Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 10:57:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089401.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_SRR089401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089401.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 10:57:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,962,820
Mapped reads	20,254,887 / 92.22%
Unmapped reads	1,707,933 / 7.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	93,860 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	3,909,111 / 17.8%
Duplication rate	12.69%
Clipped reads	9,520,706 / 43.35%

2.2. ACGT Content

Number/percentage of A's	346,915,781 / 26.01%
Number/percentage of C's	258,137,138 / 19.35%
Number/percentage of T's	407,159,694 / 30.52%
Number/percentage of G's	321,093,359 / 24.07%
Number/percentage of N's	725,551 / 0.05%
GC Percentage	43.42%

2.3. Coverage

Mean	0.4311

Standard Deviation	2.7955

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

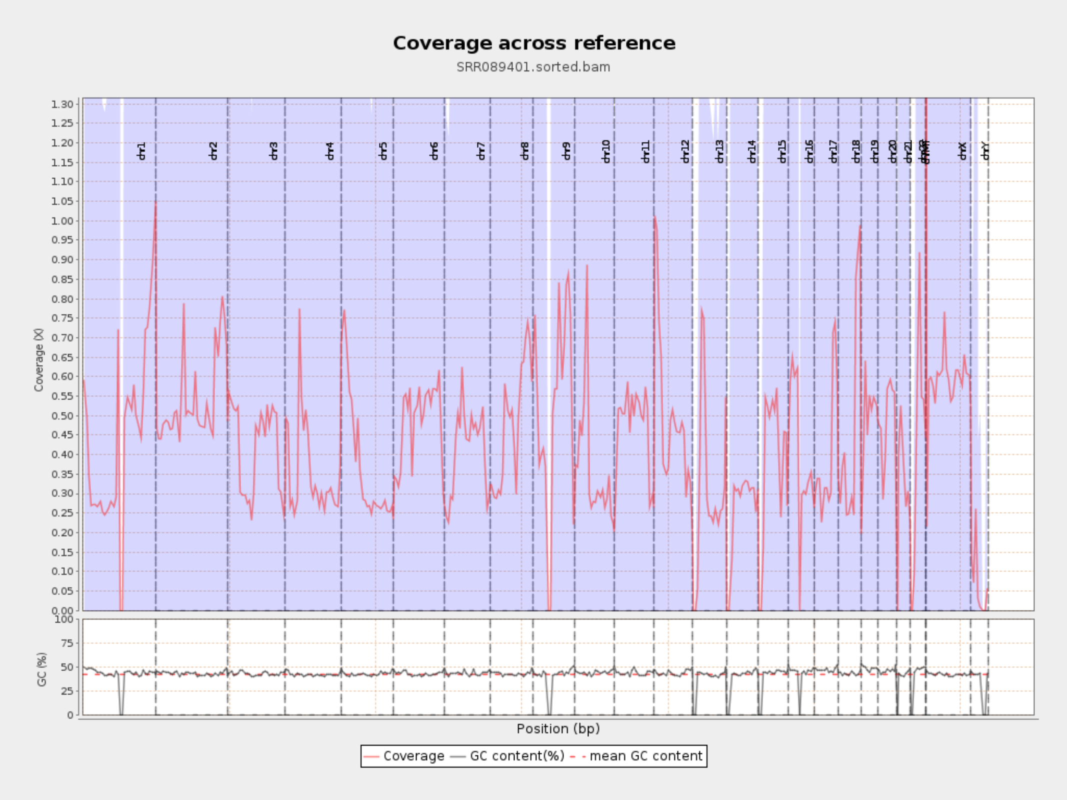
General error rate	0.77%
Mismatches	10,113,571
Insertions	90,181
Mapped reads with at least one insertion	0.44%
Deletions	260,582
Mapped reads with at least one deletion	1.27%
Homopolymer indels	44.66%

2.6. Chromosome stats

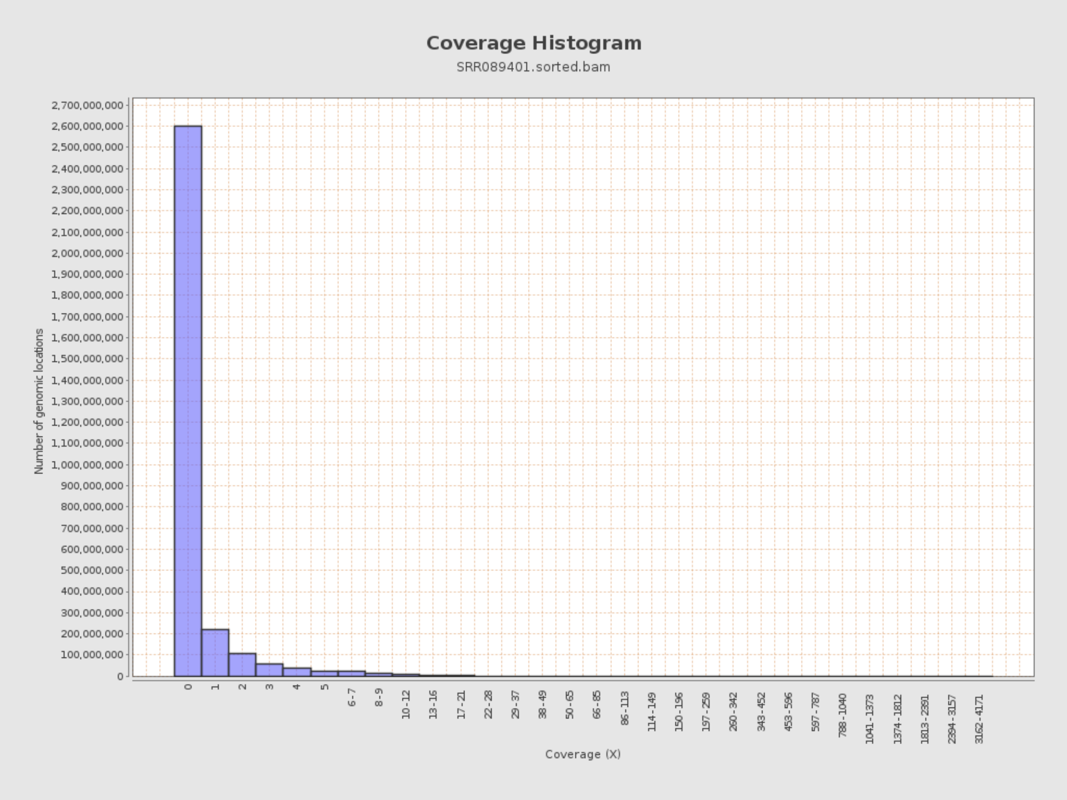
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	110767283	0.4444	4.4515
chr2	243199373	132127715	0.5433	3.7161
chr3	198022430	82383769	0.416	1.4758
chr4	191154276	68539603	0.3586	2.3327
chr5	180915260	68717021	0.3798	1.3962
chr6	171115067	83789292	0.4897	1.9531
chr7	159138663	65321712	0.4105	3.4718

chr8	146364022	70576530	0.4822	2.5478
chr9	141213431	73091411	0.5176	3.0313
chr10	135534747	49243452	0.3633	4.218
chr11	135006516	64478671	0.4776	3.0086
chr12	133851895	68131100	0.509	1.7001
chr13	115169878	34027693	0.2955	1.2218
chr14	107349540	27662238	0.2577	1.4401
chr15	102531392	38742239	0.3779	1.396
chr16	90354753	35670132	0.3948	1.8982
chr17	81195210	32325378	0.3981	1.8765
chr18	78077248	35939501	0.4603	4.62
chr19	59128983	29553924	0.4998	3.2198
chr20	63025520	30444400	0.483	1.8665
chr21	48129895	15537359	0.3228	2.2428
chr22	51304566	21919366	0.4272	1.5804
chrMT	16571	104520	6.3074	7.056
chrX	155270560	91388003	0.5886	2.3307
chrY	59373566	4014851	0.0676	2.192

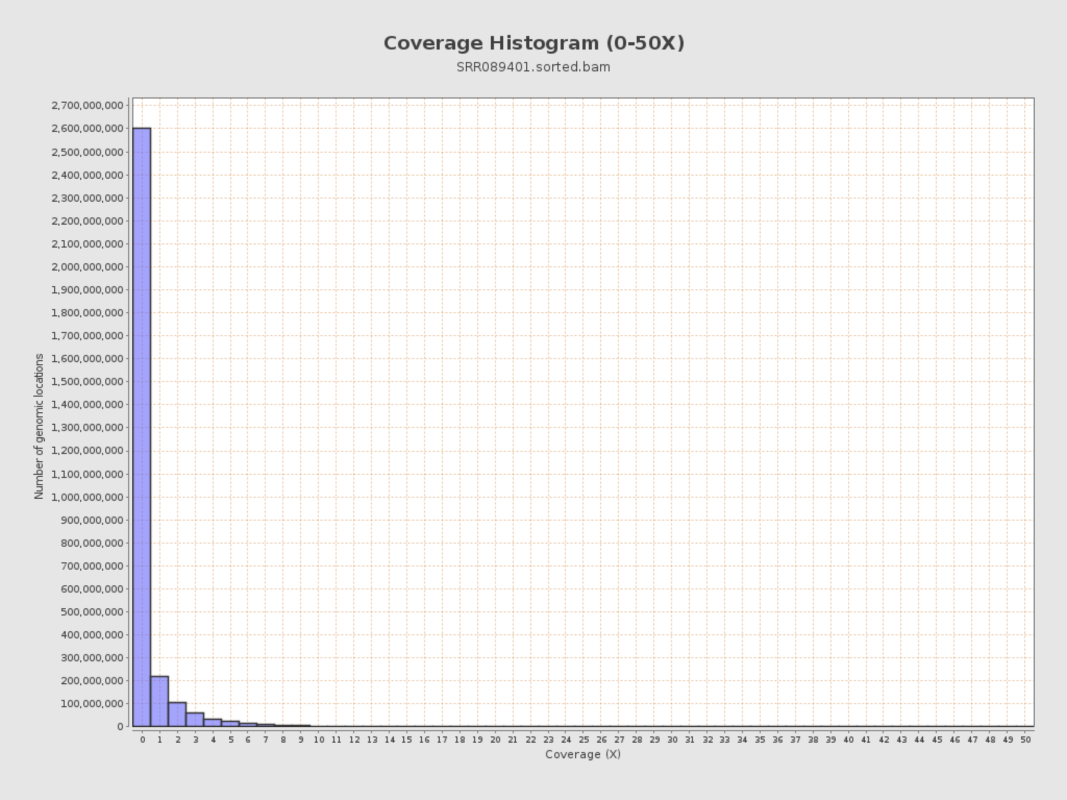
3. Results : Coverage across reference



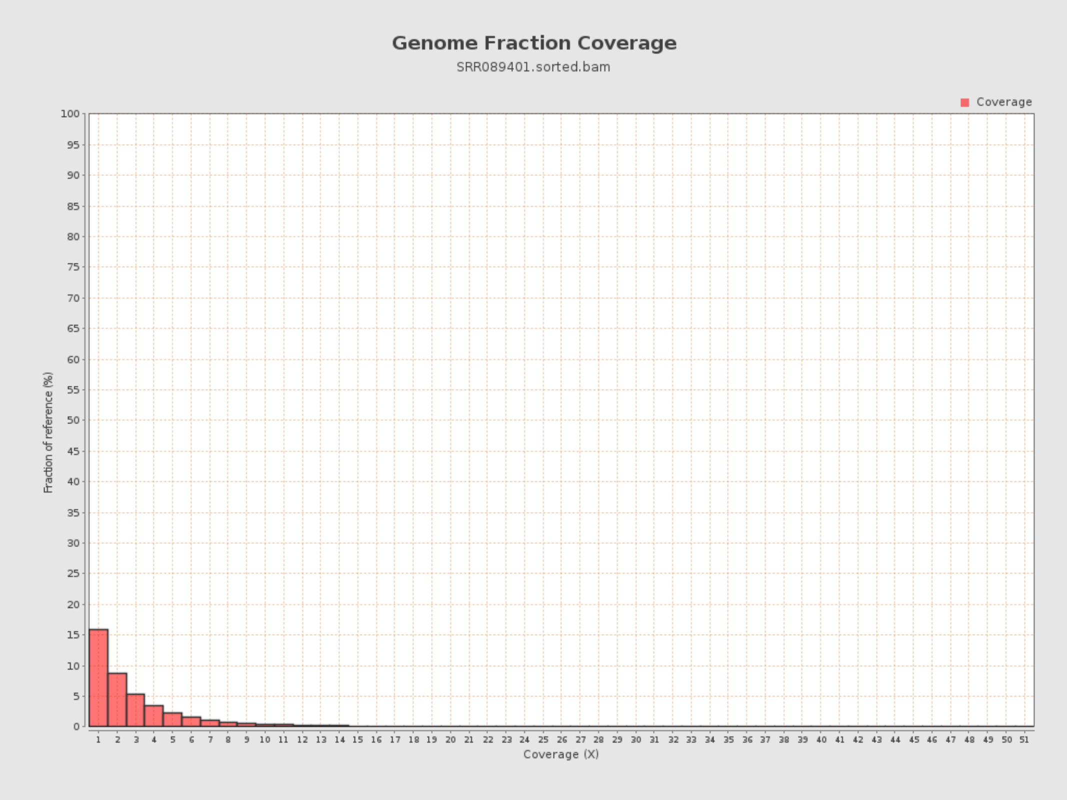
4. Results : Coverage Histogram



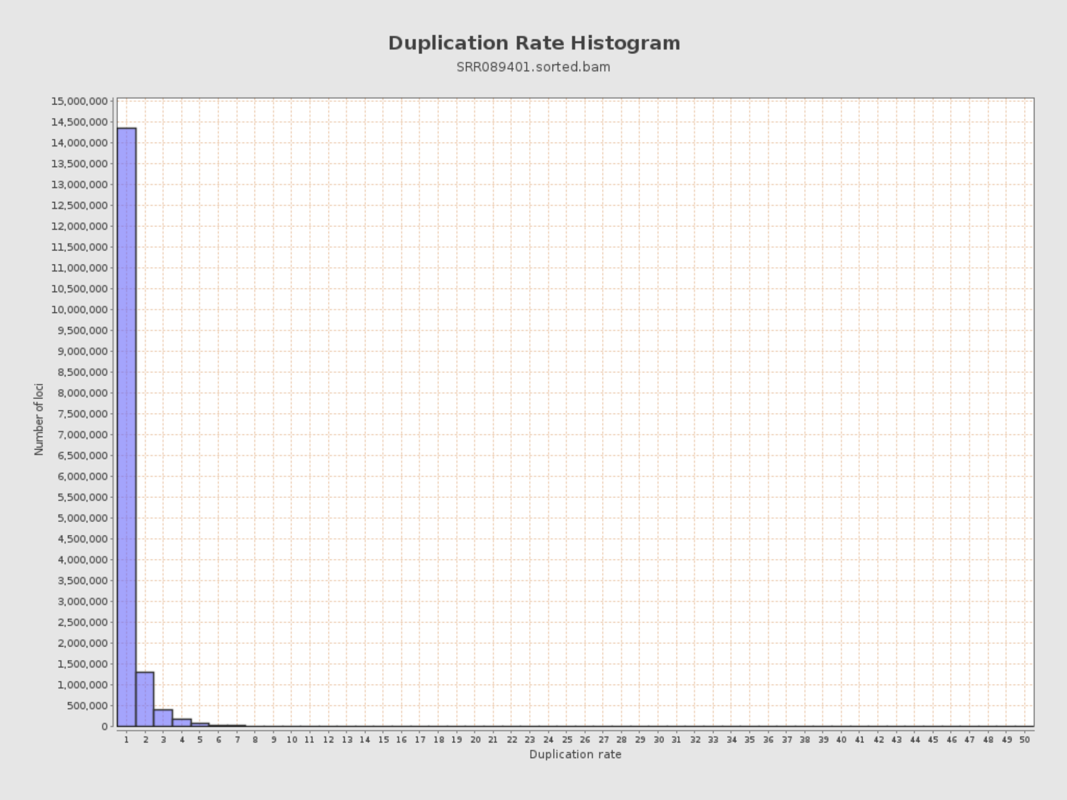
5. Results : Coverage Histogram (0-50X)



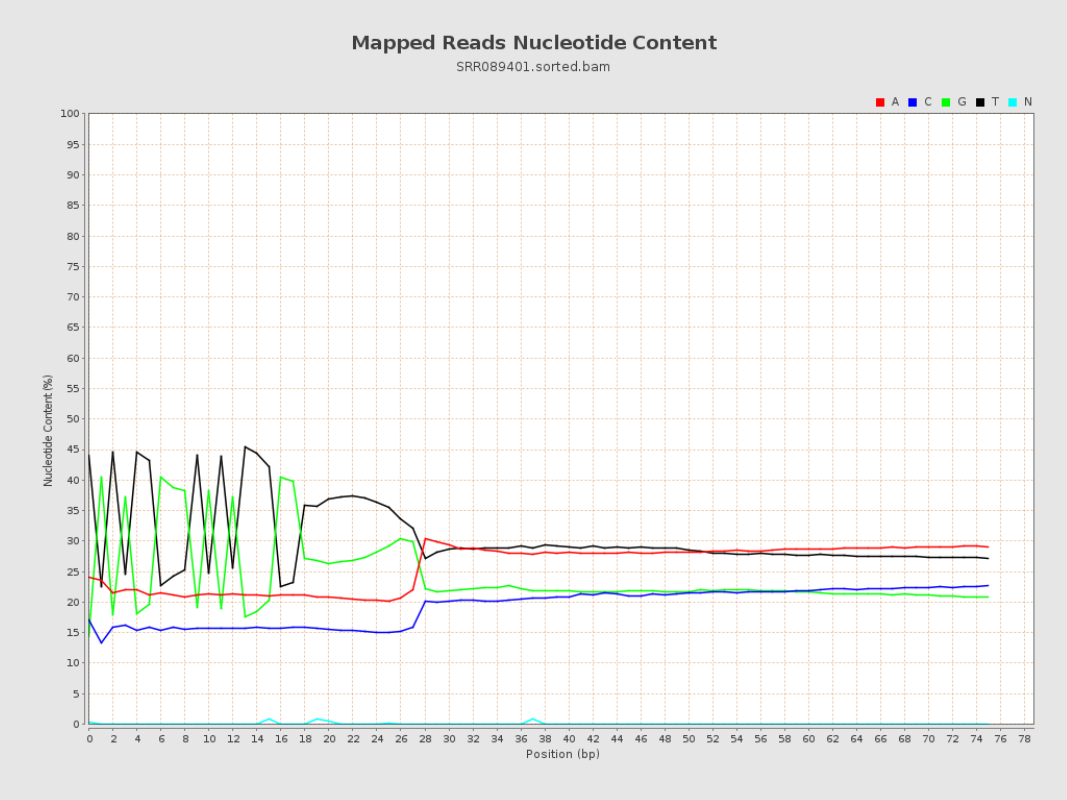
6. Results : Genome Fraction Coverage



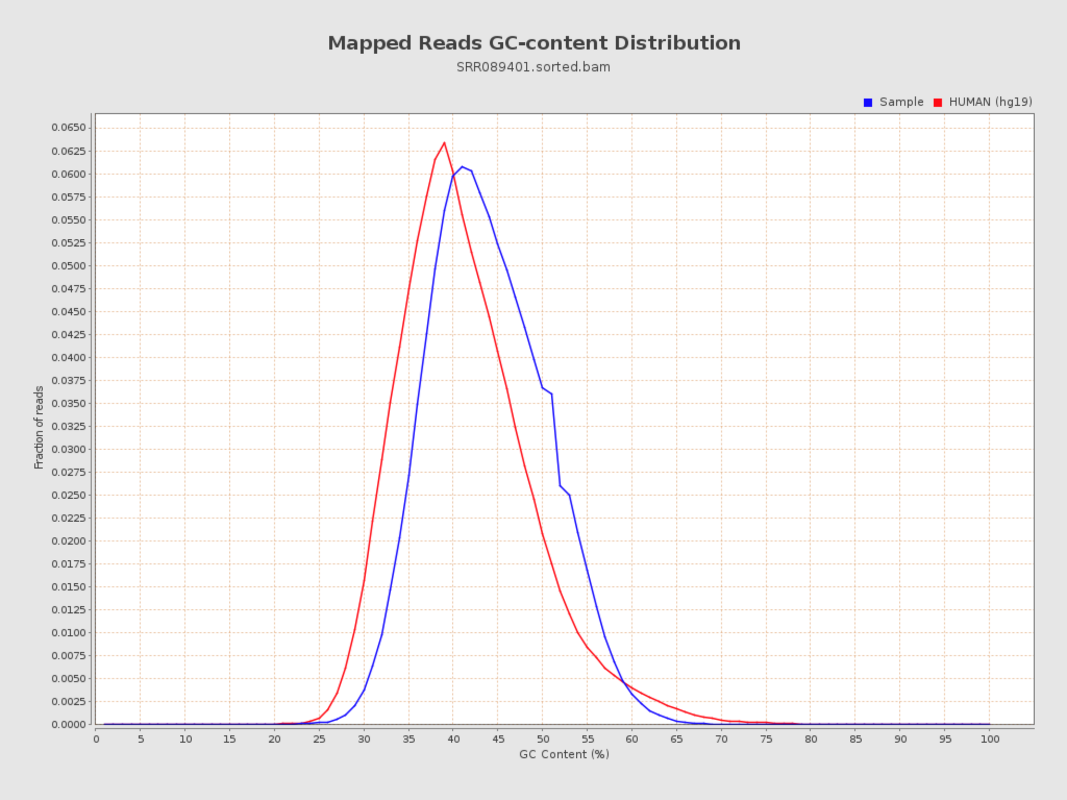
7. Results : Duplication Rate Histogram



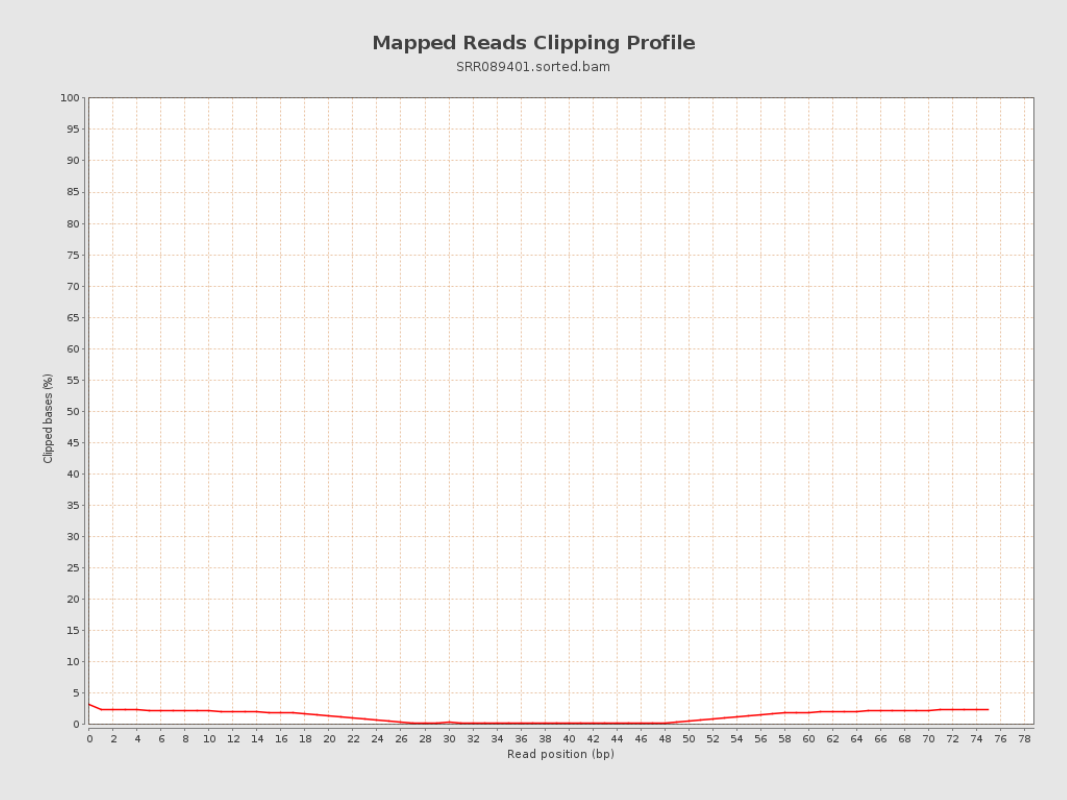
8. Results : Mapped Reads Nucleotide Content



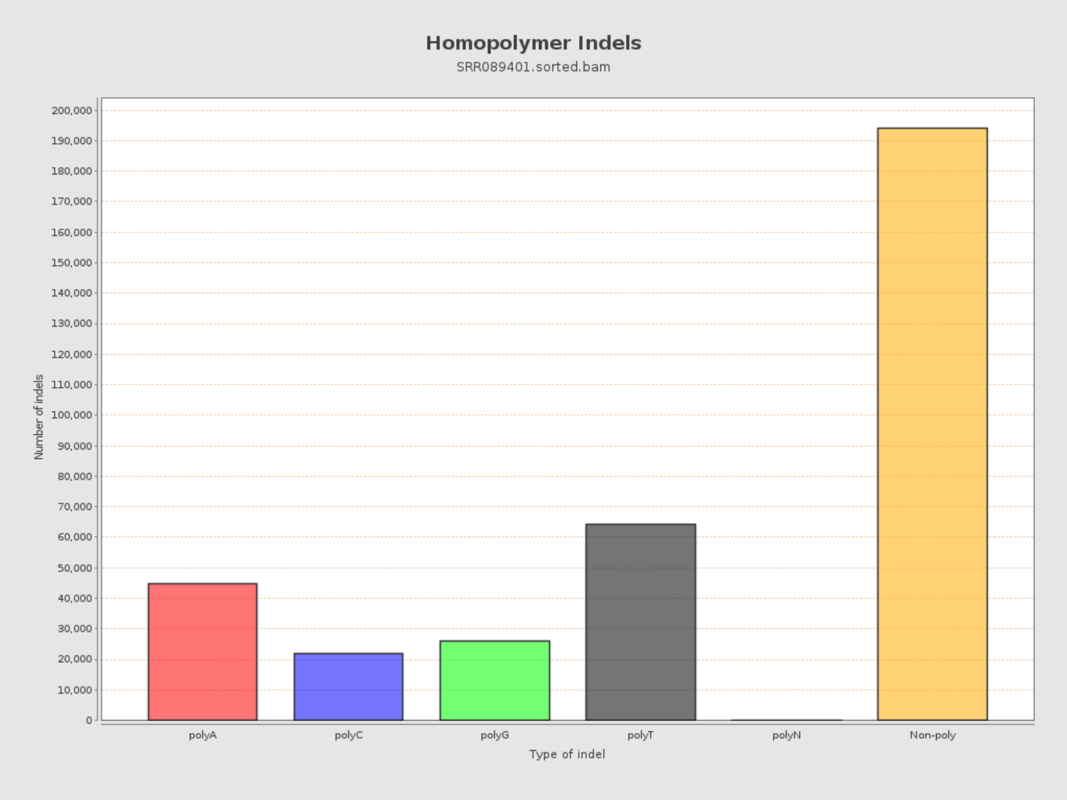
9. Results : Mapped Reads GC-content Distribution



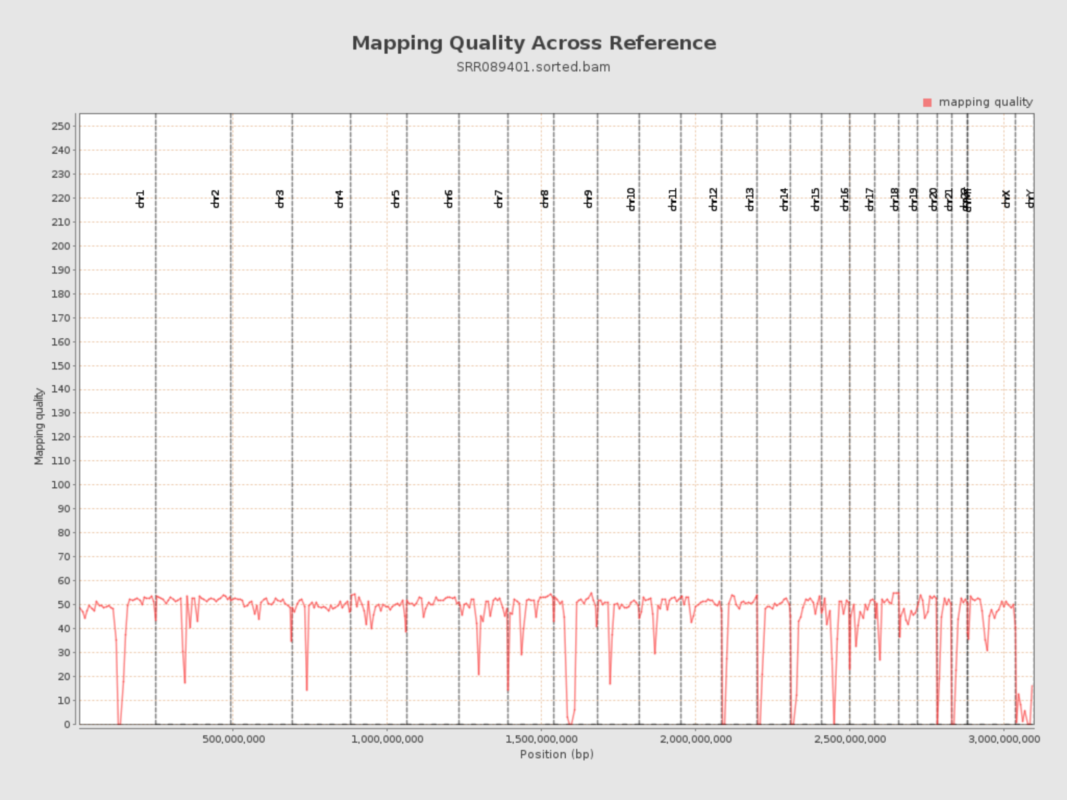
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram