Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:55:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238073.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_SRR6238073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:55:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,428,598
Mapped reads	1,176,780 / 82.37%
Unmapped reads	251,818 / 17.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,249 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	114,438 / 8.01%
Duplication rate	7.88%
Clipped reads	606,356 / 42.44%

2.2. ACGT Content

Number/percentage of A's	20,571,507 / 26.9%
Number/percentage of C's	14,399,548 / 18.83%
Number/percentage of T's	23,967,672 / 31.34%
Number/percentage of G's	17,523,054 / 22.92%
Number/percentage of N's	4,211 / 0.01%
GC Percentage	41.75%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2648

2.4. Mapping Quality

Mean Mapping Quality	44.06

2.5. Mismatches and indels

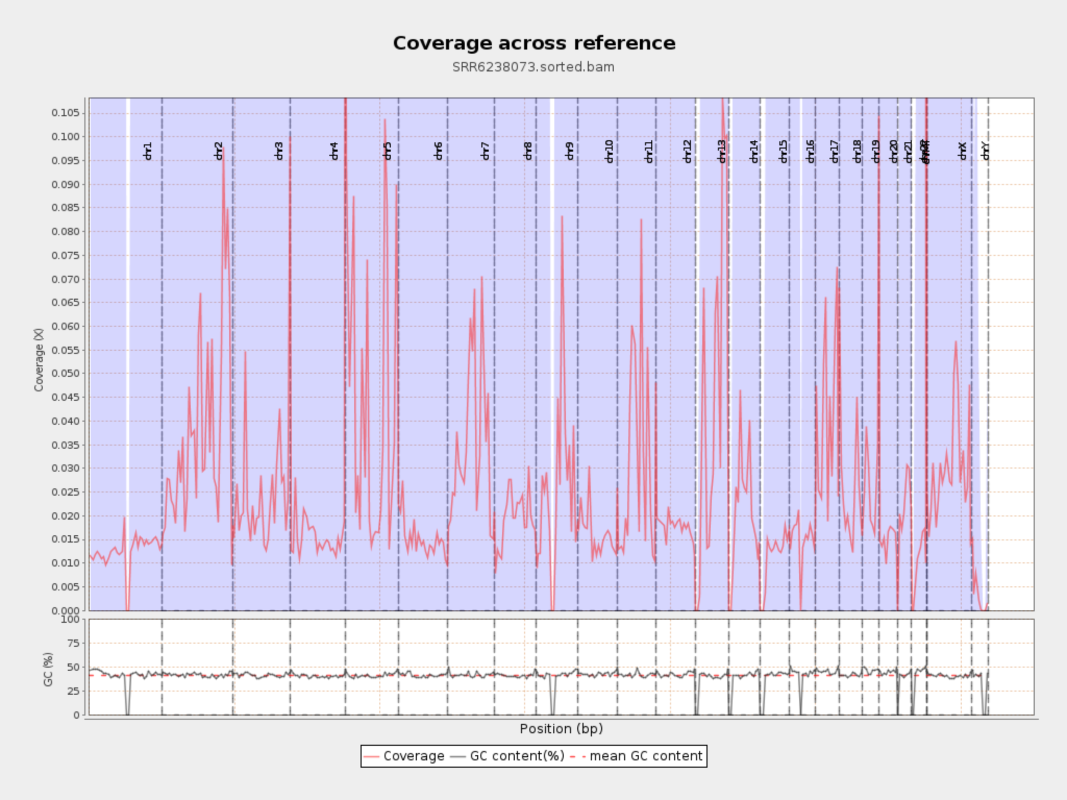
General error rate	0.8%
Mismatches	600,279
Insertions	4,900
Mapped reads with at least one insertion	0.41%
Deletions	25,279
Mapped reads with at least one deletion	2.12%
Homopolymer indels	43.36%

2.6. Chromosome stats

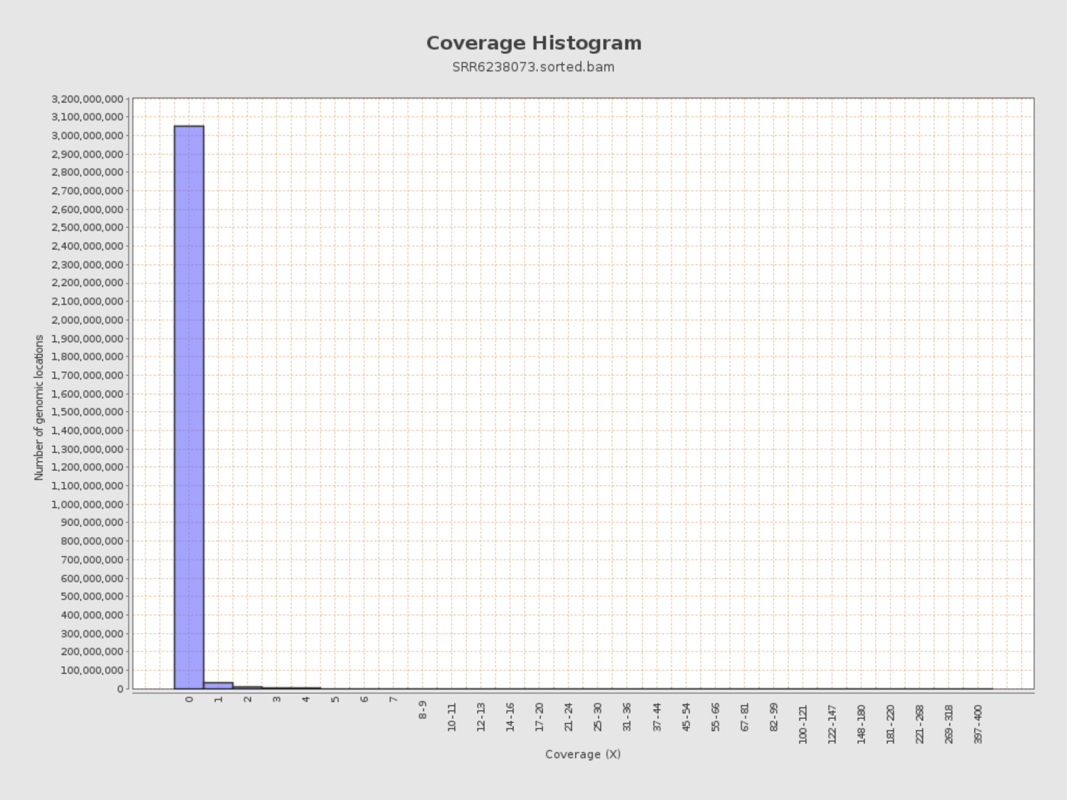
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3104357	0.0125	0.2607
chr2	243199373	9433358	0.0388	0.3536
chr3	198022430	4680286	0.0236	0.2363
chr4	191154276	2960768	0.0155	0.1844
chr5	180915260	8078508	0.0447	0.3347
chr6	171115067	2604243	0.0152	0.2016
chr7	159138663	5863890	0.0368	0.3502

chr8	146364022	2845396	0.0194	0.2367
chr9	141213431	3630677	0.0257	0.2557
chr10	135534747	2182724	0.0161	0.2228
chr11	135006516	4097401	0.0303	0.297
chr12	133851895	2386824	0.0178	0.1972
chr13	115169878	5187854	0.045	0.3425
chr14	107349540	2230171	0.0208	0.2242
chr15	102531392	1161764	0.0113	0.159
chr16	90354753	1357060	0.015	0.1775
chr17	81195210	3484632	0.0429	0.3385
chr18	78077248	2009305	0.0257	0.288
chr19	59128983	1685937	0.0285	0.302
chr20	63025520	949275	0.0151	0.1802
chr21	48129895	1023607	0.0213	0.2357
chr22	51304566	511909	0.01	0.1488
chrMT	16571	57422	3.4652	3.4989
chrX	155270560	4787178	0.0308	0.273
chrY	59373566	195636	0.0033	0.0815

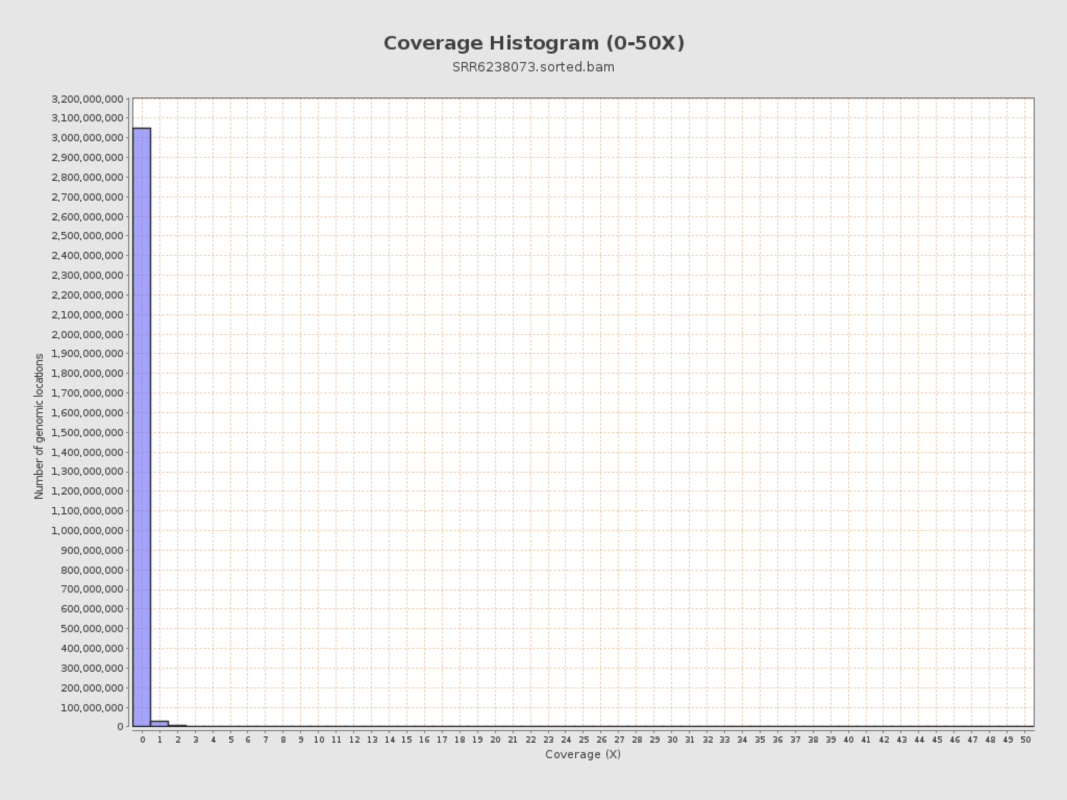
3. Results : Coverage across reference



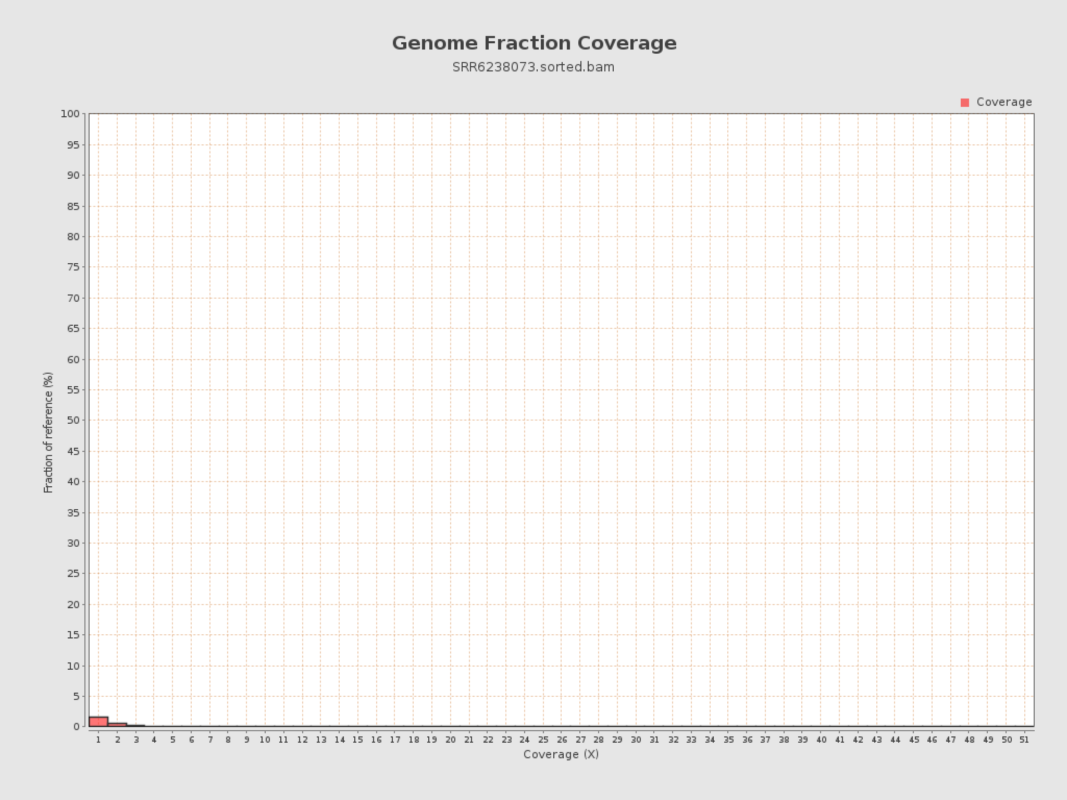
4. Results : Coverage Histogram



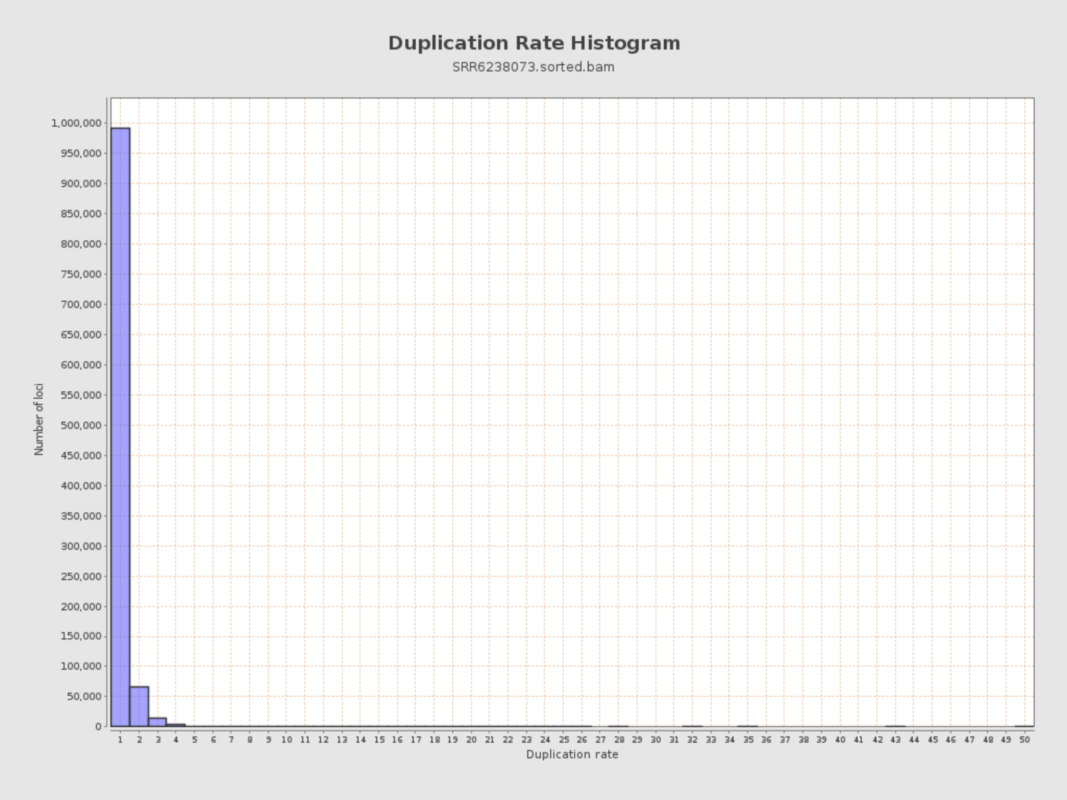
5. Results : Coverage Histogram (0-50X)



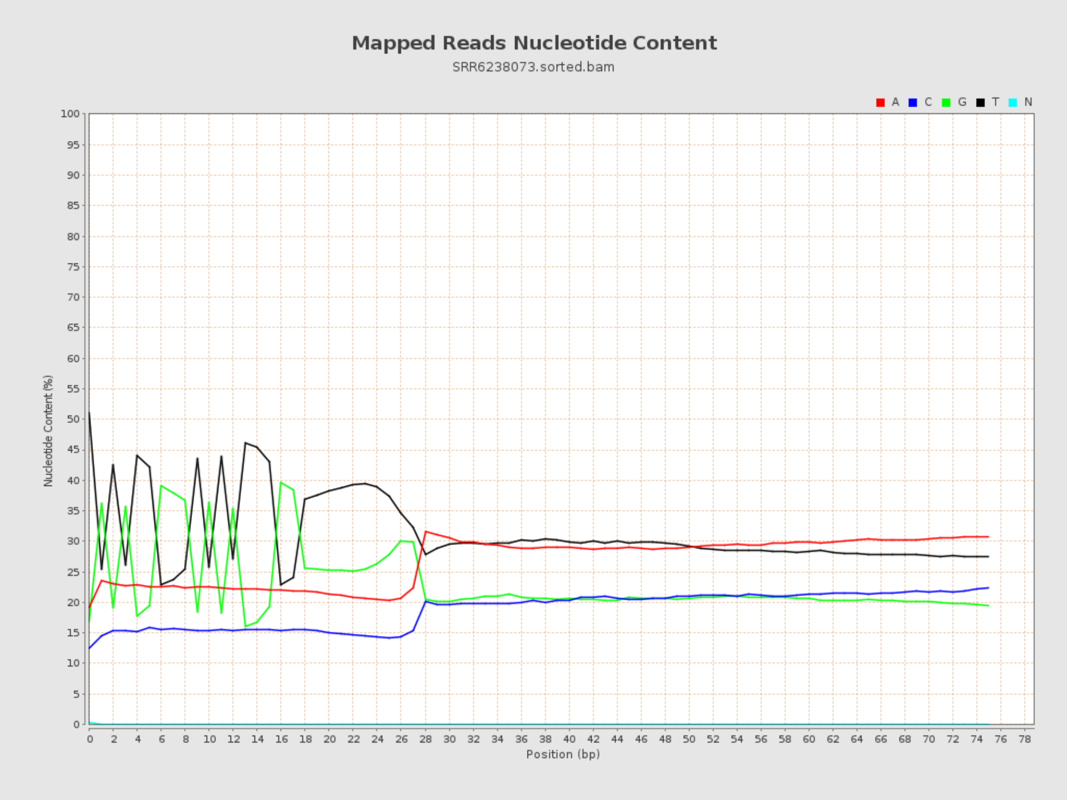
6. Results : Genome Fraction Coverage



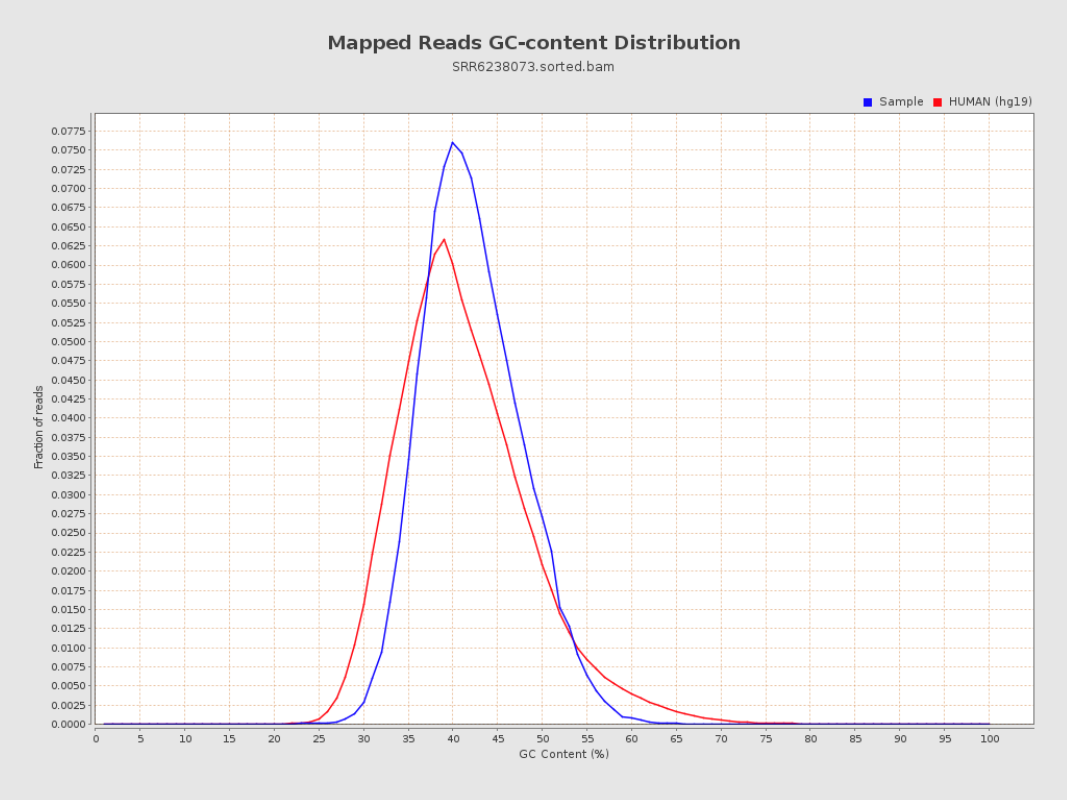
7. Results : Duplication Rate Histogram



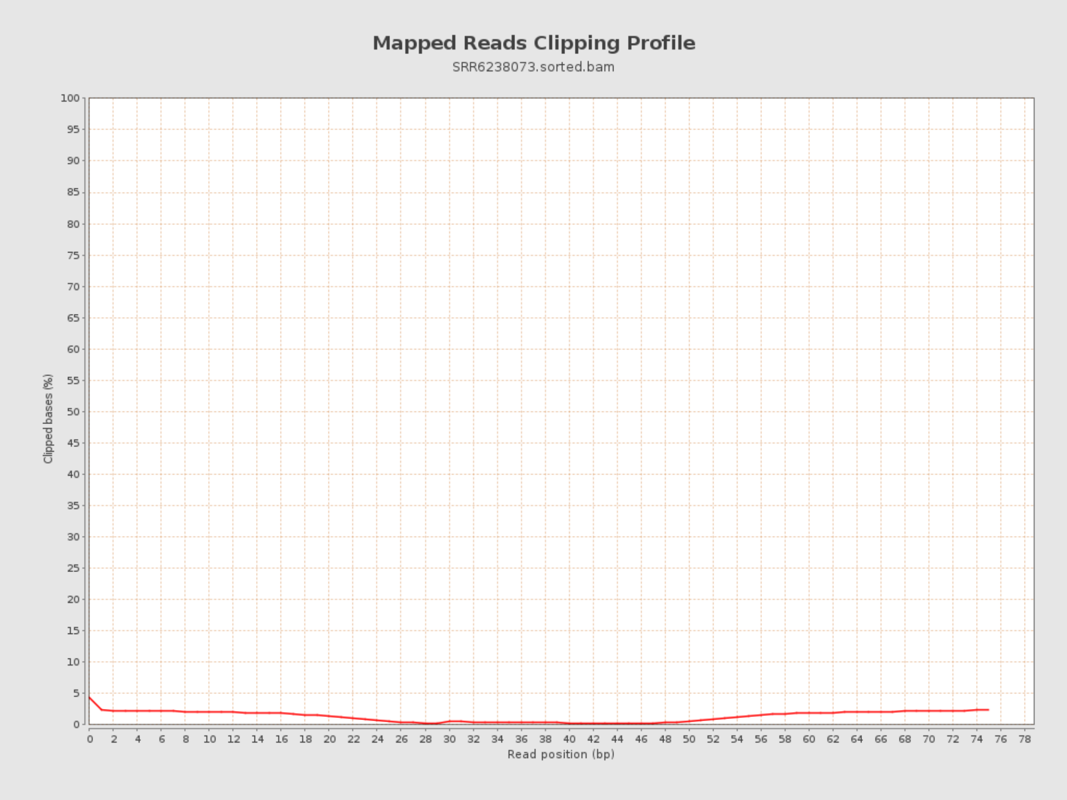
8. Results : Mapped Reads Nucleotide Content



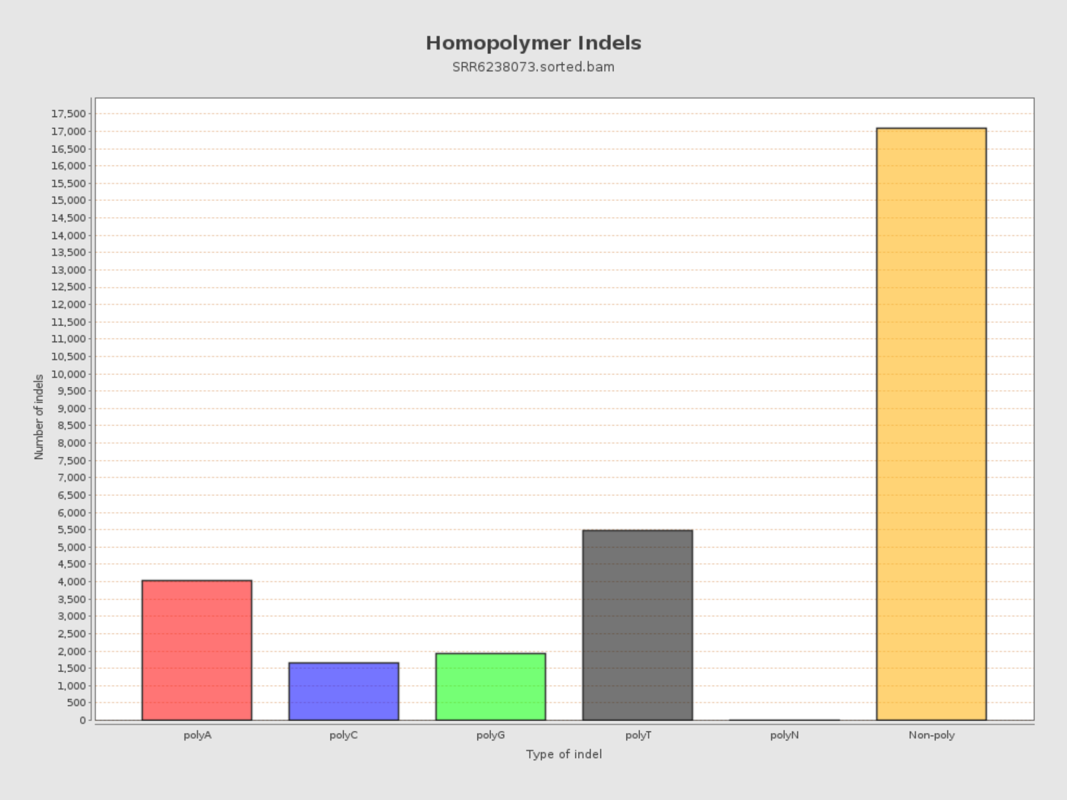
9. Results : Mapped Reads GC-content Distribution



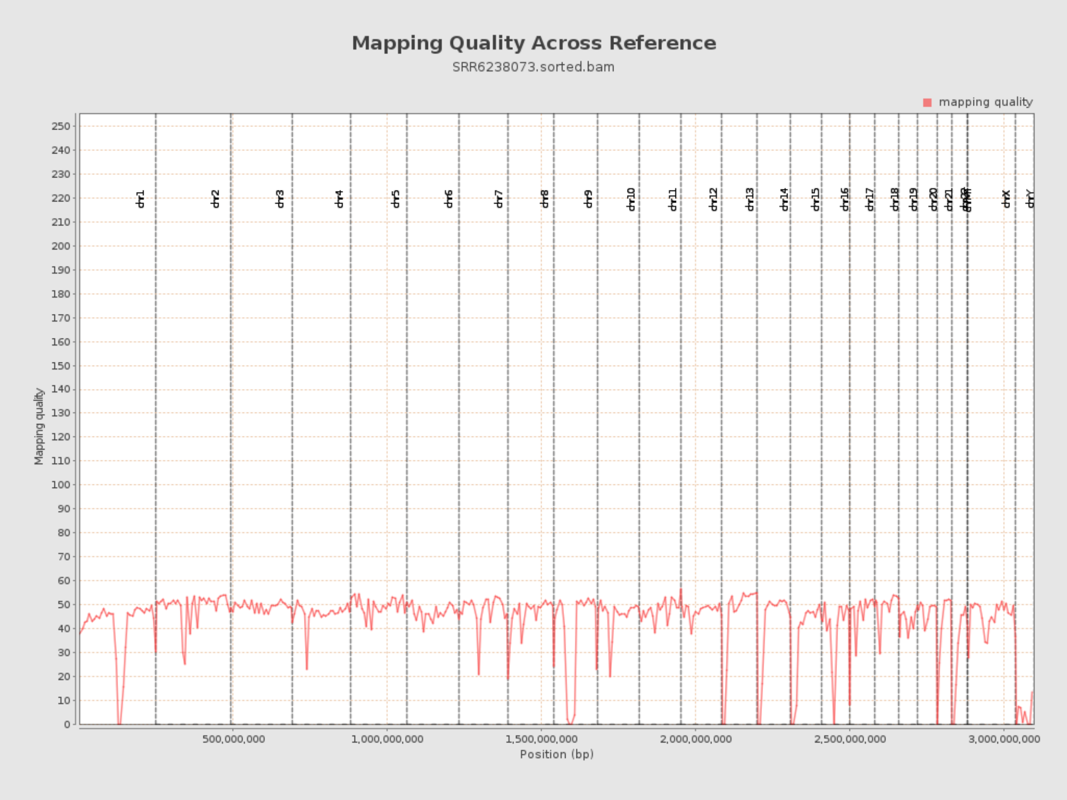
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram