Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:19:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068938.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_SRR6068938 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068938.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:19:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068938.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,838,634
Mapped reads	2,244,234 / 79.06%
Unmapped reads	594,400 / 20.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,499 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	199,462 / 7.03%
Duplication rate	7.08%
Clipped reads	1,260,909 / 44.42%

2.2. ACGT Content

Number/percentage of A's	38,022,169 / 26.68%
Number/percentage of C's	23,846,593 / 16.73%
Number/percentage of T's	48,172,496 / 33.8%
Number/percentage of G's	32,149,323 / 22.56%
Number/percentage of N's	336,741 / 0.24%
GC Percentage	39.29%

2.3. Coverage

Mean	0.0461

Standard Deviation	0.4465

2.4. Mapping Quality

Mean Mapping Quality	46.43

2.5. Mismatches and indels

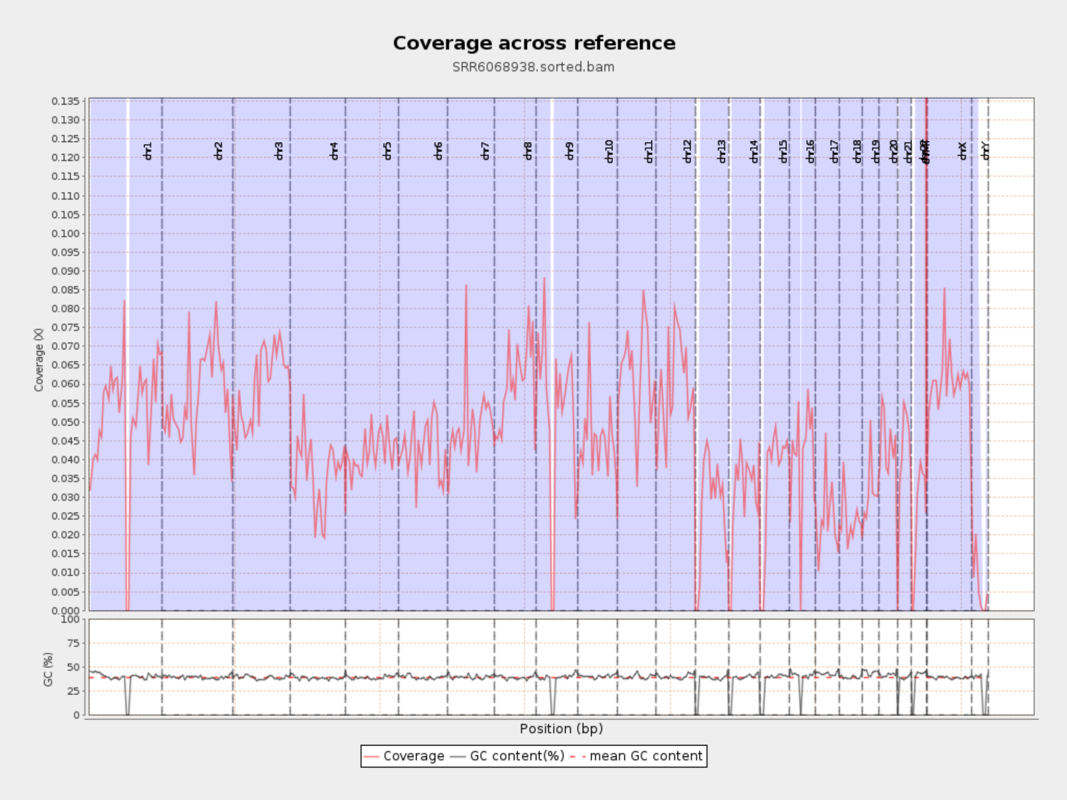
General error rate	1.13%
Mismatches	1,584,988
Insertions	12,134
Mapped reads with at least one insertion	0.54%
Deletions	50,785
Mapped reads with at least one deletion	2.24%
Homopolymer indels	49.1%

2.6. Chromosome stats

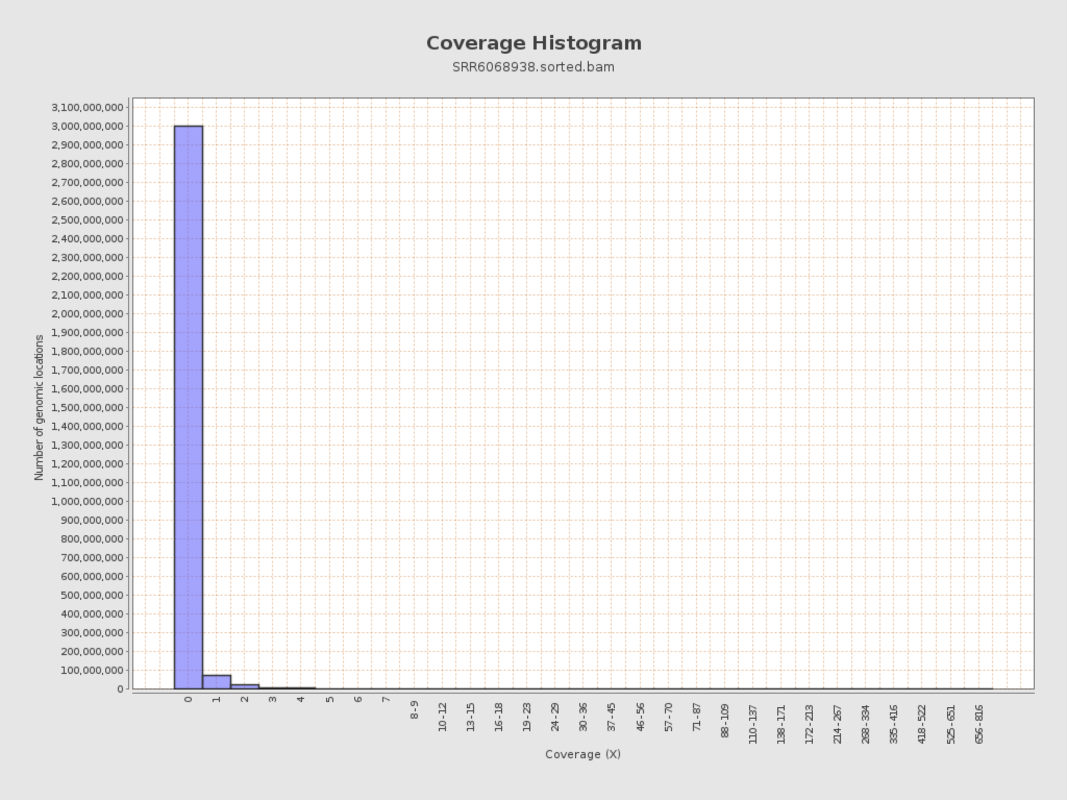
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12989828	0.0521	0.7183
chr2	243199373	13904023	0.0572	0.456
chr3	198022430	11870640	0.0599	0.34
chr4	191154276	6989664	0.0366	0.272
chr5	180915260	7625511	0.0421	0.2801
chr6	171115067	7302048	0.0427	0.3117
chr7	159138663	7876505	0.0495	0.6665

chr8	146364022	8830964	0.0603	0.5913
chr9	141213431	7533543	0.0533	0.517
chr10	135534747	6171278	0.0455	0.4246
chr11	135006516	8418753	0.0624	0.5198
chr12	133851895	7964930	0.0595	0.3473
chr13	115169878	3077838	0.0267	0.2212
chr14	107349540	3228844	0.0301	0.2974
chr15	102531392	3551993	0.0346	0.2527
chr16	90354753	3695364	0.0409	0.3107
chr17	81195210	1971786	0.0243	0.2663
chr18	78077248	1908248	0.0244	0.7083
chr19	59128983	1858988	0.0314	0.5455
chr20	63025520	2769281	0.0439	0.3046
chr21	48129895	1935455	0.0402	0.3124
chr22	51304566	1260288	0.0246	0.2057
chrMT	16571	123509	7.4533	7.7304
chrX	155270560	9361066	0.0603	0.3946
chrY	59373566	386571	0.0065	0.147

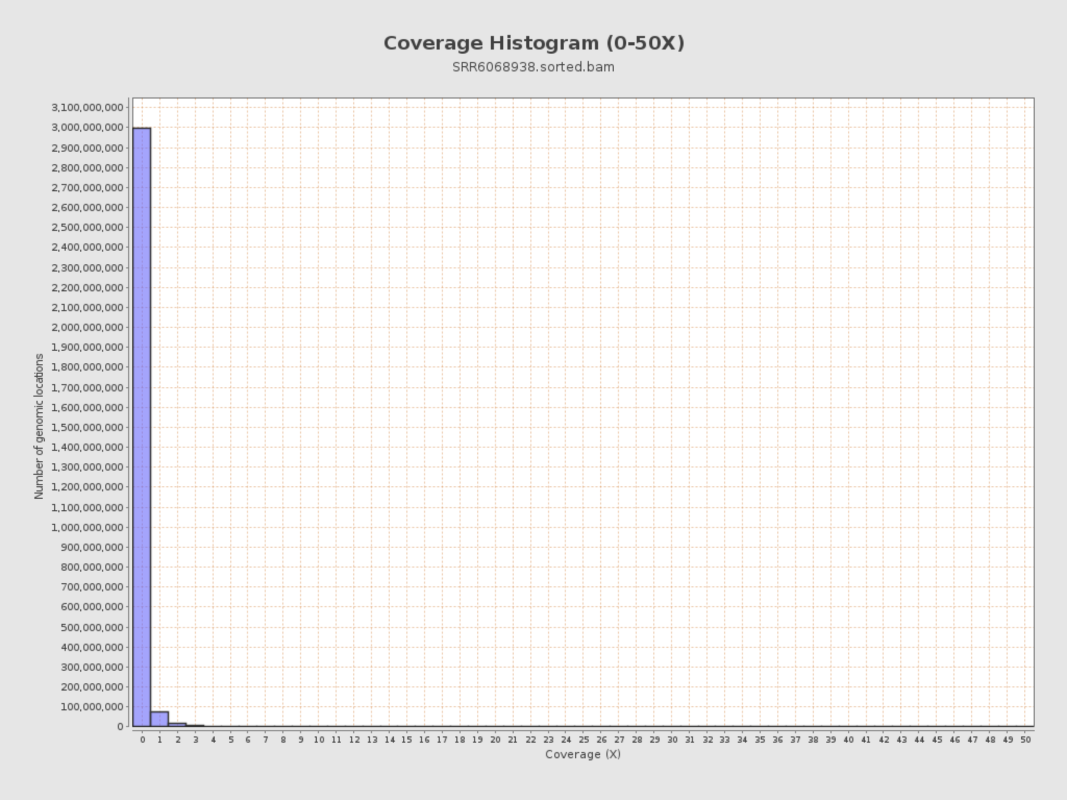
3. Results : Coverage across reference



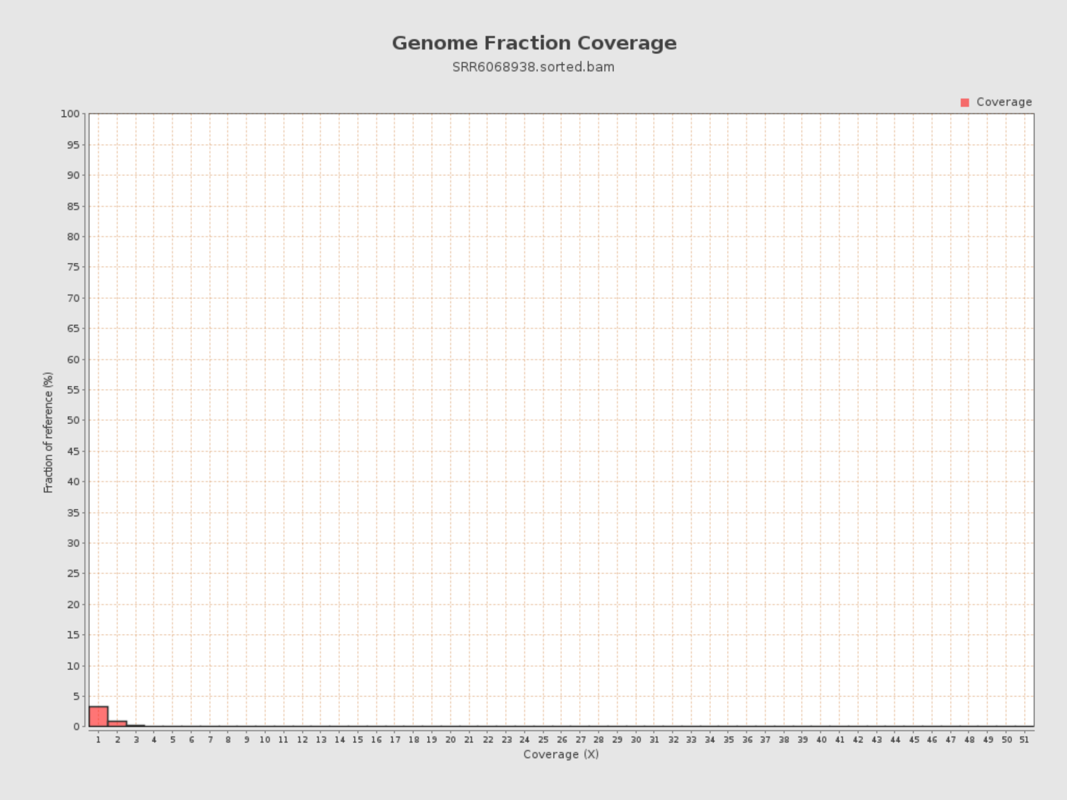
4. Results : Coverage Histogram



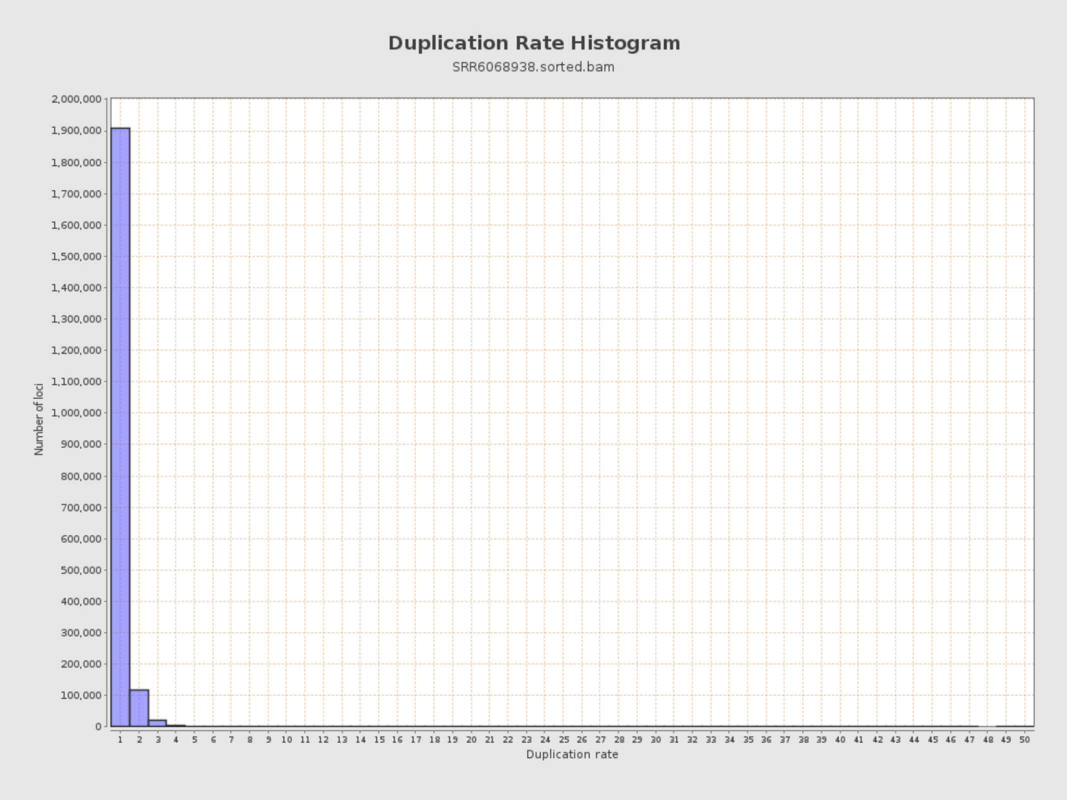
5. Results : Coverage Histogram (0-50X)



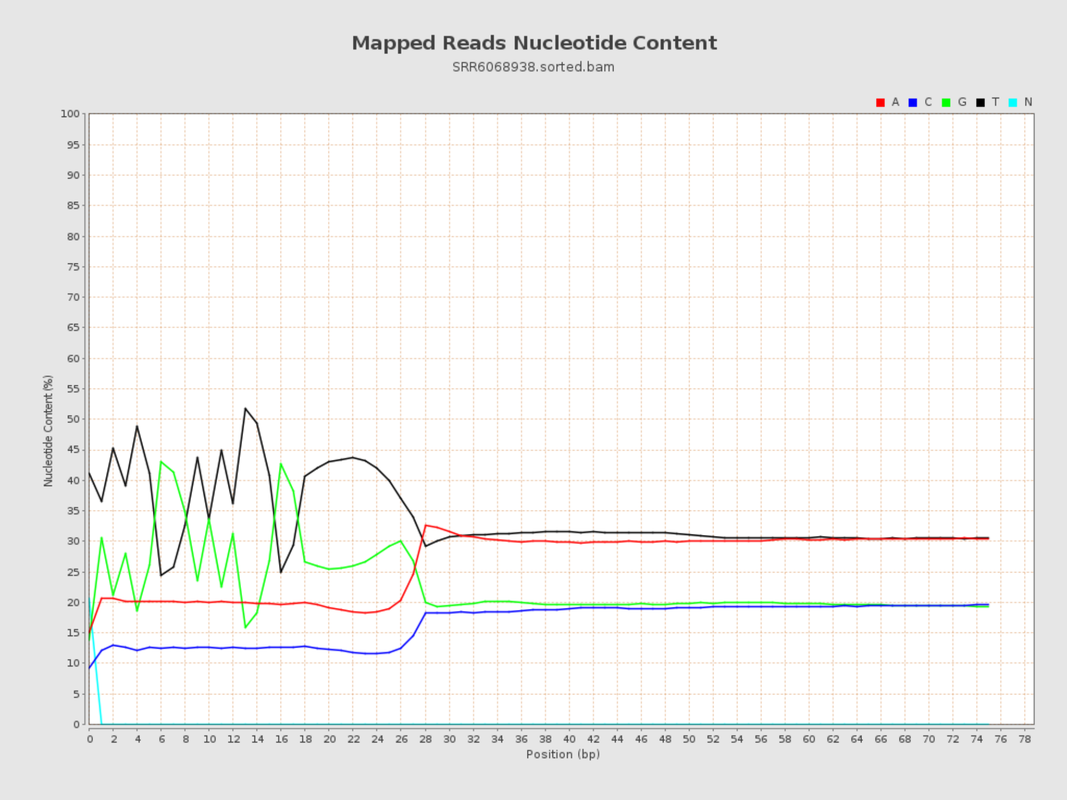
6. Results : Genome Fraction Coverage



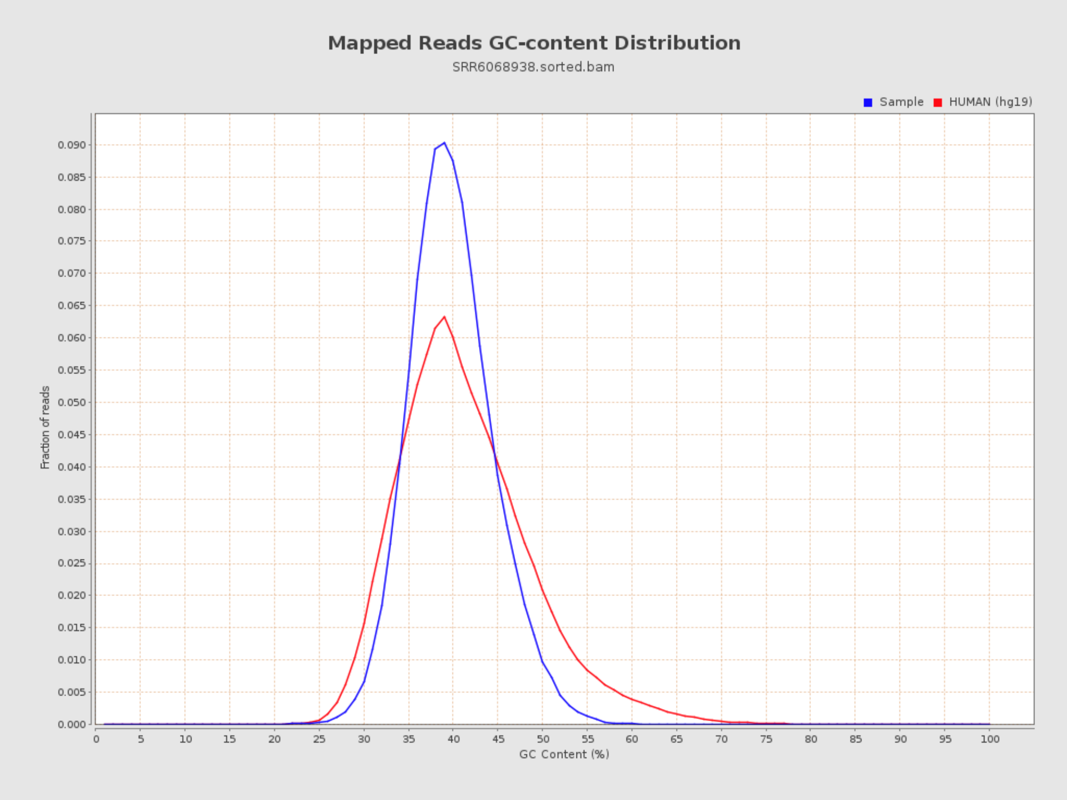
7. Results : Duplication Rate Histogram



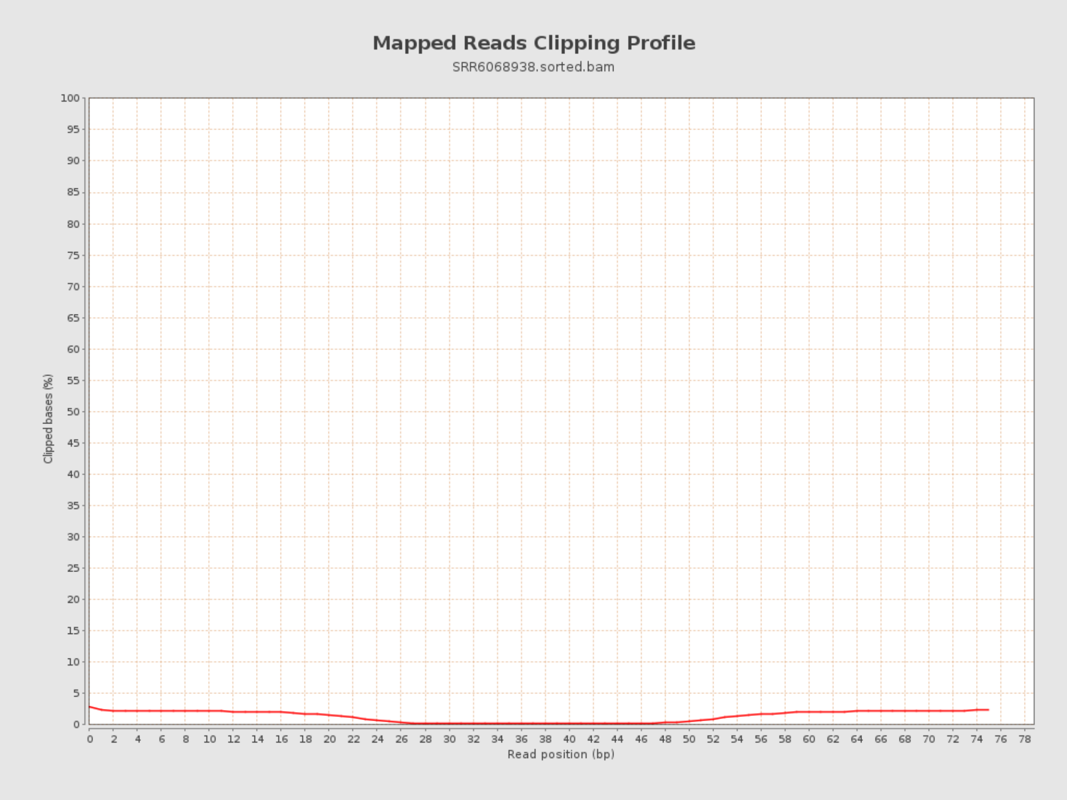
8. Results : Mapped Reads Nucleotide Content



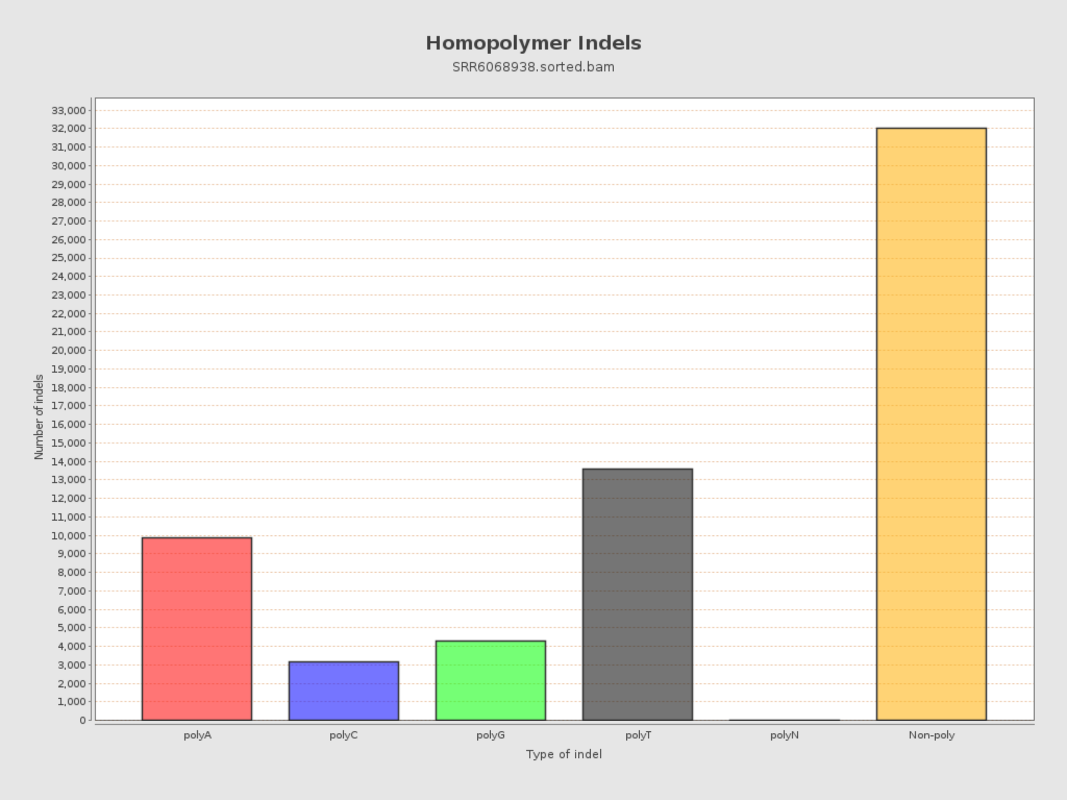
9. Results : Mapped Reads GC-content Distribution



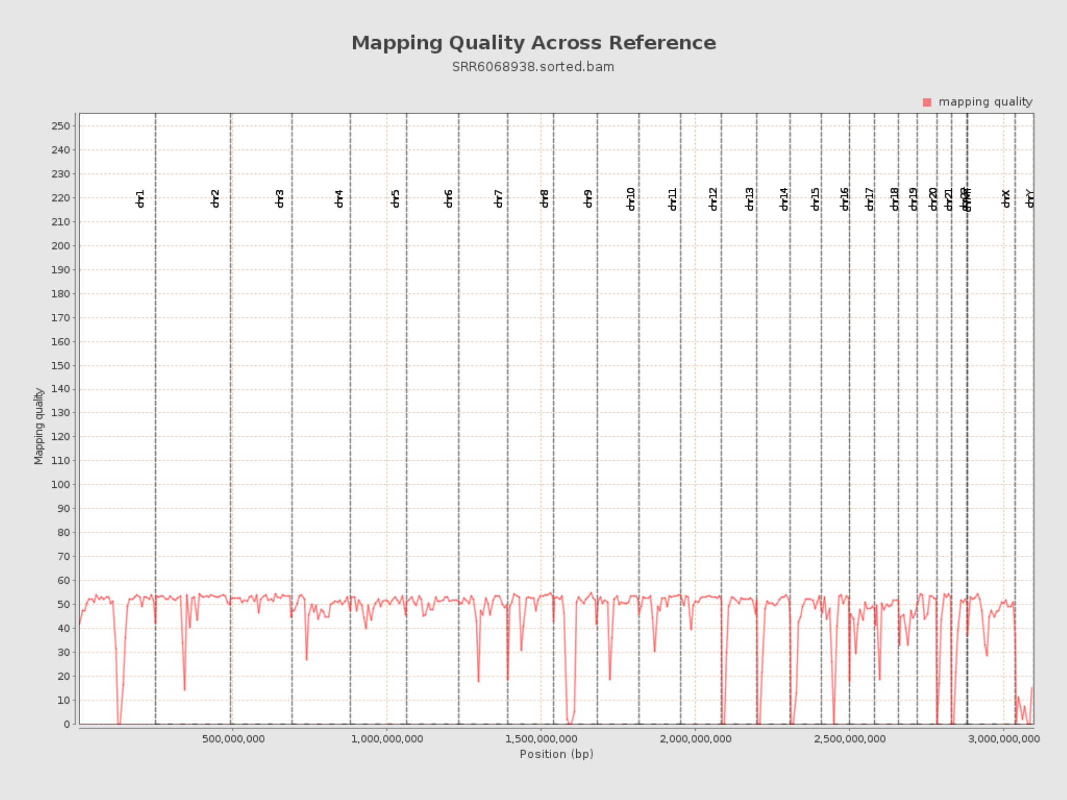
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram