Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:58:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819148.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_SRR1819148 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:58:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,984,429
Mapped reads	3,640,728 / 91.37%
Unmapped reads	343,701 / 8.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,487 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	447,738 / 11.24%
Duplication rate	8.8%
Clipped reads	3,645,996 / 91.51%

2.2. ACGT Content

Number/percentage of A's	50,517,323 / 23.84%
Number/percentage of C's	37,997,738 / 17.93%
Number/percentage of T's	69,760,727 / 32.92%
Number/percentage of G's	53,602,880 / 25.3%
Number/percentage of N's	3,117 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0685

Standard Deviation	0.6083

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

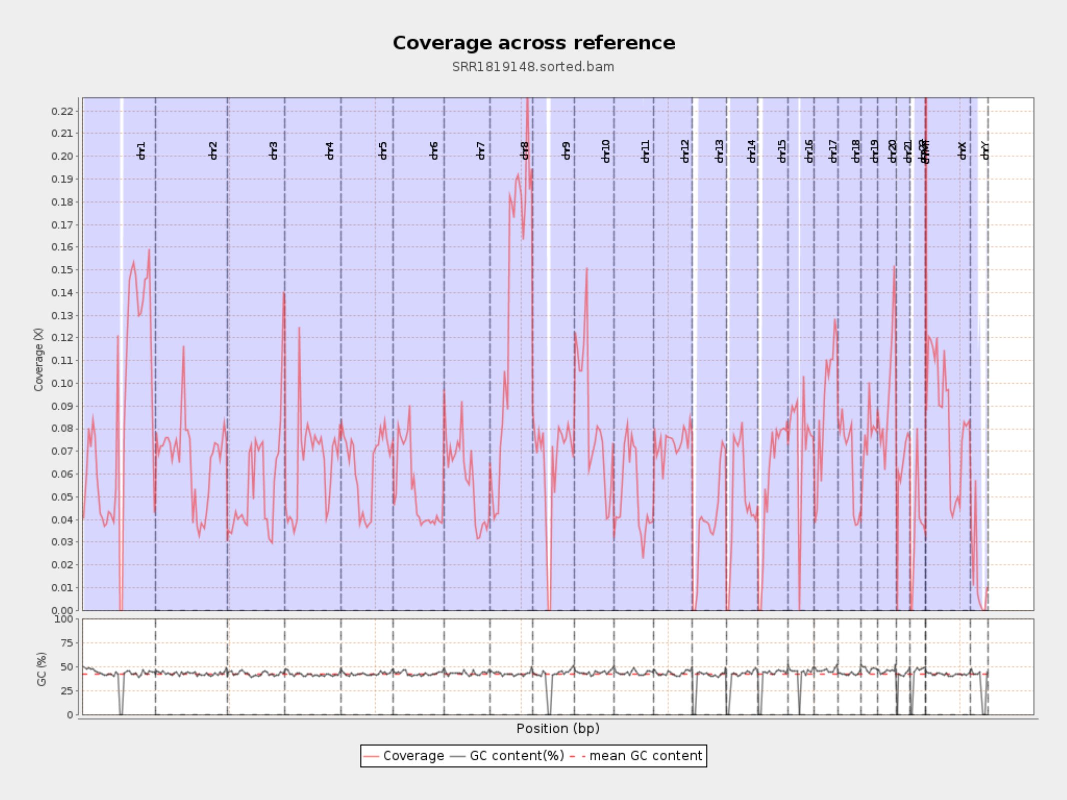
General error rate	0.53%
Mismatches	1,084,420
Insertions	14,923
Mapped reads with at least one insertion	0.41%
Deletions	38,149
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.63%

2.6. Chromosome stats

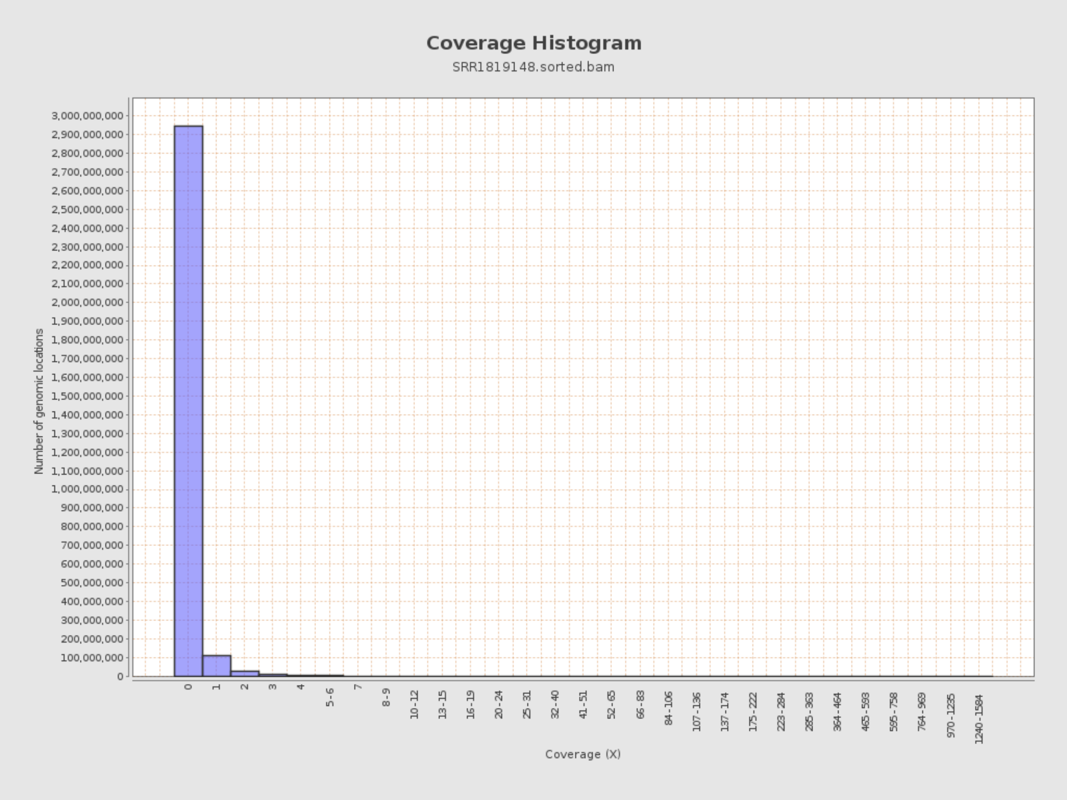
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21044040	0.0844	1.2137
chr2	243199373	16304987	0.067	0.7854
chr3	198022430	11107161	0.0561	0.321
chr4	191154276	12387953	0.0648	0.4824
chr5	180915260	11553327	0.0639	0.3438
chr6	171115067	9029885	0.0528	0.4072
chr7	159138663	9298017	0.0584	0.56

chr8	146364022	19869441	0.1358	0.6803
chr9	141213431	9100568	0.0644	0.4669
chr10	135534747	11184706	0.0825	0.6922
chr11	135006516	6835997	0.0506	0.4918
chr12	133851895	9939201	0.0743	0.3726
chr13	115169878	4554741	0.0395	0.2719
chr14	107349540	5266625	0.0491	0.3075
chr15	102531392	5791025	0.0565	0.3241
chr16	90354753	6690268	0.074	0.4075
chr17	81195210	7316117	0.0901	0.4448
chr18	78077248	5094569	0.0653	0.9858
chr19	59128983	4533412	0.0767	0.8258
chr20	63025520	6125390	0.0972	0.442
chr21	48129895	2980386	0.0619	0.4484
chr22	51304566	1784435	0.0348	0.2565
chrMT	16571	29310	1.7688	1.9859
chrX	155270560	13256270	0.0854	0.4453
chrY	59373566	868685	0.0146	0.4953

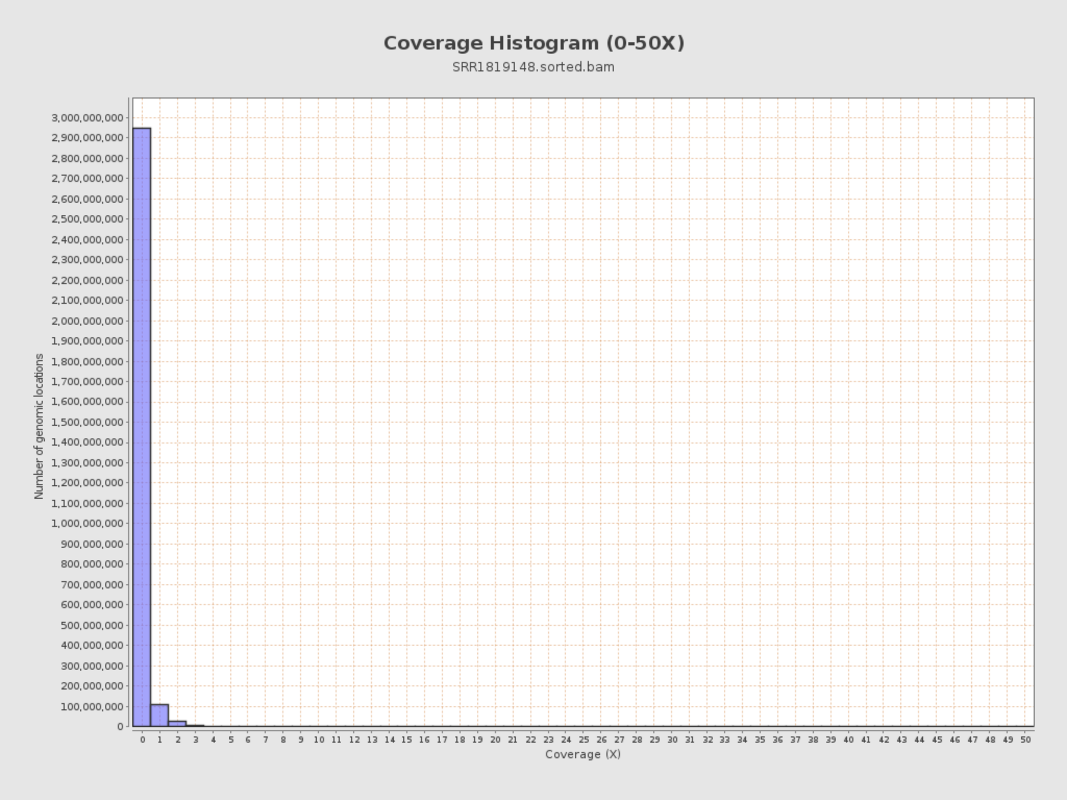
3. Results : Coverage across reference



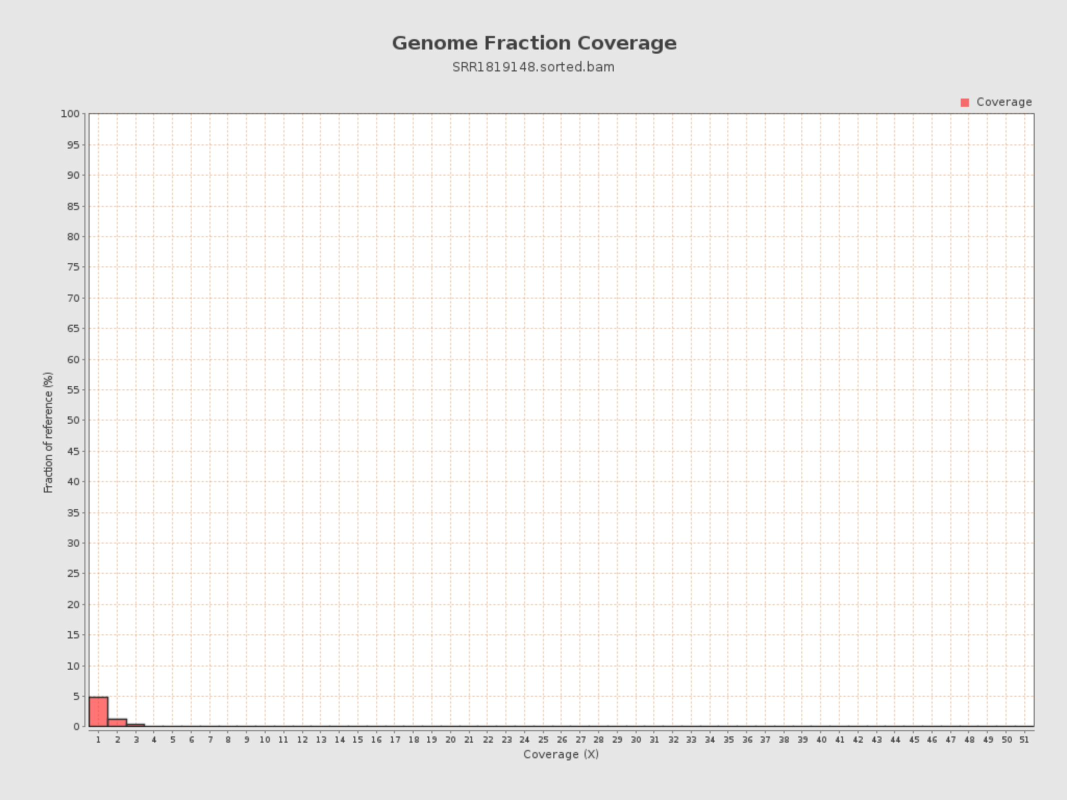
4. Results : Coverage Histogram



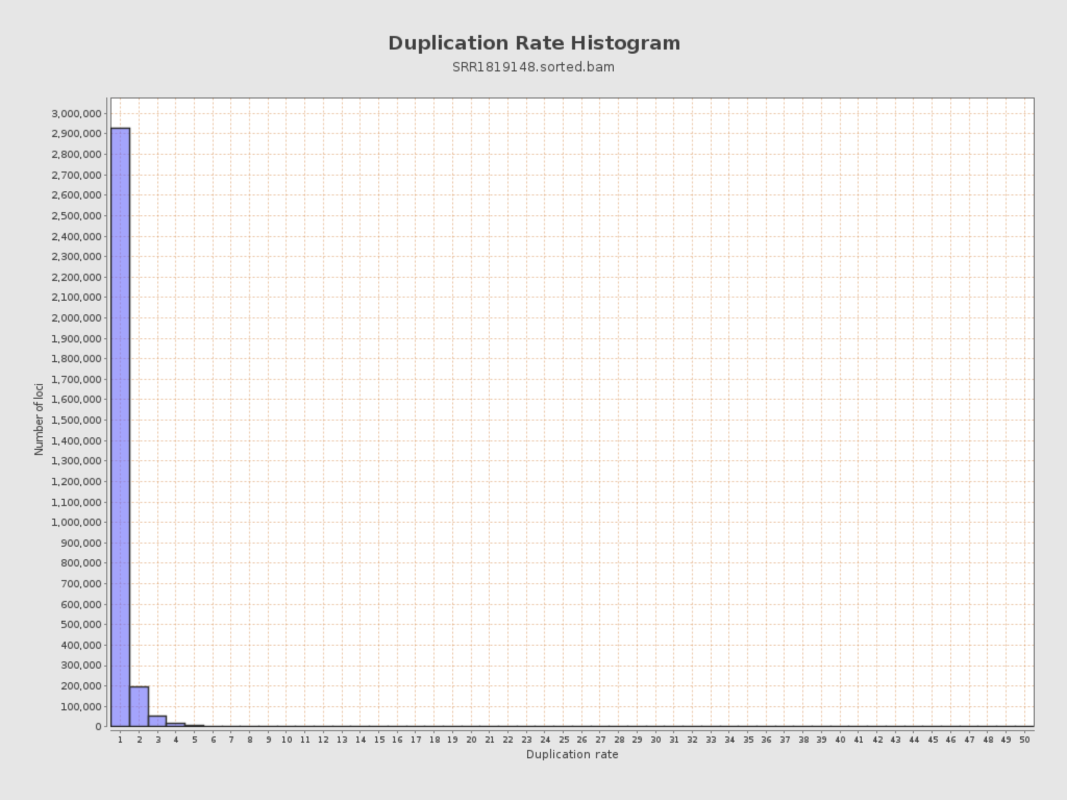
5. Results : Coverage Histogram (0-50X)



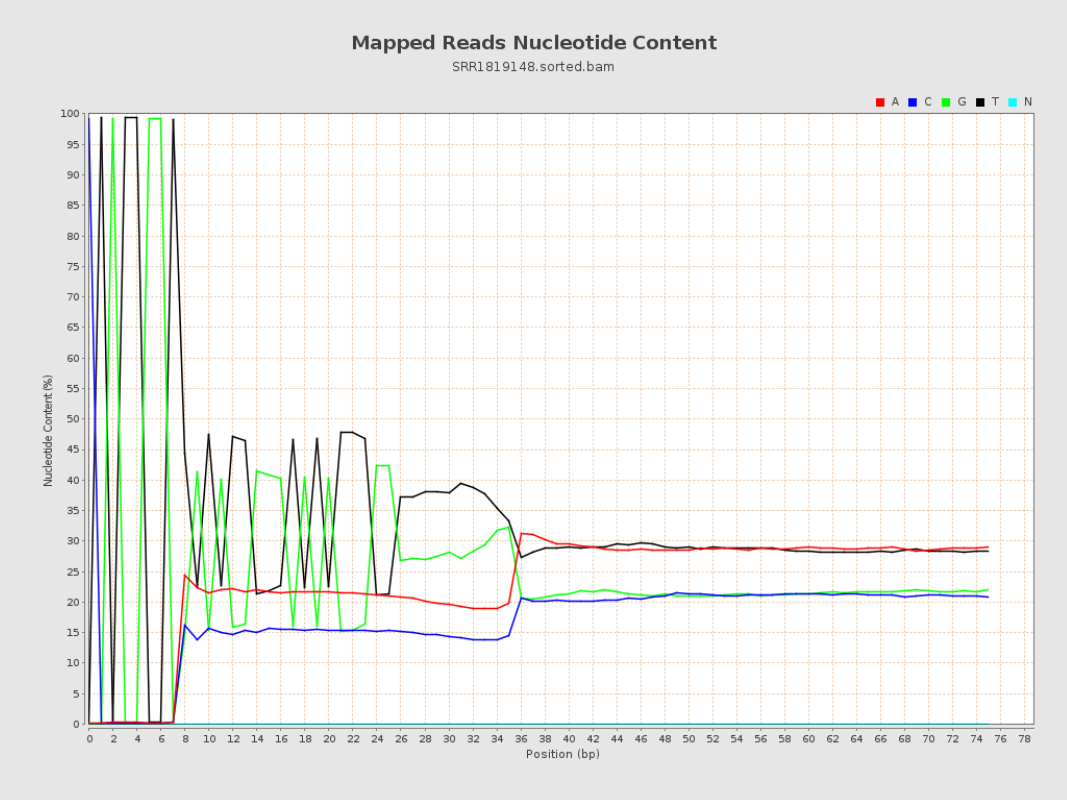
6. Results : Genome Fraction Coverage



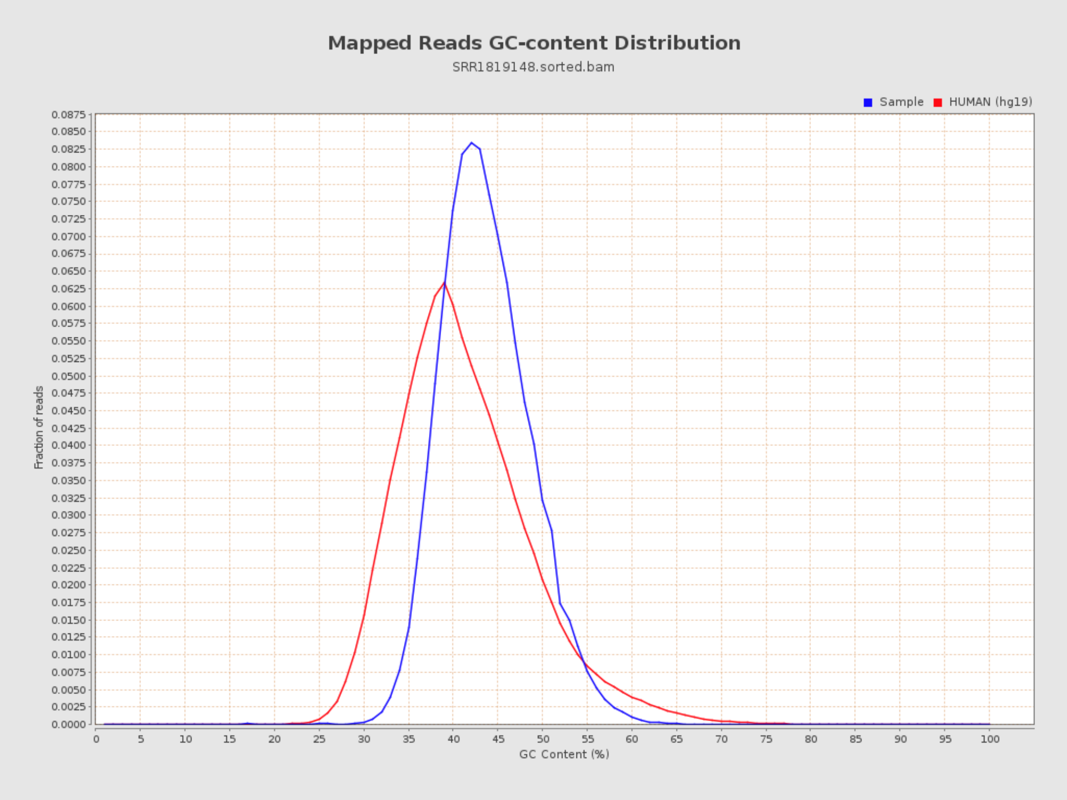
7. Results : Duplication Rate Histogram



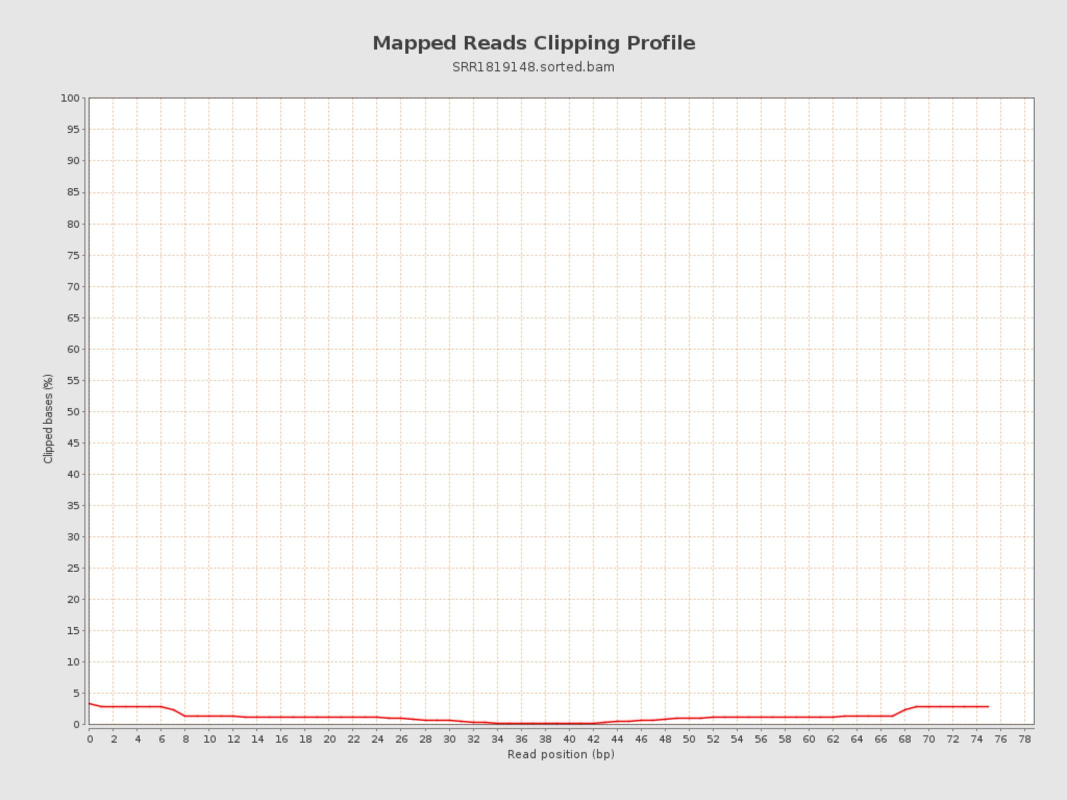
8. Results : Mapped Reads Nucleotide Content



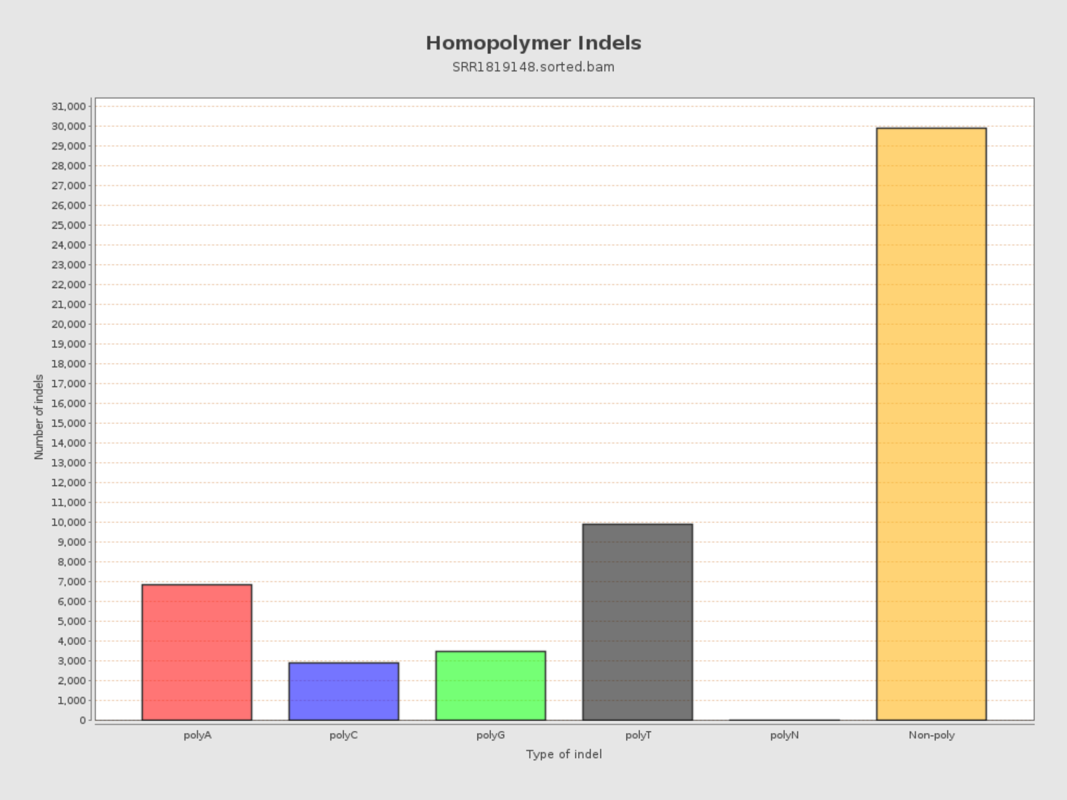
9. Results : Mapped Reads GC-content Distribution



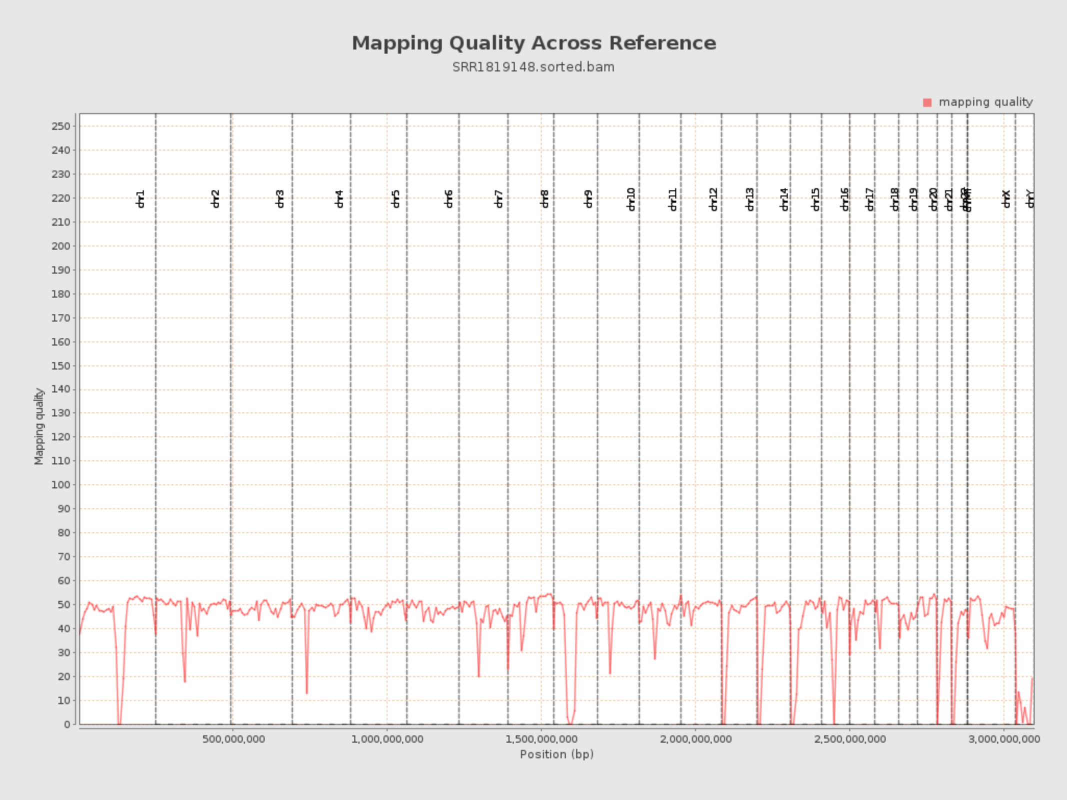
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram