Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:08:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238078.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_SRR6238078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238078.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:08:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,178,783
Mapped reads	1,046,549 / 88.78%
Unmapped reads	132,234 / 11.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,343 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	36,413 / 3.09%
Duplication rate	2.02%
Clipped reads	529,396 / 44.91%

2.2. ACGT Content

Number/percentage of A's	18,238,766 / 26.78%
Number/percentage of C's	12,541,613 / 18.42%
Number/percentage of T's	20,882,228 / 30.66%
Number/percentage of G's	16,315,497 / 23.96%
Number/percentage of N's	121,649 / 0.18%
GC Percentage	42.37%

2.3. Coverage

Mean	0.022

Standard Deviation	0.3142

2.4. Mapping Quality

Mean Mapping Quality	42.33

2.5. Mismatches and indels

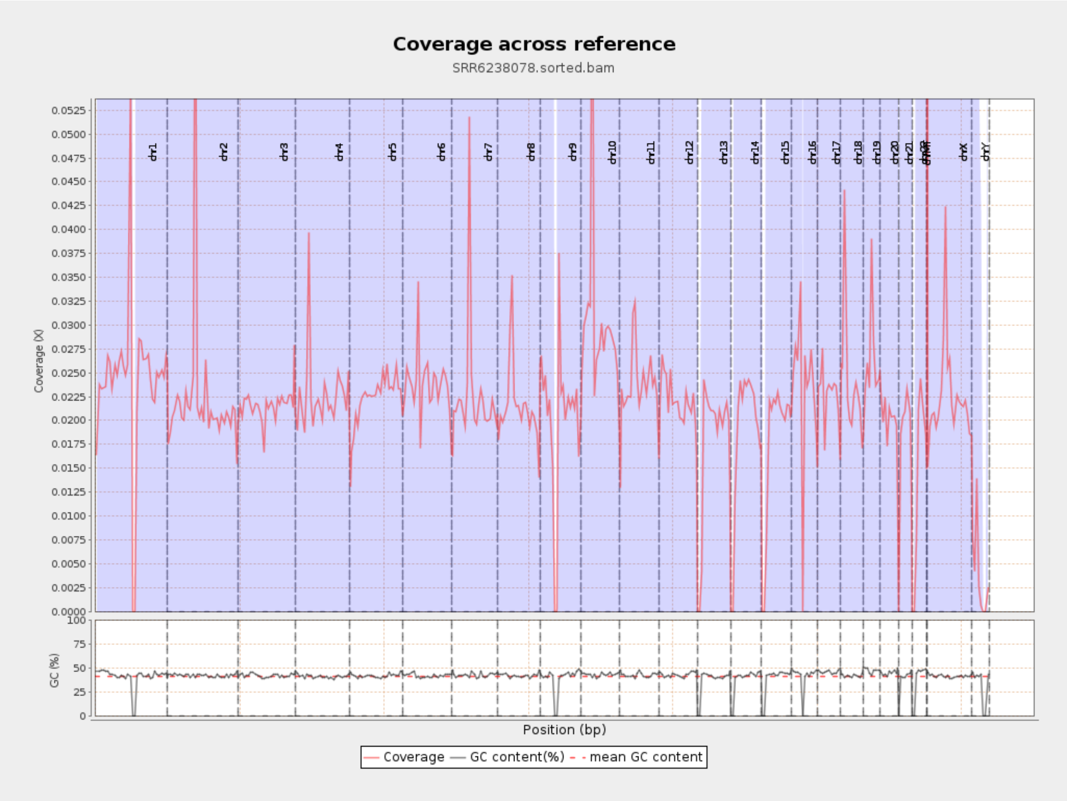
General error rate	0.96%
Mismatches	638,971
Insertions	6,578
Mapped reads with at least one insertion	0.62%
Deletions	19,365
Mapped reads with at least one deletion	1.83%
Homopolymer indels	46.19%

2.6. Chromosome stats

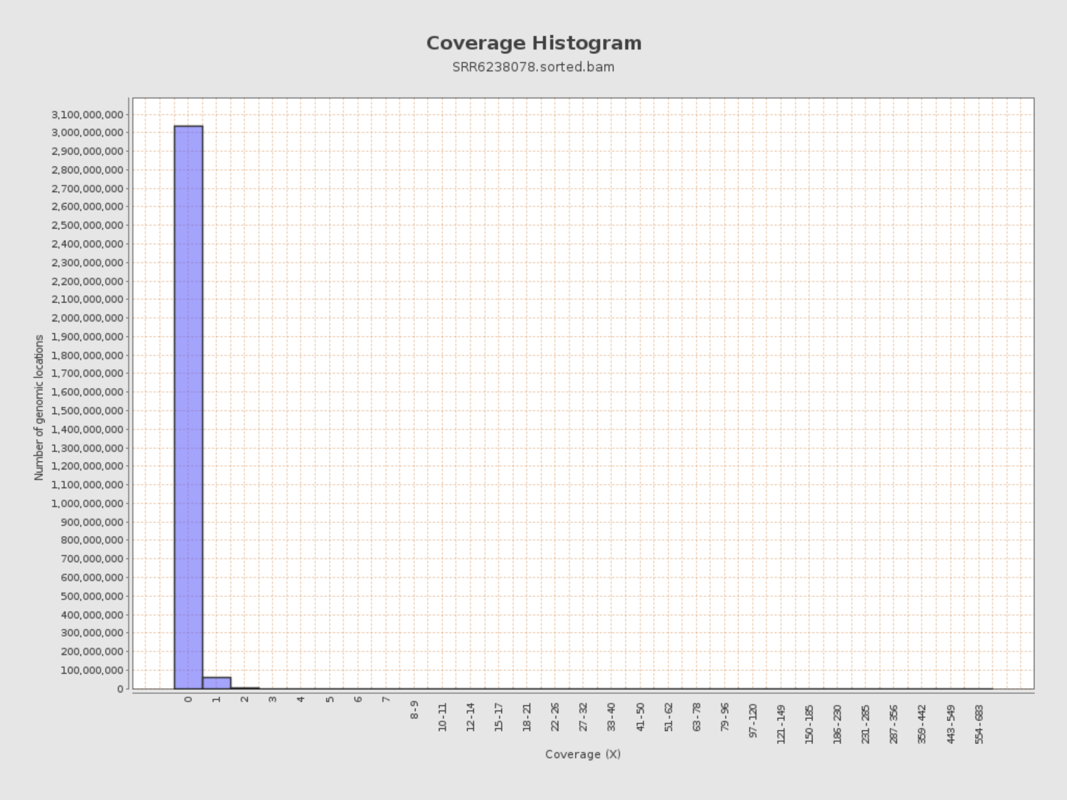
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6046065	0.0243	0.5947
chr2	243199373	5462762	0.0225	0.4012
chr3	198022430	4253101	0.0215	0.1646
chr4	191154276	4339632	0.0227	0.1815
chr5	180915260	4075976	0.0225	0.1612
chr6	171115067	4056144	0.0237	0.2106
chr7	159138663	3606639	0.0227	0.3825

chr8	146364022	3159836	0.0216	0.287
chr9	141213431	2859224	0.0202	0.3409
chr10	135534747	4174354	0.0308	0.4013
chr11	135006516	3258014	0.0241	0.281
chr12	133851895	2967281	0.0222	0.1631
chr13	115169878	2016130	0.0175	0.1376
chr14	107349540	1994809	0.0186	0.1837
chr15	102531392	1785446	0.0174	0.14
chr16	90354753	2106775	0.0233	0.2092
chr17	81195210	1842069	0.0227	0.1984
chr18	78077248	1895815	0.0243	0.6116
chr19	59128983	1560598	0.0264	0.4292
chr20	63025520	1260371	0.02	0.1653
chr21	48129895	879435	0.0183	0.1664
chr22	51304566	750233	0.0146	0.1265
chrMT	16571	38863	2.3452	2.0823
chrX	155270560	3517538	0.0227	0.2055
chrY	59373566	225170	0.0038	0.1147

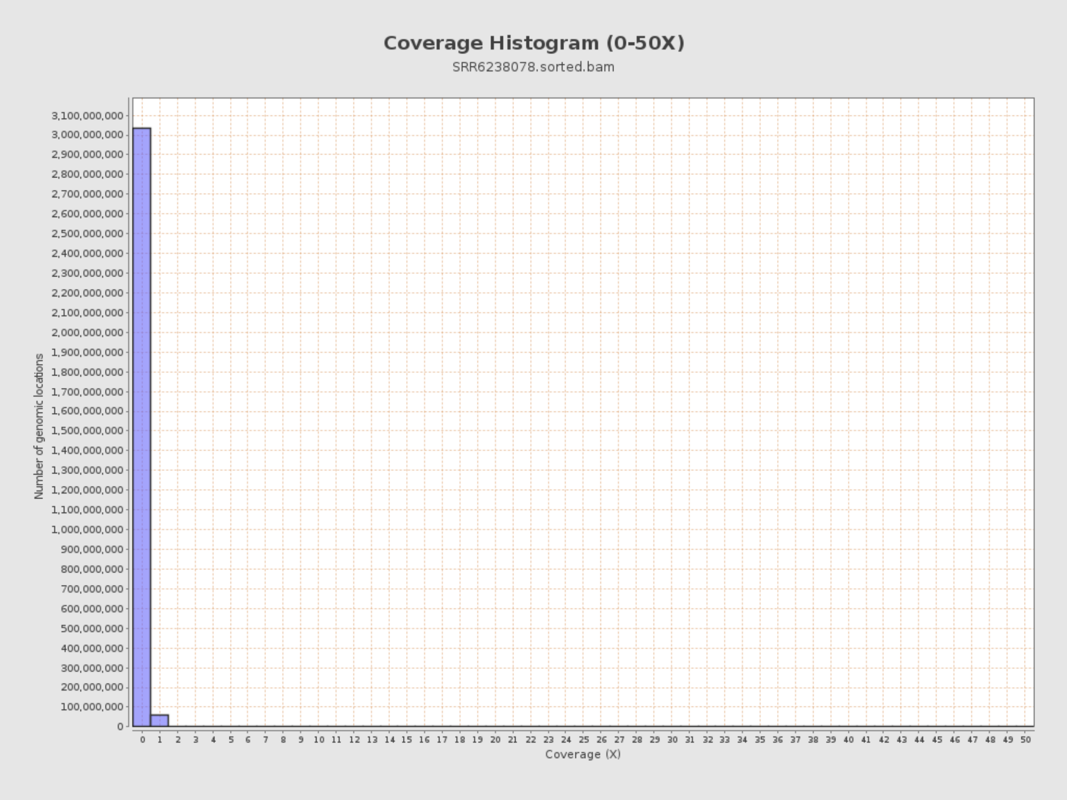
3. Results : Coverage across reference



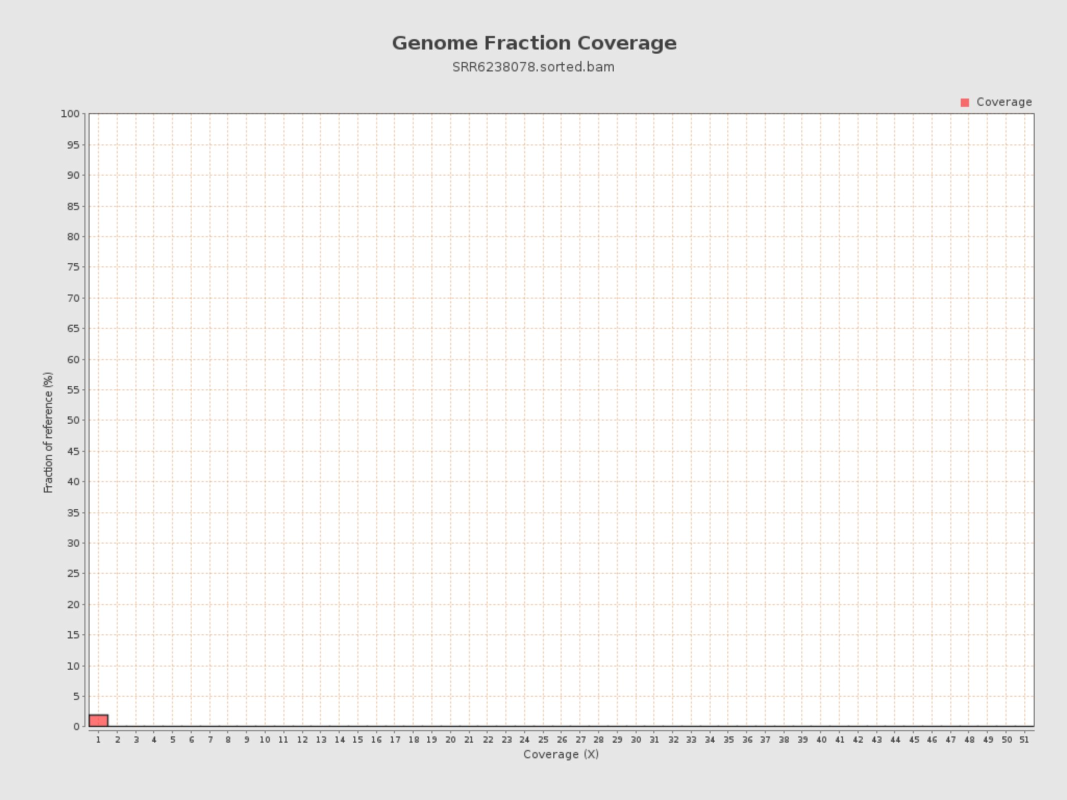
4. Results : Coverage Histogram



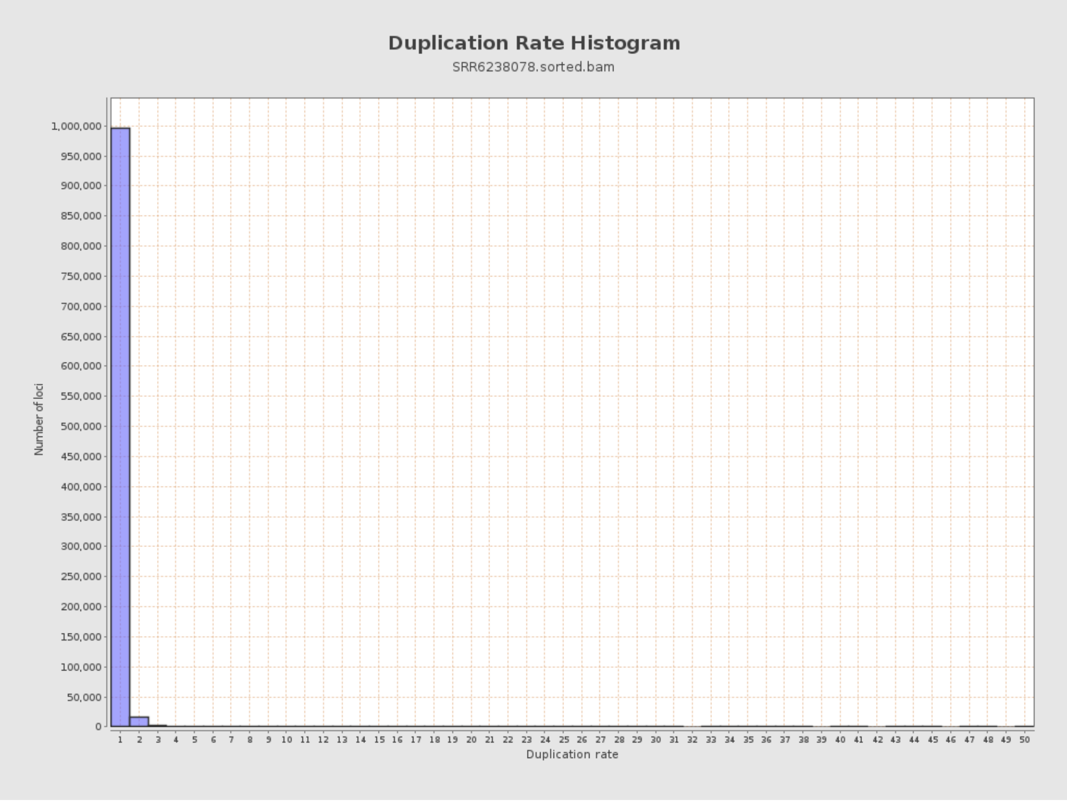
5. Results : Coverage Histogram (0-50X)



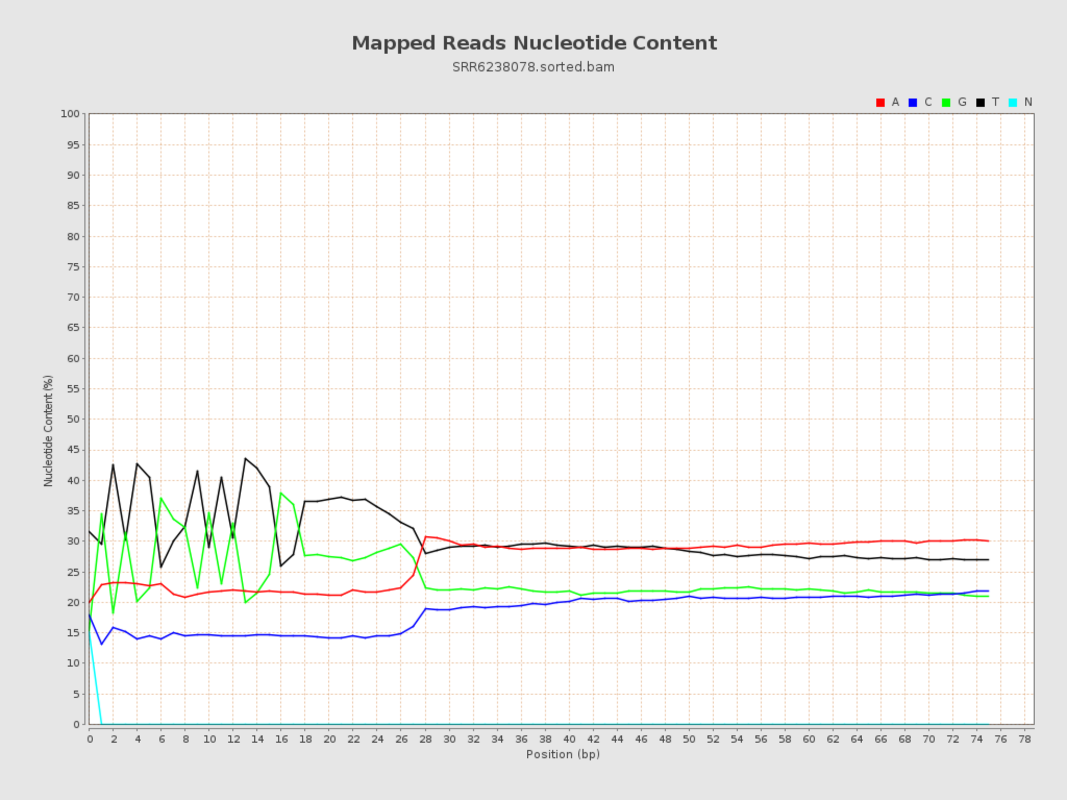
6. Results : Genome Fraction Coverage



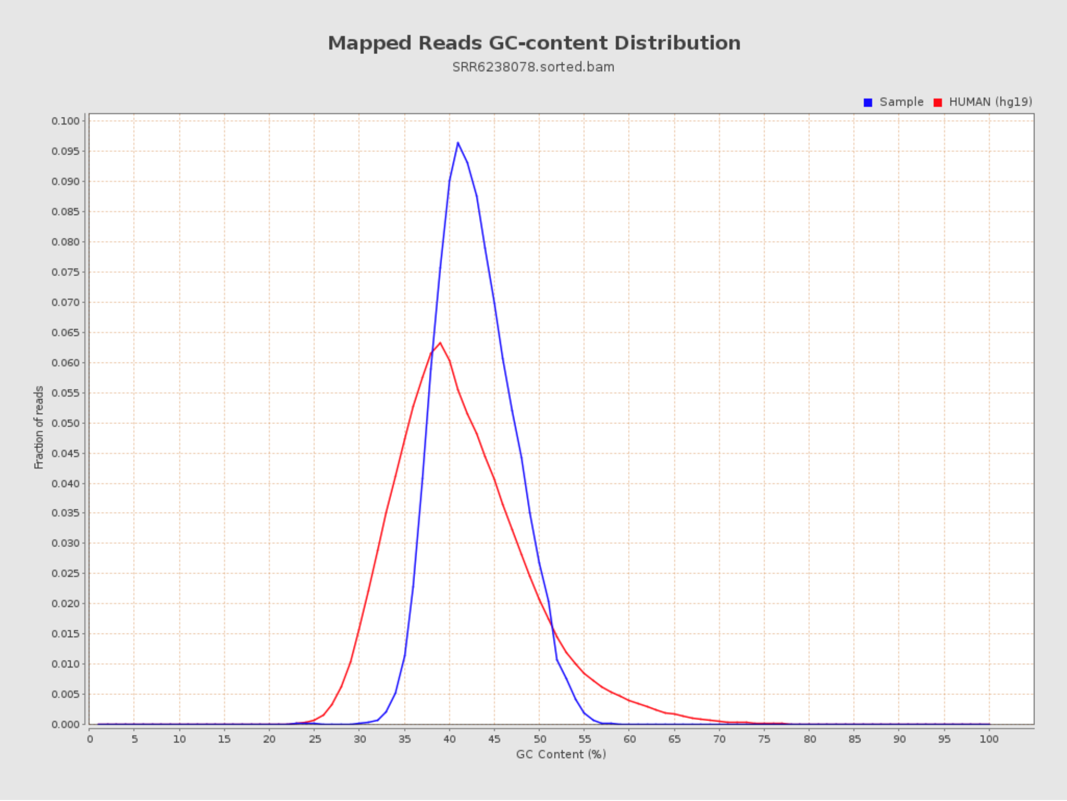
7. Results : Duplication Rate Histogram



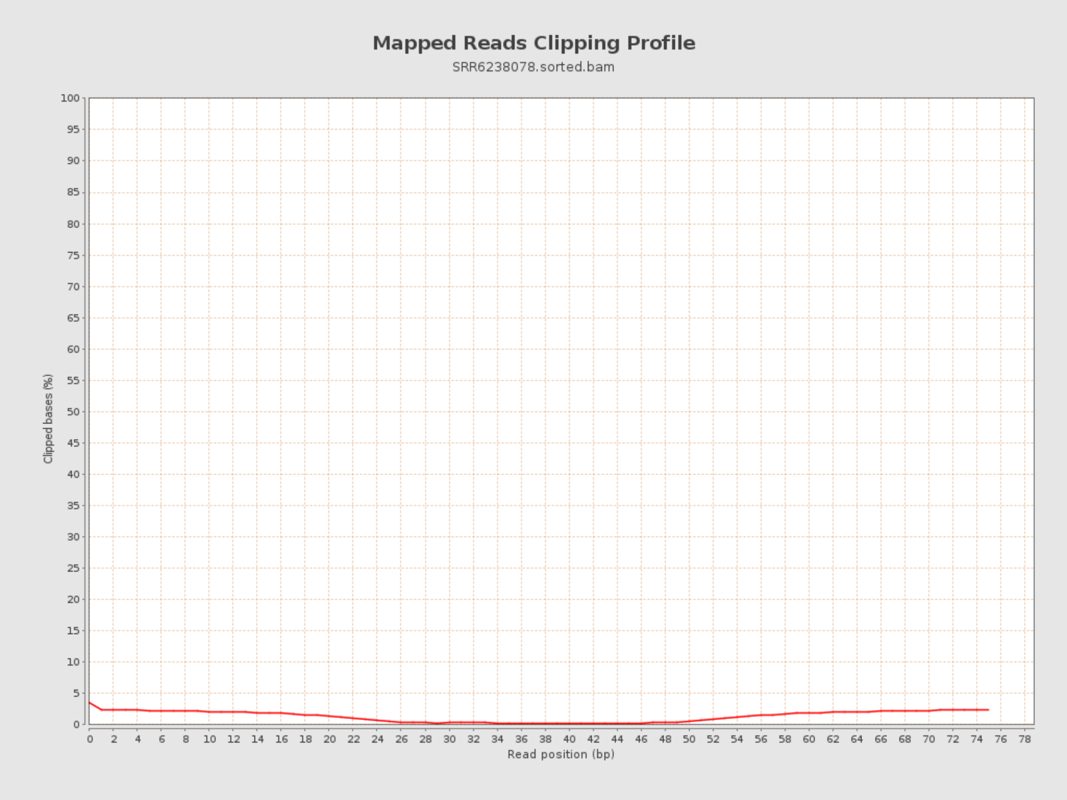
8. Results : Mapped Reads Nucleotide Content



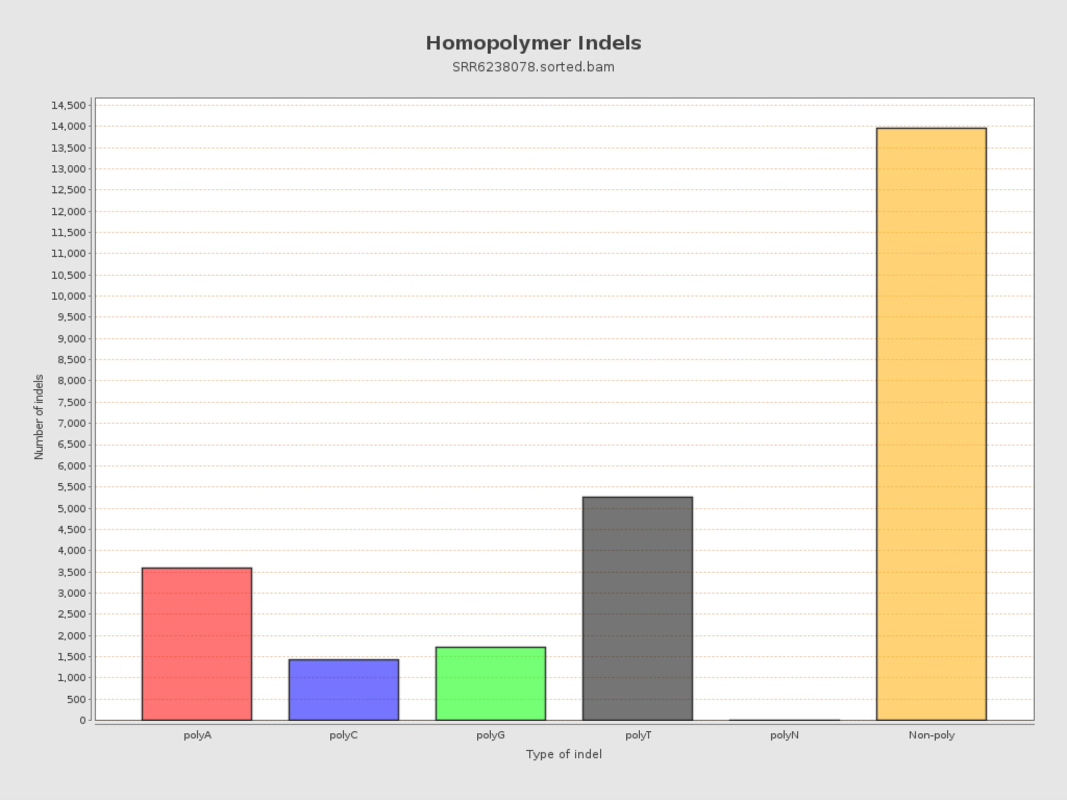
9. Results : Mapped Reads GC-content Distribution



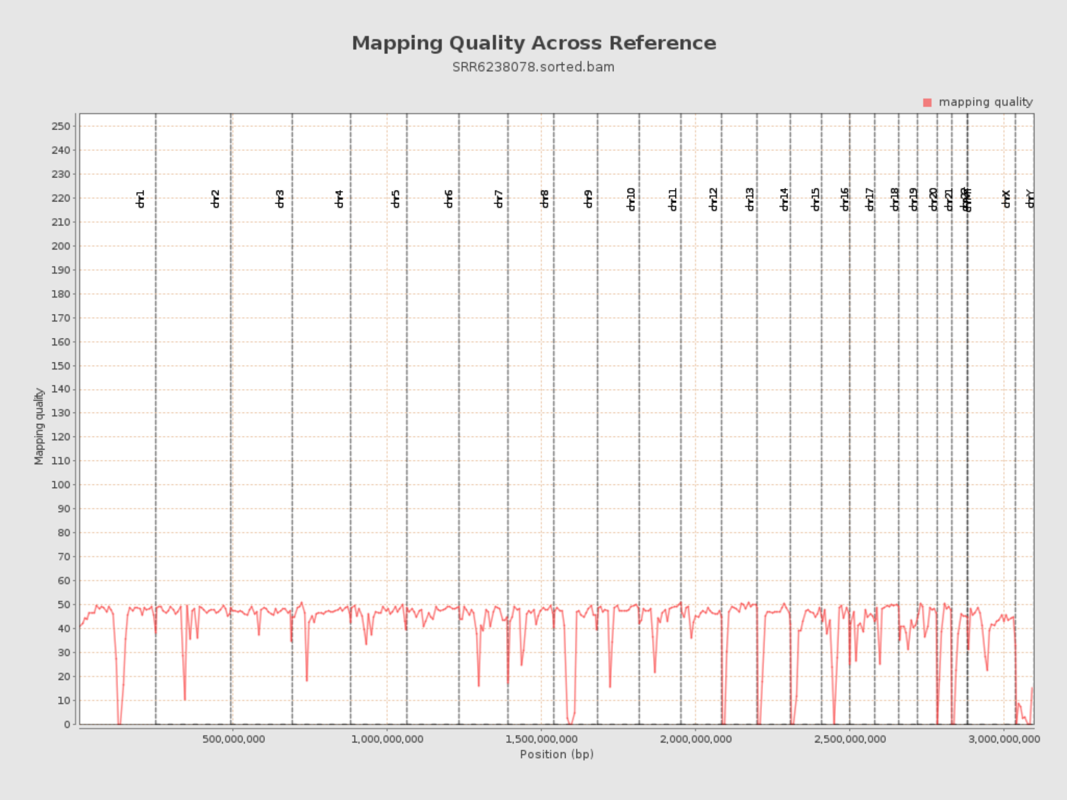
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram