Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:59:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238654.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_SRR6238654 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238654.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:59:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238654.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,583,041
Mapped reads	3,196,537 / 89.21%
Unmapped reads	386,504 / 10.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,580 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	1,148,095 / 32.04%
Duplication rate	21.26%
Clipped reads	2,031,453 / 56.7%

2.2. ACGT Content

Number/percentage of A's	49,274,127 / 25.01%
Number/percentage of C's	33,965,063 / 17.24%
Number/percentage of T's	67,267,827 / 34.15%
Number/percentage of G's	46,483,265 / 23.6%
Number/percentage of N's	4,433 / 0%
GC Percentage	40.84%

2.3. Coverage

Mean	0.0637

Standard Deviation	1.0212

2.4. Mapping Quality

Mean Mapping Quality	31.32

2.5. Mismatches and indels

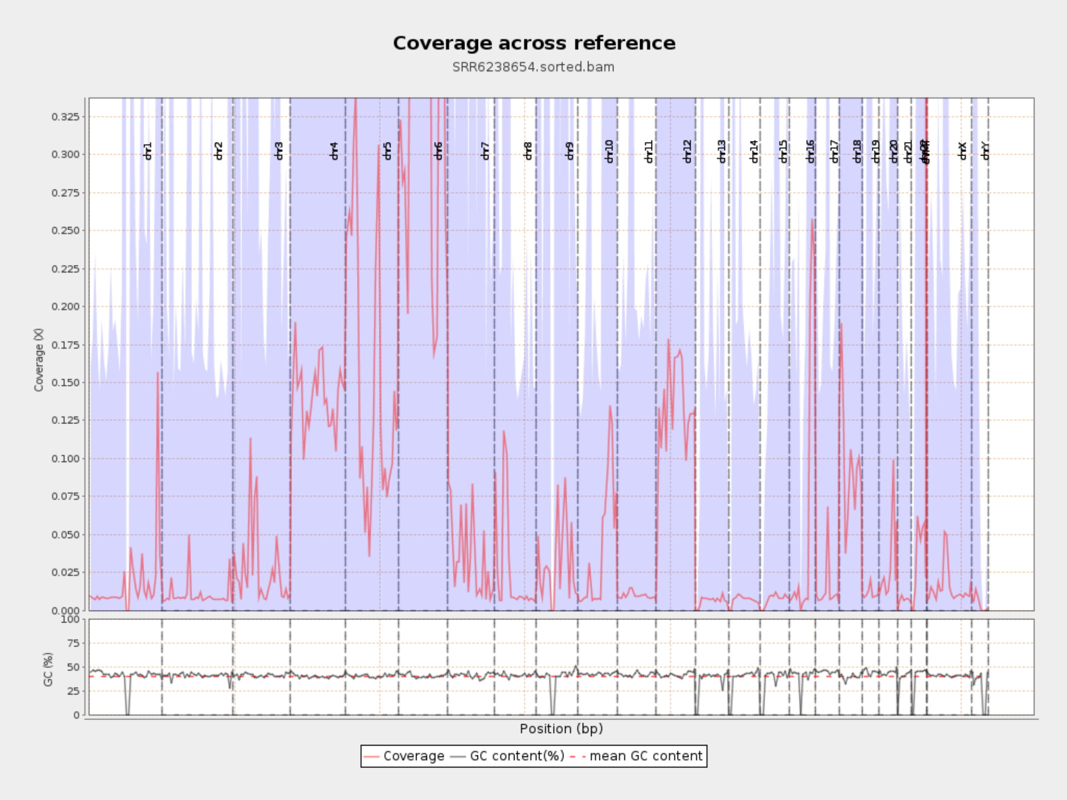
General error rate	0.55%
Mismatches	1,055,897
Insertions	12,048
Mapped reads with at least one insertion	0.37%
Deletions	49,170
Mapped reads with at least one deletion	1.53%
Homopolymer indels	42.54%

2.6. Chromosome stats

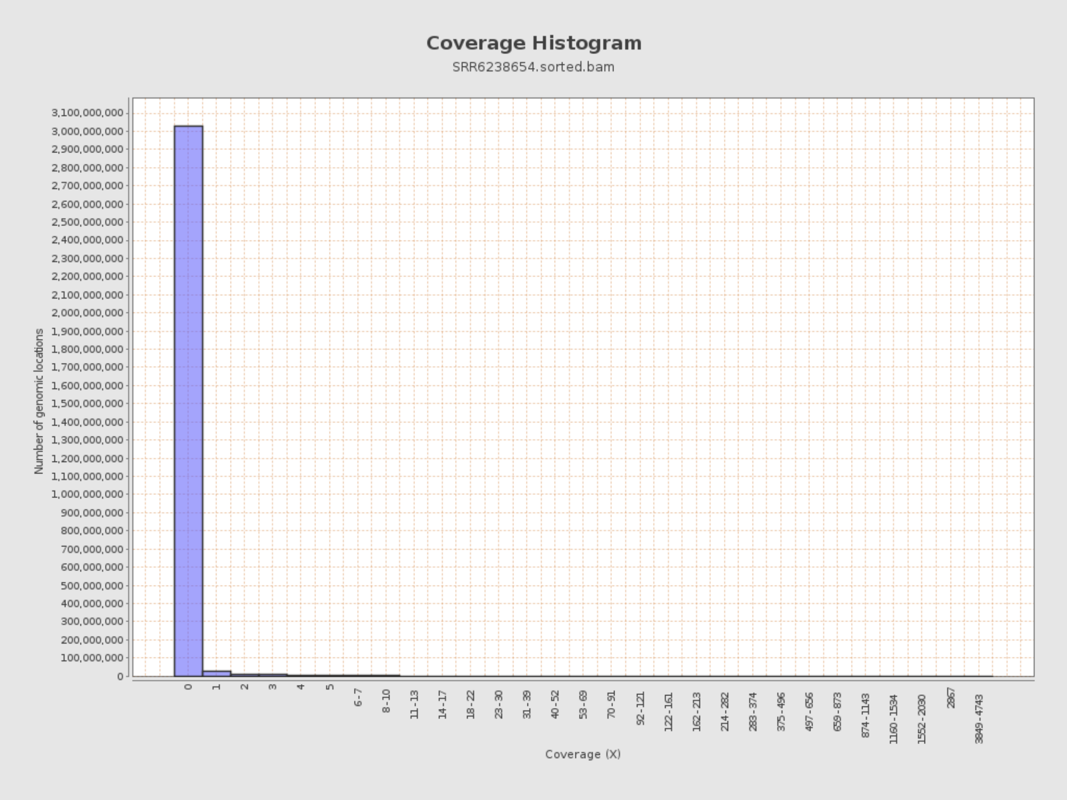
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4472008	0.0179	0.4181
chr2	243199373	2558977	0.0105	2.1219
chr3	198022430	5423282	0.0274	0.4009
chr4	191154276	27137058	0.142	0.8861
chr5	180915260	27857269	0.154	0.9446
chr6	171115067	66770920	0.3902	2.2137
chr7	159138663	5647090	0.0355	0.6747

chr8	146364022	3711345	0.0254	0.874
chr9	141213431	4502812	0.0319	0.5222
chr10	135534747	5331324	0.0393	0.528
chr11	135006516	1356357	0.01	0.2778
chr12	133851895	17828533	0.1332	0.8845
chr13	115169878	733890	0.0064	0.4922
chr14	107349540	738682	0.0069	0.2452
chr15	102531392	751226	0.0073	0.4539
chr16	90354753	5961279	0.066	0.6457
chr17	81195210	1191455	0.0147	0.2593
chr18	78077248	7663085	0.0981	2.1056
chr19	59128983	692058	0.0117	0.5033
chr20	63025520	1870257	0.0297	0.4257
chr21	48129895	327311	0.0068	0.1719
chr22	51304566	1879744	0.0366	0.4578
chrMT	16571	56897	3.4335	4.1127
chrX	155270560	2358932	0.0152	0.3251
chrY	59373566	255601	0.0043	0.3166

3. Results : Coverage across reference



4. Results : Coverage Histogram



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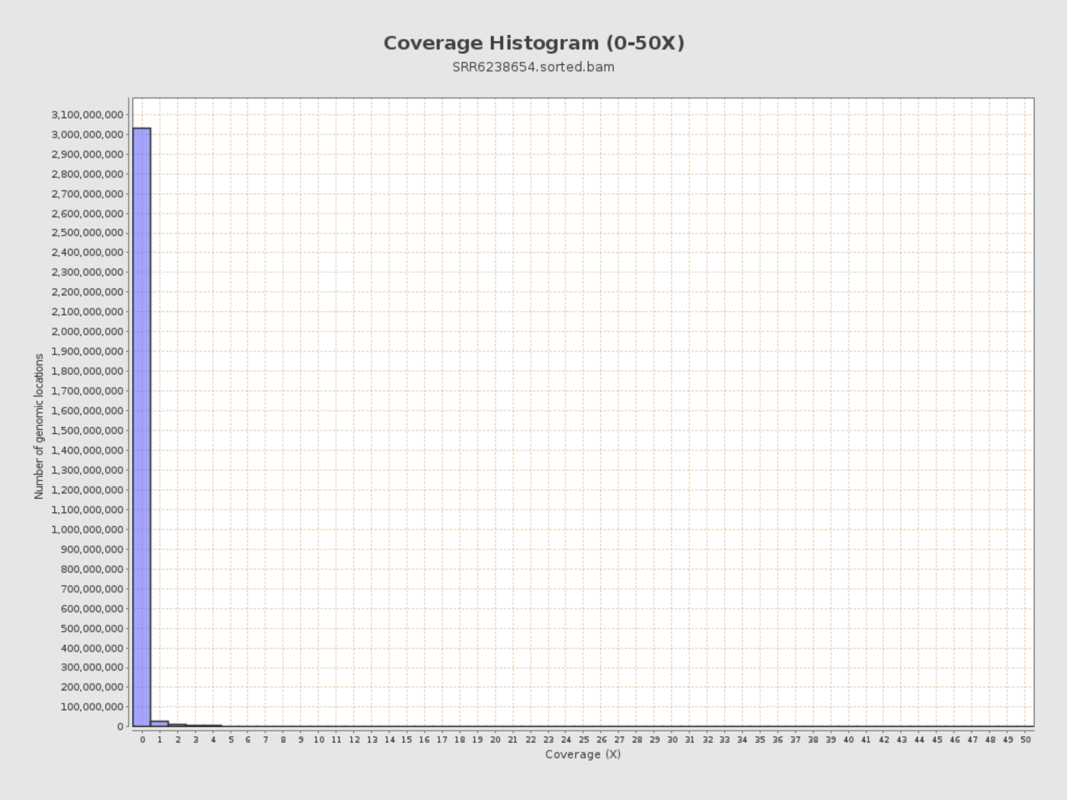
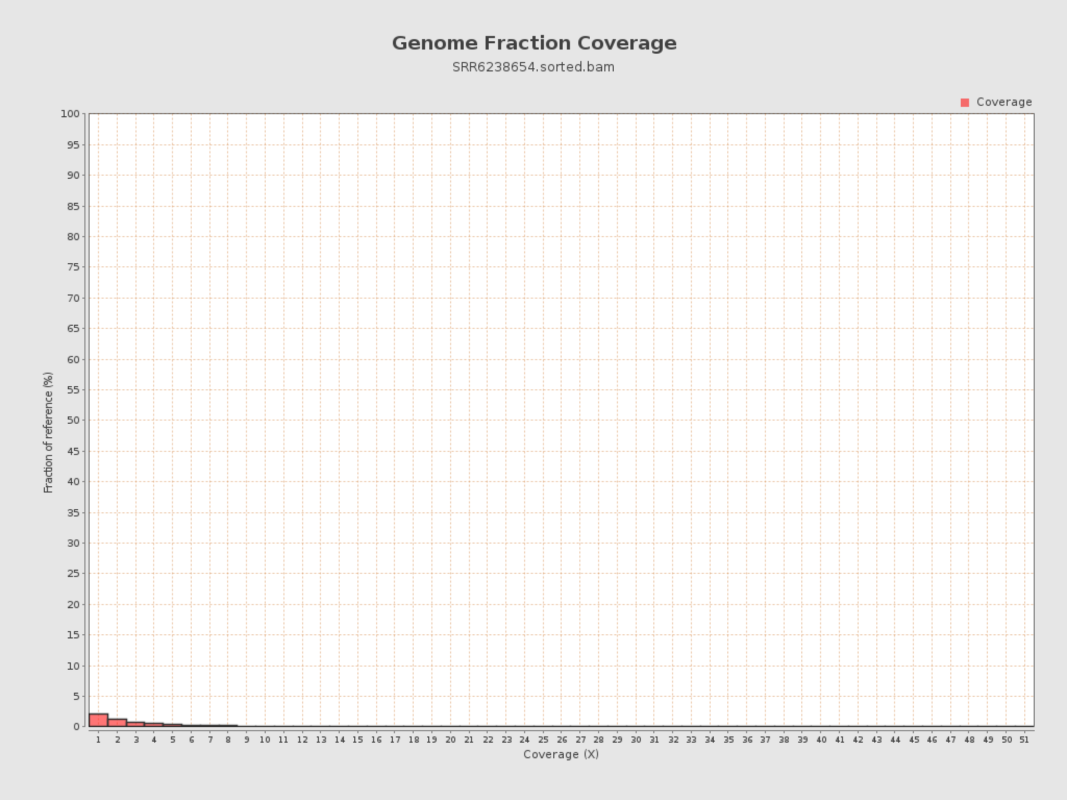
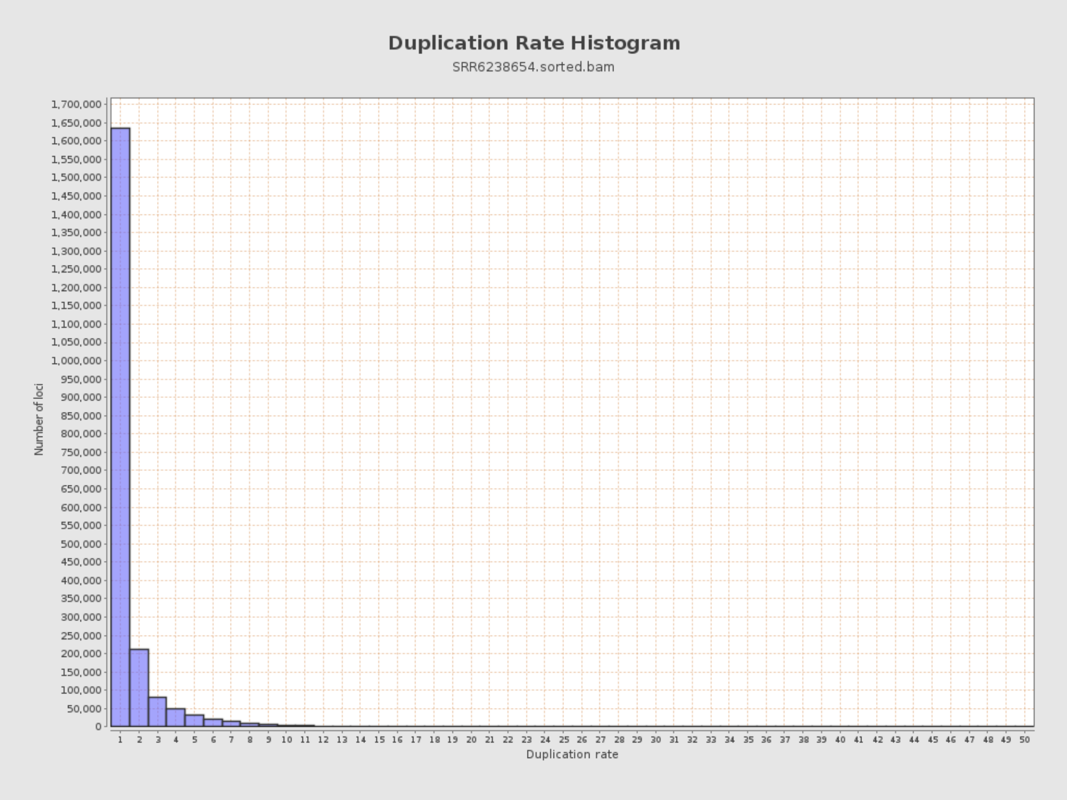
5. Results : Coverage Histogram (0-50X)



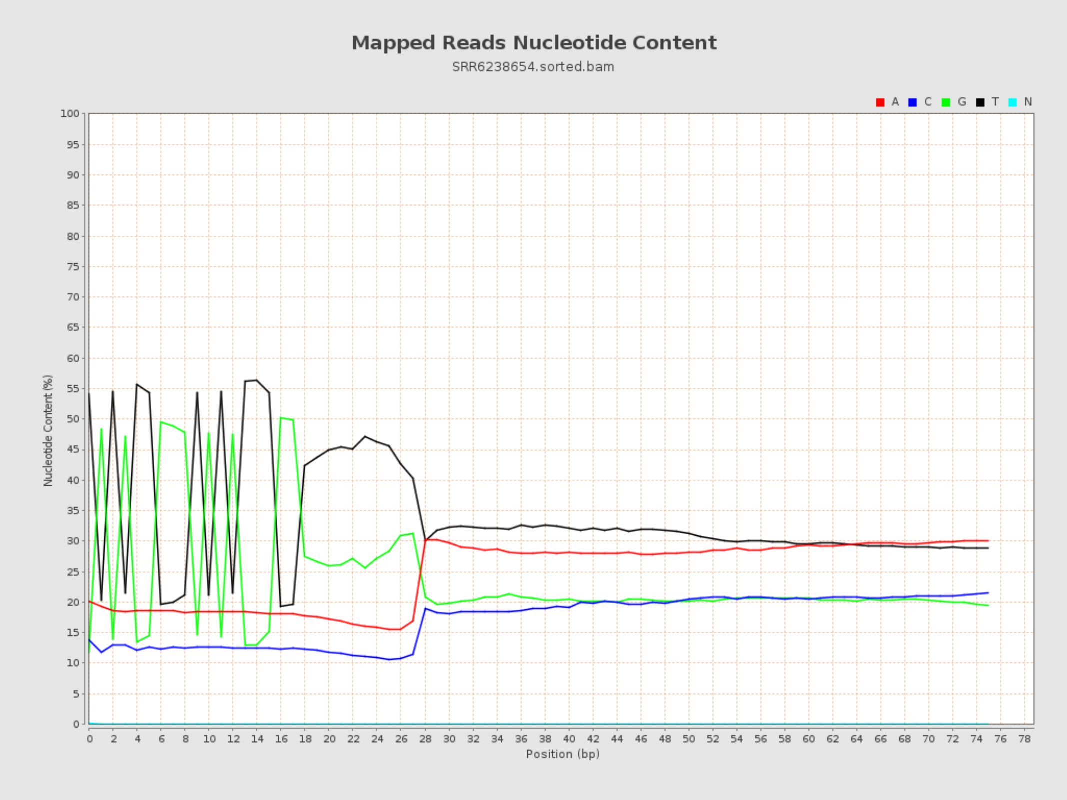
6. Results : Genome Fraction Coverage



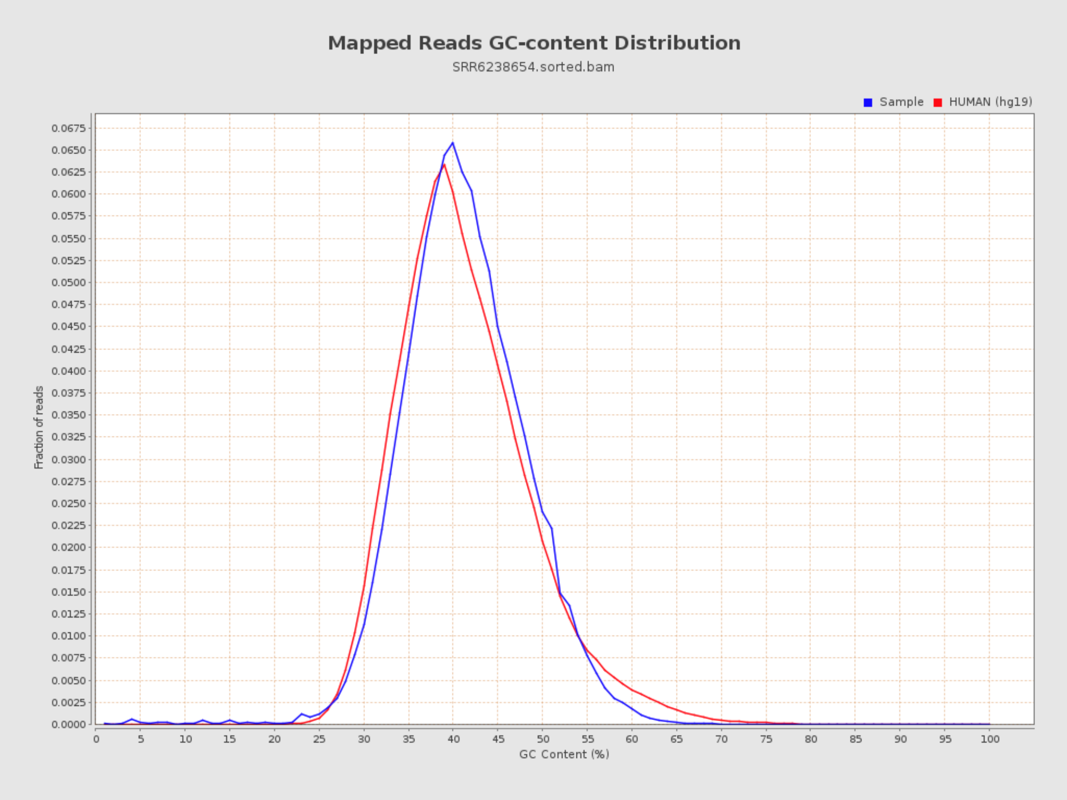
7. Results : Duplication Rate Histogram



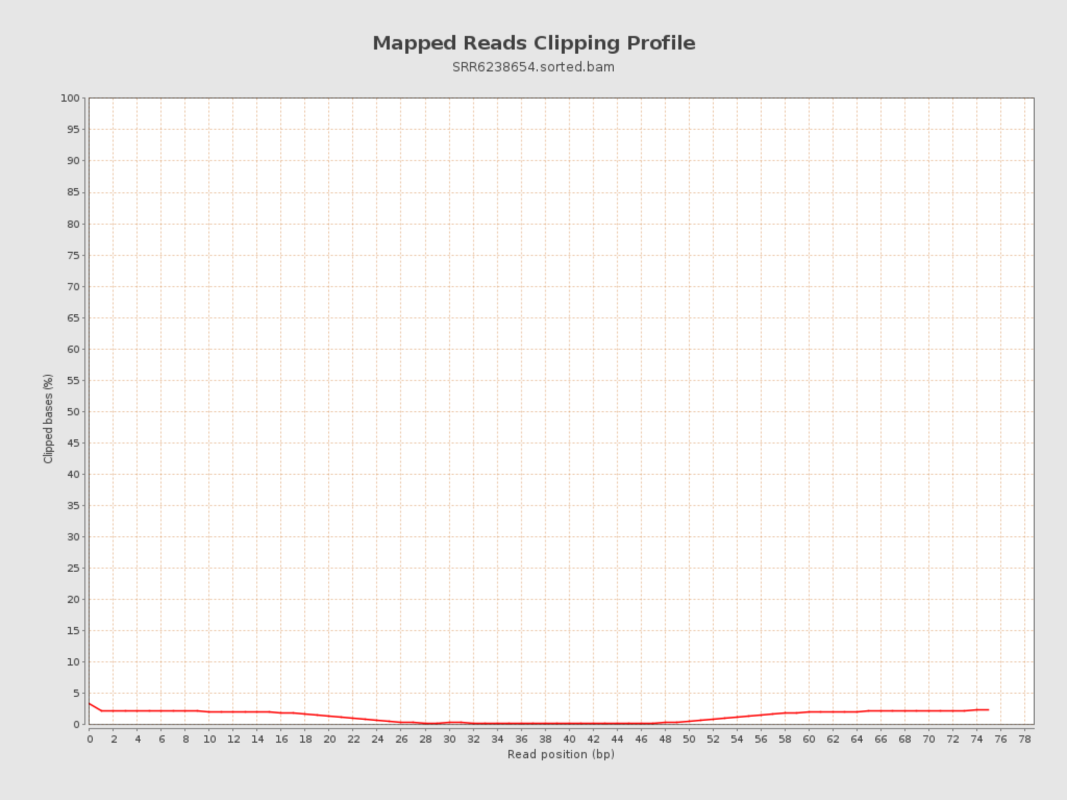
8. Results : Mapped Reads Nucleotide Content



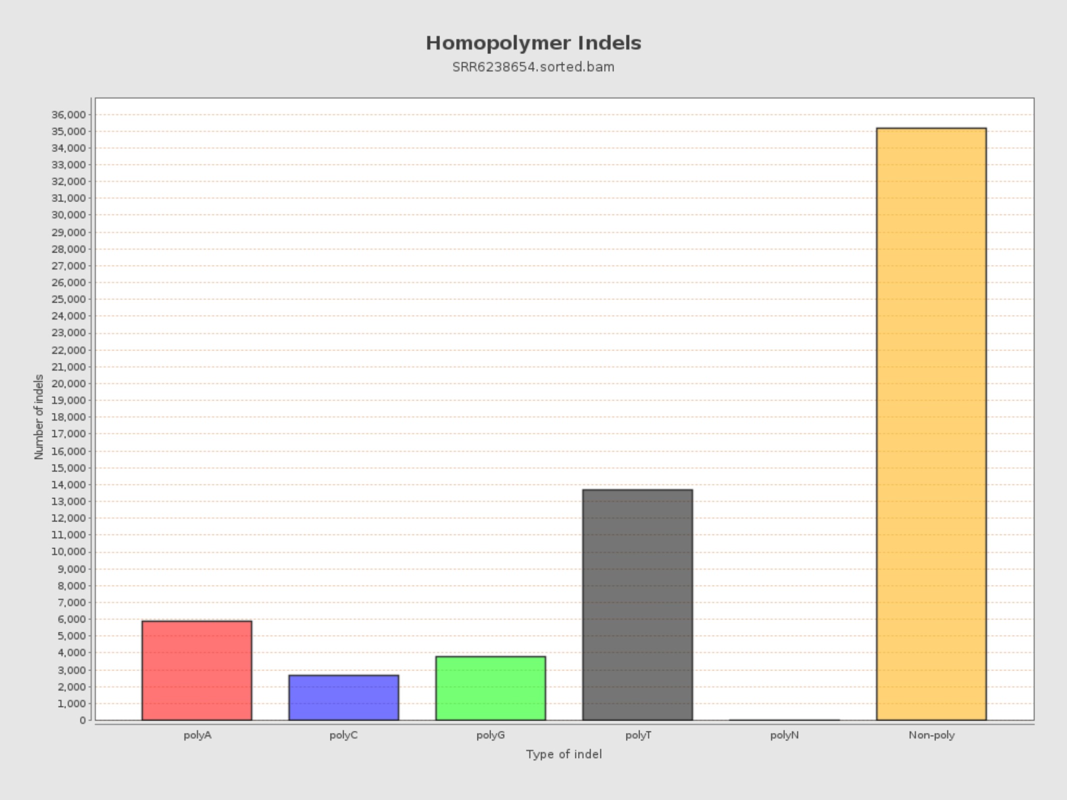
9. Results : Mapped Reads GC-content Distribution



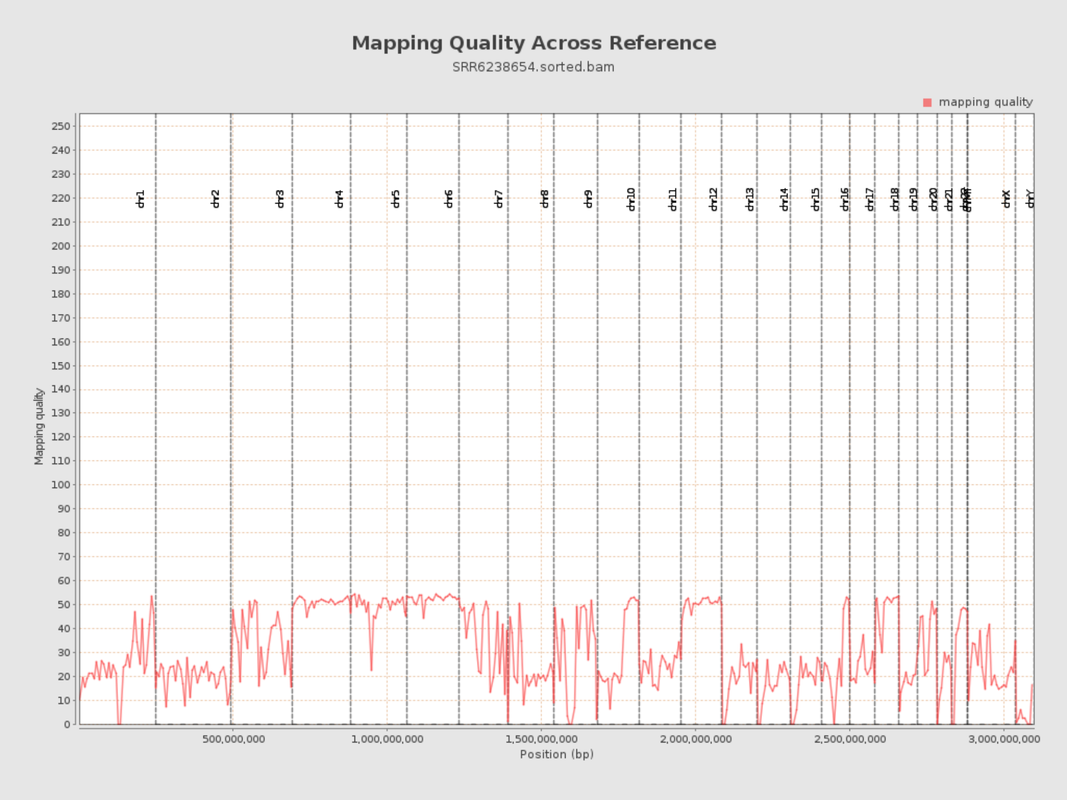
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram