Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:37:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238306.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_SRR6238306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238306.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:37:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,217,267
Mapped reads	2,041,919 / 92.09%
Unmapped reads	175,348 / 7.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,340 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	87,999 / 3.97%
Duplication rate	3.28%
Clipped reads	940,917 / 42.44%

2.2. ACGT Content

Number/percentage of A's	38,419,579 / 28.25%
Number/percentage of C's	25,258,865 / 18.57%
Number/percentage of T's	42,883,380 / 31.54%
Number/percentage of G's	29,381,077 / 21.61%
Number/percentage of N's	43,344 / 0.03%
GC Percentage	40.18%

2.3. Coverage

Mean	0.0439

Standard Deviation	0.3985

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

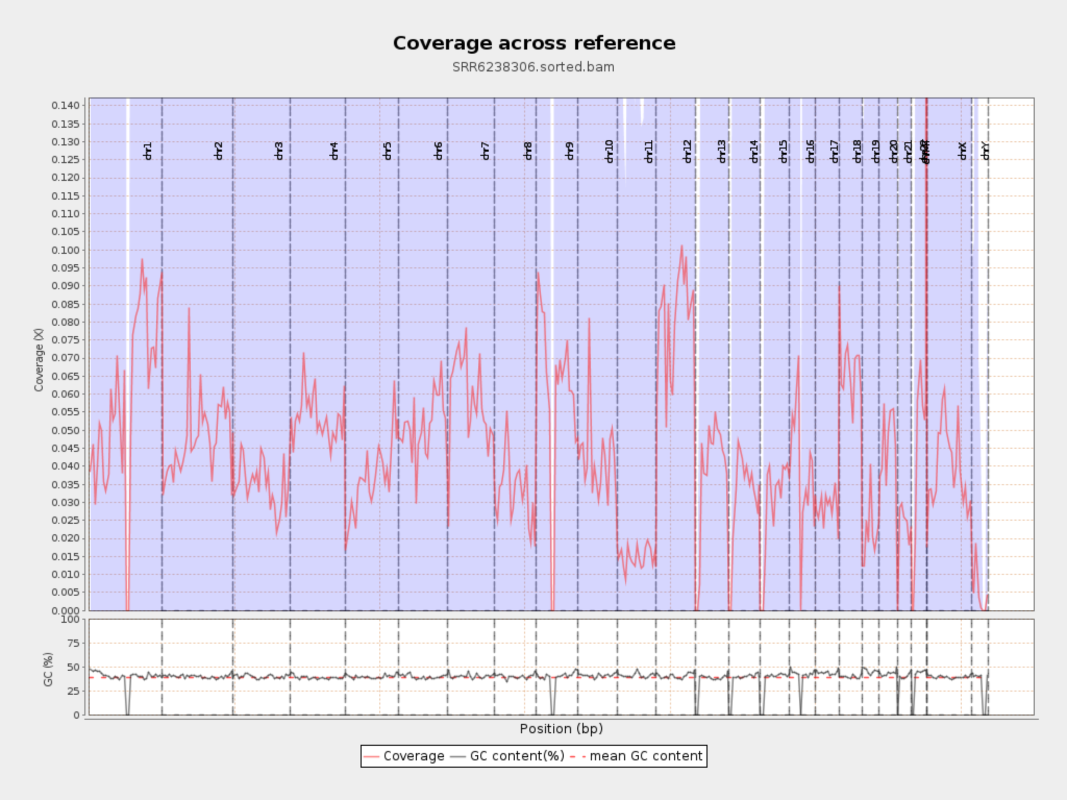
General error rate	0.84%
Mismatches	1,117,669
Insertions	10,480
Mapped reads with at least one insertion	0.51%
Deletions	34,686
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.1%

2.6. Chromosome stats

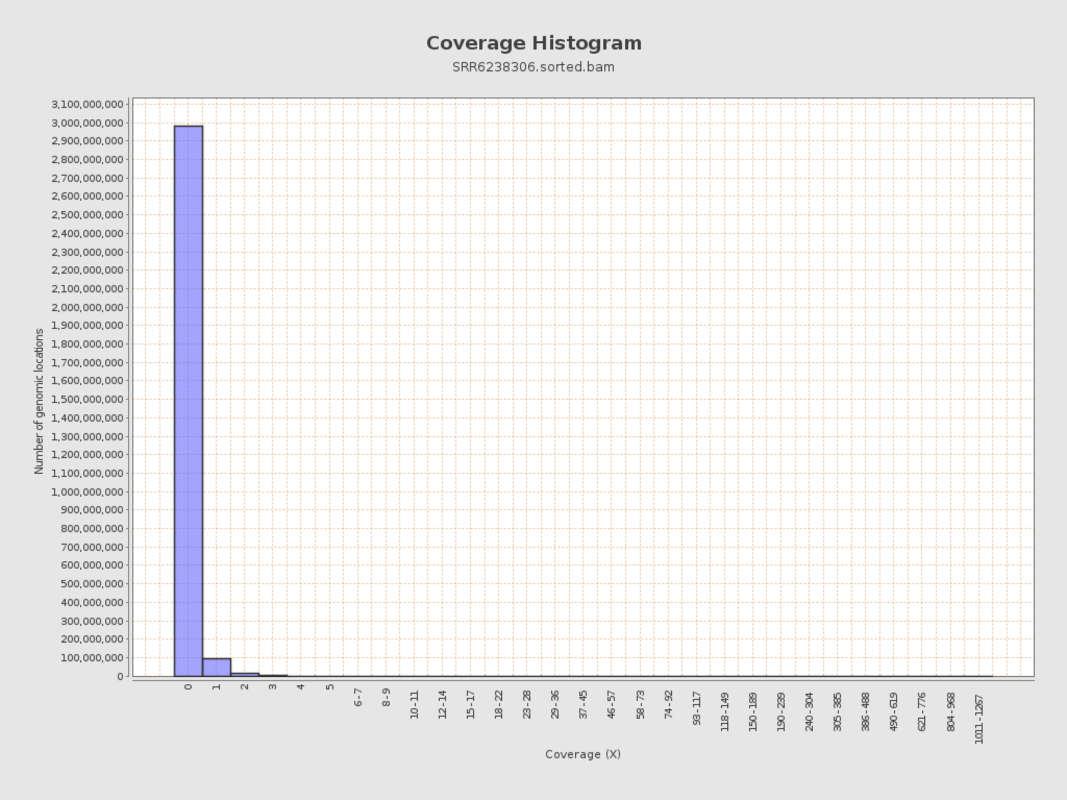
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14641300	0.0587	0.603
chr2	243199373	11628470	0.0478	0.4429
chr3	198022430	6961877	0.0352	0.2169
chr4	191154276	10246780	0.0536	0.2986
chr5	180915260	6656104	0.0368	0.2259
chr6	171115067	8758448	0.0512	0.3027
chr7	159138663	9462397	0.0595	0.5437

chr8	146364022	4812855	0.0329	0.7656
chr9	141213431	8682613	0.0615	0.4267
chr10	135534747	5731236	0.0423	0.4267
chr11	135006516	1995555	0.0148	0.1945
chr12	133851895	10853682	0.0811	0.3383
chr13	115169878	4321918	0.0375	0.223
chr14	107349540	3347754	0.0312	0.2562
chr15	102531392	2964269	0.0289	0.201
chr16	90354753	3587434	0.0397	0.2601
chr17	81195210	2317429	0.0285	0.2037
chr18	78077248	5213843	0.0668	0.6977
chr19	59128983	1299581	0.022	0.4467
chr20	63025520	2888220	0.0458	0.2528
chr21	48129895	1098081	0.0228	0.2138
chr22	51304566	2108763	0.0411	0.2339
chrMT	16571	11105	0.6701	1.1305
chrX	155270560	6170244	0.0397	0.2652
chrY	59373566	287070	0.0048	0.1547

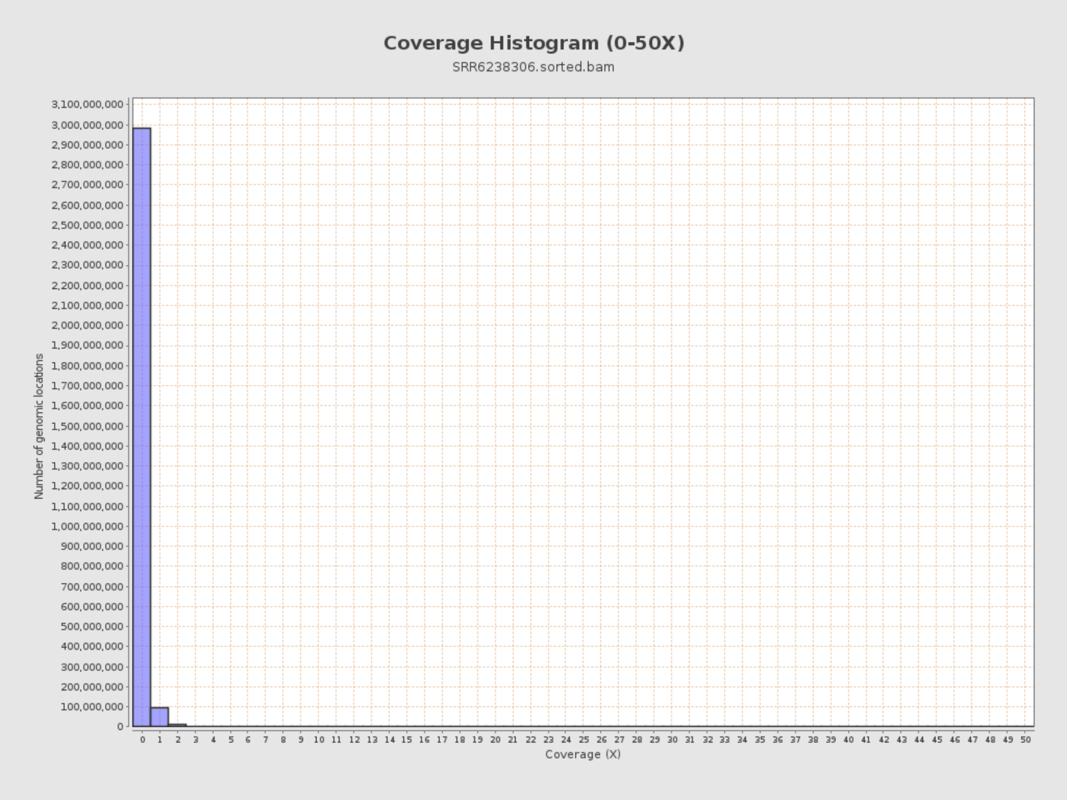
3. Results : Coverage across reference



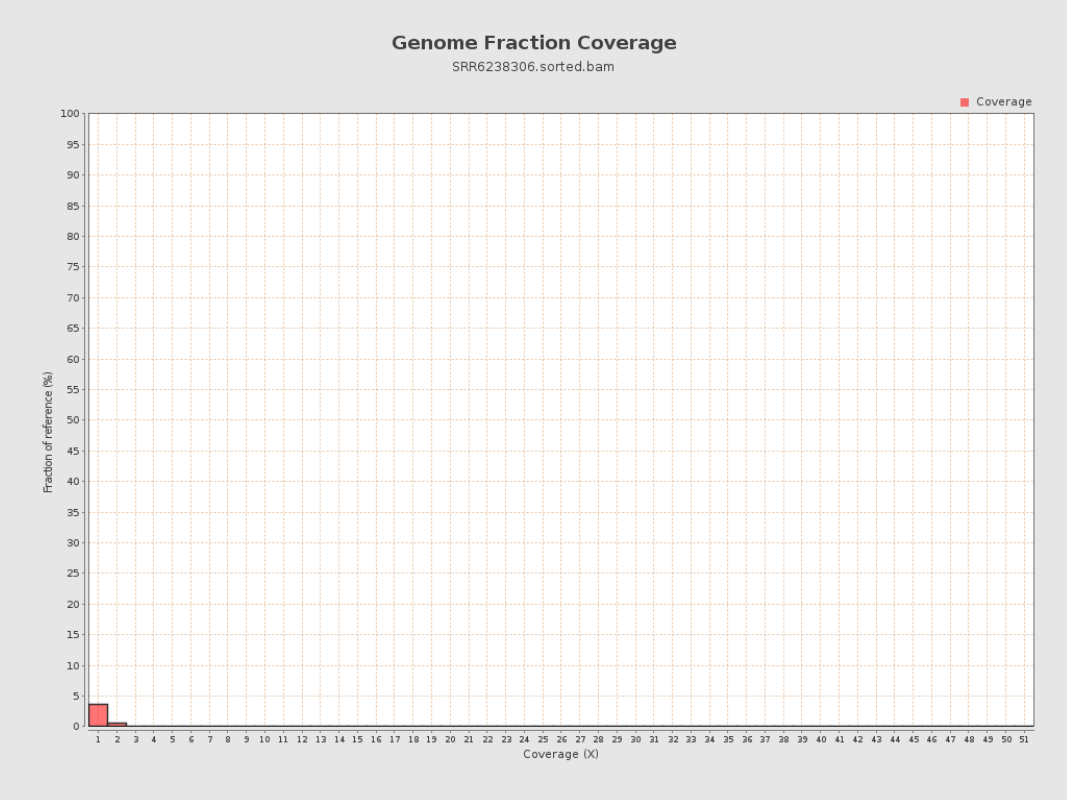
4. Results : Coverage Histogram



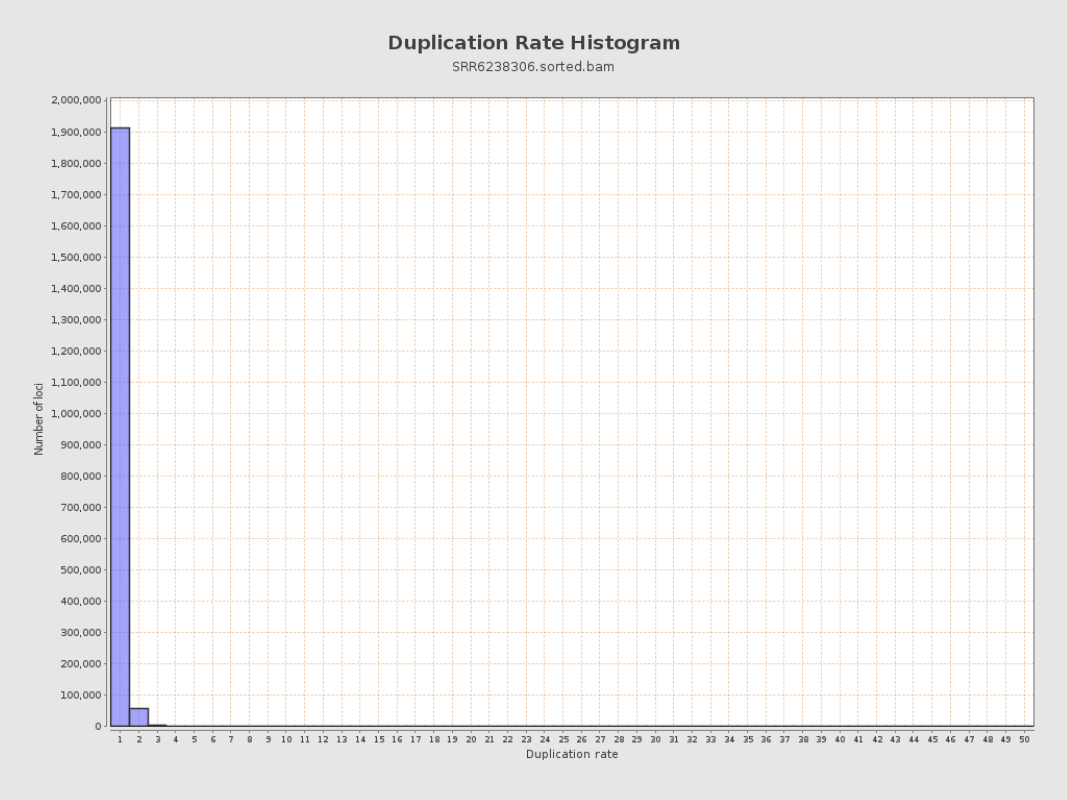
5. Results : Coverage Histogram (0-50X)



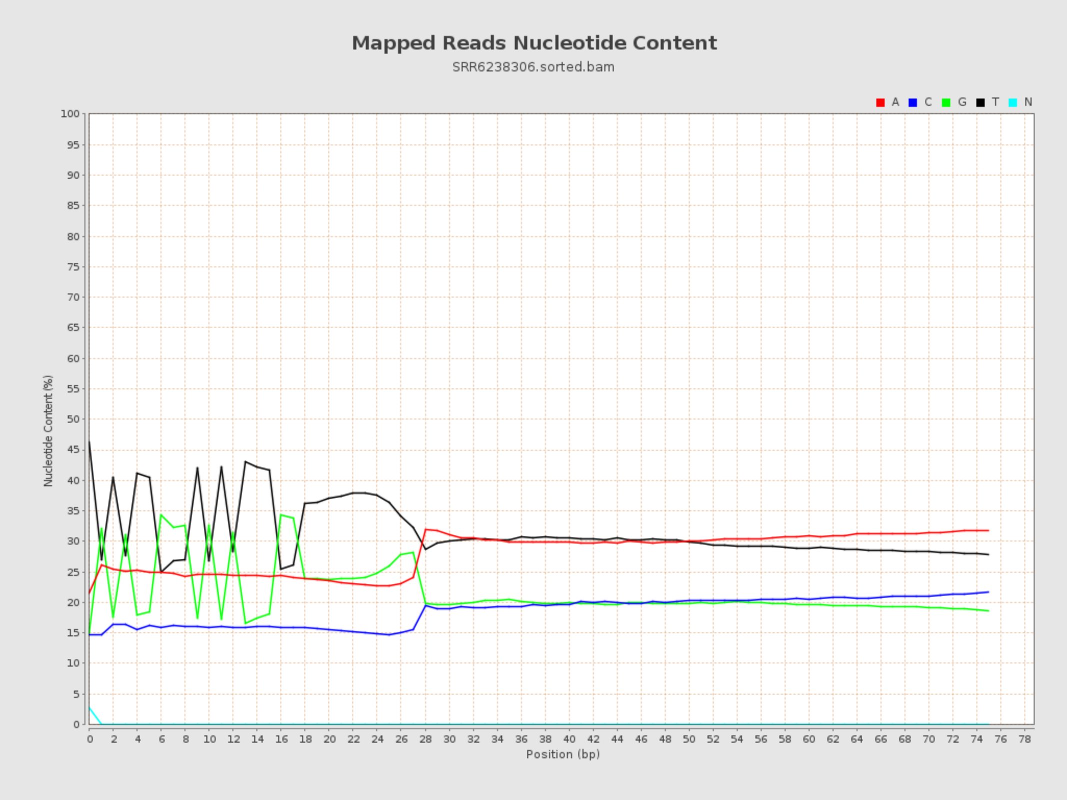
6. Results : Genome Fraction Coverage



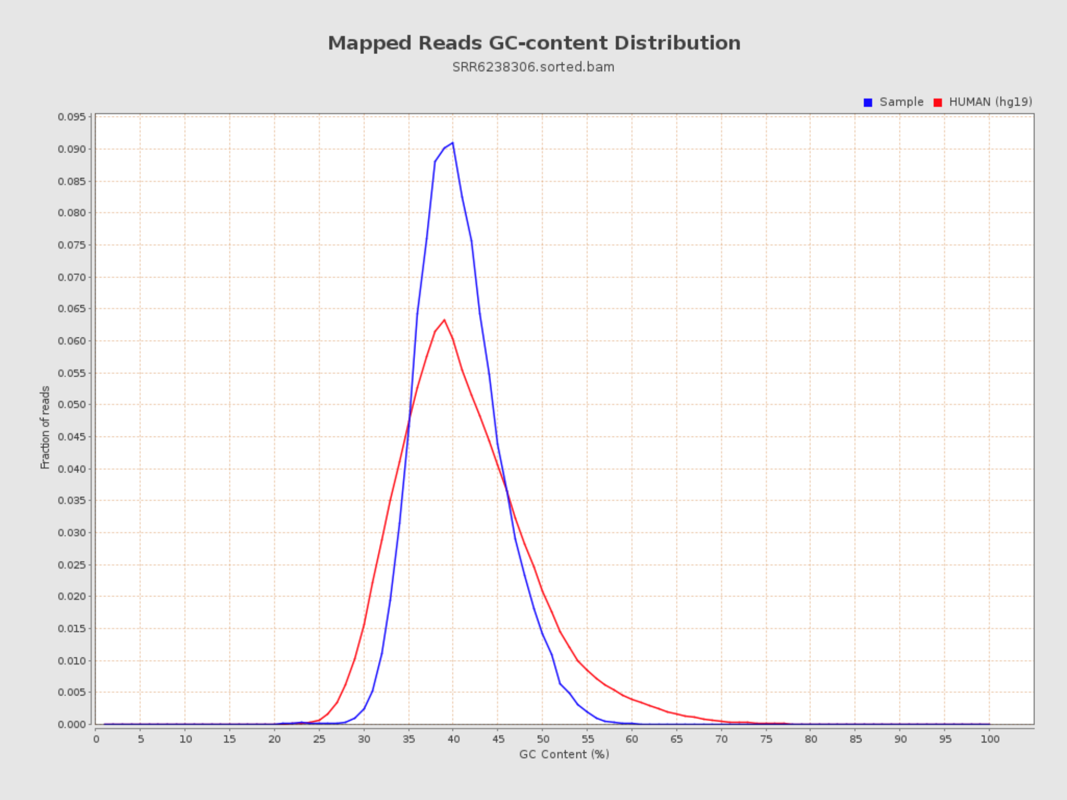
7. Results : Duplication Rate Histogram



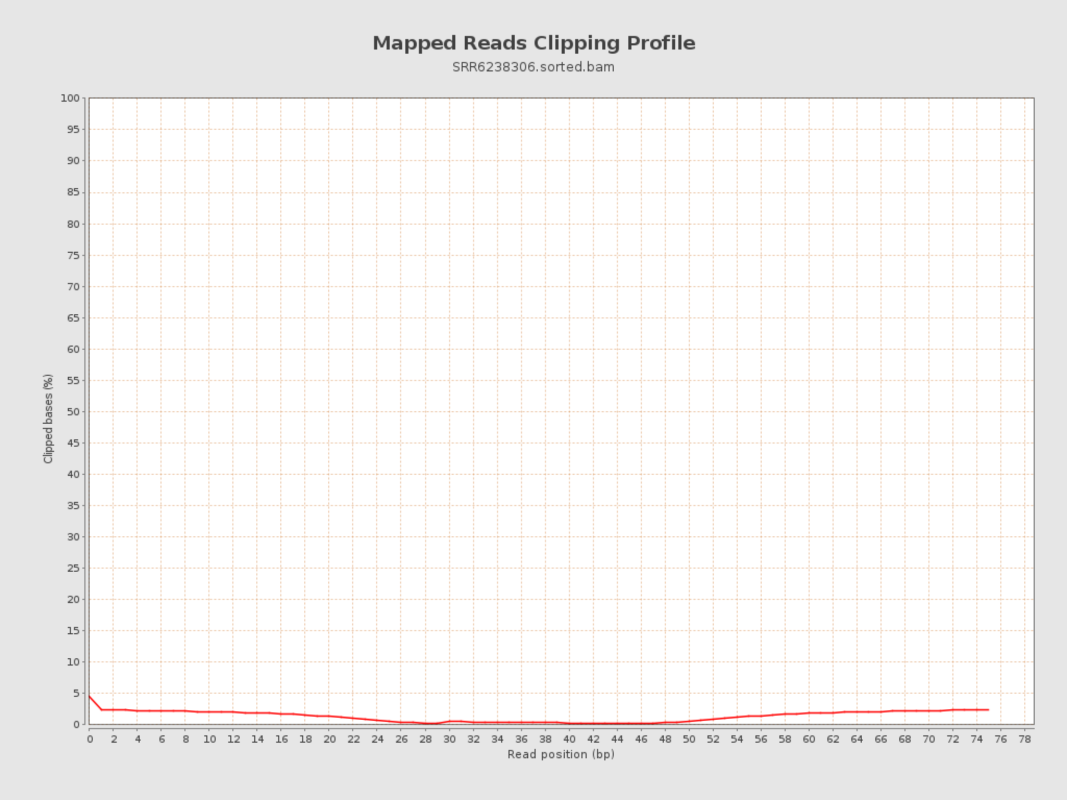
8. Results : Mapped Reads Nucleotide Content



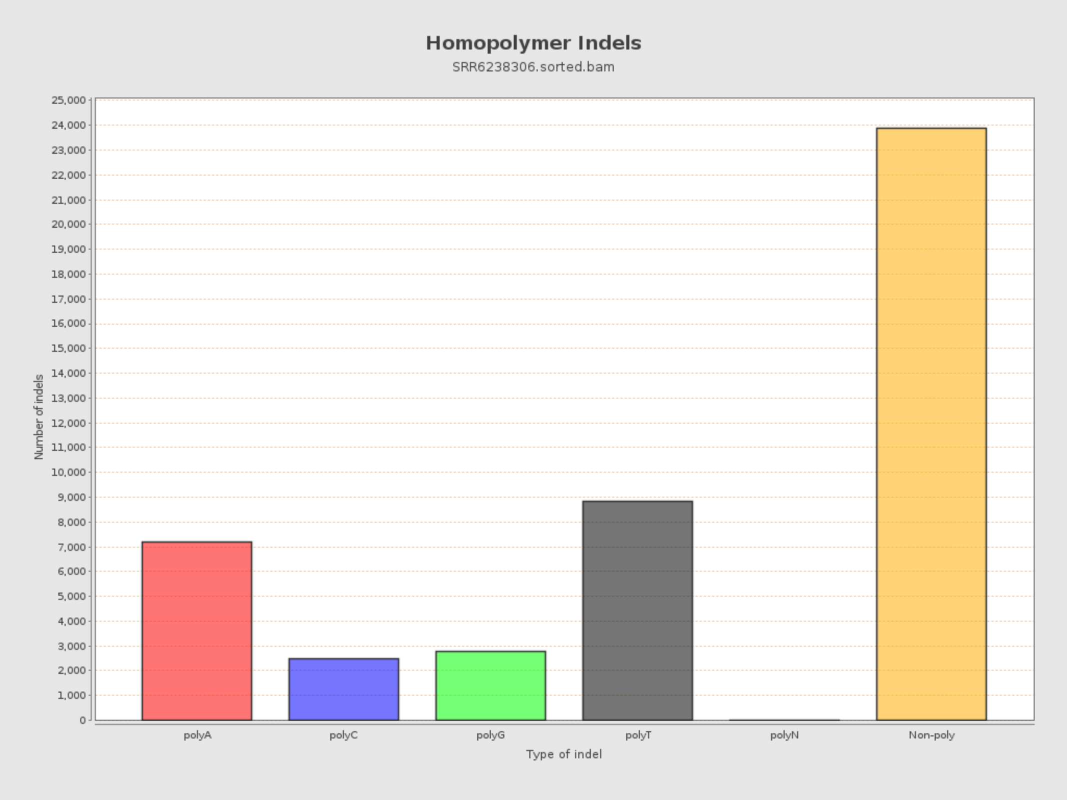
9. Results : Mapped Reads GC-content Distribution



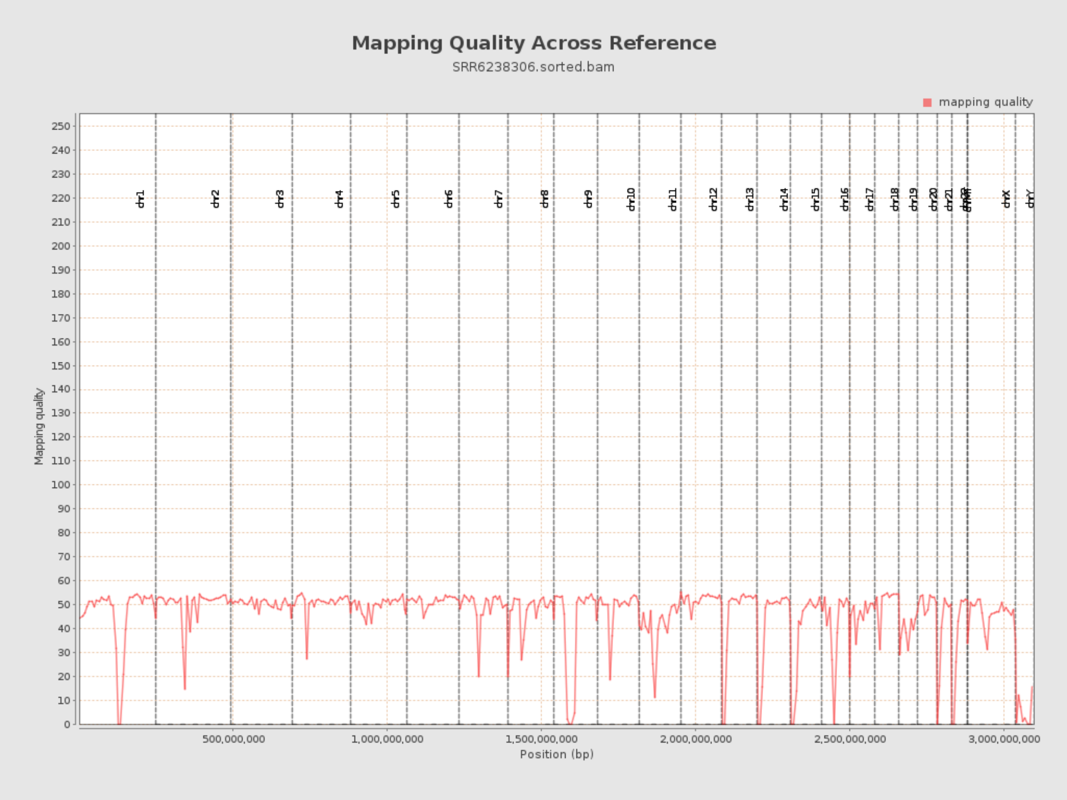
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram