Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 04:32:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3087918.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_SRR3087918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3087918.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 04:32:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3087918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,860,912
Mapped reads	1,666,811 / 89.57%
Unmapped reads	194,101 / 10.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,744 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	81,851 / 4.4%
Duplication rate	4.22%
Clipped reads	782,463 / 42.05%

2.2. ACGT Content

Number/percentage of A's	29,258,651 / 26.6%
Number/percentage of C's	20,688,581 / 18.81%
Number/percentage of T's	34,437,128 / 31.31%
Number/percentage of G's	25,596,223 / 23.27%
Number/percentage of N's	5,105 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0355

Standard Deviation	0.2931

2.4. Mapping Quality

Mean Mapping Quality	45.03

2.5. Mismatches and indels

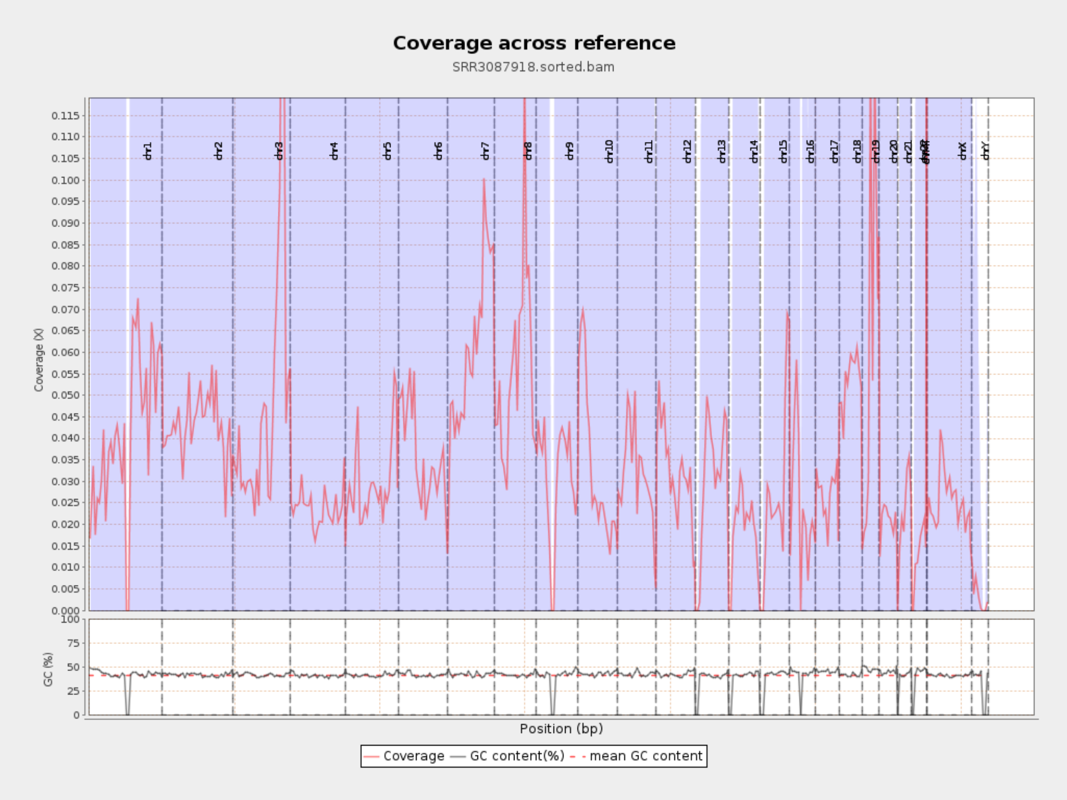
General error rate	0.7%
Mismatches	754,544
Insertions	7,689
Mapped reads with at least one insertion	0.46%
Deletions	23,777
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.15%

2.6. Chromosome stats

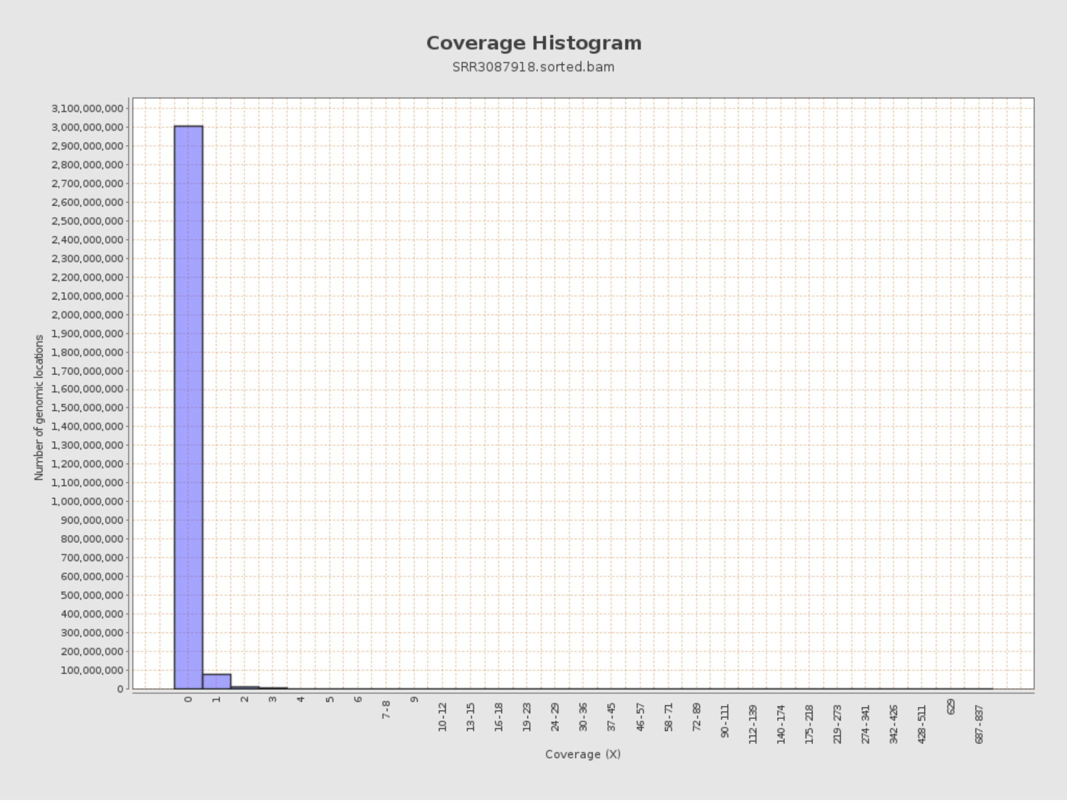
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10164336	0.0408	0.4902
chr2	243199373	10470256	0.0431	0.4414
chr3	198022430	9727783	0.0491	0.2663
chr4	191154276	4545004	0.0238	0.1841
chr5	180915260	5428180	0.03	0.2039
chr6	171115067	6223882	0.0364	0.2582
chr7	159138663	9821015	0.0617	0.4182

chr8	146364022	8336462	0.057	0.3054
chr9	141213431	4337100	0.0307	0.2308
chr10	135534747	4613628	0.034	0.2426
chr11	135006516	4275569	0.0317	0.2382
chr12	133851895	4354502	0.0325	0.2125
chr13	115169878	3473120	0.0302	0.2044
chr14	107349540	2011205	0.0187	0.1605
chr15	102531392	2631308	0.0257	0.1973
chr16	90354753	2257023	0.025	0.1884
chr17	81195210	2178781	0.0268	0.2035
chr18	78077248	4207468	0.0539	0.3519
chr19	59128983	3734724	0.0632	0.4078
chr20	63025520	1329221	0.0211	0.1712
chr21	48129895	1087690	0.0226	0.1781
chr22	51304566	652155	0.0127	0.1324
chrMT	16571	3795	0.229	0.5741
chrX	155270560	3980532	0.0256	0.195
chrY	59373566	179118	0.003	0.0665

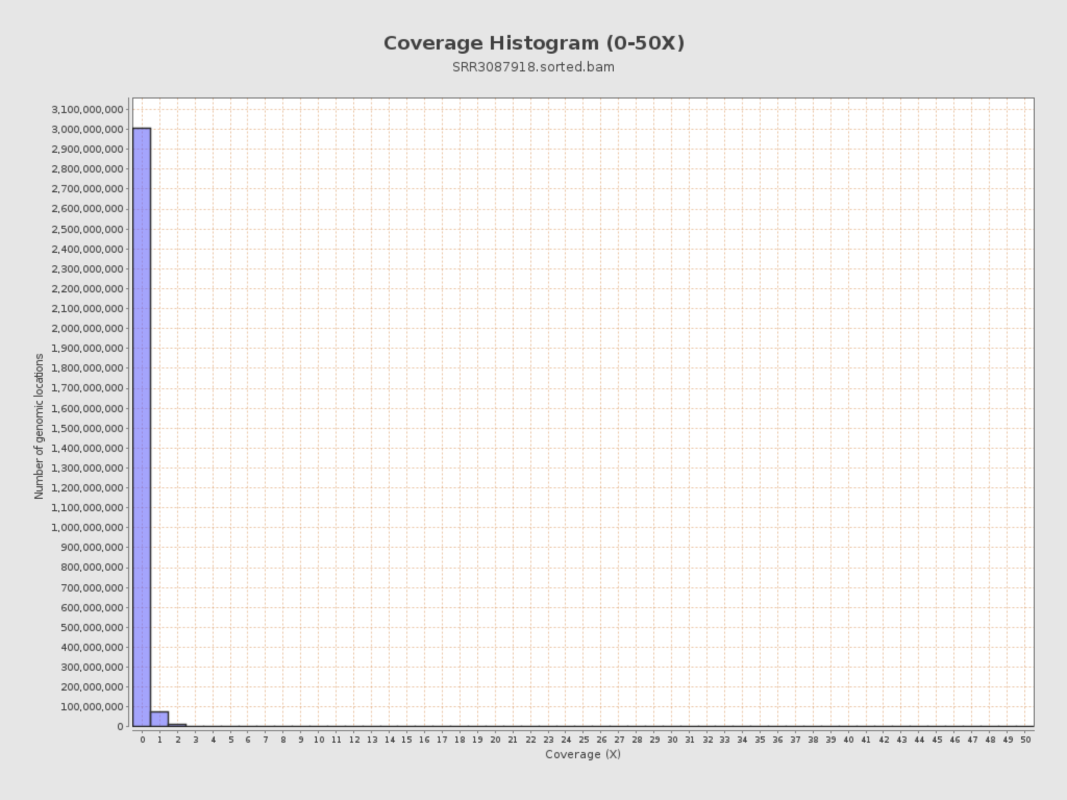
3. Results : Coverage across reference



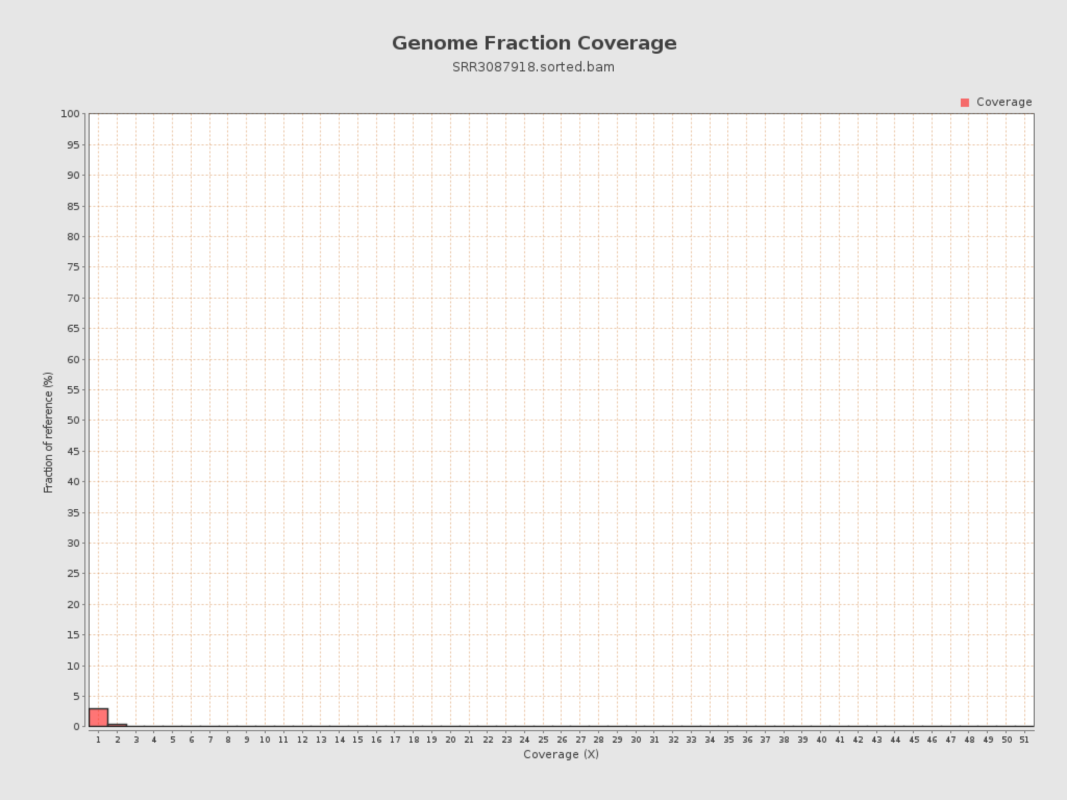
4. Results : Coverage Histogram



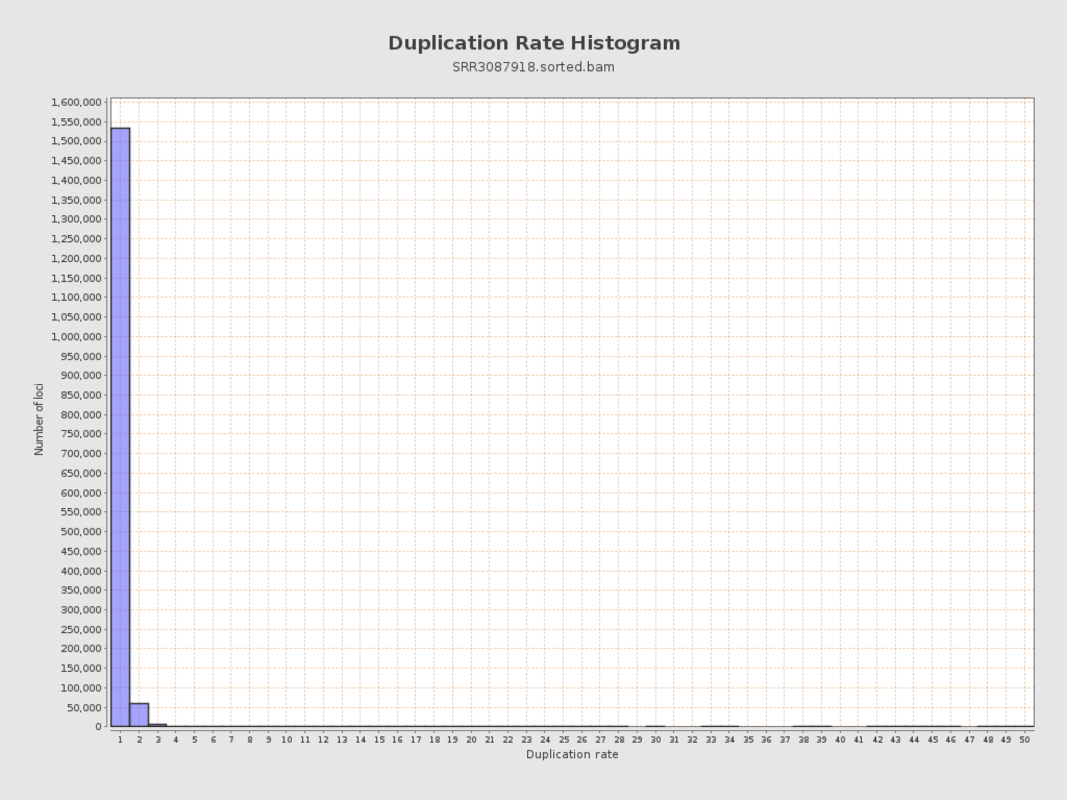
5. Results : Coverage Histogram (0-50X)



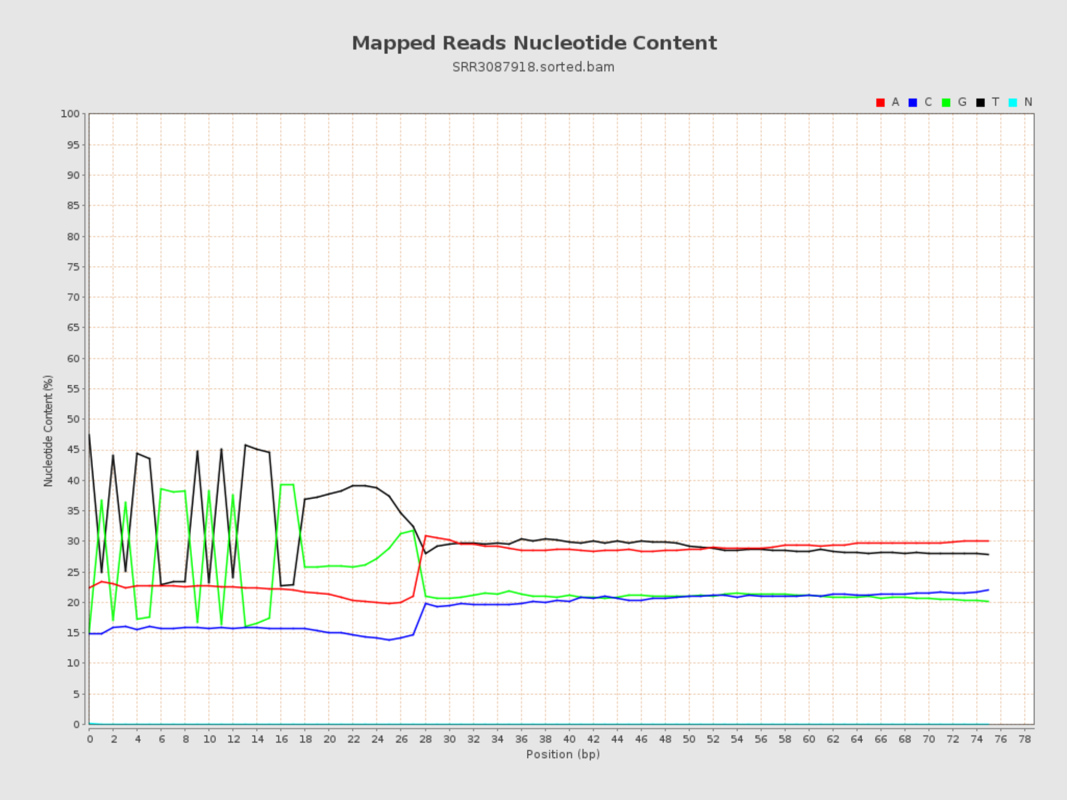
6. Results : Genome Fraction Coverage



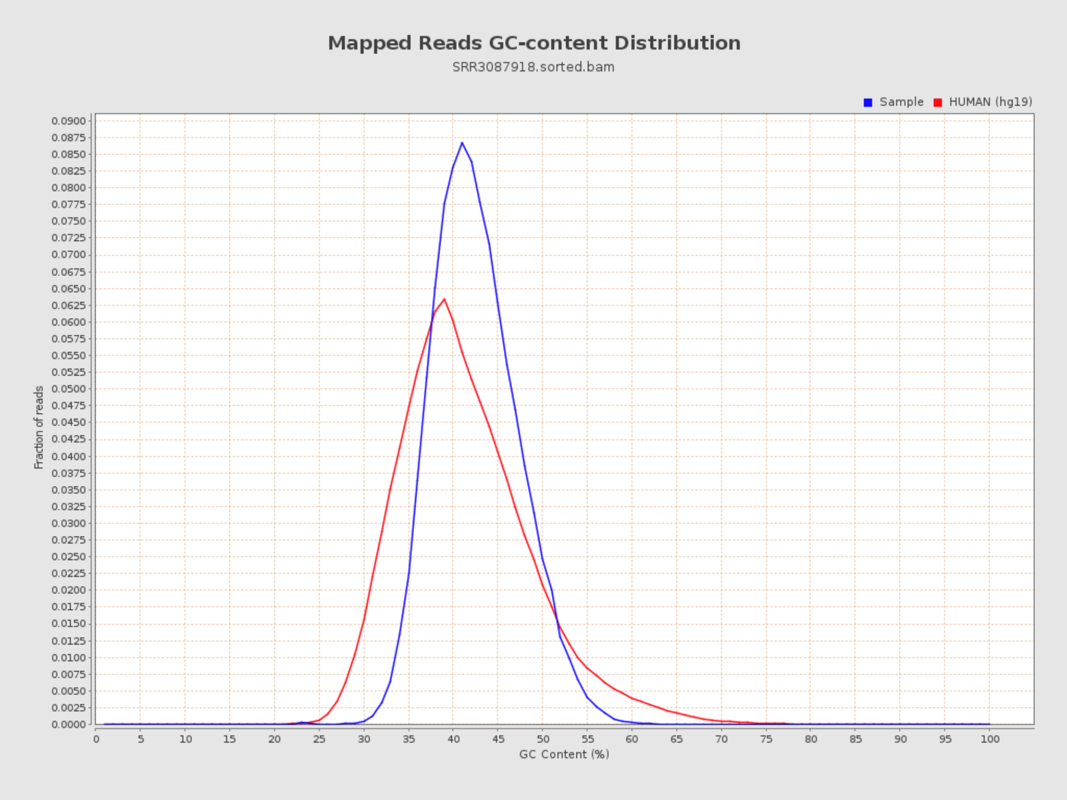
7. Results : Duplication Rate Histogram



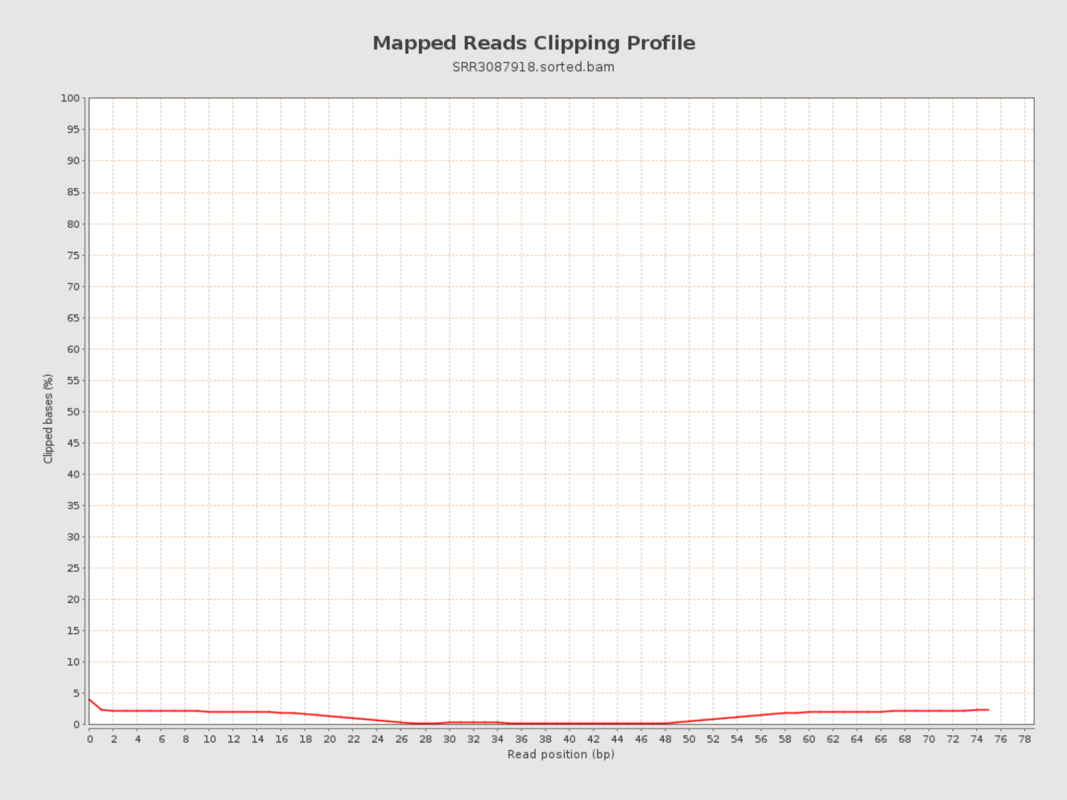
8. Results : Mapped Reads Nucleotide Content



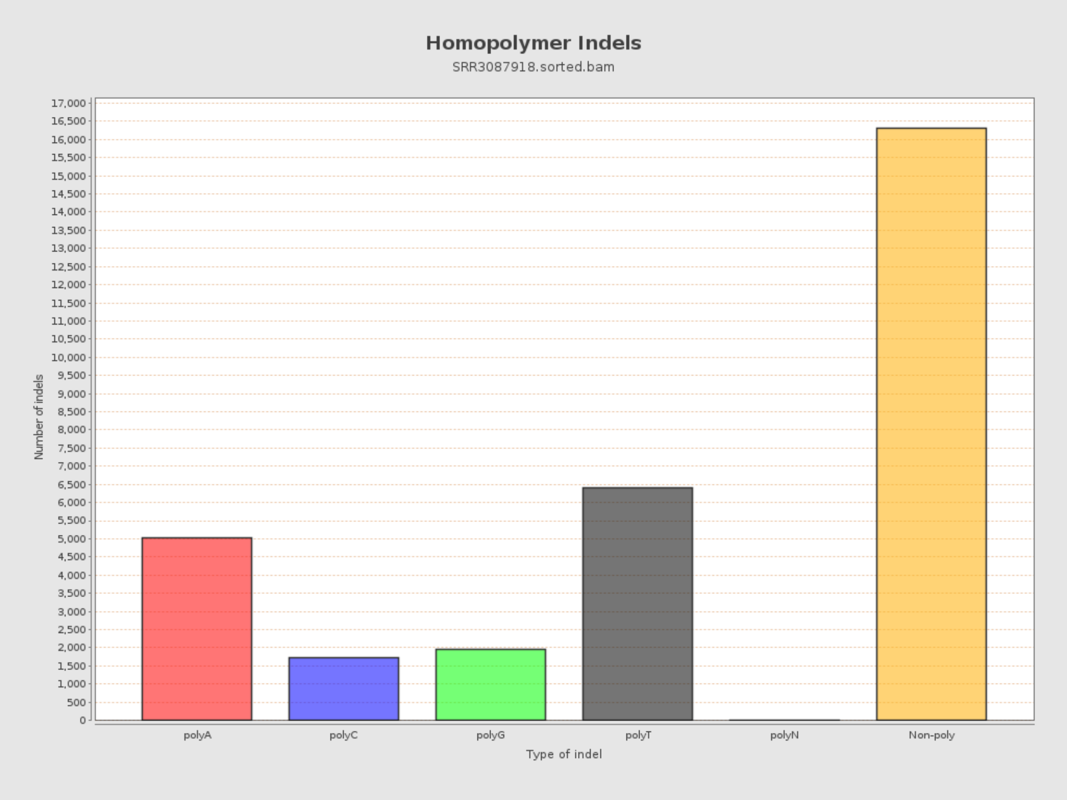
9. Results : Mapped Reads GC-content Distribution



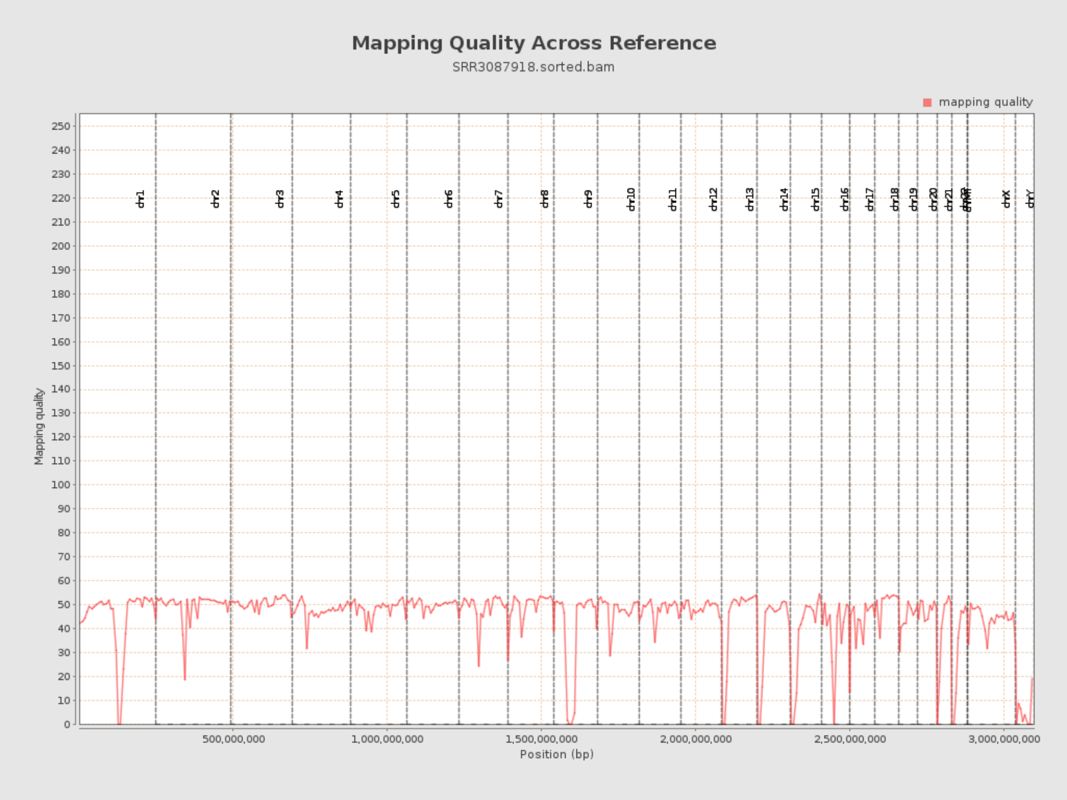
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram