Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 04:13:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089752.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_SRR089752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089752.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 04:13:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,432,098
Mapped reads	29,712,225 / 83.86%
Unmapped reads	5,719,873 / 16.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,339 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	5,404,679 / 15.25%
Duplication rate	11.41%
Clipped reads	2,025,982 / 5.72%

2.2. ACGT Content

Number/percentage of A's	434,656,366 / 30.9%
Number/percentage of C's	275,242,819 / 19.57%
Number/percentage of T's	407,863,143 / 29%
Number/percentage of G's	288,684,718 / 20.52%
Number/percentage of N's	205,260 / 0.01%
GC Percentage	40.09%

2.3. Coverage

Mean	0.4545

Standard Deviation	3.5021

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

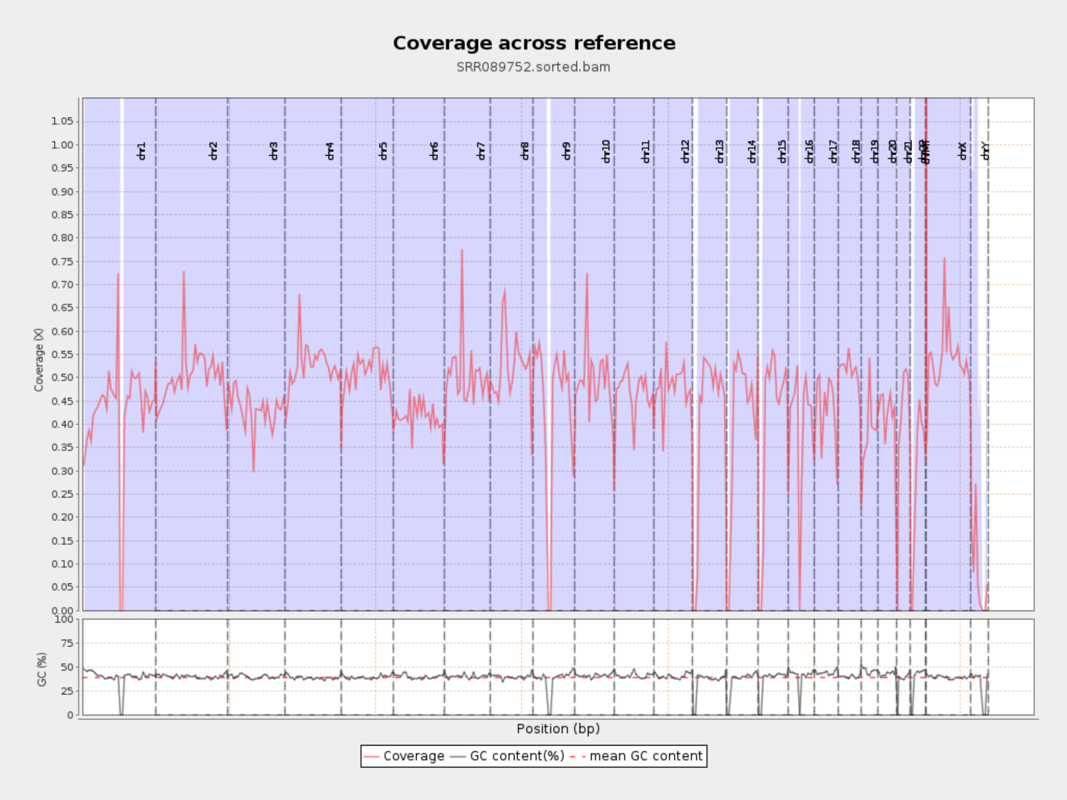
General error rate	0.45%
Mismatches	6,195,656
Insertions	53,685
Mapped reads with at least one insertion	0.18%
Deletions	172,750
Mapped reads with at least one deletion	0.58%
Homopolymer indels	47.87%

2.6. Chromosome stats

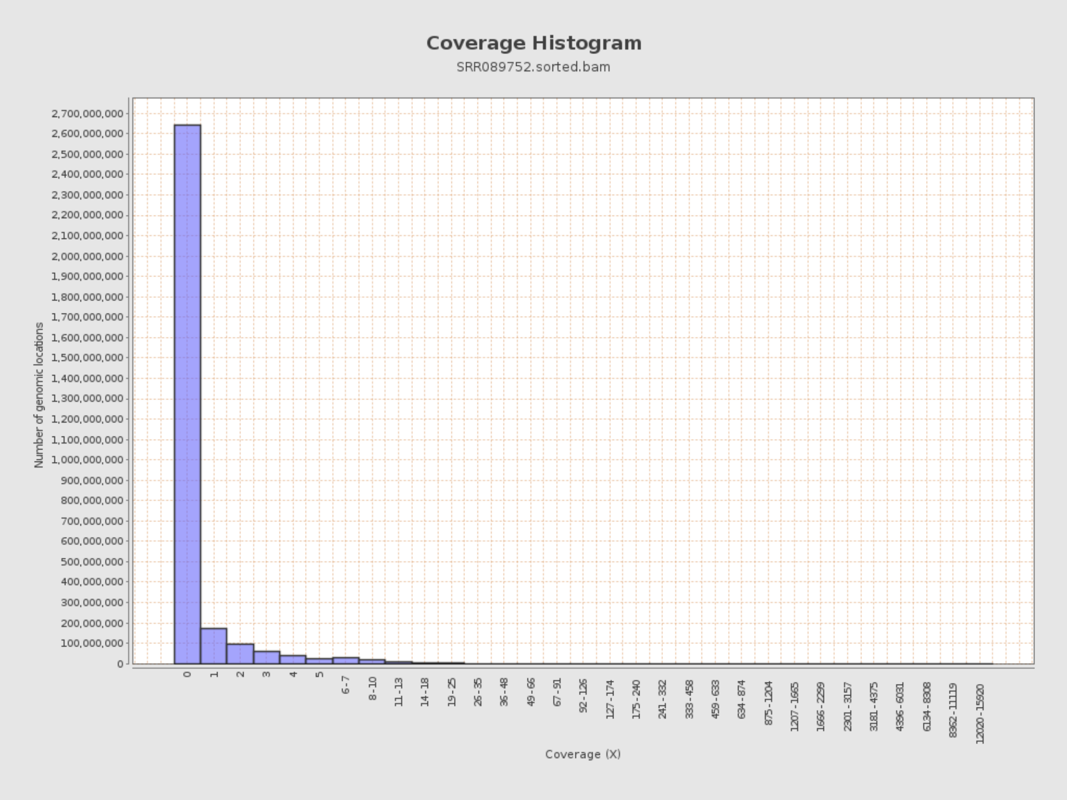
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	106183244	0.426	6.2376
chr2	243199373	122593999	0.5041	2.8122
chr3	198022430	85814366	0.4334	1.5601
chr4	191154276	100620703	0.5264	1.9903
chr5	180915260	91838678	0.5076	1.734
chr6	171115067	71338828	0.4169	1.7689
chr7	159138663	80009098	0.5028	4.2613

chr8	146364022	76336612	0.5216	8.5854
chr9	141213431	61815548	0.4377	2.7668
chr10	135534747	67359561	0.497	2.7783
chr11	135006516	63100496	0.4674	2.8058
chr12	133851895	64385353	0.481	1.7943
chr13	115169878	47257634	0.4103	1.5185
chr14	107349540	43789566	0.4079	1.7266
chr15	102531392	41087854	0.4007	1.4864
chr16	90354753	35137473	0.3889	1.668
chr17	81195210	35524684	0.4375	2.0724
chr18	78077248	40304683	0.5162	6.0141
chr19	59128983	22842204	0.3863	4.0655
chr20	63025520	26646691	0.4228	1.7102
chr21	48129895	19509875	0.4054	2.0251
chr22	51304566	14503502	0.2827	1.2067
chrMT	16571	536916	32.4009	21.1987
chrX	155270560	83757182	0.5394	2.2148
chrY	59373566	4618232	0.0778	2.0762

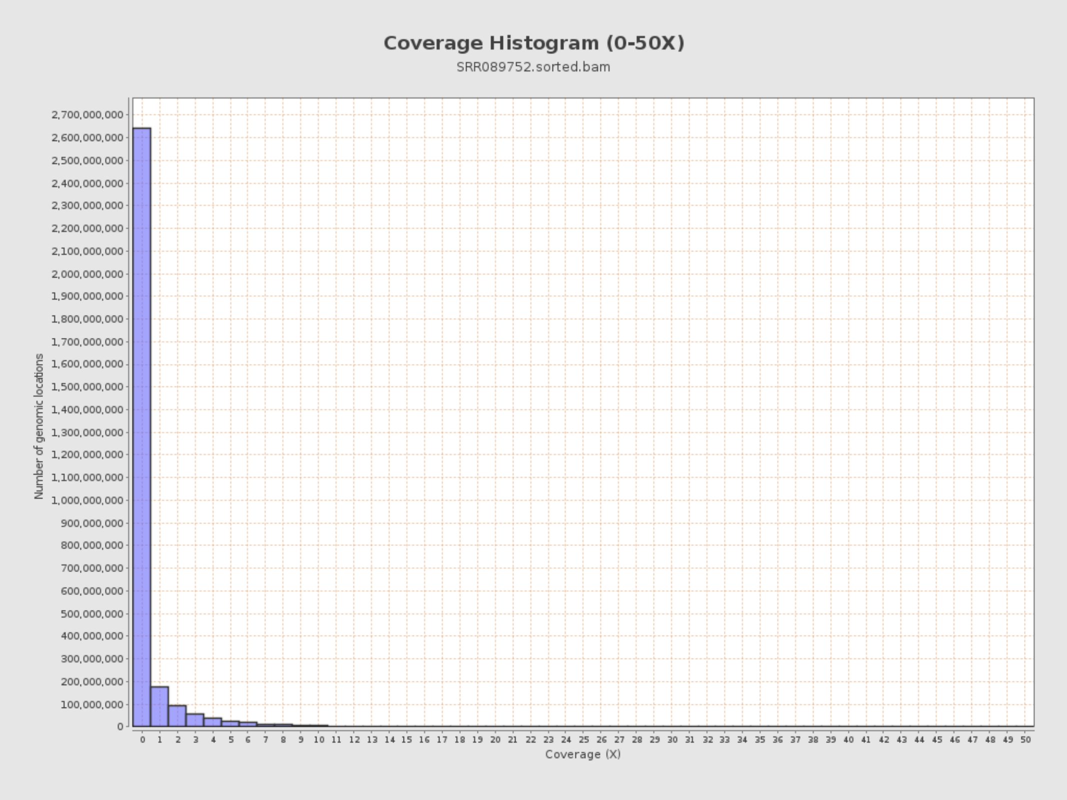
3. Results : Coverage across reference



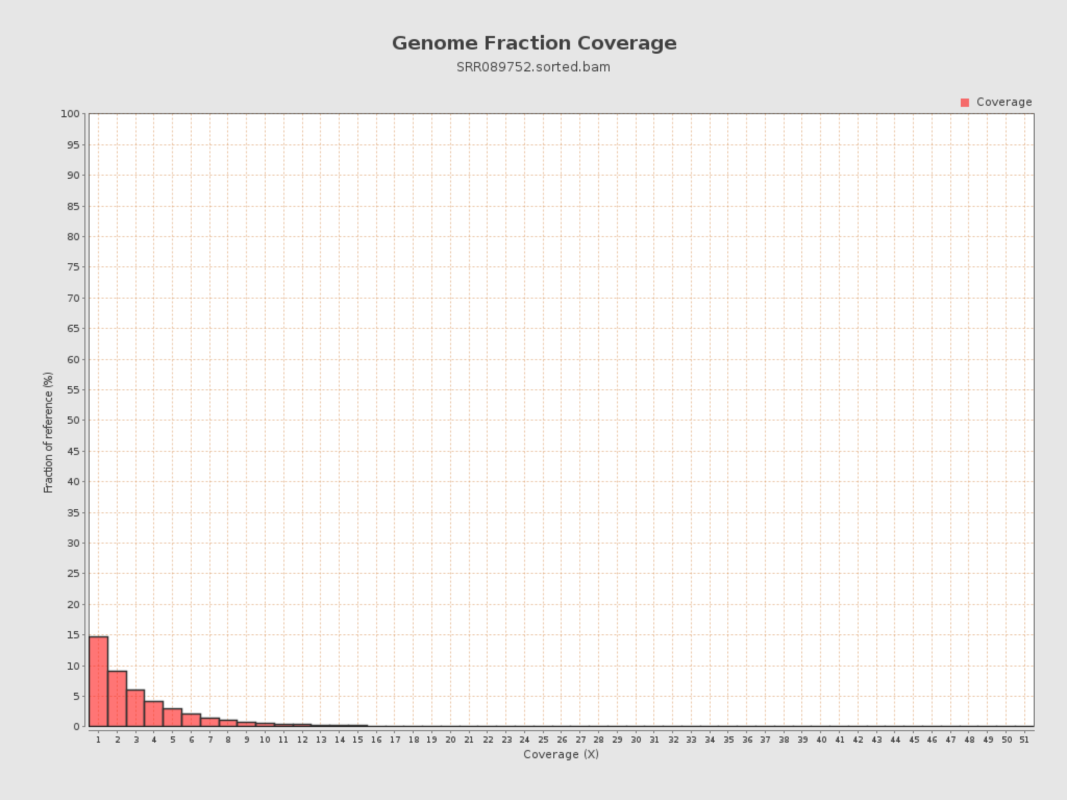
4. Results : Coverage Histogram



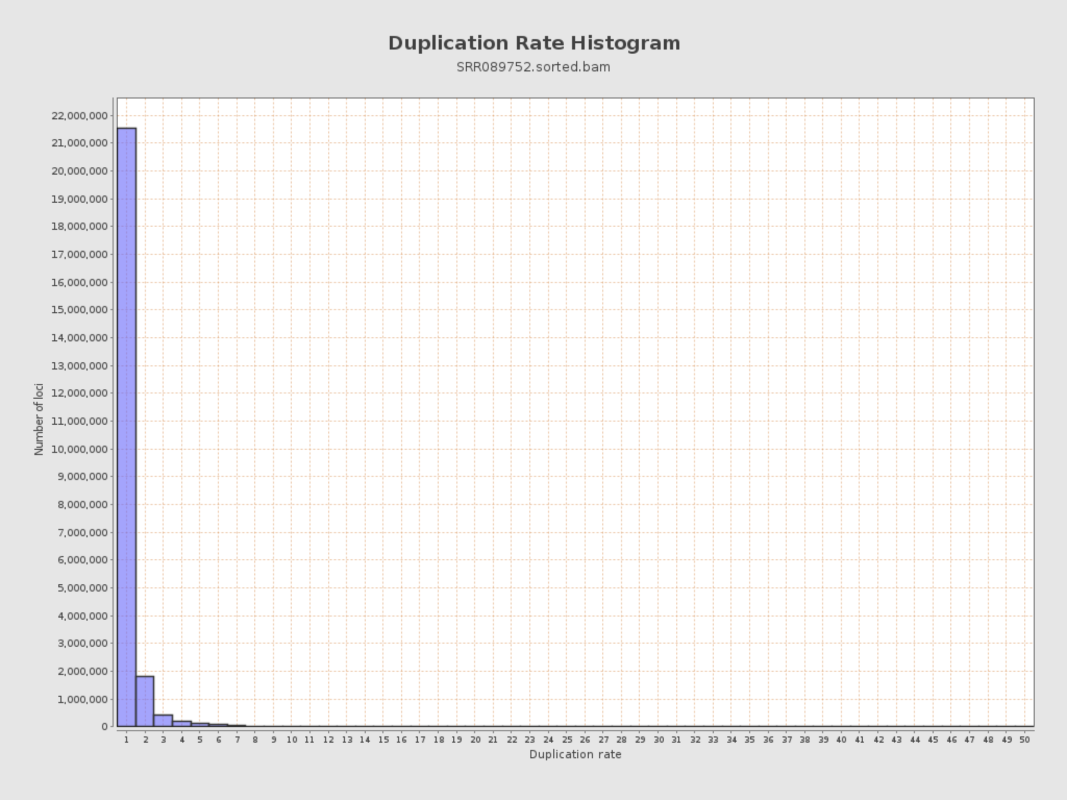
5. Results : Coverage Histogram (0-50X)



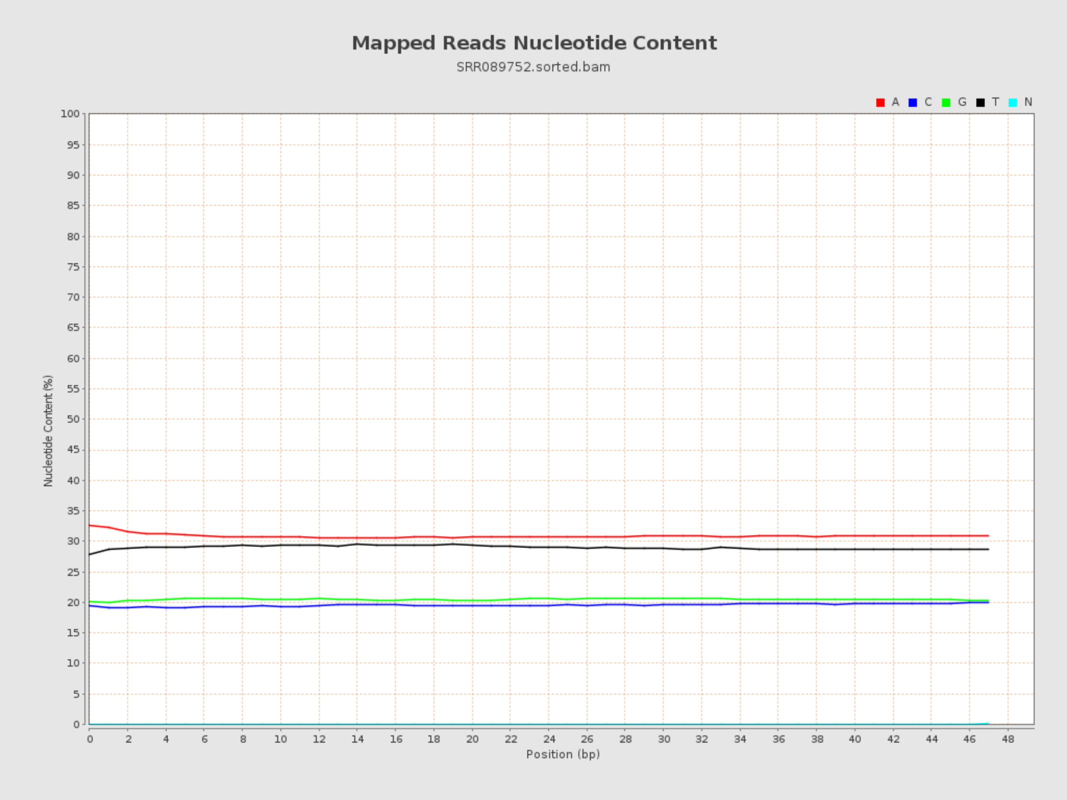
6. Results : Genome Fraction Coverage



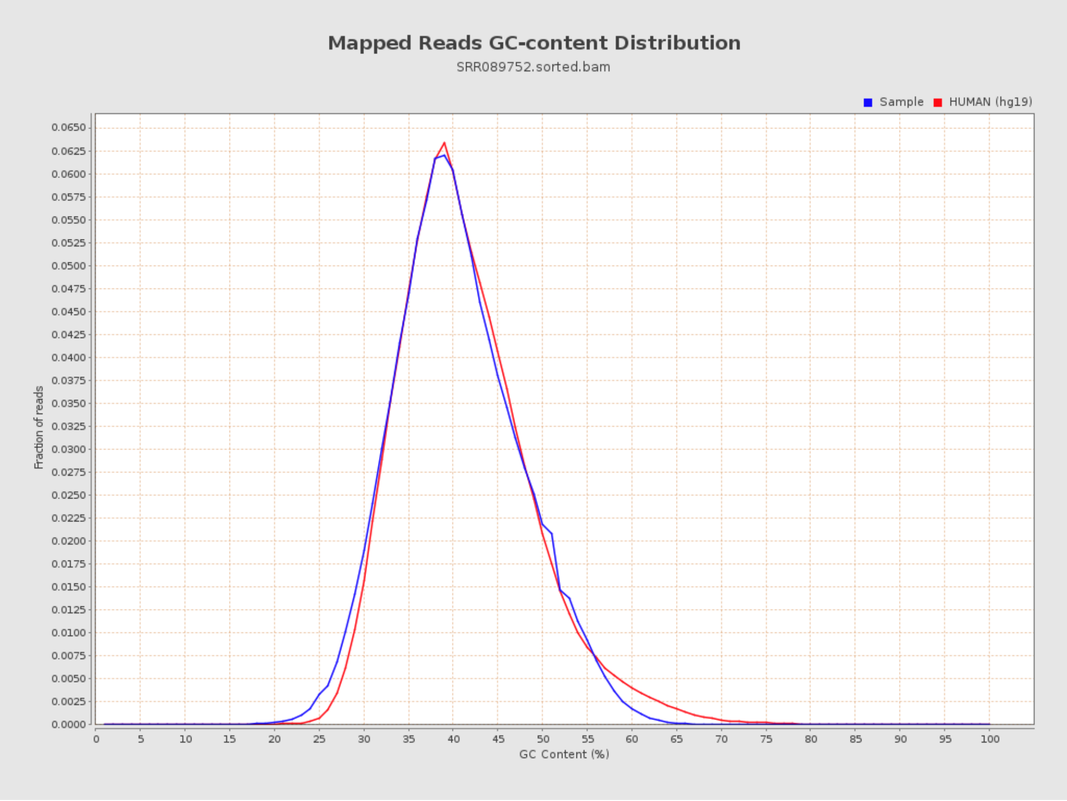
7. Results : Duplication Rate Histogram



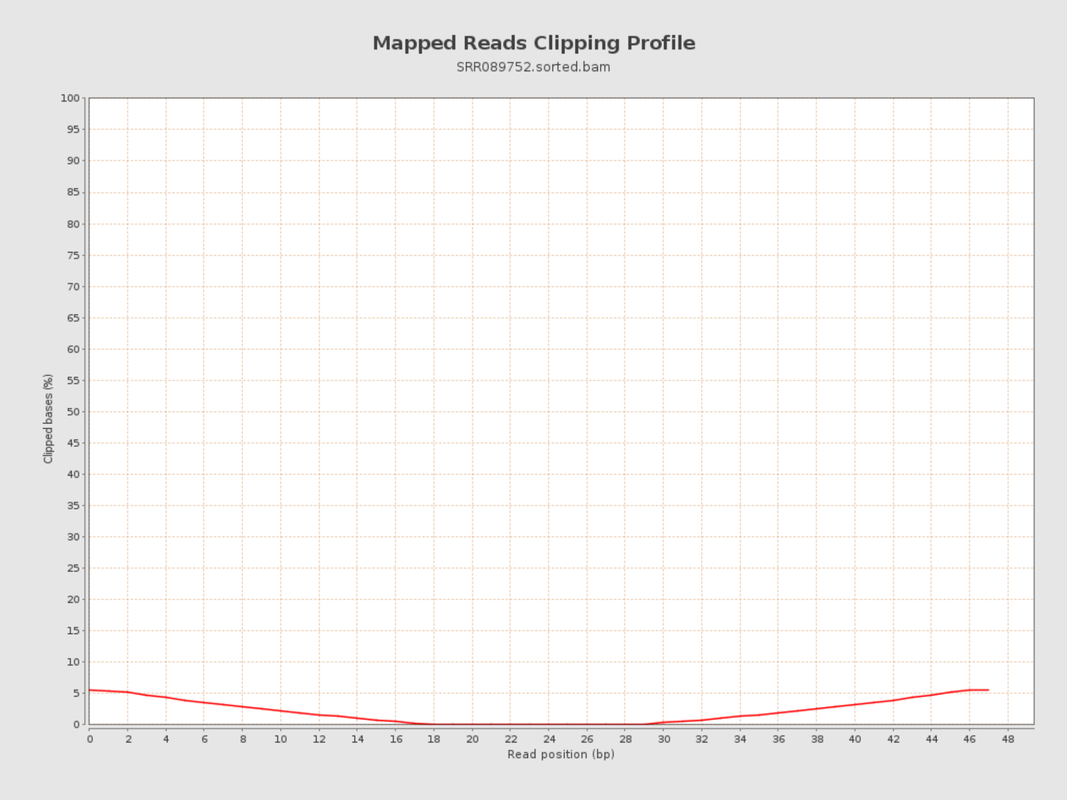
8. Results : Mapped Reads Nucleotide Content



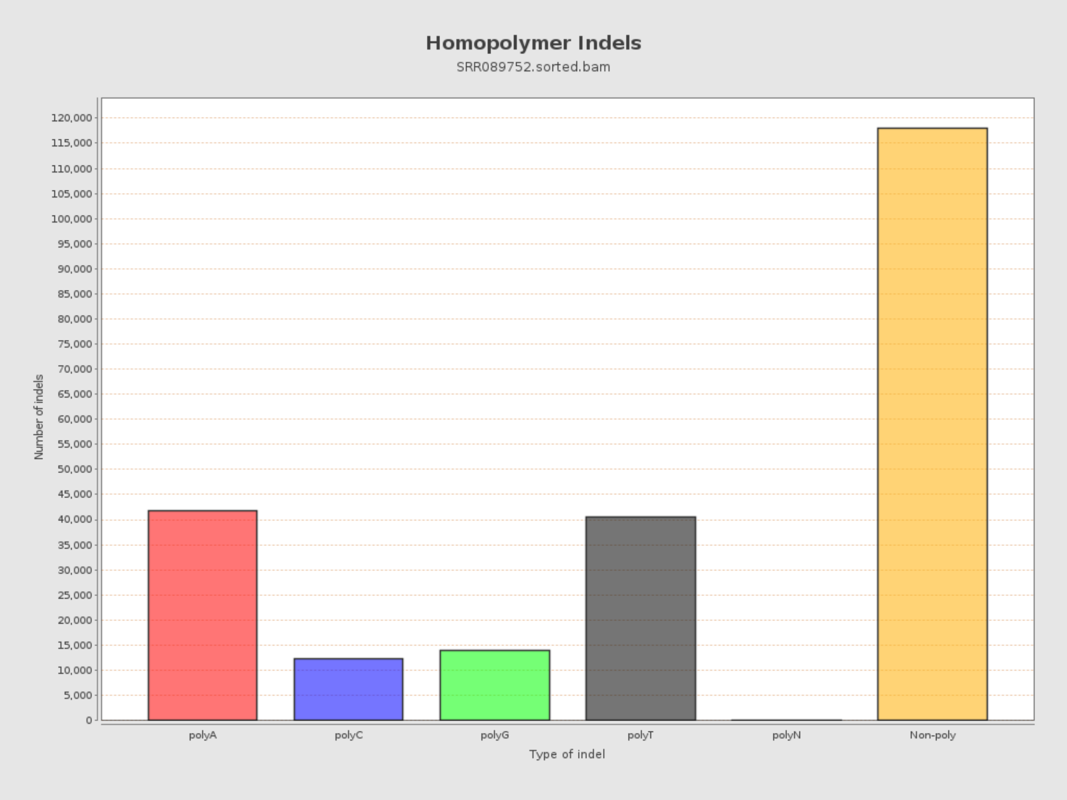
9. Results : Mapped Reads GC-content Distribution



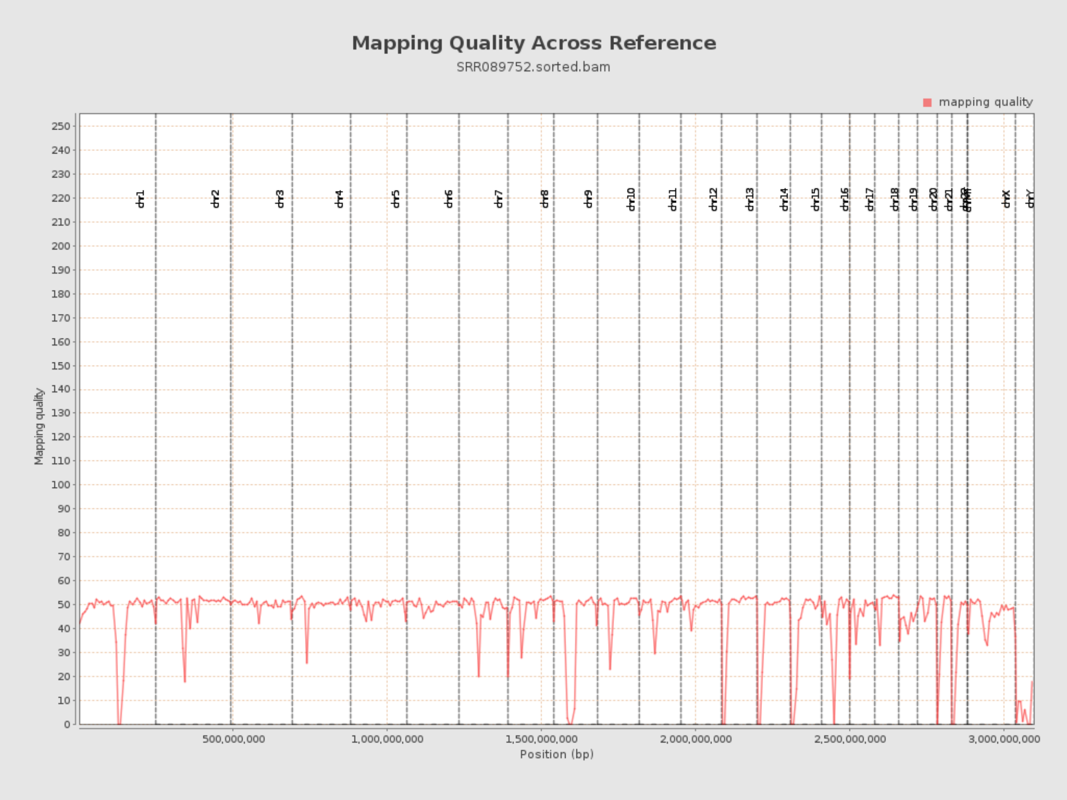
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram