Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:46:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238538.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_SRR6238538 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238538.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:46:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238538.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,726,988
Mapped reads	6,868,696 / 88.89%
Unmapped reads	858,292 / 11.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	71,095 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	3,023,675 / 39.13%
Duplication rate	21.91%
Clipped reads	4,366,685 / 56.51%

2.2. ACGT Content

Number/percentage of A's	104,609,737 / 24.63%
Number/percentage of C's	75,796,760 / 17.85%
Number/percentage of T's	142,003,057 / 33.43%
Number/percentage of G's	102,279,746 / 24.08%
Number/percentage of N's	28,915 / 0.01%
GC Percentage	41.93%

2.3. Coverage

Mean	0.1373

Standard Deviation	2.341

2.4. Mapping Quality

Mean Mapping Quality	38.28

2.5. Mismatches and indels

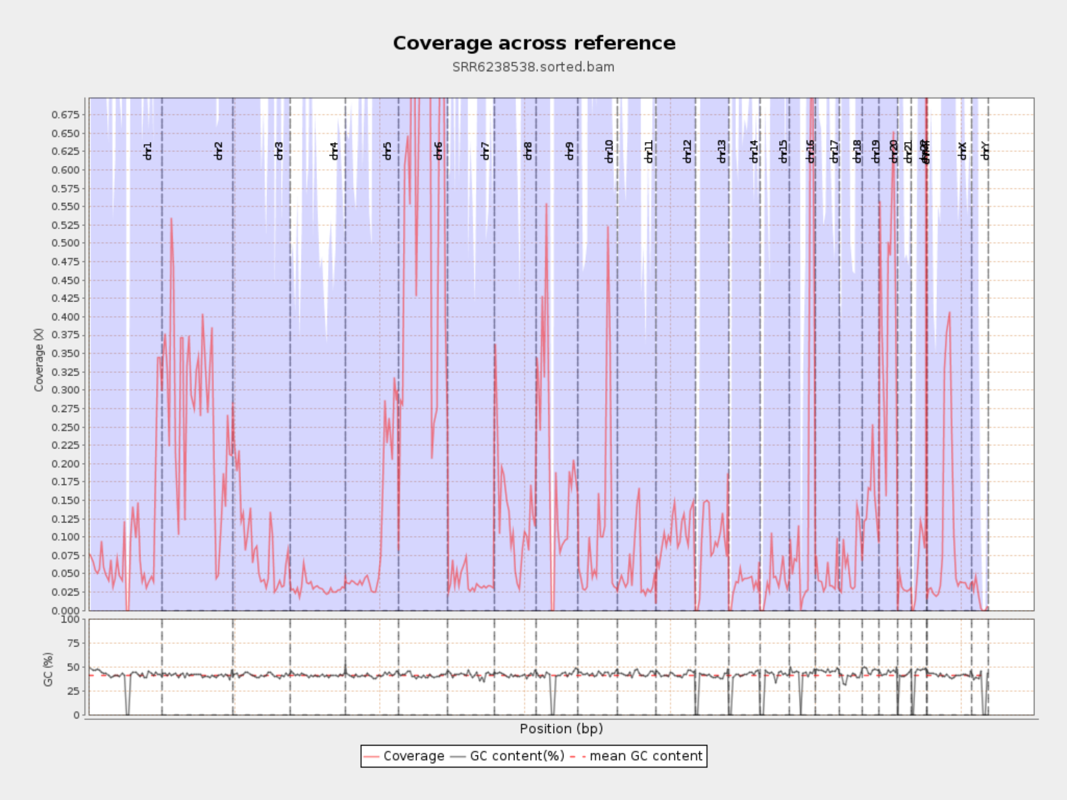
General error rate	0.63%
Mismatches	2,624,741
Insertions	27,534
Mapped reads with at least one insertion	0.4%
Deletions	143,215
Mapped reads with at least one deletion	2.06%
Homopolymer indels	40.61%

2.6. Chromosome stats

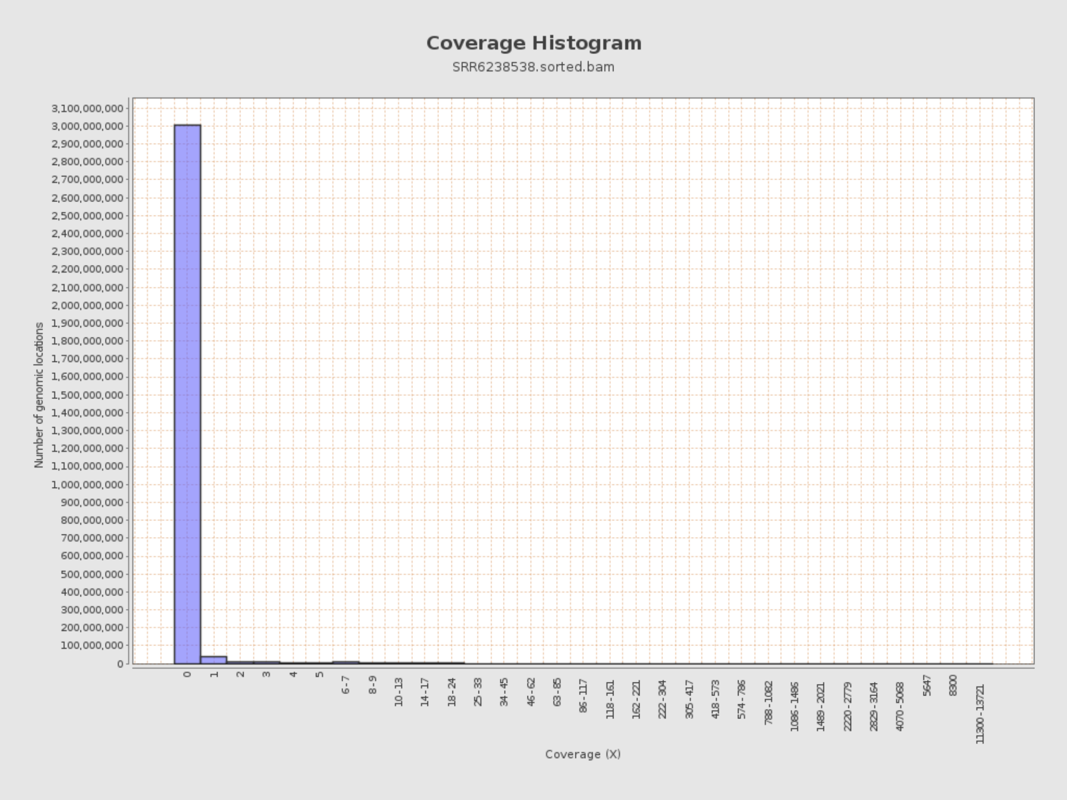
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21043134	0.0844	1.7312
chr2	243199373	67275889	0.2766	6.1436
chr3	198022430	17964192	0.0907	1.0168
chr4	191154276	5866052	0.0307	0.5412
chr5	180915260	19188587	0.1061	1.1158
chr6	171115067	103481786	0.6047	3.7953
chr7	159138663	6216045	0.0391	0.9947

chr8	146364022	19168879	0.131	1.4242
chr9	141213431	27238576	0.1929	1.7304
chr10	135534747	14611830	0.1078	1.2368
chr11	135006516	7321935	0.0542	0.7792
chr12	133851895	13930605	0.1041	1.1007
chr13	115169878	10446551	0.0907	1.414
chr14	107349540	3753533	0.035	0.7613
chr15	102531392	4031981	0.0393	1.2072
chr16	90354753	17844816	0.1975	1.6568
chr17	81195210	3788912	0.0467	0.7008
chr18	78077248	5338887	0.0684	3.9642
chr19	59128983	8860975	0.1499	1.5222
chr20	63025520	26365734	0.4183	2.2735
chr21	48129895	1433720	0.0298	0.6088
chr22	51304566	3203020	0.0624	0.8139
chrMT	16571	341562	20.612	19.5755
chrX	155270560	15255933	0.0983	1.085
chrY	59373566	984407	0.0166	0.7492

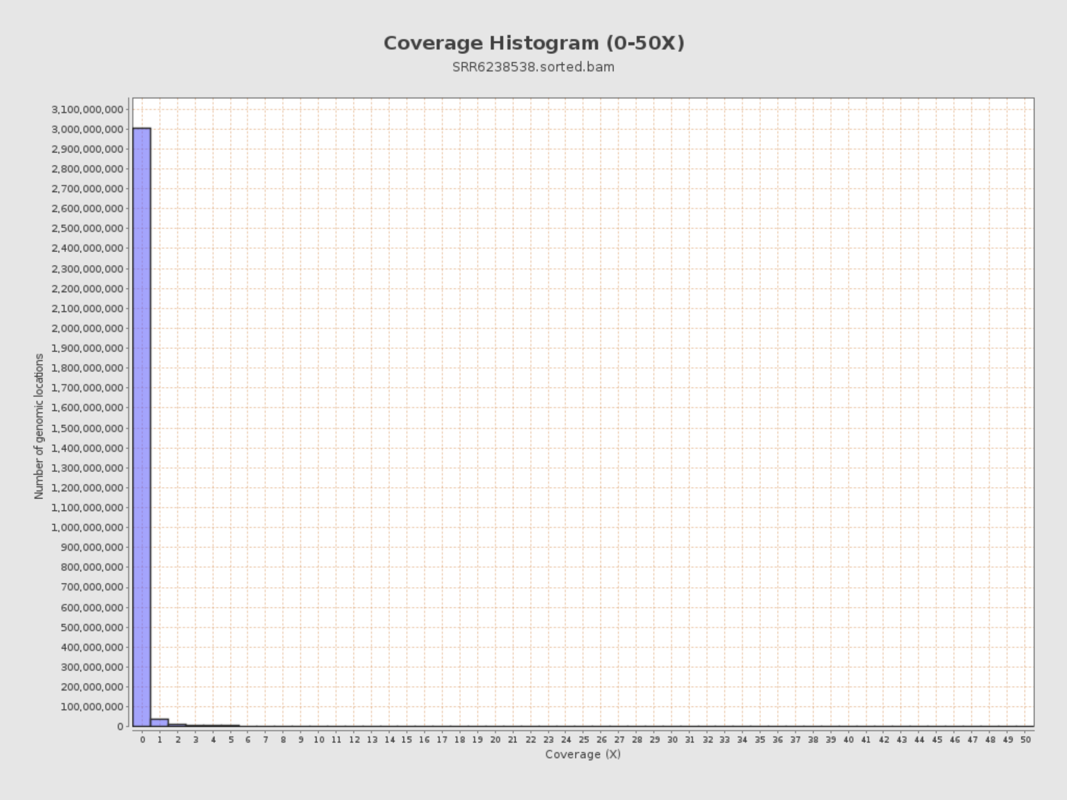
3. Results : Coverage across reference



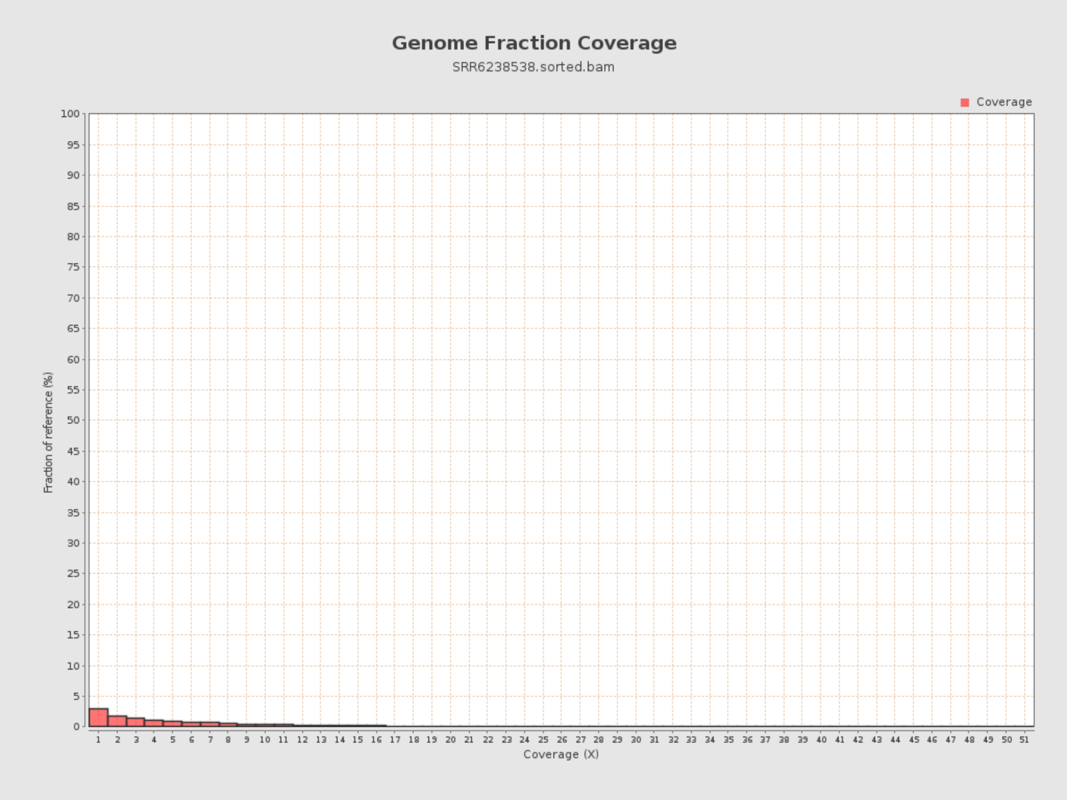
4. Results : Coverage Histogram



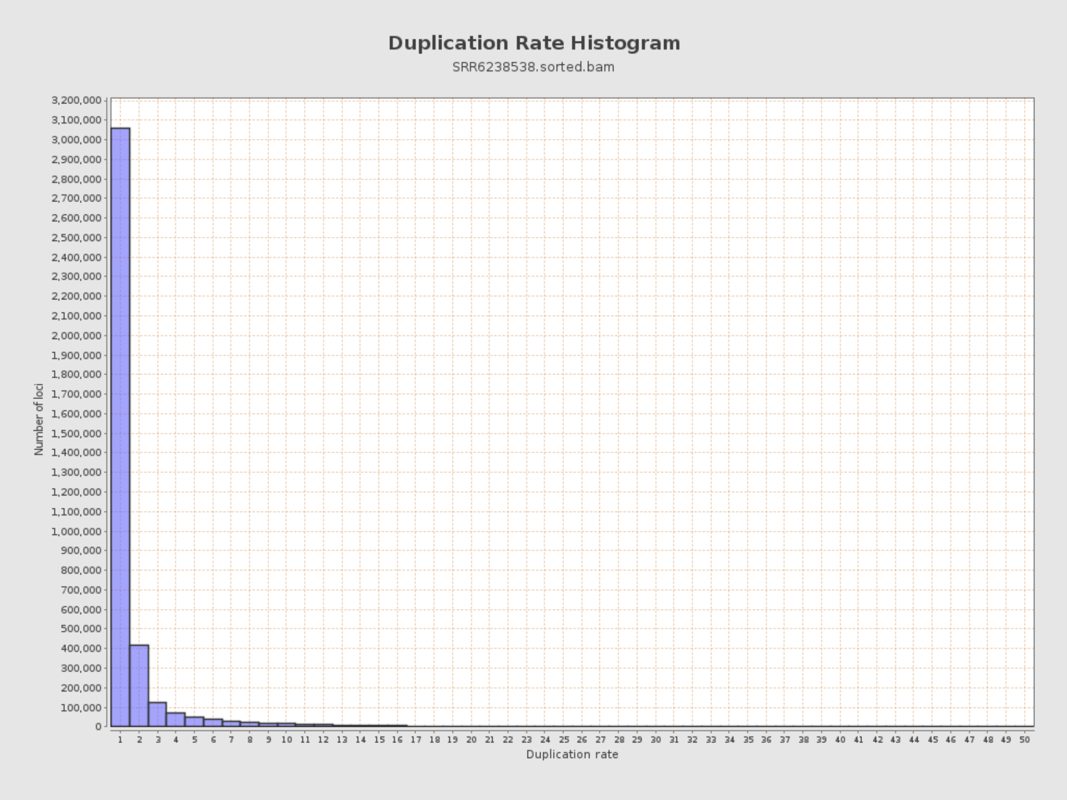
5. Results : Coverage Histogram (0-50X)



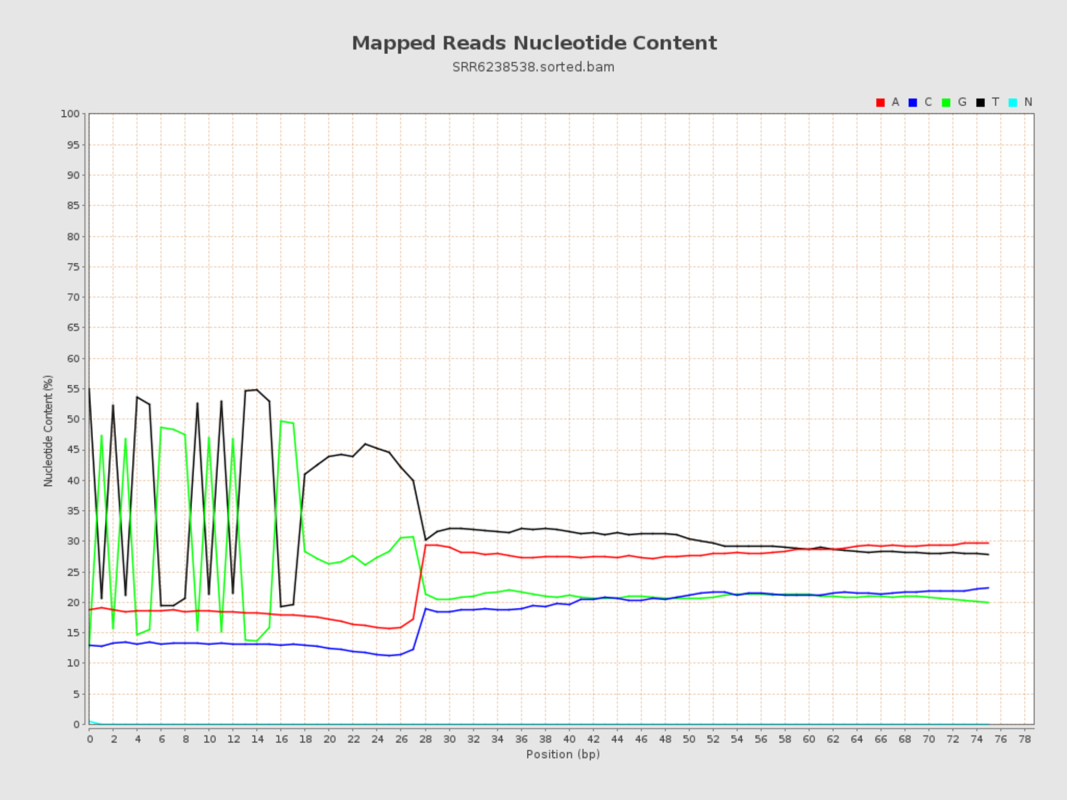
6. Results : Genome Fraction Coverage



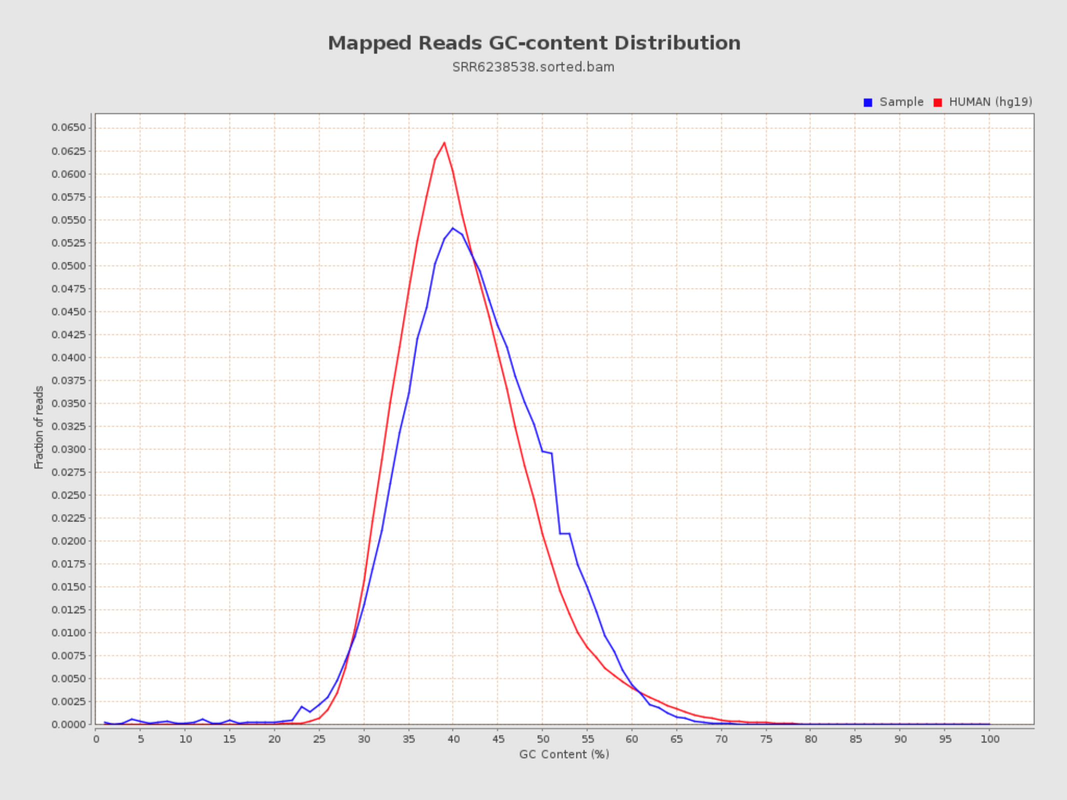
7. Results : Duplication Rate Histogram



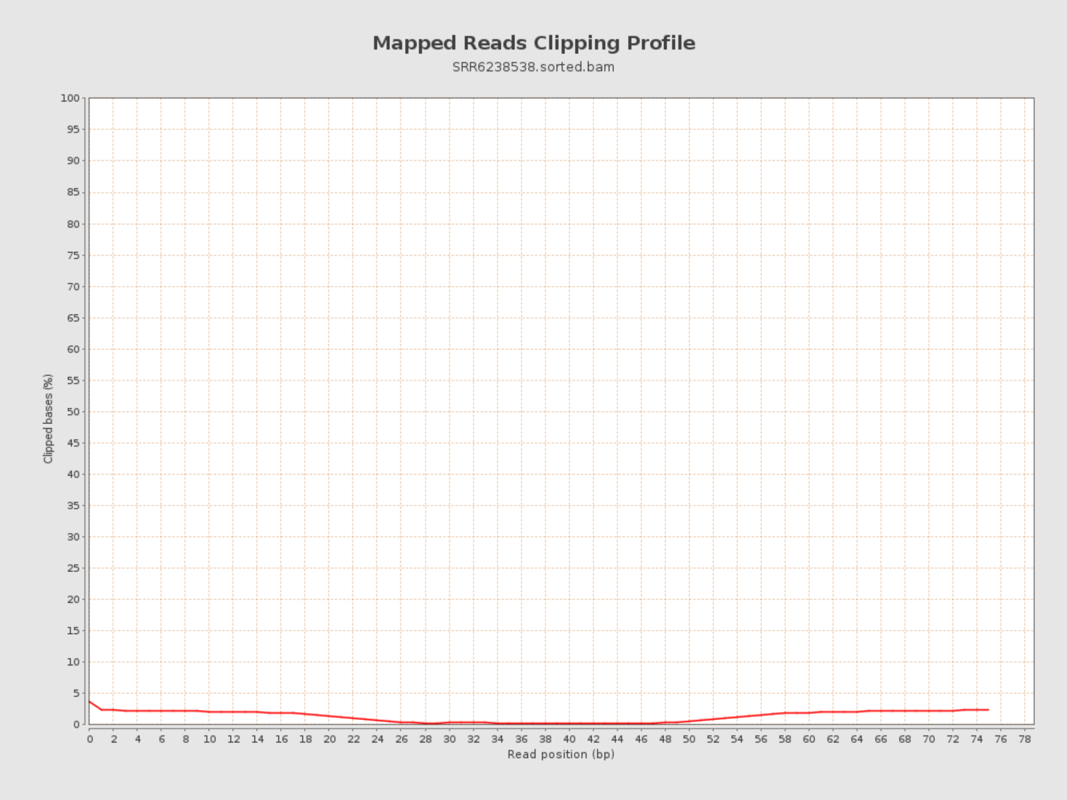
8. Results : Mapped Reads Nucleotide Content



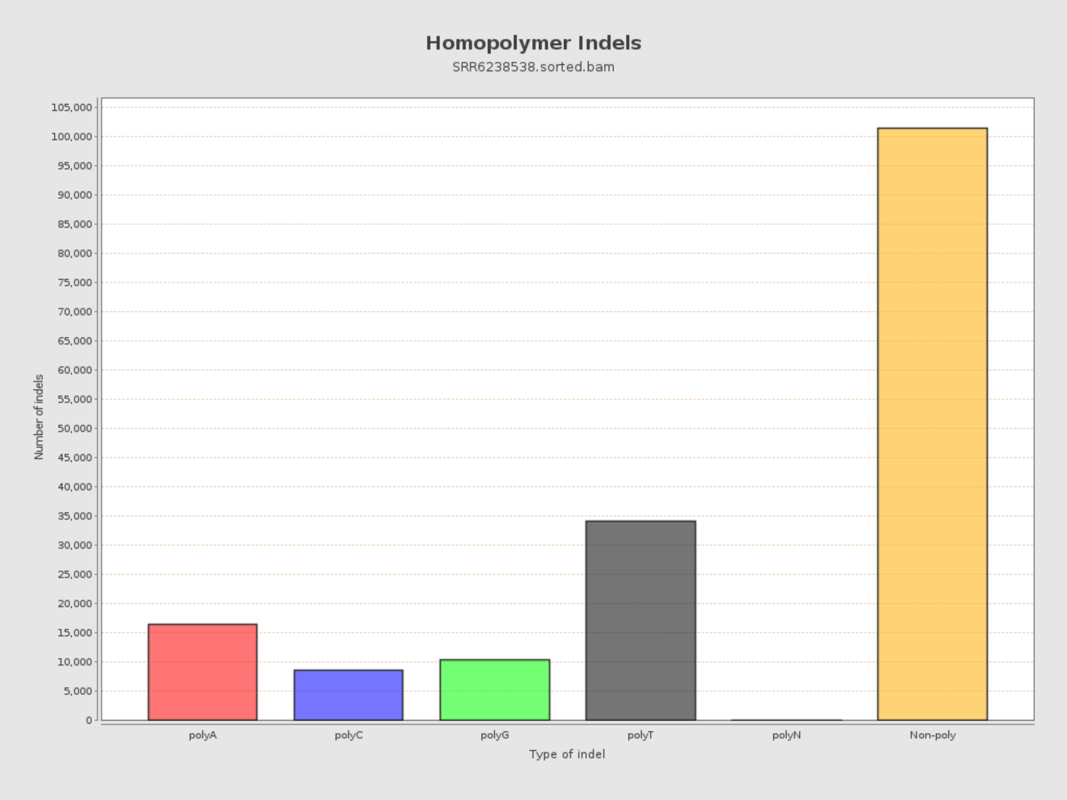
9. Results : Mapped Reads GC-content Distribution



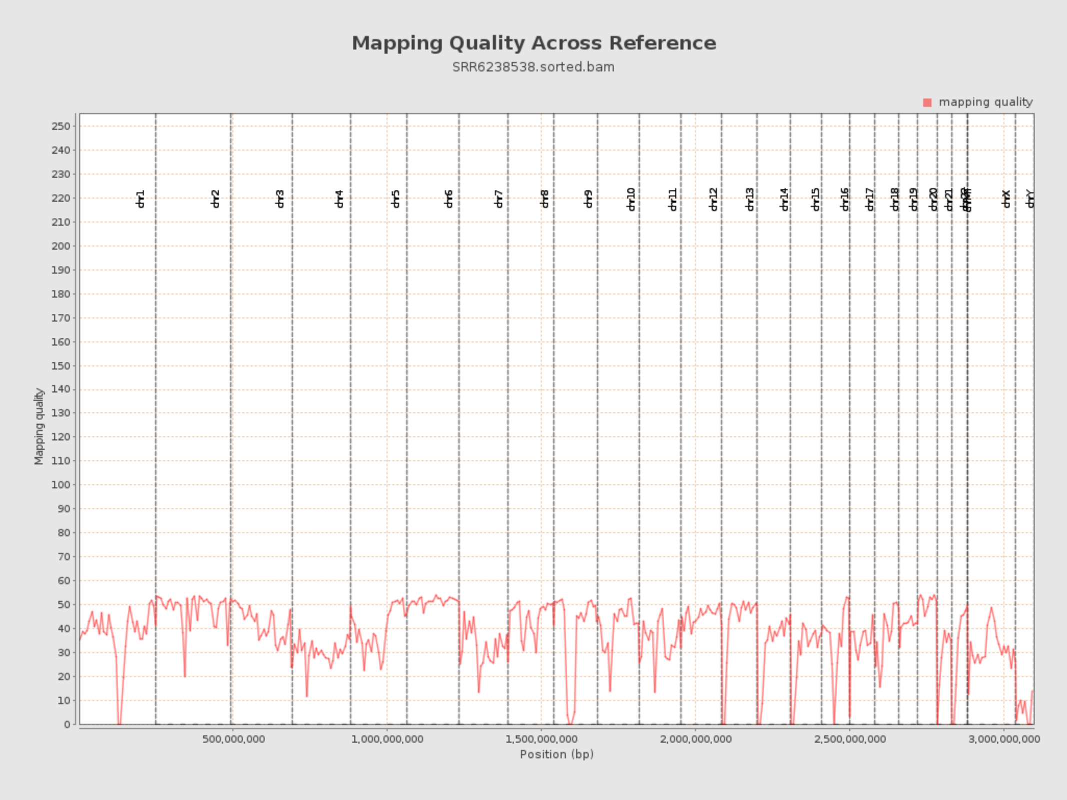
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram