Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:19:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819138.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_SRR1819138 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819138.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:19:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,666,266
Mapped reads	1,519,885 / 91.22%
Unmapped reads	146,381 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,993 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	94,950 / 5.7%
Duplication rate	4.87%
Clipped reads	1,522,172 / 91.35%

2.2. ACGT Content

Number/percentage of A's	23,203,013 / 26.19%
Number/percentage of C's	16,746,638 / 18.9%
Number/percentage of T's	26,934,304 / 30.4%
Number/percentage of G's	21,710,901 / 24.51%
Number/percentage of N's	1,309 / 0%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0286

Standard Deviation	0.2815

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

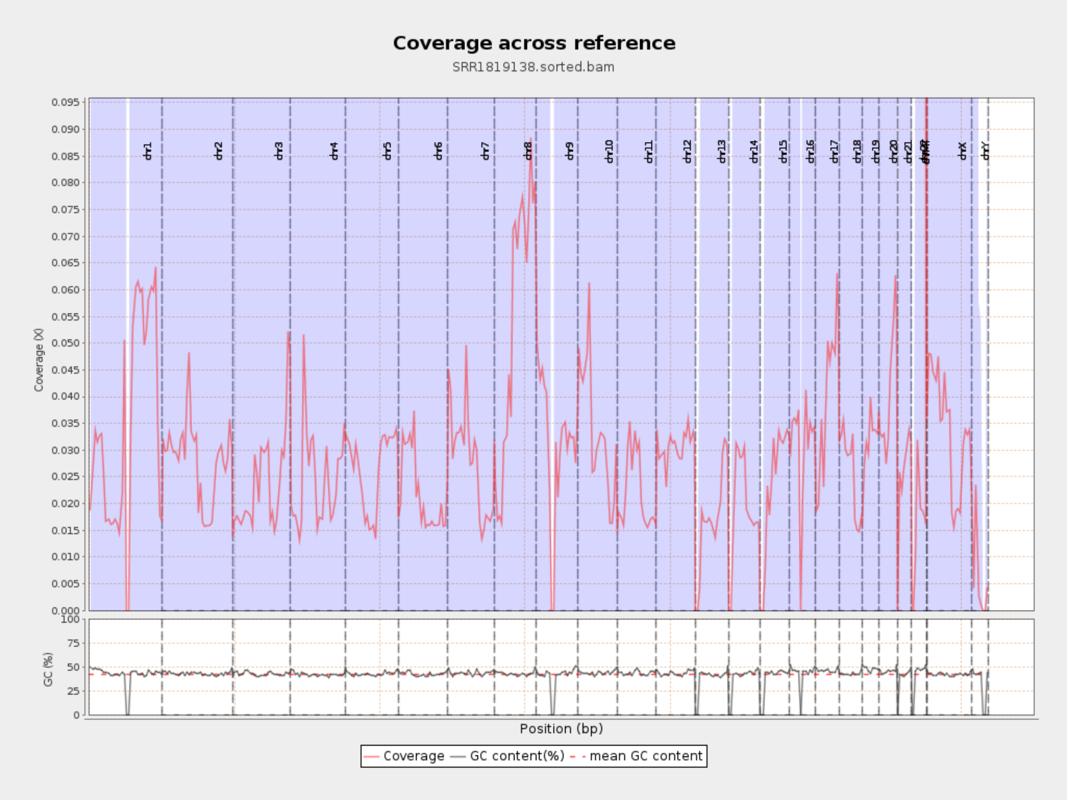
General error rate	0.54%
Mismatches	464,544
Insertions	6,818
Mapped reads with at least one insertion	0.45%
Deletions	16,920
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.43%

2.6. Chromosome stats

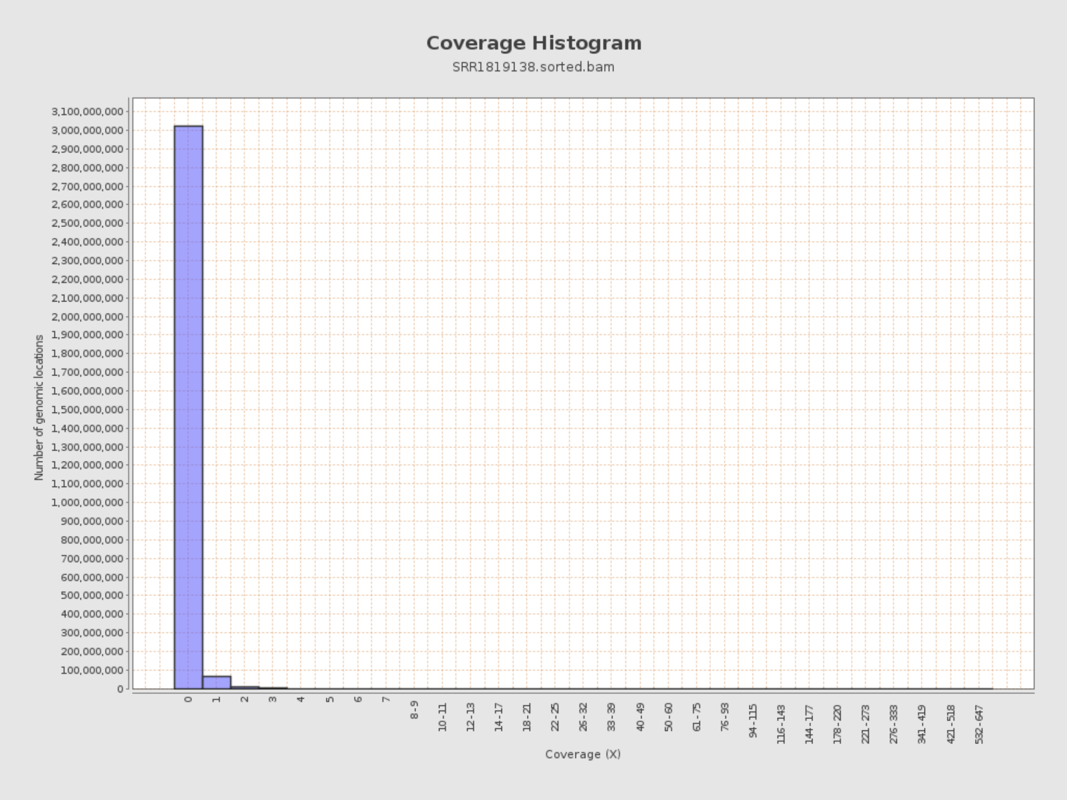
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8662482	0.0348	0.5089
chr2	243199373	6871487	0.0283	0.3474
chr3	198022430	4681121	0.0236	0.1762
chr4	191154276	4651359	0.0243	0.229
chr5	180915260	4783760	0.0264	0.1862
chr6	171115067	3747174	0.0219	0.1998
chr7	159138663	4465999	0.0281	0.3269

chr8	146364022	7971697	0.0545	0.3177
chr9	141213431	4331591	0.0307	0.2368
chr10	135534747	4594696	0.0339	0.3166
chr11	135006516	3009378	0.0223	0.2236
chr12	133851895	4121187	0.0308	0.2017
chr13	115169878	1978403	0.0172	0.1516
chr14	107349540	2065373	0.0192	0.1628
chr15	102531392	2371841	0.0231	0.175
chr16	90354753	2787372	0.0308	0.212
chr17	81195210	3273058	0.0403	0.2422
chr18	78077248	2028395	0.026	0.3963
chr19	59128983	1895152	0.0321	0.3579
chr20	63025520	2584369	0.041	0.2393
chr21	48129895	1238117	0.0257	0.2169
chr22	51304566	778364	0.0152	0.1429
chrMT	16571	123043	7.4252	4.9928
chrX	155270560	5259012	0.0339	0.2283
chrY	59373566	350393	0.0059	0.2147

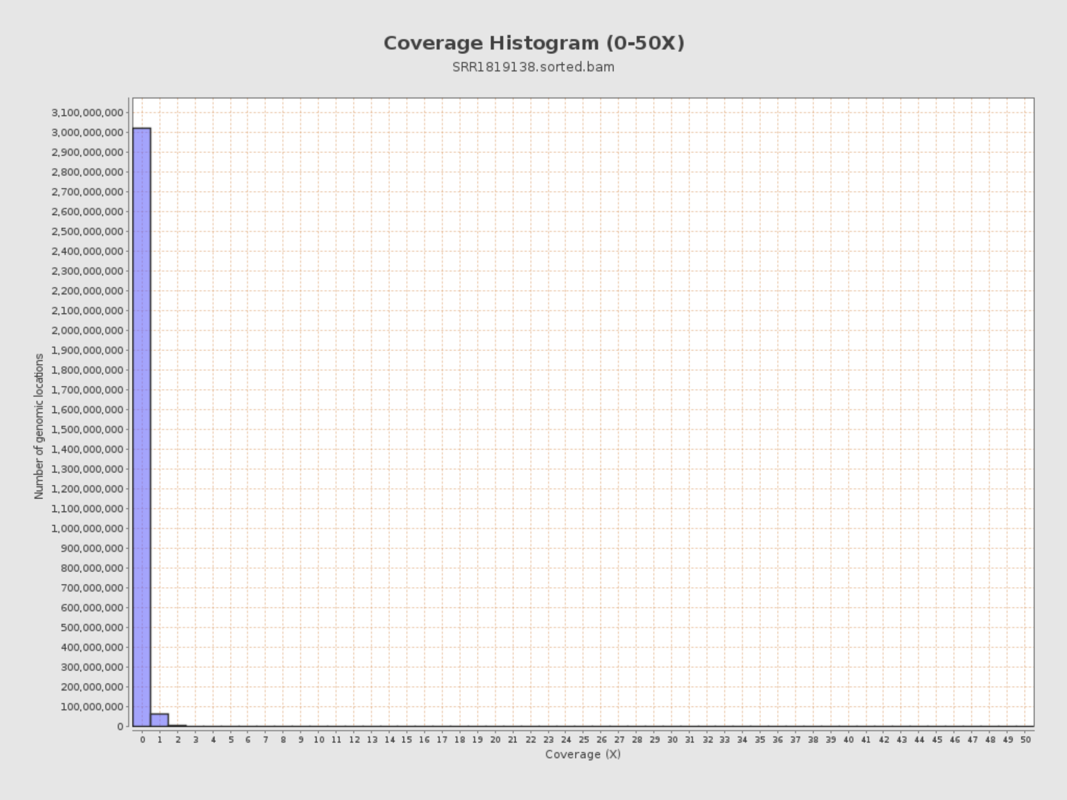
3. Results : Coverage across reference



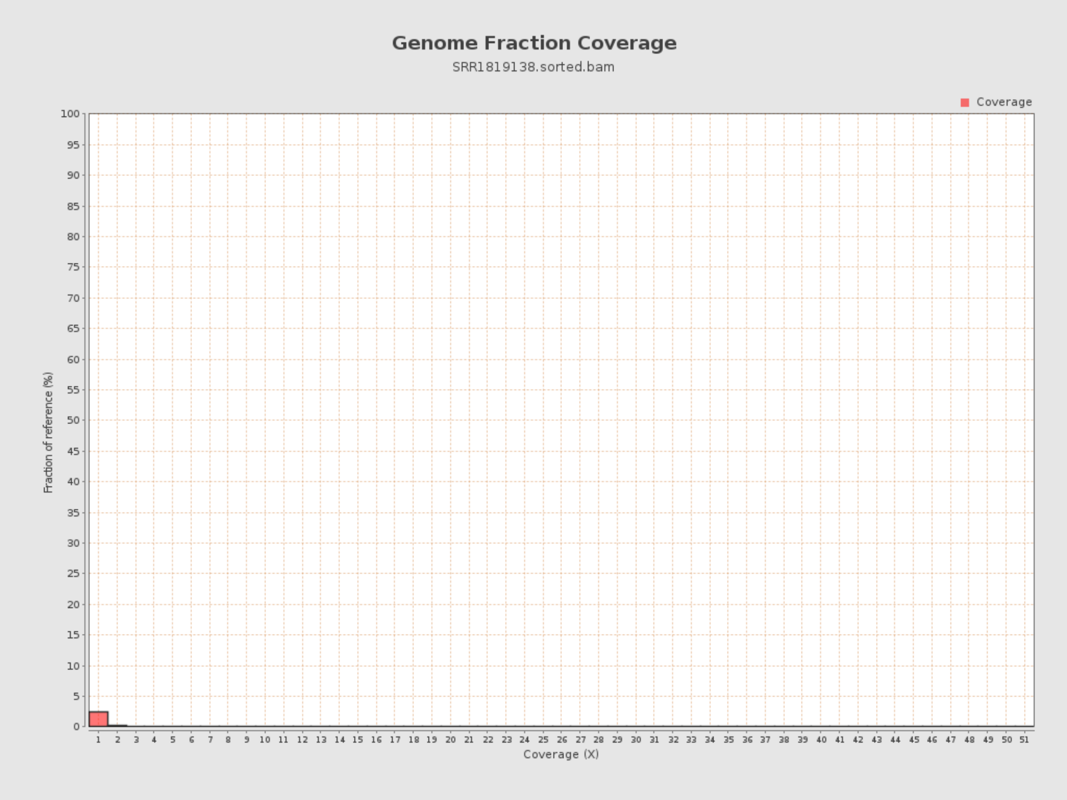
4. Results : Coverage Histogram



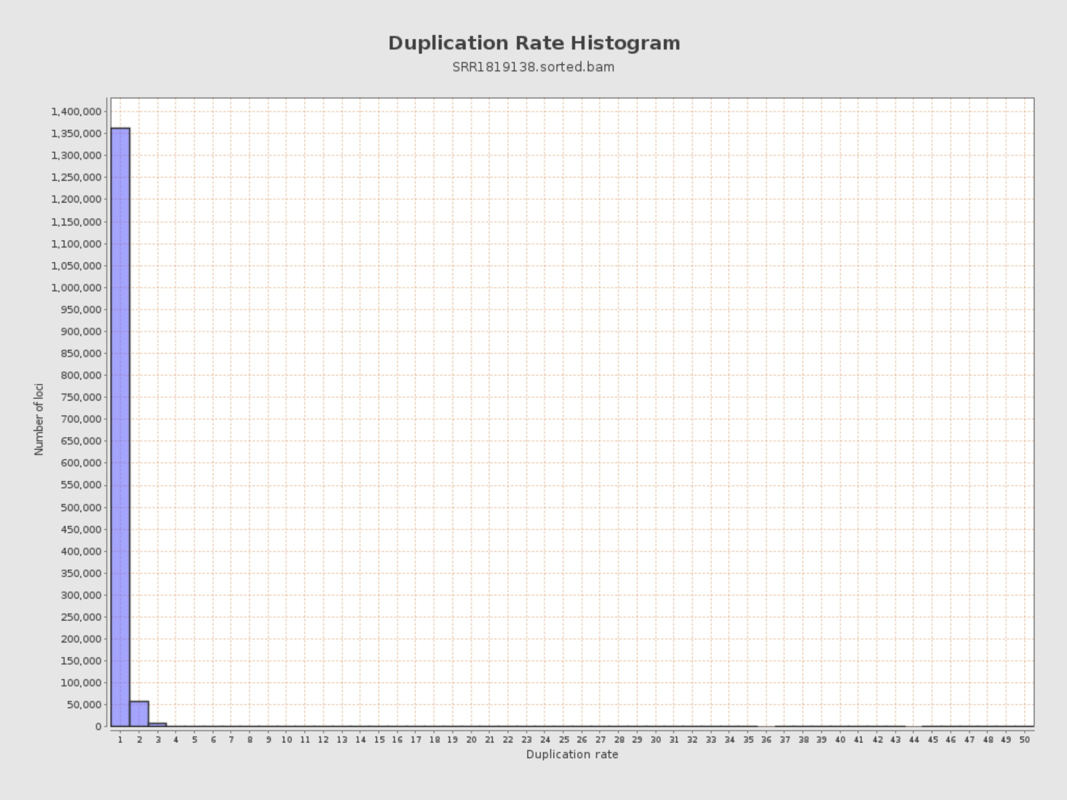
5. Results : Coverage Histogram (0-50X)



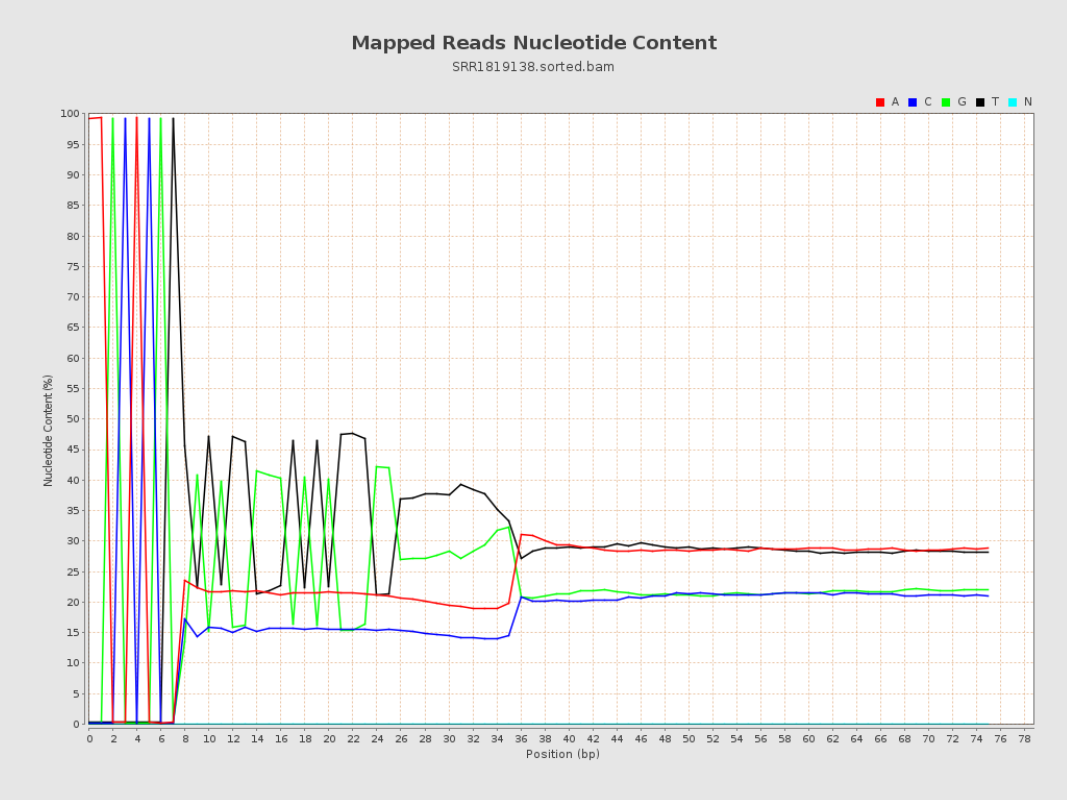
6. Results : Genome Fraction Coverage



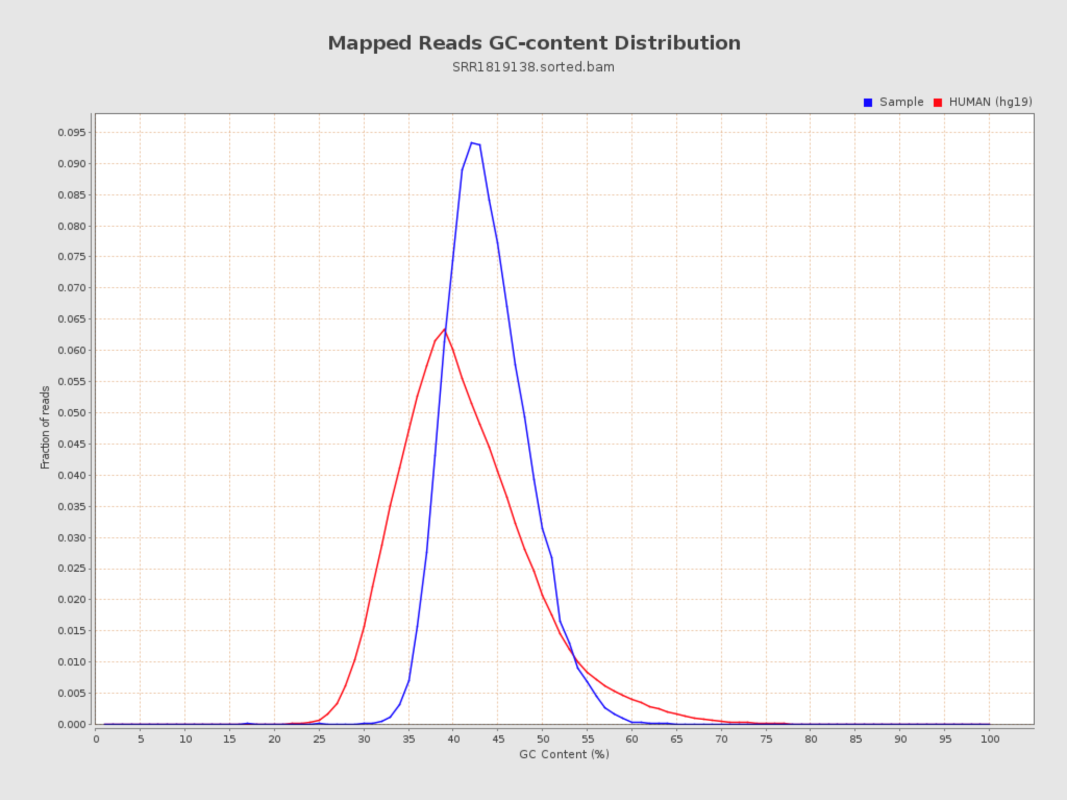
7. Results : Duplication Rate Histogram



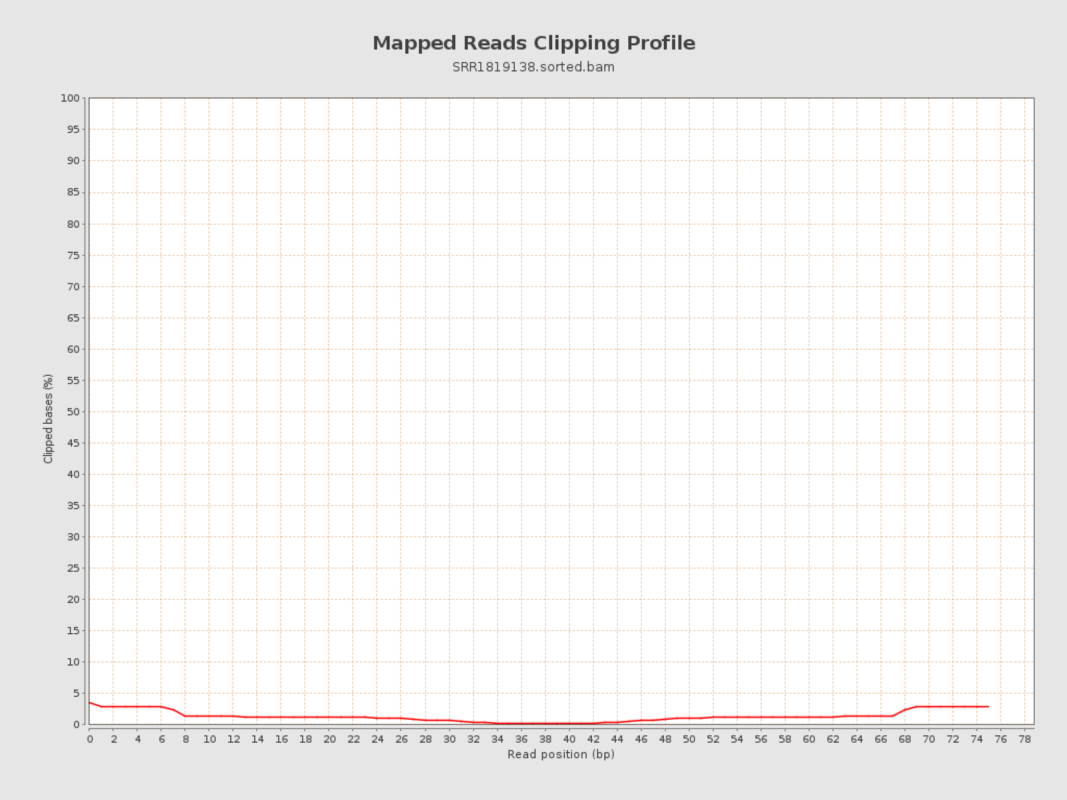
8. Results : Mapped Reads Nucleotide Content



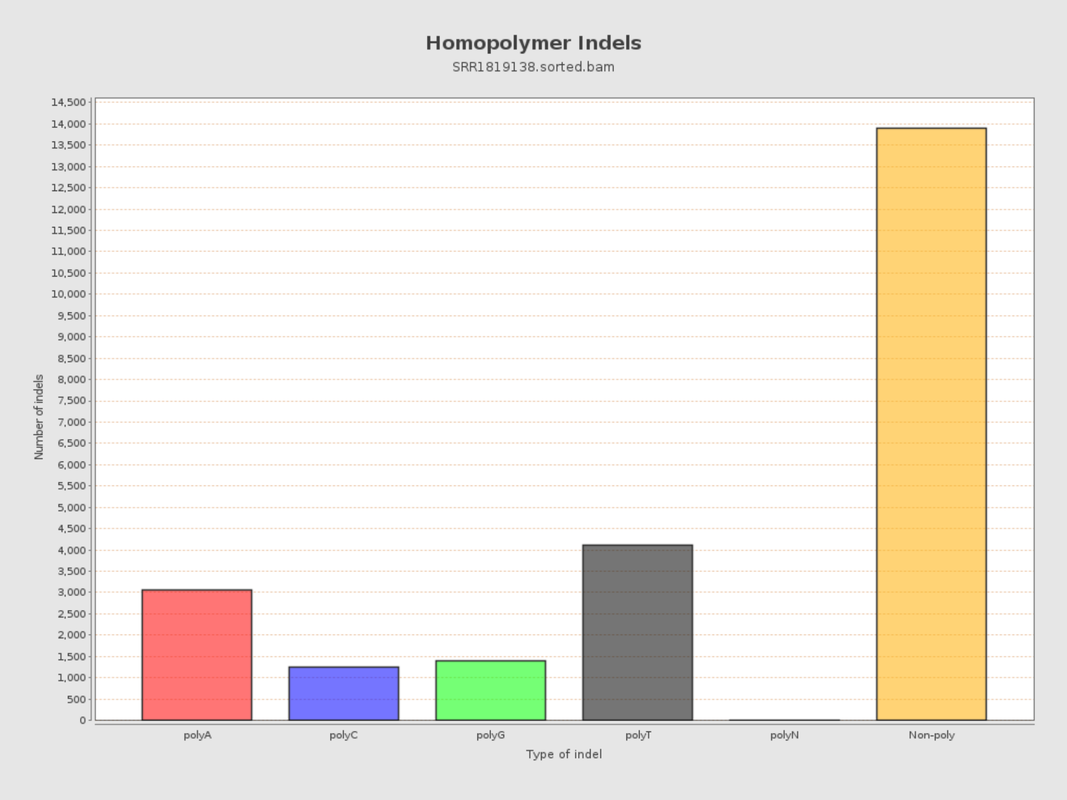
9. Results : Mapped Reads GC-content Distribution



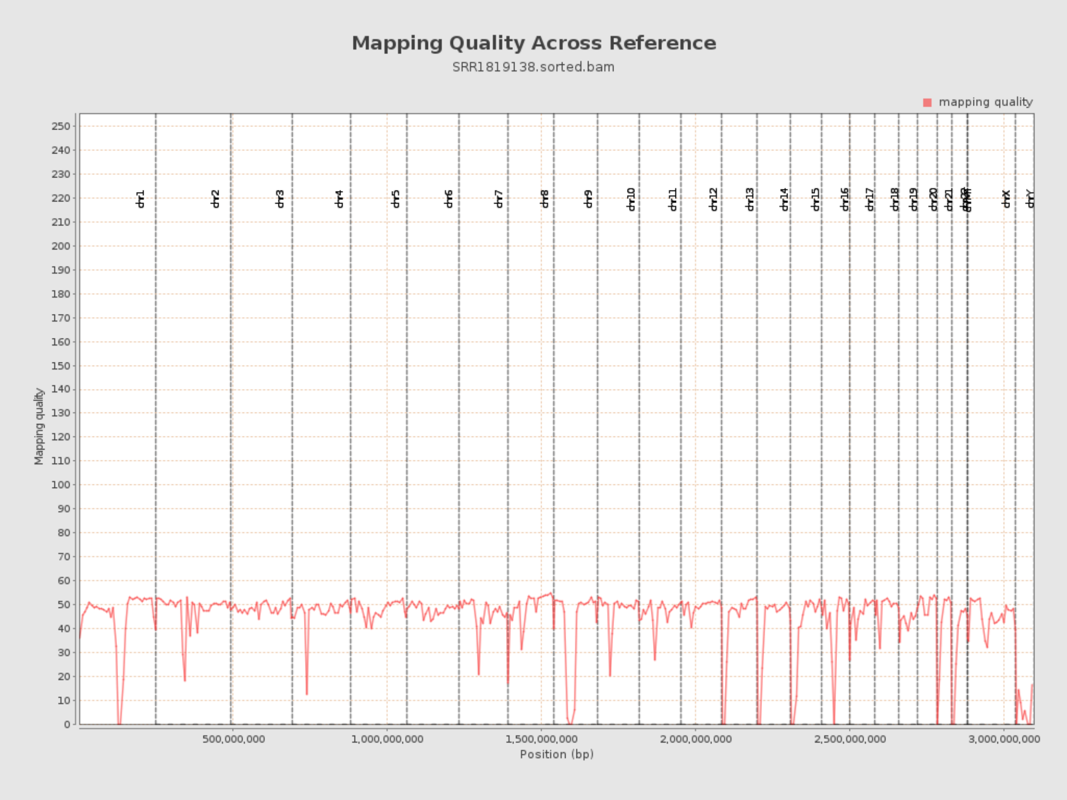
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram