Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:27:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084380.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_SRR3084380 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084380.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:27:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084380.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,951,435
Mapped reads	1,735,853 / 58.81%
Unmapped reads	1,215,582 / 41.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,625 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	65,668 / 2.22%
Duplication rate	3.14%
Clipped reads	939,577 / 31.83%

2.2. ACGT Content

Number/percentage of A's	30,708,357 / 27.89%
Number/percentage of C's	20,880,791 / 18.96%
Number/percentage of T's	33,794,346 / 30.69%
Number/percentage of G's	24,734,094 / 22.46%
Number/percentage of N's	1,276 / 0%
GC Percentage	41.42%

2.3. Coverage

Mean	0.0356

Standard Deviation	0.2804

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

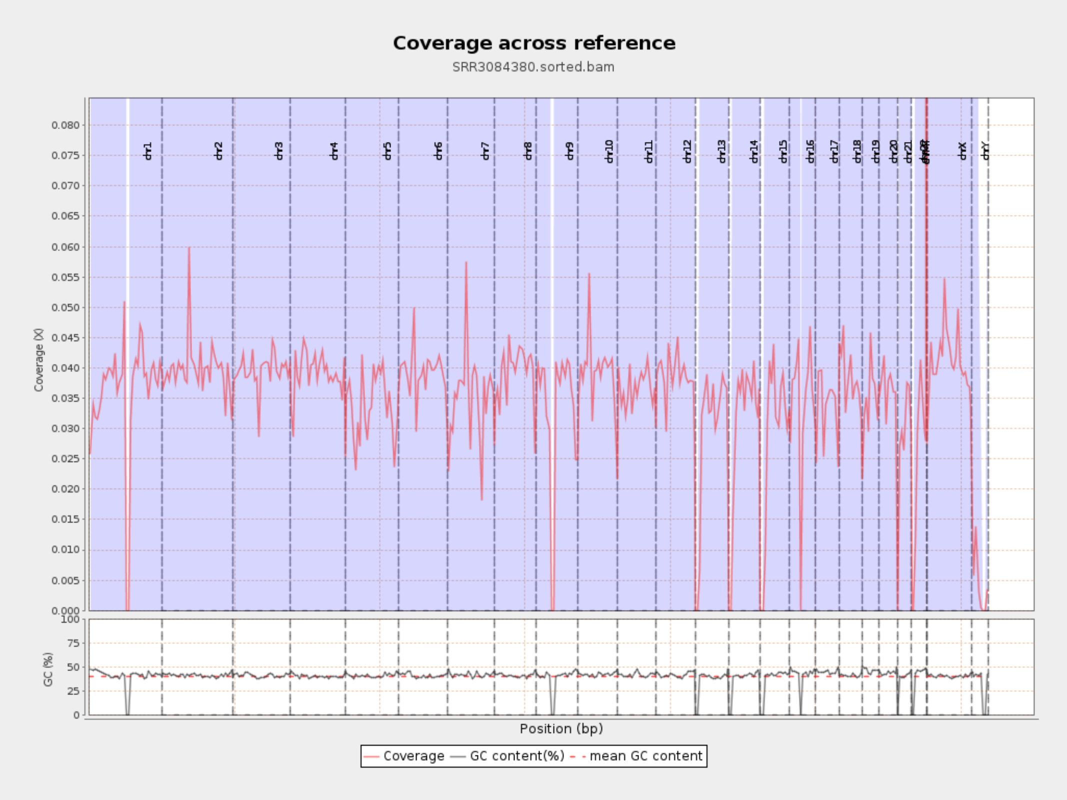
General error rate	0.83%
Mismatches	900,084
Insertions	8,070
Mapped reads with at least one insertion	0.46%
Deletions	22,918
Mapped reads with at least one deletion	1.31%
Homopolymer indels	46.72%

2.6. Chromosome stats

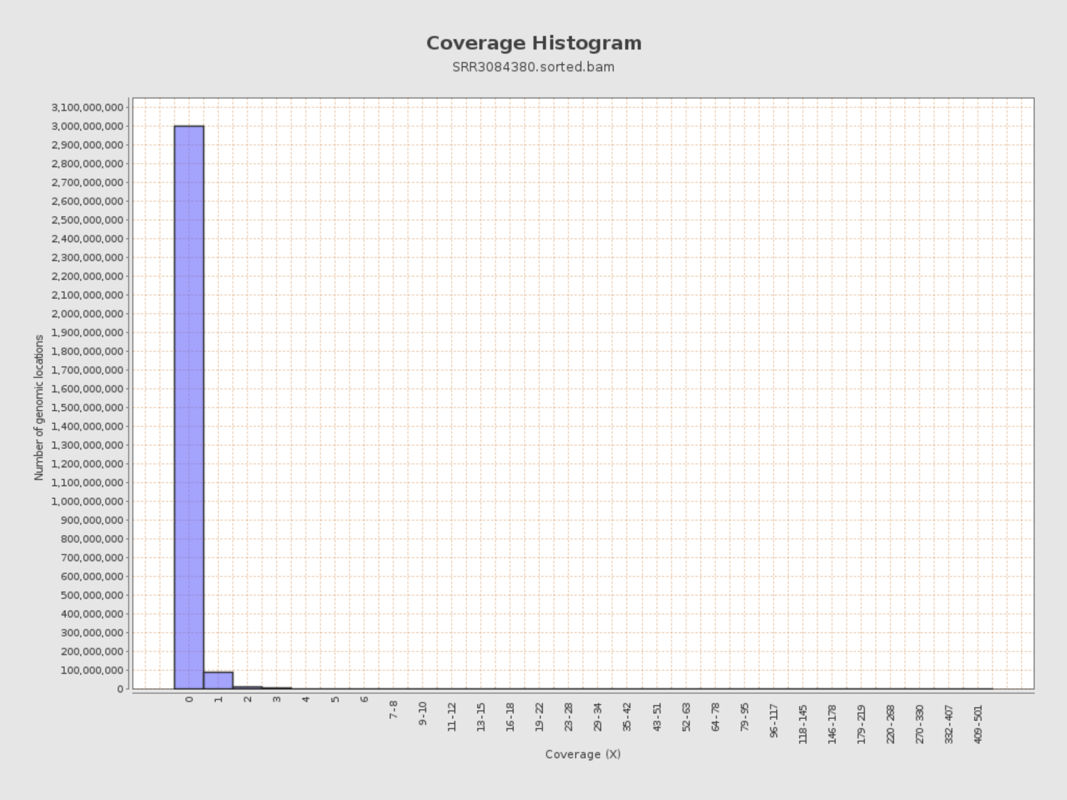
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8939657	0.0359	0.411
chr2	243199373	9700069	0.0399	0.3597
chr3	198022430	7833904	0.0396	0.2208
chr4	191154276	7474739	0.0391	0.2285
chr5	180915260	6066554	0.0335	0.2044
chr6	171115067	6722155	0.0393	0.2581
chr7	159138663	5616712	0.0353	0.3511

chr8	146364022	5751408	0.0393	0.2813
chr9	141213431	4652845	0.0329	0.2768
chr10	135534747	5373774	0.0396	0.2882
chr11	135006516	4924426	0.0365	0.2584
chr12	133851895	5194088	0.0388	0.2223
chr13	115169878	3338933	0.029	0.1898
chr14	107349540	3239128	0.0302	0.2014
chr15	102531392	2927259	0.0285	0.1928
chr16	90354753	3105748	0.0344	0.2205
chr17	81195210	2677655	0.033	0.2178
chr18	78077248	2992890	0.0383	0.4877
chr19	59128983	2074257	0.0351	0.3372
chr20	63025520	2281250	0.0362	0.2185
chr21	48129895	1365965	0.0284	0.1964
chr22	51304566	1186330	0.0231	0.1683
chrMT	16571	55651	3.3583	2.622
chrX	155270560	6389336	0.0411	0.243
chrY	59373566	270882	0.0046	0.1014

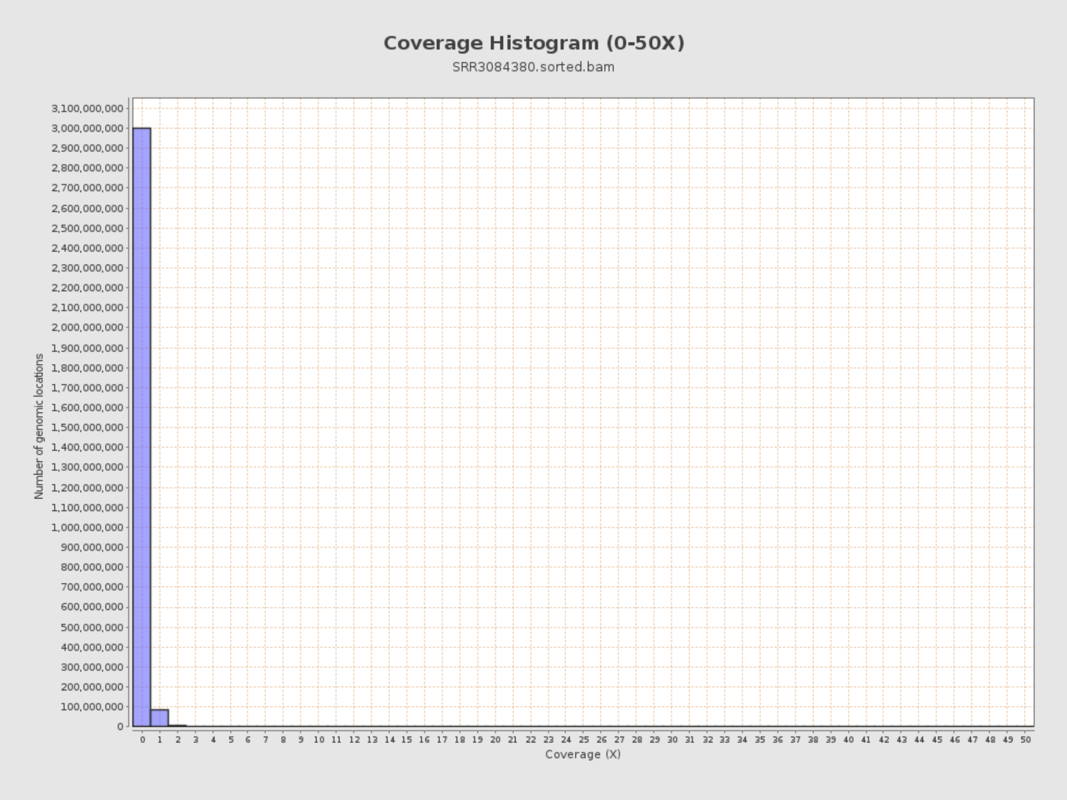
3. Results : Coverage across reference



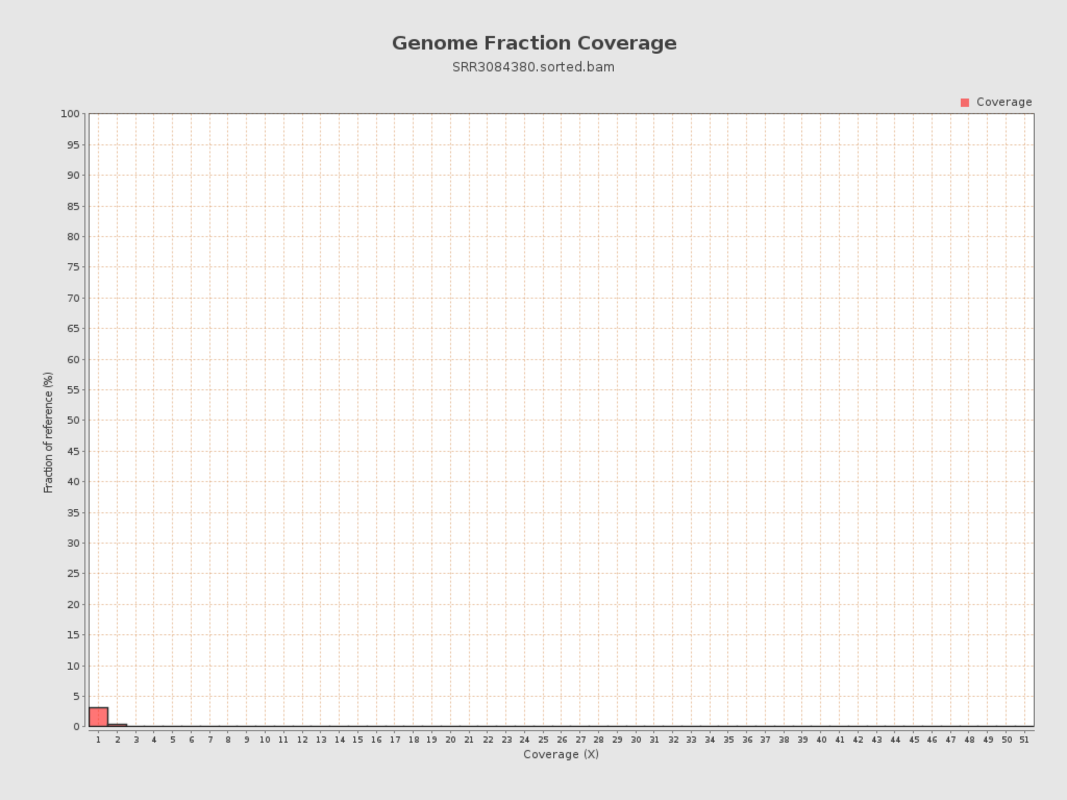
4. Results : Coverage Histogram



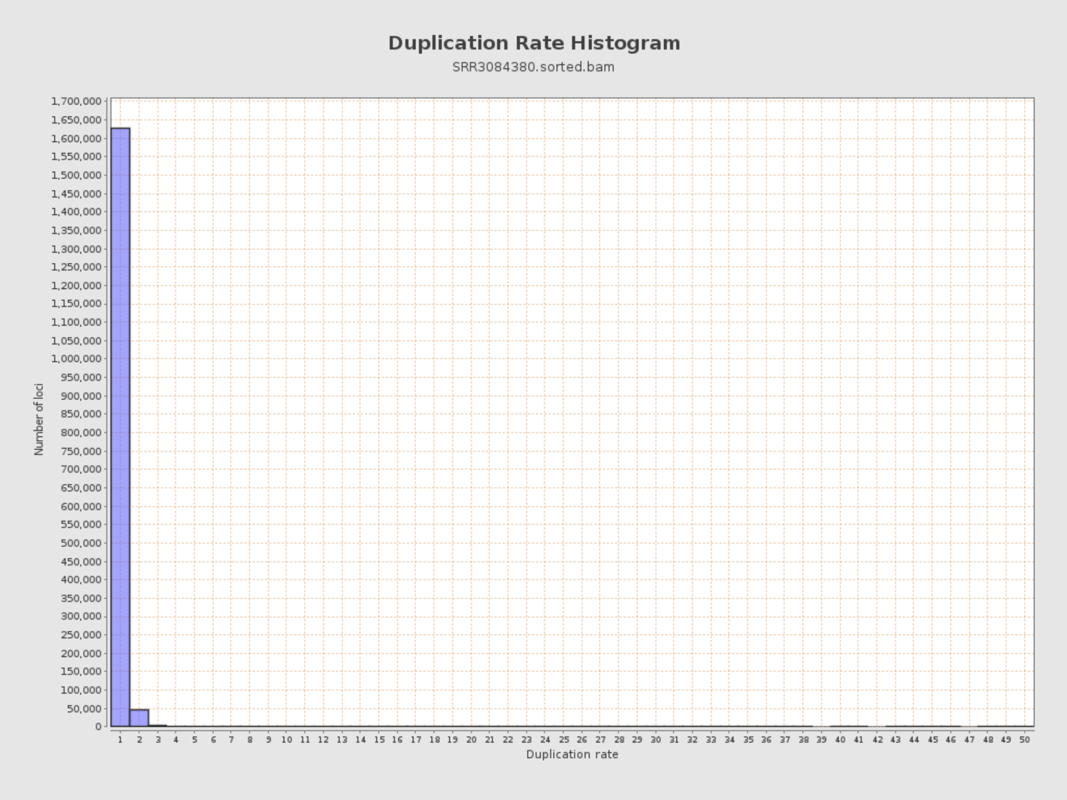
5. Results : Coverage Histogram (0-50X)



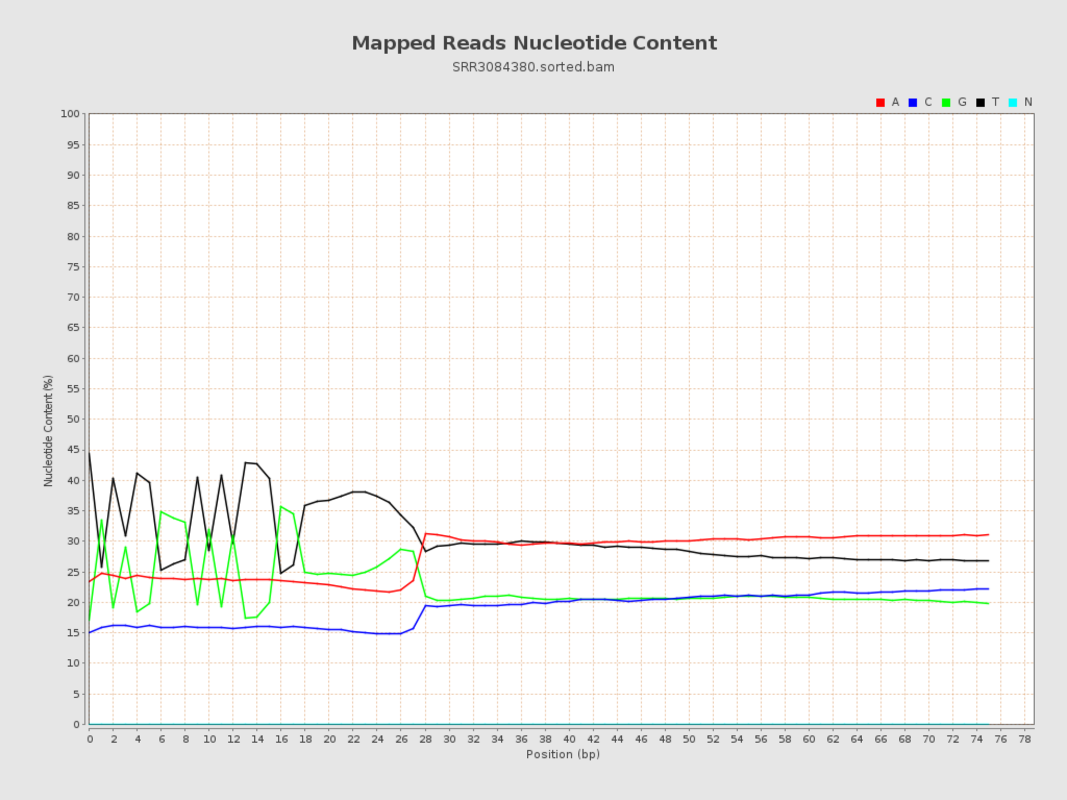
6. Results : Genome Fraction Coverage



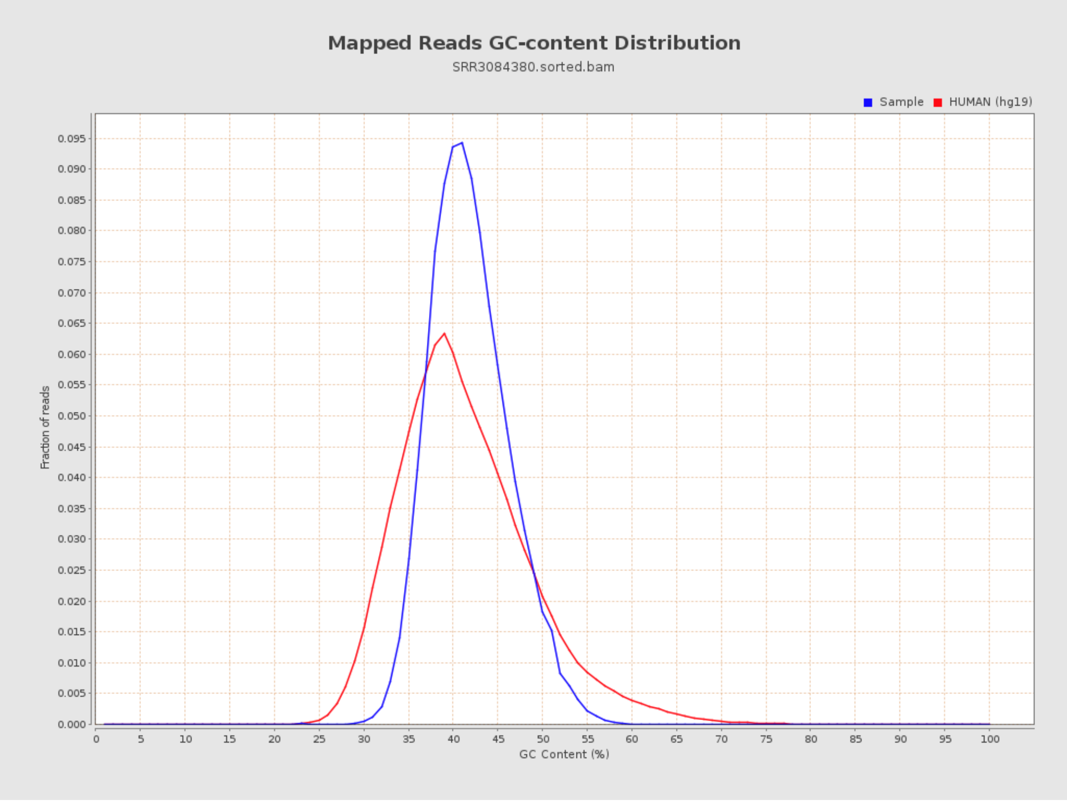
7. Results : Duplication Rate Histogram



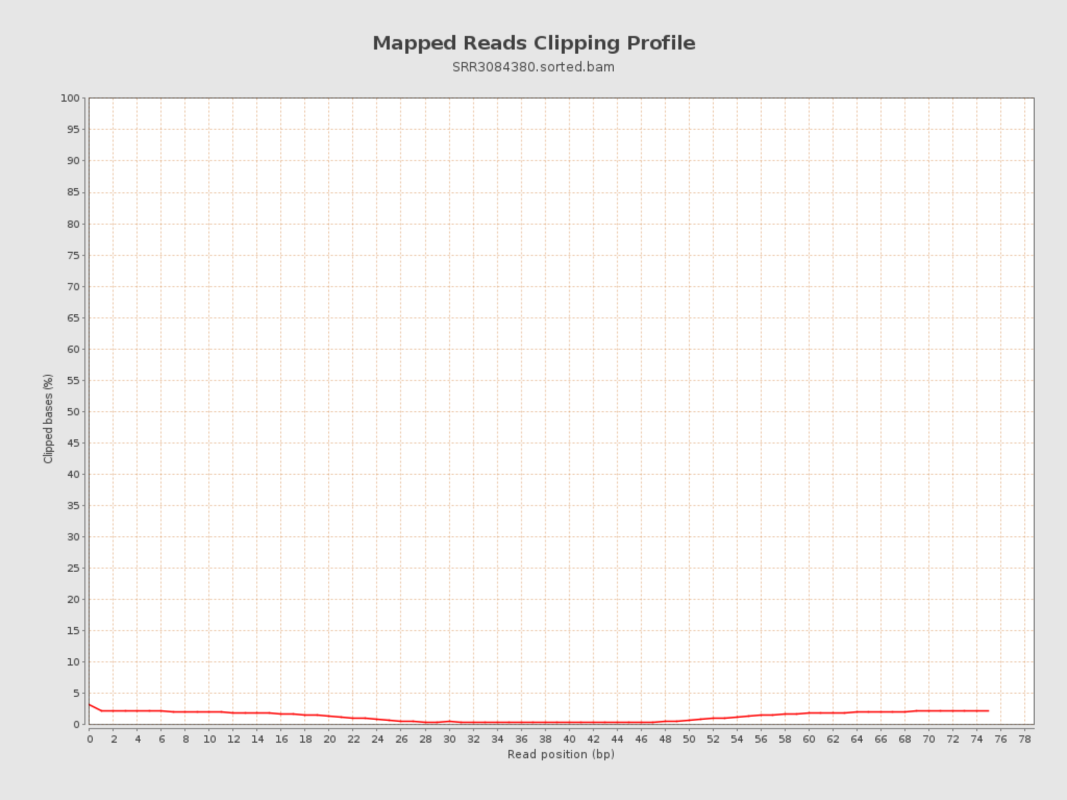
8. Results : Mapped Reads Nucleotide Content



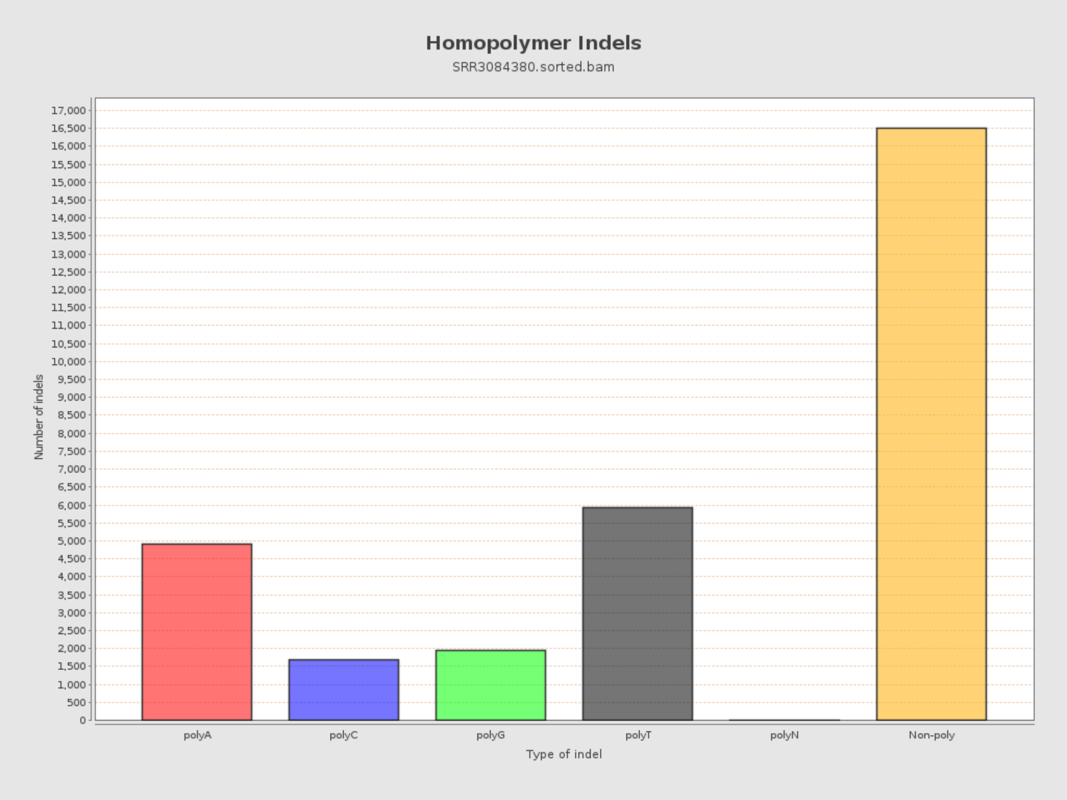
9. Results : Mapped Reads GC-content Distribution



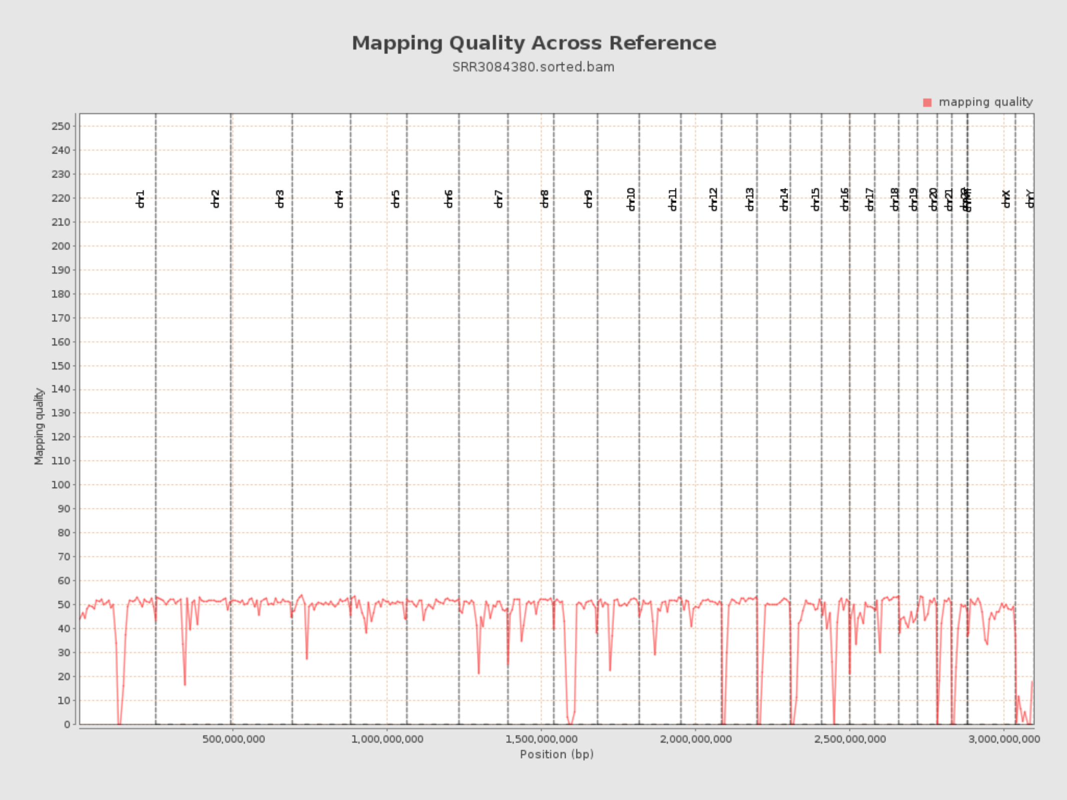
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram