Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:12:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819136.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_SRR1819136 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819136.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:12:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,911,501
Mapped reads	1,752,485 / 91.68%
Unmapped reads	159,016 / 8.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,621 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	127,150 / 6.65%
Duplication rate	5.63%
Clipped reads	1,756,469 / 91.89%

2.2. ACGT Content

Number/percentage of A's	24,926,602 / 24.46%
Number/percentage of C's	20,118,318 / 19.74%
Number/percentage of T's	31,798,859 / 31.2%
Number/percentage of G's	25,070,119 / 24.6%
Number/percentage of N's	1,554 / 0%
GC Percentage	44.34%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.3254

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

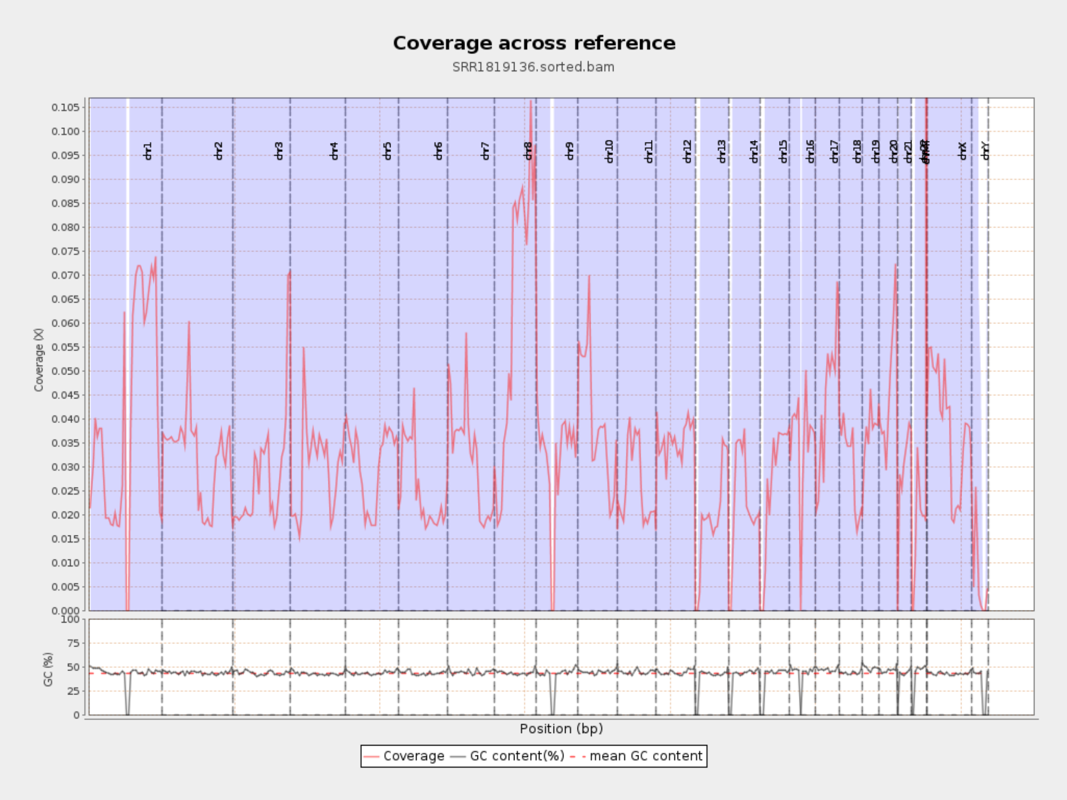
General error rate	0.53%
Mismatches	525,619
Insertions	6,475
Mapped reads with at least one insertion	0.37%
Deletions	18,484
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.24%

2.6. Chromosome stats

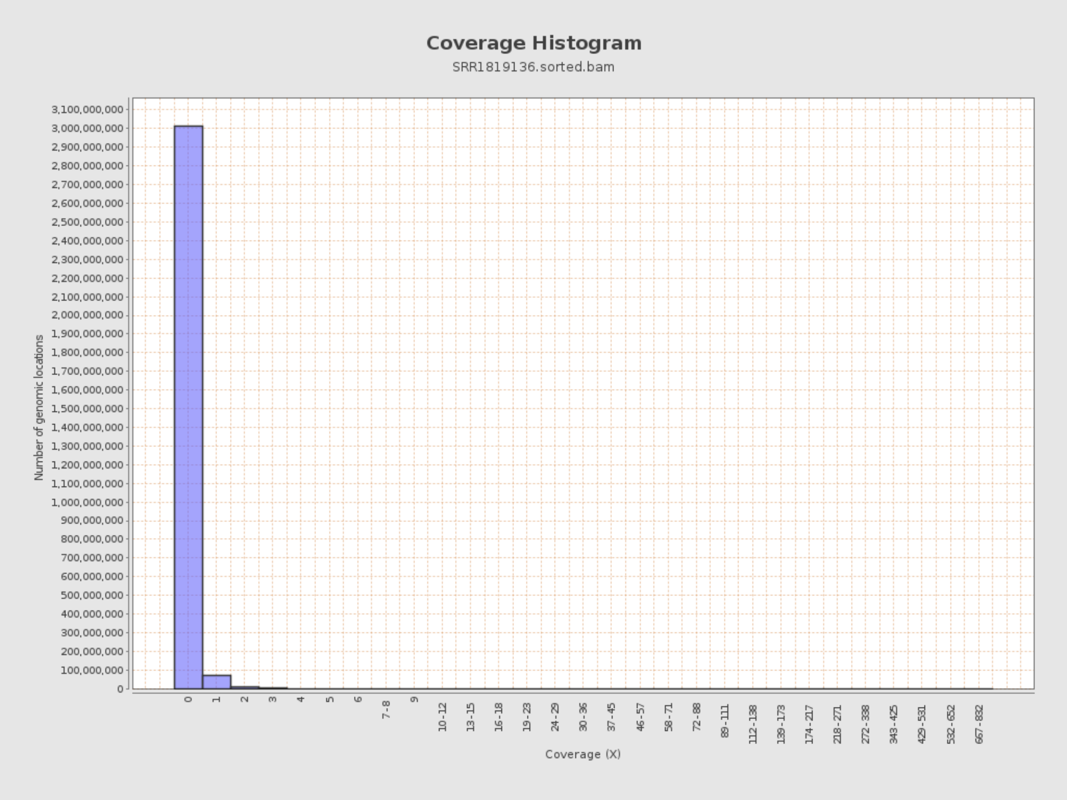
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10094471	0.0405	0.6366
chr2	243199373	7915298	0.0325	0.3935
chr3	198022430	5502715	0.0278	0.1953
chr4	191154276	5658371	0.0296	0.2503
chr5	180915260	5533546	0.0306	0.2055
chr6	171115067	4329077	0.0253	0.2322
chr7	159138663	5123721	0.0322	0.3709

chr8	146364022	9292723	0.0635	0.3576
chr9	141213431	4342947	0.0308	0.2502
chr10	135534747	5420086	0.04	0.3609
chr11	135006516	3531024	0.0262	0.2535
chr12	133851895	4784793	0.0357	0.2231
chr13	115169878	2217206	0.0193	0.1627
chr14	107349540	2410505	0.0225	0.1801
chr15	102531392	2697958	0.0263	0.1915
chr16	90354753	3182477	0.0352	0.2321
chr17	81195210	3622873	0.0446	0.2619
chr18	78077248	2389343	0.0306	0.466
chr19	59128983	2213970	0.0374	0.4364
chr20	63025520	2955462	0.0469	0.2584
chr21	48129895	1414870	0.0294	0.2328
chr22	51304566	855090	0.0167	0.1517
chrMT	16571	58705	3.5426	2.7382
chrX	155270560	6006932	0.0387	0.2488
chrY	59373566	392293	0.0066	0.2275

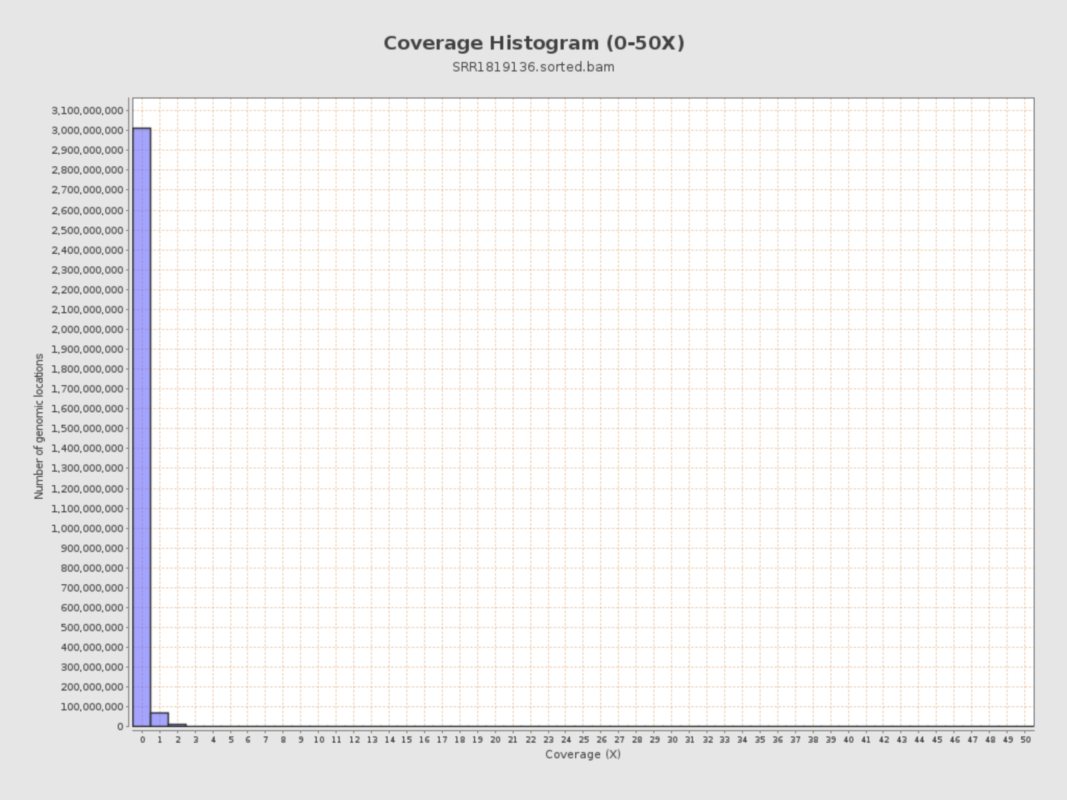
3. Results : Coverage across reference



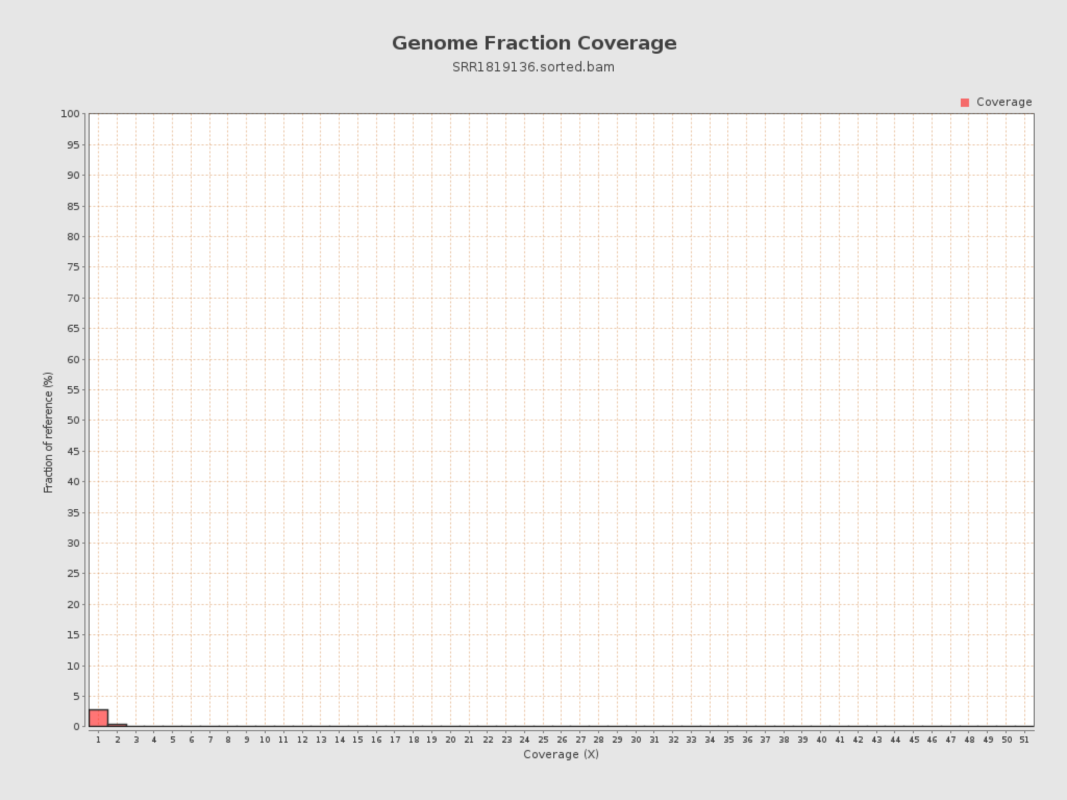
4. Results : Coverage Histogram



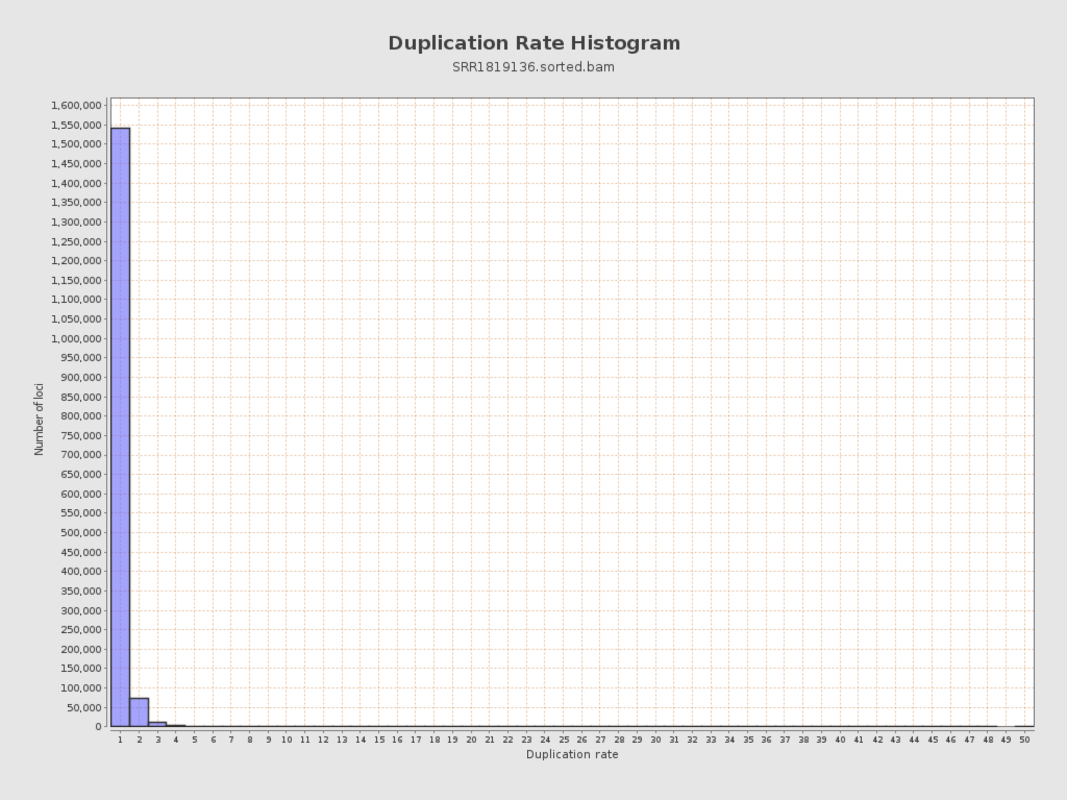
5. Results : Coverage Histogram (0-50X)



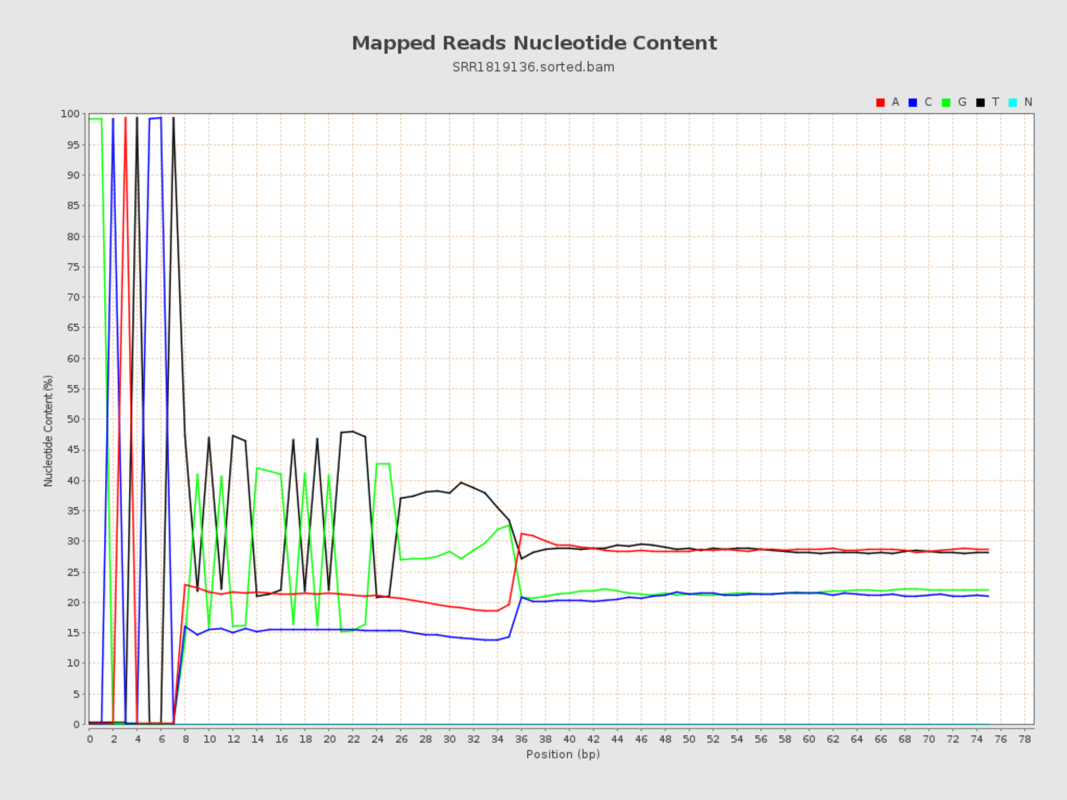
6. Results : Genome Fraction Coverage



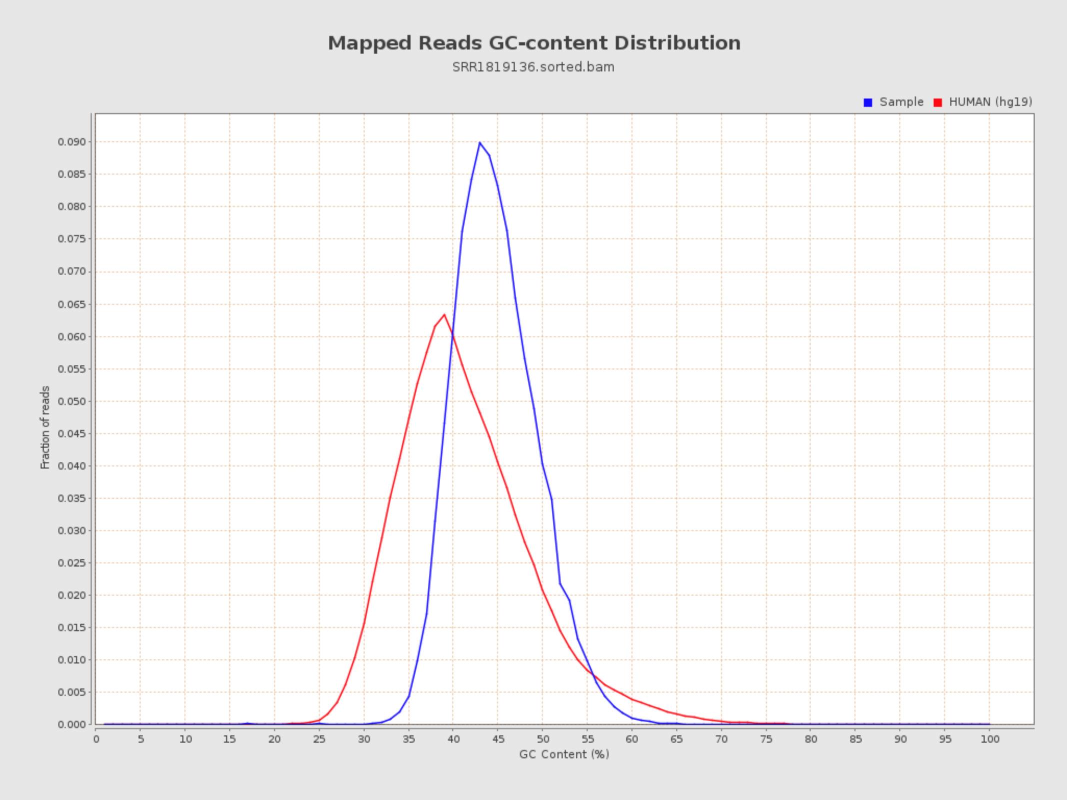
7. Results : Duplication Rate Histogram



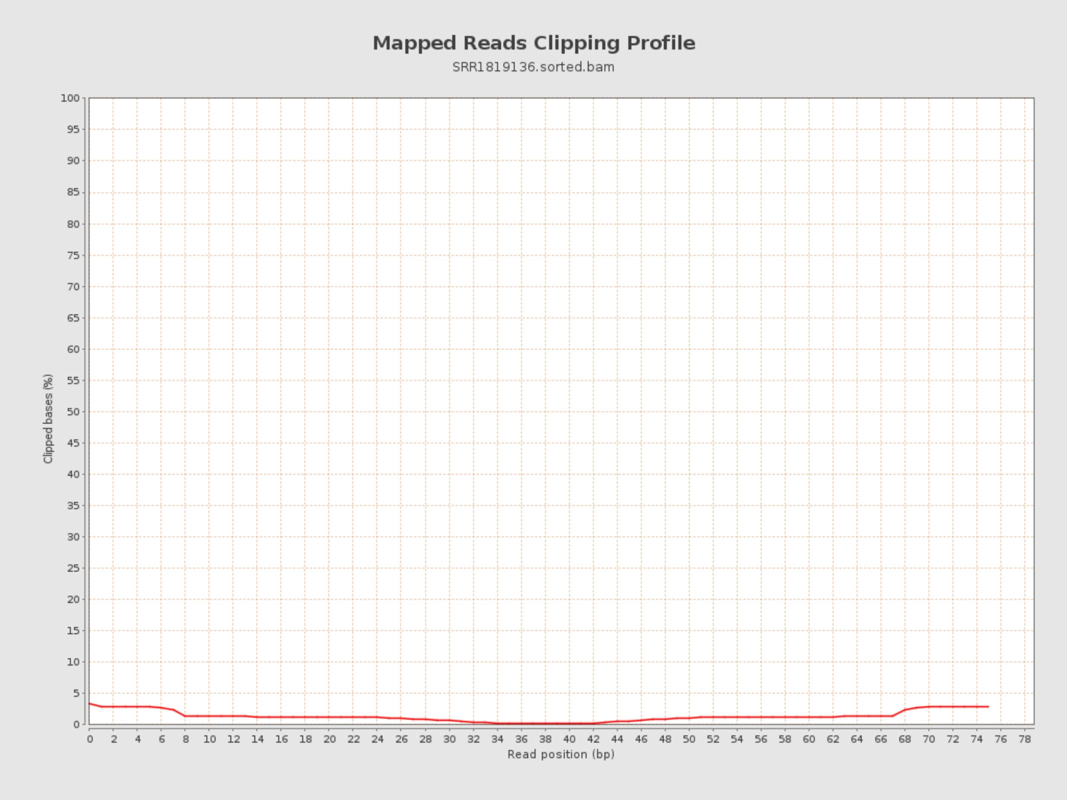
8. Results : Mapped Reads Nucleotide Content



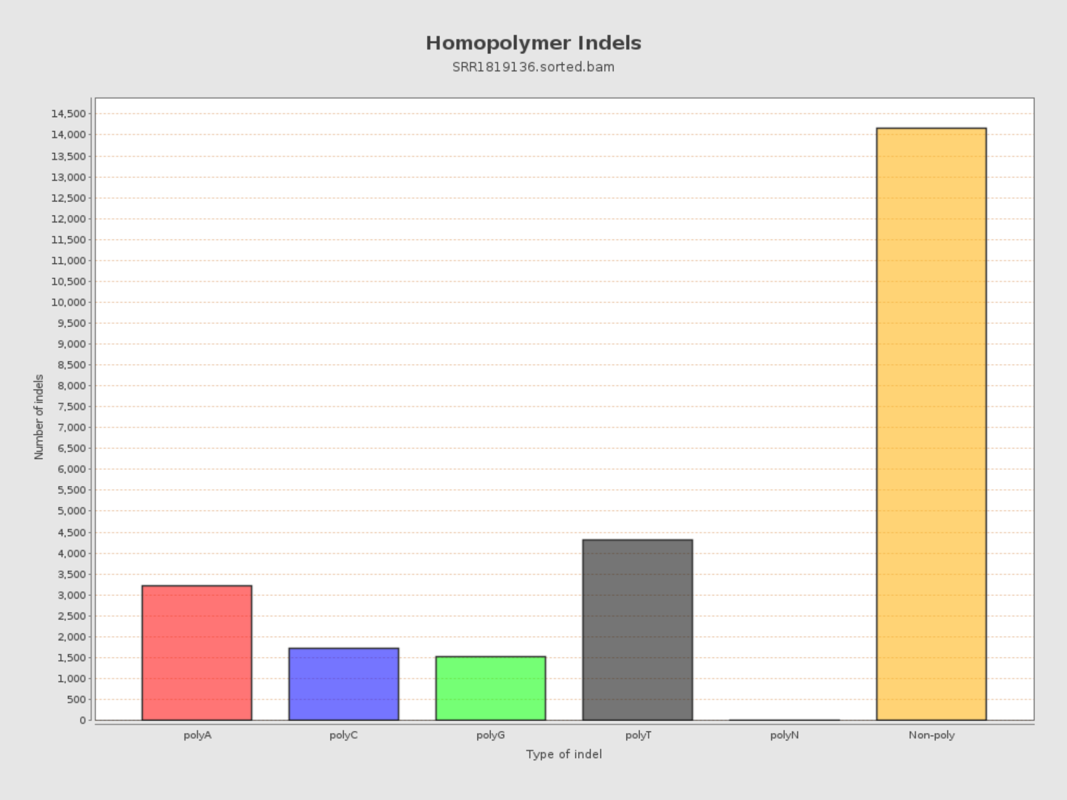
9. Results : Mapped Reads GC-content Distribution



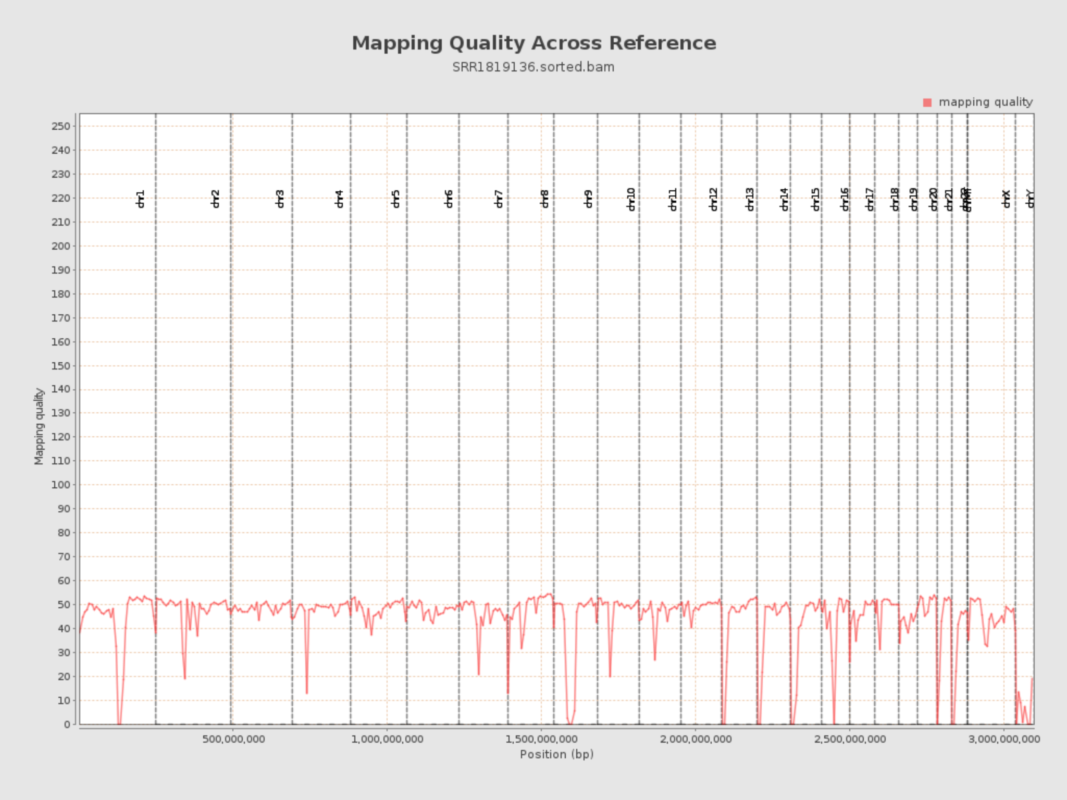
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram