Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:36:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819042.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_SRR1819042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819042.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:36:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,969,405
Mapped reads	2,644,684 / 89.06%
Unmapped reads	324,721 / 10.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,346 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	100,095 / 3.37%
Duplication rate	2.86%
Clipped reads	2,649,217 / 89.22%

2.2. ACGT Content

Number/percentage of A's	37,896,888 / 25.21%
Number/percentage of C's	27,707,577 / 18.43%
Number/percentage of T's	46,143,217 / 30.7%
Number/percentage of G's	38,567,091 / 25.66%
Number/percentage of N's	3,343 / 0%
GC Percentage	44.09%

2.3. Coverage

Mean	0.0486

Standard Deviation	0.3367

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Mismatches and indels

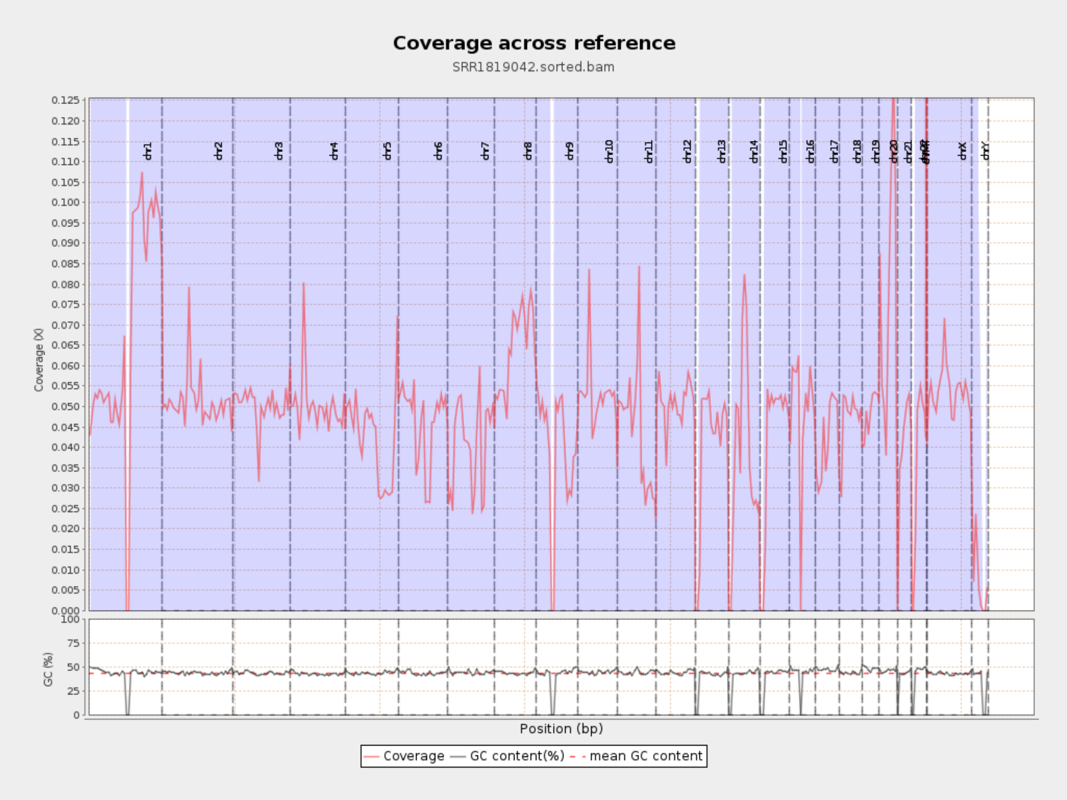
General error rate	0.5%
Mismatches	740,671
Insertions	9,210
Mapped reads with at least one insertion	0.35%
Deletions	24,123
Mapped reads with at least one deletion	0.91%
Homopolymer indels	40.93%

2.6. Chromosome stats

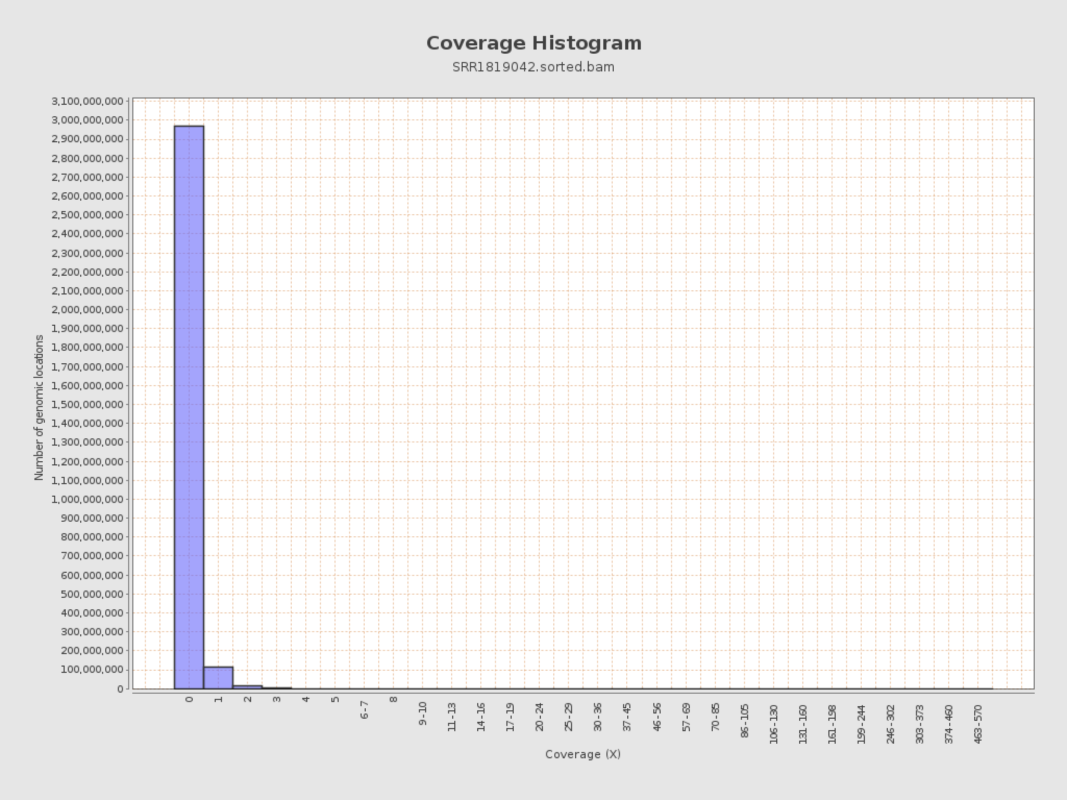
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16829471	0.0675	0.5129
chr2	243199373	12473026	0.0513	0.3928
chr3	198022430	9911703	0.0501	0.2566
chr4	191154276	9575829	0.0501	0.2893
chr5	180915260	7621774	0.0421	0.2369
chr6	171115067	7905785	0.0462	0.2687
chr7	159138663	6446892	0.0405	0.2956

chr8	146364022	9470907	0.0647	0.3448
chr9	141213431	5433742	0.0385	0.3534
chr10	135534747	7206015	0.0532	0.3836
chr11	135006516	5935242	0.044	0.3295
chr12	133851895	6806221	0.0508	0.2617
chr13	115169878	4616919	0.0401	0.2255
chr14	107349540	4072347	0.0379	0.2433
chr15	102531392	4253610	0.0415	0.2326
chr16	90354753	4438669	0.0491	0.287
chr17	81195210	3427155	0.0422	0.244
chr18	78077248	3670775	0.047	0.6747
chr19	59128983	2859709	0.0484	0.3707
chr20	63025520	4858535	0.0771	0.332
chr21	48129895	1937025	0.0402	0.2672
chr22	51304566	1790656	0.0349	0.2125
chrMT	16571	16276	0.9822	1.1013
chrX	155270560	8365284	0.0539	0.314
chrY	59373566	435685	0.0073	0.1564

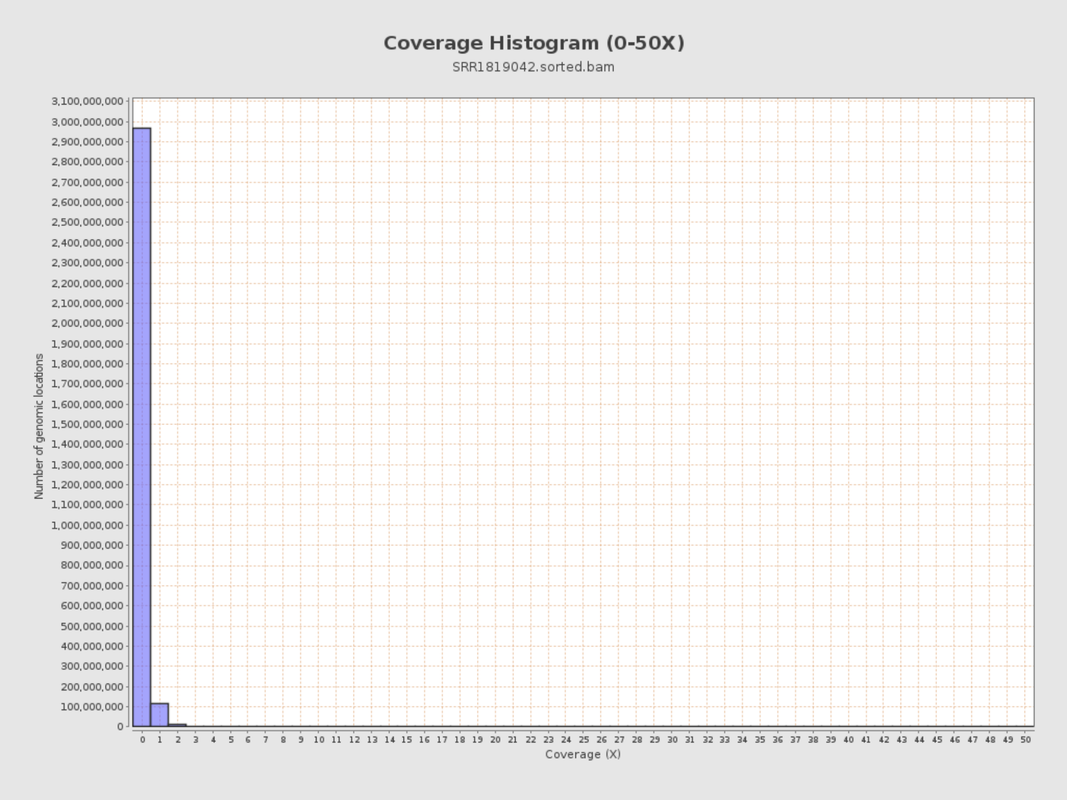
3. Results : Coverage across reference



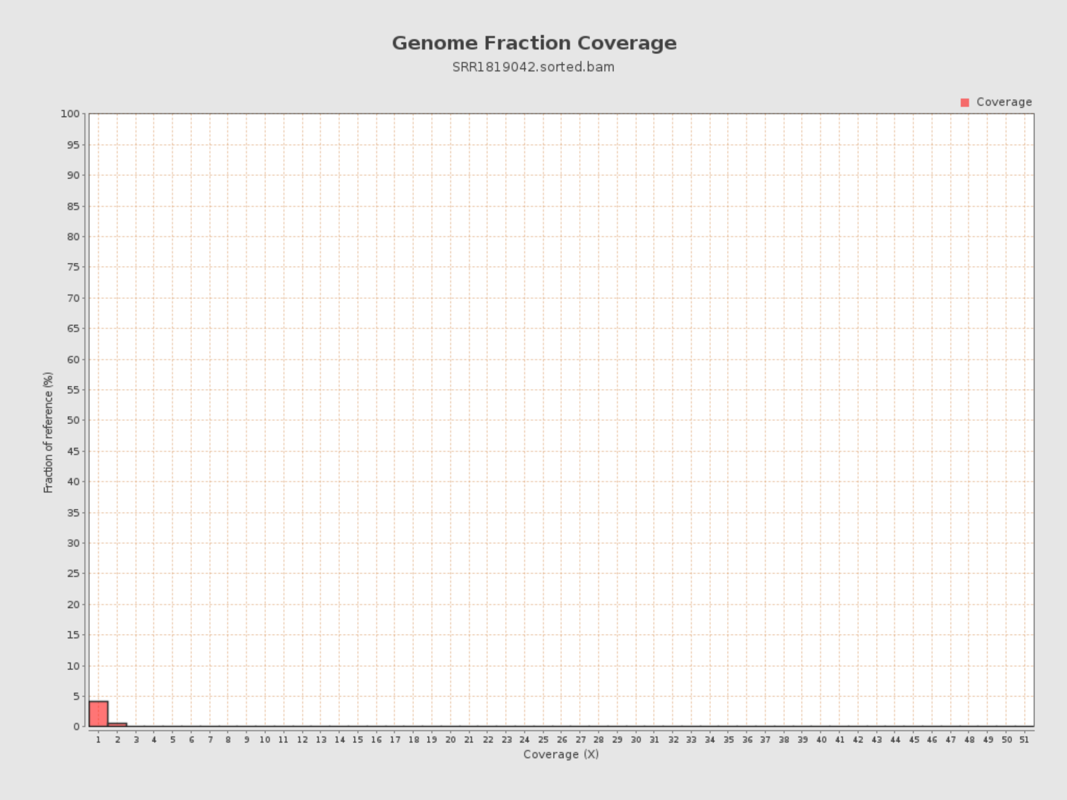
4. Results : Coverage Histogram



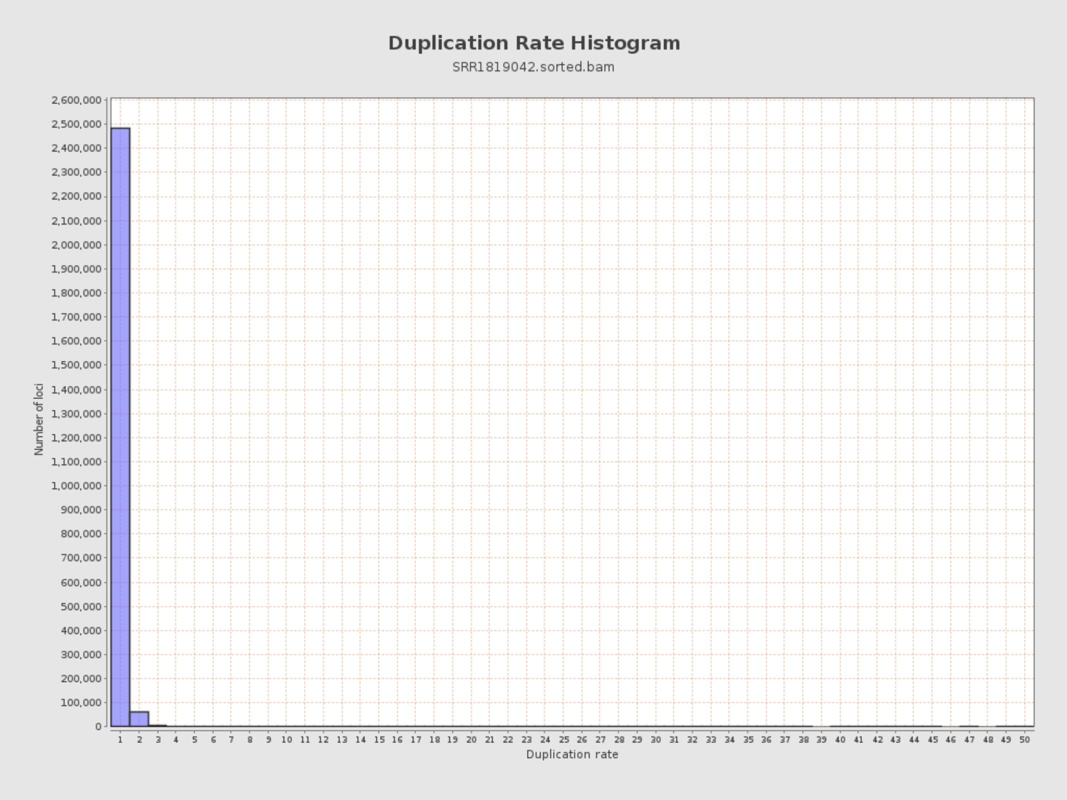
5. Results : Coverage Histogram (0-50X)



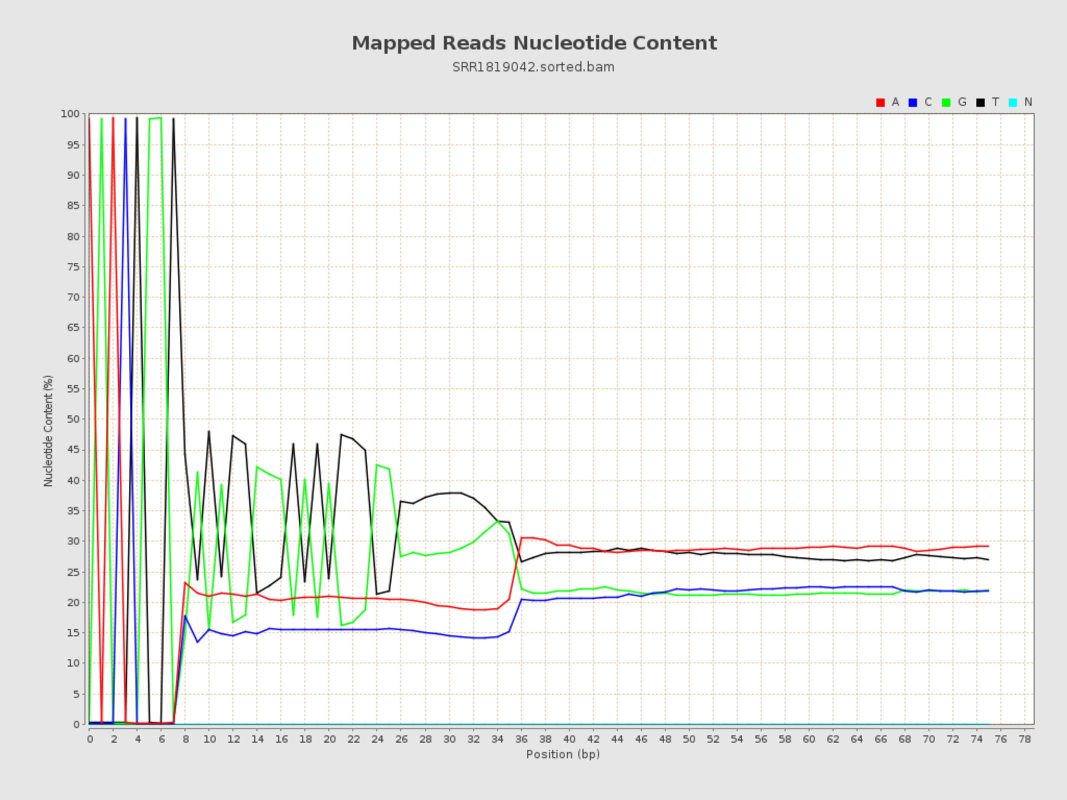
6. Results : Genome Fraction Coverage



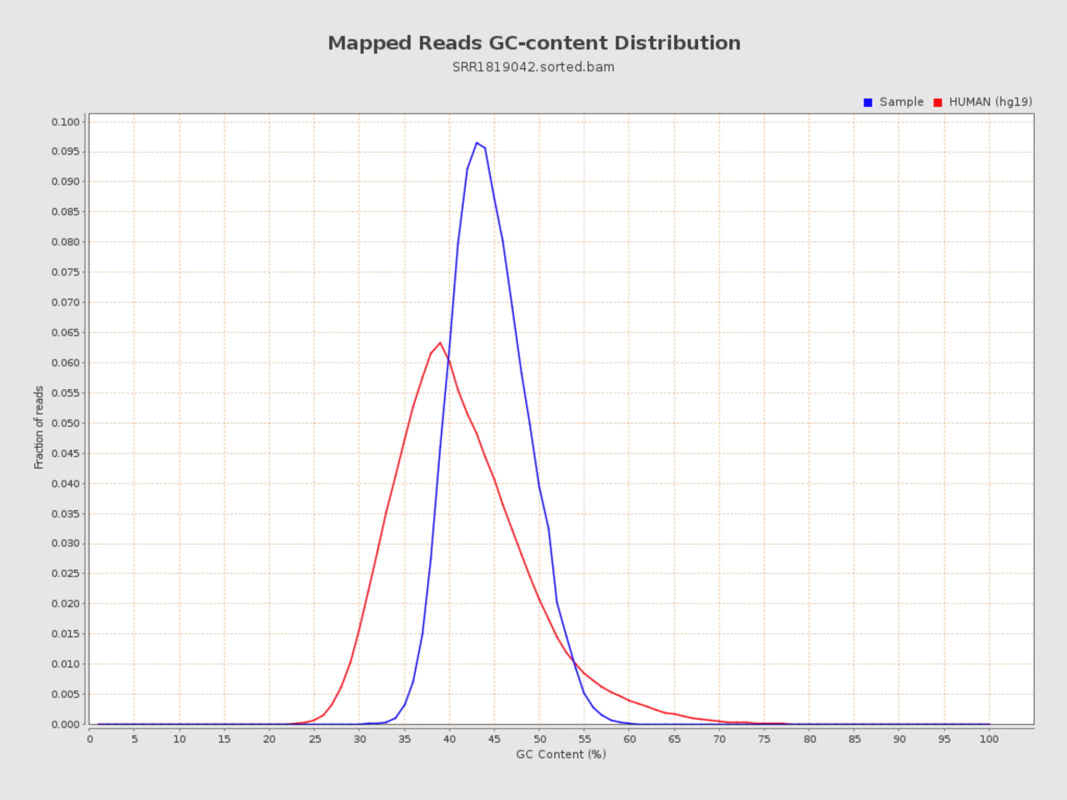
7. Results : Duplication Rate Histogram



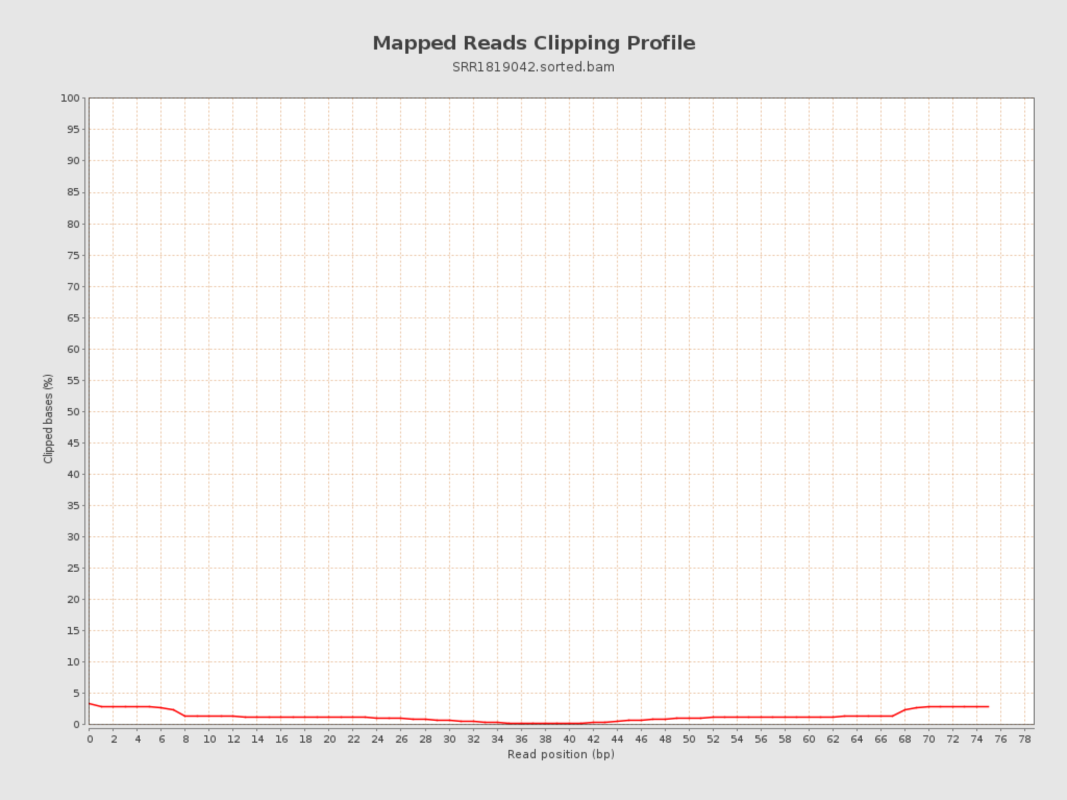
8. Results : Mapped Reads Nucleotide Content



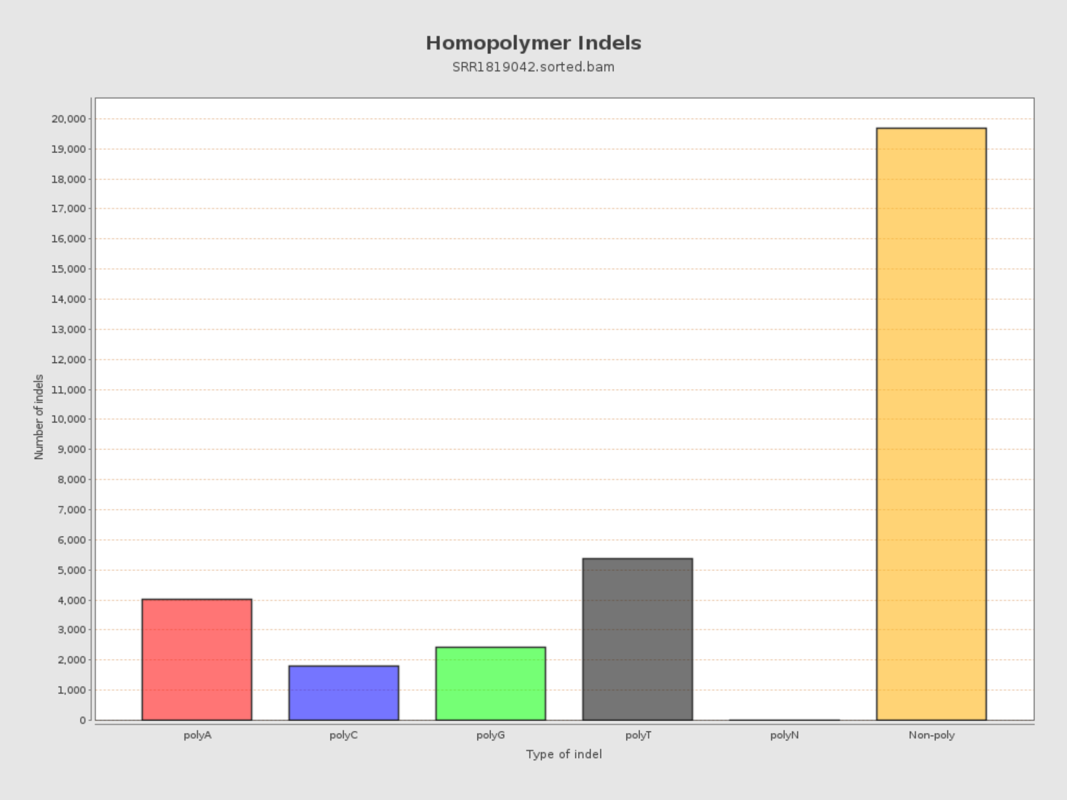
9. Results : Mapped Reads GC-content Distribution



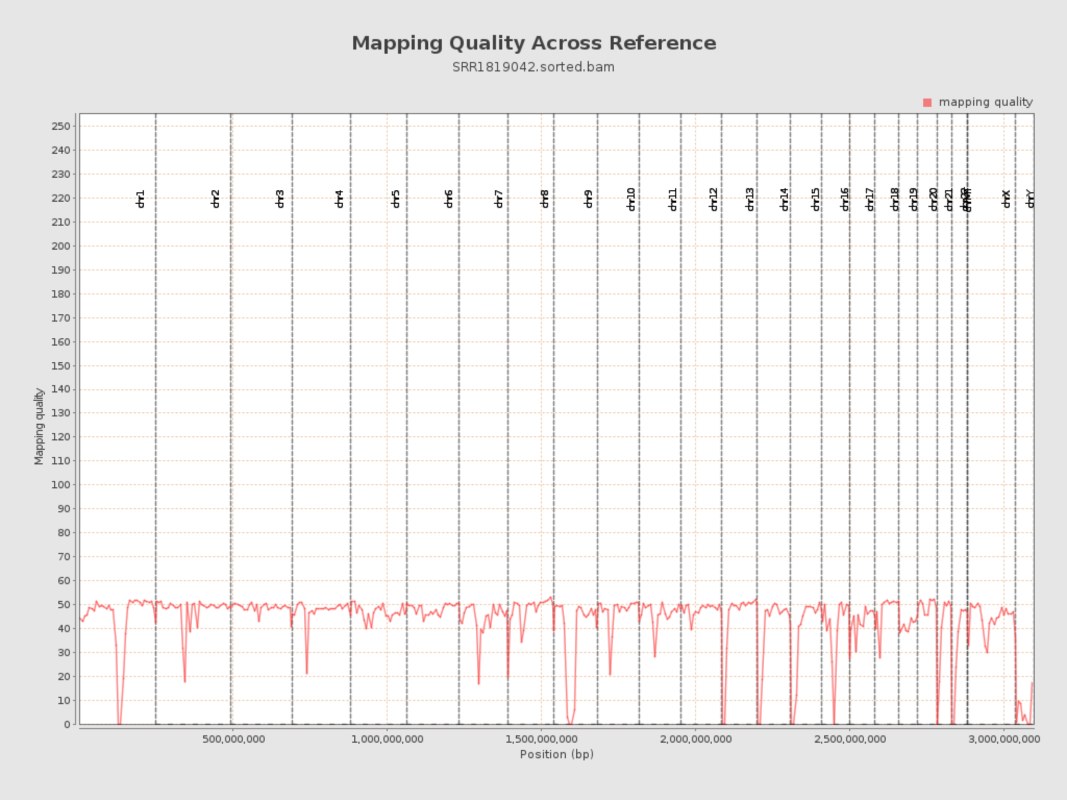
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram