Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:48:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238269.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_SRR6238269 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238269.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:48:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238269.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,082,023
Mapped reads	1,867,631 / 89.7%
Unmapped reads	214,392 / 10.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,932 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	59,661 / 2.87%
Duplication rate	2.1%
Clipped reads	906,960 / 43.56%

2.2. ACGT Content

Number/percentage of A's	34,820,868 / 28.27%
Number/percentage of C's	23,449,218 / 19.04%
Number/percentage of T's	37,068,739 / 30.1%
Number/percentage of G's	27,787,698 / 22.56%
Number/percentage of N's	34,773 / 0.03%
GC Percentage	41.6%

2.3. Coverage

Mean	0.0398

Standard Deviation	0.3945

2.4. Mapping Quality

Mean Mapping Quality	43.44

2.5. Mismatches and indels

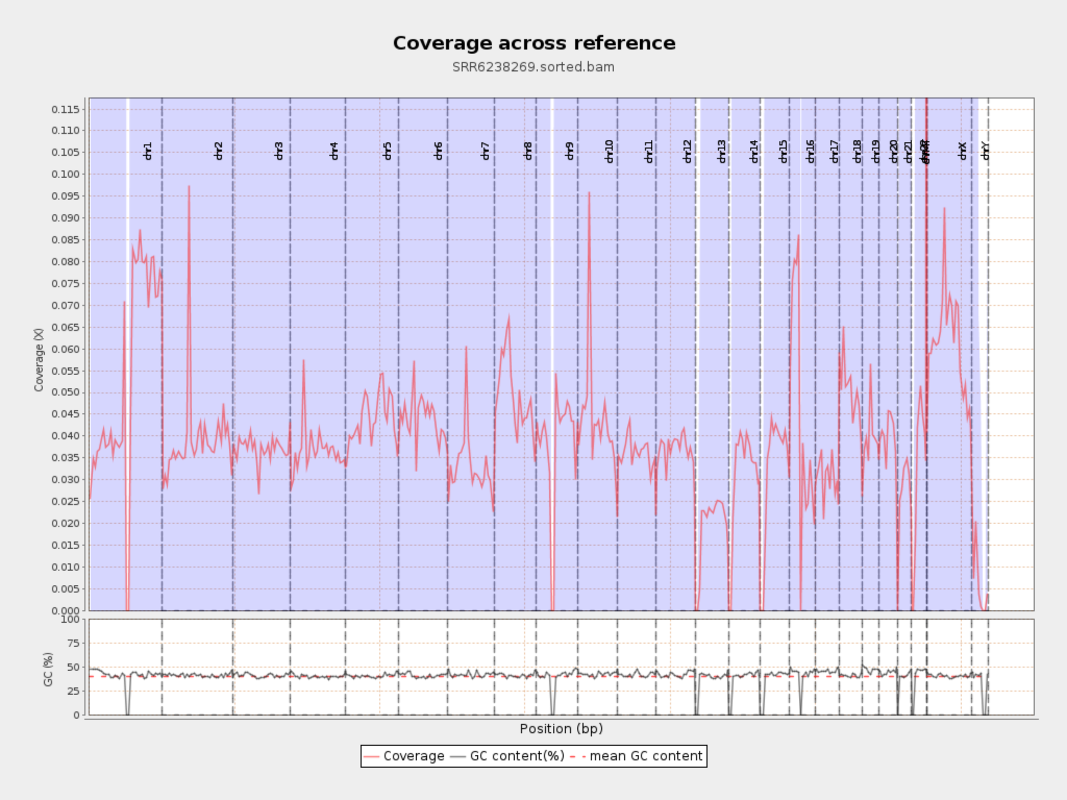
General error rate	0.94%
Mismatches	1,132,922
Insertions	10,728
Mapped reads with at least one insertion	0.57%
Deletions	39,320
Mapped reads with at least one deletion	2.08%
Homopolymer indels	44.53%

2.6. Chromosome stats

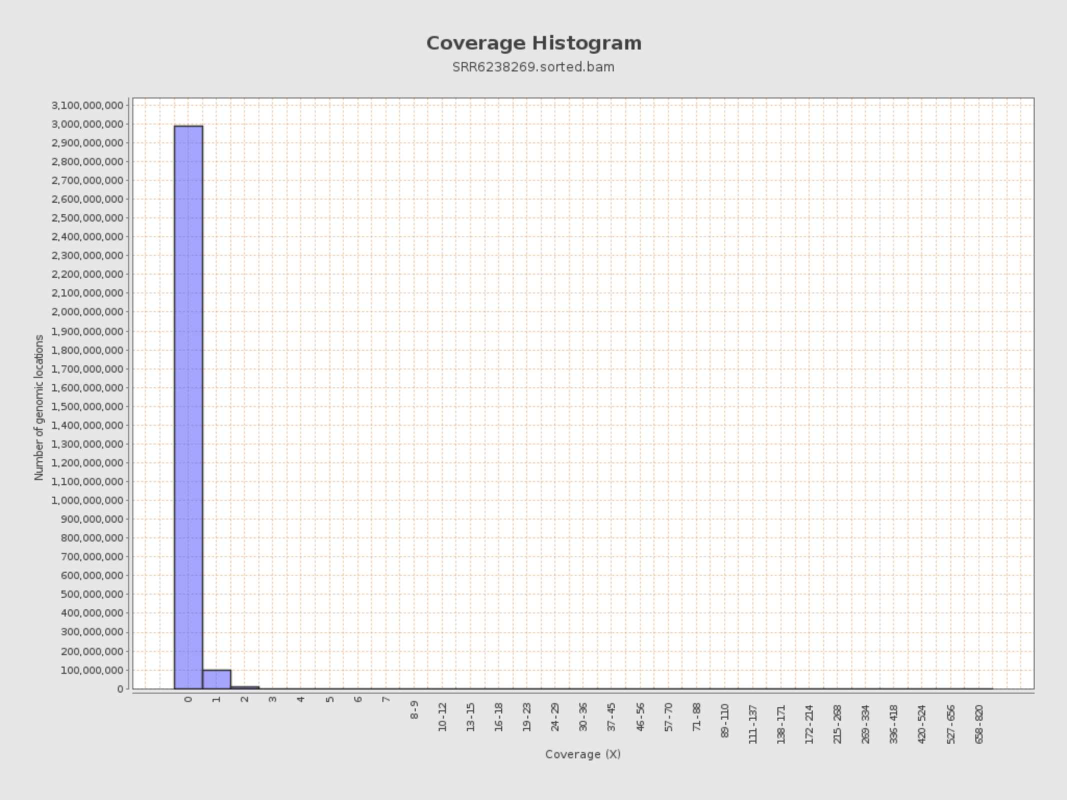
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13248585	0.0532	0.7323
chr2	243199373	9558185	0.0393	0.4977
chr3	198022430	7333147	0.037	0.2122
chr4	191154276	7006096	0.0367	0.2351
chr5	180915260	7958309	0.044	0.2302
chr6	171115067	7507804	0.0439	0.2878
chr7	159138663	5291720	0.0333	0.4193

chr8	146364022	7201702	0.0492	0.4995
chr9	141213431	5345089	0.0379	0.4076
chr10	135534747	6025112	0.0445	0.4623
chr11	135006516	4879526	0.0361	0.2937
chr12	133851895	4951105	0.037	0.2191
chr13	115169878	2205086	0.0191	0.1485
chr14	107349540	3305535	0.0308	0.2539
chr15	102531392	3293174	0.0321	0.1982
chr16	90354753	4071320	0.0451	0.2989
chr17	81195210	2466835	0.0304	0.2228
chr18	78077248	3959022	0.0507	0.7163
chr19	59128983	2360274	0.0399	0.5554
chr20	63025520	2501642	0.0397	0.223
chr21	48129895	1285588	0.0267	0.216
chr22	51304566	1575427	0.0307	0.1894
chrMT	16571	8313	0.5017	0.8037
chrX	155270560	9507662	0.0612	0.3237
chrY	59373566	381703	0.0064	0.1836

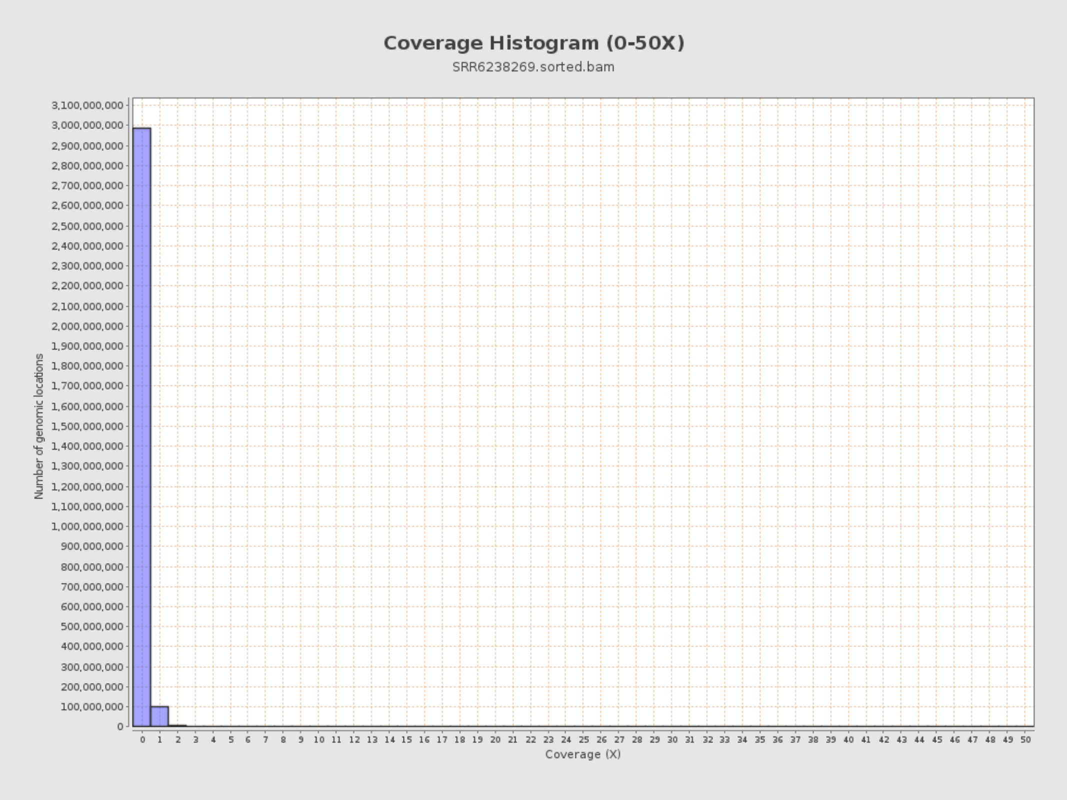
3. Results : Coverage across reference



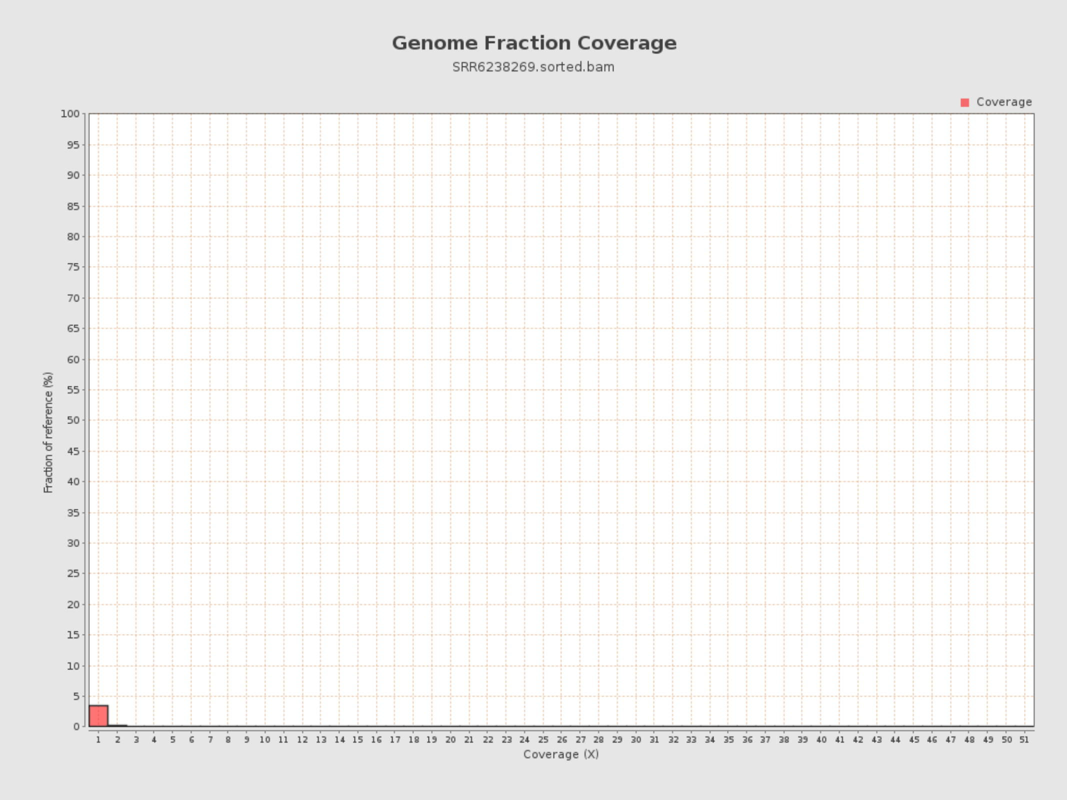
4. Results : Coverage Histogram



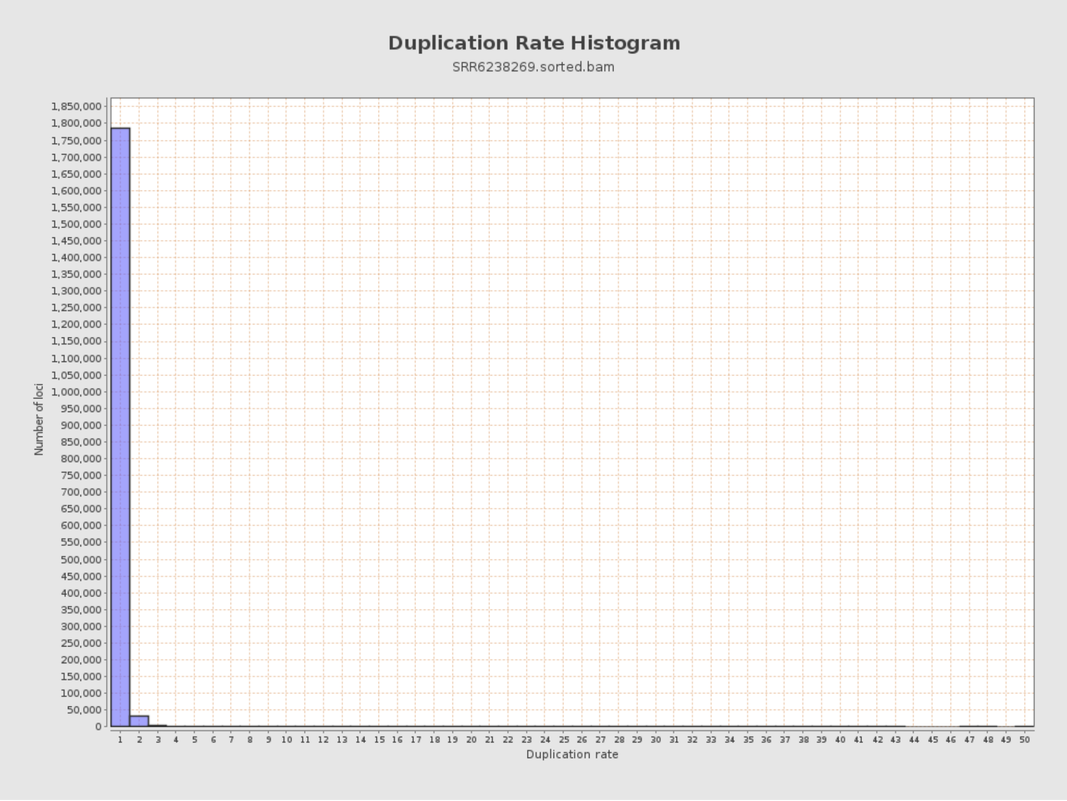
5. Results : Coverage Histogram (0-50X)



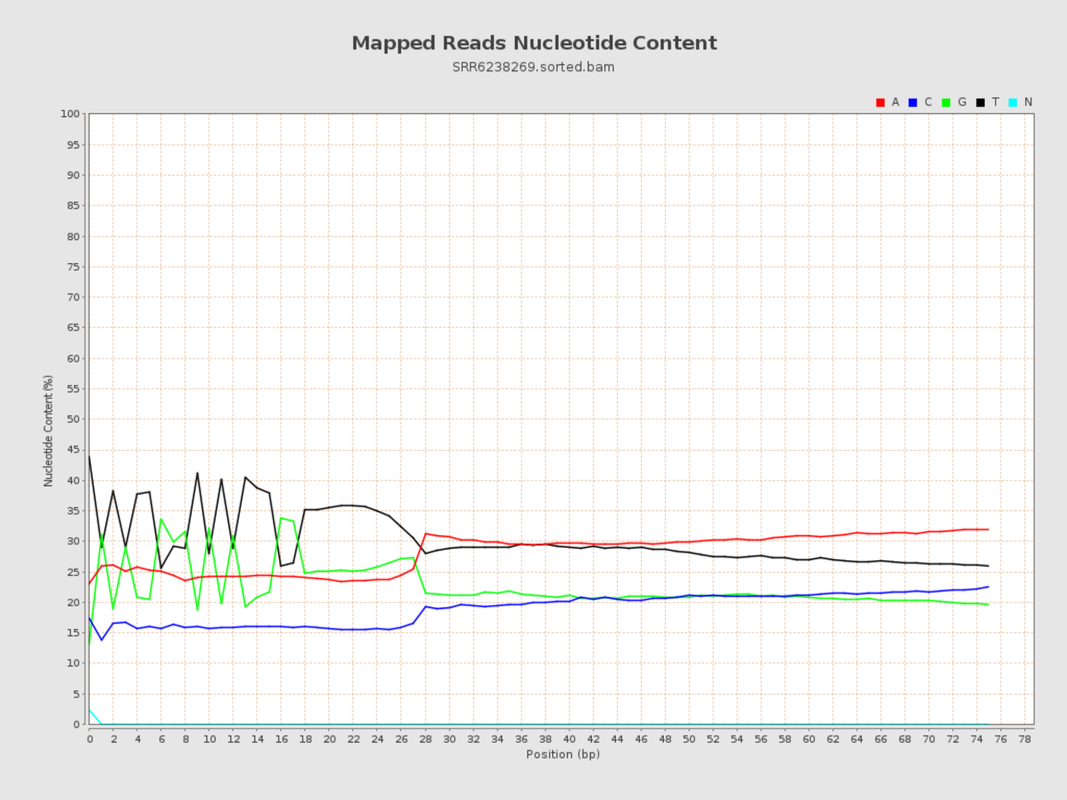
6. Results : Genome Fraction Coverage



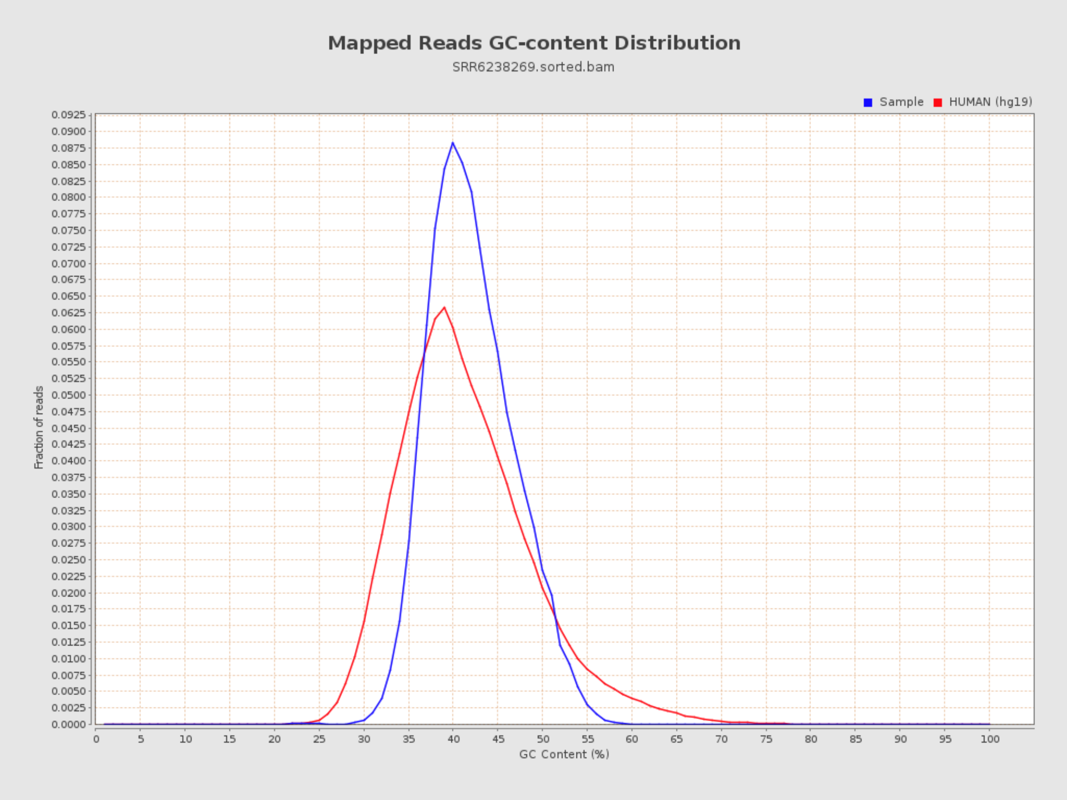
7. Results : Duplication Rate Histogram



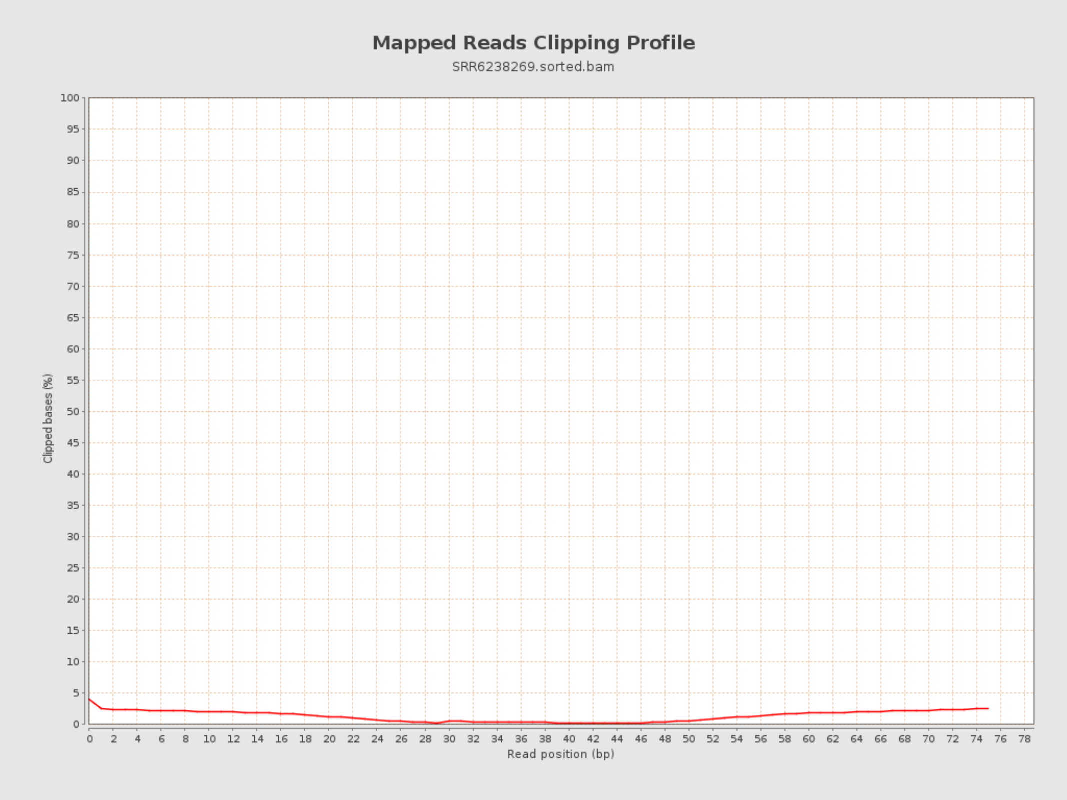
8. Results : Mapped Reads Nucleotide Content



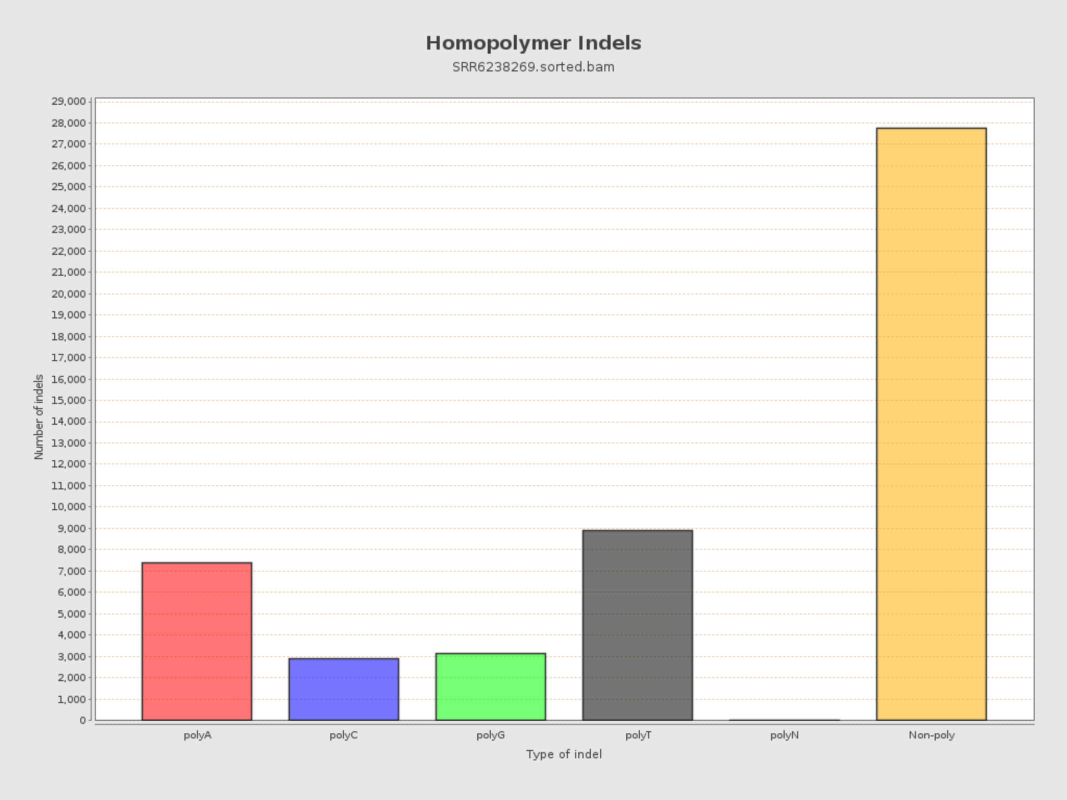
9. Results : Mapped Reads GC-content Distribution



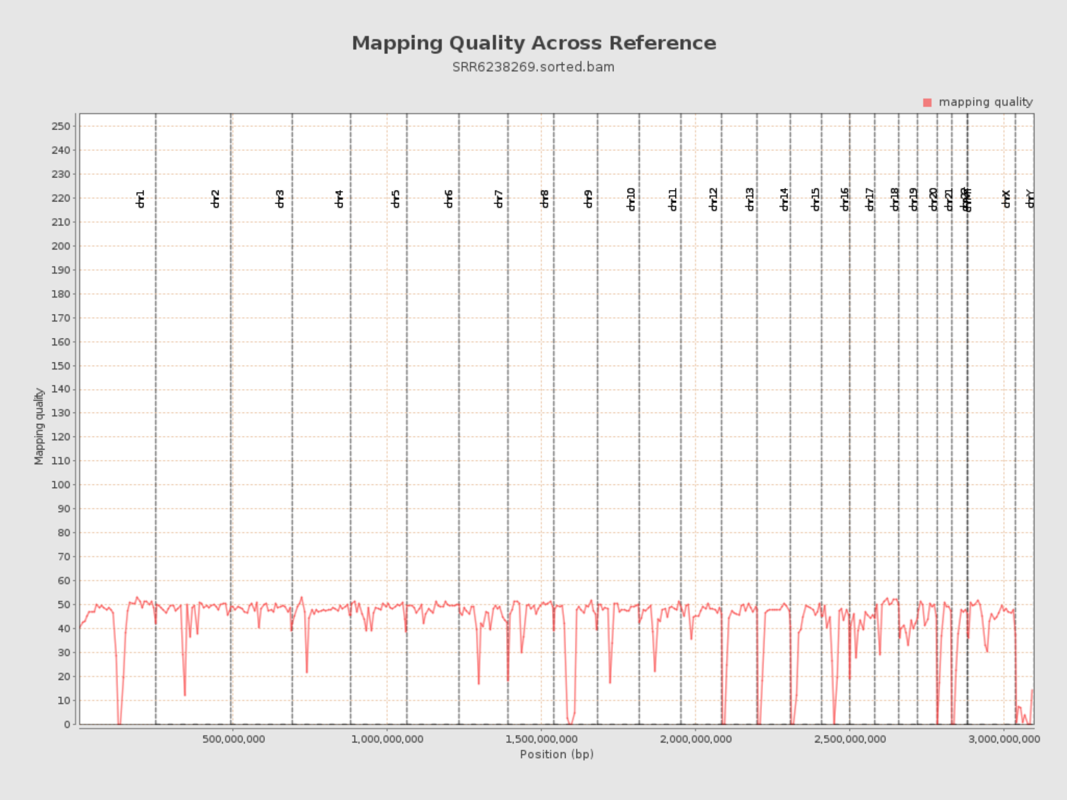
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram