Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:02:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080738.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_SRR3080738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080738.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:02:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,077,611
Mapped reads	4,260,935 / 70.11%
Unmapped reads	1,816,676 / 29.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,761 / 0.52%
Read min/max/mean length	30 / 66 / 66.17
Duplicated reads (estimated)	593,641 / 9.77%
Duplication rate	11.13%
Clipped reads	672,354 / 11.06%

2.2. ACGT Content

Number/percentage of A's	82,100,450 / 30.21%
Number/percentage of C's	54,876,255 / 20.19%
Number/percentage of T's	74,481,043 / 27.41%
Number/percentage of G's	60,209,733 / 22.16%
Number/percentage of N's	84,568 / 0.03%
GC Percentage	42.35%

2.3. Coverage

Mean	0.0878

Standard Deviation	0.6285

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

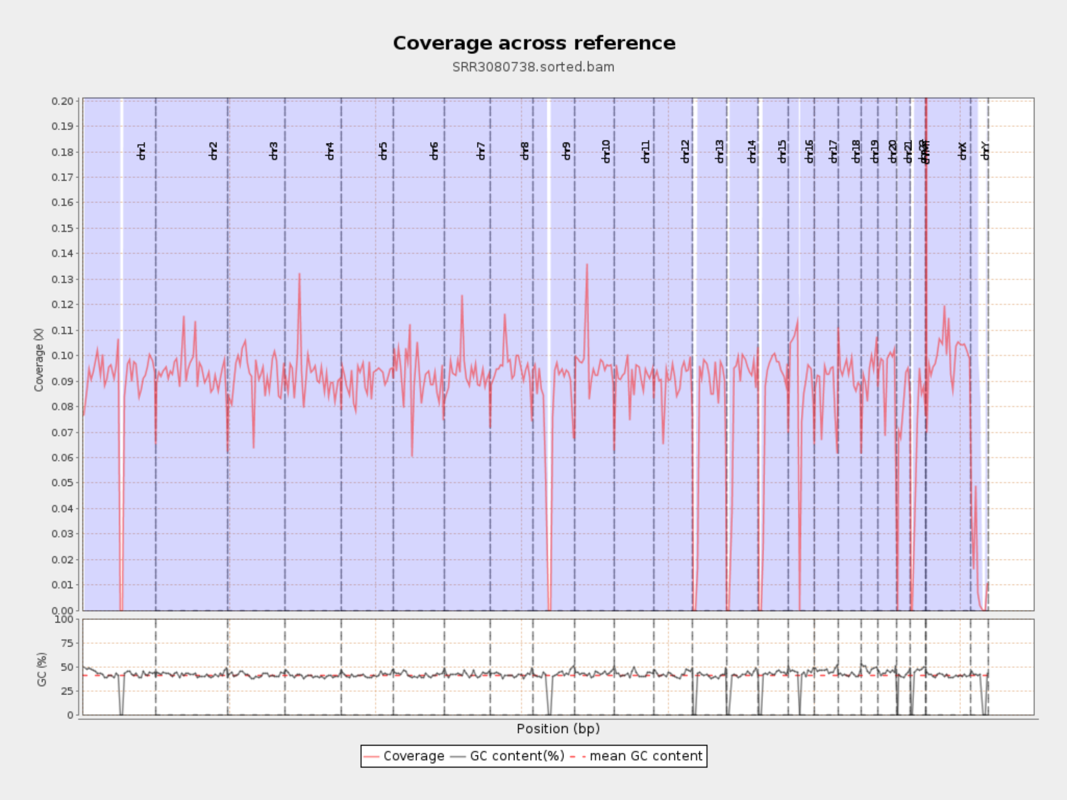
General error rate	0.91%
Mismatches	2,428,988
Insertions	20,290
Mapped reads with at least one insertion	0.47%
Deletions	51,712
Mapped reads with at least one deletion	1.2%
Homopolymer indels	43.38%

2.6. Chromosome stats

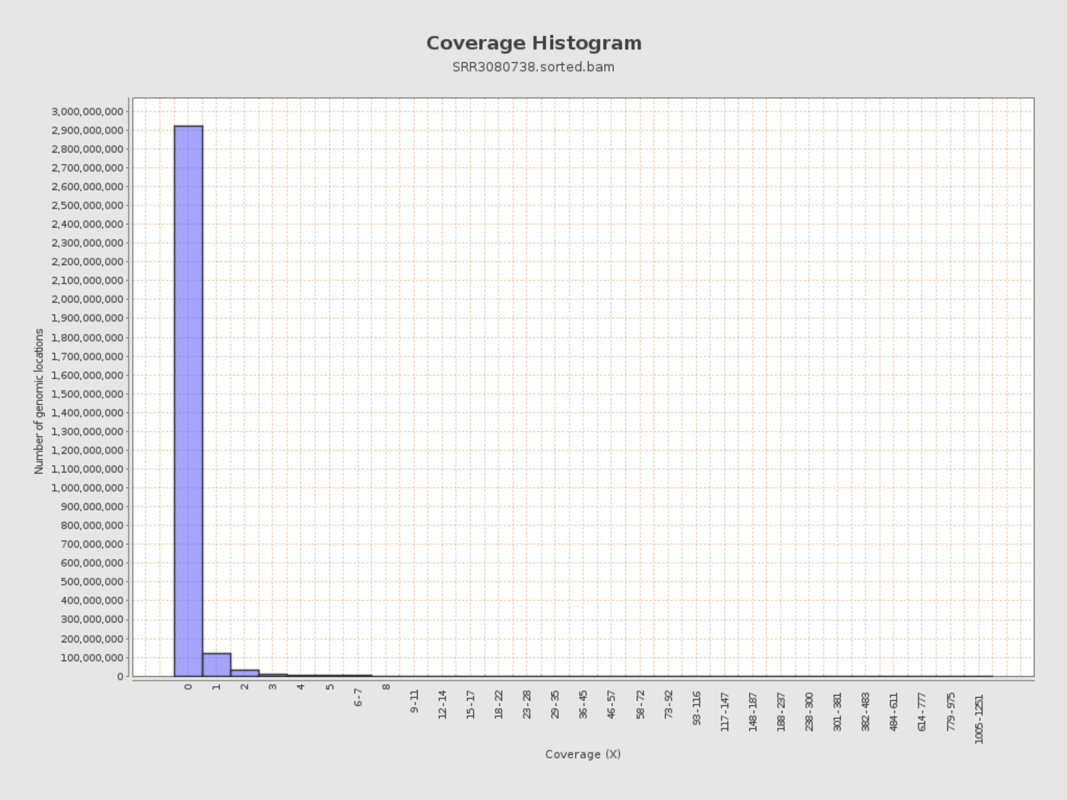
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21799292	0.0875	0.7306
chr2	243199373	22911133	0.0942	0.6478
chr3	198022430	18169830	0.0918	0.4536
chr4	191154276	17685613	0.0925	0.5077
chr5	180915260	16470688	0.091	0.4534
chr6	171115067	15675541	0.0916	0.8114
chr7	159138663	14880864	0.0935	0.8847

chr8	146364022	13886963	0.0949	0.9677
chr9	141213431	10973917	0.0777	0.5347
chr10	135534747	13189845	0.0973	0.6574
chr11	135006516	12301156	0.0911	0.6654
chr12	133851895	12145585	0.0907	0.4576
chr13	115169878	8824755	0.0766	0.4093
chr14	107349540	8495409	0.0791	0.4804
chr15	102531392	7834811	0.0764	0.4164
chr16	90354753	7745625	0.0857	0.4814
chr17	81195210	7093346	0.0874	0.4618
chr18	78077248	7294985	0.0934	0.9886
chr19	59128983	5486484	0.0928	0.7892
chr20	63025520	5901589	0.0936	0.4759
chr21	48129895	3584317	0.0745	0.4646
chr22	51304566	3037458	0.0592	0.3655
chrMT	16571	71629	4.3226	4.391
chrX	155270560	15533753	0.1	0.524
chrY	59373566	851942	0.0143	0.4307

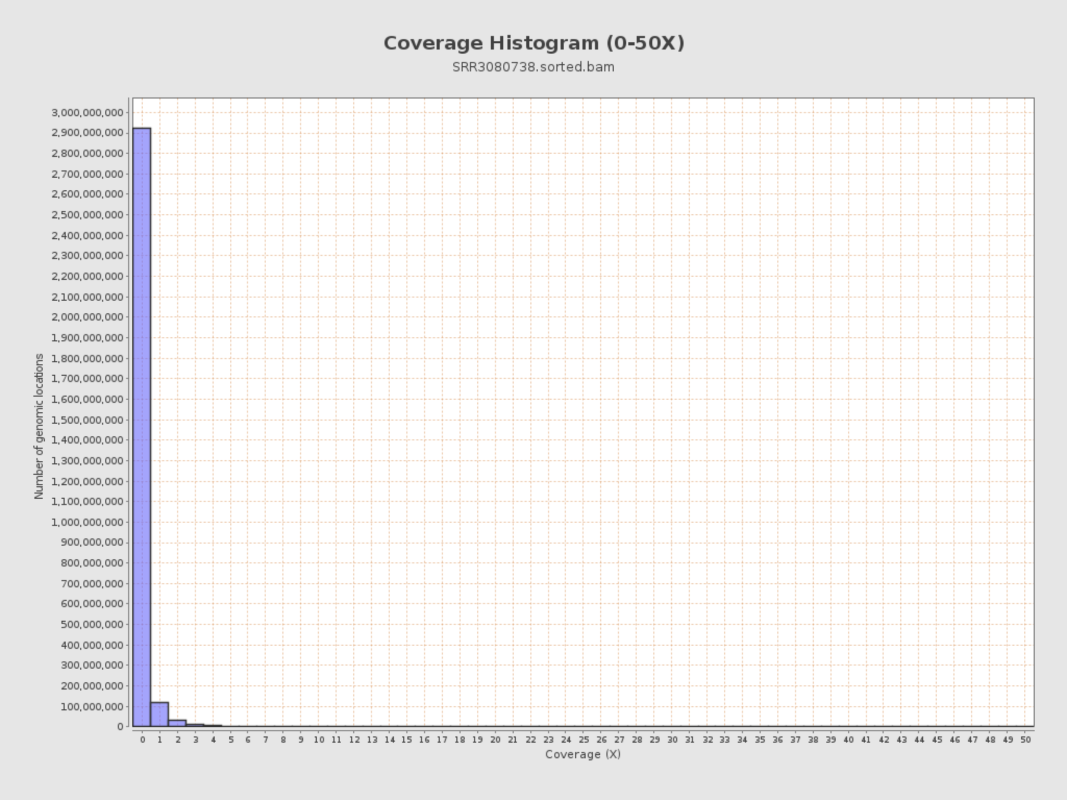
3. Results : Coverage across reference



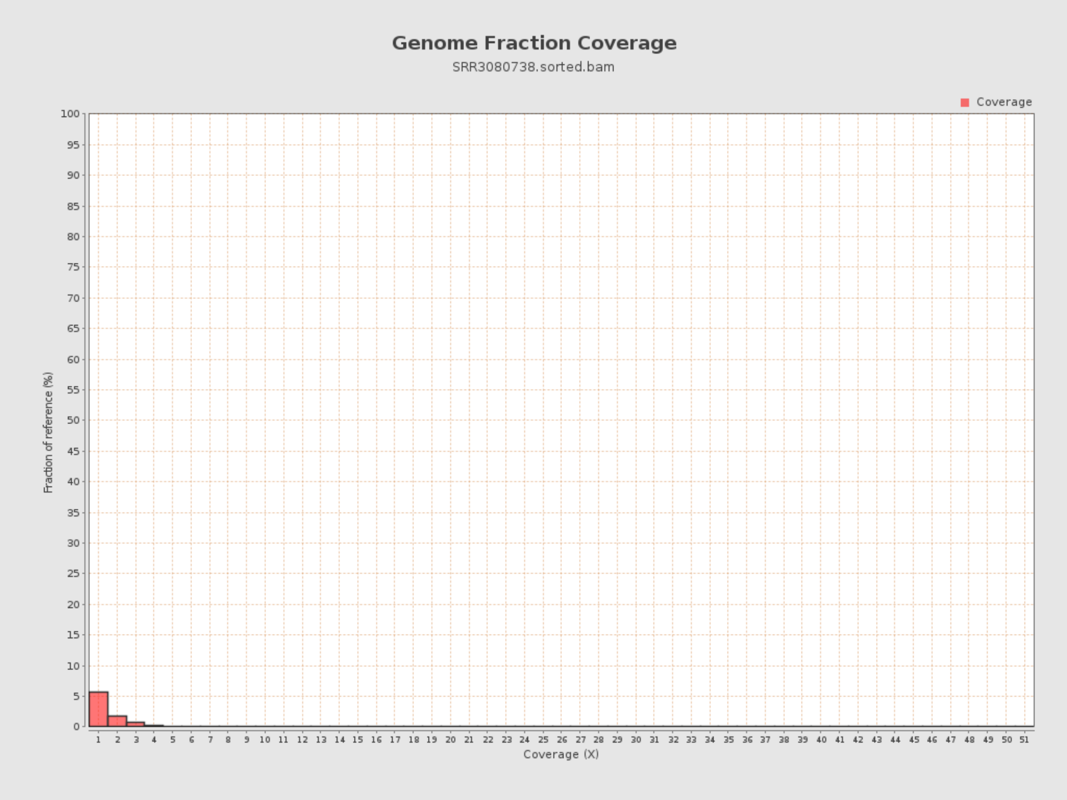
4. Results : Coverage Histogram



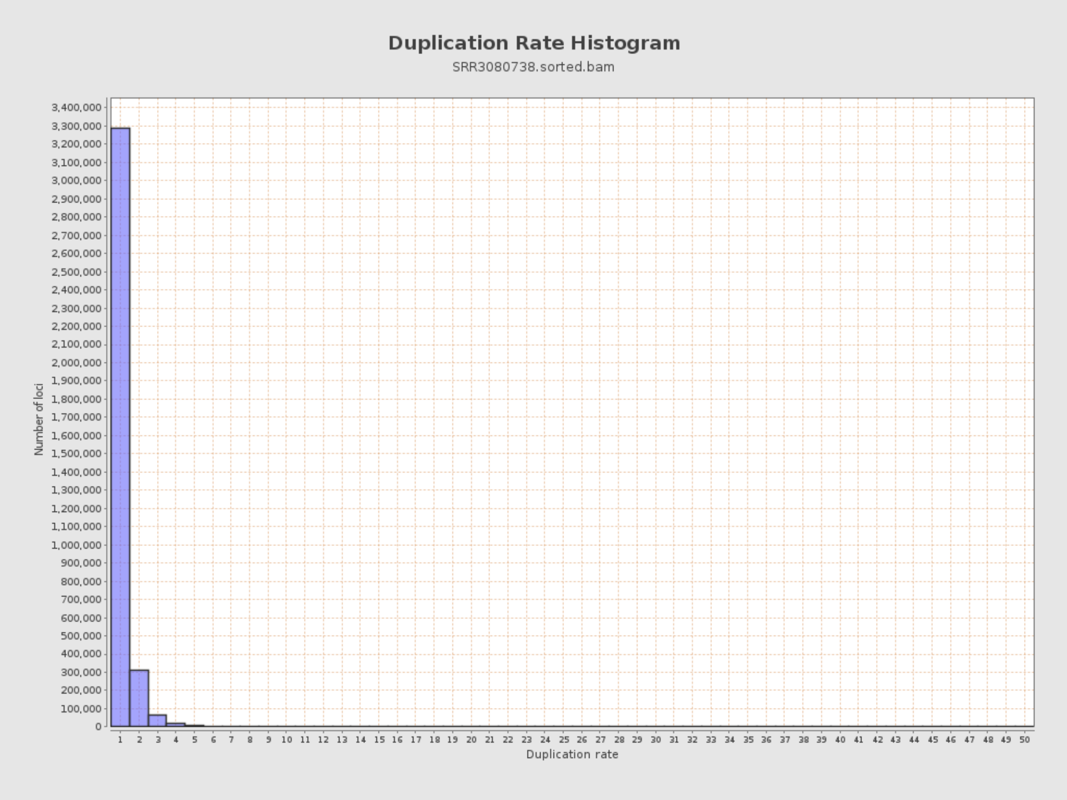
5. Results : Coverage Histogram (0-50X)



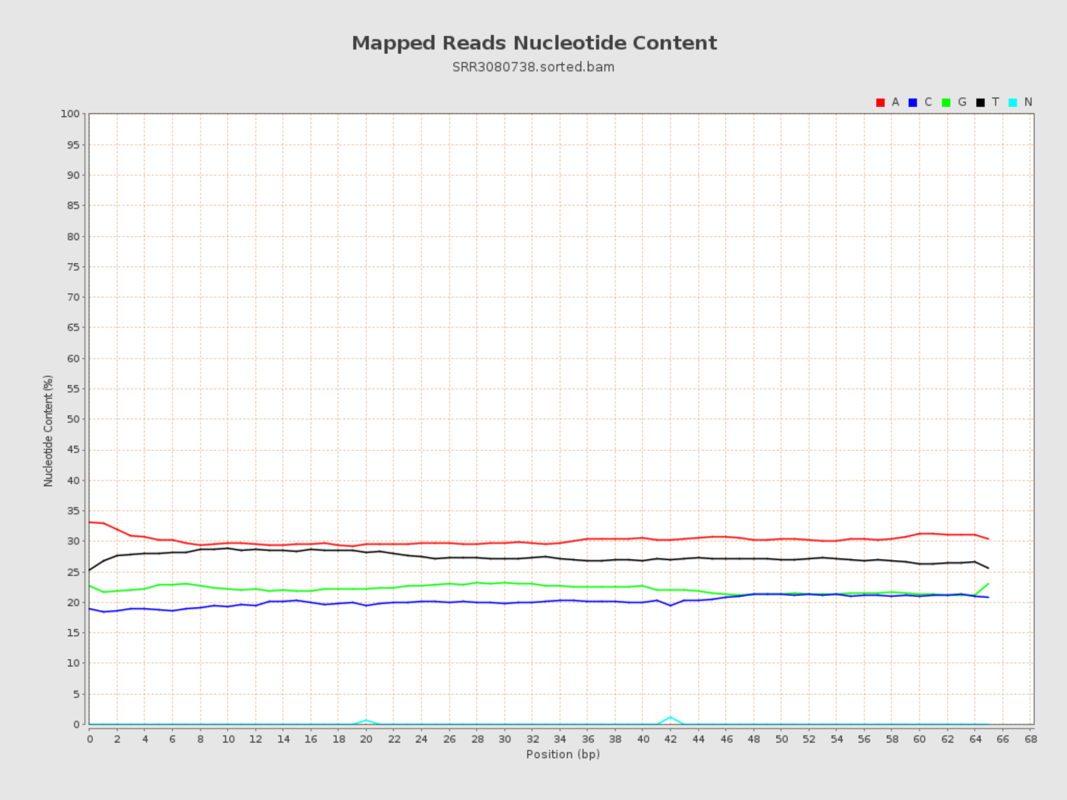
6. Results : Genome Fraction Coverage



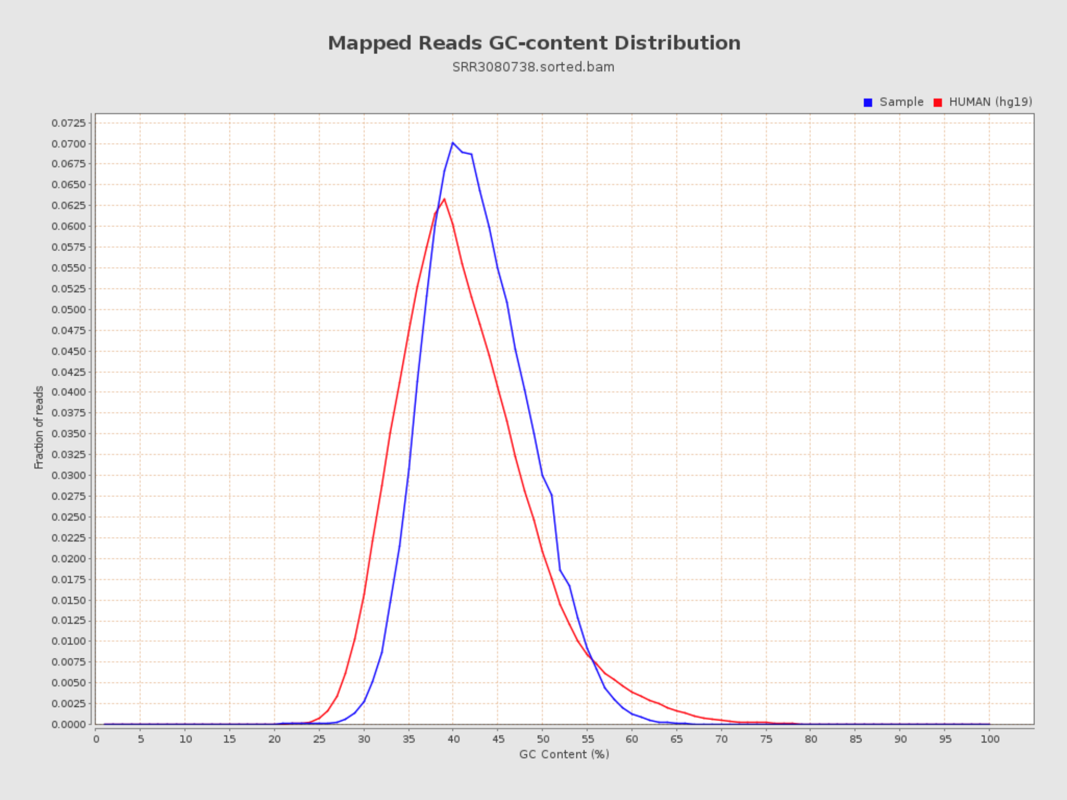
7. Results : Duplication Rate Histogram



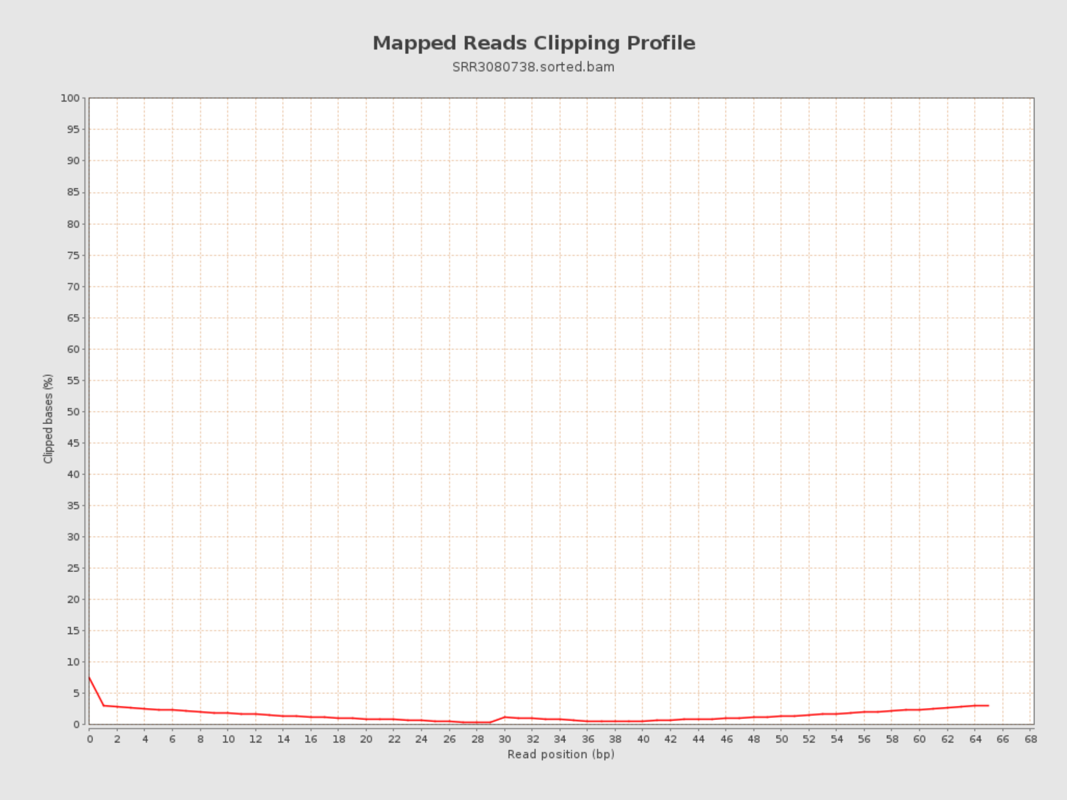
8. Results : Mapped Reads Nucleotide Content



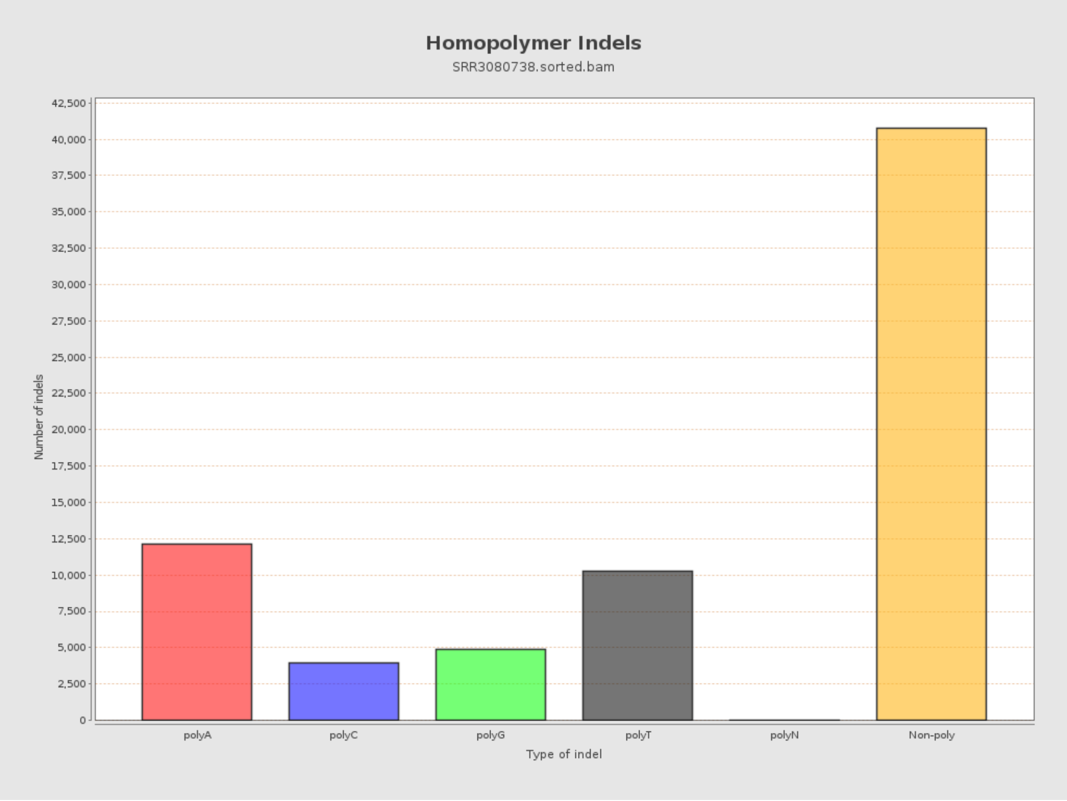
9. Results : Mapped Reads GC-content Distribution



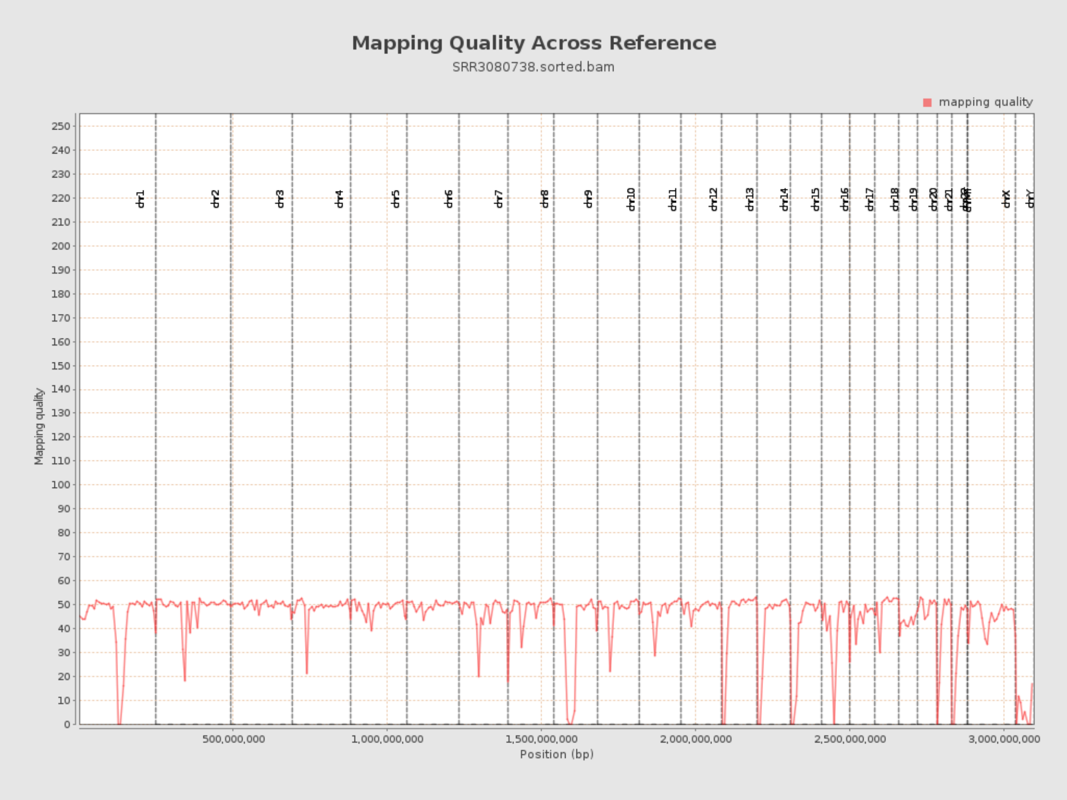
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram