Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:09:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819135.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_SRR1819135 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819135.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:09:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,244,613
Mapped reads	1,136,905 / 91.35%
Unmapped reads	107,708 / 8.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,682 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	64,547 / 5.19%
Duplication rate	4.49%
Clipped reads	1,138,835 / 91.5%

2.2. ACGT Content

Number/percentage of A's	16,728,747 / 25.39%
Number/percentage of C's	12,918,000 / 19.61%
Number/percentage of T's	20,610,063 / 31.28%
Number/percentage of G's	15,632,825 / 23.73%
Number/percentage of N's	1,003 / 0%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2298

2.4. Mapping Quality

Mean Mapping Quality	44.63

2.5. Mismatches and indels

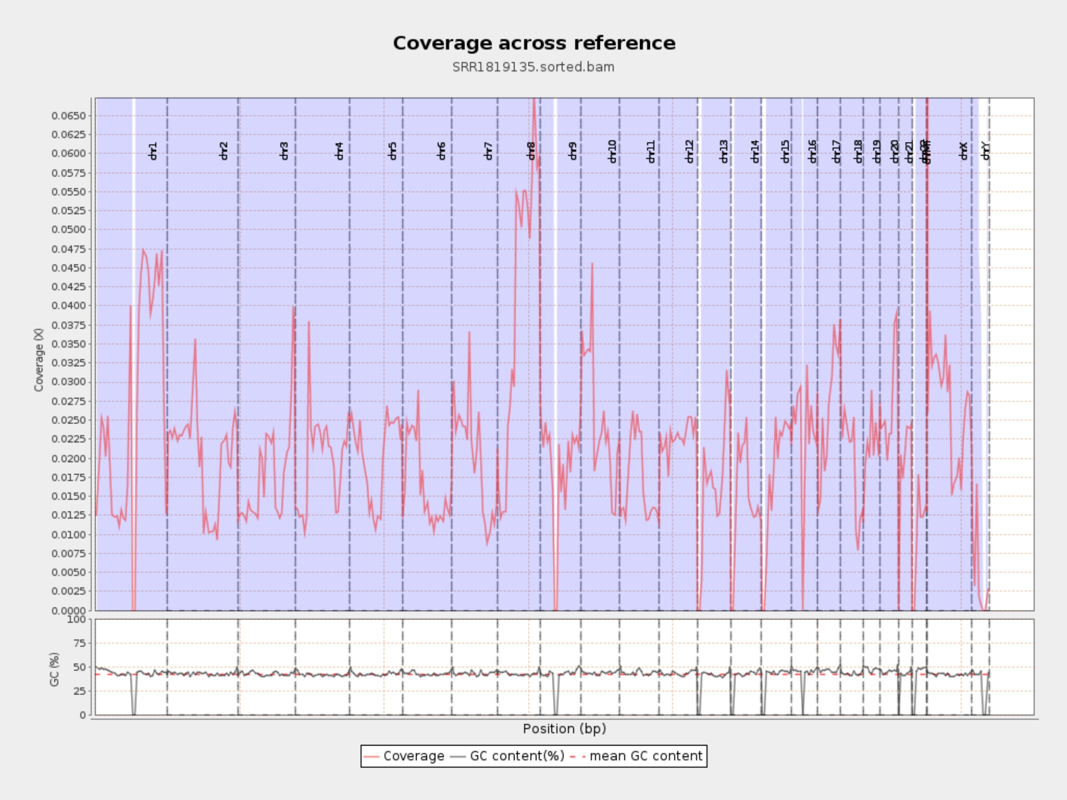
General error rate	0.53%
Mismatches	342,992
Insertions	4,409
Mapped reads with at least one insertion	0.39%
Deletions	11,952
Mapped reads with at least one deletion	1.04%
Homopolymer indels	44.01%

2.6. Chromosome stats

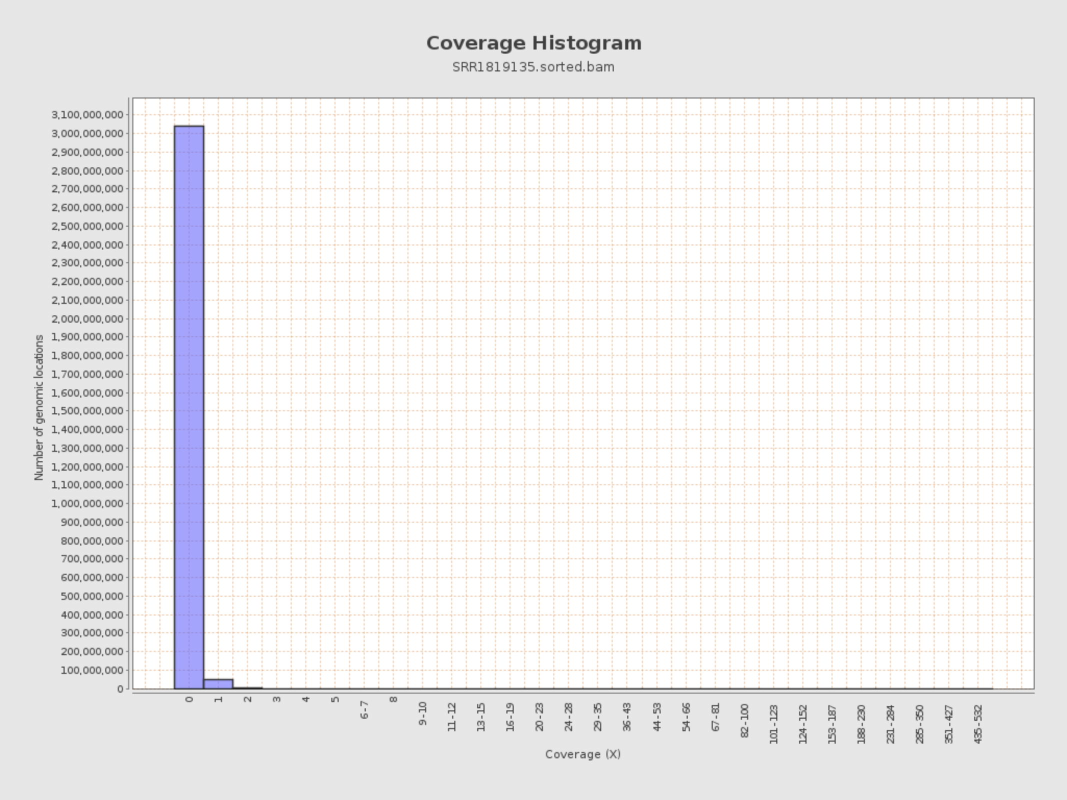
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6491589	0.026	0.4183
chr2	243199373	4985156	0.0205	0.2754
chr3	198022430	3524802	0.0178	0.1499
chr4	191154276	3780527	0.0198	0.1864
chr5	180915260	3674445	0.0203	0.1603
chr6	171115067	2800516	0.0164	0.1675
chr7	159138663	3228793	0.0203	0.2678

chr8	146364022	5981023	0.0409	0.2653
chr9	141213431	2617899	0.0185	0.1802
chr10	135534747	3482088	0.0257	0.2512
chr11	135006516	2305568	0.0171	0.1953
chr12	133851895	3050740	0.0228	0.1699
chr13	115169878	1889789	0.0164	0.144
chr14	107349540	1559128	0.0145	0.1364
chr15	102531392	1773790	0.0173	0.1478
chr16	90354753	2081838	0.023	0.1786
chr17	81195210	2133064	0.0263	0.194
chr18	78077248	1494854	0.0191	0.3086
chr19	59128983	1297003	0.0219	0.2749
chr20	63025520	1722030	0.0273	0.1883
chr21	48129895	944696	0.0196	0.1807
chr22	51304566	521153	0.0102	0.1138
chrMT	16571	92284	5.569	3.8195
chrX	155270560	4226517	0.0272	0.196
chrY	59373566	251230	0.0042	0.1435

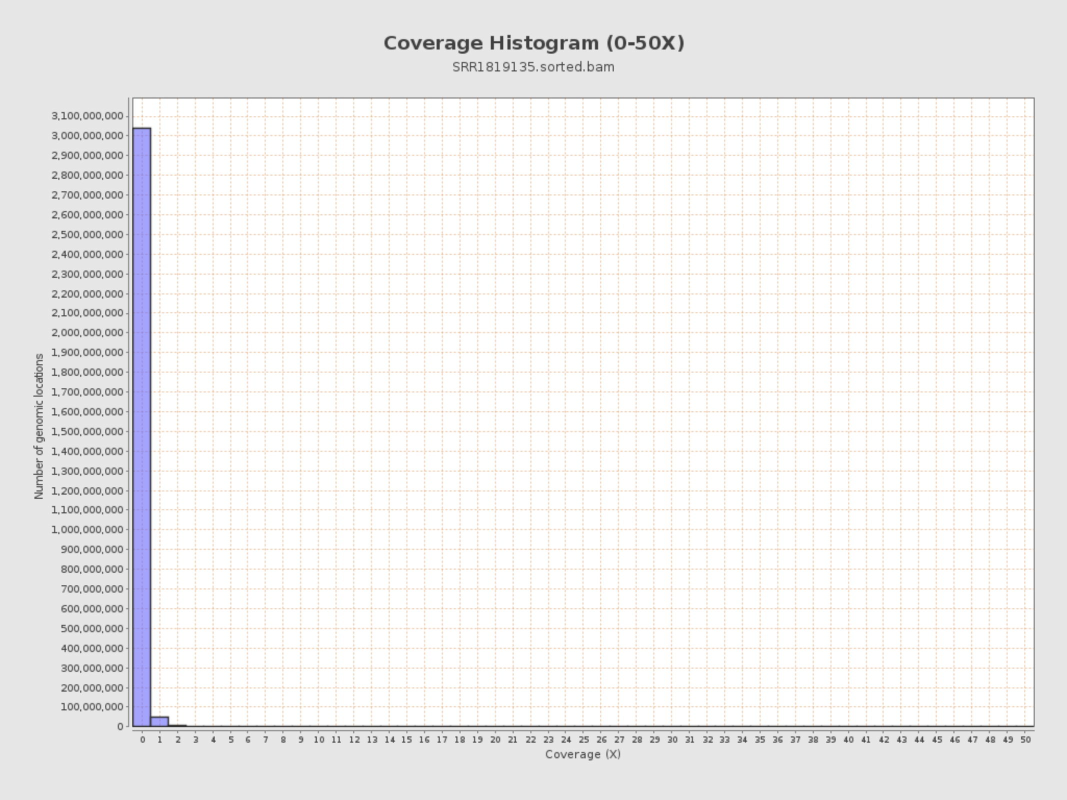
3. Results : Coverage across reference



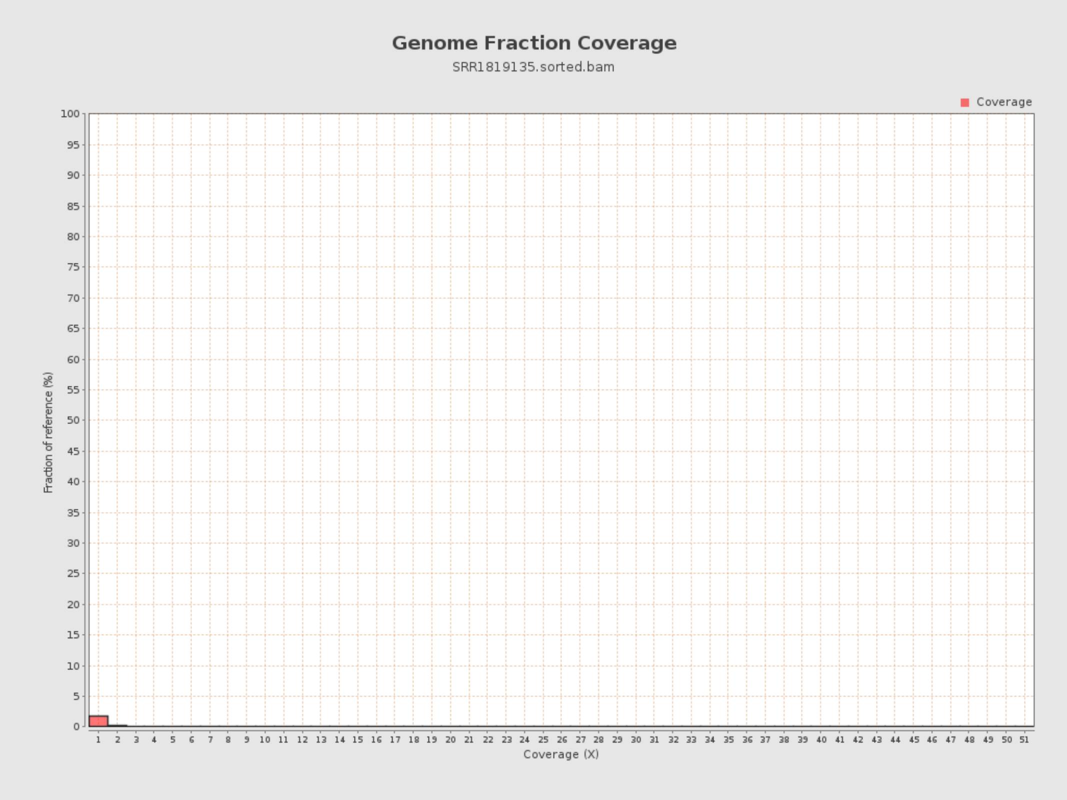
4. Results : Coverage Histogram



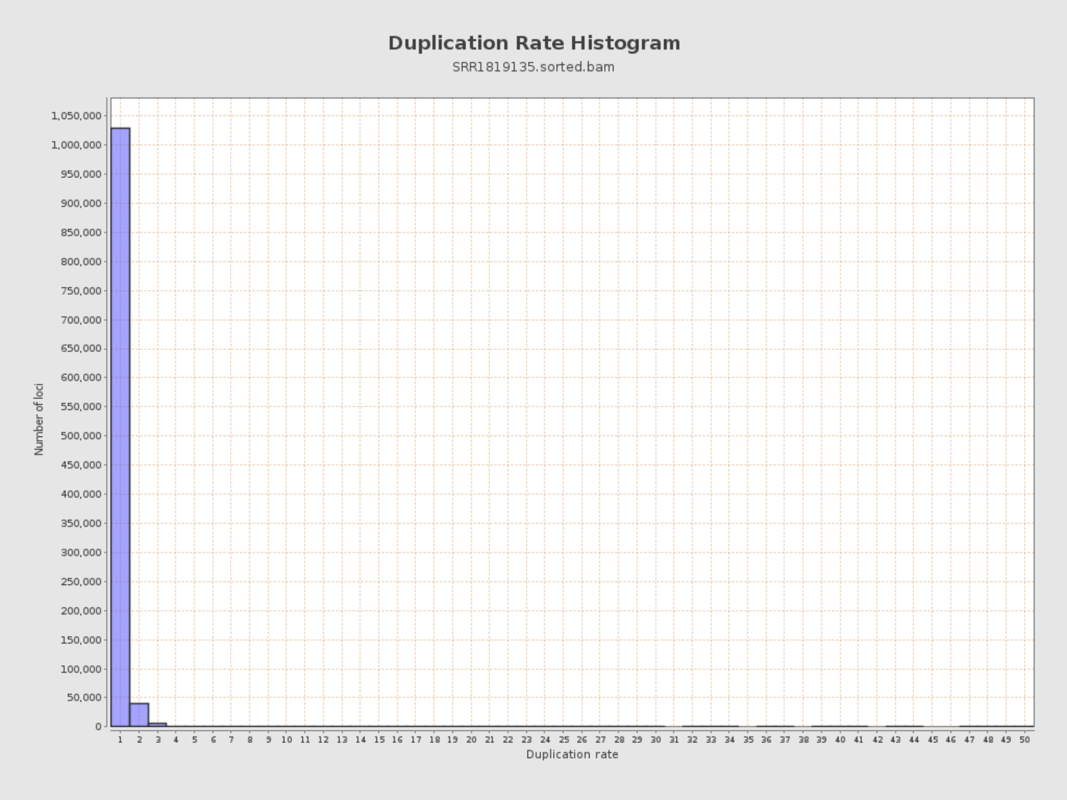
5. Results : Coverage Histogram (0-50X)



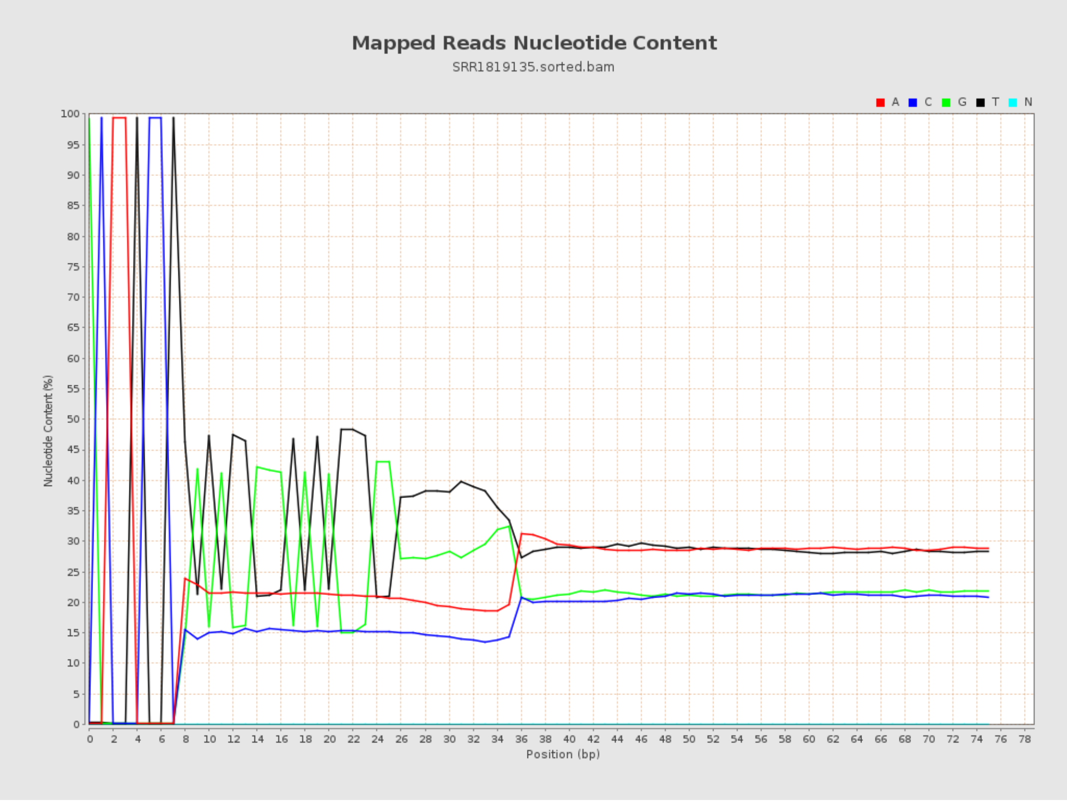
6. Results : Genome Fraction Coverage



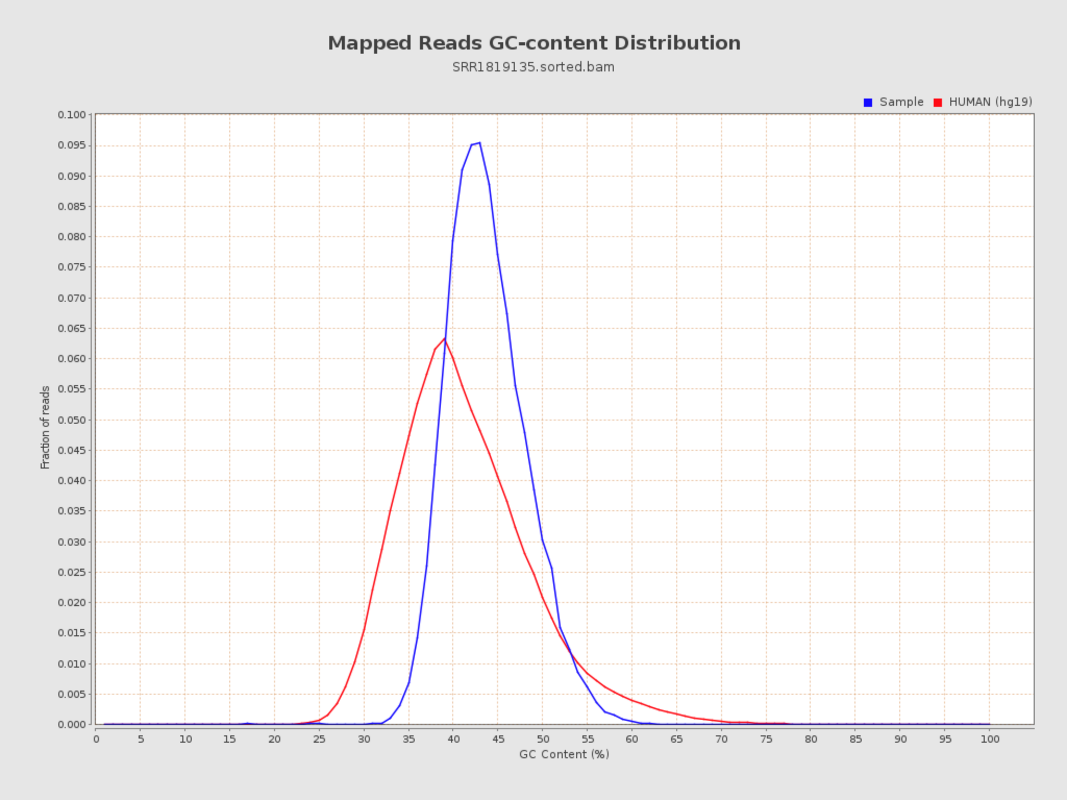
7. Results : Duplication Rate Histogram



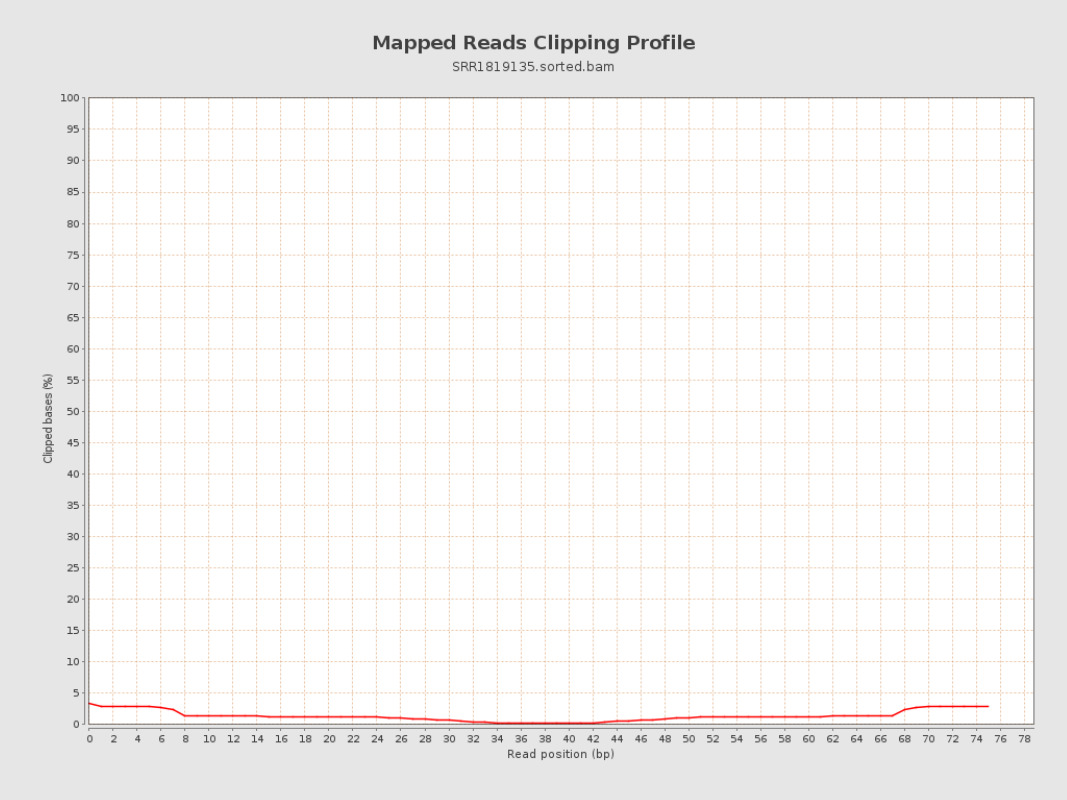
8. Results : Mapped Reads Nucleotide Content



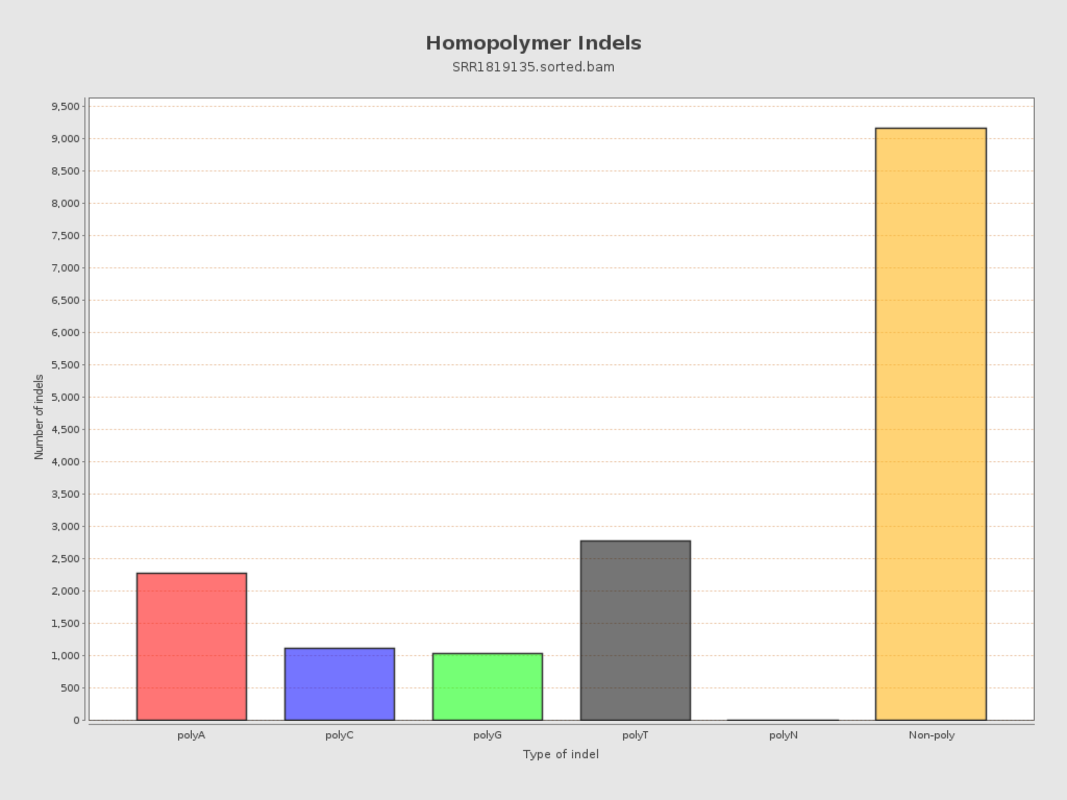
9. Results : Mapped Reads GC-content Distribution



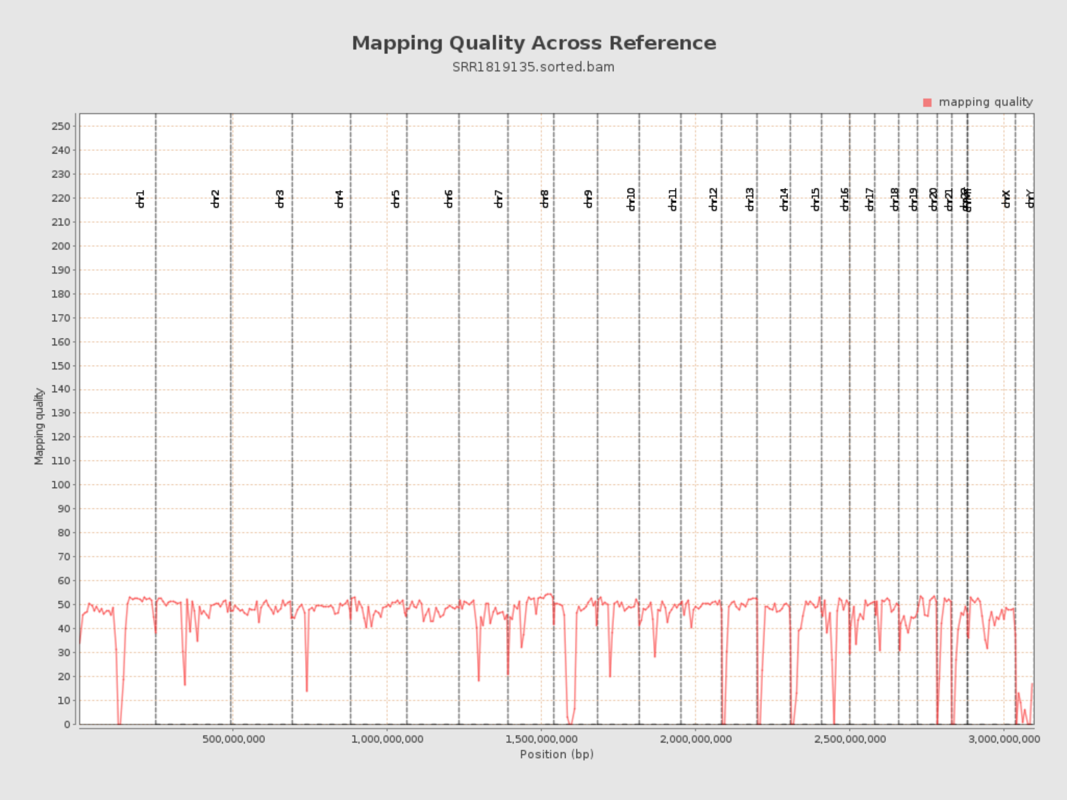
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram