Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:17:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717022.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_SRR9717022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:17:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,015,658
Mapped reads	2,652,012 / 87.94%
Unmapped reads	363,646 / 12.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,987 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	95,539 / 3.17%
Duplication rate	2.64%
Clipped reads	2,661,170 / 88.25%

2.2. ACGT Content

Number/percentage of A's	38,185,068 / 25.47%
Number/percentage of C's	30,452,126 / 20.31%
Number/percentage of T's	45,598,027 / 30.41%
Number/percentage of G's	35,711,377 / 23.82%
Number/percentage of N's	3,205 / 0%
GC Percentage	44.12%

2.3. Coverage

Mean	0.0485

Standard Deviation	0.3433

2.4. Mapping Quality

Mean Mapping Quality	43.2

2.5. Mismatches and indels

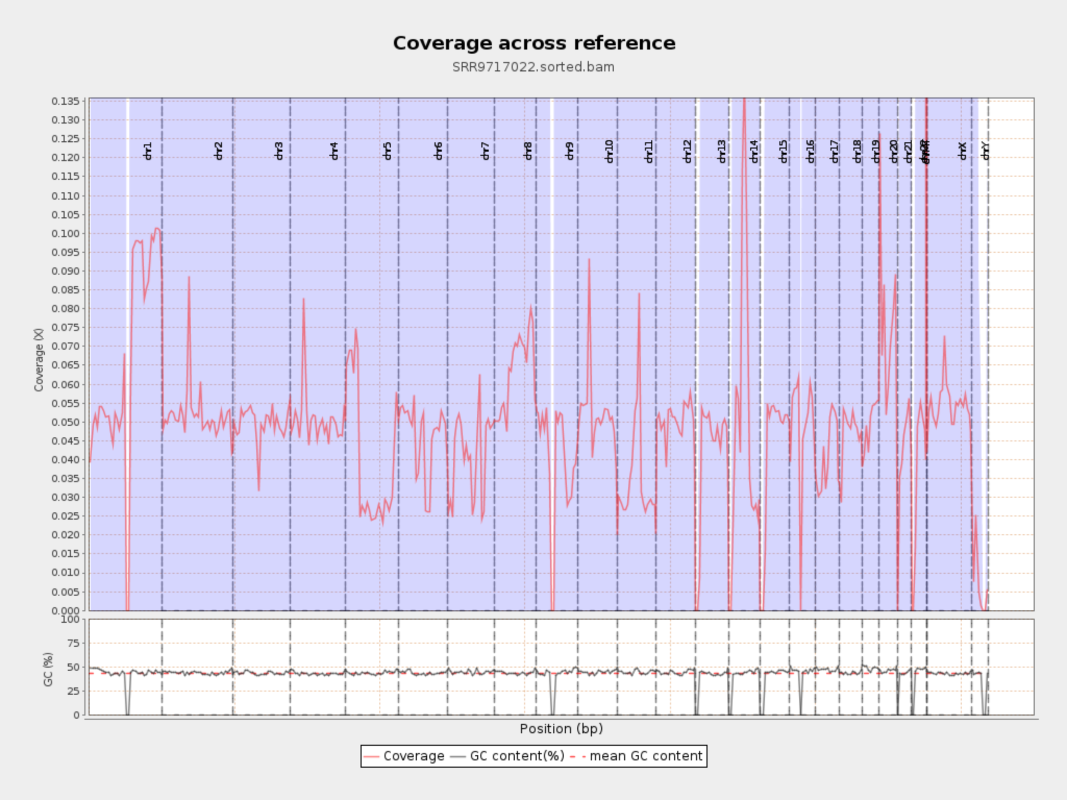
General error rate	0.51%
Mismatches	741,072
Insertions	10,317
Mapped reads with at least one insertion	0.39%
Deletions	23,104
Mapped reads with at least one deletion	0.87%
Homopolymer indels	40.66%

2.6. Chromosome stats

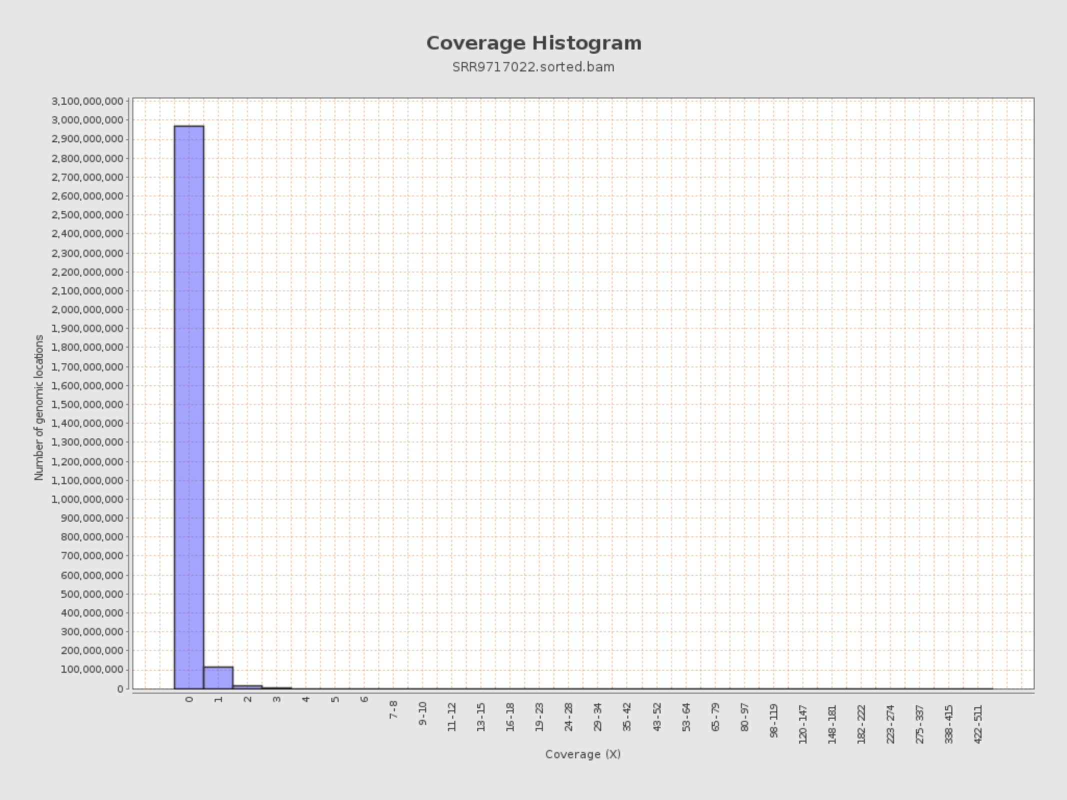
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16551321	0.0664	0.4844
chr2	243199373	12688283	0.0522	0.4287
chr3	198022430	9778102	0.0494	0.2544
chr4	191154276	9658984	0.0505	0.2951
chr5	180915260	7207626	0.0398	0.2328
chr6	171115067	7873070	0.046	0.2668
chr7	159138663	6487858	0.0408	0.3055

chr8	146364022	9336383	0.0638	0.342
chr9	141213431	5494073	0.0389	0.372
chr10	135534747	7157510	0.0528	0.4397
chr11	135006516	4761854	0.0353	0.3161
chr12	133851895	6774143	0.0506	0.2622
chr13	115169878	4678878	0.0406	0.2257
chr14	107349540	5347589	0.0498	0.288
chr15	102531392	4322005	0.0422	0.2334
chr16	90354753	4422262	0.0489	0.2909
chr17	81195210	3372003	0.0415	0.2426
chr18	78077248	3666954	0.047	0.6878
chr19	59128983	2924962	0.0495	0.3989
chr20	63025520	4778555	0.0758	0.3344
chr21	48129895	1978629	0.0411	0.2644
chr22	51304566	1780380	0.0347	0.2118
chrMT	16571	23246	1.4028	1.4688
chrX	155270560	8477309	0.0546	0.318
chrY	59373566	446891	0.0075	0.1734

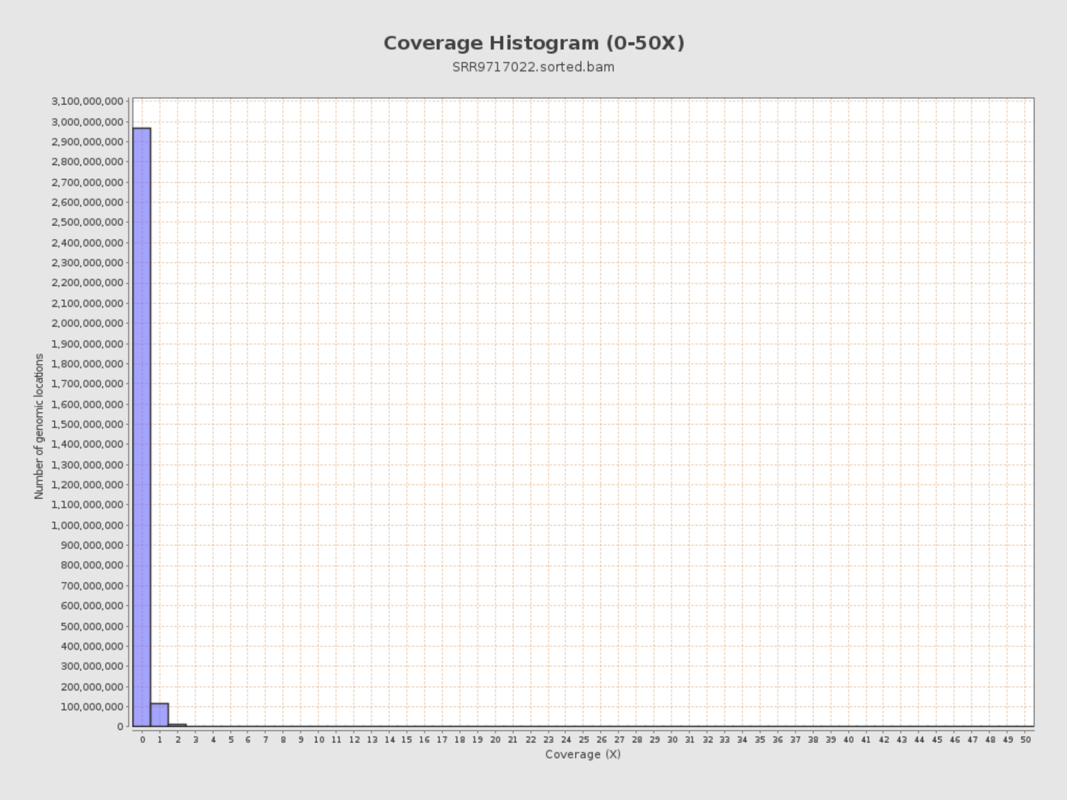
3. Results : Coverage across reference



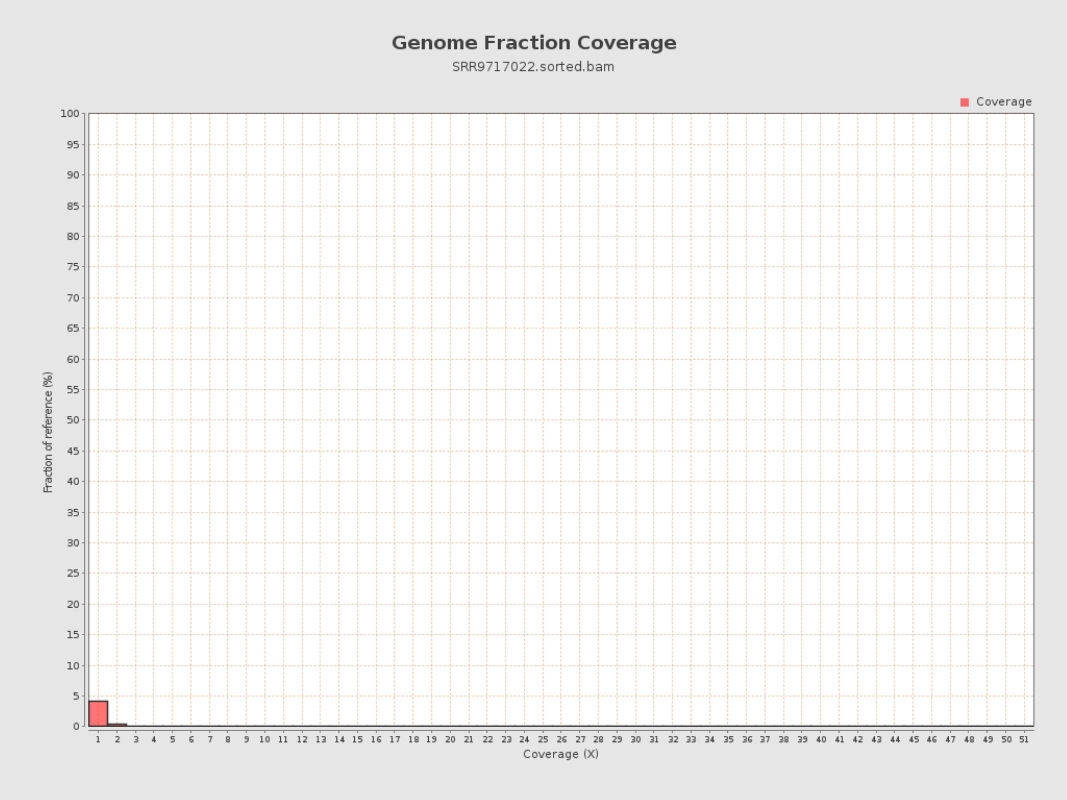
4. Results : Coverage Histogram



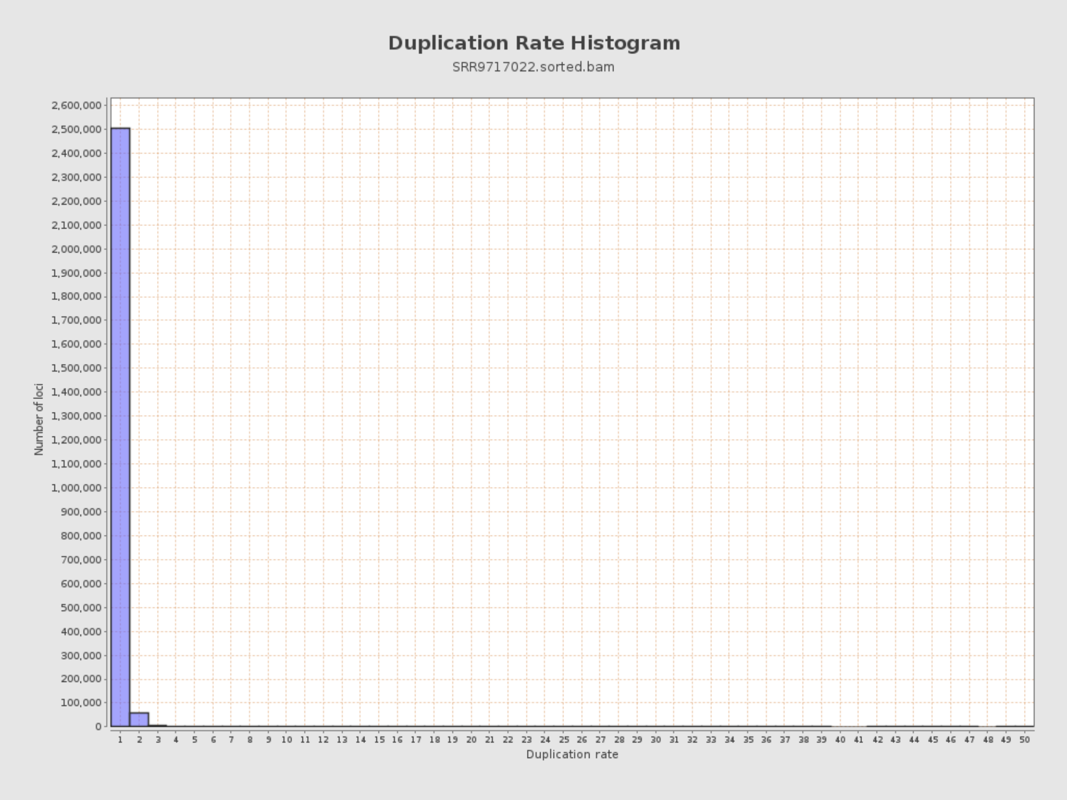
5. Results : Coverage Histogram (0-50X)



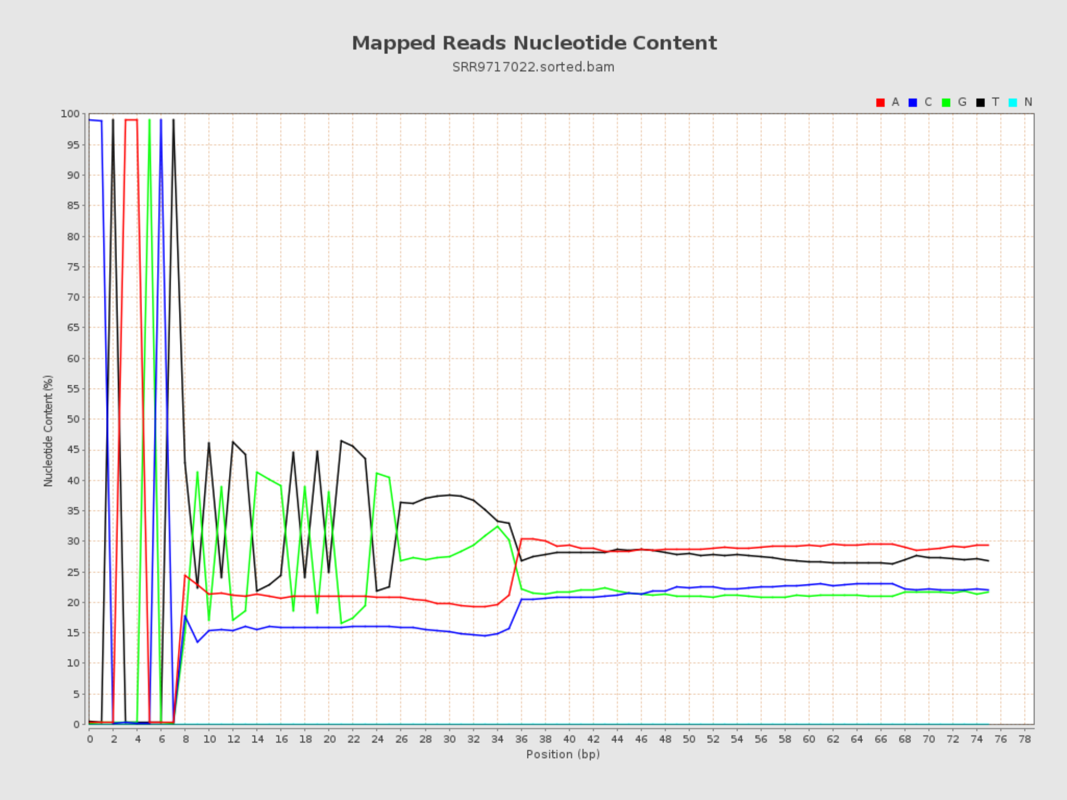
6. Results : Genome Fraction Coverage



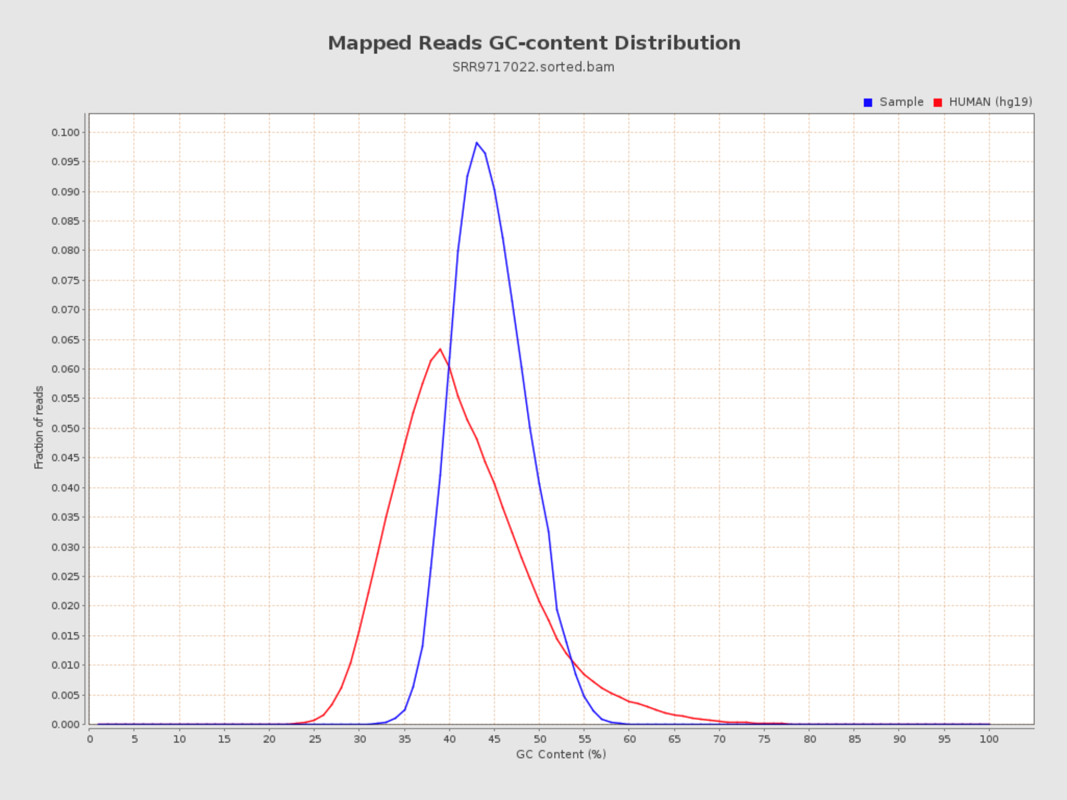
7. Results : Duplication Rate Histogram



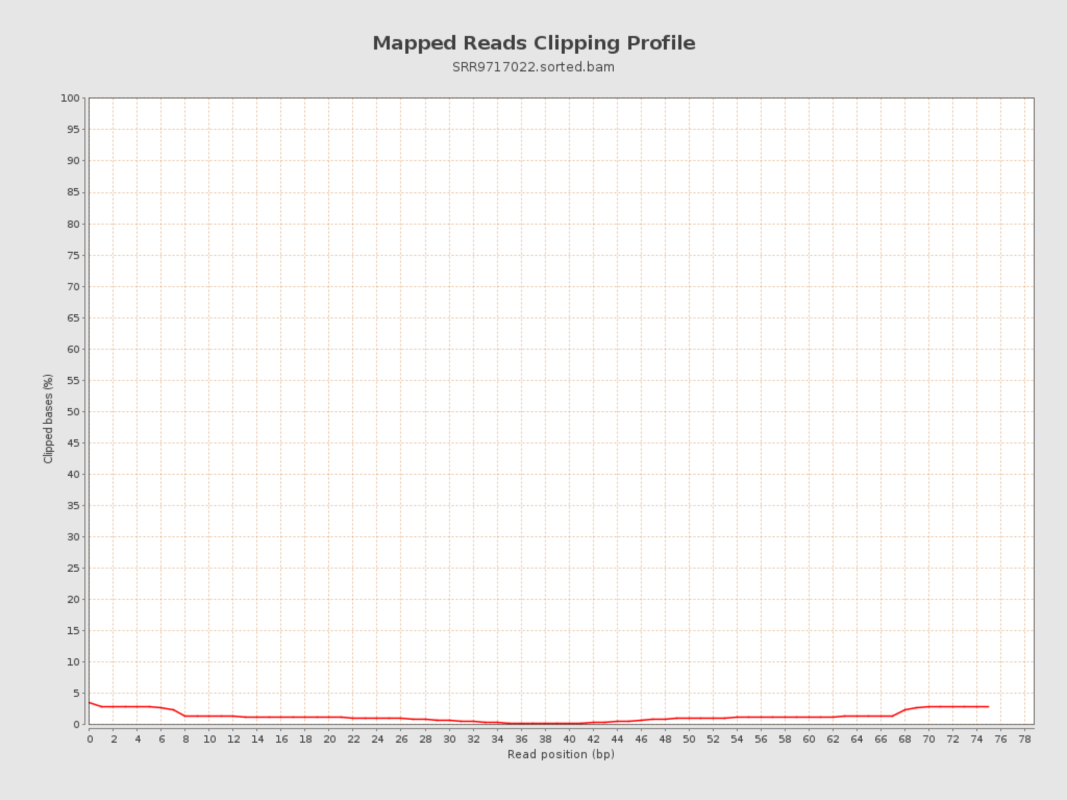
8. Results : Mapped Reads Nucleotide Content



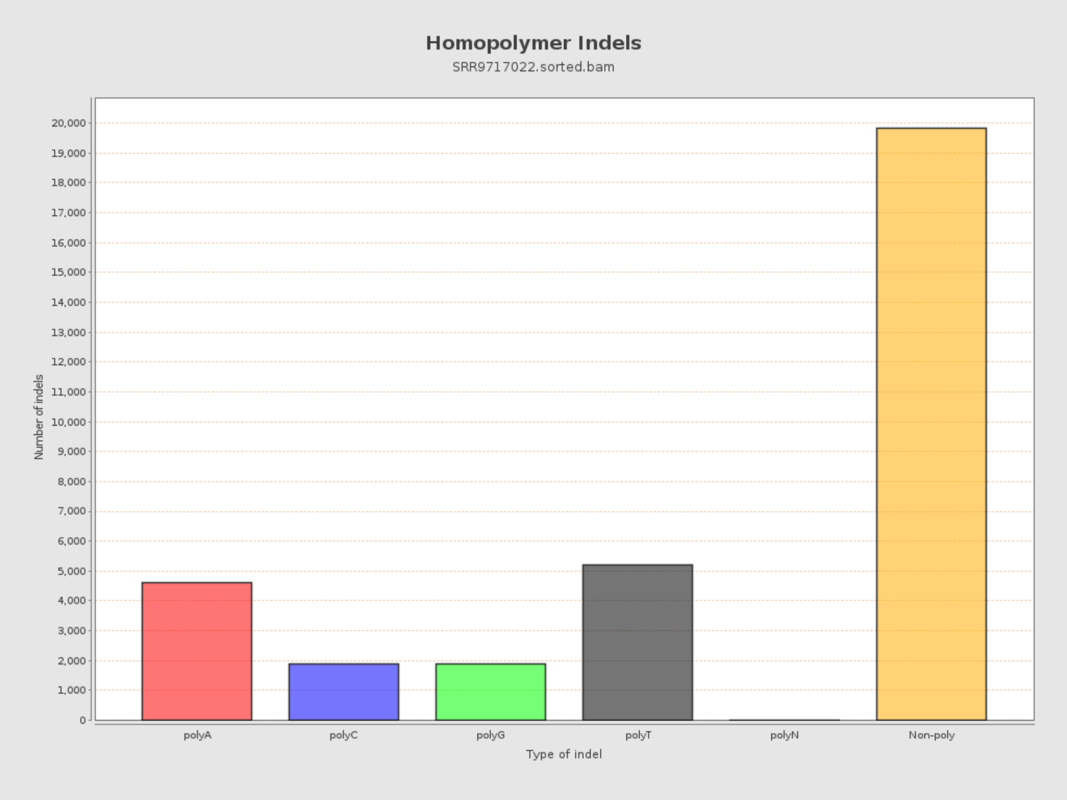
9. Results : Mapped Reads GC-content Distribution



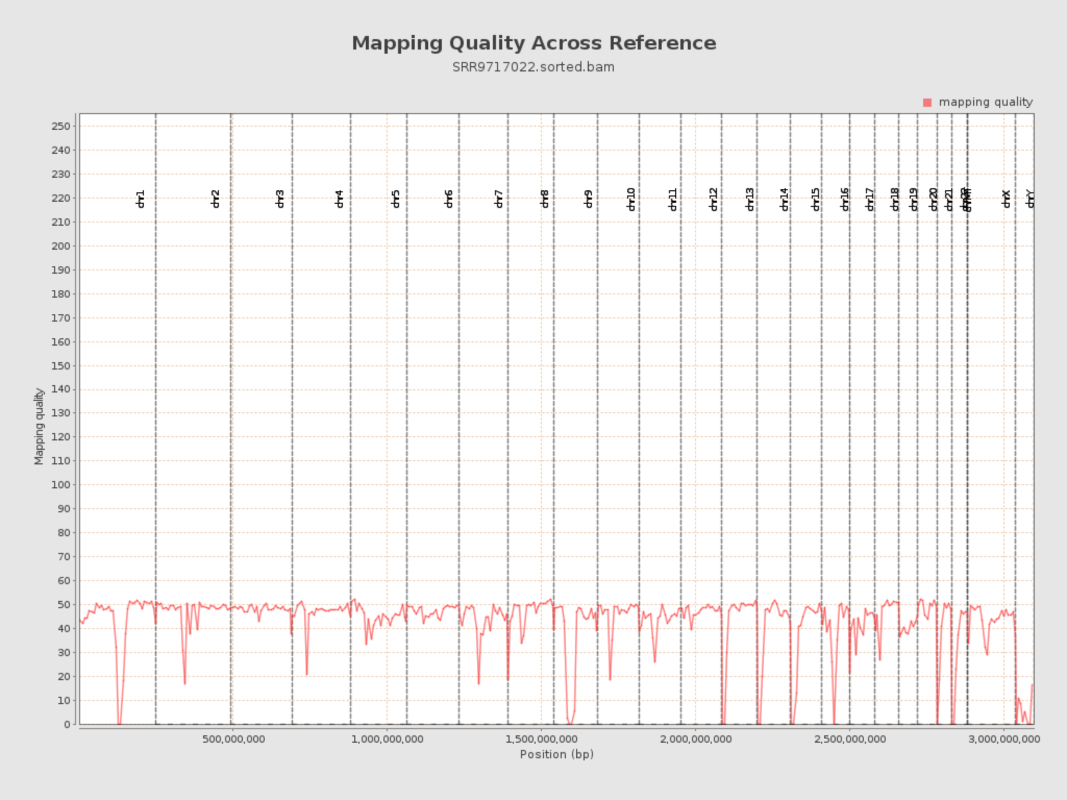
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram