Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 04:19:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3087911.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_SRR3087911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3087911.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 04:19:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3087911.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,894,225
Mapped reads	1,701,015 / 89.8%
Unmapped reads	193,210 / 10.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,982 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	80,095 / 4.23%
Duplication rate	3.99%
Clipped reads	807,164 / 42.61%

2.2. ACGT Content

Number/percentage of A's	29,820,389 / 26.6%
Number/percentage of C's	20,916,044 / 18.66%
Number/percentage of T's	35,245,199 / 31.44%
Number/percentage of G's	26,108,389 / 23.29%
Number/percentage of N's	5,575 / 0%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.2933

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

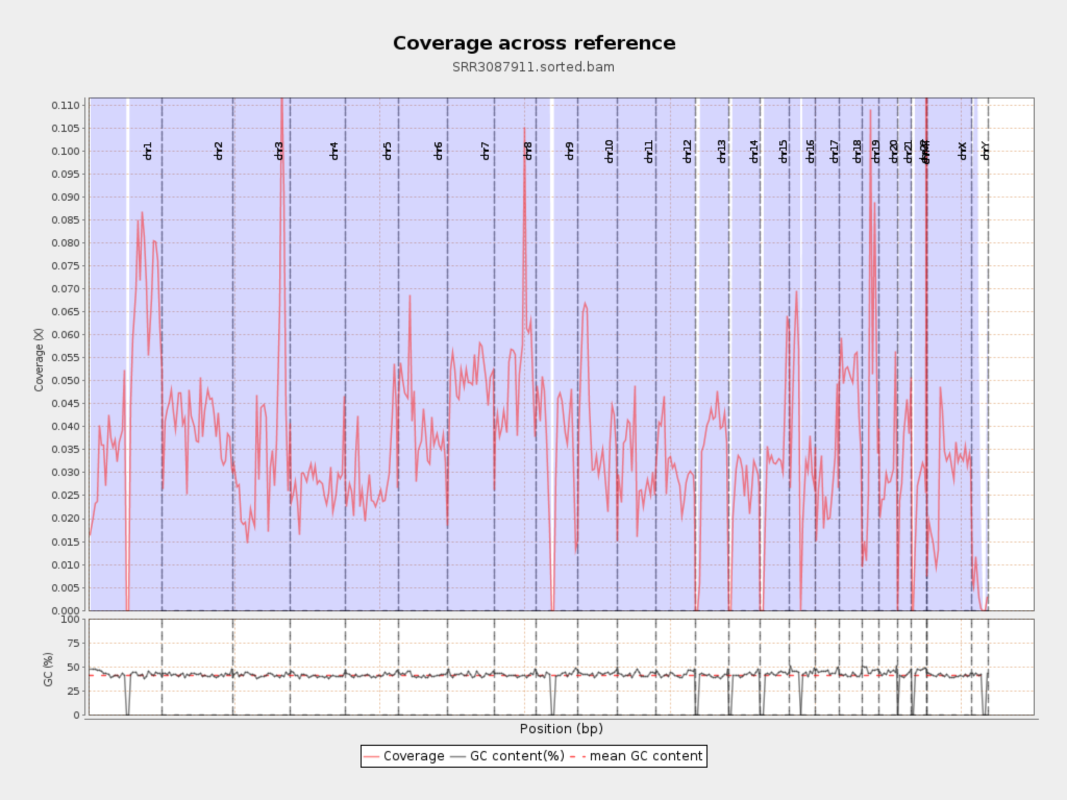
General error rate	0.71%
Mismatches	786,556
Insertions	8,370
Mapped reads with at least one insertion	0.49%
Deletions	25,162
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.86%

2.6. Chromosome stats

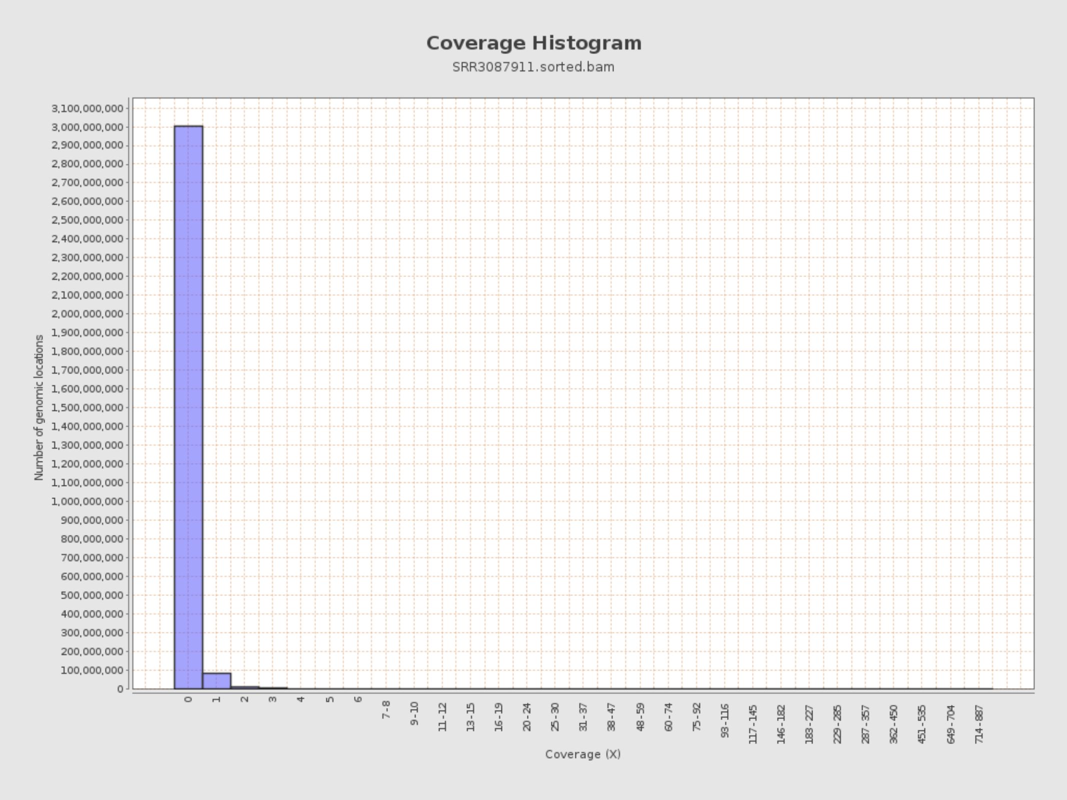
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11911077	0.0478	0.499
chr2	243199373	9886065	0.0407	0.4518
chr3	198022430	7234103	0.0365	0.223
chr4	191154276	5326811	0.0279	0.197
chr5	180915260	5198530	0.0287	0.1961
chr6	171115067	6970931	0.0407	0.2624
chr7	159138663	8099109	0.0509	0.3156

chr8	146364022	7623920	0.0521	0.2948
chr9	141213431	4870458	0.0345	0.258
chr10	135534747	5558389	0.041	0.26
chr11	135006516	4038229	0.0299	0.2363
chr12	133851895	4185283	0.0313	0.2041
chr13	115169878	3847733	0.0334	0.2107
chr14	107349540	2706626	0.0252	0.1846
chr15	102531392	3202522	0.0312	0.2132
chr16	90354753	3289669	0.0364	0.2297
chr17	81195210	2163519	0.0266	0.1965
chr18	78077248	3967153	0.0508	0.4525
chr19	59128983	2704096	0.0457	0.3542
chr20	63025520	1945597	0.0309	0.205
chr21	48129895	1601382	0.0333	0.2161
chr22	51304566	1095078	0.0213	0.1672
chrMT	16571	6325	0.3817	0.6677
chrX	155270560	4493939	0.0289	0.2042
chrY	59373566	209973	0.0035	0.0883

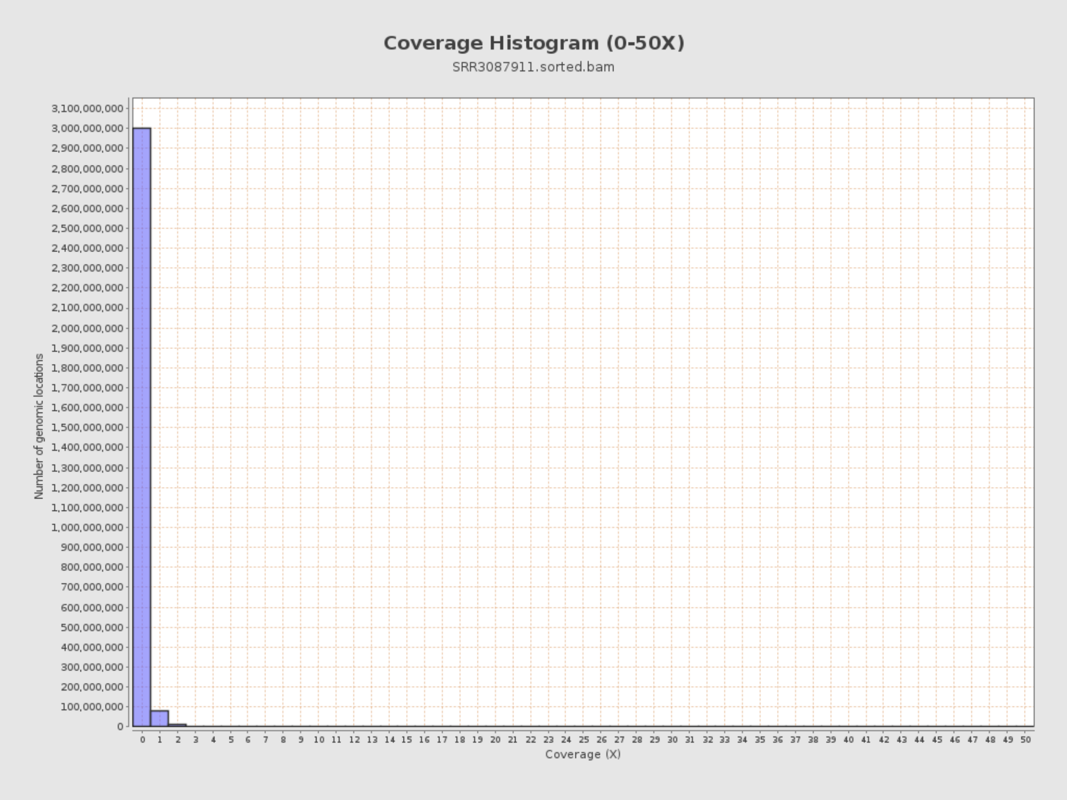
3. Results : Coverage across reference



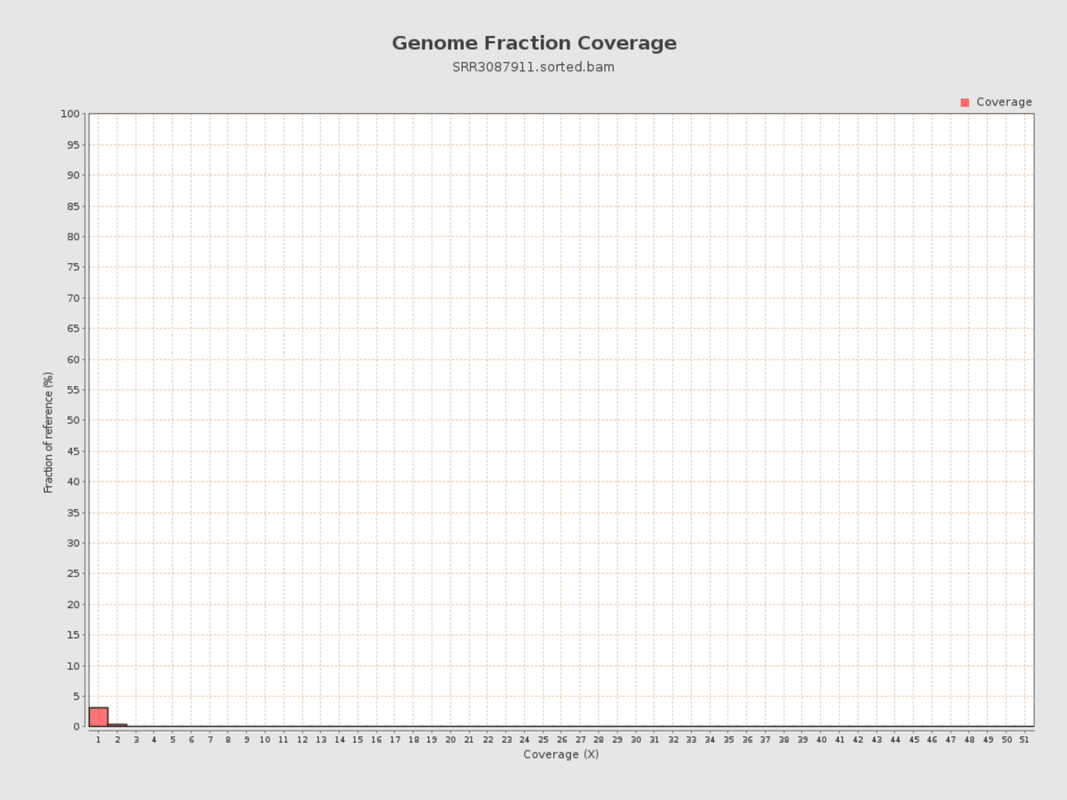
4. Results : Coverage Histogram



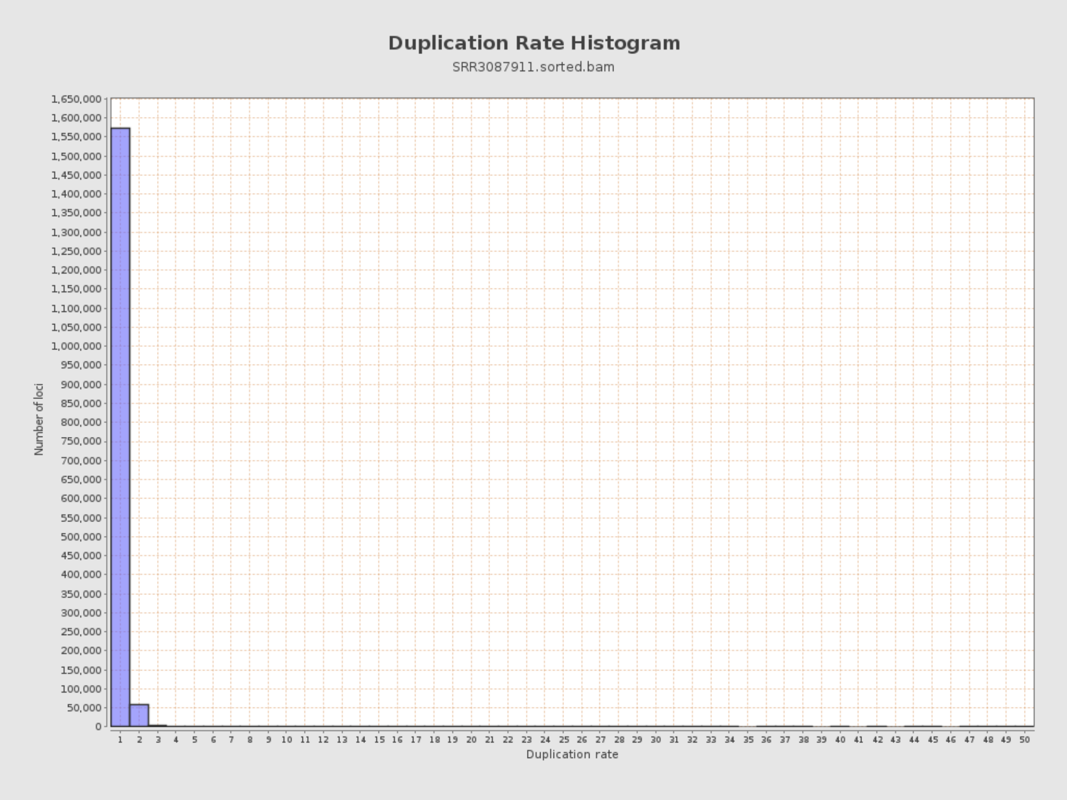
5. Results : Coverage Histogram (0-50X)



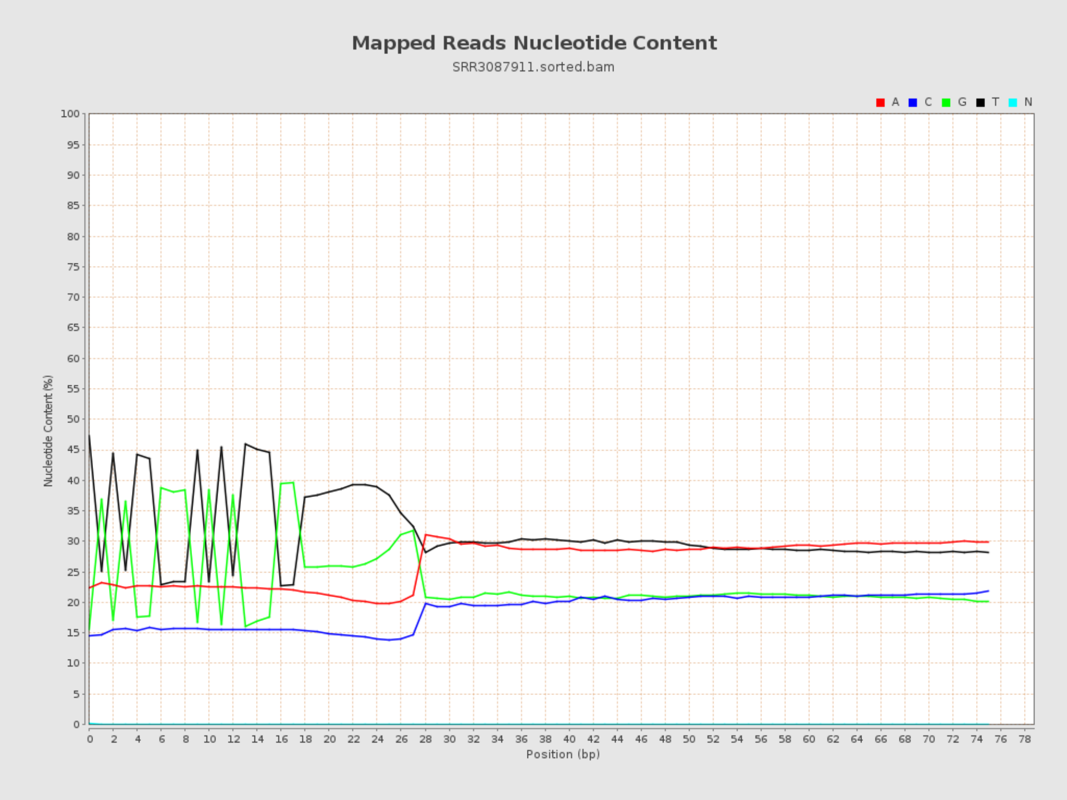
6. Results : Genome Fraction Coverage



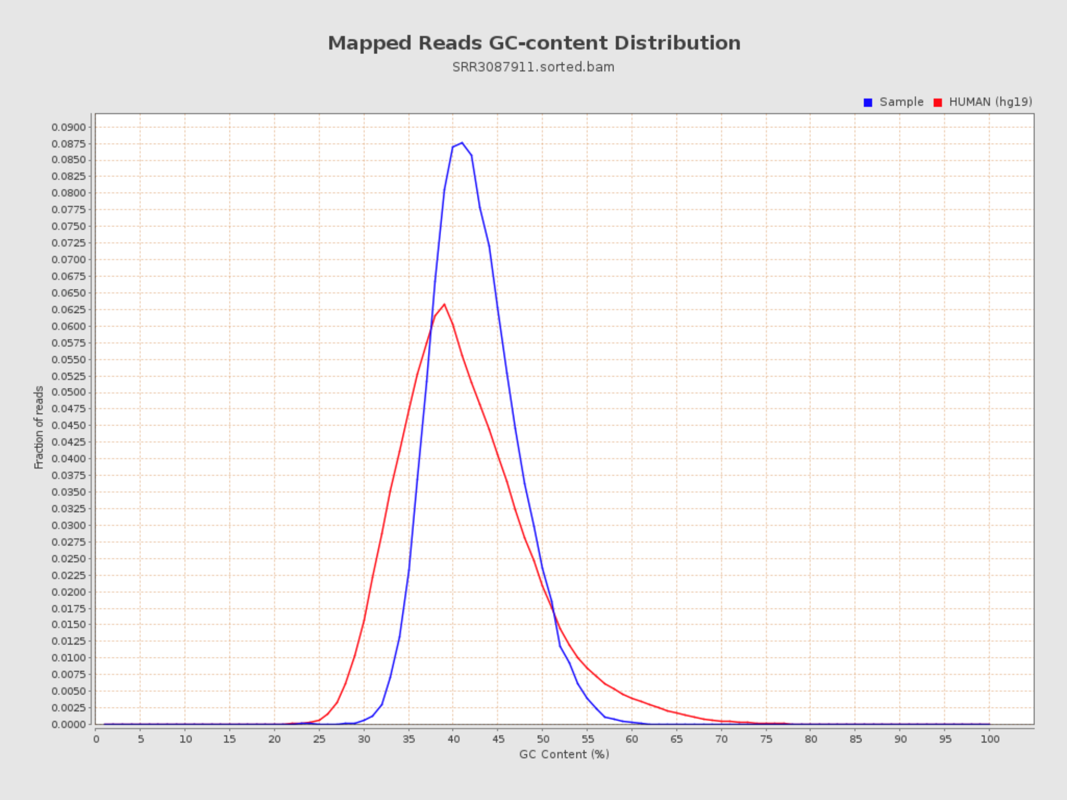
7. Results : Duplication Rate Histogram



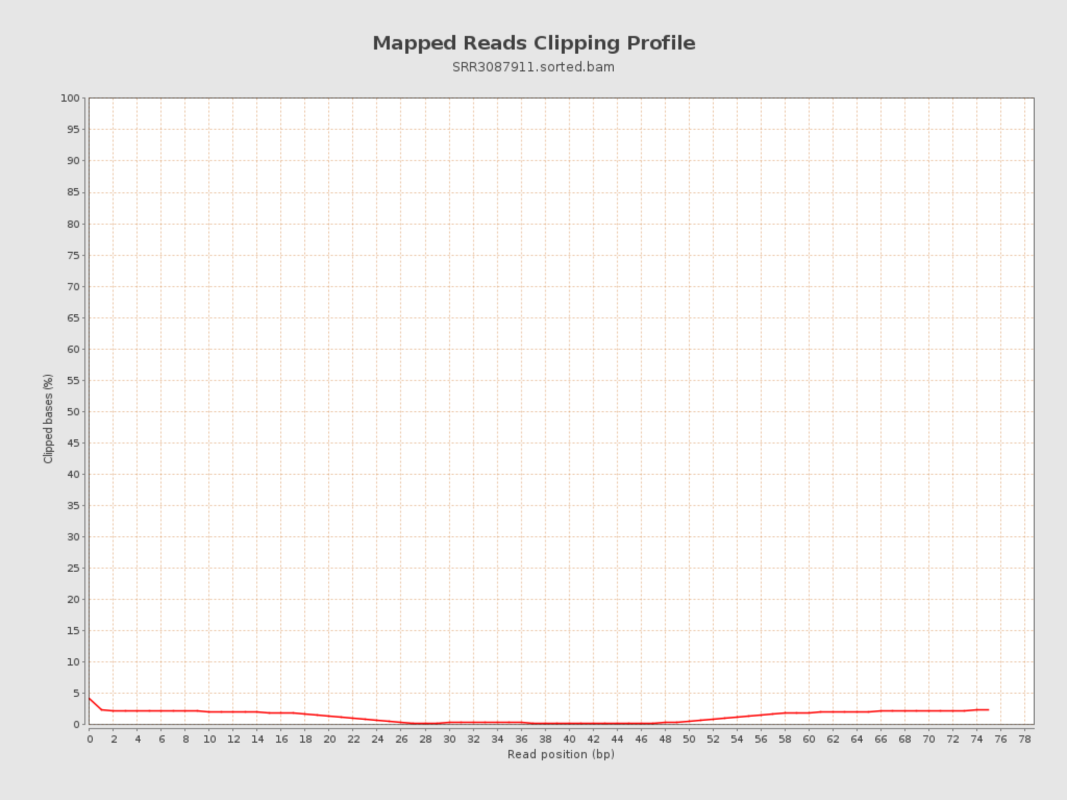
8. Results : Mapped Reads Nucleotide Content



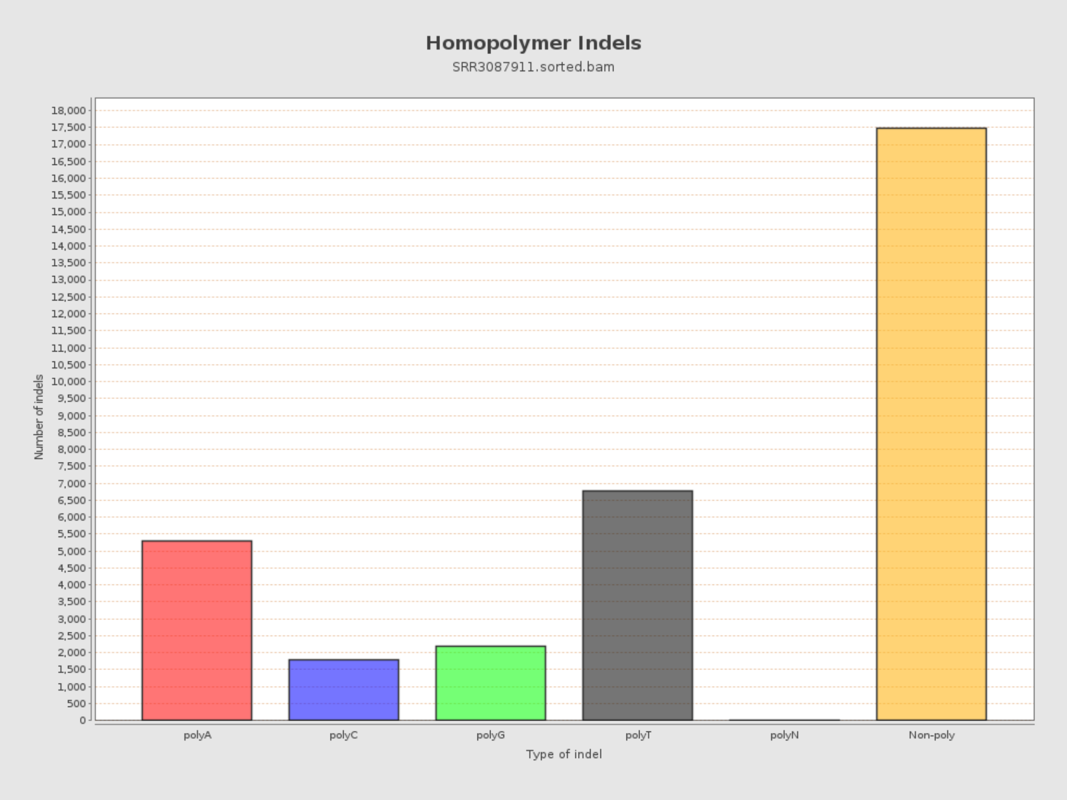
9. Results : Mapped Reads GC-content Distribution



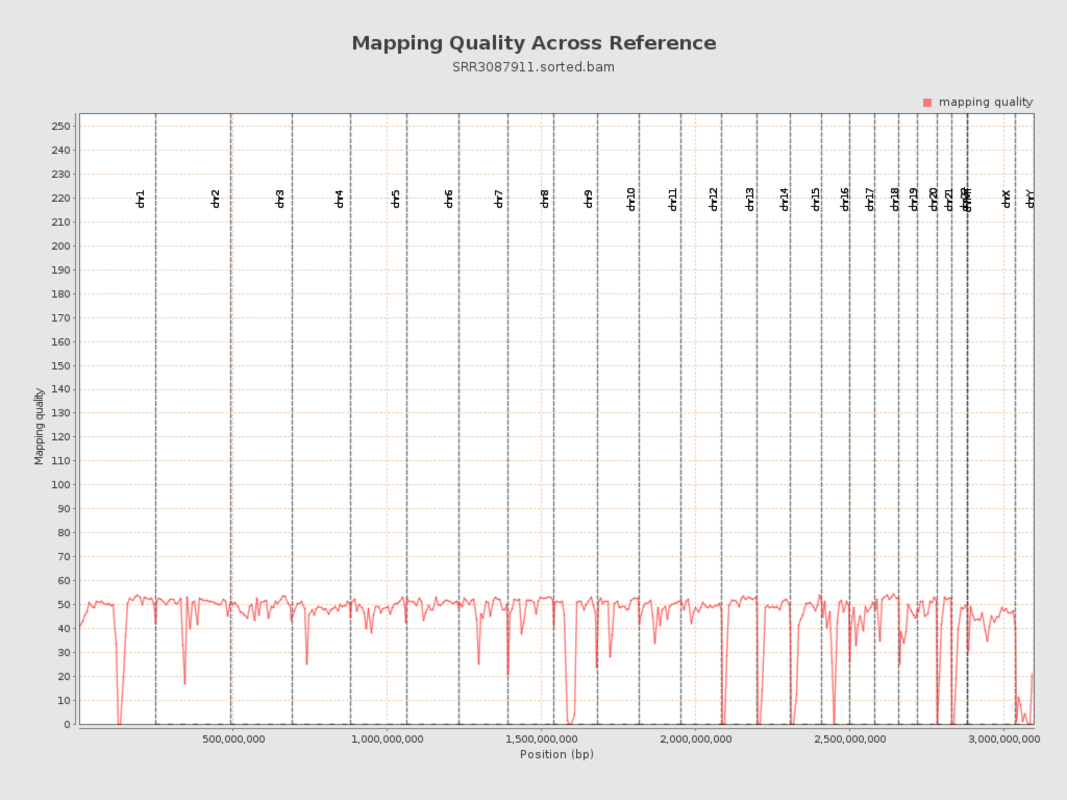
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram