Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 01:09:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089716.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_SRR089716 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089716.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 01:09:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089716.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,954,616
Mapped reads	19,081,921 / 86.92%
Unmapped reads	2,872,695 / 13.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	816 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,971,982 / 18.09%
Duplication rate	11.26%
Clipped reads	1,306,009 / 5.95%

2.2. ACGT Content

Number/percentage of A's	265,949,985 / 29.42%
Number/percentage of C's	184,078,938 / 20.37%
Number/percentage of T's	265,625,380 / 29.39%
Number/percentage of G's	187,748,653 / 20.77%
Number/percentage of N's	467,119 / 0.05%
GC Percentage	41.14%

2.3. Coverage

Mean	0.292

Standard Deviation	2.1413

2.4. Mapping Quality

Mean Mapping Quality	45.62

2.5. Mismatches and indels

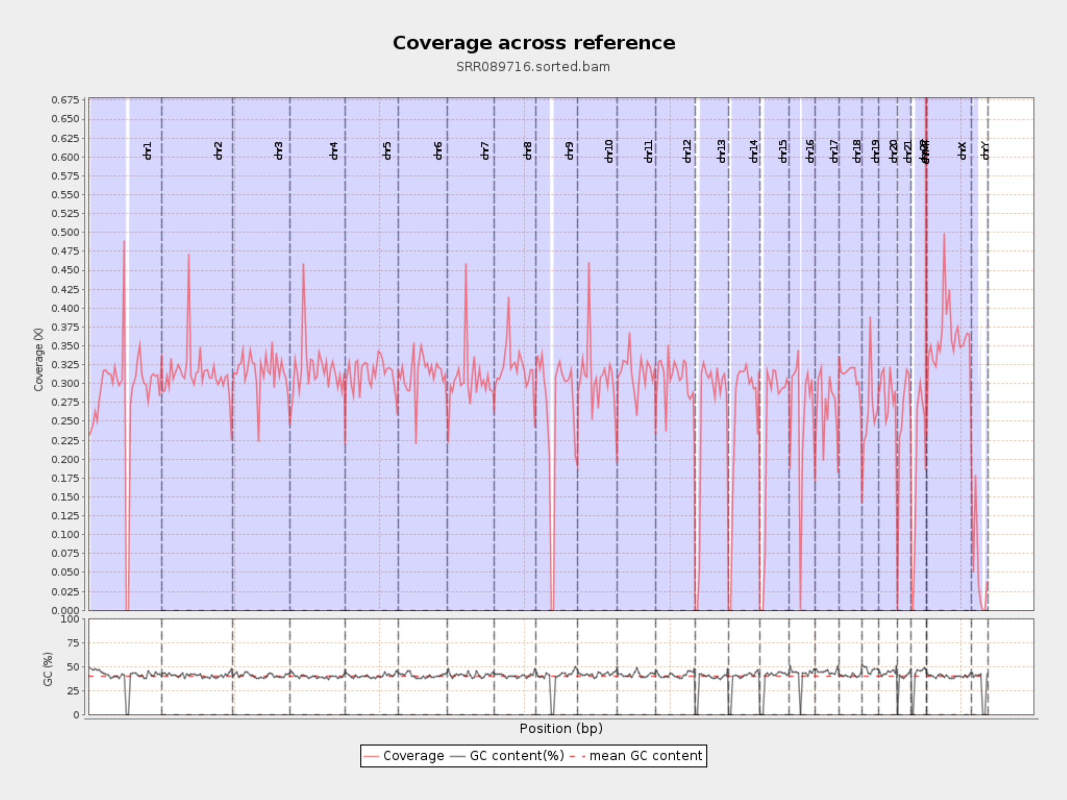
General error rate	0.52%
Mismatches	4,631,679
Insertions	36,282
Mapped reads with at least one insertion	0.19%
Deletions	112,059
Mapped reads with at least one deletion	0.59%
Homopolymer indels	47.85%

2.6. Chromosome stats

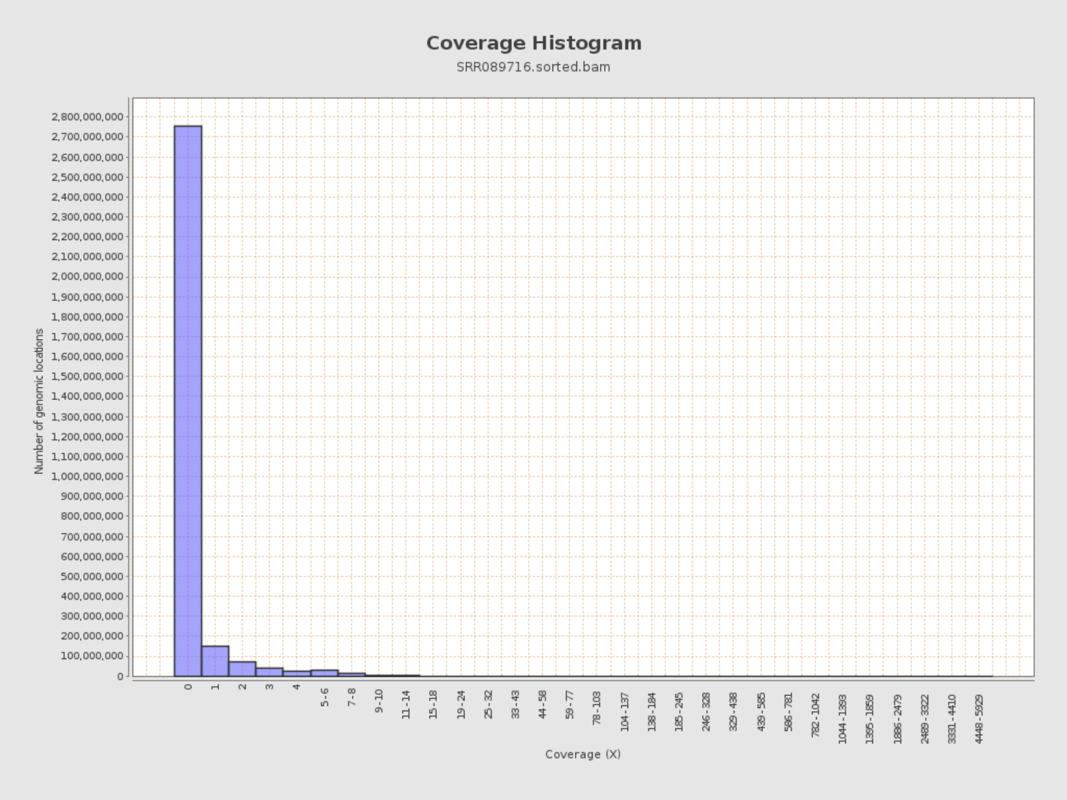
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	71185429	0.2856	4.2922
chr2	243199373	76303759	0.3137	2.0307
chr3	198022430	62493894	0.3156	1.2008
chr4	191154276	60799097	0.3181	1.4037
chr5	180915260	56640318	0.3131	1.2148
chr6	171115067	53547103	0.3129	1.3383
chr7	159138663	48878229	0.3071	2.6066

chr8	146364022	46861896	0.3202	3.1607
chr9	141213431	37360481	0.2646	1.7846
chr10	135534747	41855136	0.3088	1.8682
chr11	135006516	42225823	0.3128	1.9799
chr12	133851895	41005039	0.3063	1.3092
chr13	115169878	29207582	0.2536	1.0773
chr14	107349540	27082205	0.2523	1.1821
chr15	102531392	24819119	0.2421	1.0548
chr16	90354753	23617024	0.2614	1.1985
chr17	81195210	21696110	0.2672	1.4503
chr18	78077248	24302936	0.3113	3.9091
chr19	59128983	15710046	0.2657	2.9174
chr20	63025520	17907368	0.2841	1.2663
chr21	48129895	11864578	0.2465	1.3797
chr22	51304566	9675635	0.1886	0.9307
chrMT	16571	98576	5.9487	5.614
chrX	155270560	55882241	0.3599	1.5904
chrY	59373566	3020302	0.0509	1.3419

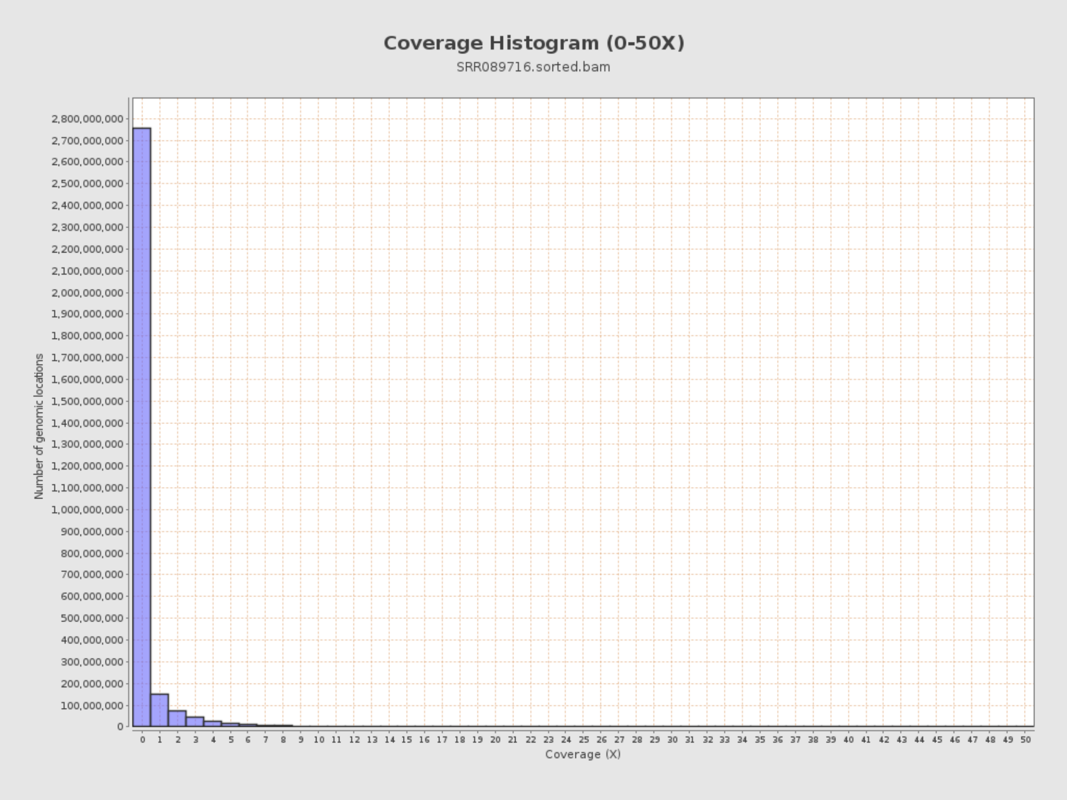
3. Results : Coverage across reference



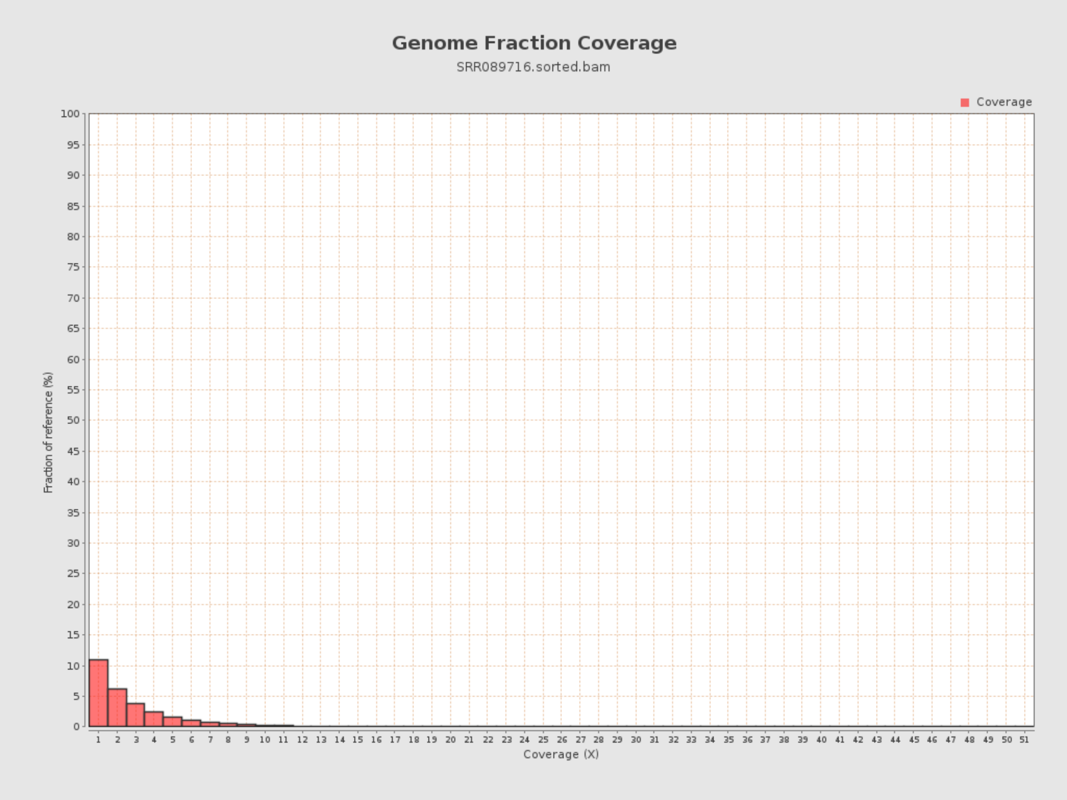
4. Results : Coverage Histogram



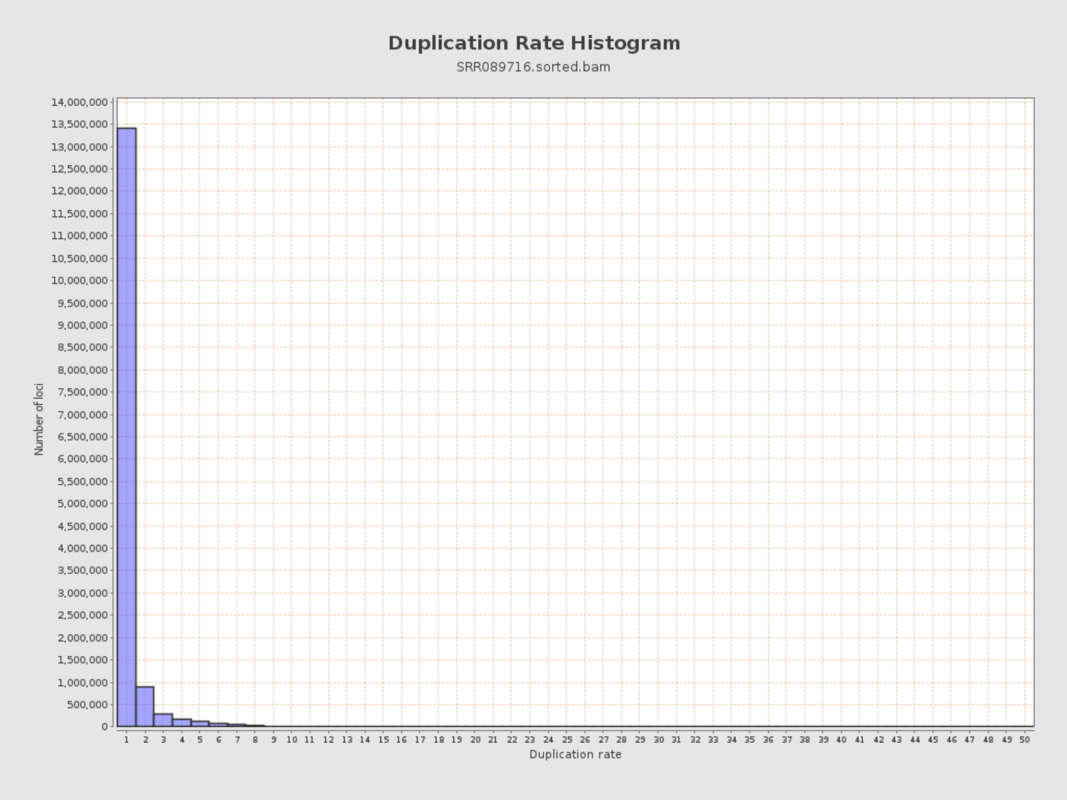
5. Results : Coverage Histogram (0-50X)



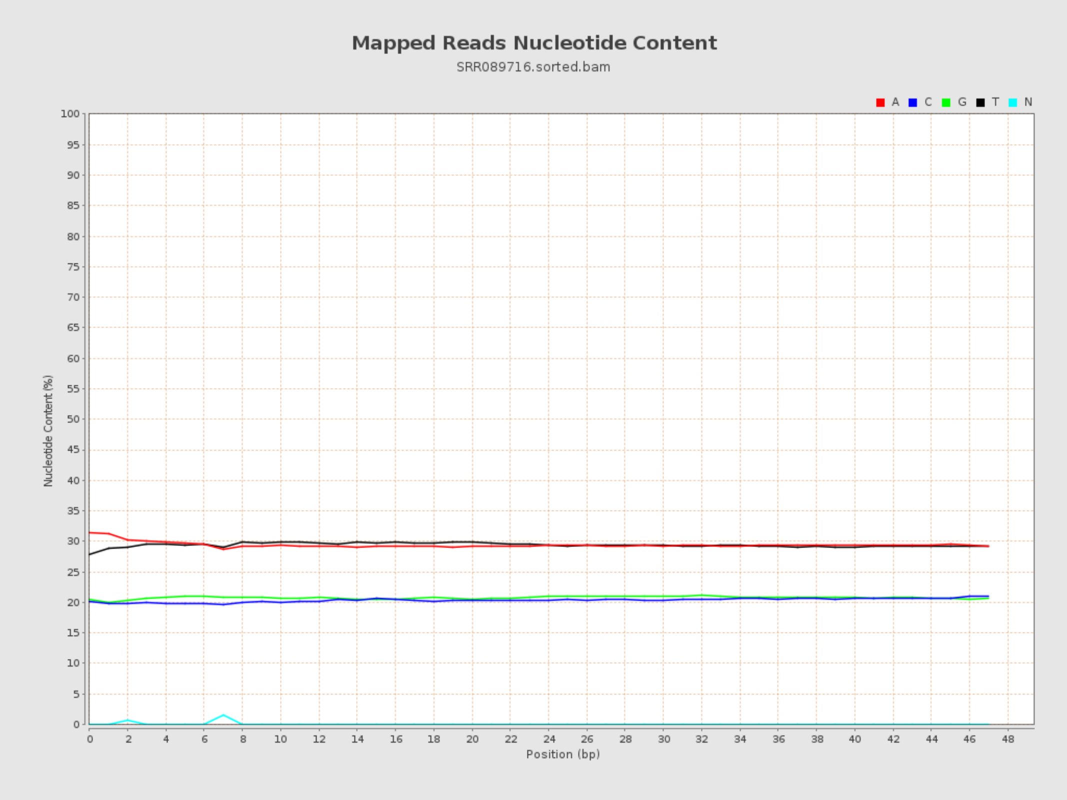
6. Results : Genome Fraction Coverage



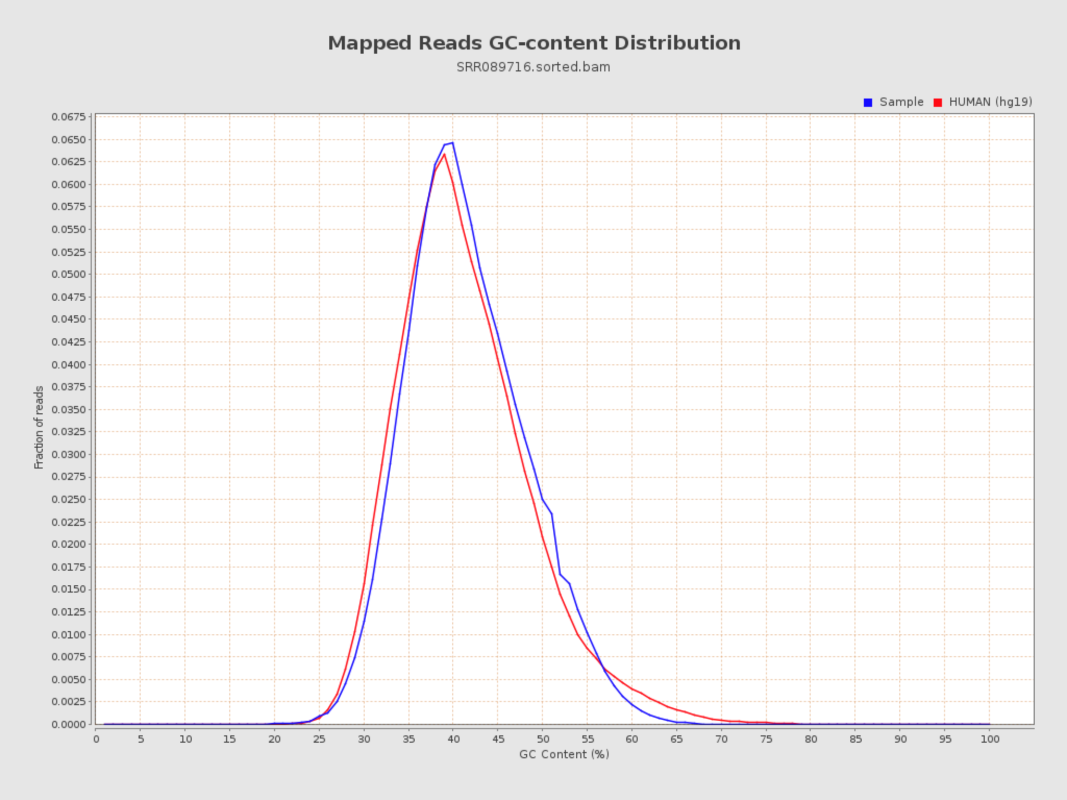
7. Results : Duplication Rate Histogram



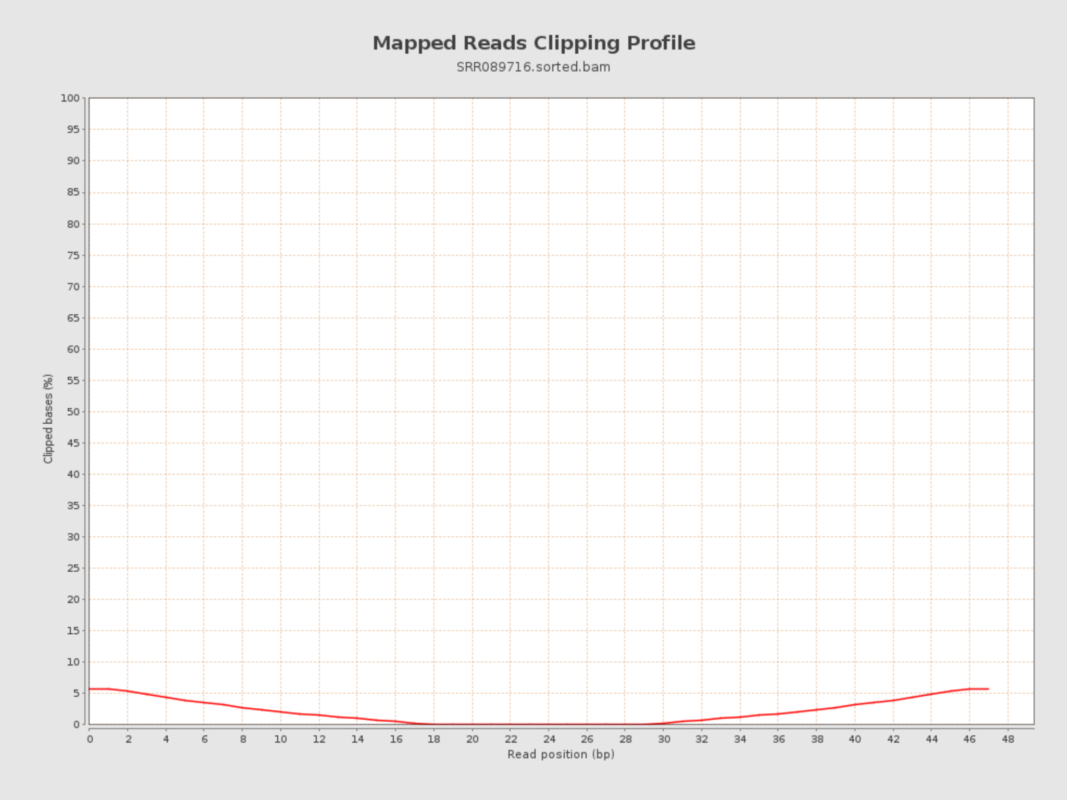
8. Results : Mapped Reads Nucleotide Content



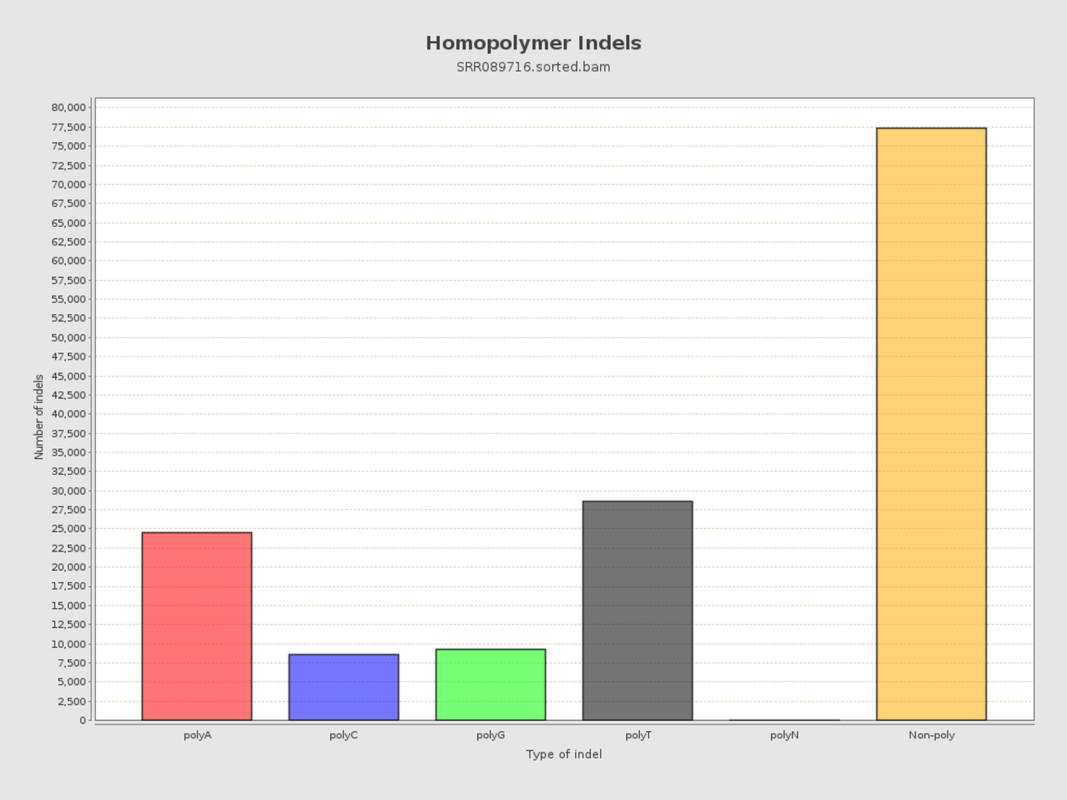
9. Results : Mapped Reads GC-content Distribution



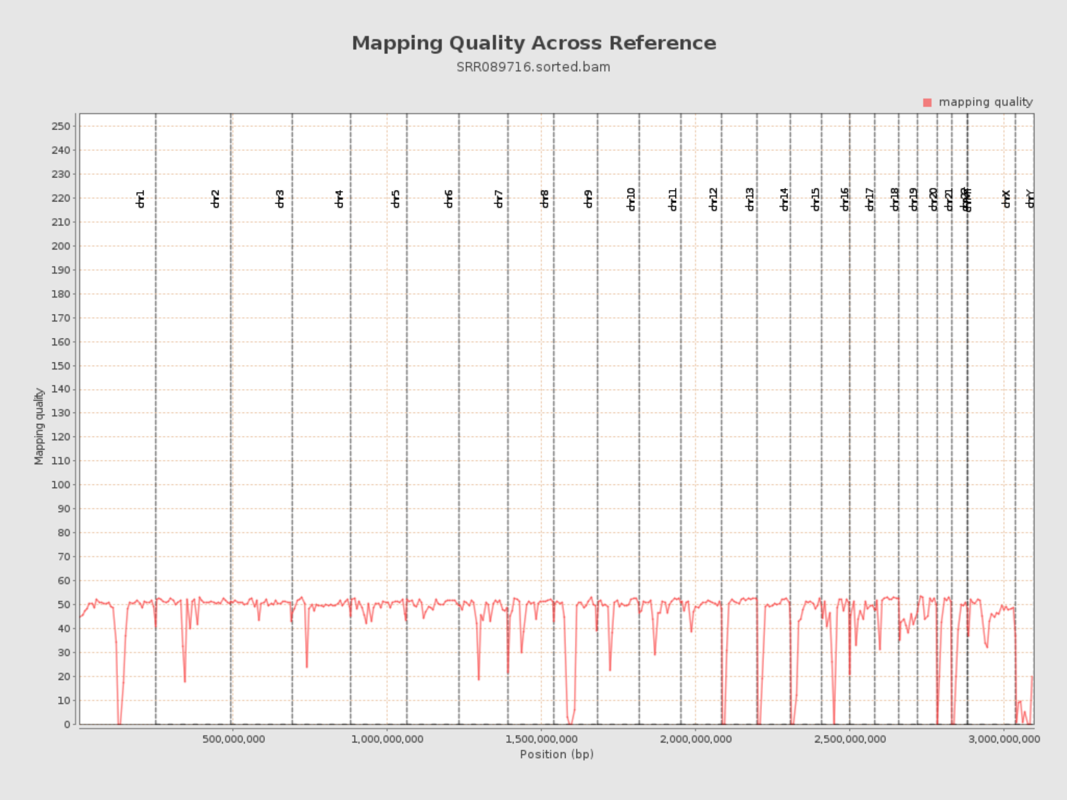
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram