Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 15:31:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089594.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_SRR089594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089594.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 15:31:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,863,389
Mapped reads	14,893,688 / 83.38%
Unmapped reads	2,969,701 / 16.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	597 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,350,042 / 18.75%
Duplication rate	14.66%
Clipped reads	1,321,052 / 7.4%

2.2. ACGT Content

Number/percentage of A's	204,193,473 / 29.06%
Number/percentage of C's	147,543,783 / 21%
Number/percentage of T's	201,461,173 / 28.67%
Number/percentage of G's	149,371,891 / 21.26%
Number/percentage of N's	43,781 / 0.01%
GC Percentage	42.26%

2.3. Coverage

Mean	0.227

Standard Deviation	1.452

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

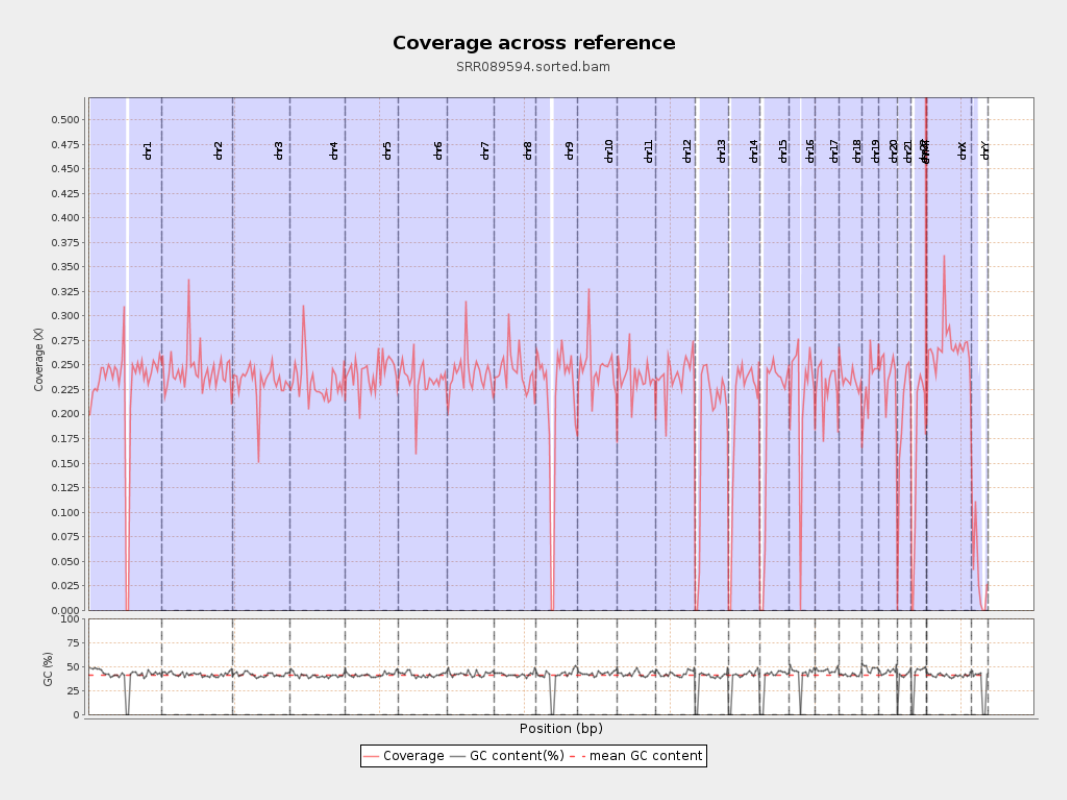
General error rate	0.57%
Mismatches	3,965,139
Insertions	28,532
Mapped reads with at least one insertion	0.19%
Deletions	88,595
Mapped reads with at least one deletion	0.59%
Homopolymer indels	44.8%

2.6. Chromosome stats

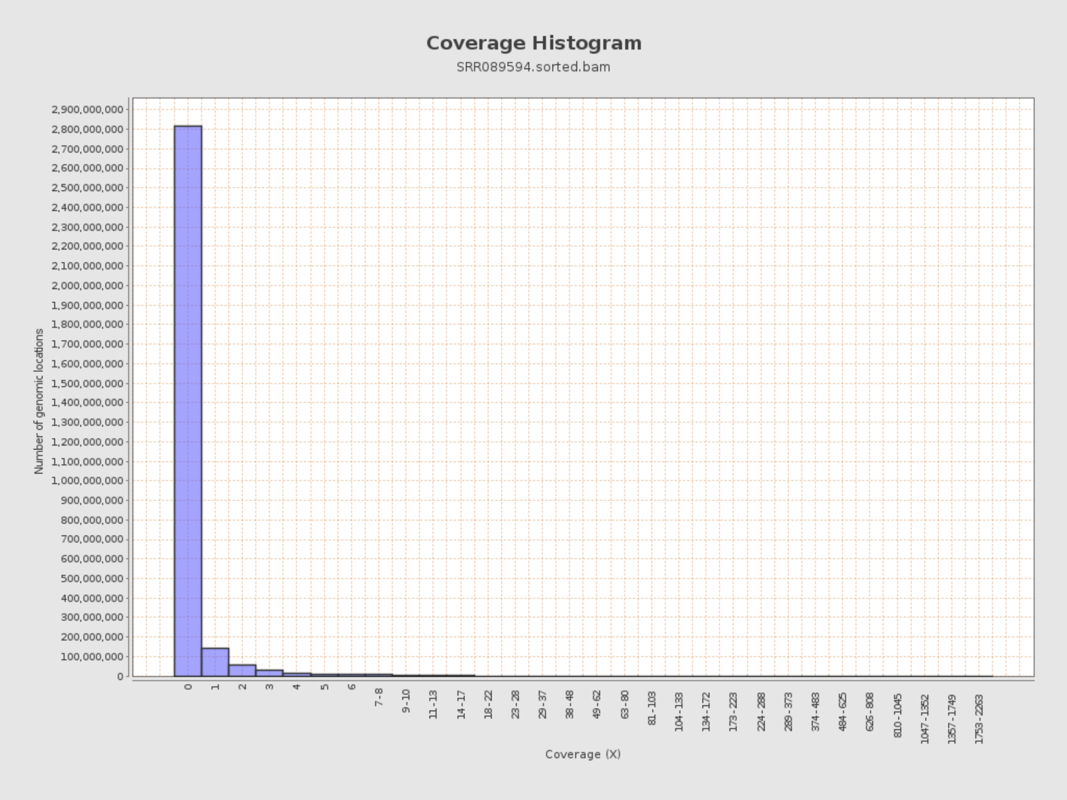
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	56697494	0.2275	2.0329
chr2	243199373	59487500	0.2446	1.7812
chr3	198022430	46107258	0.2328	1.1074
chr4	191154276	44546853	0.233	1.1783
chr5	180915260	43799863	0.2421	1.126
chr6	171115067	40213797	0.235	1.2808
chr7	159138663	38514223	0.242	1.8601

chr8	146364022	35626984	0.2434	1.6741
chr9	141213431	30118023	0.2133	1.3374
chr10	135534747	33559573	0.2476	1.5262
chr11	135006516	32028753	0.2372	1.4337
chr12	133851895	32144737	0.2402	1.1581
chr13	115169878	21704419	0.1885	0.998
chr14	107349540	21318815	0.1986	1.2417
chr15	102531392	19834825	0.1935	1.0085
chr16	90354753	20016029	0.2215	1.1764
chr17	81195210	18459854	0.2274	1.2428
chr18	78077248	18456313	0.2364	2.0272
chr19	59128983	13713495	0.2319	2.0128
chr20	63025520	15057139	0.2389	1.2109
chr21	48129895	9262632	0.1925	1.149
chr22	51304566	8109605	0.1581	0.9144
chrMT	16571	205823	12.4207	11.092
chrX	155270560	41632491	0.2681	1.3722
chrY	59373566	2130151	0.0359	0.665

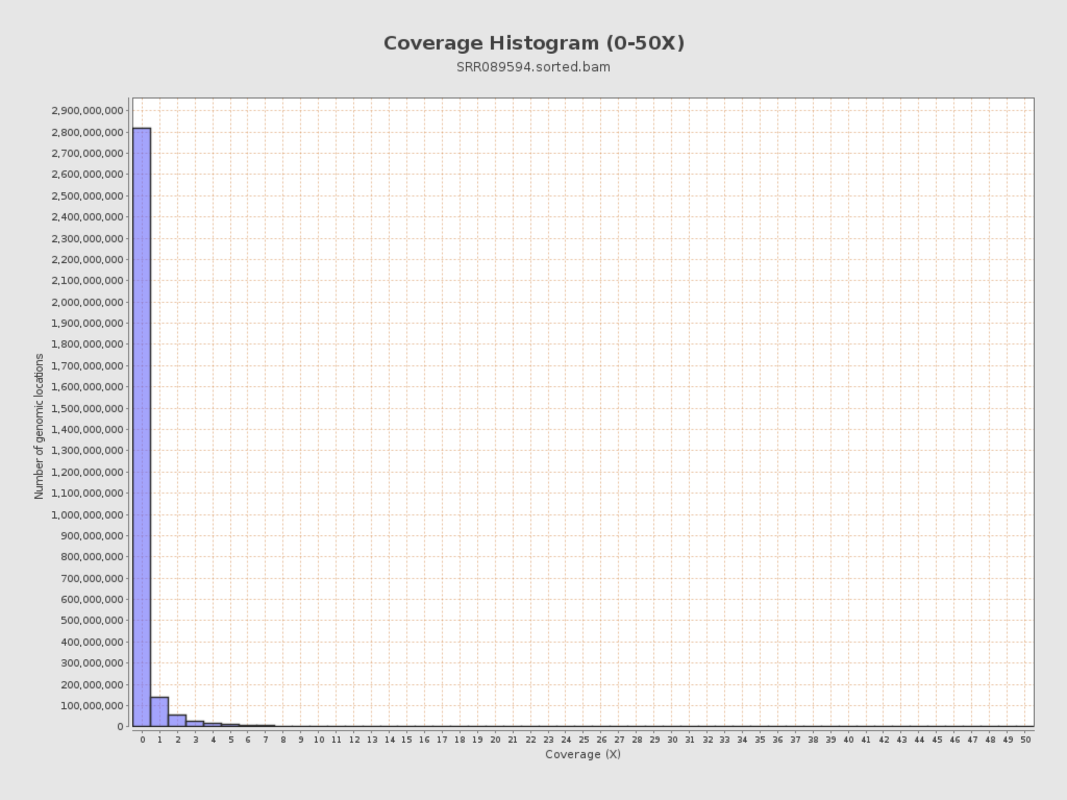
3. Results : Coverage across reference



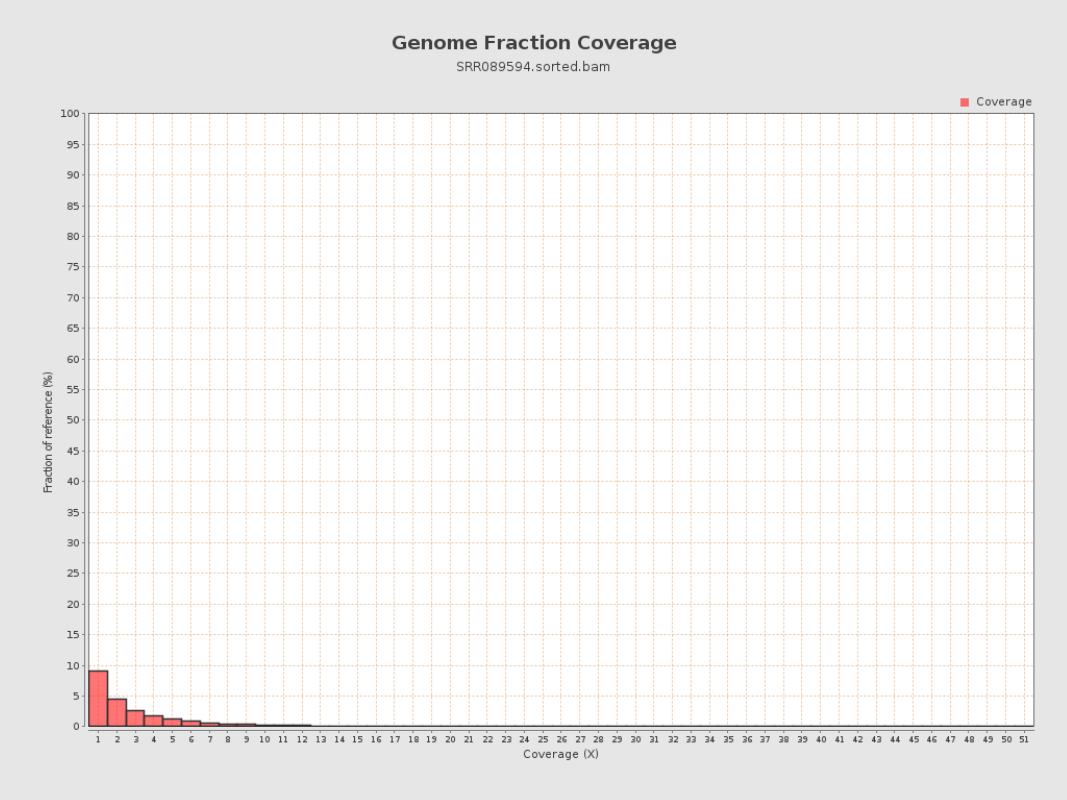
4. Results : Coverage Histogram



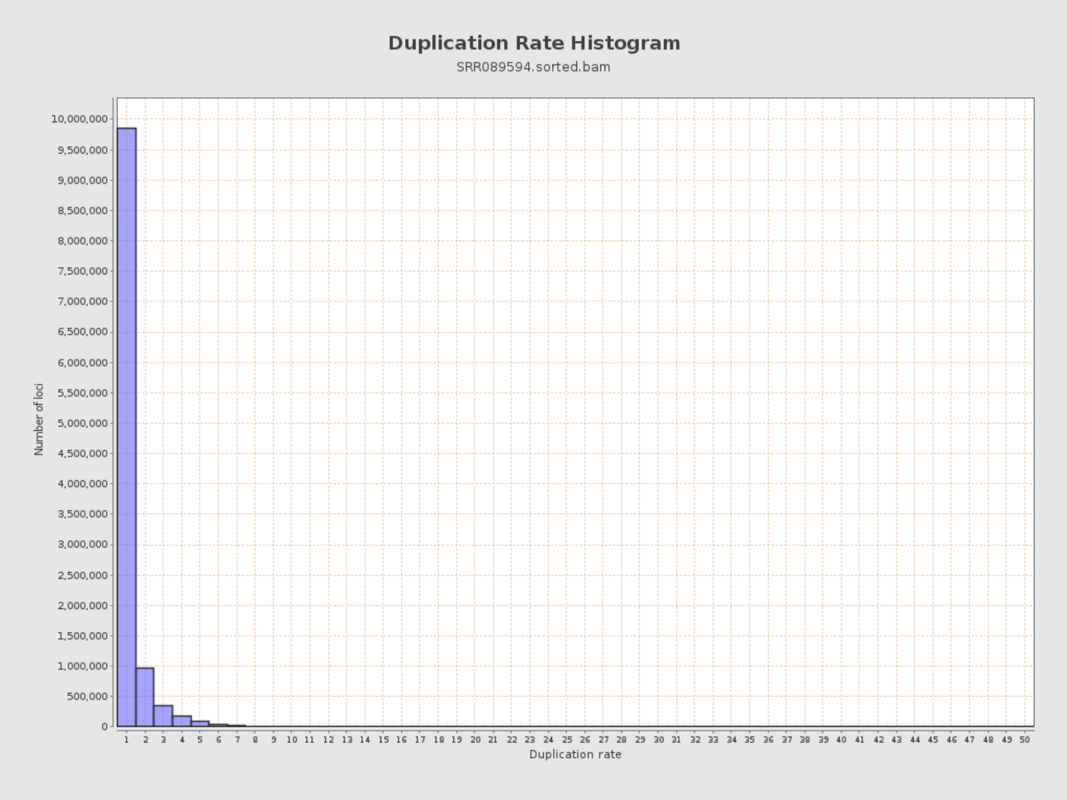
5. Results : Coverage Histogram (0-50X)



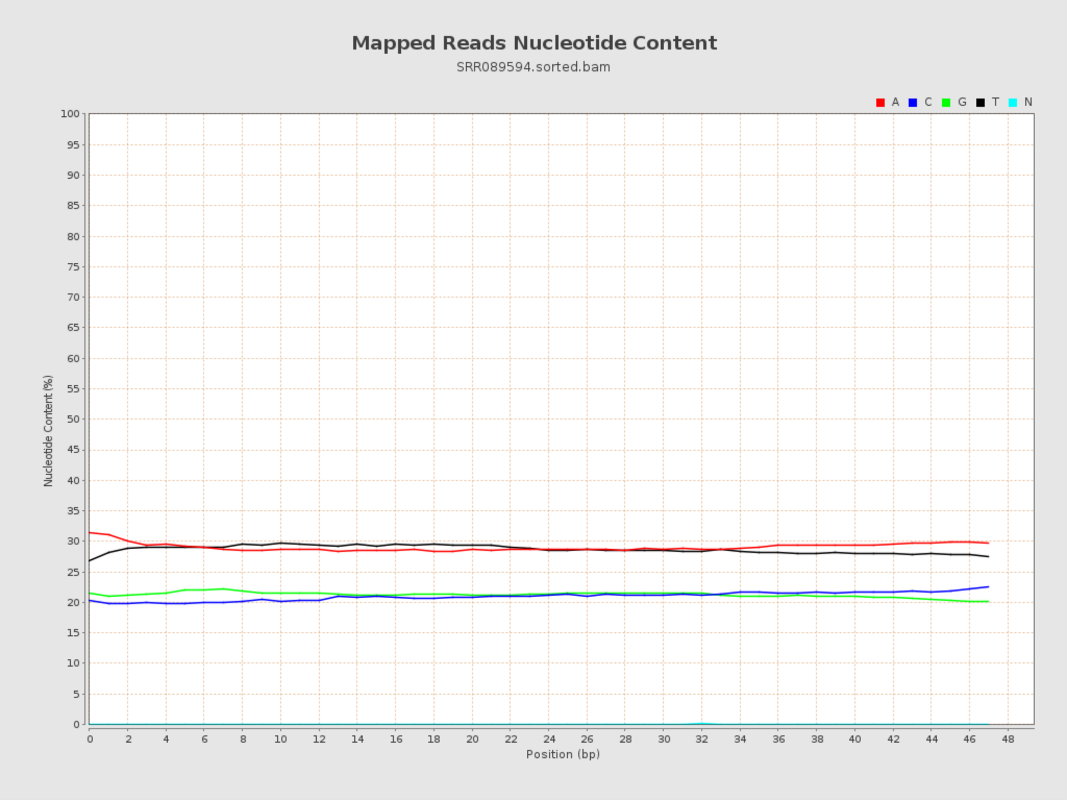
6. Results : Genome Fraction Coverage



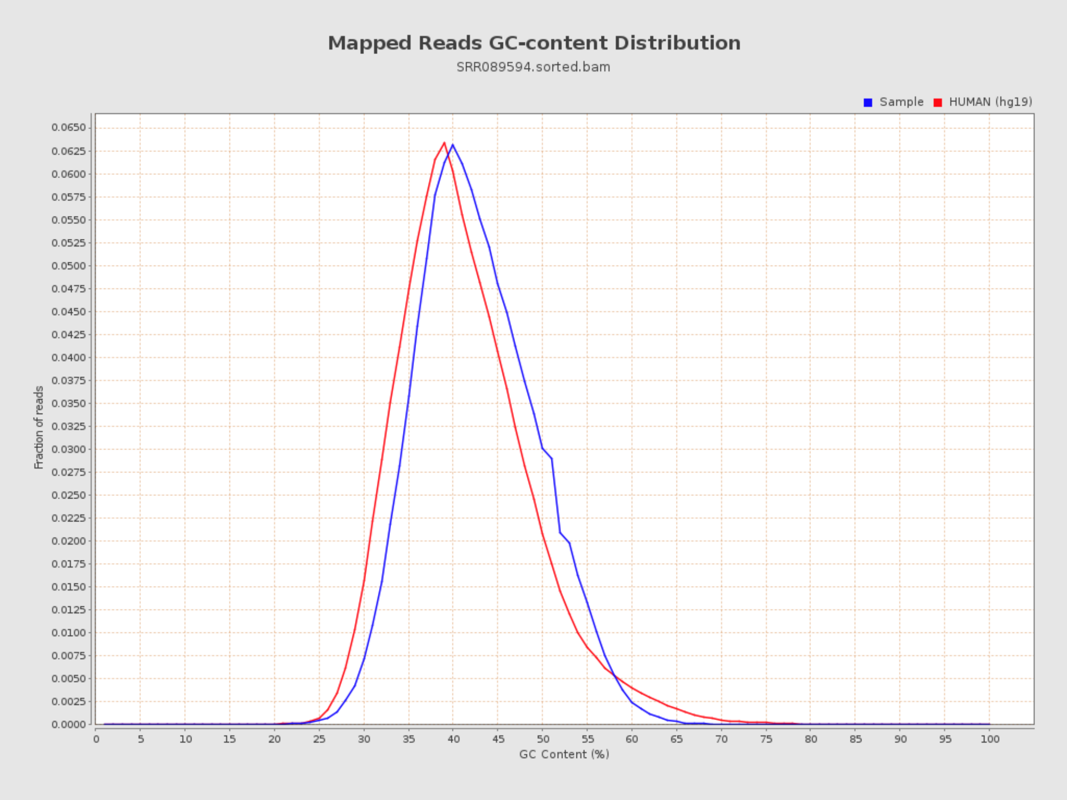
7. Results : Duplication Rate Histogram



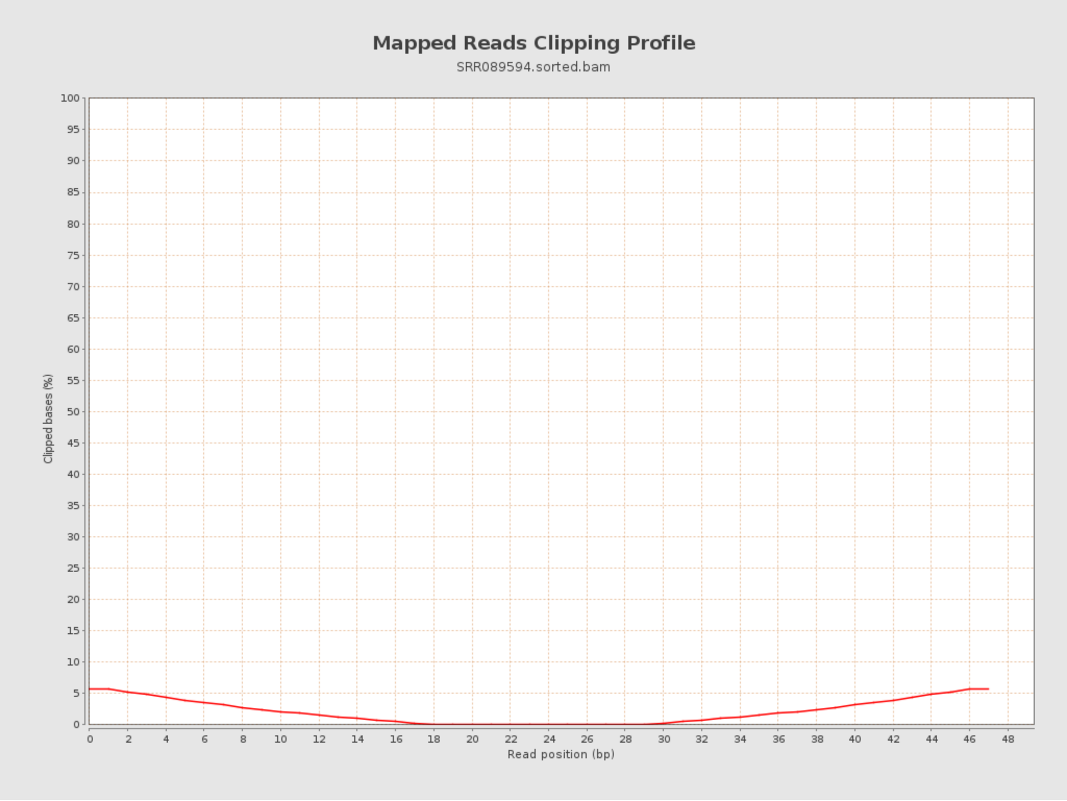
8. Results : Mapped Reads Nucleotide Content



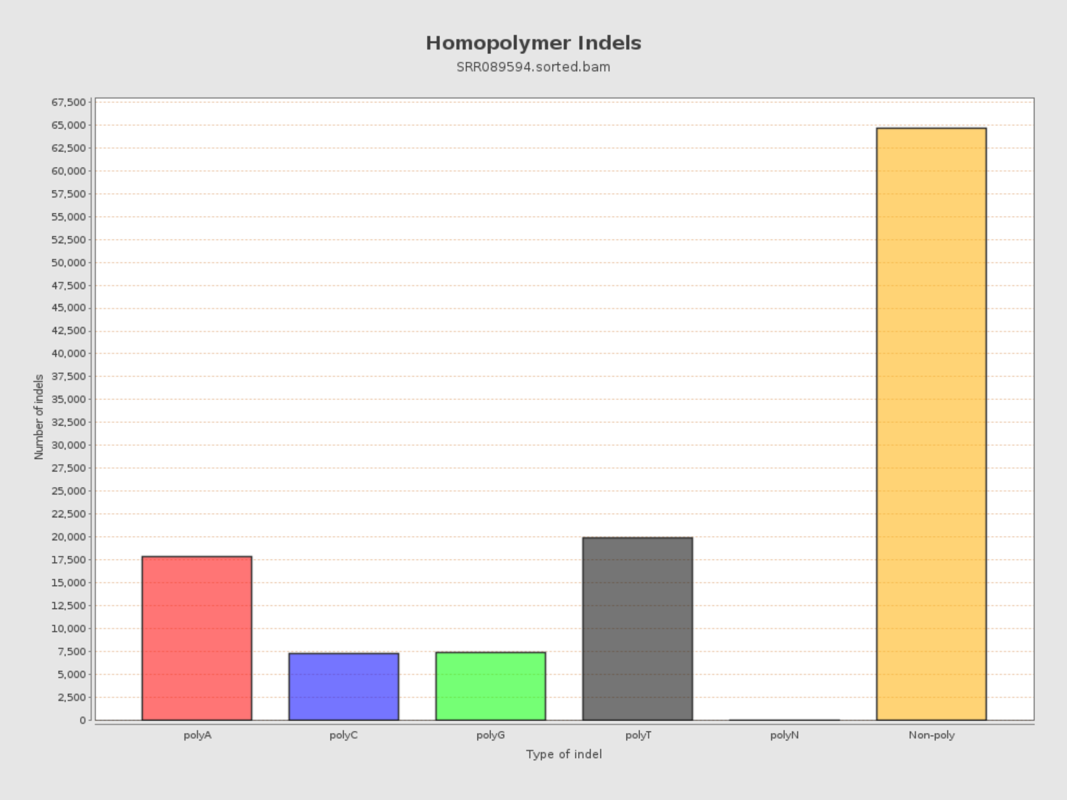
9. Results : Mapped Reads GC-content Distribution



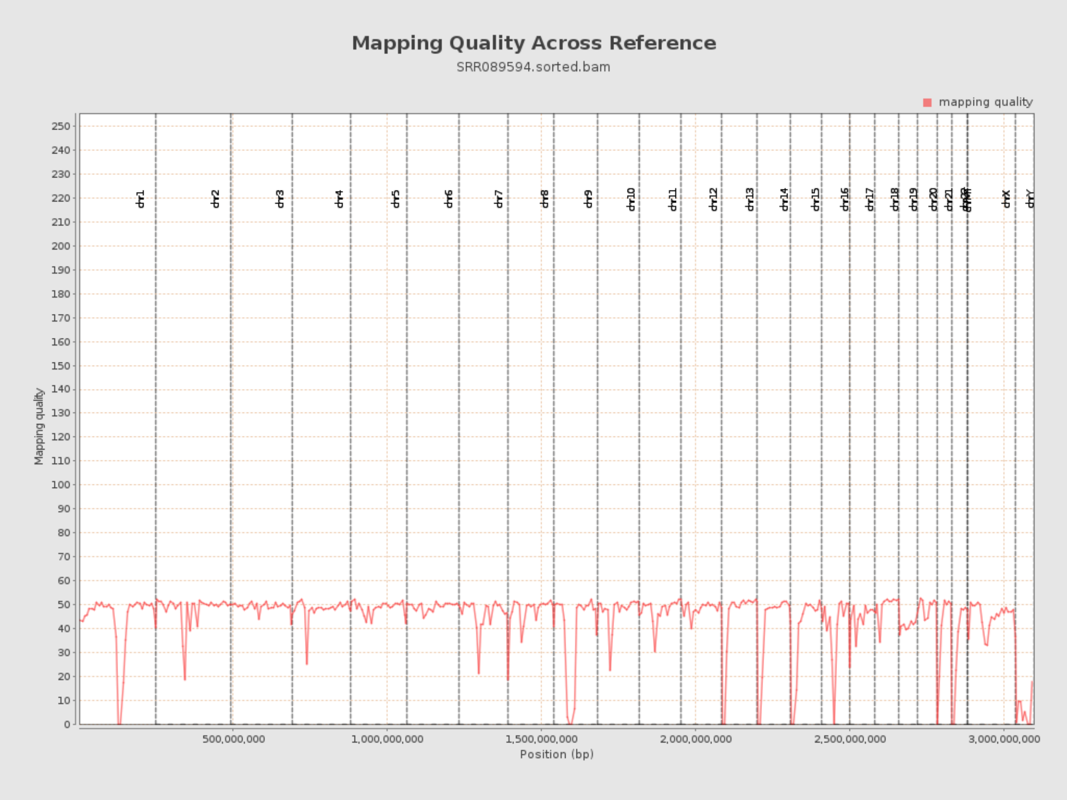
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram