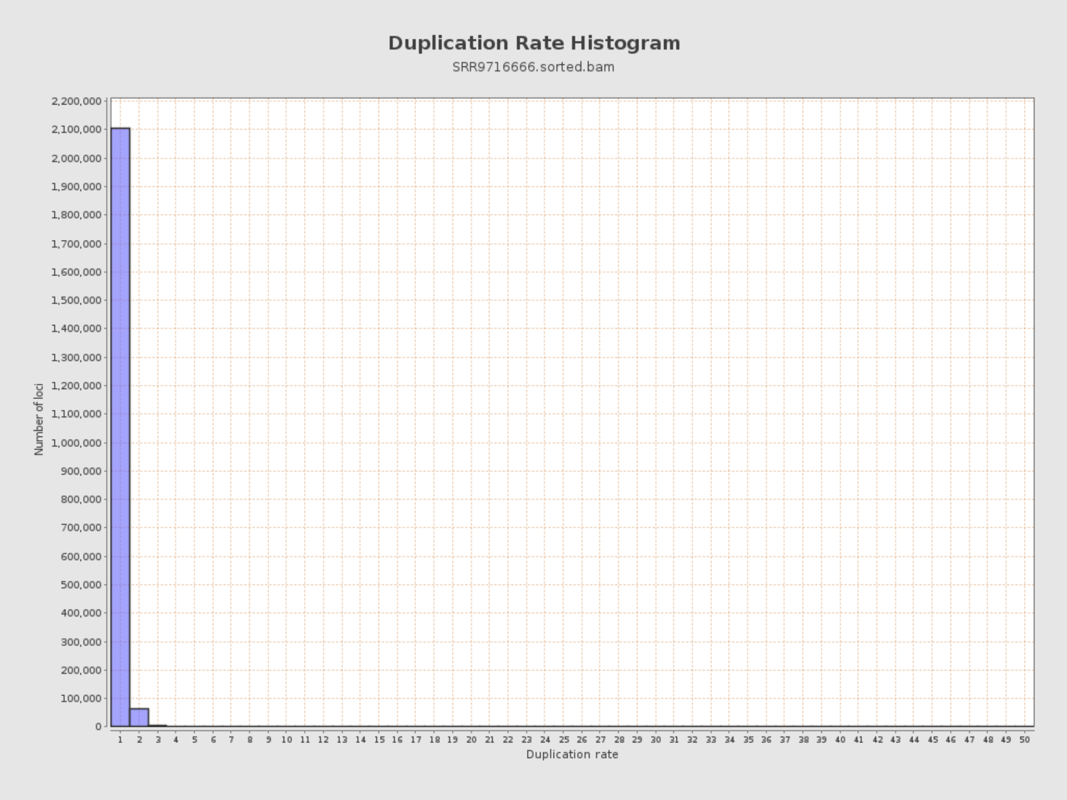
5. Results : Coverage Histogram (0-50X)



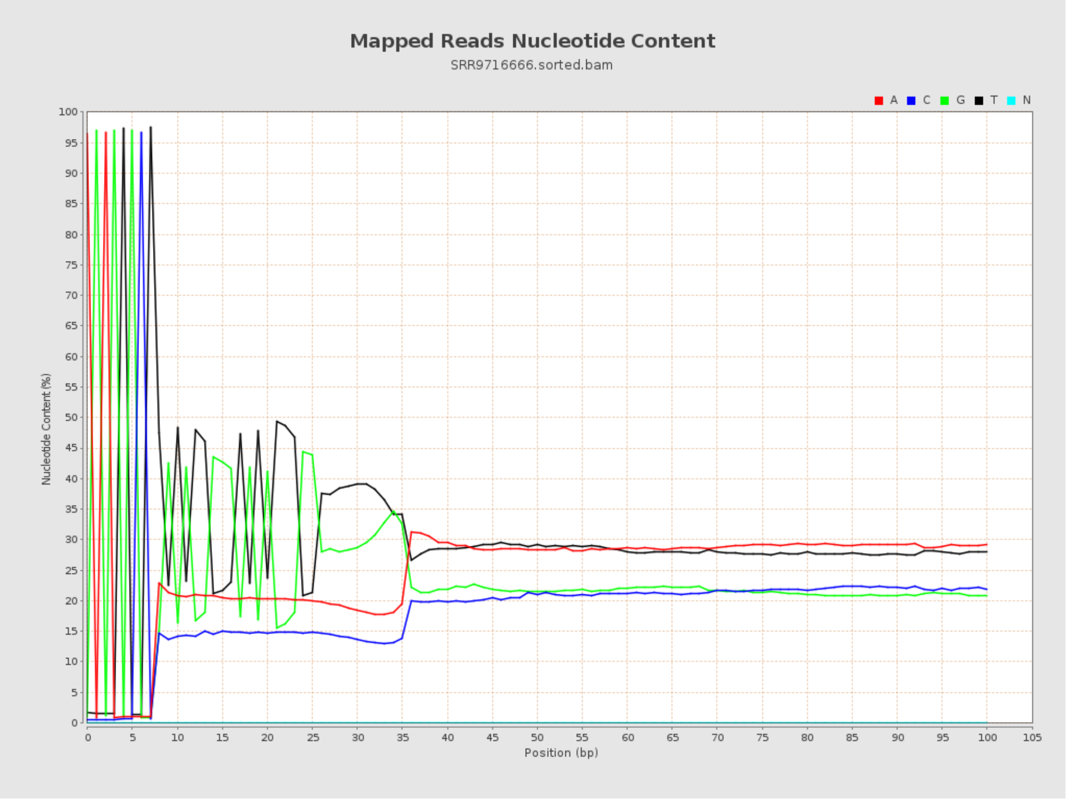
6. Results : Genome Fraction Coverage



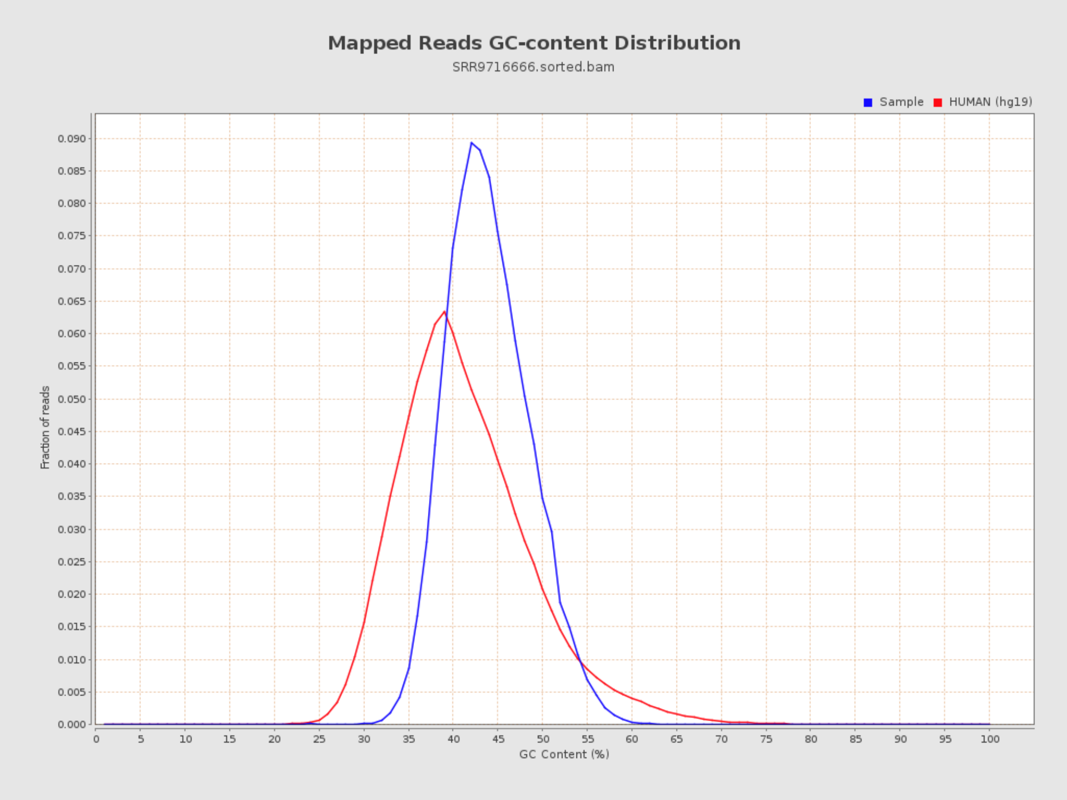
7. Results : Duplication Rate Histogram



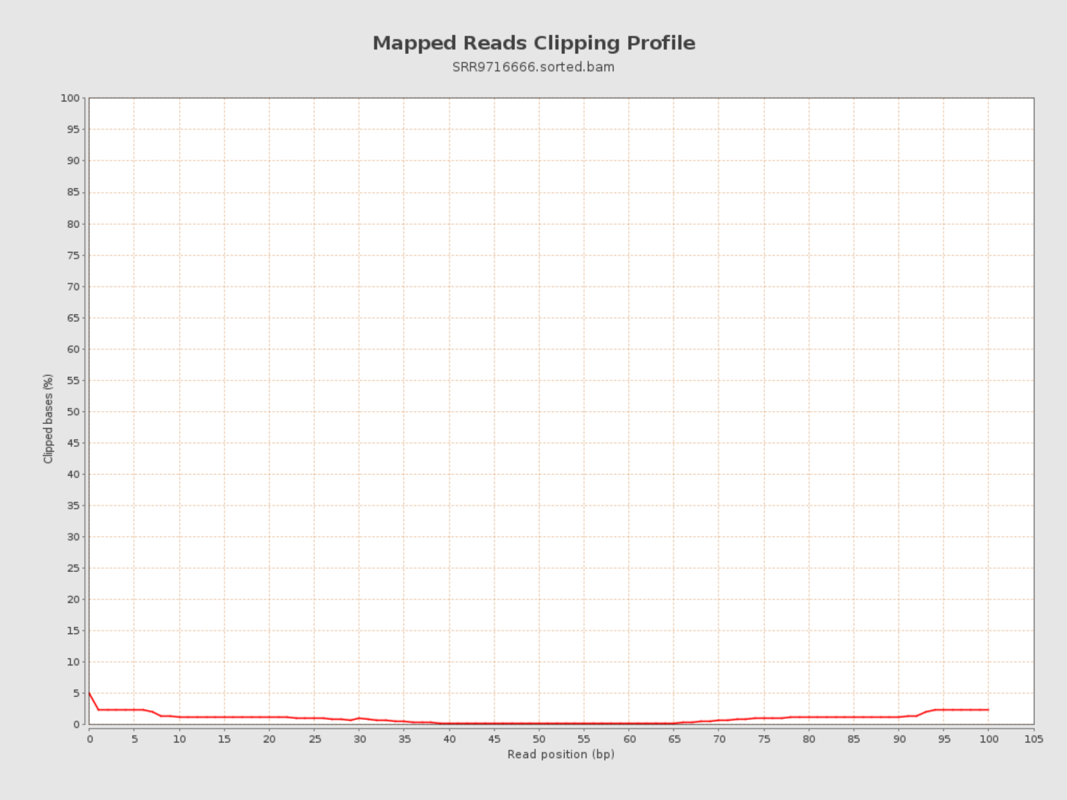
8. Results : Mapped Reads Nucleotide Content



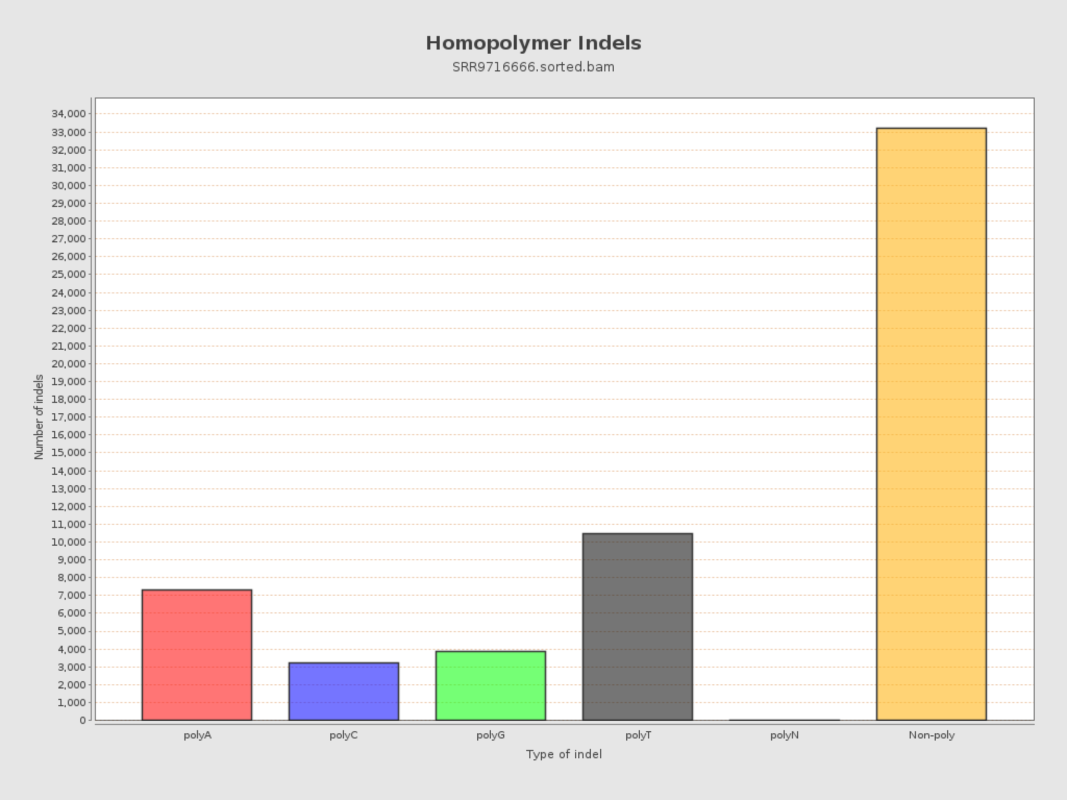
9. Results : Mapped Reads GC-content Distribution



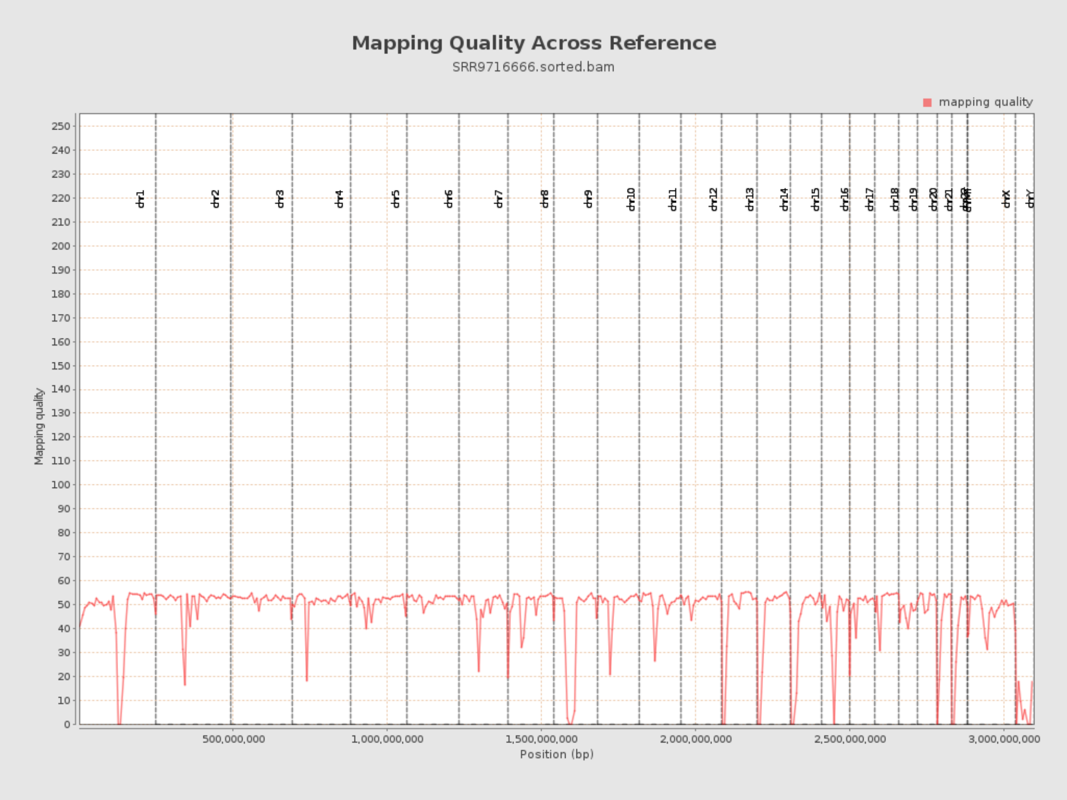
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram