Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 04:26:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3087917.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_SRR3087917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3087917.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 04:26:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3087917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,621,739
Mapped reads	1,436,769 / 88.59%
Unmapped reads	184,970 / 11.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,768 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	68,145 / 4.2%
Duplication rate	4.14%
Clipped reads	656,428 / 40.48%

2.2. ACGT Content

Number/percentage of A's	25,313,391 / 26.6%
Number/percentage of C's	17,972,779 / 18.89%
Number/percentage of T's	29,695,352 / 31.21%
Number/percentage of G's	22,174,473 / 23.3%
Number/percentage of N's	4,429 / 0%
GC Percentage	42.19%

2.3. Coverage

Mean	0.0308

Standard Deviation	0.2497

2.4. Mapping Quality

Mean Mapping Quality	45.33

2.5. Mismatches and indels

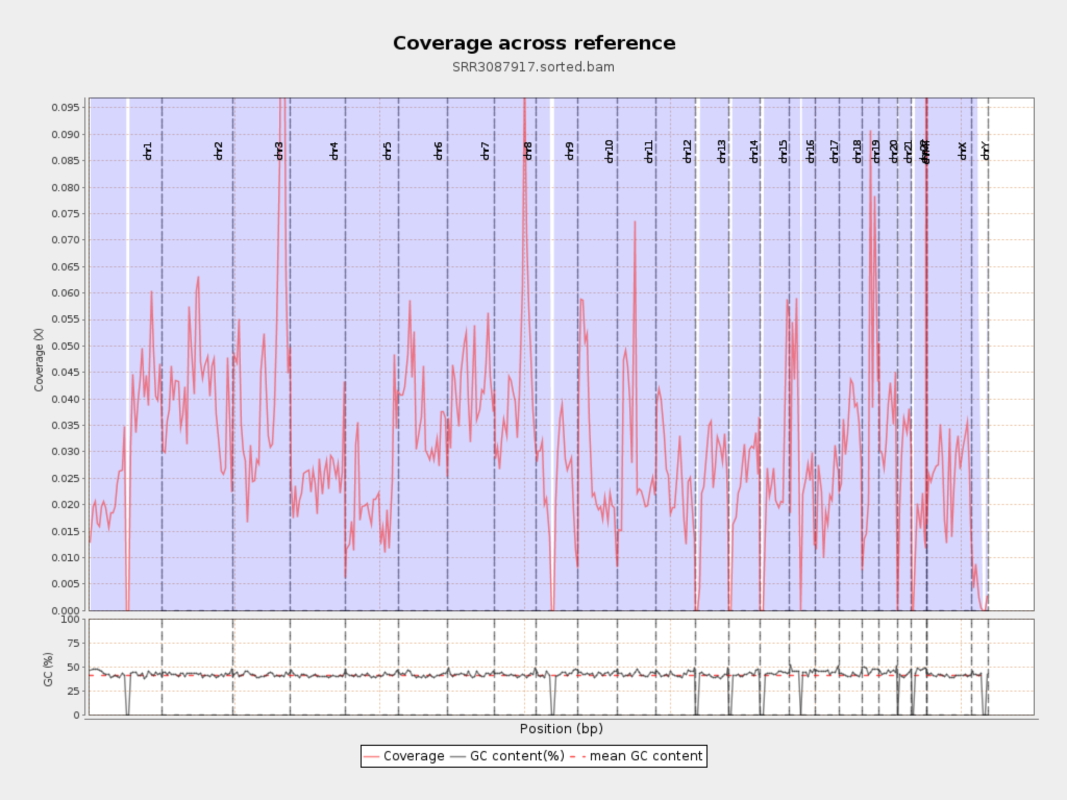
General error rate	0.68%
Mismatches	640,167
Insertions	6,646
Mapped reads with at least one insertion	0.46%
Deletions	19,909
Mapped reads with at least one deletion	1.37%
Homopolymer indels	48.23%

2.6. Chromosome stats

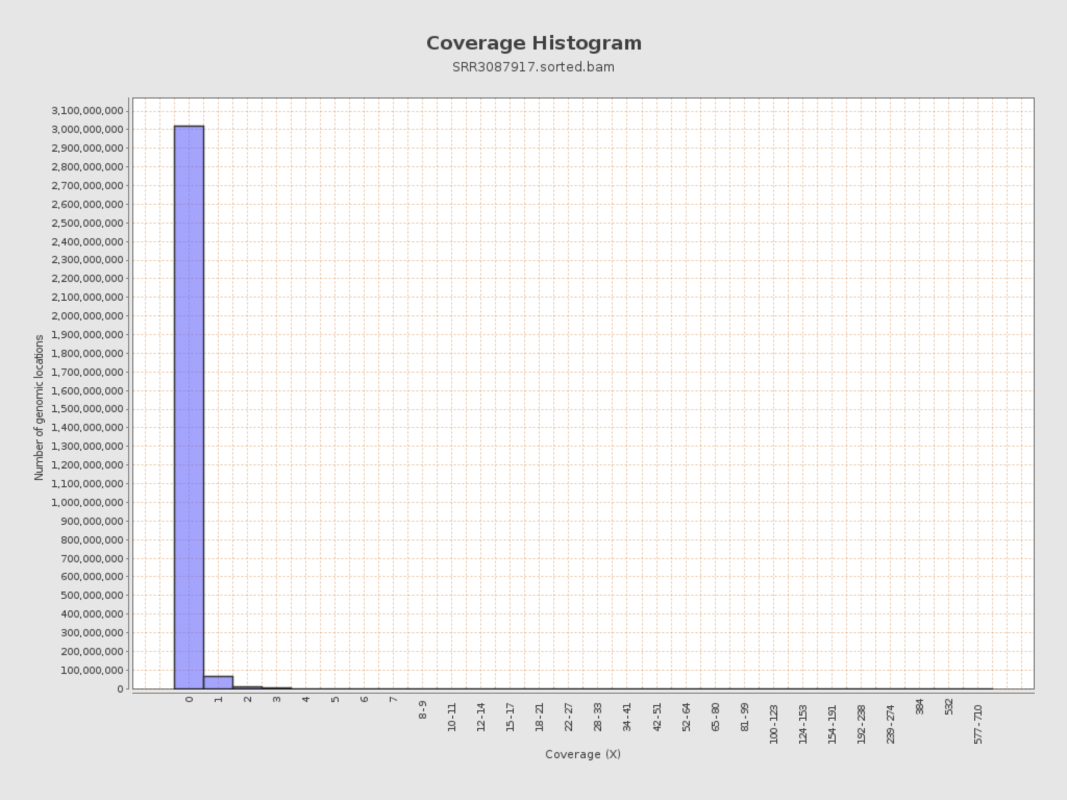
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7259660	0.0291	0.3178
chr2	243199373	9948115	0.0409	0.3857
chr3	198022430	9332451	0.0471	0.2601
chr4	191154276	4781584	0.025	0.1877
chr5	180915260	3751754	0.0207	0.1681
chr6	171115067	6438151	0.0376	0.2534
chr7	159138663	6755356	0.0424	0.3377

chr8	146364022	6483252	0.0443	0.2741
chr9	141213431	3254887	0.023	0.201
chr10	135534747	4017556	0.0296	0.216
chr11	135006516	4011405	0.0297	0.2272
chr12	133851895	3454798	0.0258	0.1884
chr13	115169878	2777408	0.0241	0.1811
chr14	107349540	2469638	0.023	0.1785
chr15	102531392	2441341	0.0238	0.188
chr16	90354753	2652975	0.0294	0.2071
chr17	81195210	1712184	0.0211	0.1721
chr18	78077248	2713546	0.0348	0.3195
chr19	59128983	2444092	0.0413	0.2907
chr20	63025520	2169417	0.0344	0.2218
chr21	48129895	1372394	0.0285	0.2041
chr22	51304566	657657	0.0128	0.131
chrMT	16571	7855	0.474	1.2692
chrX	155270560	4097466	0.0264	0.1933
chrY	59373566	188840	0.0032	0.0735

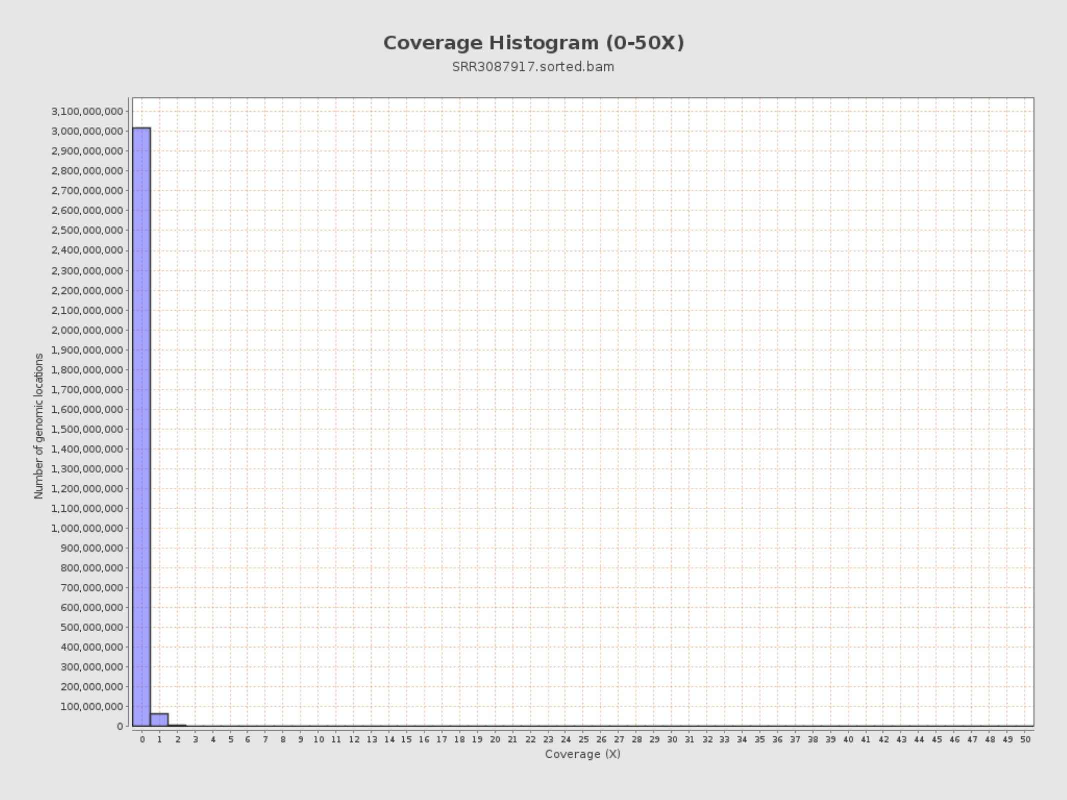
3. Results : Coverage across reference



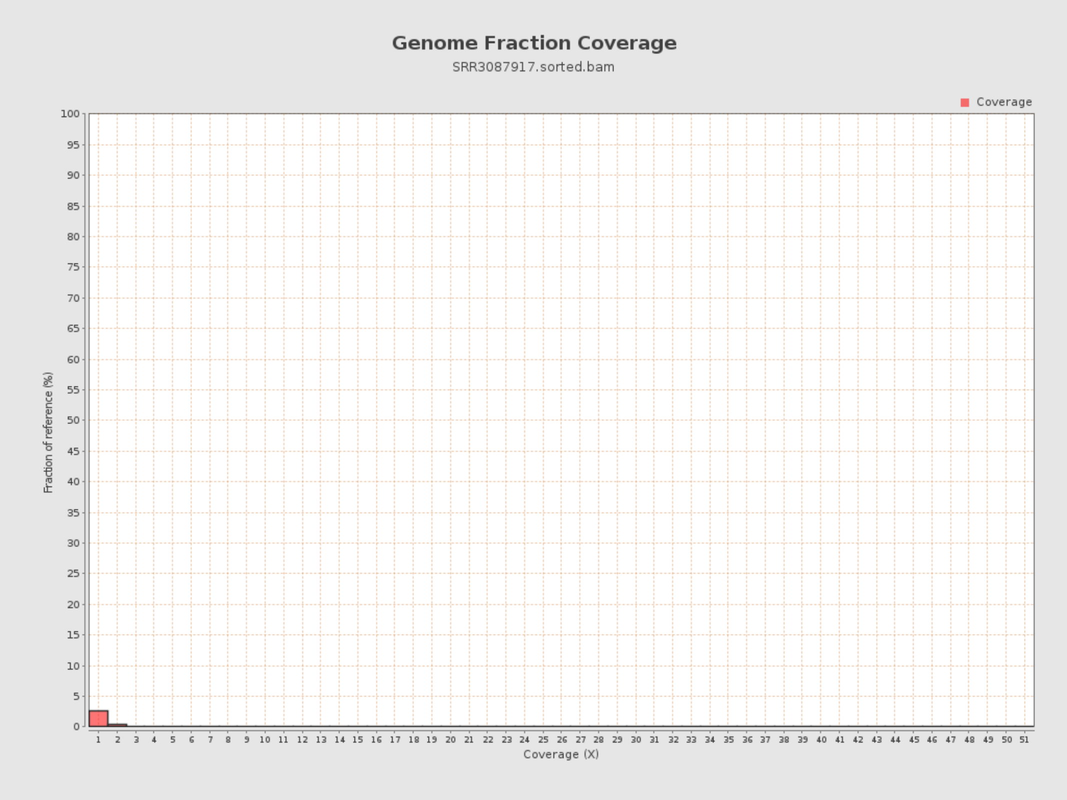
4. Results : Coverage Histogram



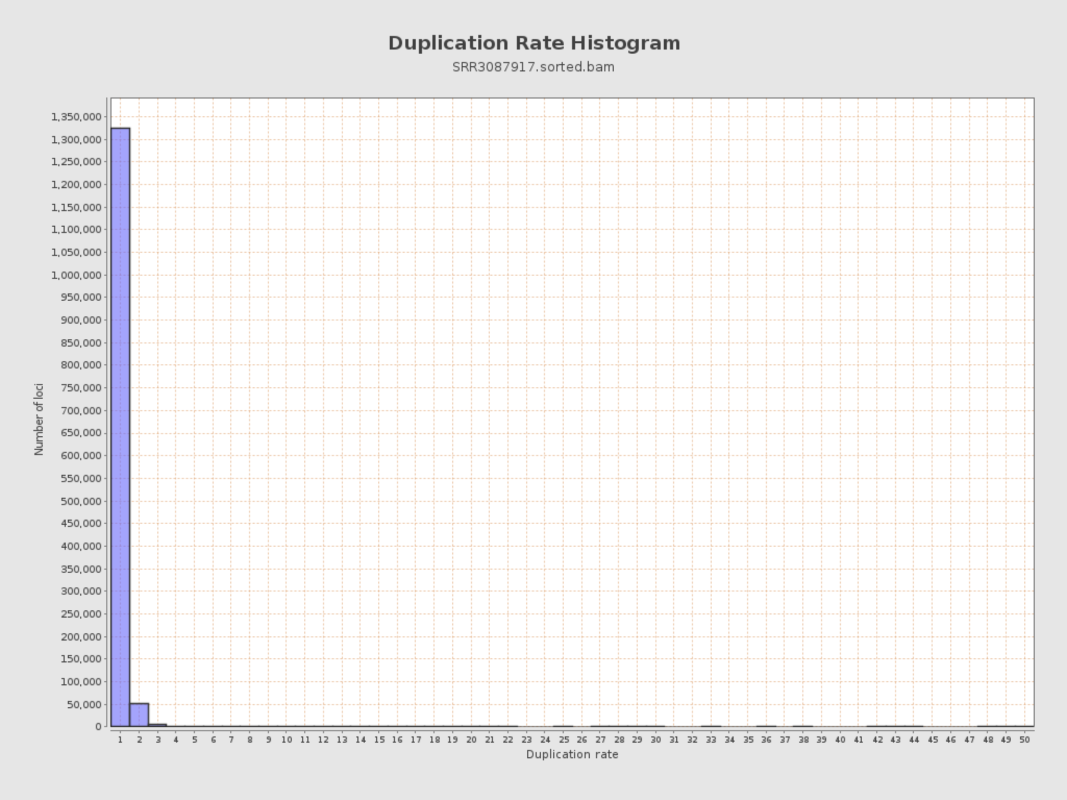
5. Results : Coverage Histogram (0-50X)



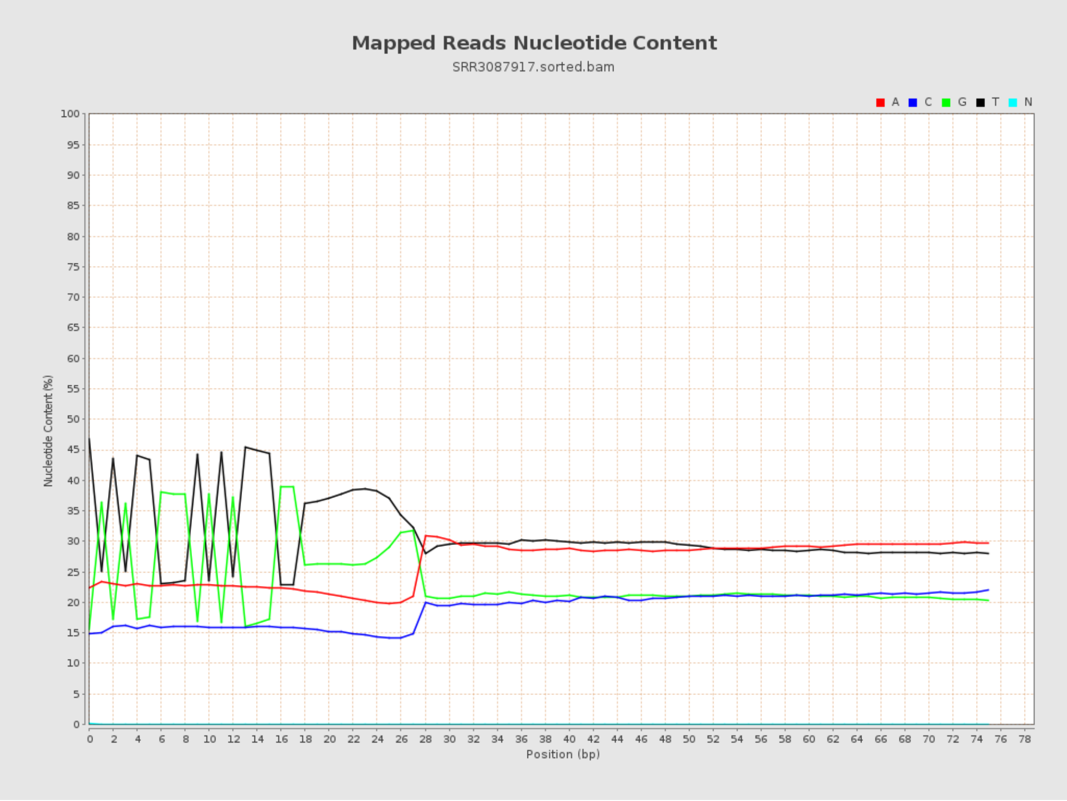
6. Results : Genome Fraction Coverage



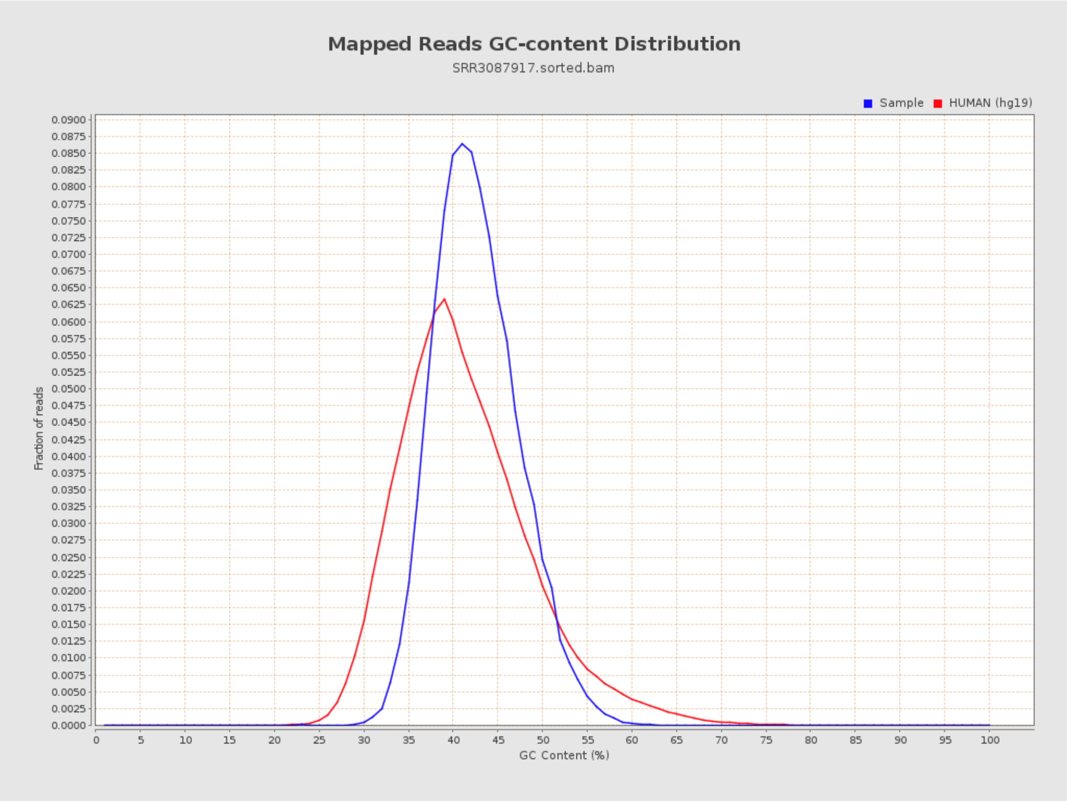
7. Results : Duplication Rate Histogram



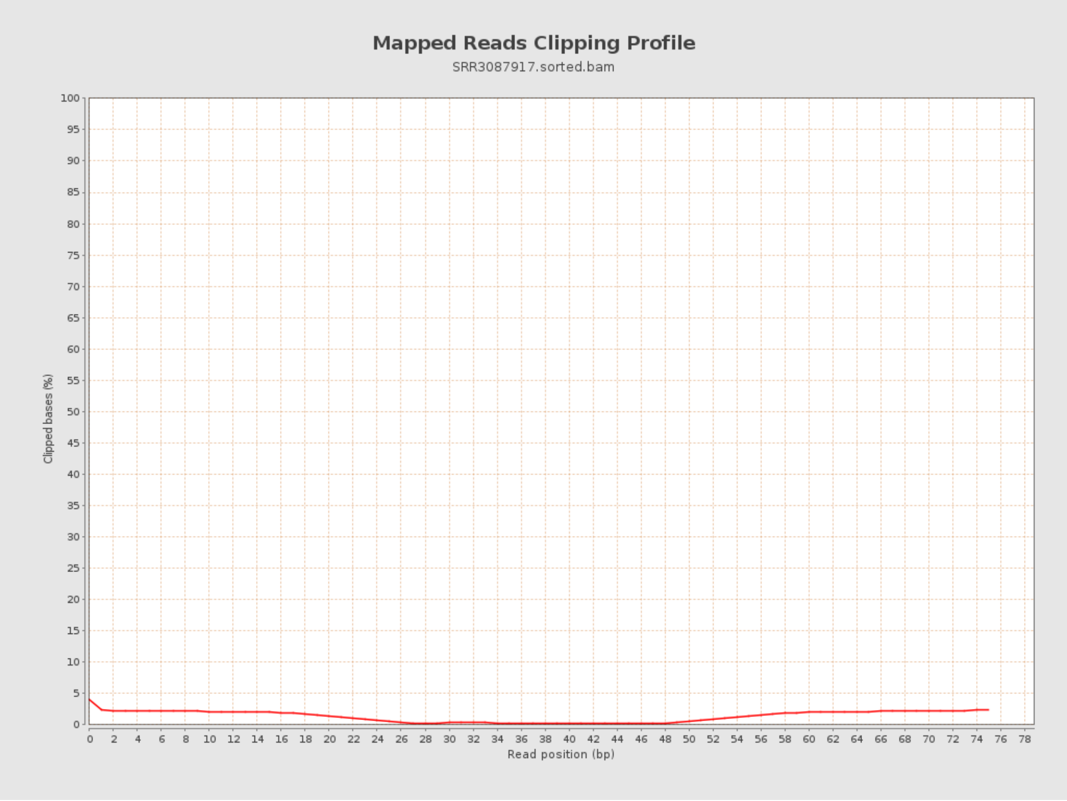
8. Results : Mapped Reads Nucleotide Content



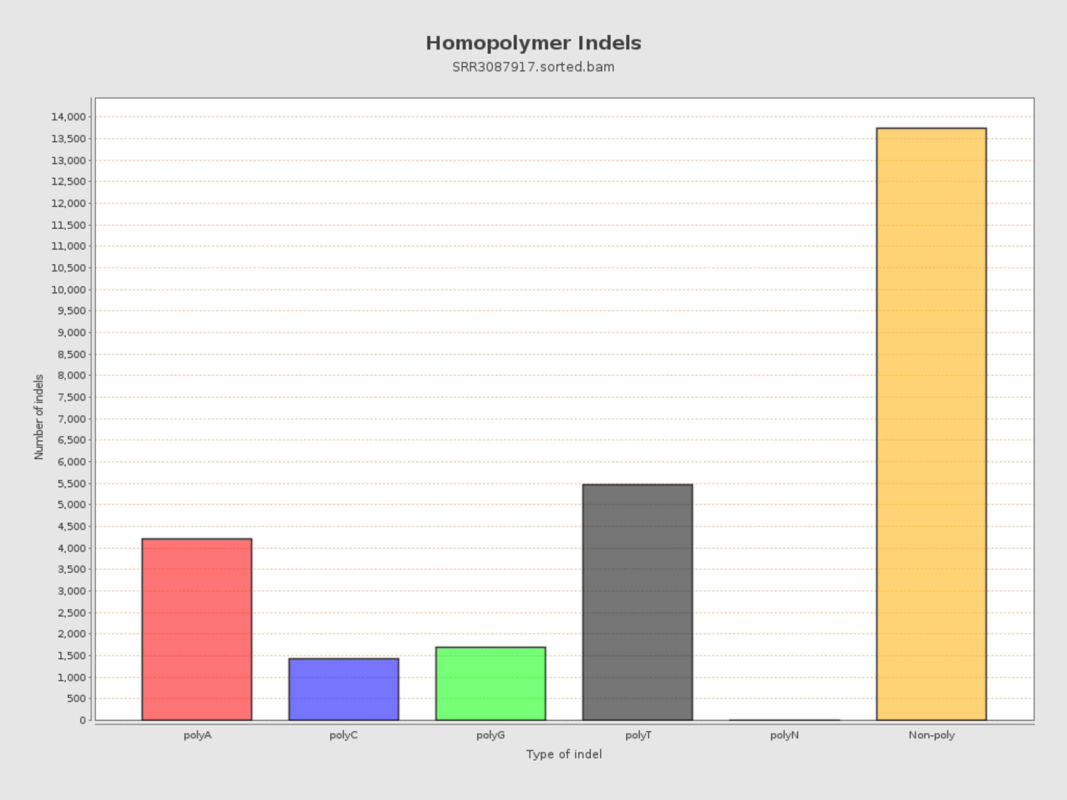
9. Results : Mapped Reads GC-content Distribution



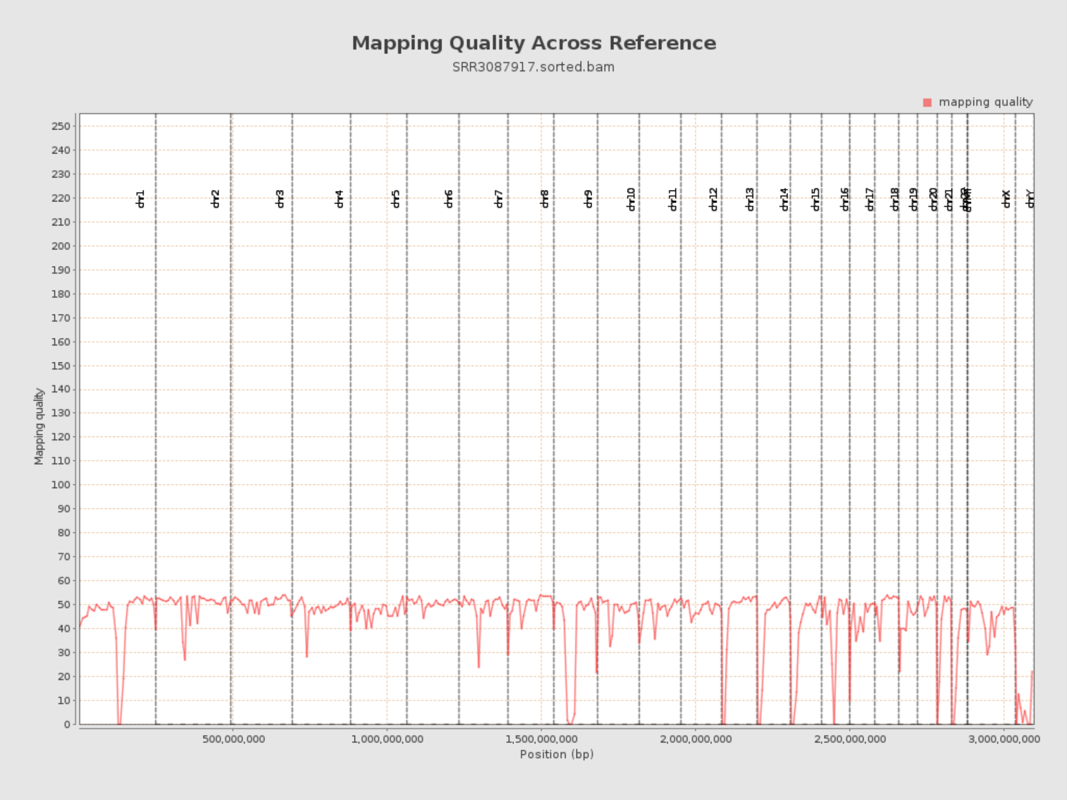
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram