Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 05:35:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089756.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_SRR089756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 05:35:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,106,029
Mapped reads	19,372,062 / 91.78%
Unmapped reads	1,733,967 / 8.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	140,394 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	5,154,934 / 24.42%
Duplication rate	15.29%
Clipped reads	8,764,930 / 41.53%

2.2. ACGT Content

Number/percentage of A's	342,820,158 / 26.69%
Number/percentage of C's	236,891,682 / 18.44%
Number/percentage of T's	405,456,711 / 31.57%
Number/percentage of G's	298,413,400 / 23.23%
Number/percentage of N's	809,879 / 0.06%
GC Percentage	41.68%

2.3. Coverage

Mean	0.4151

Standard Deviation	2.5413

2.4. Mapping Quality

Mean Mapping Quality	47.15

2.5. Mismatches and indels

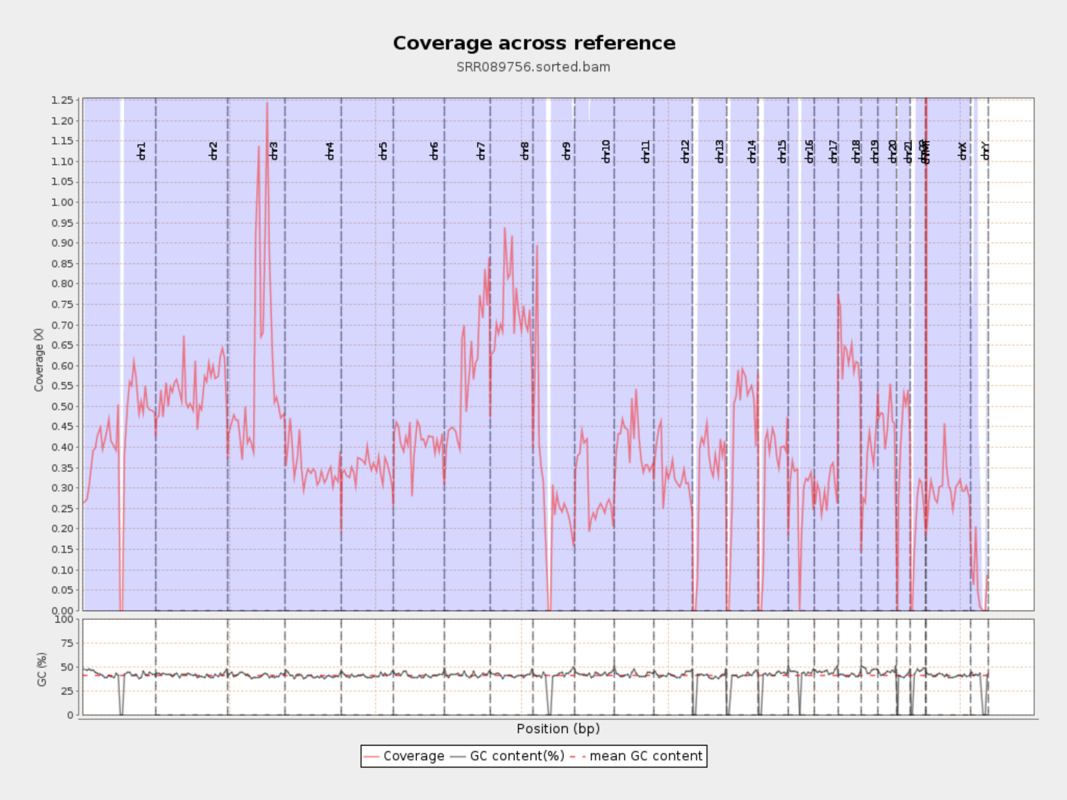
General error rate	0.66%
Mismatches	8,373,575
Insertions	83,468
Mapped reads with at least one insertion	0.43%
Deletions	269,025
Mapped reads with at least one deletion	1.37%
Homopolymer indels	48.1%

2.6. Chromosome stats

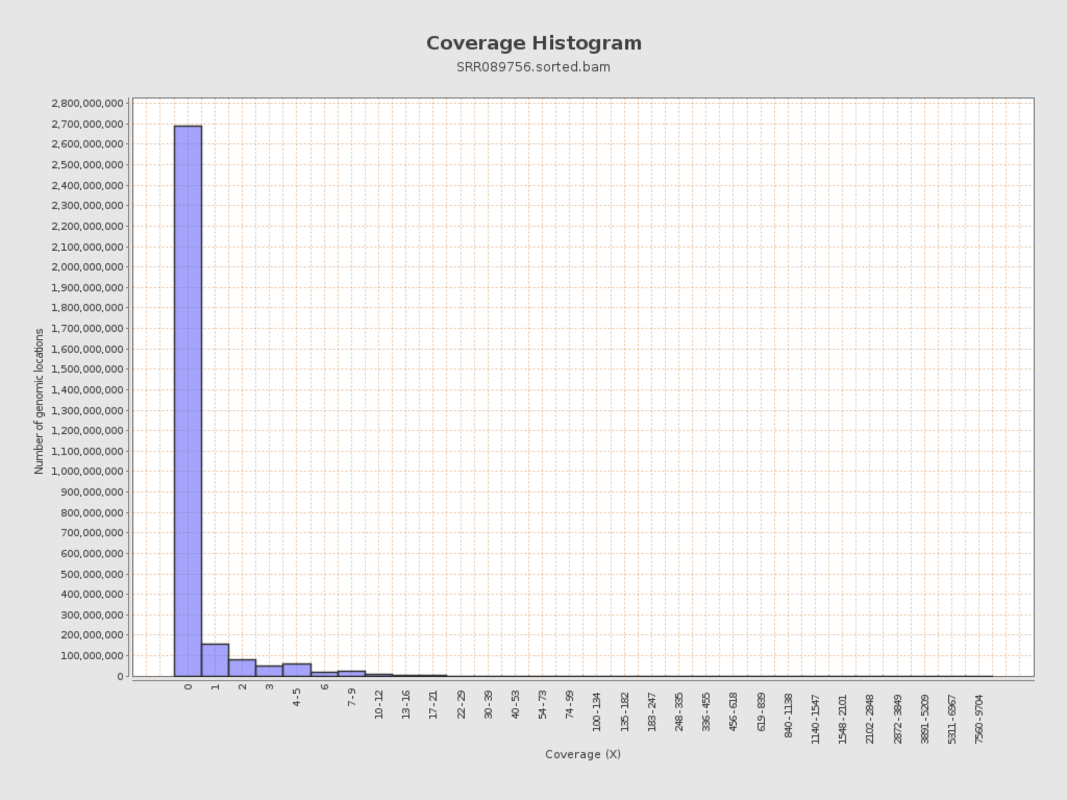
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	104926845	0.421	3.867
chr2	243199373	132920368	0.5465	2.7756
chr3	198022430	116318841	0.5874	1.8847
chr4	191154276	66977815	0.3504	1.6114
chr5	180915260	62683095	0.3465	1.4069
chr6	171115067	71012963	0.415	1.6822
chr7	159138663	92573838	0.5817	3.3309

chr8	146364022	106957417	0.7308	5.9719
chr9	141213431	40725547	0.2884	1.8462
chr10	135534747	39837282	0.2939	1.9052
chr11	135006516	55183931	0.4088	2.0823
chr12	133851895	45603523	0.3407	1.4246
chr13	115169878	37382641	0.3246	1.3591
chr14	107349540	47723360	0.4446	1.6579
chr15	102531392	33358207	0.3253	1.3727
chr16	90354753	25042432	0.2772	1.3494
chr17	81195210	24053895	0.2962	1.5619
chr18	78077248	49182082	0.6299	3.5409
chr19	59128983	21568915	0.3648	2.3925
chr20	63025520	28916347	0.4588	1.7414
chr21	48129895	19598799	0.4072	1.7377
chr22	51304566	10590538	0.2064	1.1066
chrMT	16571	1674667	101.0601	55.6119
chrX	155270560	46332010	0.2984	1.4291
chrY	59373566	3728720	0.0628	1.6483

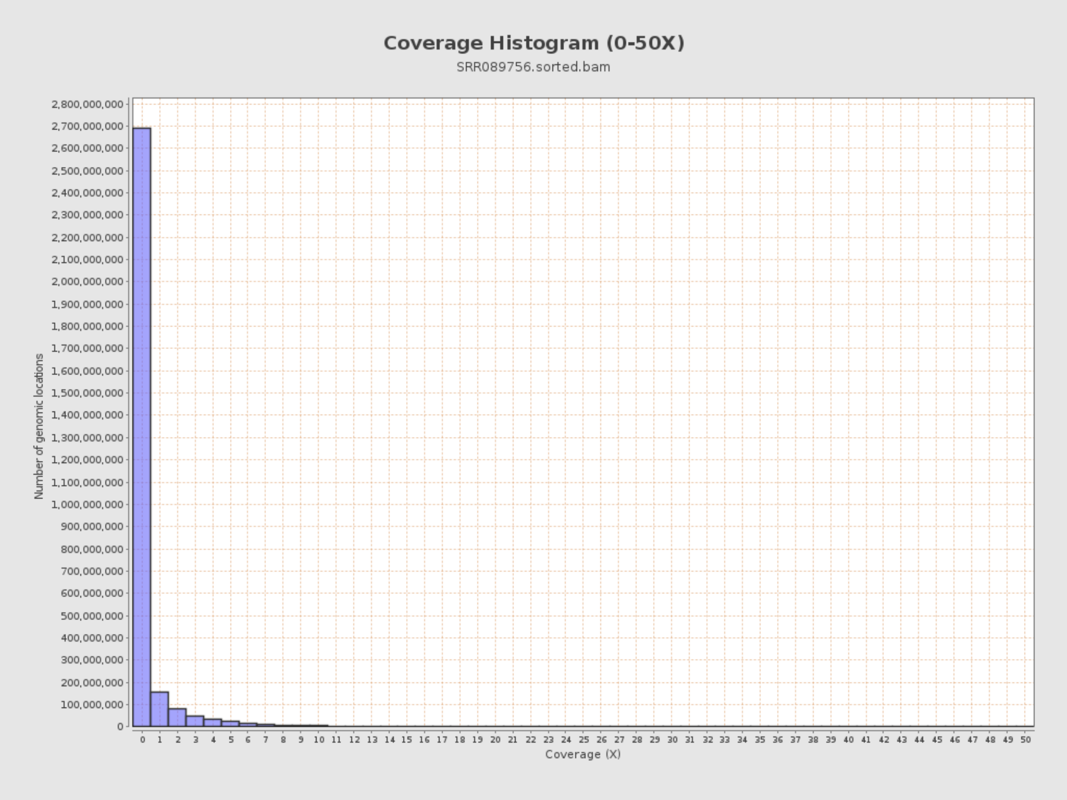
3. Results : Coverage across reference



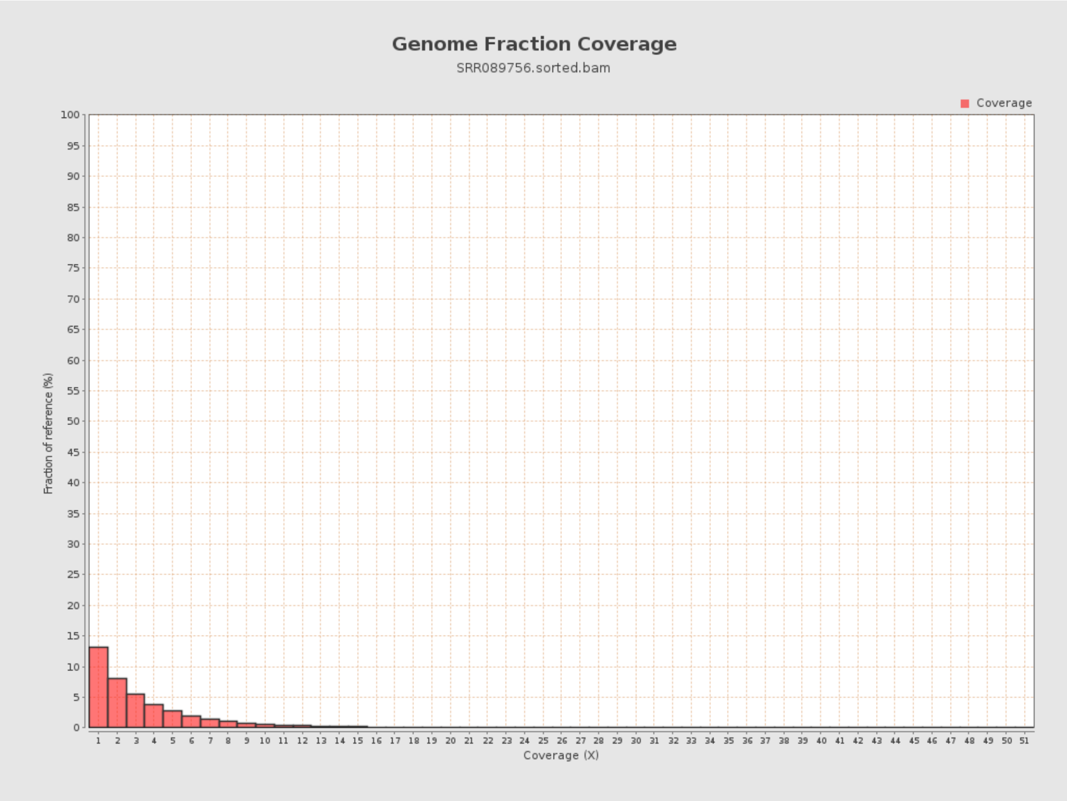
4. Results : Coverage Histogram



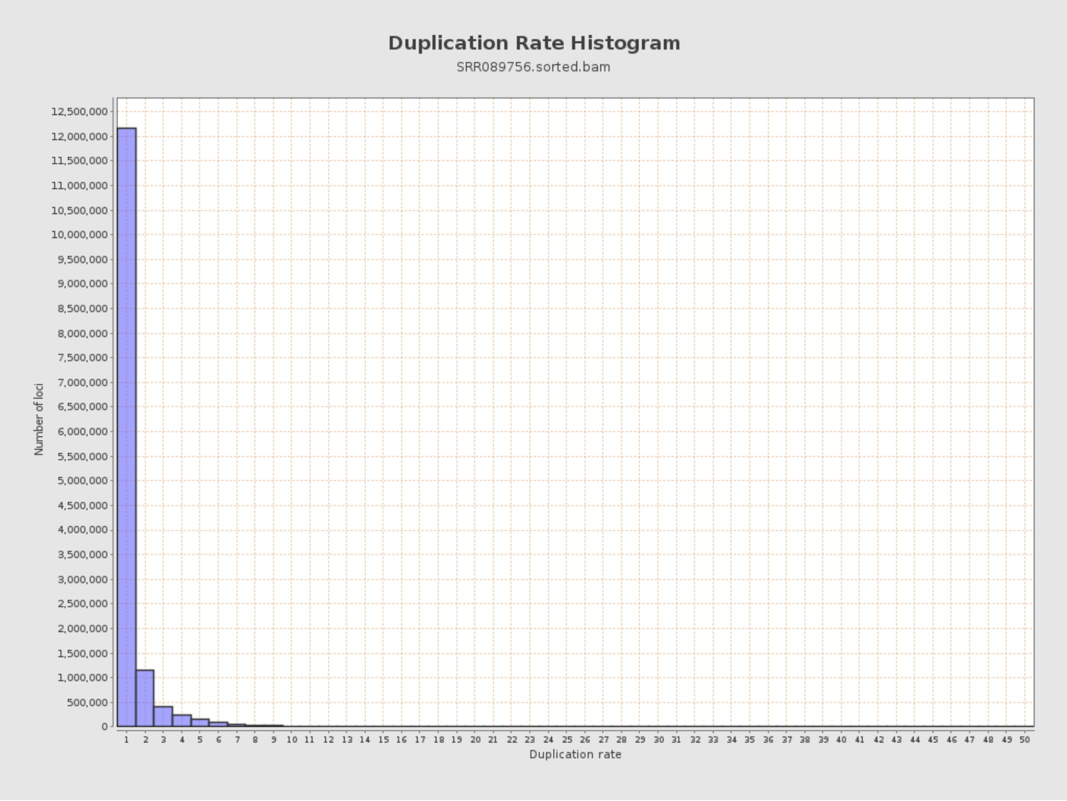
5. Results : Coverage Histogram (0-50X)



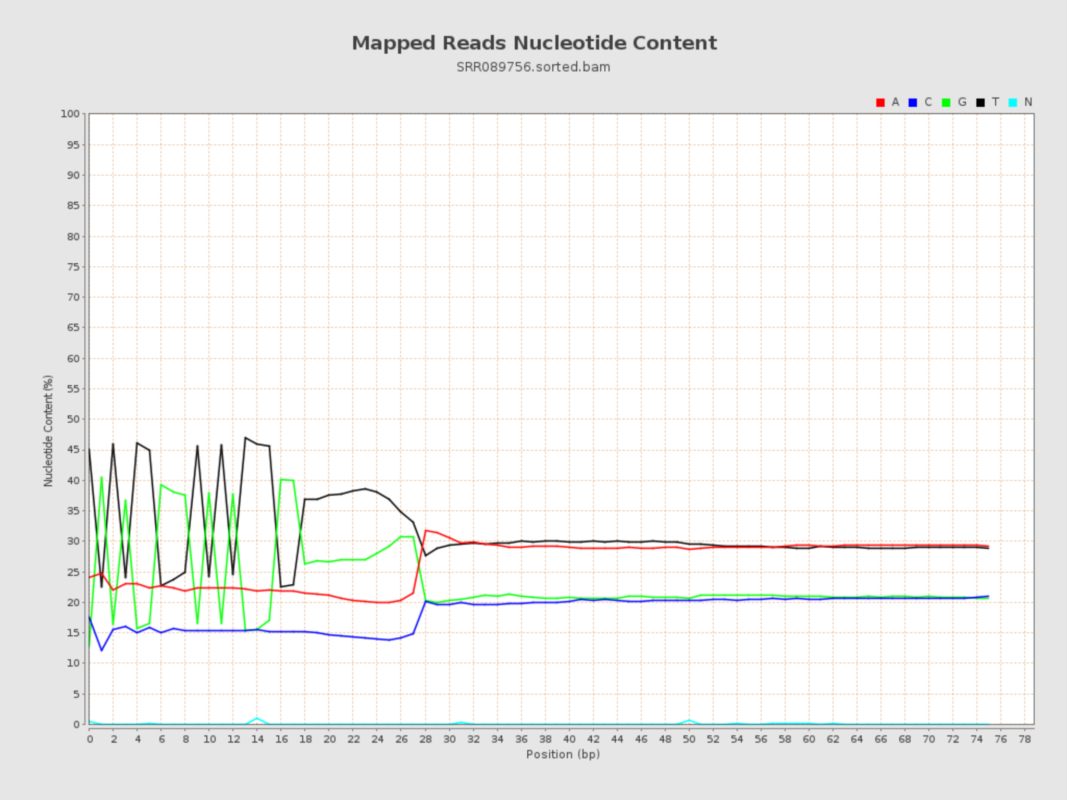
6. Results : Genome Fraction Coverage



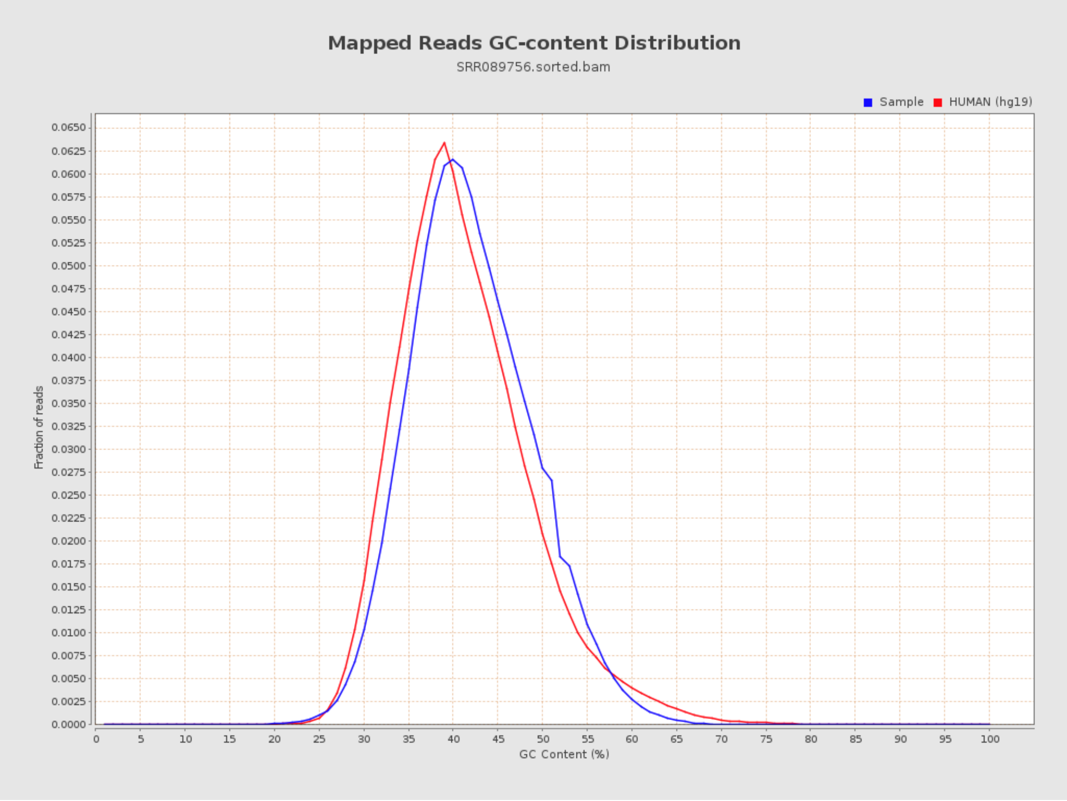
7. Results : Duplication Rate Histogram



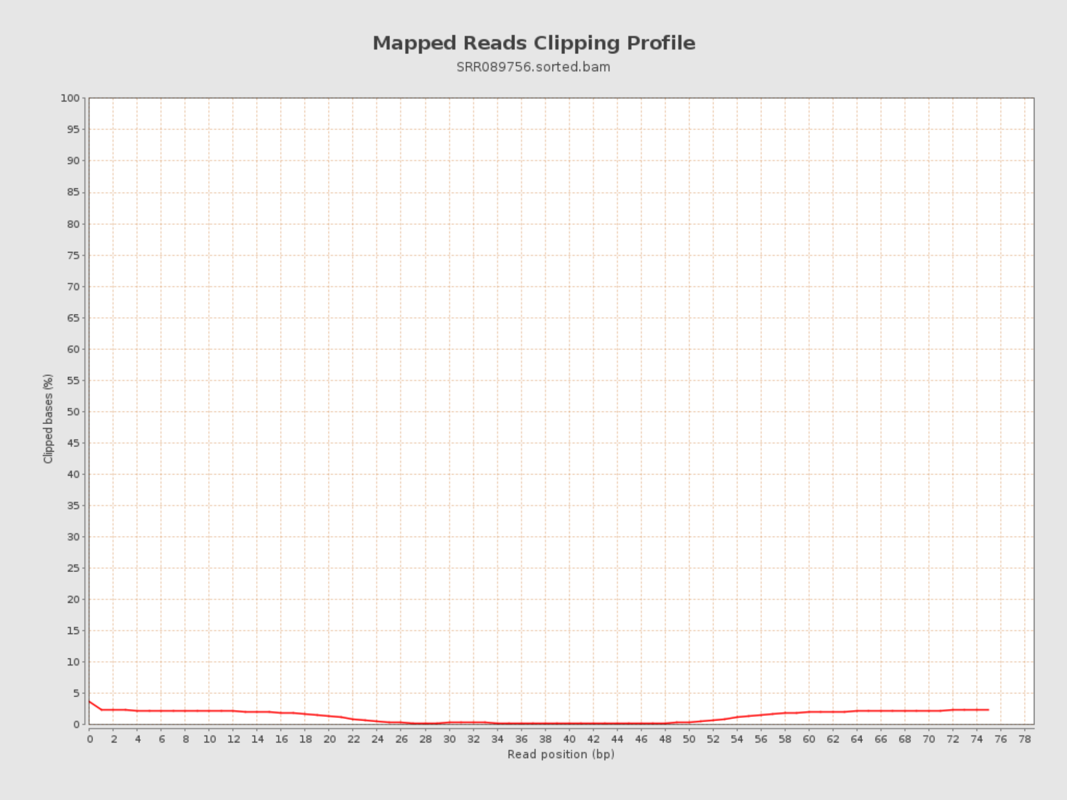
8. Results : Mapped Reads Nucleotide Content



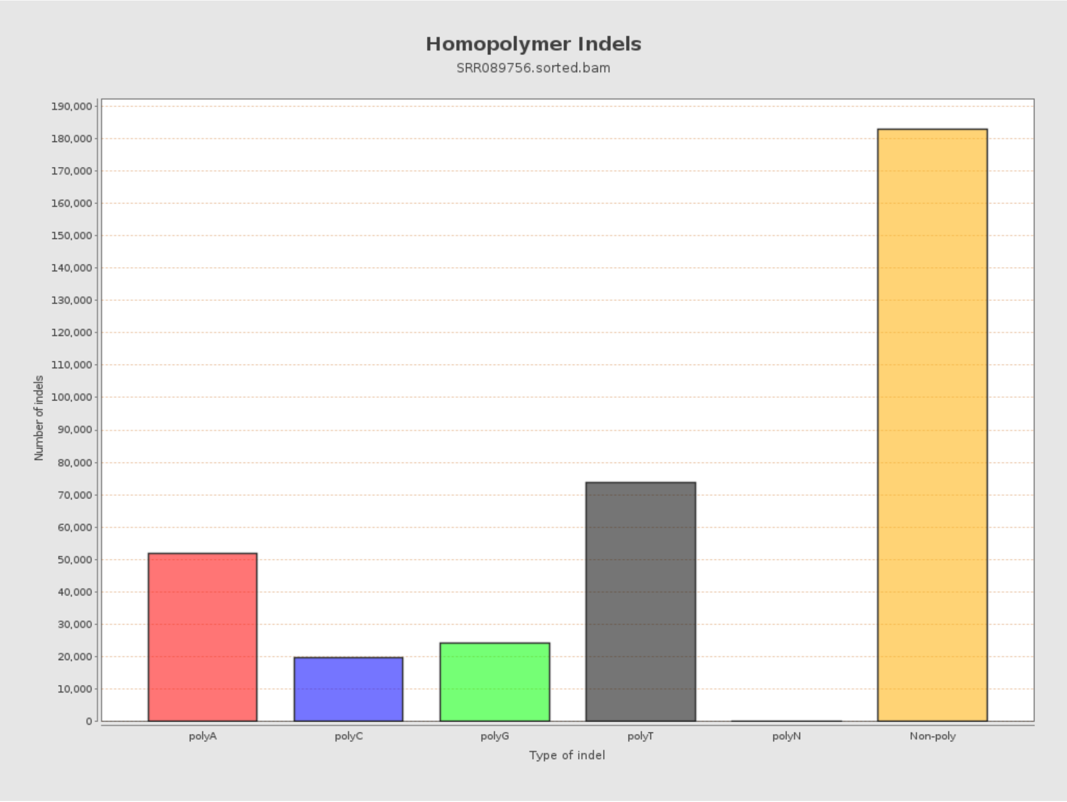
9. Results : Mapped Reads GC-content Distribution



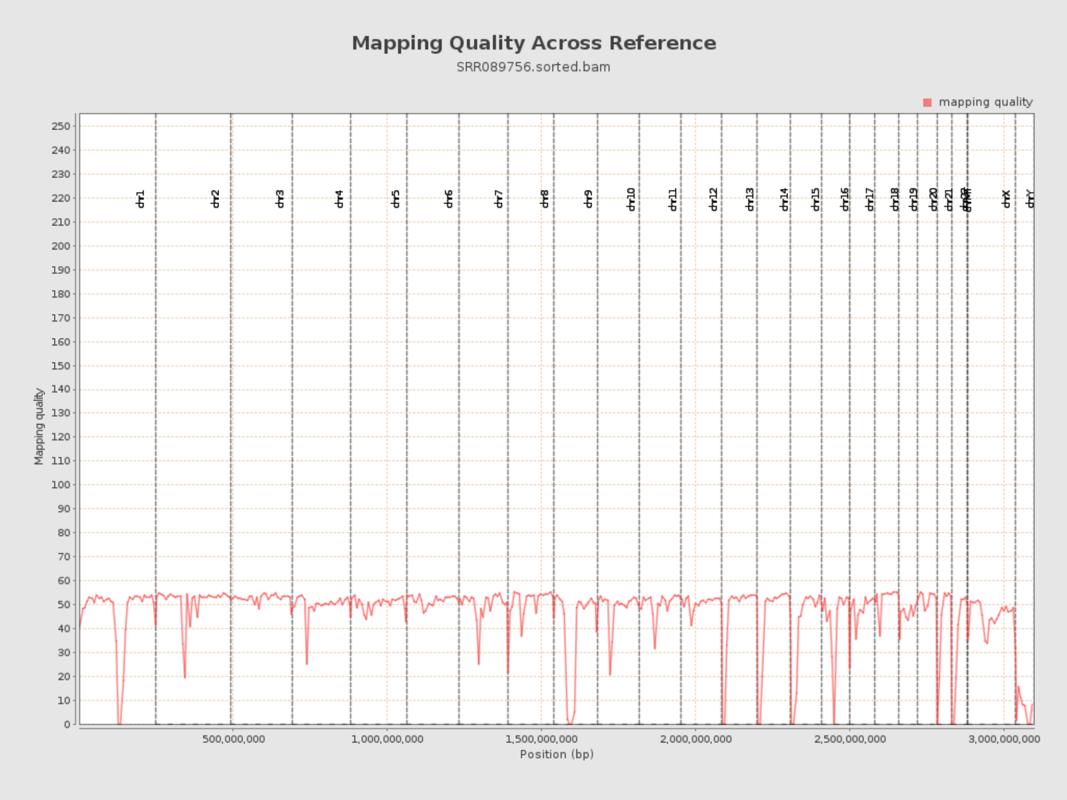
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram