Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 16:02:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089596.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_SRR089596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089596.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 16:02:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,688,972
Mapped reads	18,776,767 / 79.26%
Unmapped reads	4,912,205 / 20.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	726 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,850,950 / 7.81%
Duplication rate	7.34%
Clipped reads	2,370,434 / 10.01%

2.2. ACGT Content

Number/percentage of A's	280,511,717 / 31.92%
Number/percentage of C's	178,514,505 / 20.31%
Number/percentage of T's	223,422,329 / 25.42%
Number/percentage of G's	195,906,224 / 22.29%
Number/percentage of N's	397,873 / 0.05%
GC Percentage	42.61%

2.3. Coverage

Mean	0.2839

Standard Deviation	1.3801

2.4. Mapping Quality

Mean Mapping Quality	42.74

2.5. Mismatches and indels

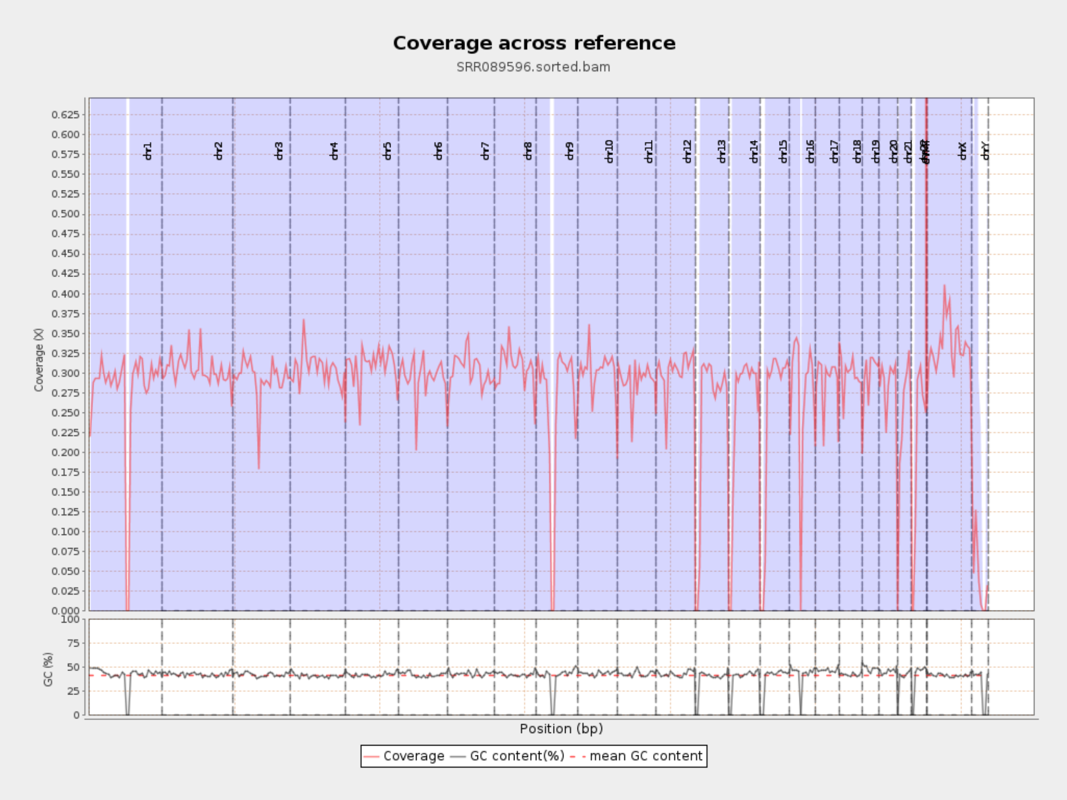
General error rate	0.57%
Mismatches	4,977,979
Insertions	40,206
Mapped reads with at least one insertion	0.21%
Deletions	118,297
Mapped reads with at least one deletion	0.63%
Homopolymer indels	43.23%

2.6. Chromosome stats

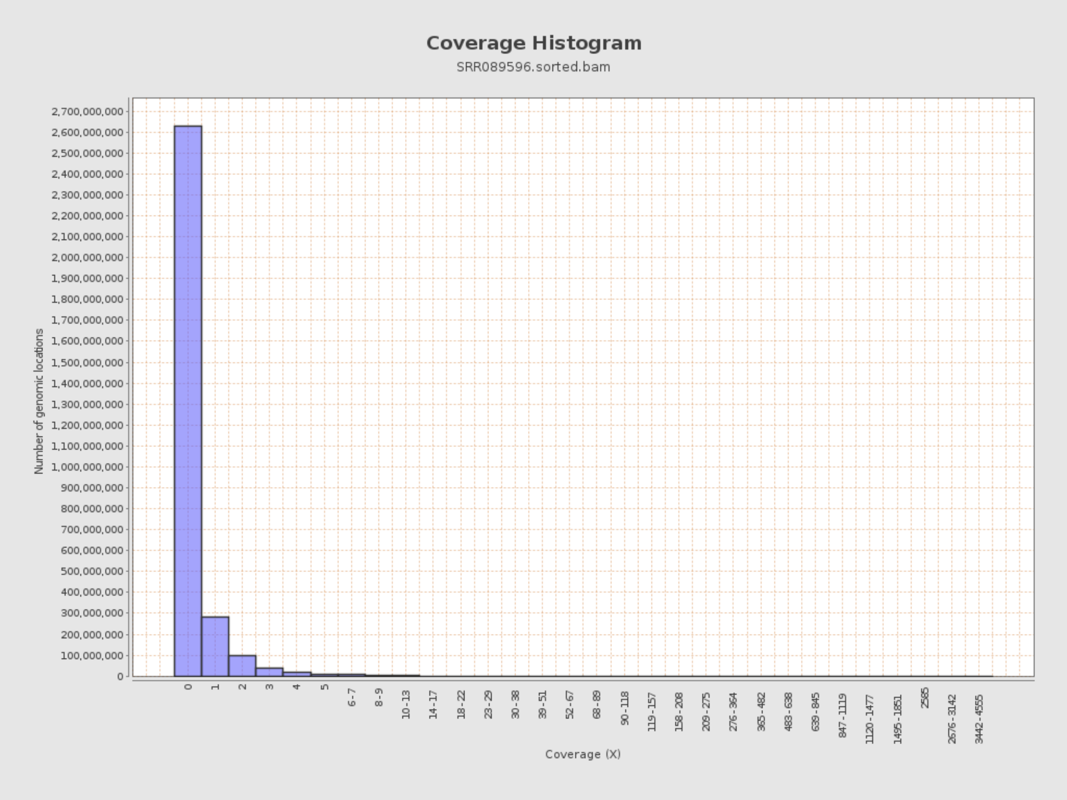
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	68902636	0.2764	1.8042
chr2	243199373	74243959	0.3053	1.5513
chr3	198022430	58052673	0.2932	0.9712
chr4	191154276	58274006	0.3049	1.0939
chr5	180915260	55922777	0.3091	1.0109
chr6	171115067	50407646	0.2946	1.1301
chr7	159138663	48407494	0.3042	1.6636

chr8	146364022	44873404	0.3066	2.7132
chr9	141213431	36420462	0.2579	1.2227
chr10	135534747	41217342	0.3041	1.4386
chr11	135006516	39015717	0.289	1.2468
chr12	133851895	40358235	0.3015	1.0137
chr13	115169878	28081053	0.2438	0.8904
chr14	107349540	26614989	0.2479	1.0406
chr15	102531392	25071897	0.2445	0.8955
chr16	90354753	24765770	0.2741	1.0763
chr17	81195210	23421568	0.2885	1.0801
chr18	78077248	23277163	0.2981	1.7134
chr19	59128983	17686534	0.2991	1.7674
chr20	63025520	17923172	0.2844	1.0585
chr21	48129895	11363031	0.2361	1.086
chr22	51304566	10052715	0.1959	0.8188
chrMT	16571	151331	9.1323	9.5324
chrX	155270560	51829403	0.3338	1.2094
chrY	59373566	2597211	0.0437	0.6334

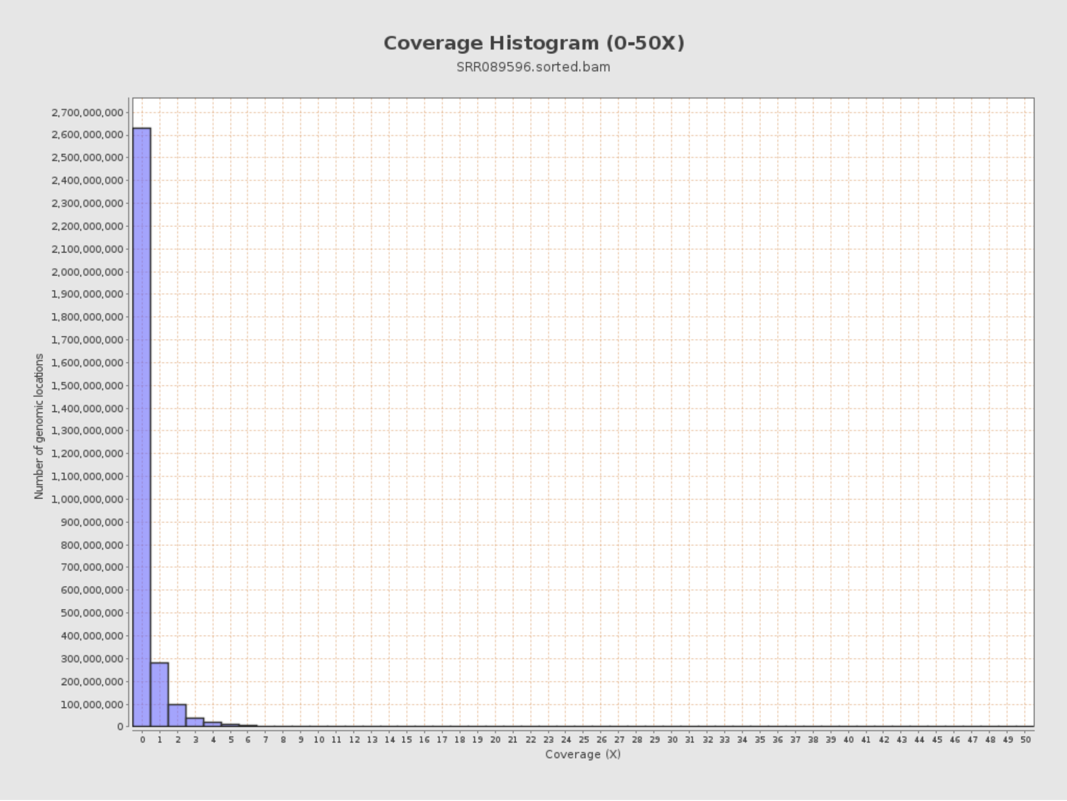
3. Results : Coverage across reference



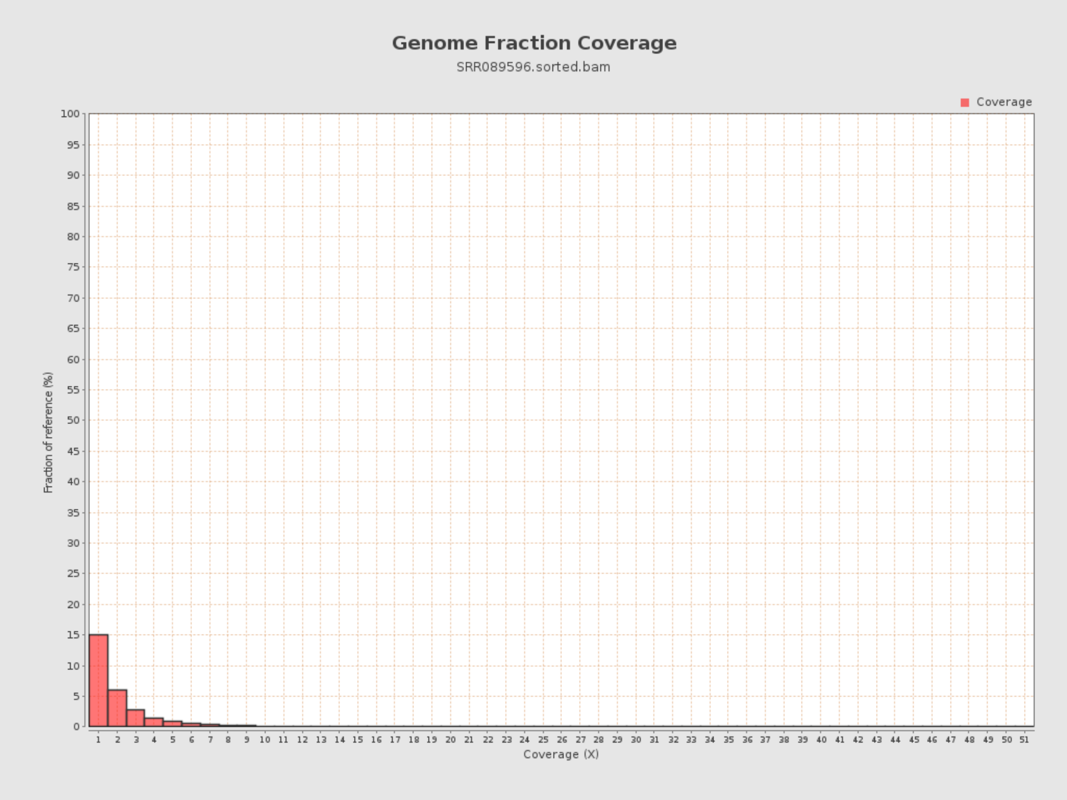
4. Results : Coverage Histogram



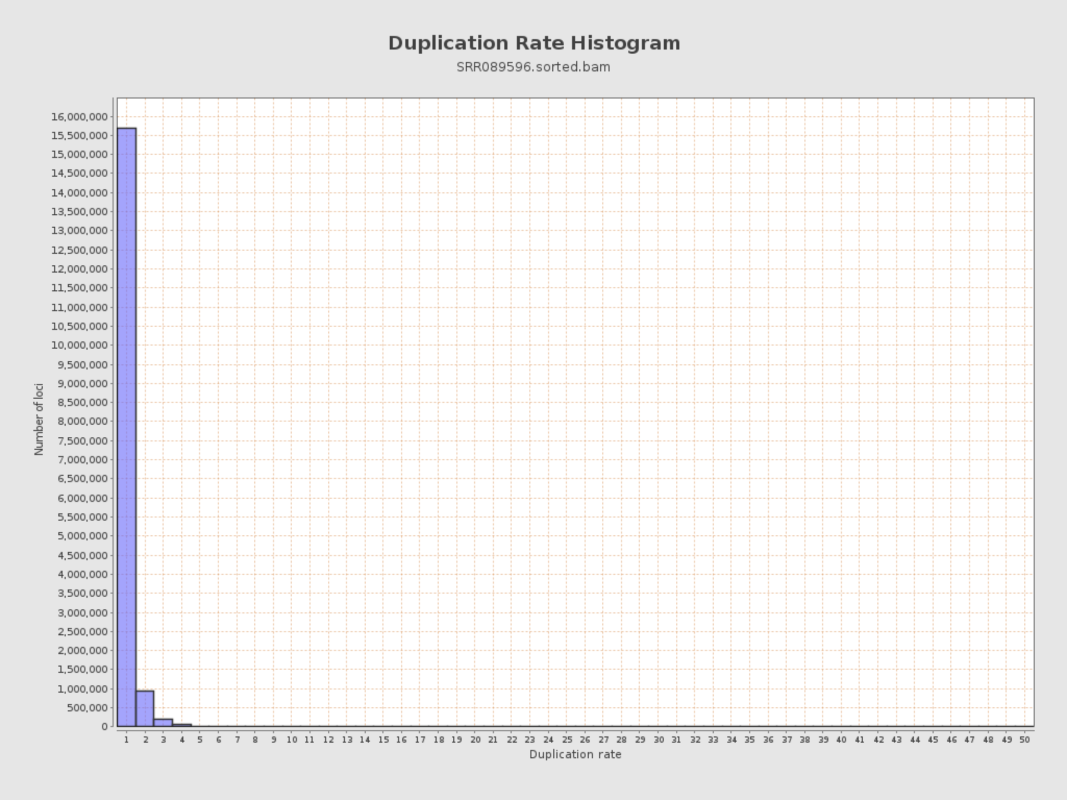
5. Results : Coverage Histogram (0-50X)



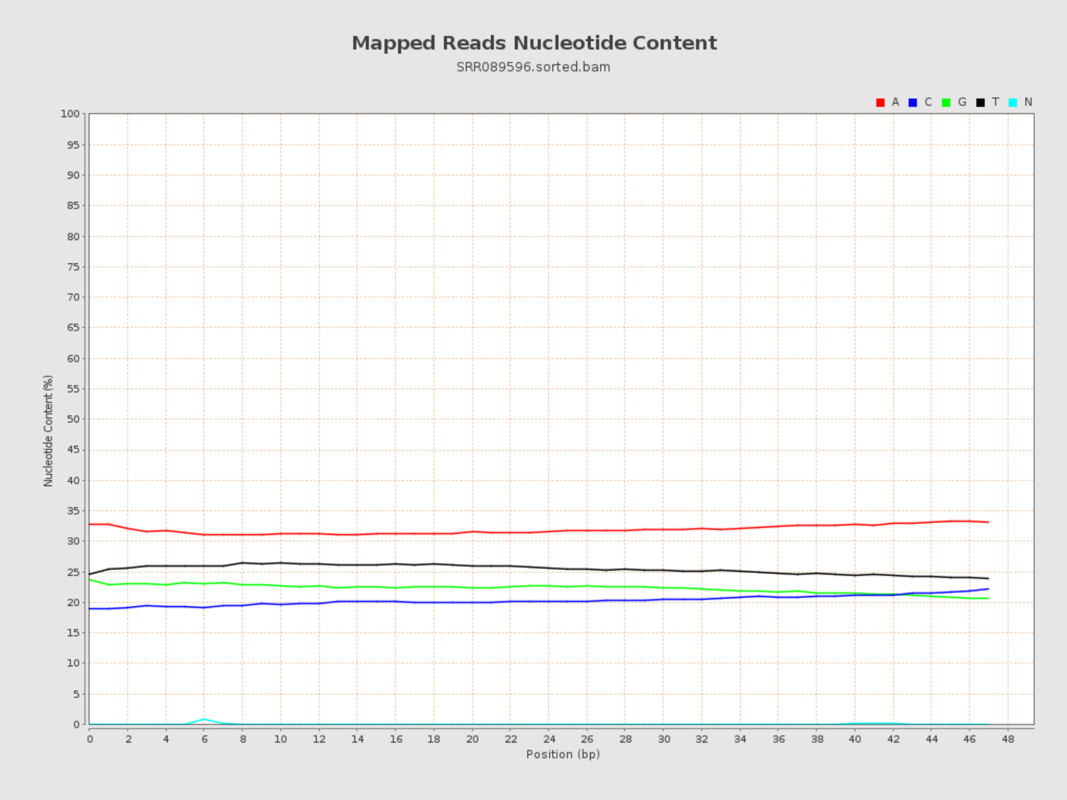
6. Results : Genome Fraction Coverage



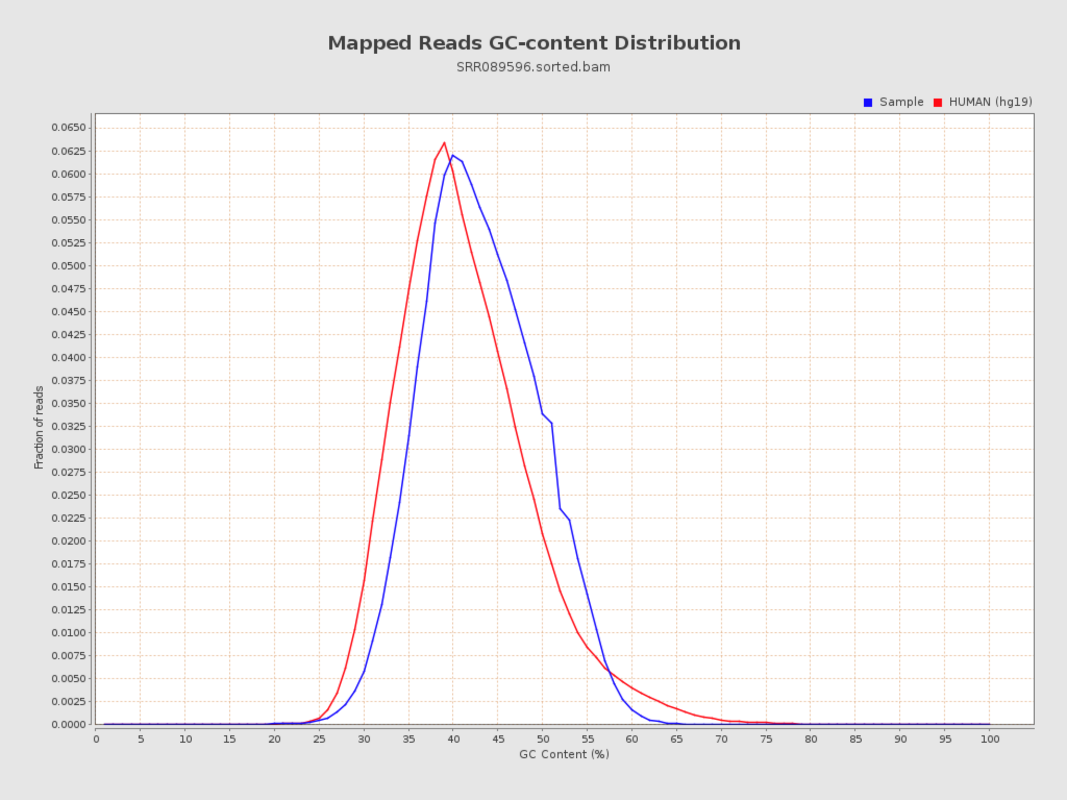
7. Results : Duplication Rate Histogram



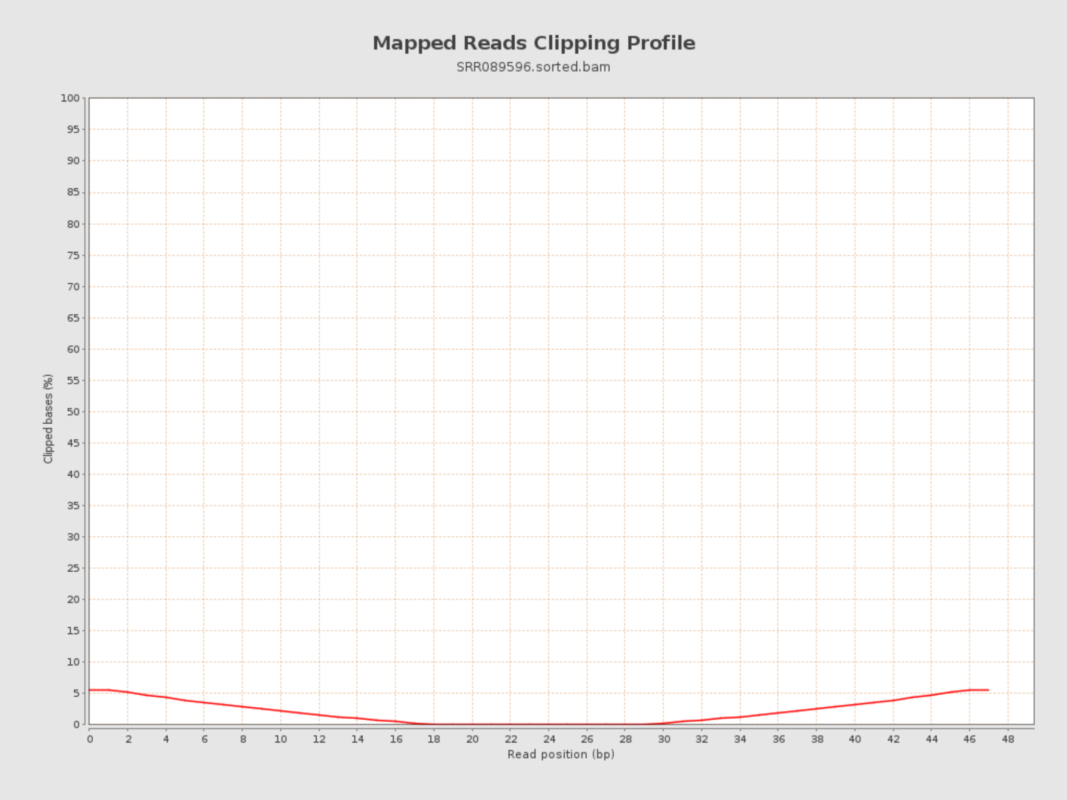
8. Results : Mapped Reads Nucleotide Content



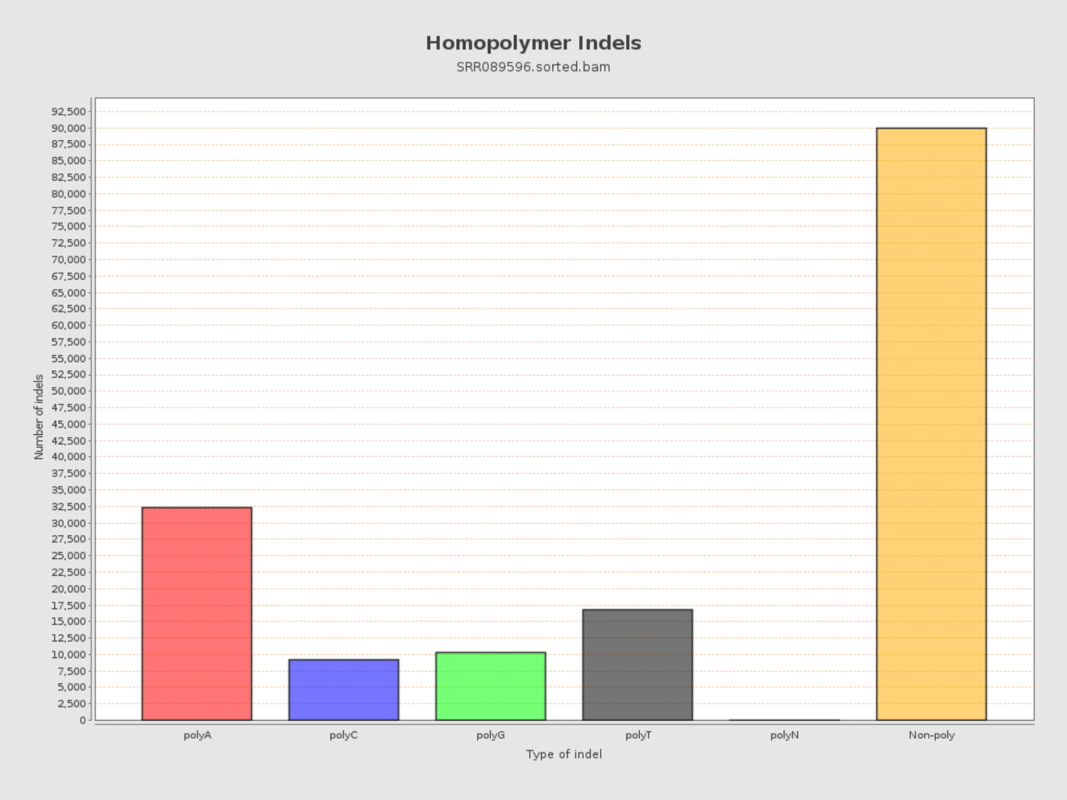
9. Results : Mapped Reads GC-content Distribution



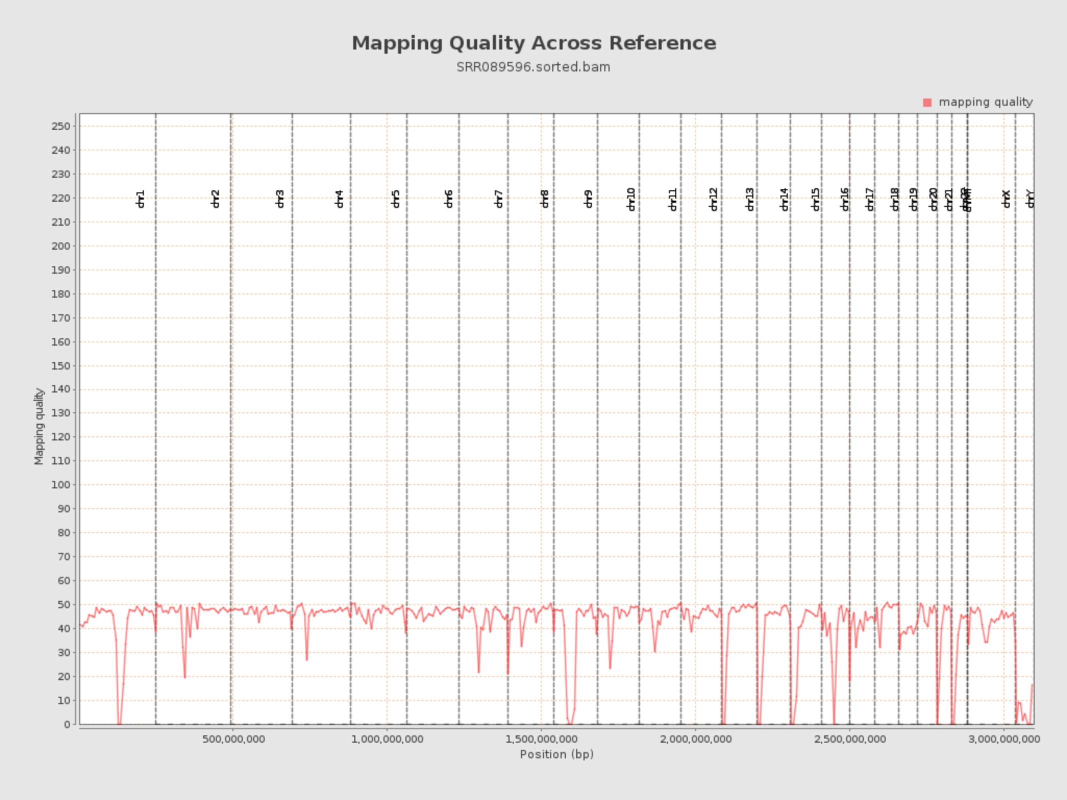
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram