Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:06:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238077.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_SRR6238077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238077.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:06:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,557,119
Mapped reads	1,320,054 / 84.78%
Unmapped reads	237,065 / 15.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,728 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	74,782 / 4.8%
Duplication rate	4.12%
Clipped reads	848,008 / 54.46%

2.2. ACGT Content

Number/percentage of A's	20,184,713 / 24.78%
Number/percentage of C's	14,194,692 / 17.43%
Number/percentage of T's	26,081,007 / 32.02%
Number/percentage of G's	20,858,707 / 25.61%
Number/percentage of N's	136,253 / 0.17%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0263

Standard Deviation	0.2725

2.4. Mapping Quality

Mean Mapping Quality	42.07

2.5. Mismatches and indels

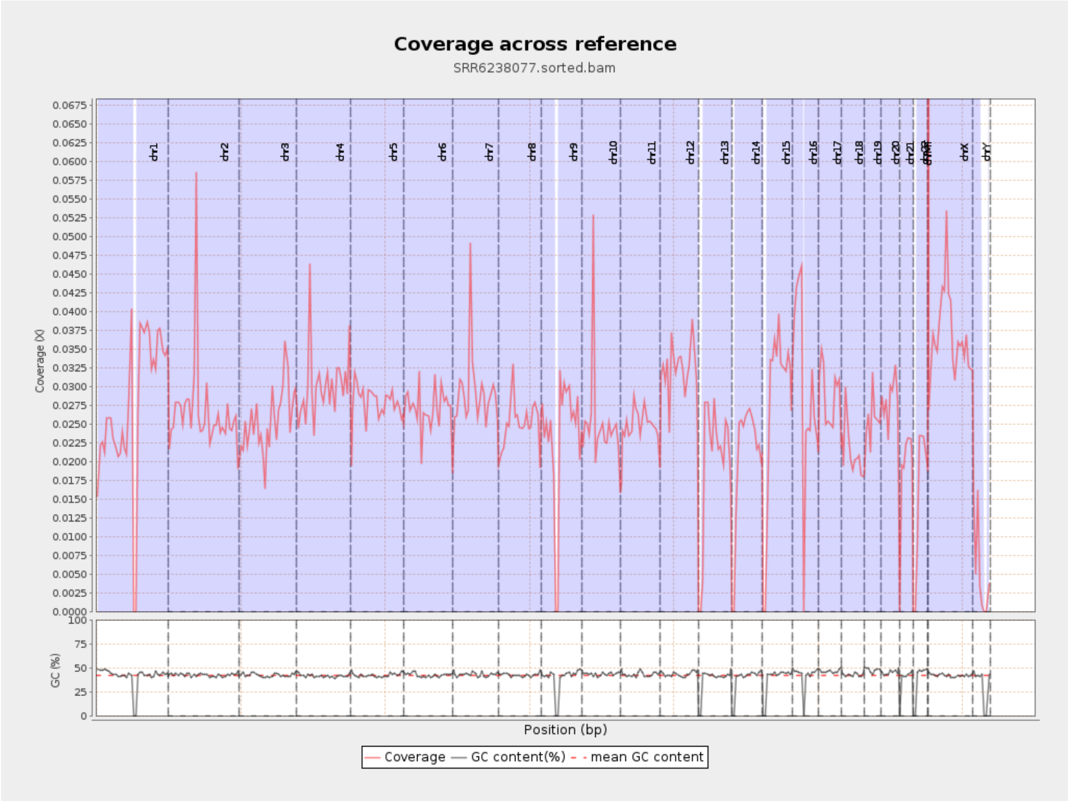
General error rate	0.89%
Mismatches	712,224
Insertions	7,021
Mapped reads with at least one insertion	0.53%
Deletions	26,867
Mapped reads with at least one deletion	2.01%
Homopolymer indels	47.06%

2.6. Chromosome stats

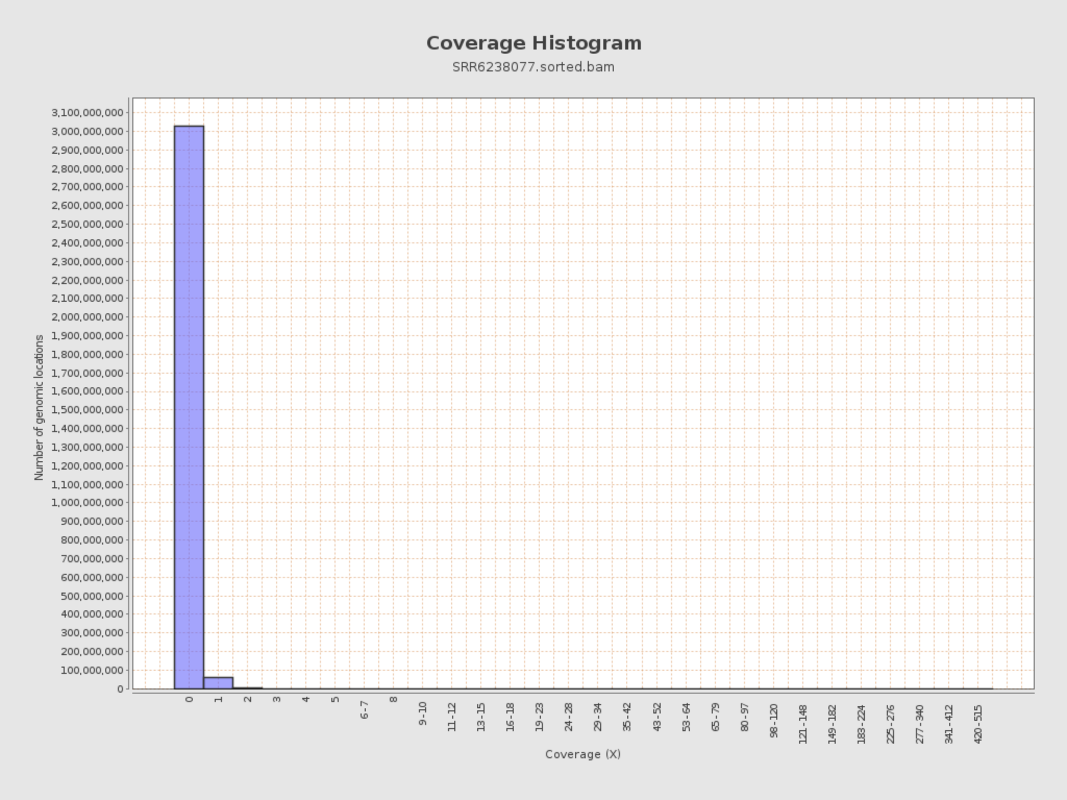
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6810901	0.0273	0.3839
chr2	243199373	6474922	0.0266	0.3932
chr3	198022430	5027052	0.0254	0.1891
chr4	191154276	5745863	0.0301	0.2187
chr5	180915260	5088483	0.0281	0.1915
chr6	171115067	4616159	0.027	0.2391
chr7	159138663	4637104	0.0291	0.3677

chr8	146364022	3675247	0.0251	0.251
chr9	141213431	3287309	0.0233	0.2924
chr10	135534747	3402638	0.0251	0.2935
chr11	135006516	3372697	0.025	0.2365
chr12	133851895	4330860	0.0324	0.2192
chr13	115169878	2281579	0.0198	0.1665
chr14	107349540	2207322	0.0206	0.1885
chr15	102531392	2822475	0.0275	0.193
chr16	90354753	2696274	0.0298	0.2217
chr17	81195210	2339389	0.0288	0.2181
chr18	78077248	1650399	0.0211	0.4133
chr19	59128983	1503048	0.0254	0.3097
chr20	63025520	1749527	0.0278	0.1999
chr21	48129895	928216	0.0193	0.1802
chr22	51304566	803597	0.0157	0.1467
chrMT	16571	21079	1.272	1.6673
chrX	155270560	5722964	0.0369	0.2501
chrY	59373566	304565	0.0051	0.1418

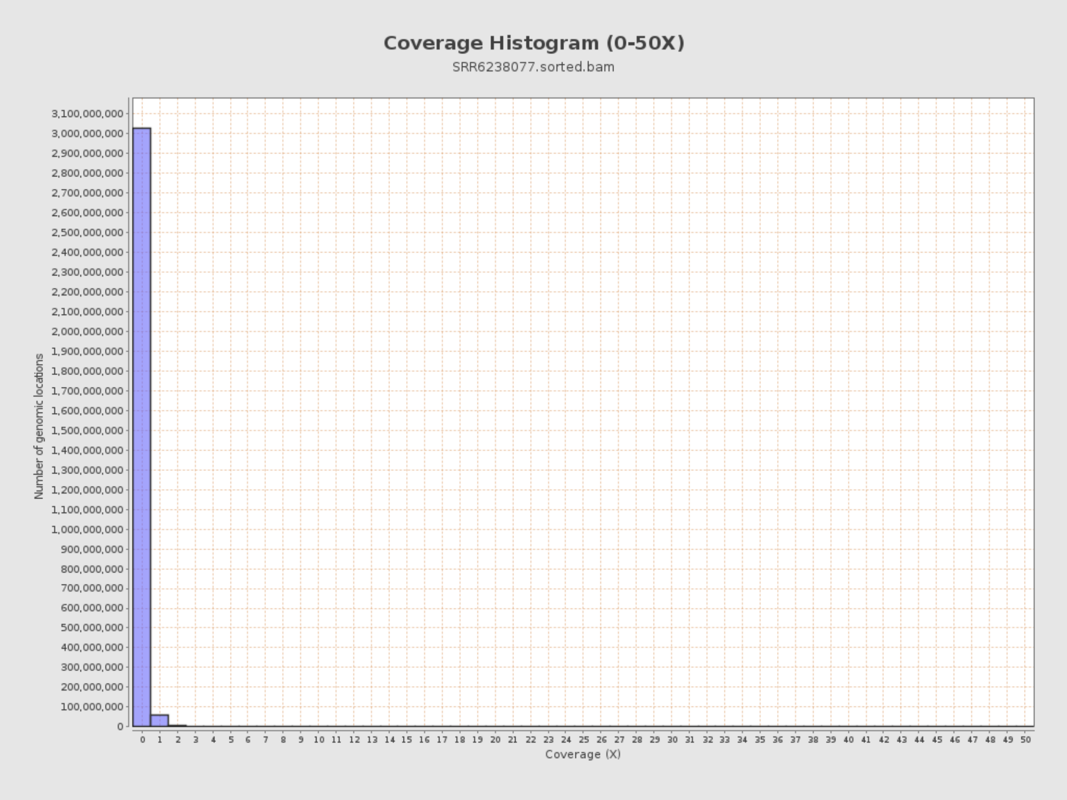
3. Results : Coverage across reference



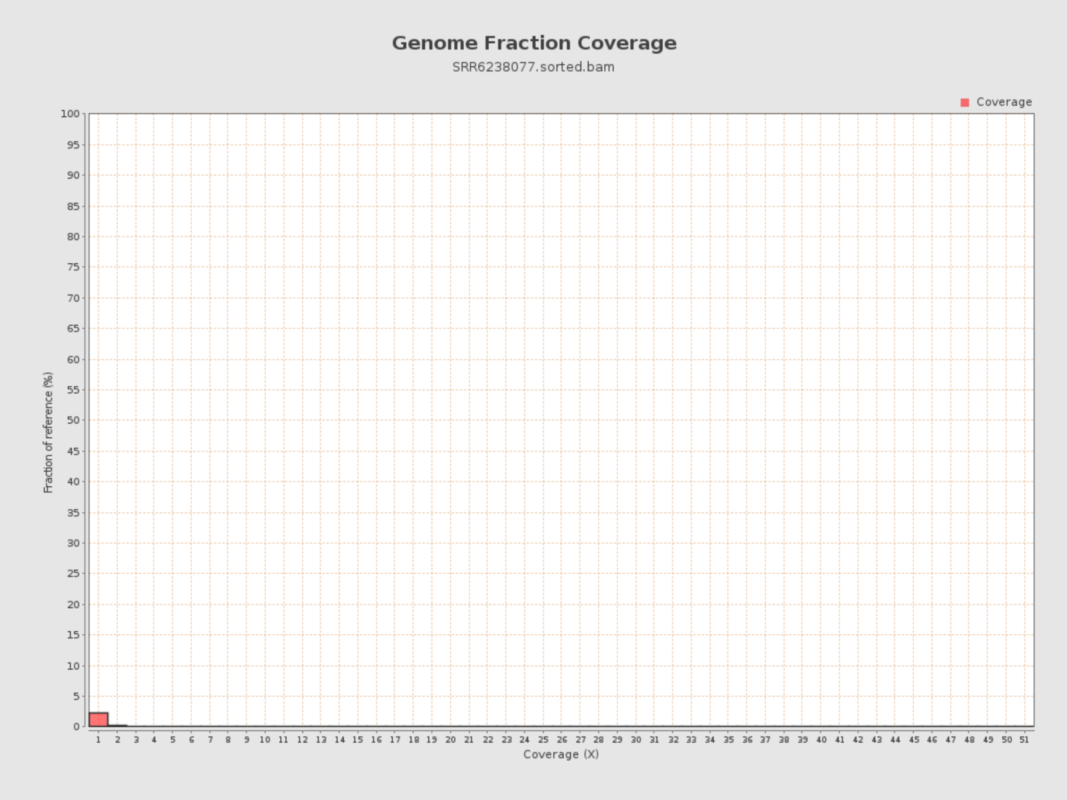
4. Results : Coverage Histogram



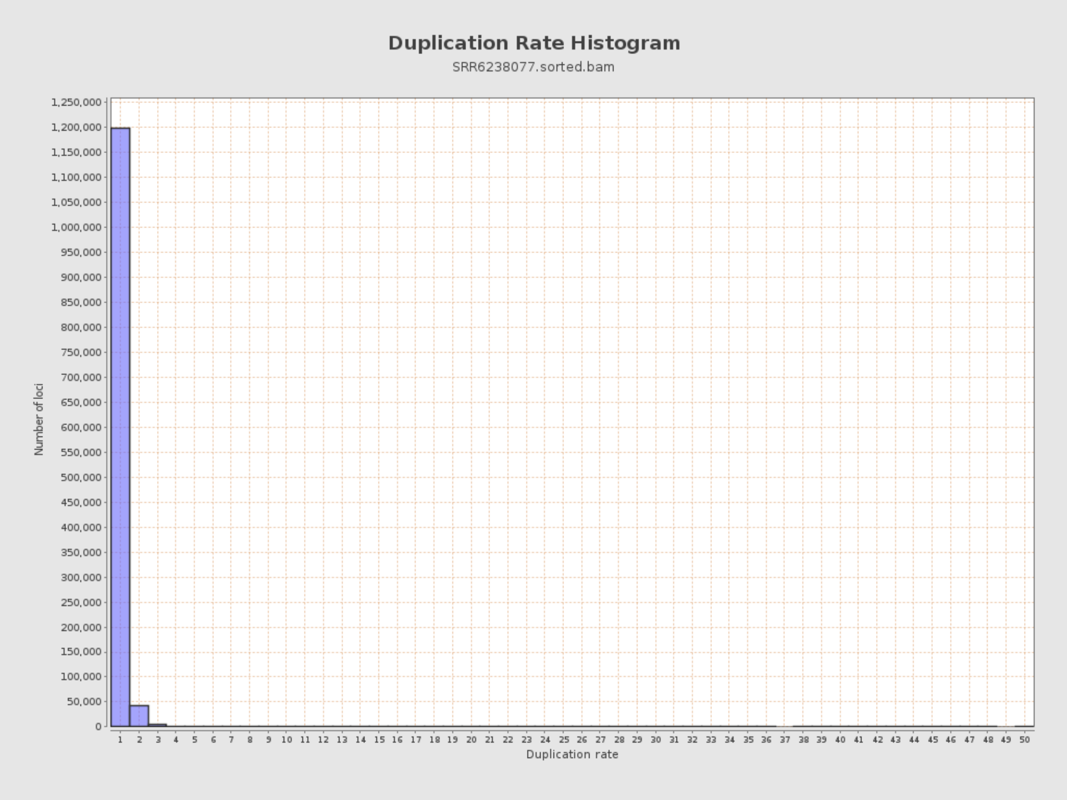
5. Results : Coverage Histogram (0-50X)



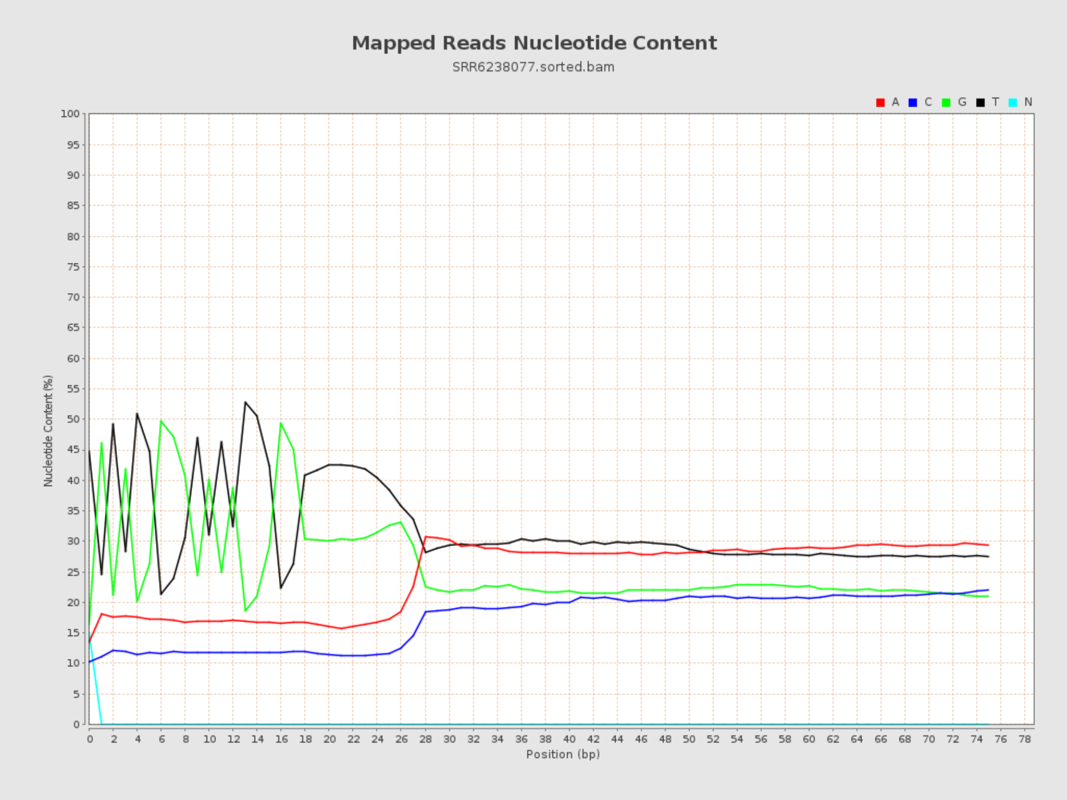
6. Results : Genome Fraction Coverage



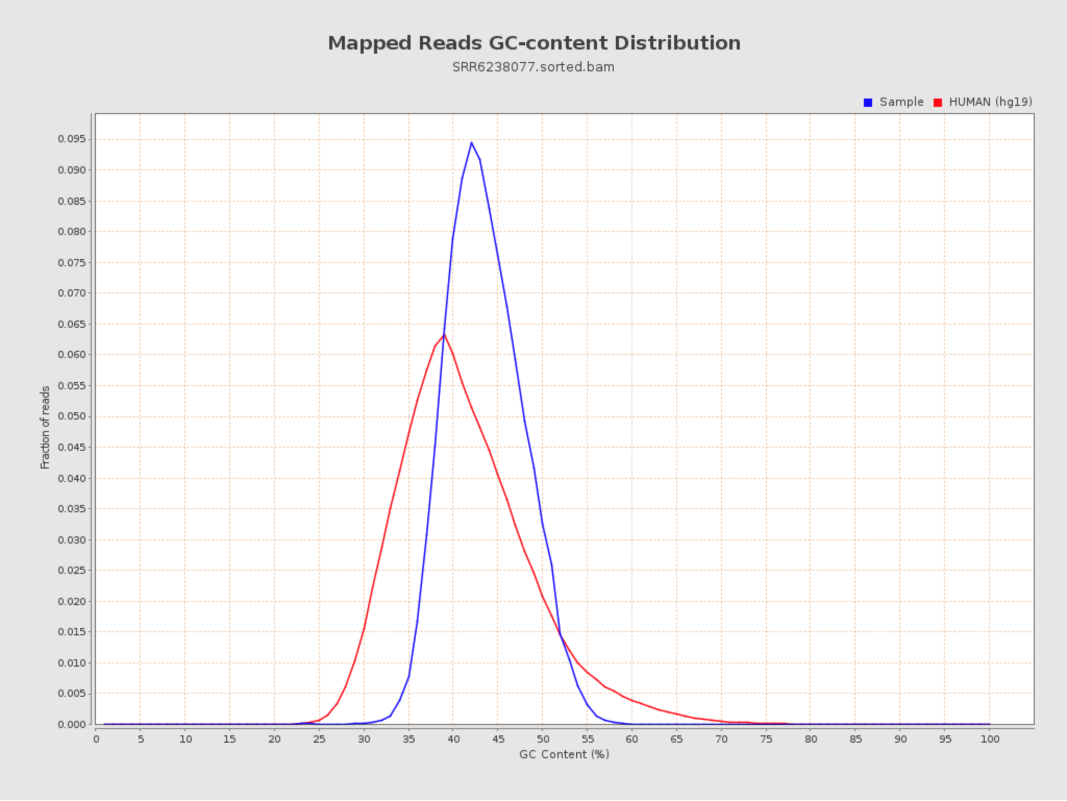
7. Results : Duplication Rate Histogram



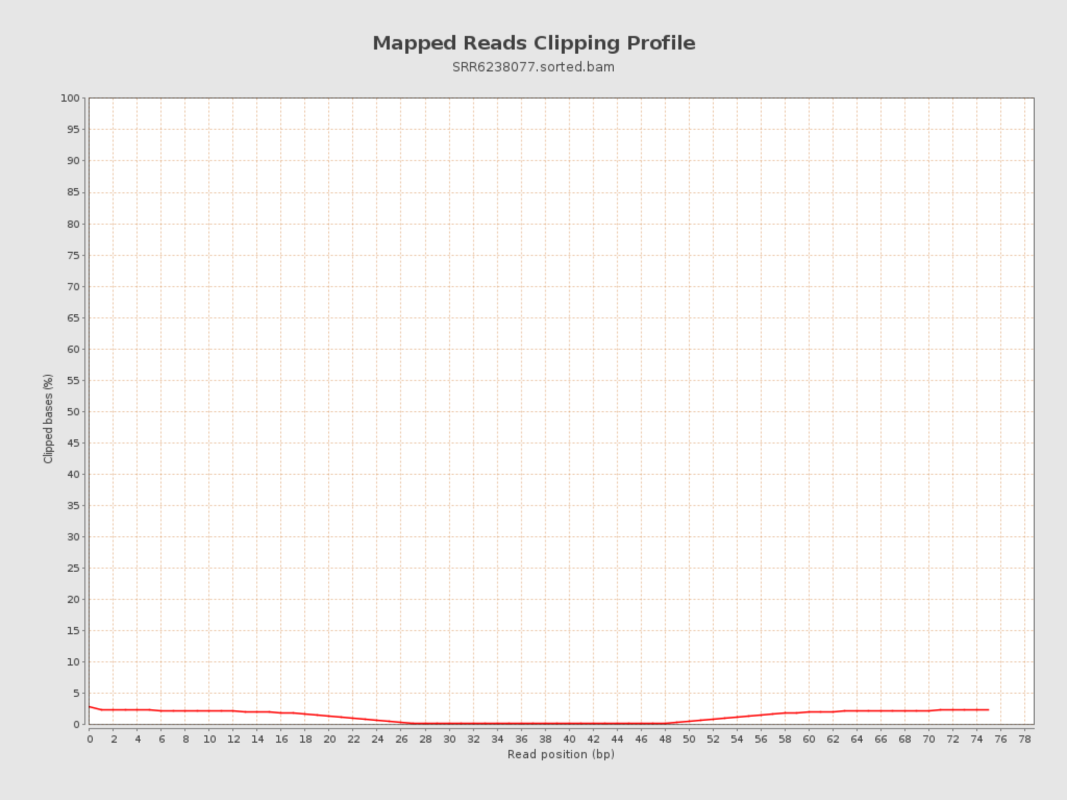
8. Results : Mapped Reads Nucleotide Content



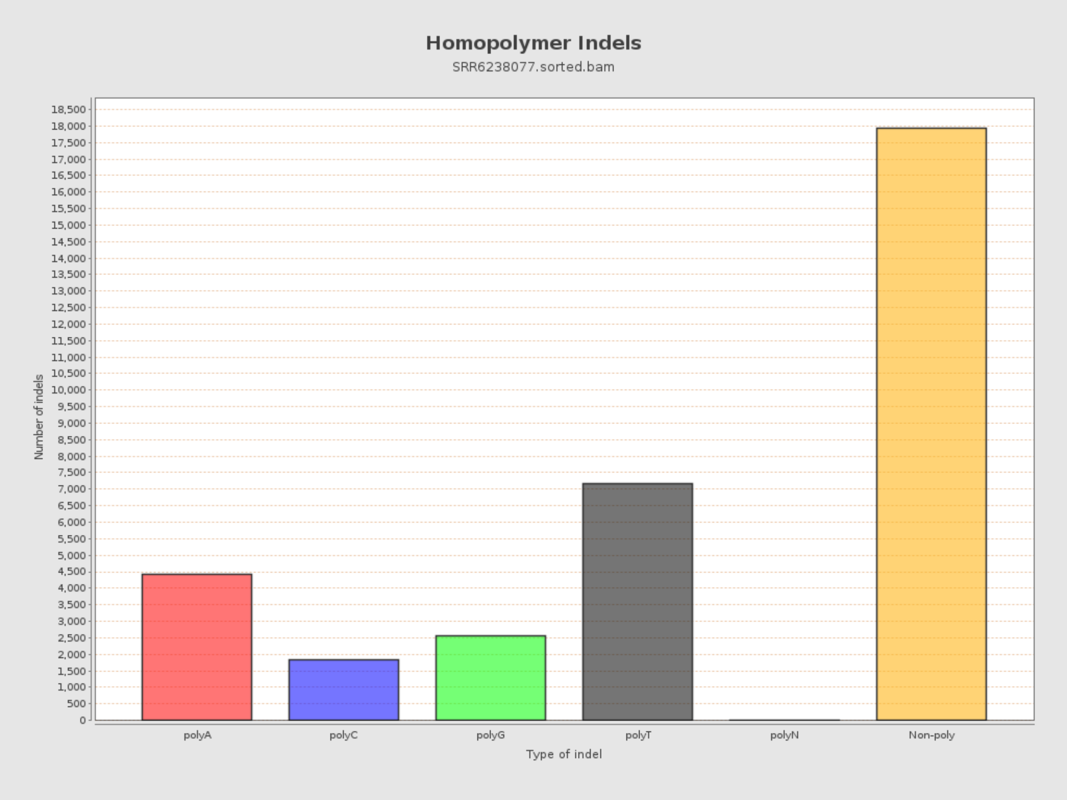
9. Results : Mapped Reads GC-content Distribution



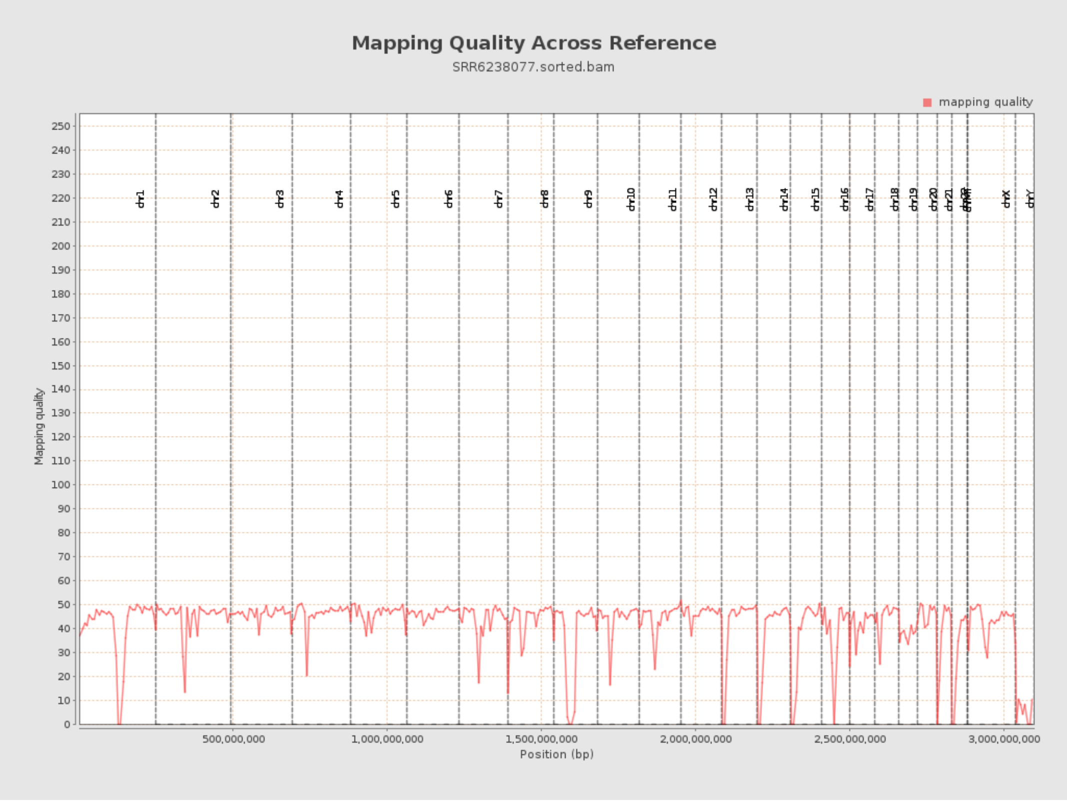
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram