Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:08:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716753.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_SRR9716753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716753.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:08:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,575,238
Mapped reads	1,190,470 / 75.57%
Unmapped reads	384,768 / 24.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,939 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	63,700 / 4.04%
Duplication rate	4.33%
Clipped reads	1,191,773 / 75.66%

2.2. ACGT Content

Number/percentage of A's	15,794,425 / 25.23%
Number/percentage of C's	13,696,919 / 21.88%
Number/percentage of T's	17,455,234 / 27.89%
Number/percentage of G's	15,647,749 / 25%
Number/percentage of N's	1,709 / 0%
GC Percentage	46.88%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.1938

2.4. Mapping Quality

Mean Mapping Quality	40.26

2.5. Mismatches and indels

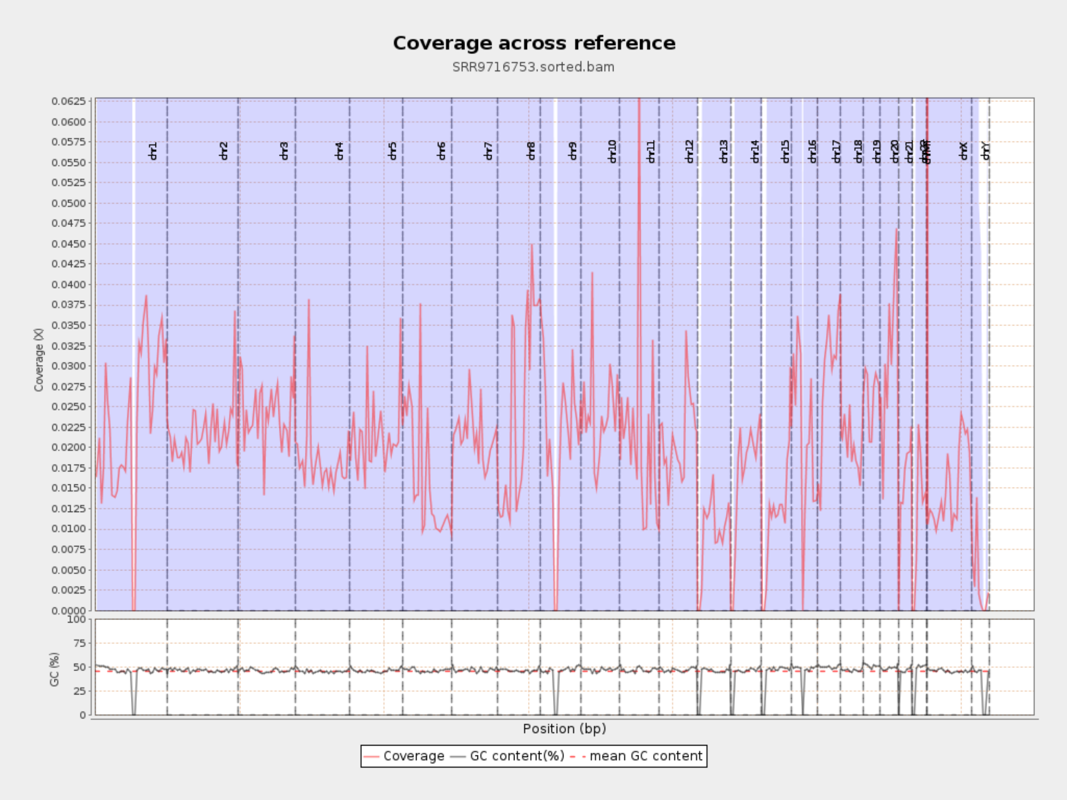
General error rate	0.54%
Mismatches	328,679
Insertions	4,684
Mapped reads with at least one insertion	0.39%
Deletions	10,384
Mapped reads with at least one deletion	0.87%
Homopolymer indels	32.83%

2.6. Chromosome stats

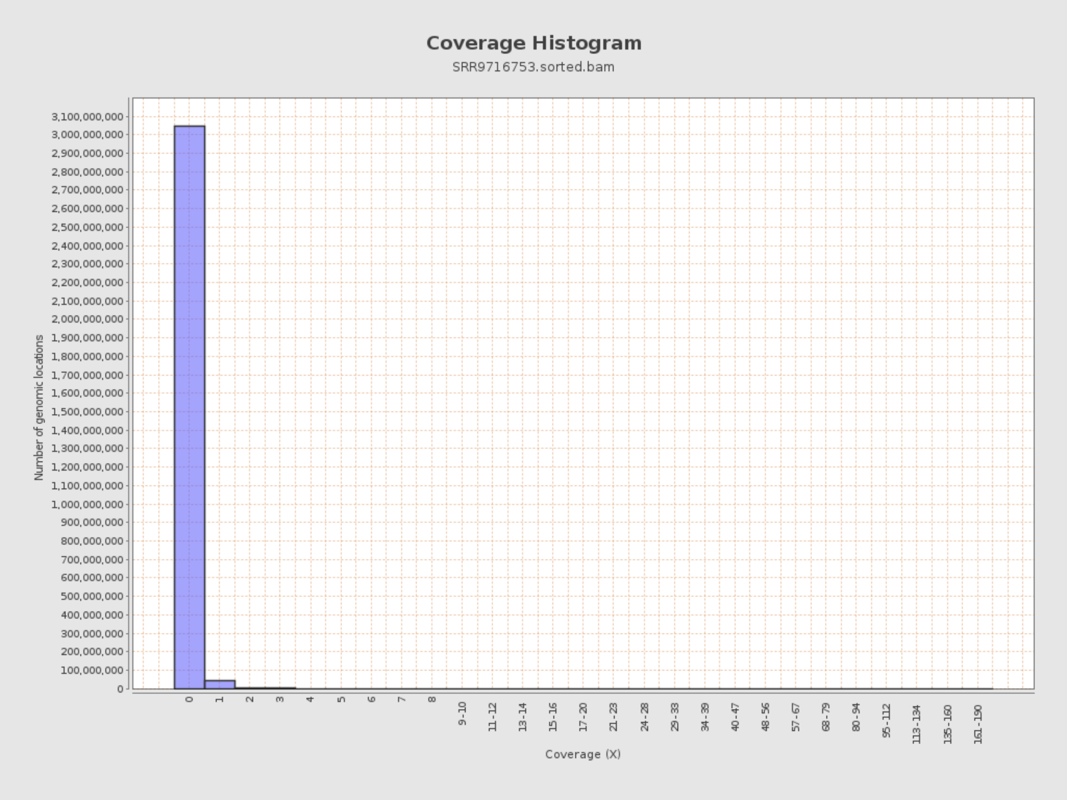
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5792320	0.0232	0.2276
chr2	243199373	5282054	0.0217	0.2222
chr3	198022430	4769890	0.0241	0.1927
chr4	191154276	3539838	0.0185	0.1845
chr5	180915260	3900226	0.0216	0.1791
chr6	171115067	2780895	0.0163	0.1584
chr7	159138663	3421826	0.0215	0.213

chr8	146364022	3596411	0.0246	0.1983
chr9	141213431	3025126	0.0214	0.1855
chr10	135534747	3286191	0.0242	0.2504
chr11	135006516	2998120	0.0222	0.213
chr12	133851895	2833126	0.0212	0.1813
chr13	115169878	1094945	0.0095	0.1179
chr14	107349540	1780805	0.0166	0.1556
chr15	102531392	1166231	0.0114	0.13
chr16	90354753	1915190	0.0212	0.1893
chr17	81195210	2341132	0.0288	0.2204
chr18	78077248	1570443	0.0201	0.2043
chr19	59128983	1550935	0.0262	0.2254
chr20	63025520	1988327	0.0315	0.2336
chr21	48129895	751854	0.0156	0.1932
chr22	51304566	611244	0.0119	0.133
chrMT	16571	51089	3.083	3.0064
chrX	155270560	2364688	0.0152	0.1557
chrY	59373566	200146	0.0034	0.1186

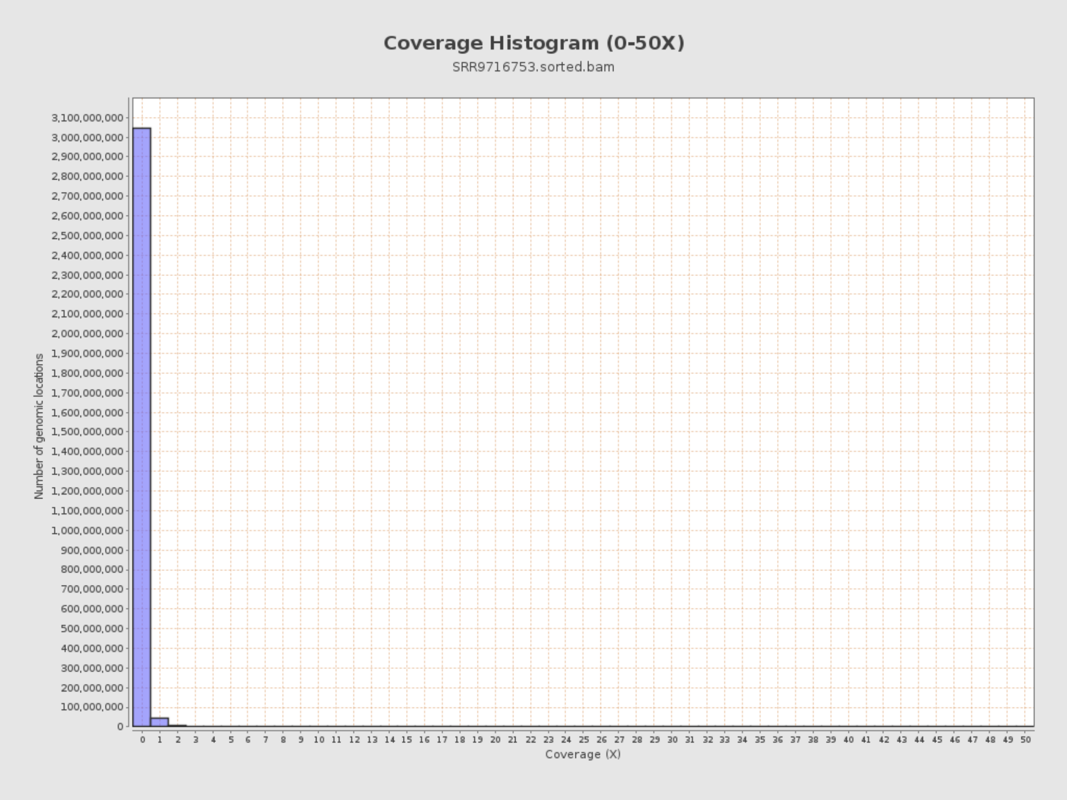
3. Results : Coverage across reference



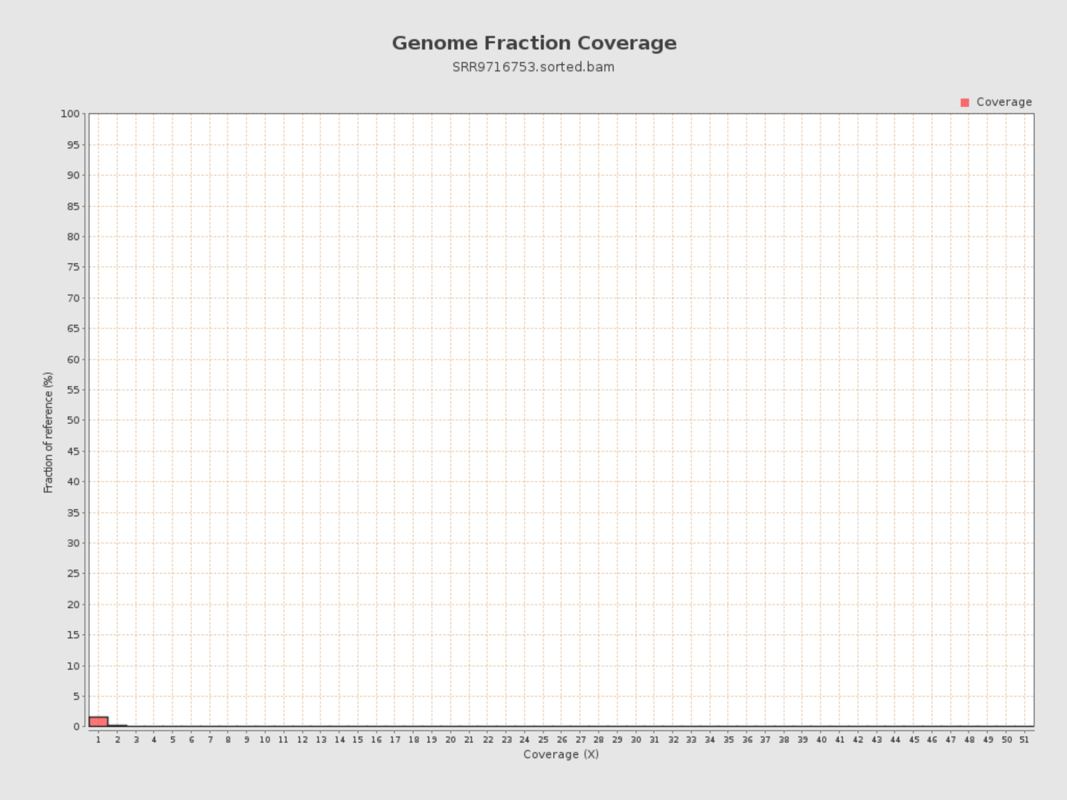
4. Results : Coverage Histogram



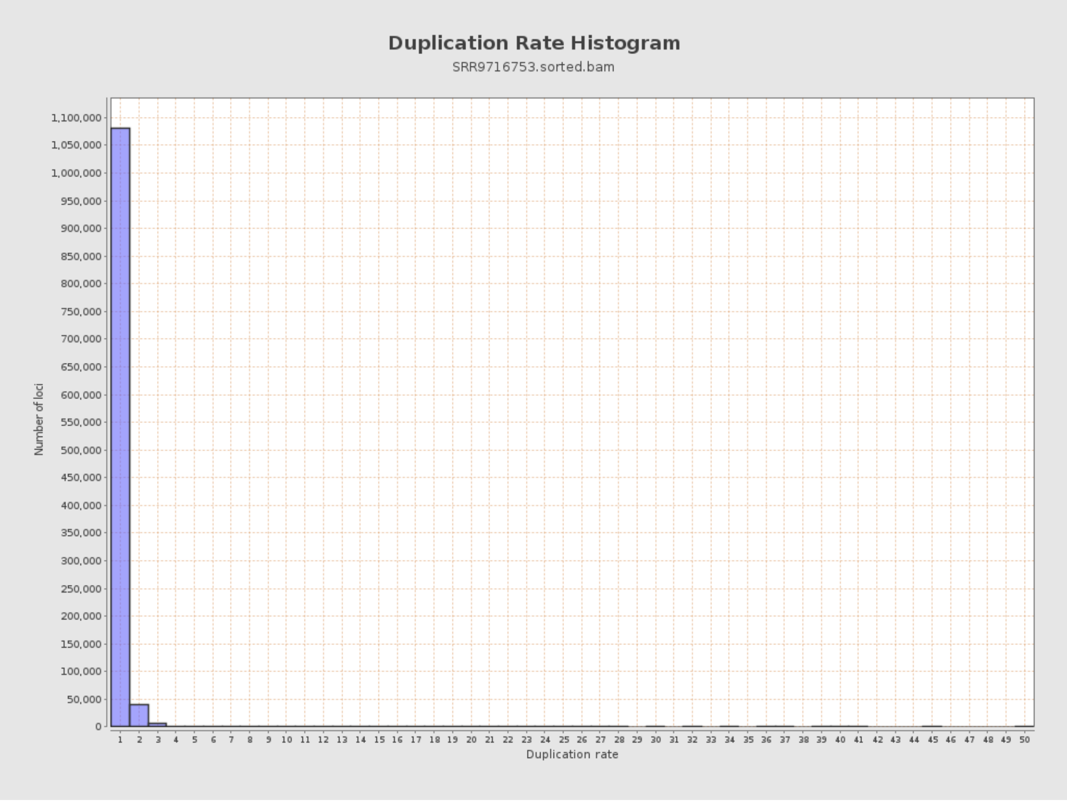
5. Results : Coverage Histogram (0-50X)



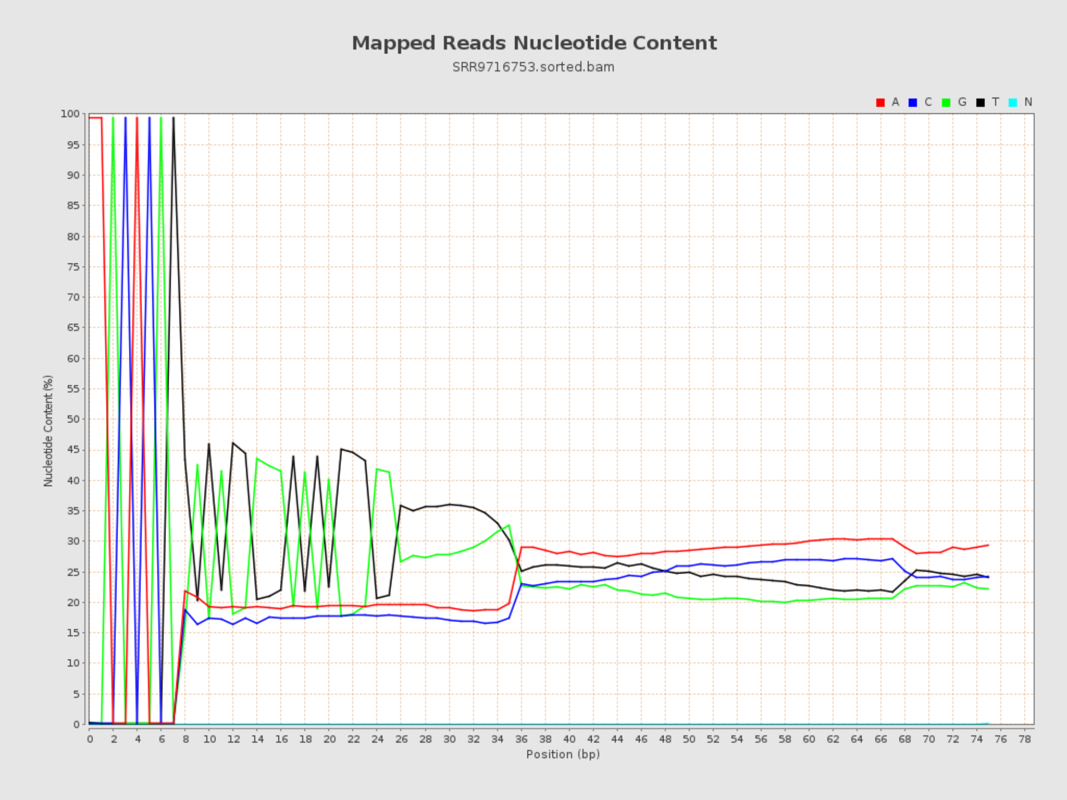
6. Results : Genome Fraction Coverage



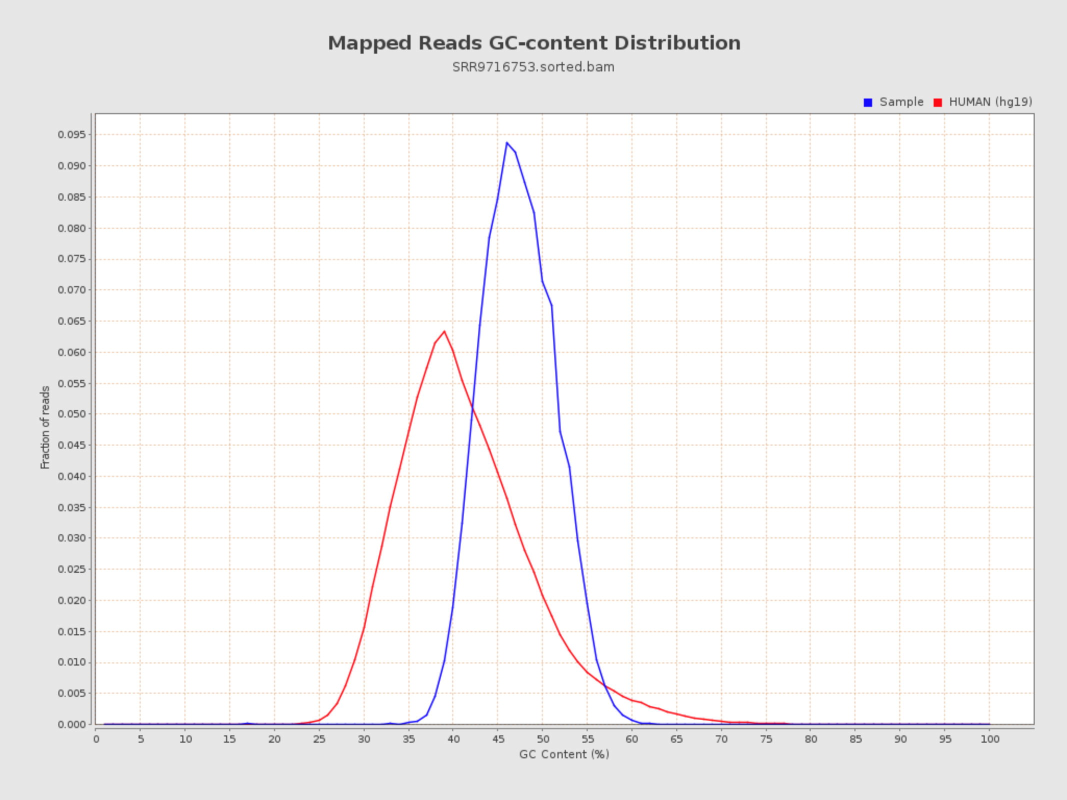
7. Results : Duplication Rate Histogram



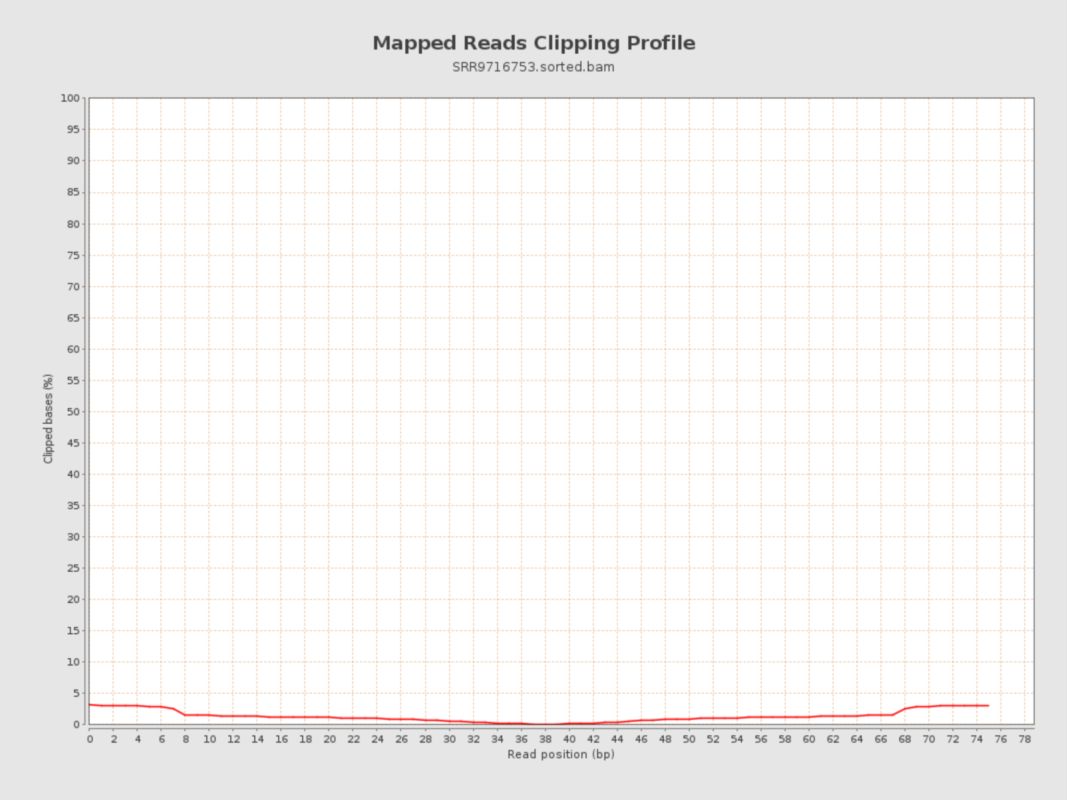
8. Results : Mapped Reads Nucleotide Content



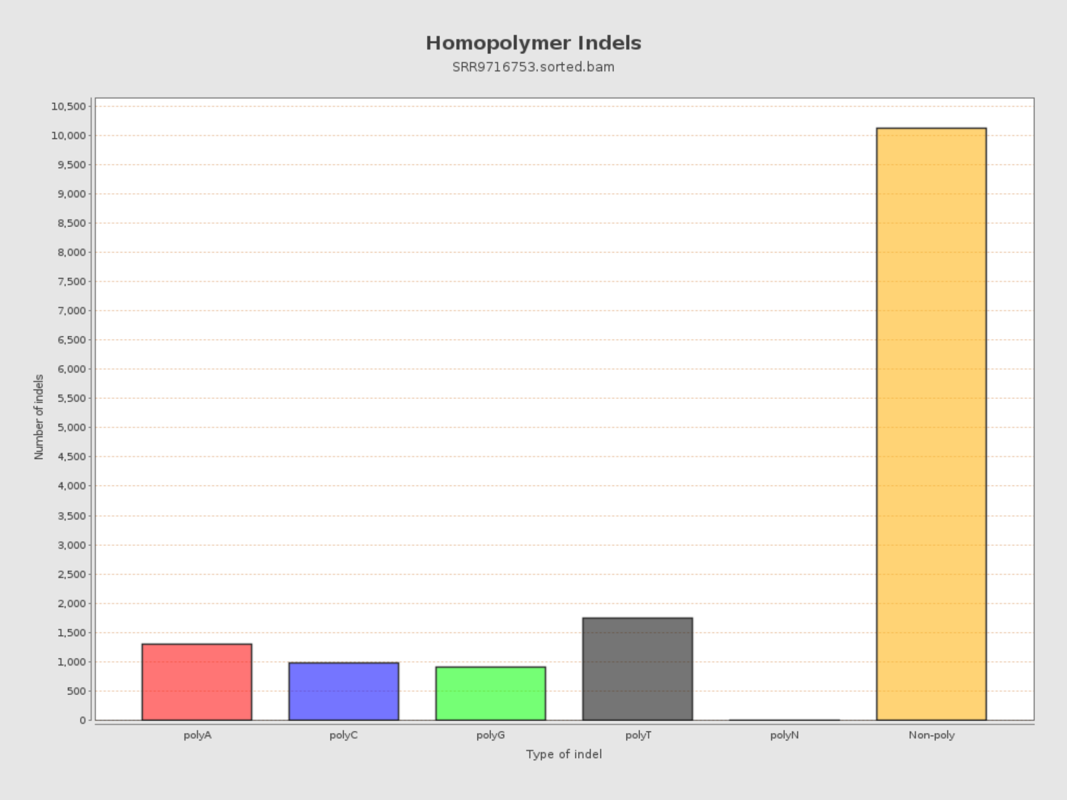
9. Results : Mapped Reads GC-content Distribution



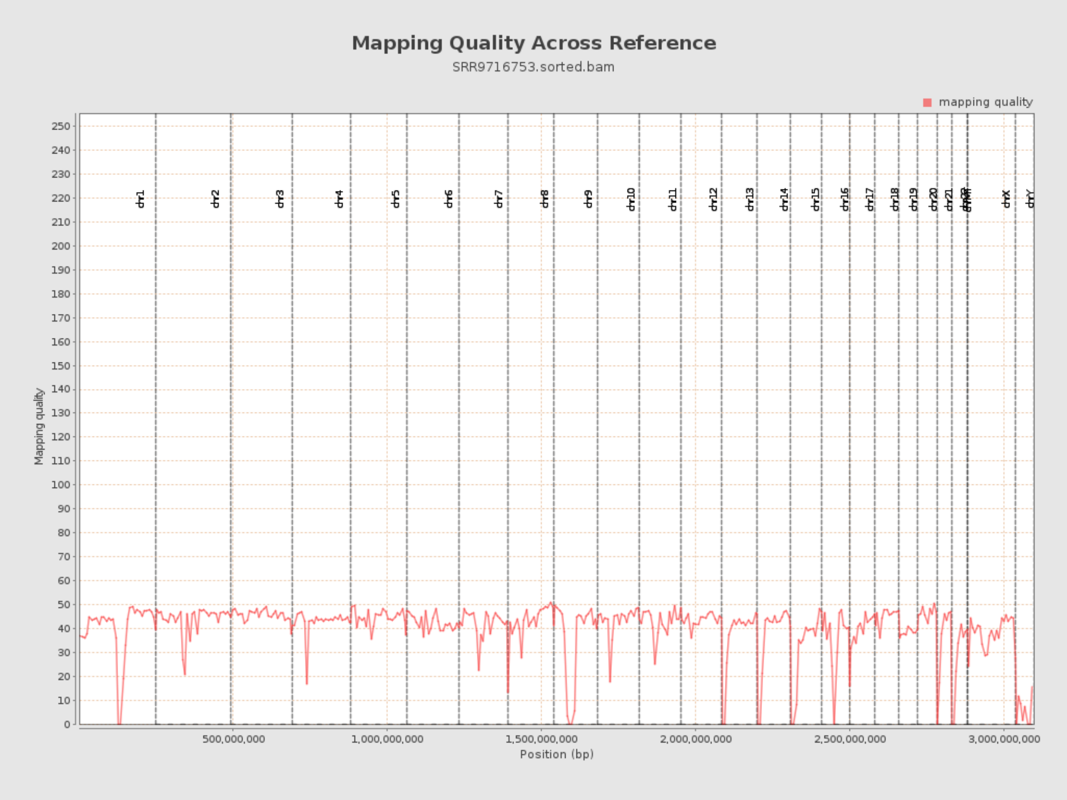
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram