Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 01:39:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089719.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_SRR089719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089719.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 01:39:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,875,704
Mapped reads	11,966,955 / 86.24%
Unmapped reads	1,908,749 / 13.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	653 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,818,740 / 13.11%
Duplication rate	11.16%
Clipped reads	934,420 / 6.73%

2.2. ACGT Content

Number/percentage of A's	169,055,185 / 29.88%
Number/percentage of C's	110,080,766 / 19.46%
Number/percentage of T's	171,728,992 / 30.36%
Number/percentage of G's	114,844,219 / 20.3%
Number/percentage of N's	5,645 / 0%
GC Percentage	39.76%

2.3. Coverage

Mean	0.1828

Standard Deviation	1.225

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

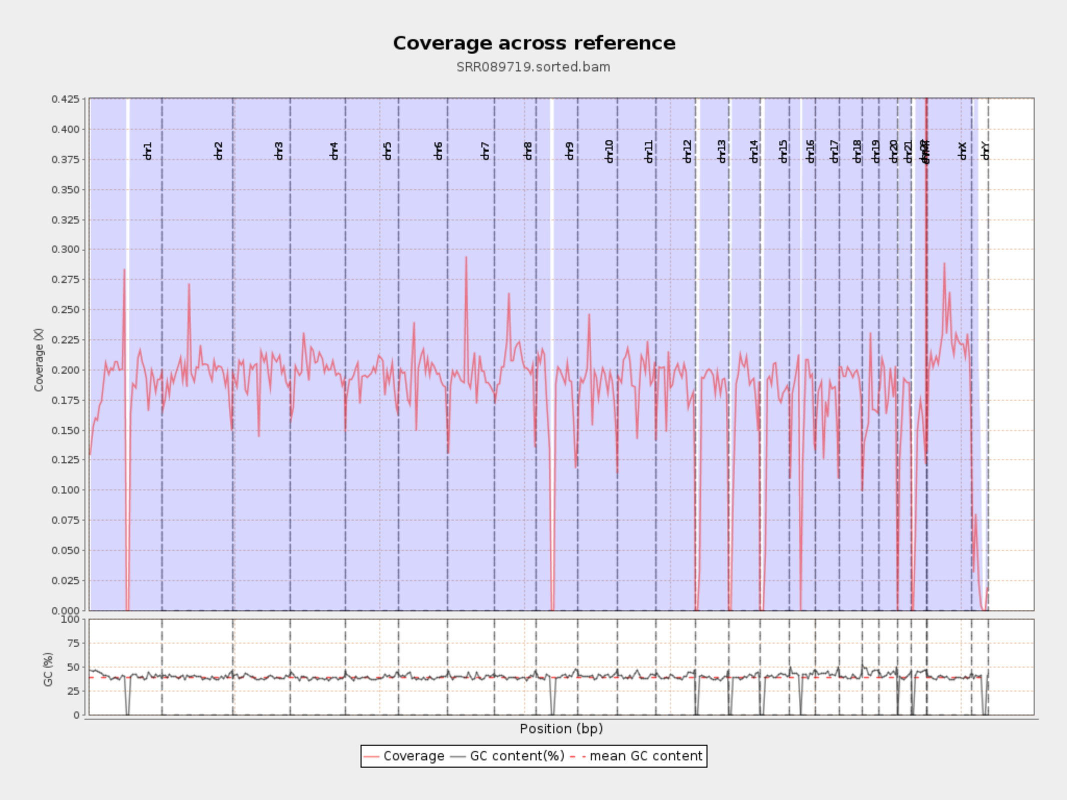
General error rate	0.52%
Mismatches	2,922,996
Insertions	26,119
Mapped reads with at least one insertion	0.22%
Deletions	77,744
Mapped reads with at least one deletion	0.65%
Homopolymer indels	49.6%

2.6. Chromosome stats

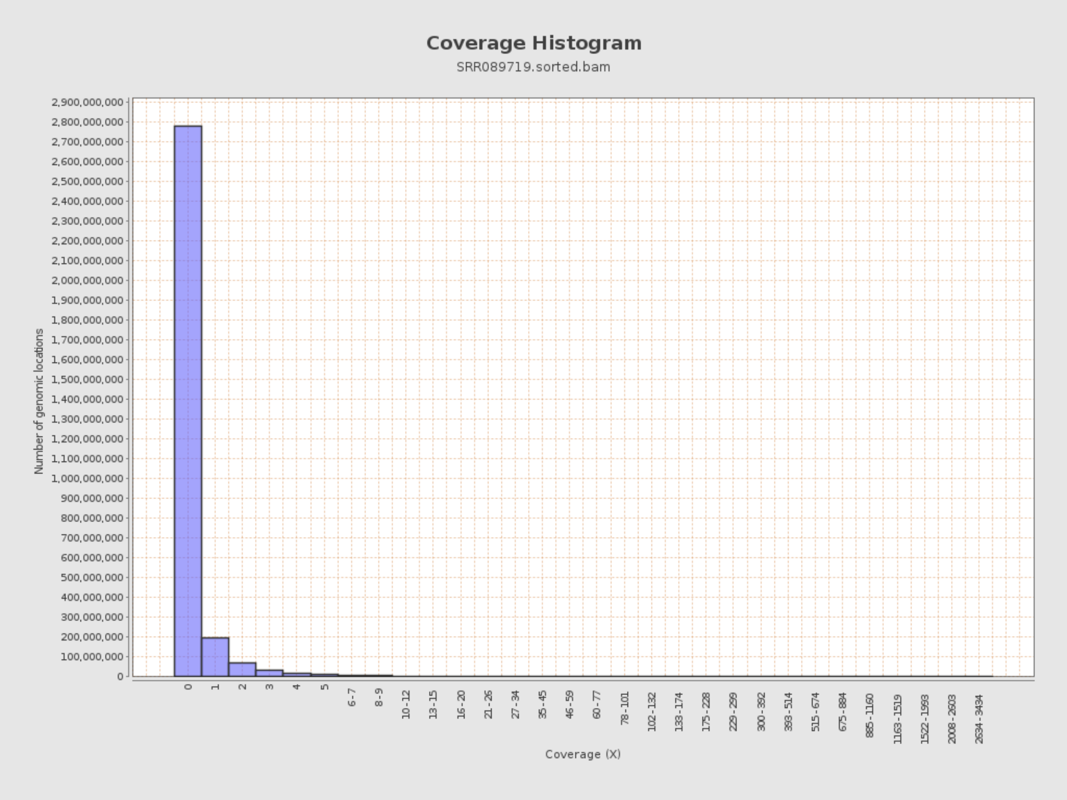
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	44663491	0.1792	2.2358
chr2	243199373	48007974	0.1974	1.1046
chr3	198022430	39260980	0.1983	0.7256
chr4	191154276	38348280	0.2006	0.7733
chr5	180915260	35062784	0.1938	0.7327
chr6	171115067	33516849	0.1959	0.8914
chr7	159138663	31271279	0.1965	1.6785

chr8	146364022	29866992	0.2041	2.0258
chr9	141213431	23541982	0.1667	1.0411
chr10	135534747	25723597	0.1898	1.0256
chr11	135006516	26398127	0.1955	1.0853
chr12	133851895	25309328	0.1891	0.7913
chr13	115169878	18325212	0.1591	0.6508
chr14	107349540	17253491	0.1607	0.725
chr15	102531392	15483910	0.151	0.6314
chr16	90354753	14914090	0.1651	0.7151
chr17	81195210	13557419	0.167	0.7828
chr18	78077248	15319934	0.1962	2.3315
chr19	59128983	9750323	0.1649	1.6525
chr20	63025520	11698975	0.1856	0.7904
chr21	48129895	7271106	0.1511	0.7412
chr22	51304566	5544576	0.1081	0.5181
chrMT	16571	66217	3.996	3.5122
chrX	155270560	34088725	0.2195	0.9447
chrY	59373566	1586871	0.0267	0.4948

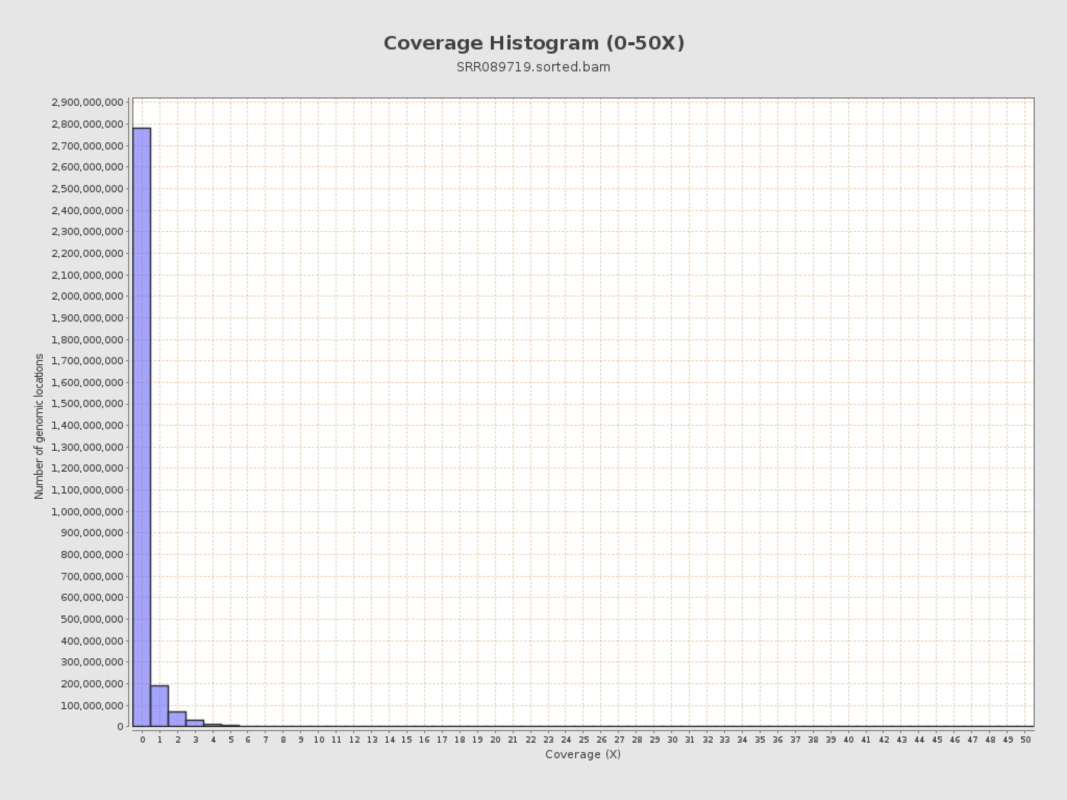
3. Results : Coverage across reference



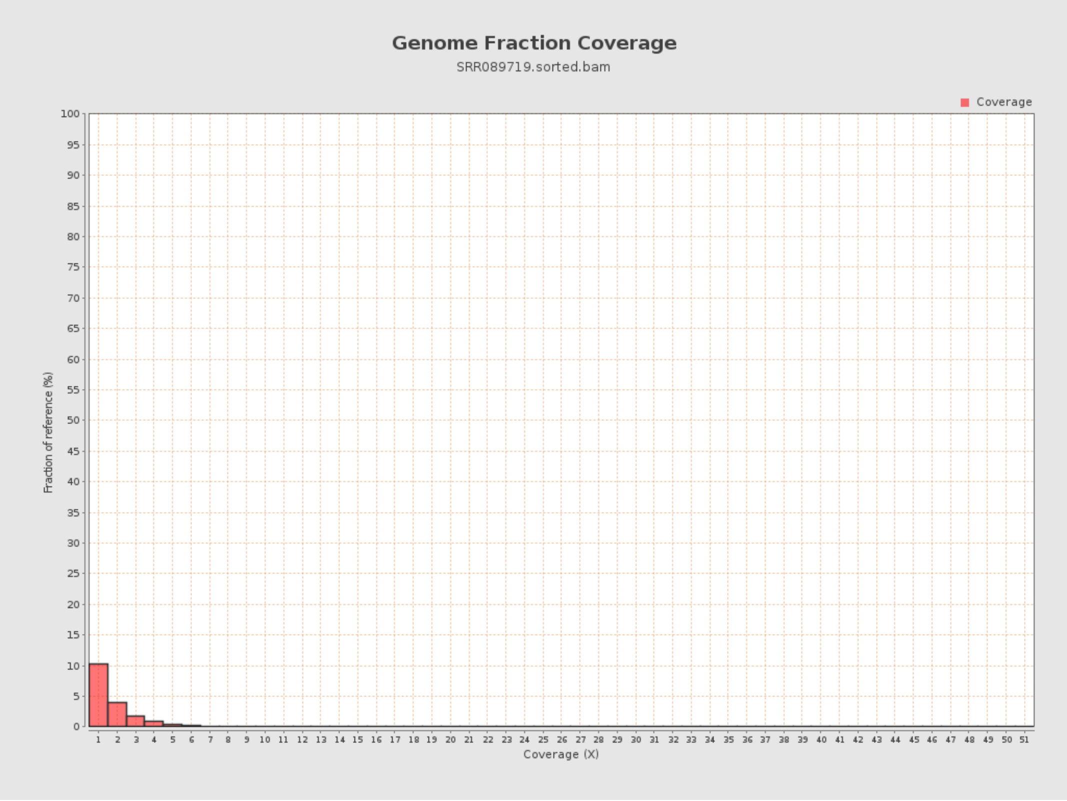
4. Results : Coverage Histogram



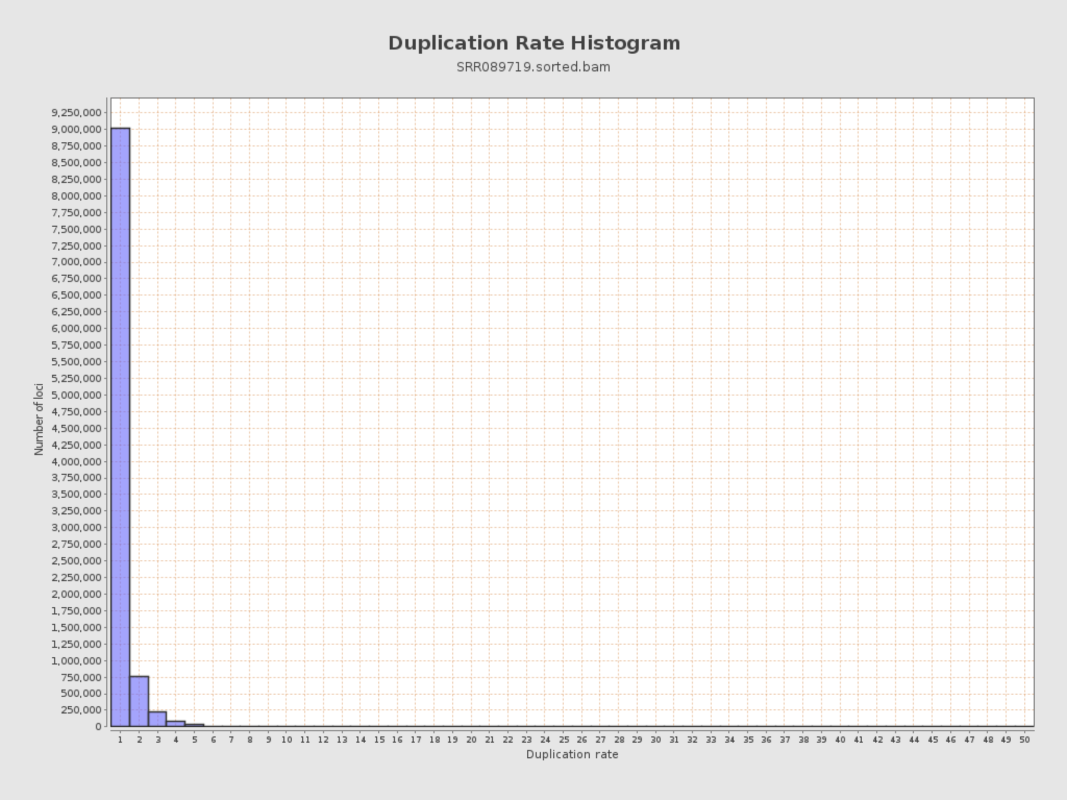
5. Results : Coverage Histogram (0-50X)



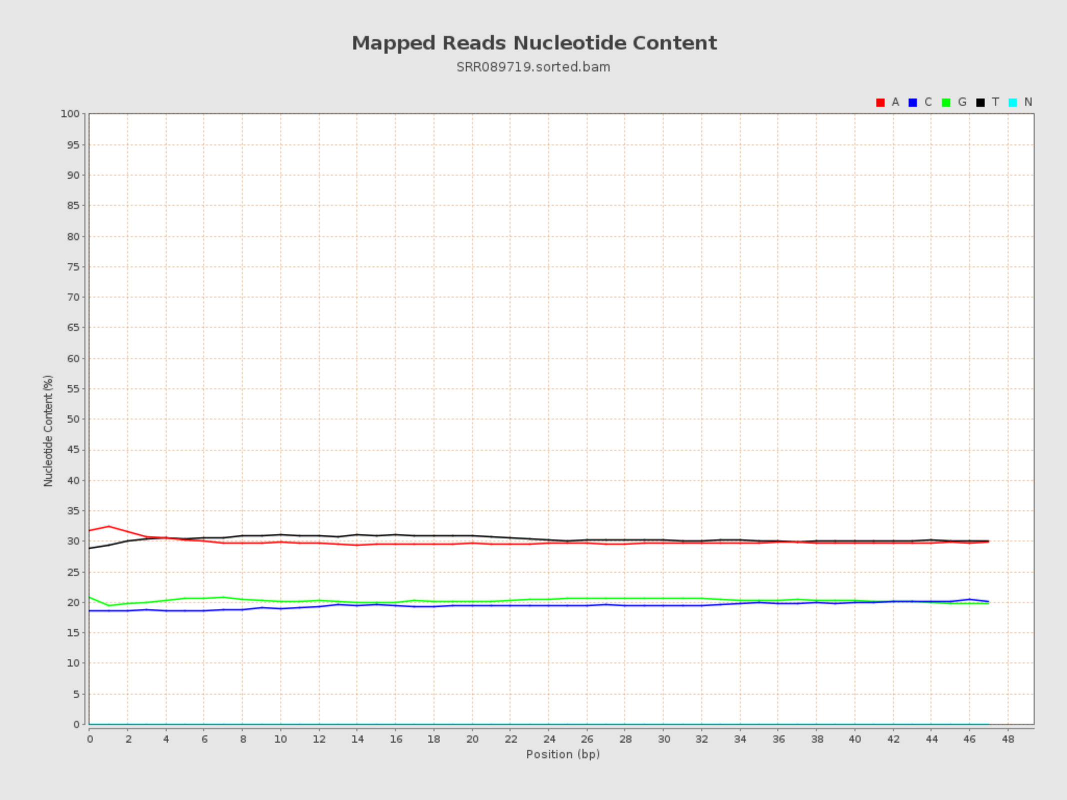
6. Results : Genome Fraction Coverage



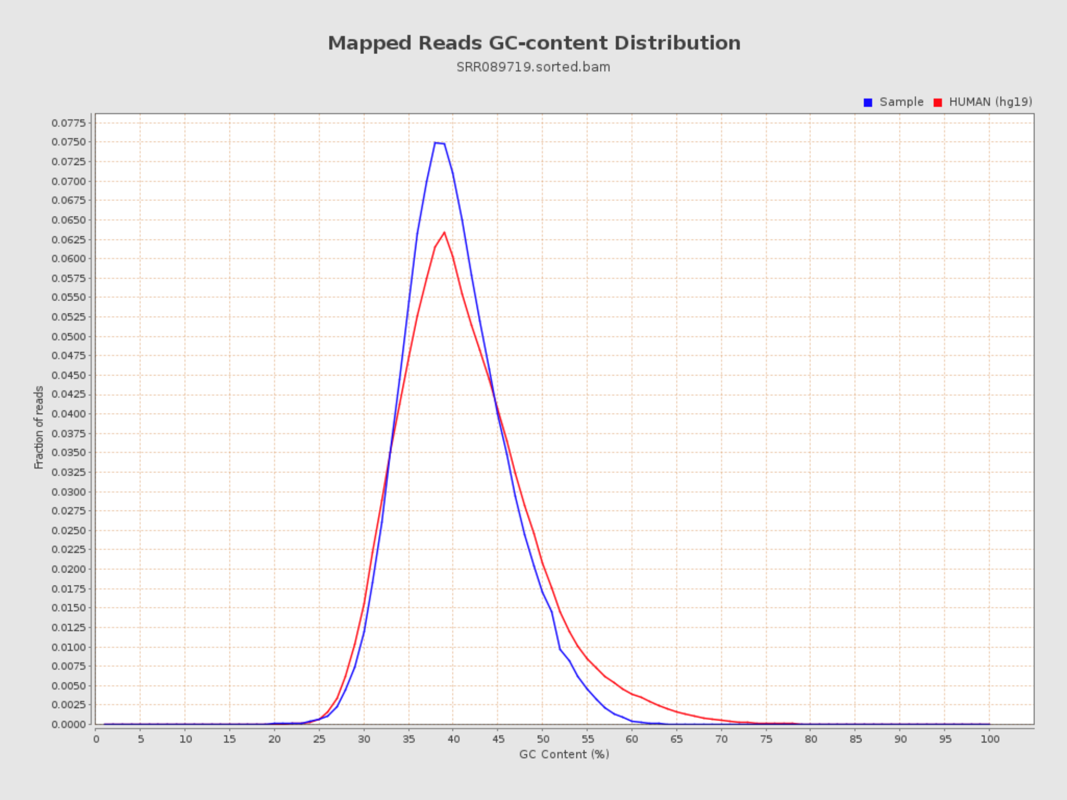
7. Results : Duplication Rate Histogram



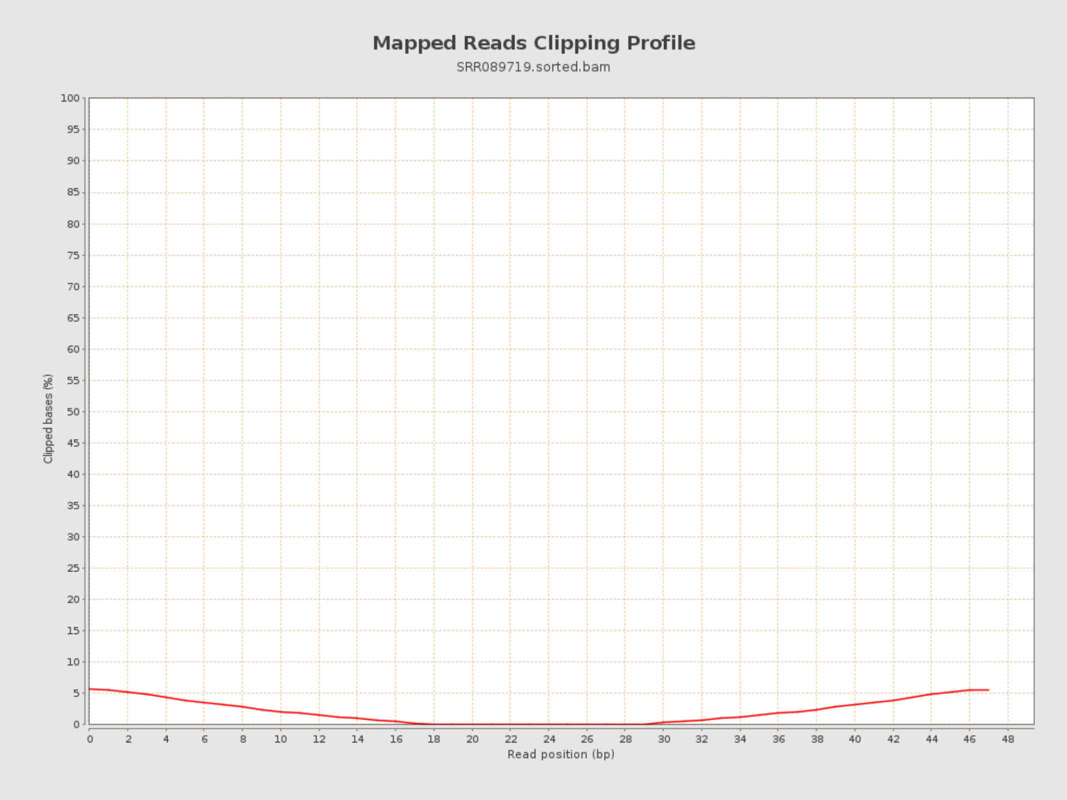
8. Results : Mapped Reads Nucleotide Content



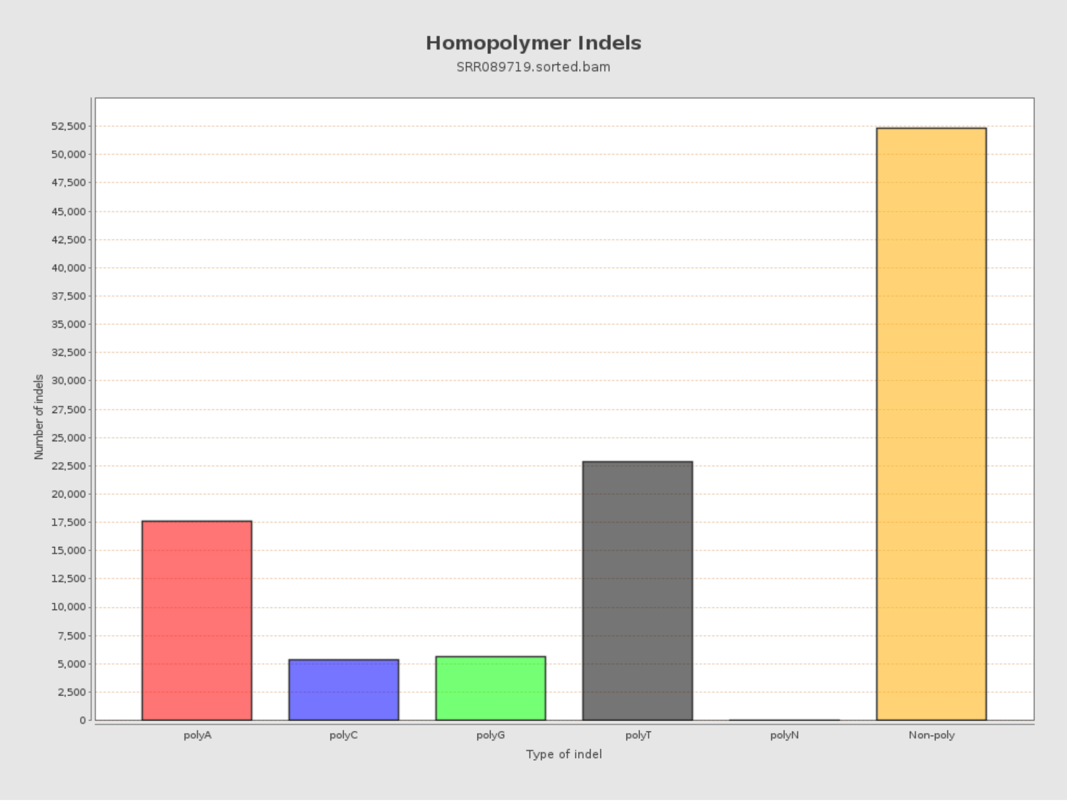
9. Results : Mapped Reads GC-content Distribution



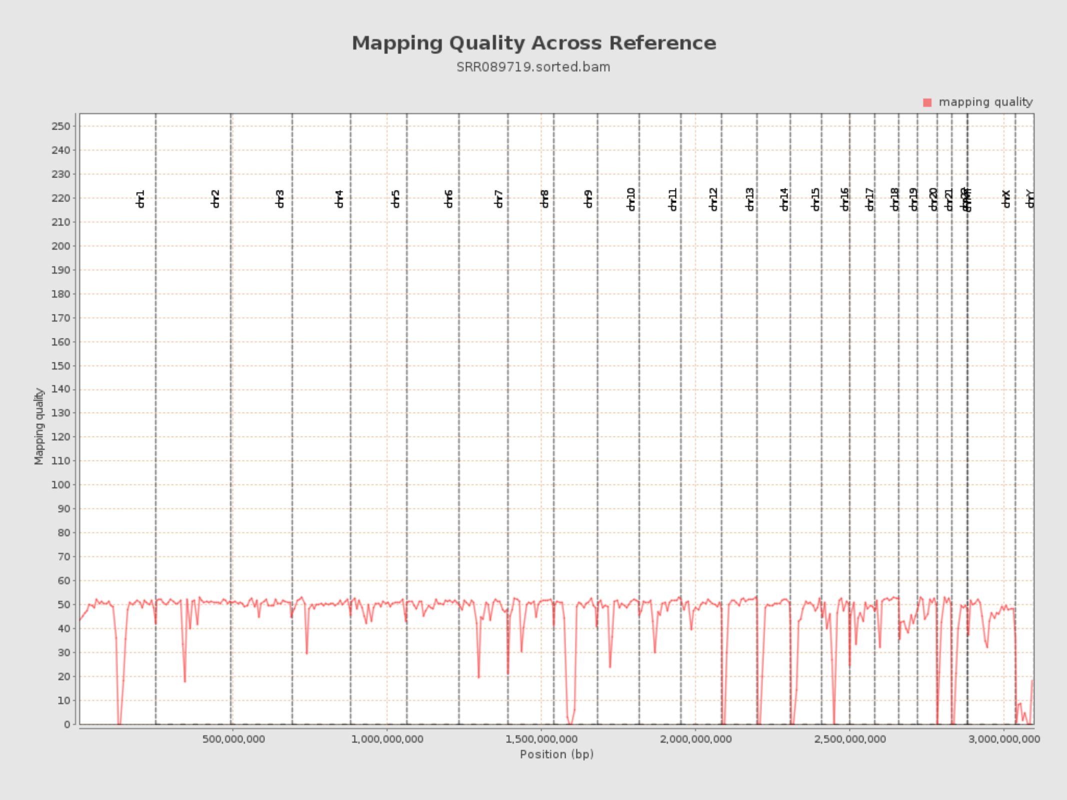
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram