Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 12:39:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089550.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_SRR089550 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089550.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 12:39:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089550.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,901,489
Mapped reads	13,001,136 / 93.52%
Unmapped reads	900,353 / 6.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	85,999 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	2,447,658 / 17.61%
Duplication rate	13.44%
Clipped reads	7,248,908 / 52.14%

2.2. ACGT Content

Number/percentage of A's	206,594,467 / 24.97%
Number/percentage of C's	153,583,993 / 18.56%
Number/percentage of T's	260,165,824 / 31.45%
Number/percentage of G's	206,862,855 / 25%
Number/percentage of N's	128,950 / 0.02%
GC Percentage	43.57%

2.3. Coverage

Mean	0.2673

Standard Deviation	1.7812

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

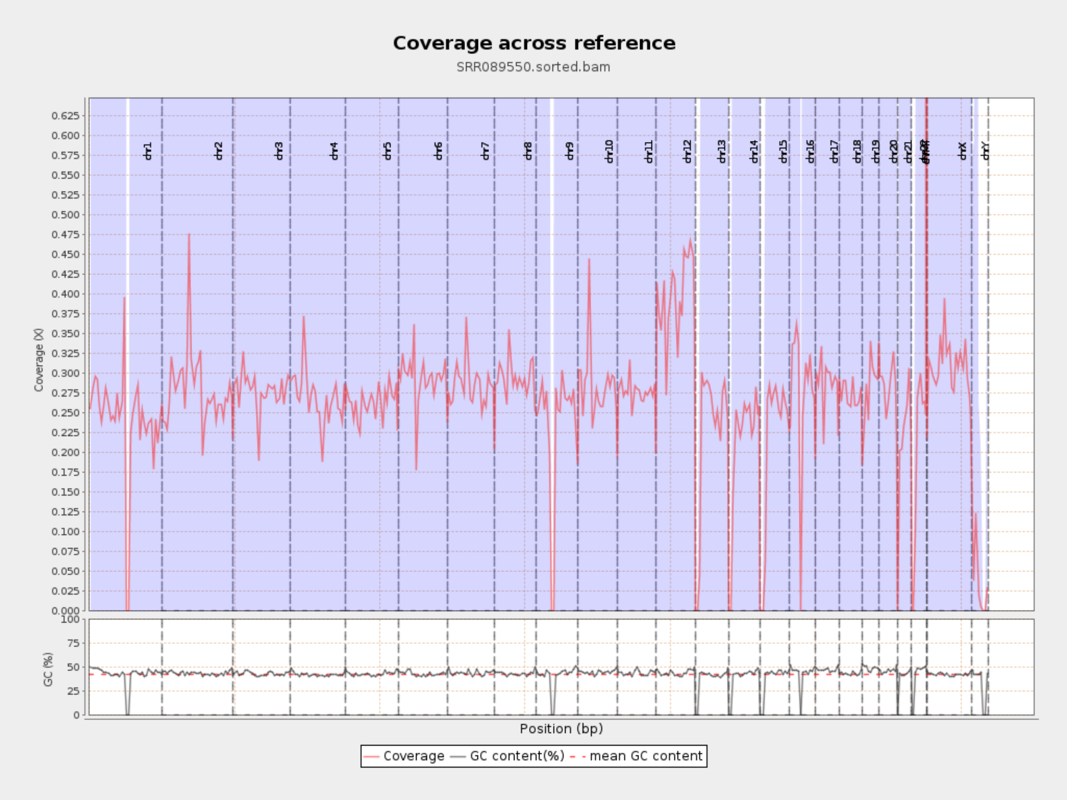
General error rate	0.74%
Mismatches	6,001,130
Insertions	51,953
Mapped reads with at least one insertion	0.4%
Deletions	167,210
Mapped reads with at least one deletion	1.27%
Homopolymer indels	46.55%

2.6. Chromosome stats

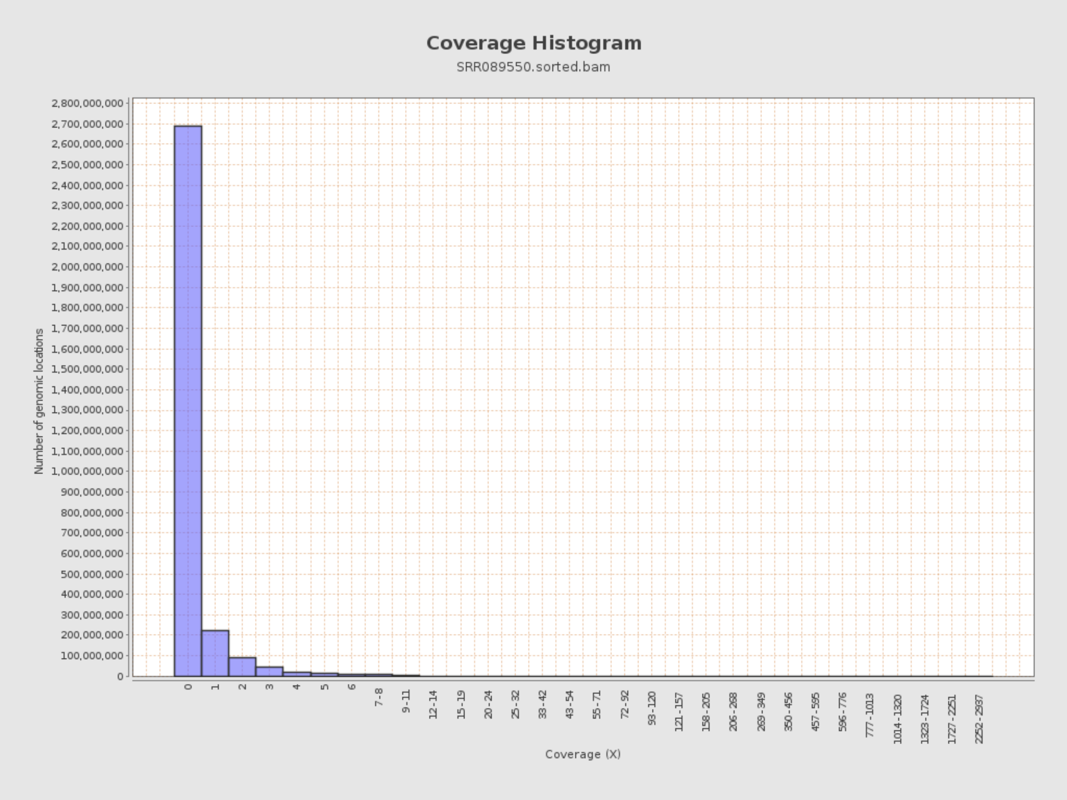
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	59490994	0.2387	2.9317
chr2	243199373	68170711	0.2803	2.2187
chr3	198022430	54883569	0.2772	0.9586
chr4	191154276	51504843	0.2694	1.1427
chr5	180915260	47527843	0.2627	0.9347
chr6	171115067	50231060	0.2936	1.8701
chr7	159138663	45587973	0.2865	1.9918

chr8	146364022	43139313	0.2947	1.8339
chr9	141213431	33048167	0.234	1.7276
chr10	135534747	38759963	0.286	2.0083
chr11	135006516	37161274	0.2753	1.6835
chr12	133851895	53336559	0.3985	1.9048
chr13	115169878	25669378	0.2229	0.8442
chr14	107349540	22288068	0.2076	0.9892
chr15	102531392	21778690	0.2124	1.9068
chr16	90354753	25181283	0.2787	1.2017
chr17	81195210	23311560	0.2871	1.3505
chr18	78077248	21343305	0.2734	2.9824
chr19	59128983	16716609	0.2827	2.3411
chr20	63025520	17795356	0.2824	1.0822
chr21	48129895	10432539	0.2168	1.1005
chr22	51304566	9734251	0.1897	0.8094
chrMT	16571	454240	27.4117	16.6077
chrX	155270560	47887020	0.3084	1.2552
chrY	59373566	2190315	0.0369	0.8397

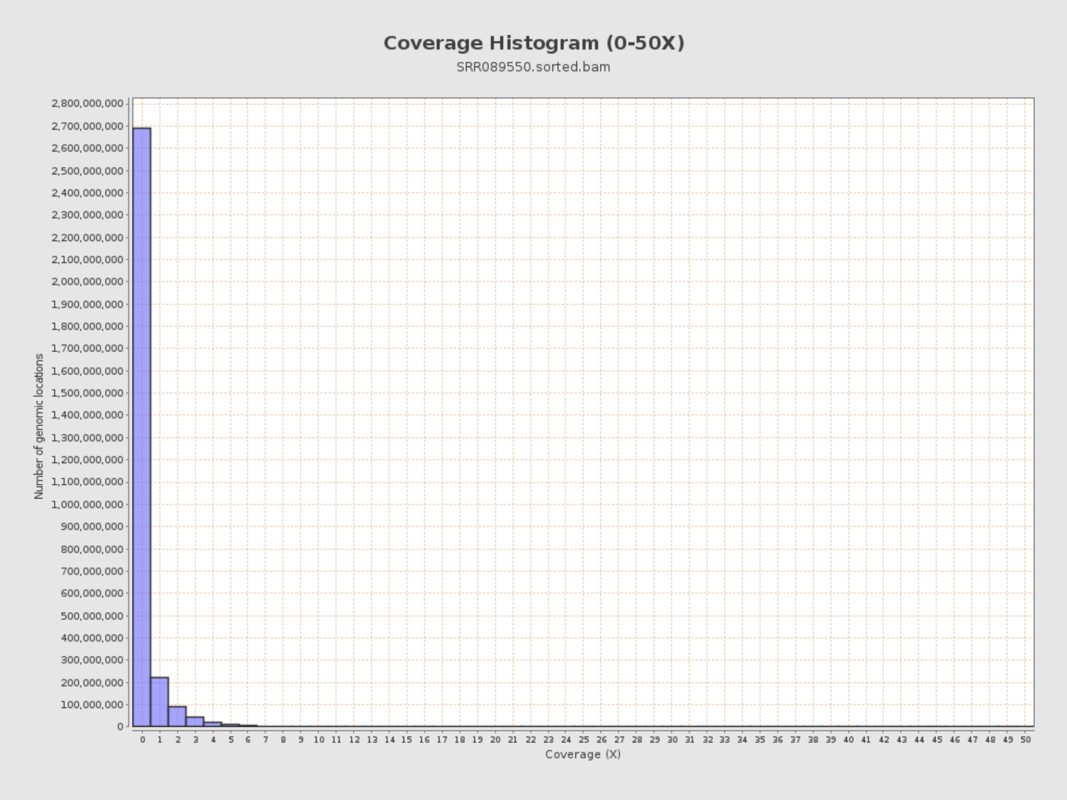
3. Results : Coverage across reference



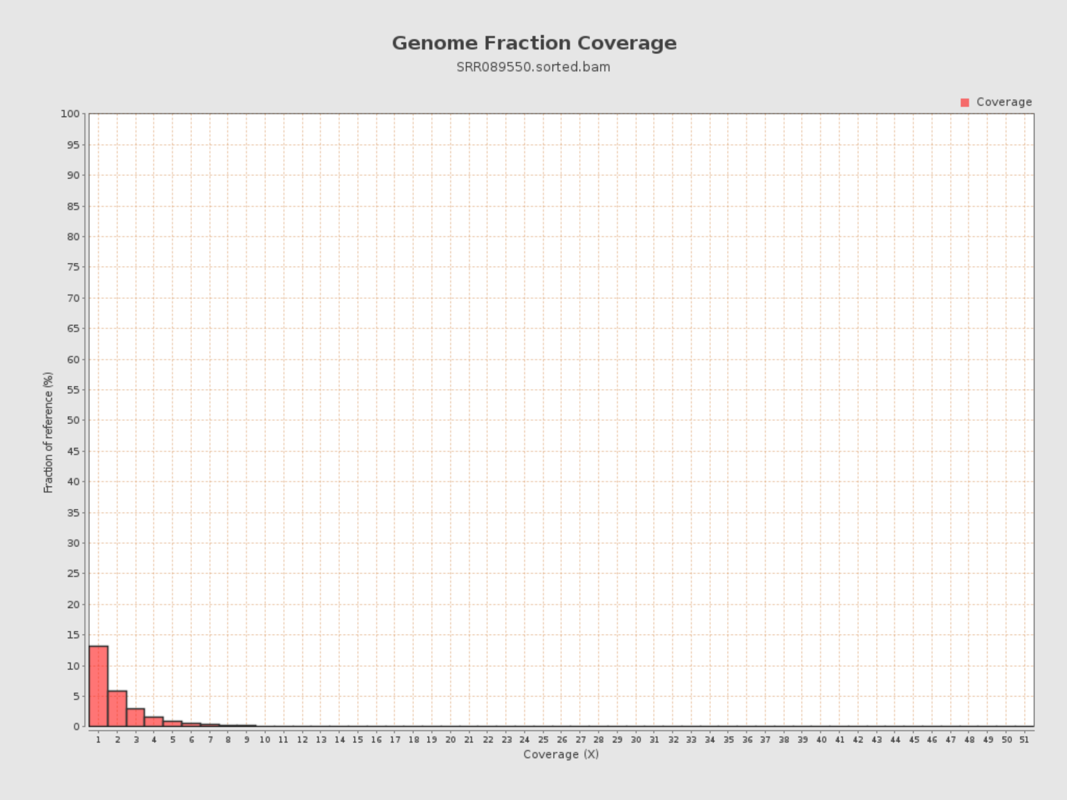
4. Results : Coverage Histogram



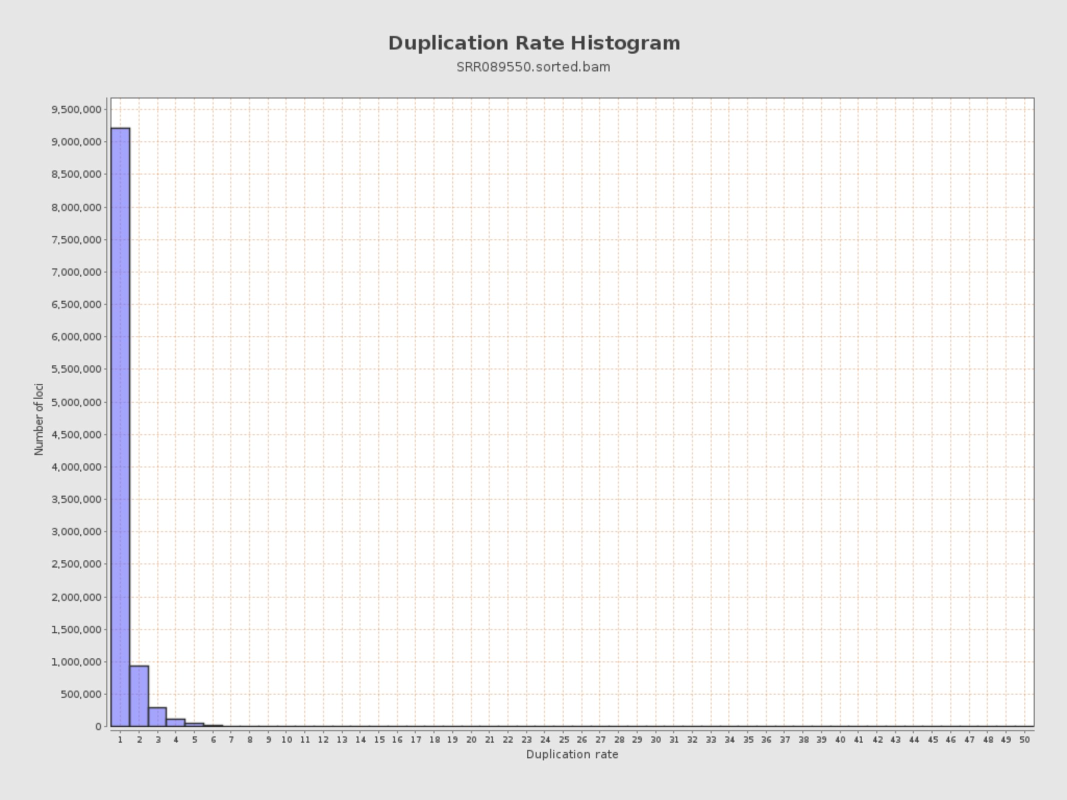
5. Results : Coverage Histogram (0-50X)



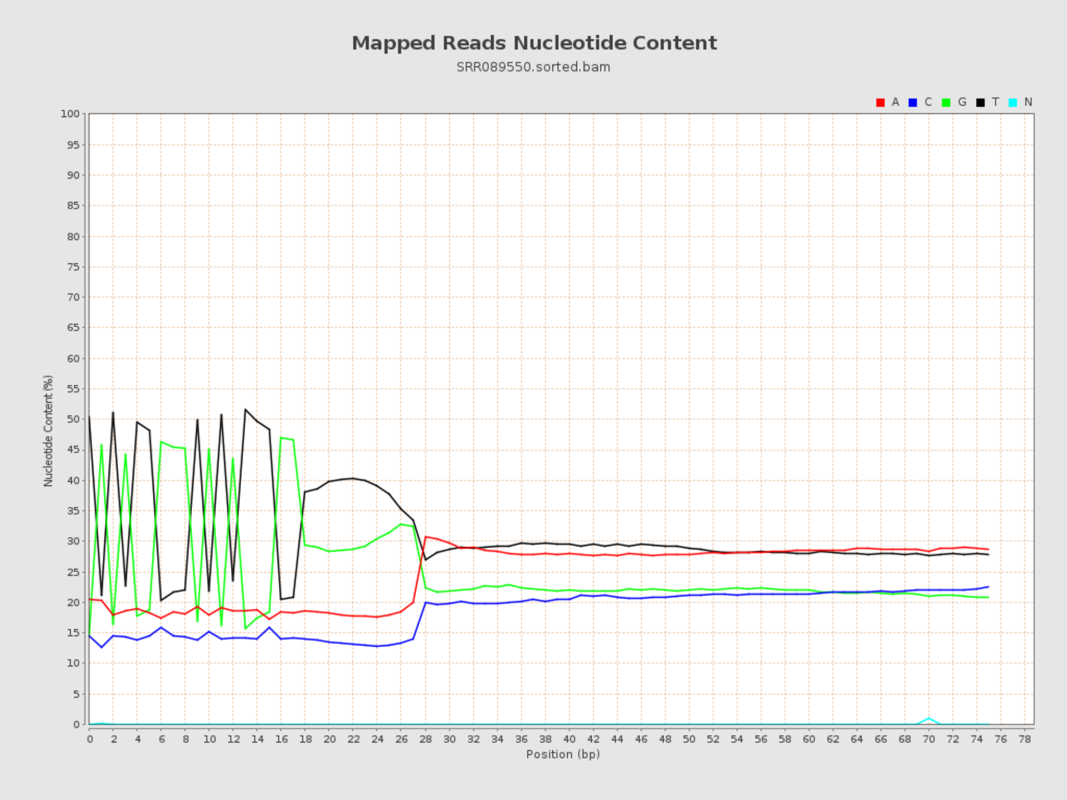
6. Results : Genome Fraction Coverage



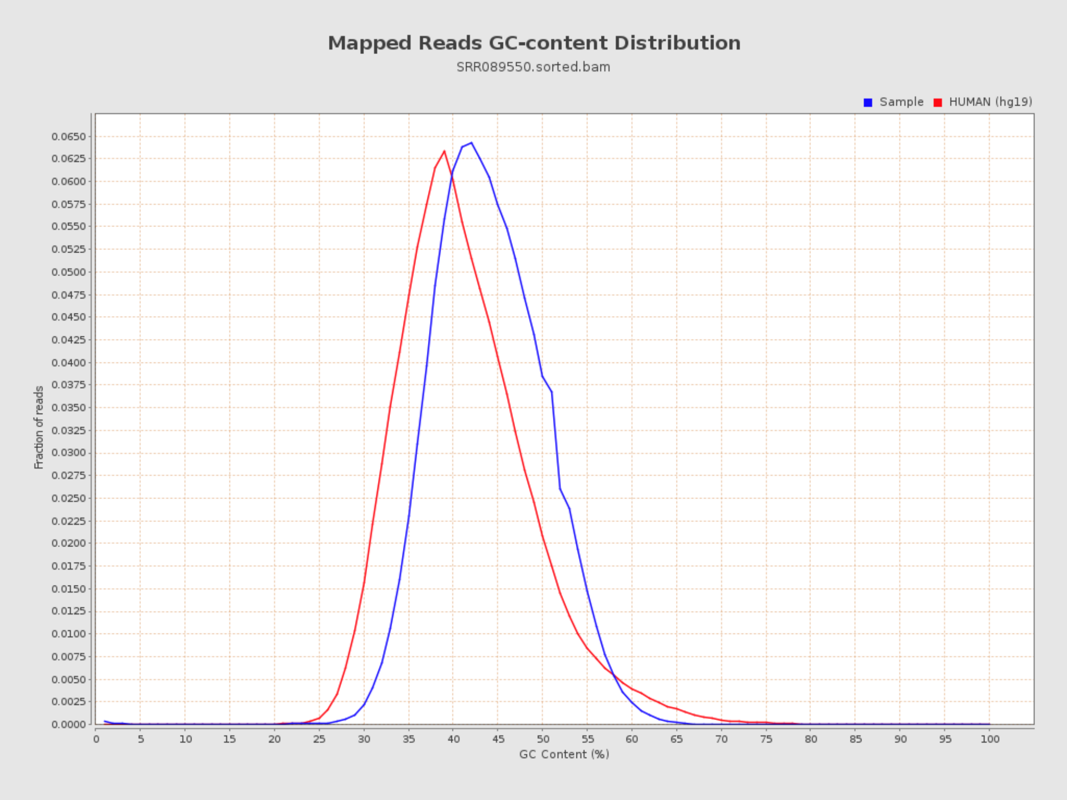
7. Results : Duplication Rate Histogram



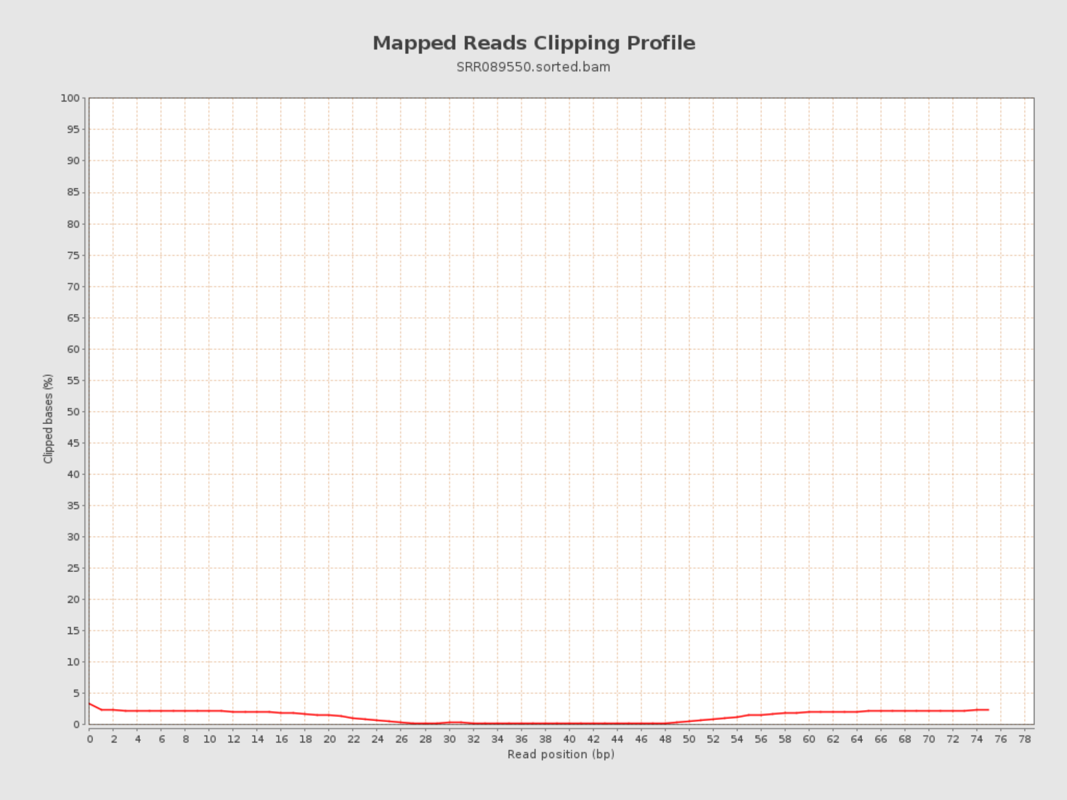
8. Results : Mapped Reads Nucleotide Content



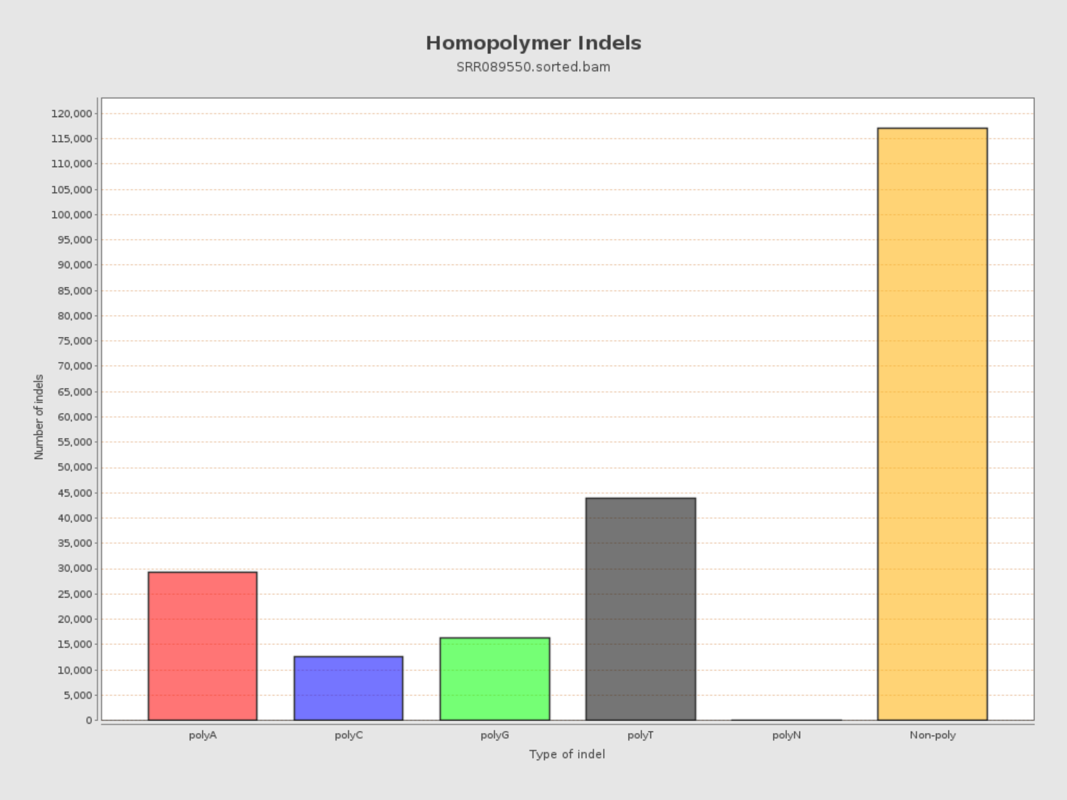
9. Results : Mapped Reads GC-content Distribution



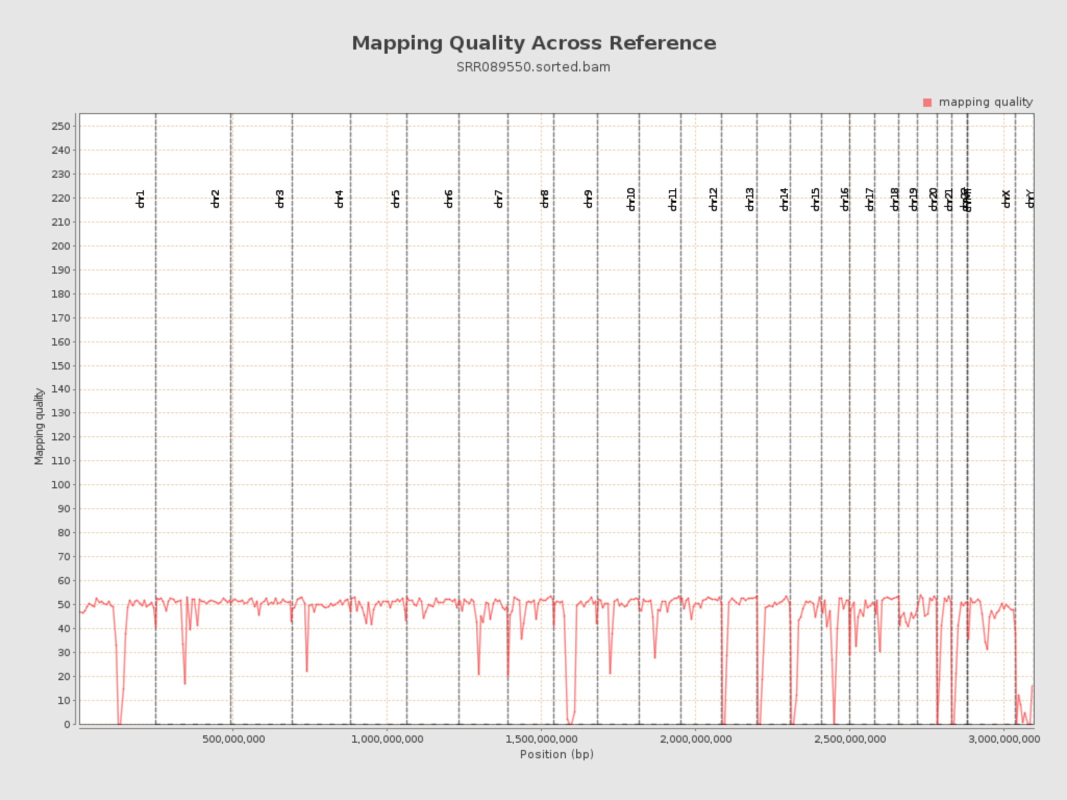
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram