Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 04:59:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716673.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_SRR9716673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716673.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 04:59:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,967,131
Mapped reads	1,844,583 / 93.77%
Unmapped reads	122,548 / 6.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,810 / 1.82%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	77,605 / 3.95%
Duplication rate	2.99%
Clipped reads	1,875,010 / 95.32%

2.2. ACGT Content

Number/percentage of A's	37,921,841 / 26.12%
Number/percentage of C's	28,598,258 / 19.7%
Number/percentage of T's	44,413,854 / 30.6%
Number/percentage of G's	34,221,517 / 23.57%
Number/percentage of N's	10,723 / 0.01%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0469

Standard Deviation	0.4419

2.4. Mapping Quality

Mean Mapping Quality	47.59

2.5. Mismatches and indels

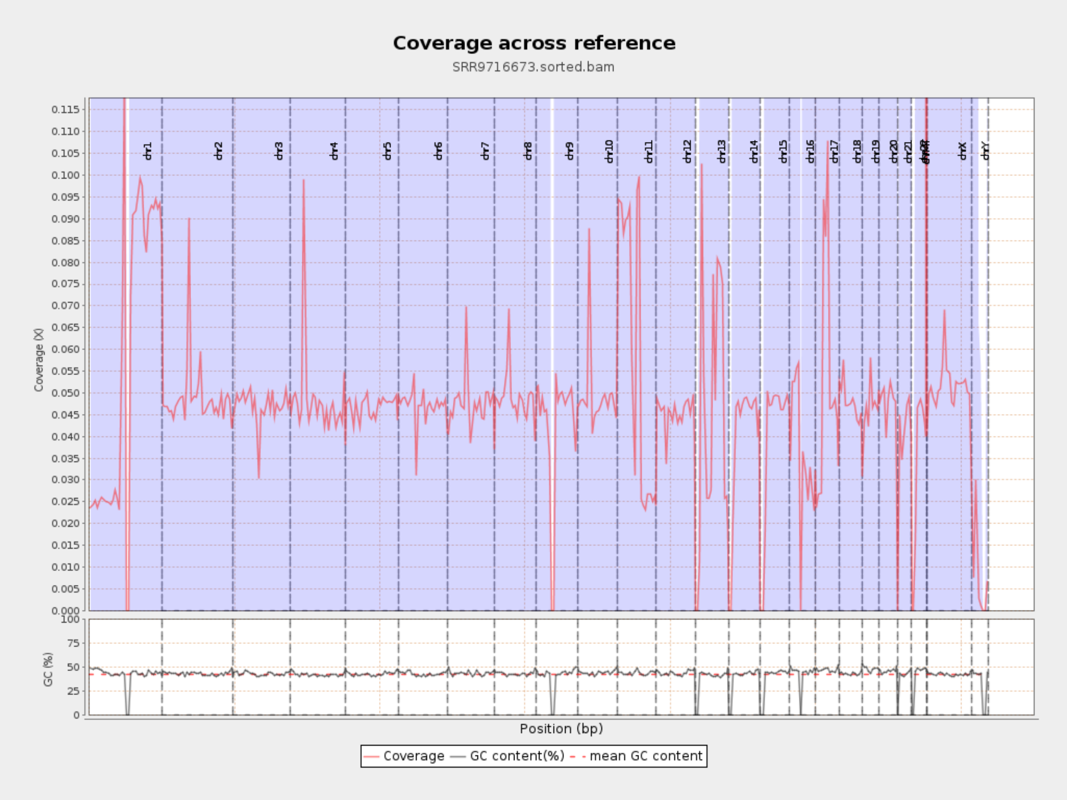
General error rate	0.66%
Mismatches	920,228
Insertions	13,614
Mapped reads with at least one insertion	0.73%
Deletions	35,263
Mapped reads with at least one deletion	1.88%
Homopolymer indels	40.59%

2.6. Chromosome stats

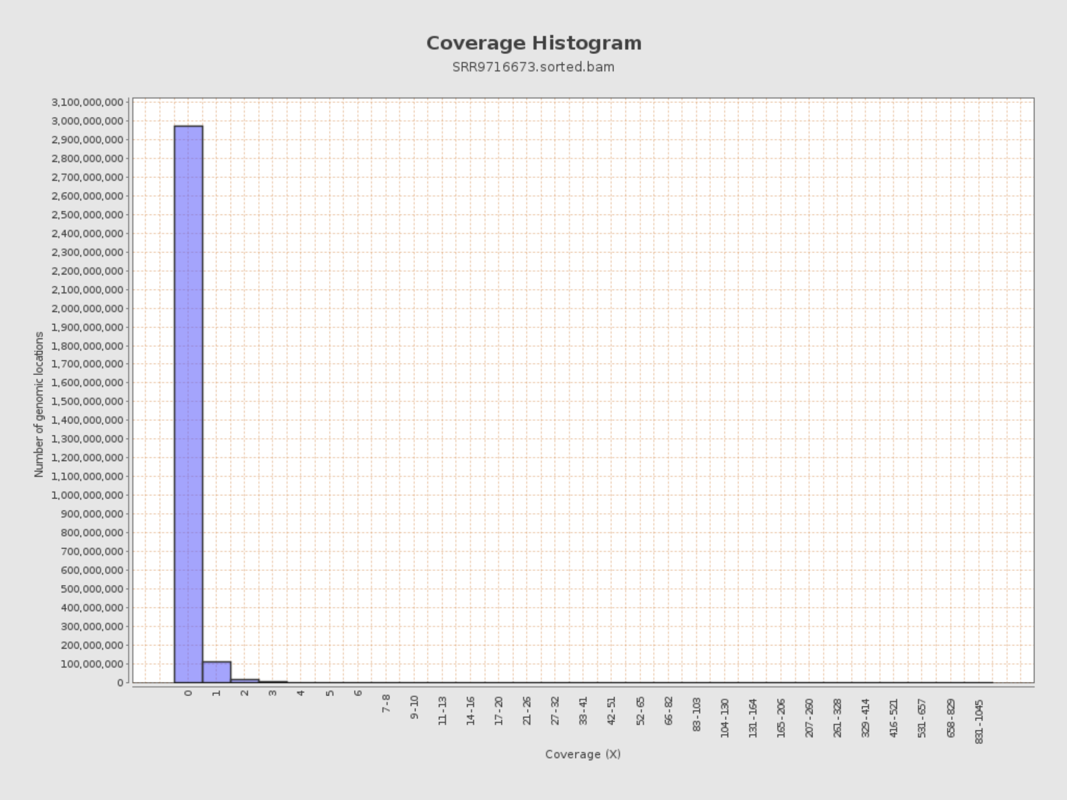
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14199018	0.057	0.9403
chr2	243199373	11959523	0.0492	0.4533
chr3	198022430	9288262	0.0469	0.2428
chr4	191154276	9265449	0.0485	0.3269
chr5	180915260	8473148	0.0468	0.2458
chr6	171115067	8058952	0.0471	0.2672
chr7	159138663	7620532	0.0479	0.4945

chr8	146364022	7168706	0.049	0.5458
chr9	141213431	5923763	0.0419	0.3592
chr10	135534747	6686312	0.0493	0.4307
chr11	135006516	8017046	0.0594	0.4862
chr12	133851895	6078117	0.0454	0.2406
chr13	115169878	5140774	0.0446	0.2398
chr14	107349540	4196692	0.0391	0.2449
chr15	102531392	4019880	0.0392	0.222
chr16	90354753	3229344	0.0357	0.2405
chr17	81195210	4394557	0.0541	0.3177
chr18	78077248	3757526	0.0481	0.5922
chr19	59128983	2758659	0.0467	0.6565
chr20	63025520	2995435	0.0475	0.2668
chr21	48129895	1866807	0.0388	0.2665
chr22	51304566	1636229	0.0319	0.201
chrMT	16571	40658	2.4536	2.0124
chrX	155270560	7996448	0.0515	0.3071
chrY	59373566	461770	0.0078	0.2614

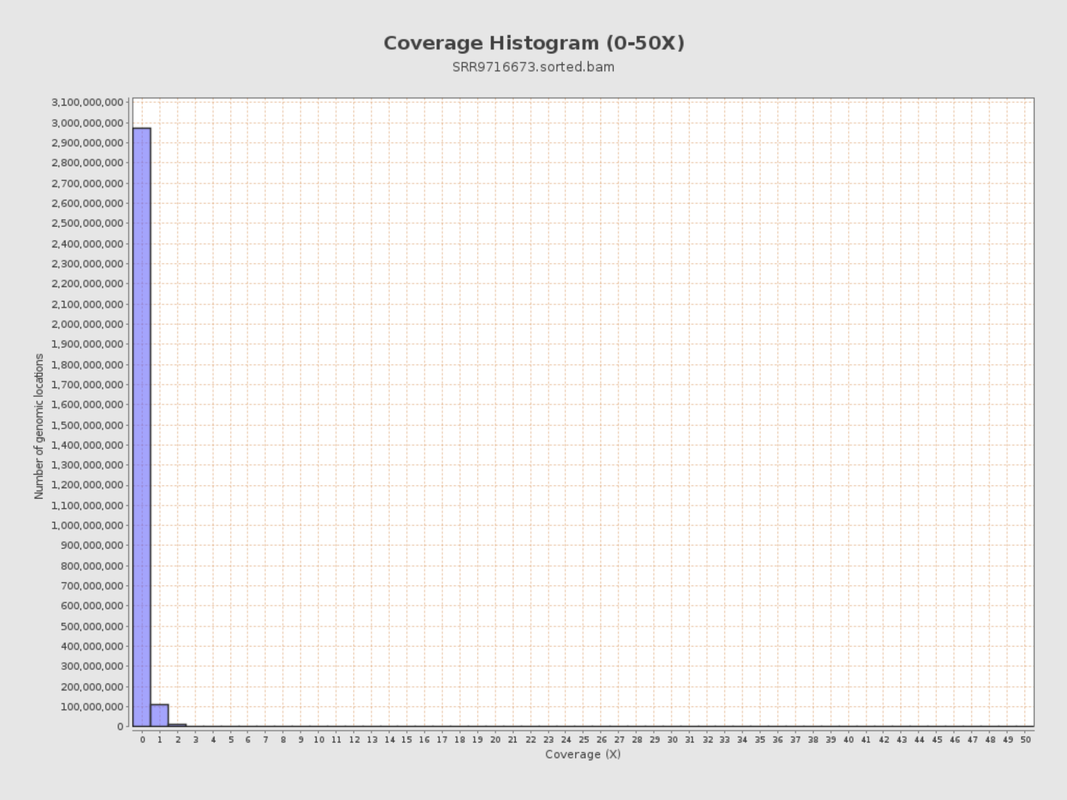
3. Results : Coverage across reference



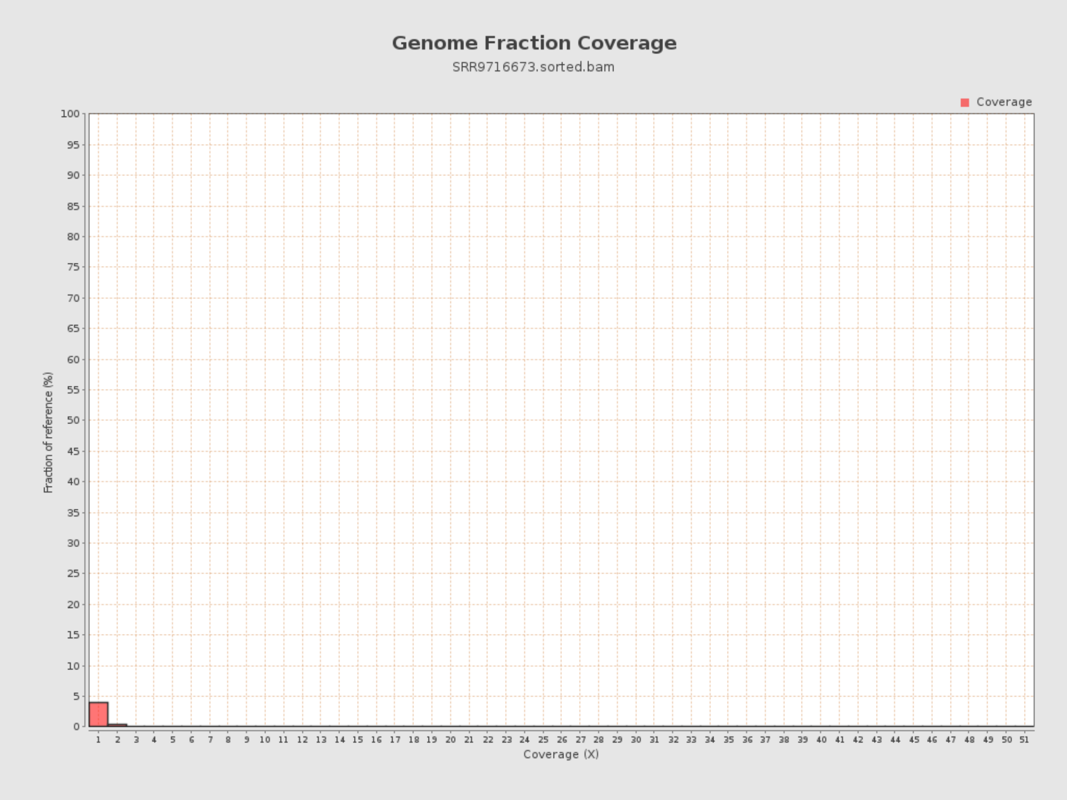
4. Results : Coverage Histogram



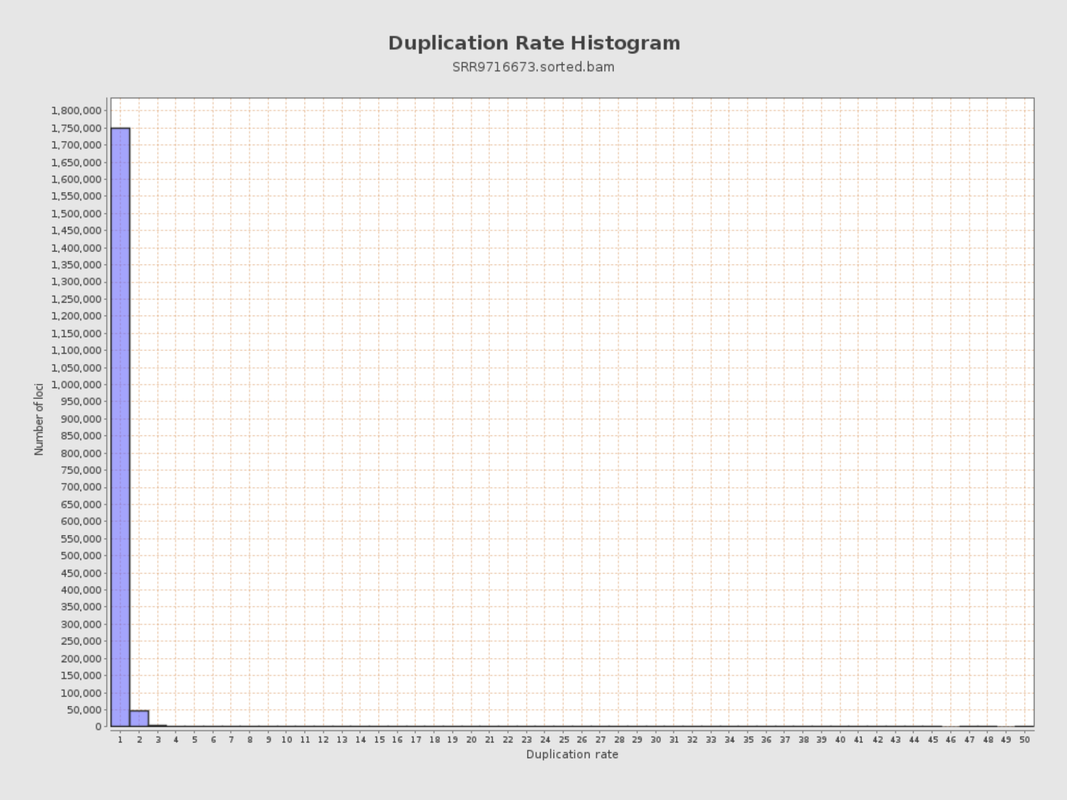
5. Results : Coverage Histogram (0-50X)



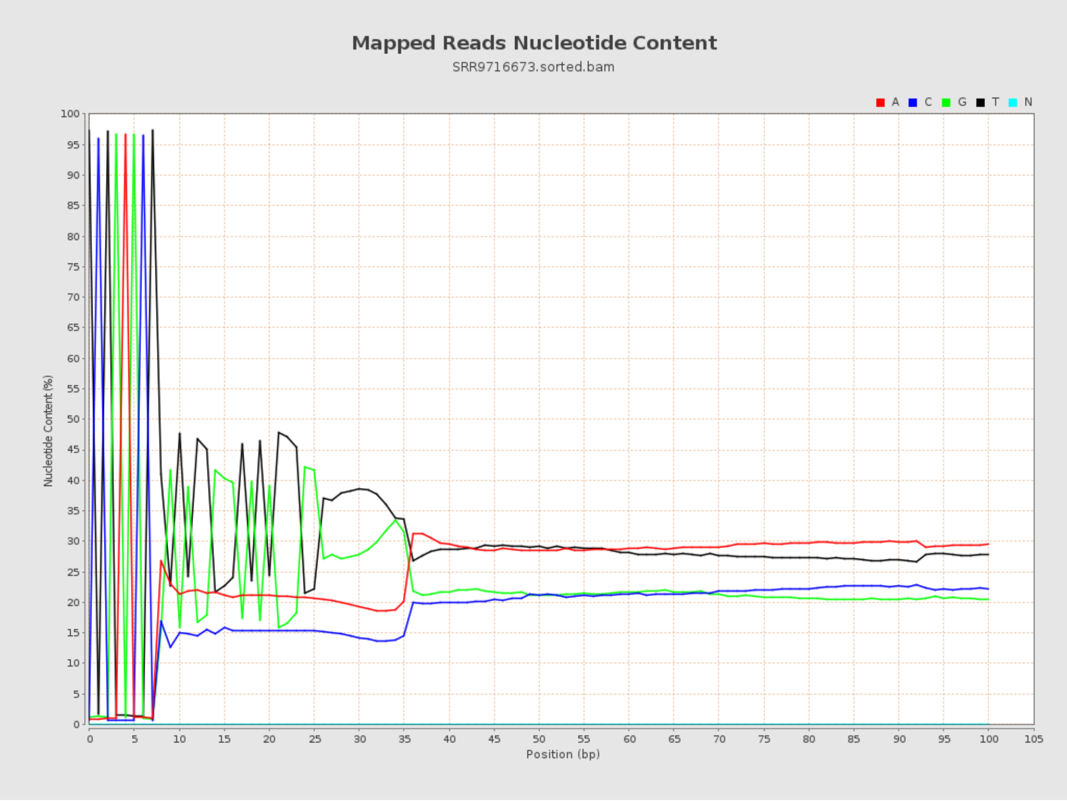
6. Results : Genome Fraction Coverage



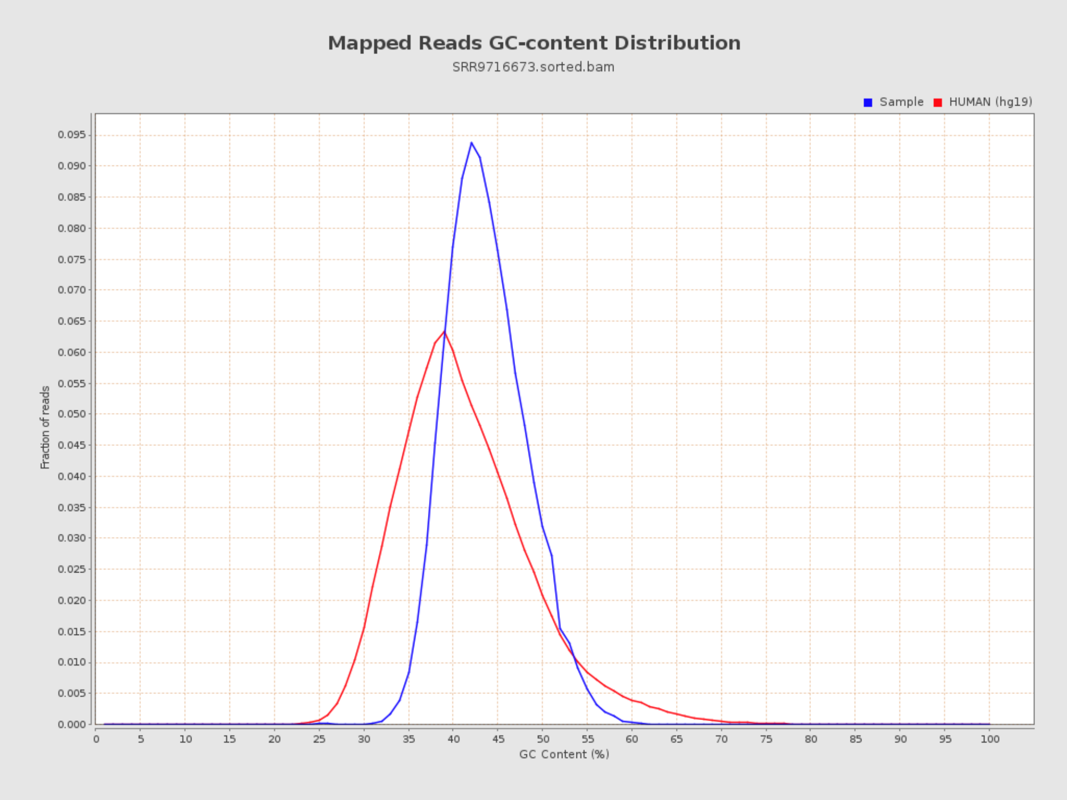
7. Results : Duplication Rate Histogram



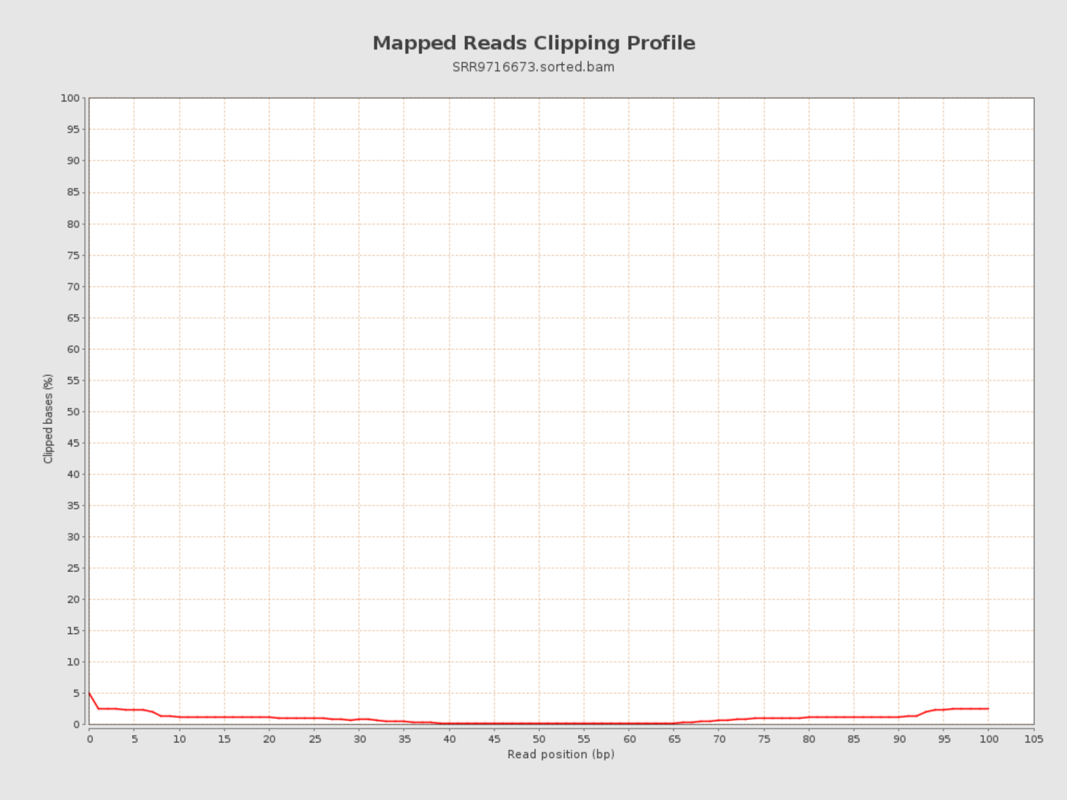
8. Results : Mapped Reads Nucleotide Content



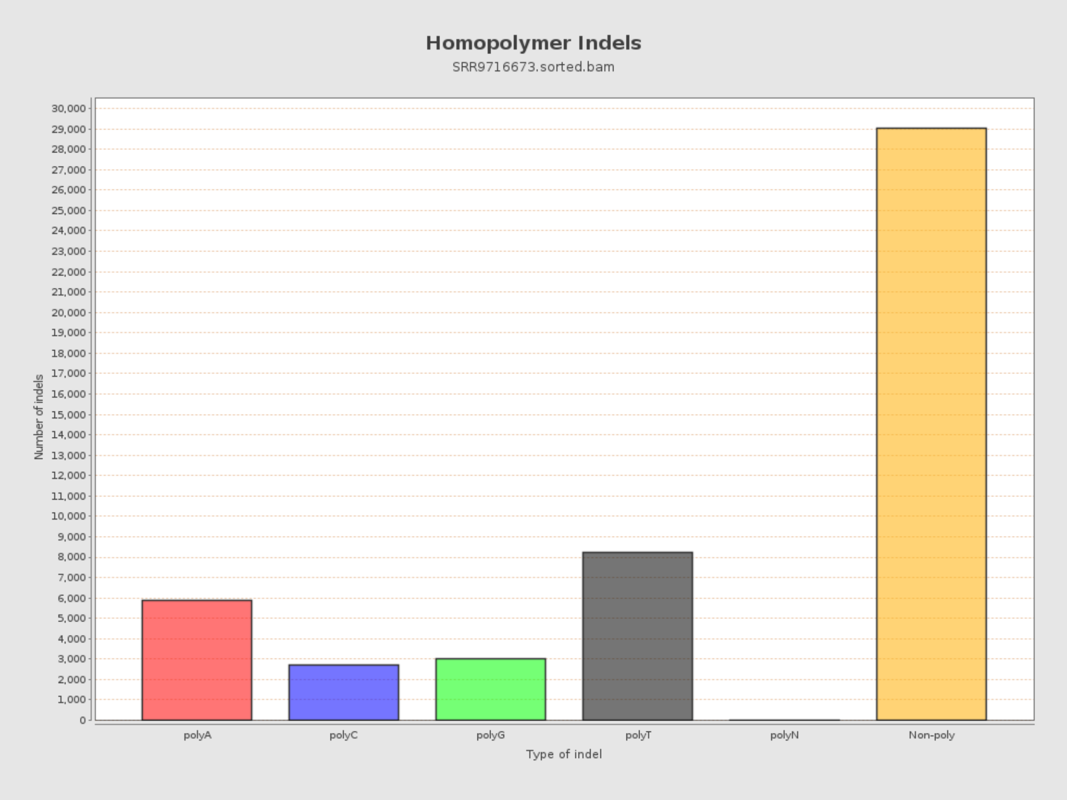
9. Results : Mapped Reads GC-content Distribution



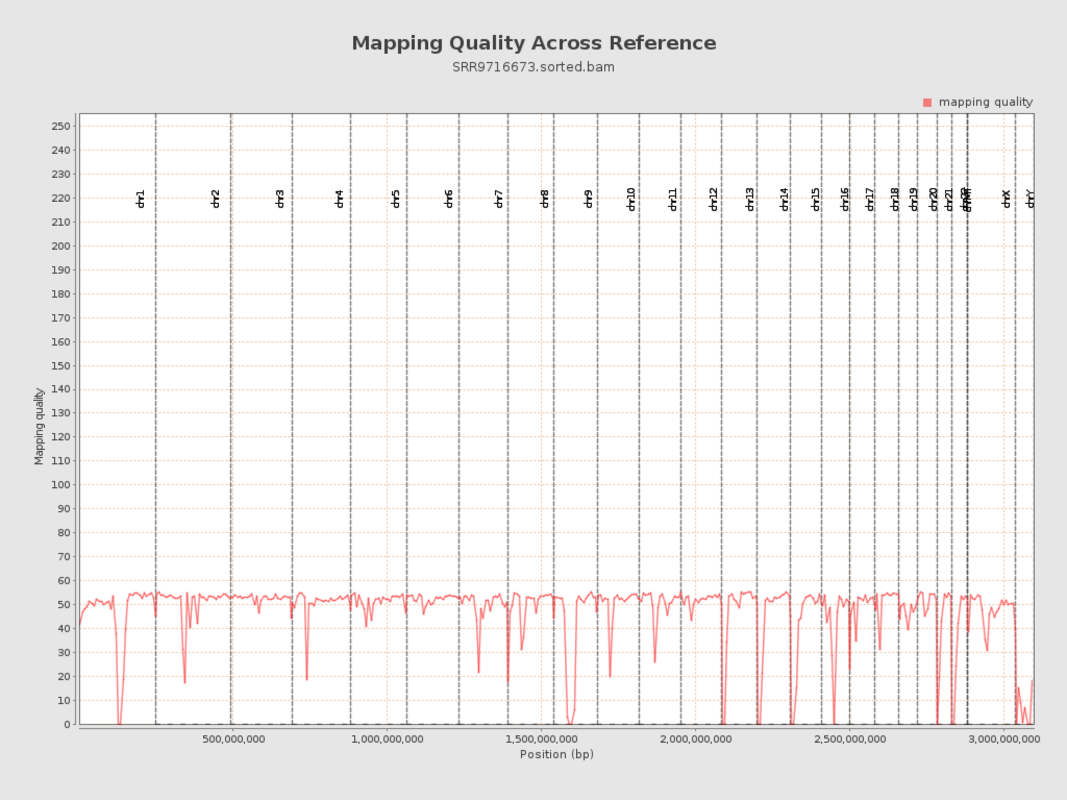
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram