Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:15:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238317.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_SRR6238317 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238317.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:15:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238317.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,010,173
Mapped reads	2,602,152 / 86.45%
Unmapped reads	408,021 / 13.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,439 / 1.11%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	188,696 / 6.27%
Duplication rate	5.67%
Clipped reads	1,497,545 / 49.75%

2.2. ACGT Content

Number/percentage of A's	45,941,725 / 27.53%
Number/percentage of C's	31,990,843 / 19.17%
Number/percentage of T's	51,363,103 / 30.78%
Number/percentage of G's	37,554,204 / 22.5%
Number/percentage of N's	44,153 / 0.03%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0539

Standard Deviation	0.5009

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

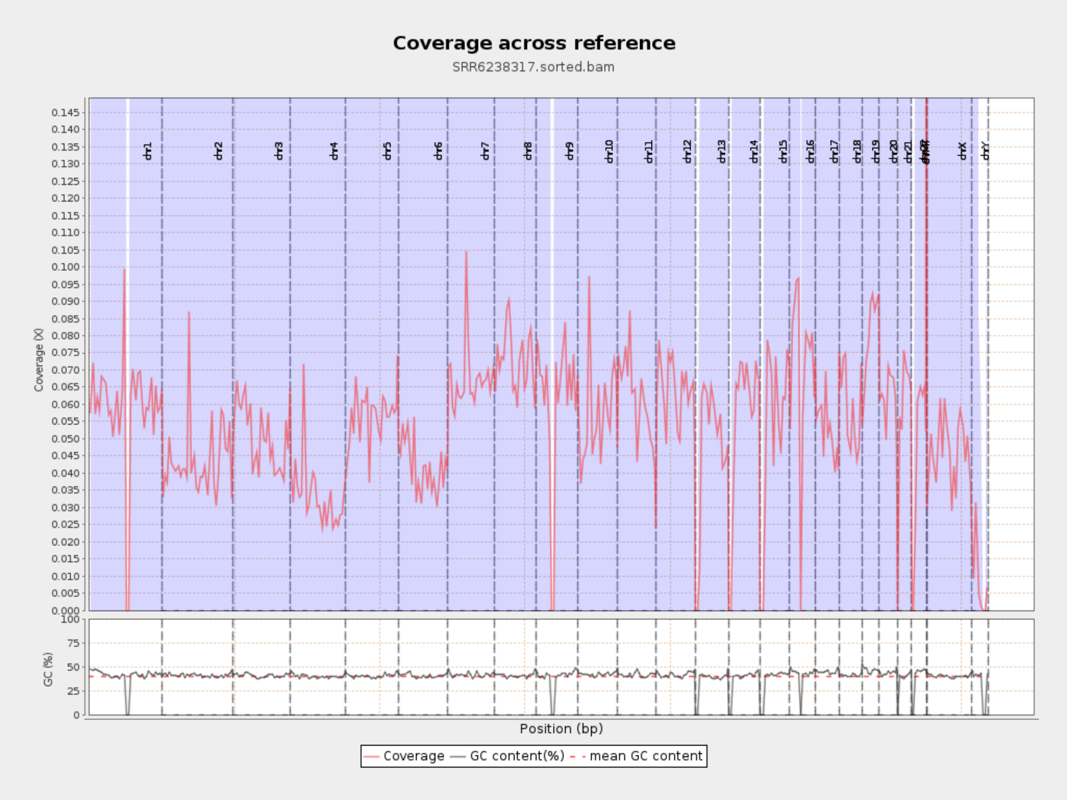
General error rate	0.95%
Mismatches	1,558,600
Insertions	13,881
Mapped reads with at least one insertion	0.53%
Deletions	56,701
Mapped reads with at least one deletion	2.15%
Homopolymer indels	44.05%

2.6. Chromosome stats

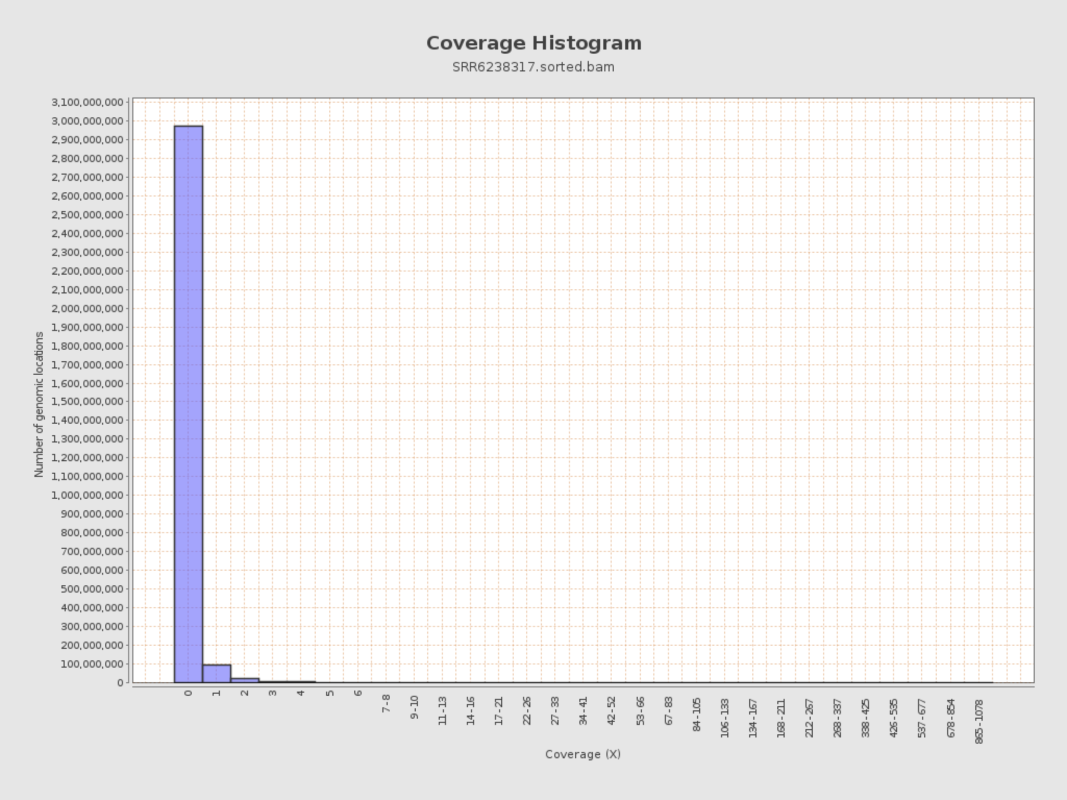
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14619801	0.0587	0.8965
chr2	243199373	10608360	0.0436	0.635
chr3	198022430	9984505	0.0504	0.2901
chr4	191154276	6388878	0.0334	0.2915
chr5	180915260	10212813	0.0565	0.3106
chr6	171115067	7133739	0.0417	0.3245
chr7	159138663	10761081	0.0676	0.624

chr8	146364022	10621536	0.0726	0.7173
chr9	141213431	8455567	0.0599	0.472
chr10	135534747	7670613	0.0566	0.4781
chr11	135006516	8324992	0.0617	0.4397
chr12	133851895	8668391	0.0648	0.3424
chr13	115169878	5355102	0.0465	0.281
chr14	107349540	5944921	0.0554	0.3457
chr15	102531392	5419457	0.0529	0.3162
chr16	90354753	6485237	0.0718	0.3798
chr17	81195210	4260304	0.0525	0.3332
chr18	78077248	4592992	0.0588	0.7915
chr19	59128983	4781324	0.0809	0.6933
chr20	63025520	3929851	0.0624	0.335
chr21	48129895	2809664	0.0584	0.3487
chr22	51304566	2259551	0.044	0.2702
chrMT	16571	7079	0.4272	0.8752
chrX	155270560	7205376	0.0464	0.3217
chrY	59373566	488105	0.0082	0.2466

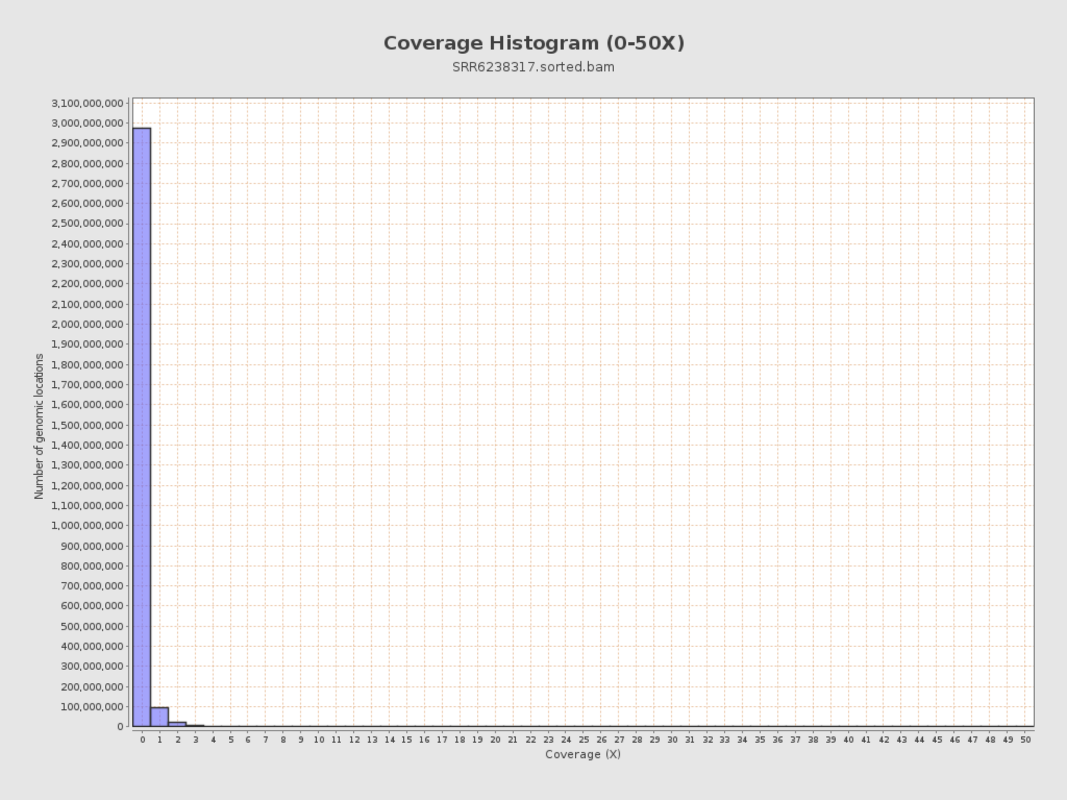
3. Results : Coverage across reference



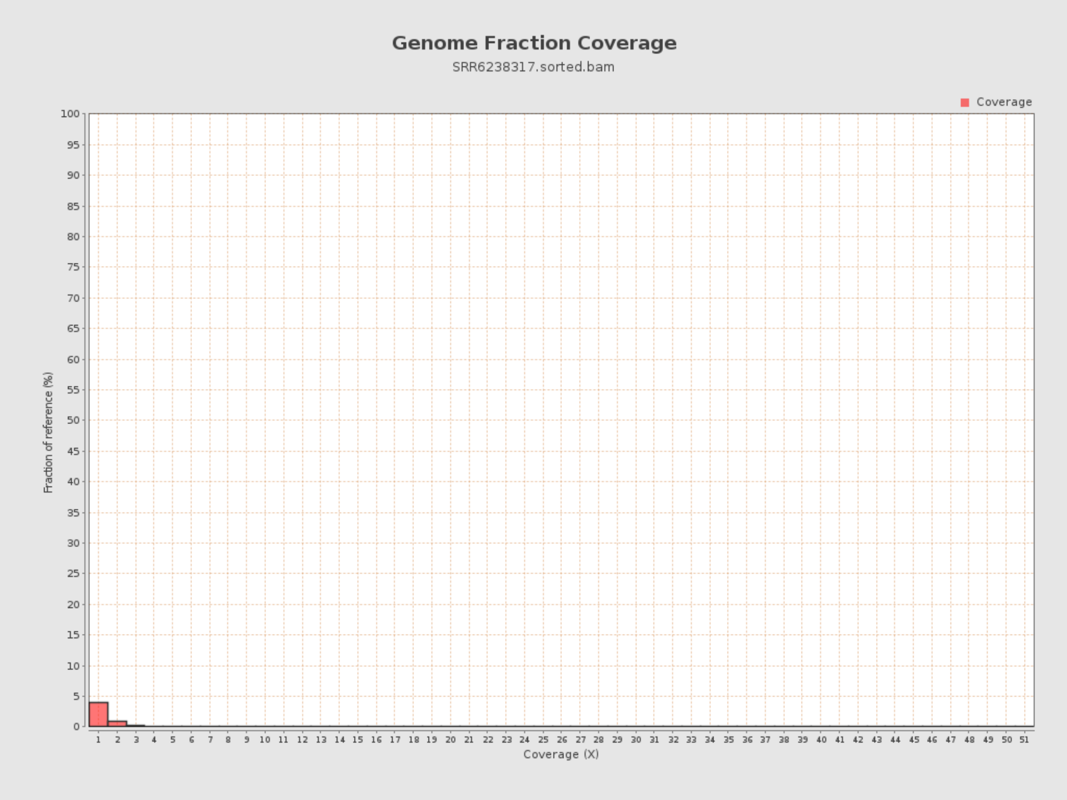
4. Results : Coverage Histogram



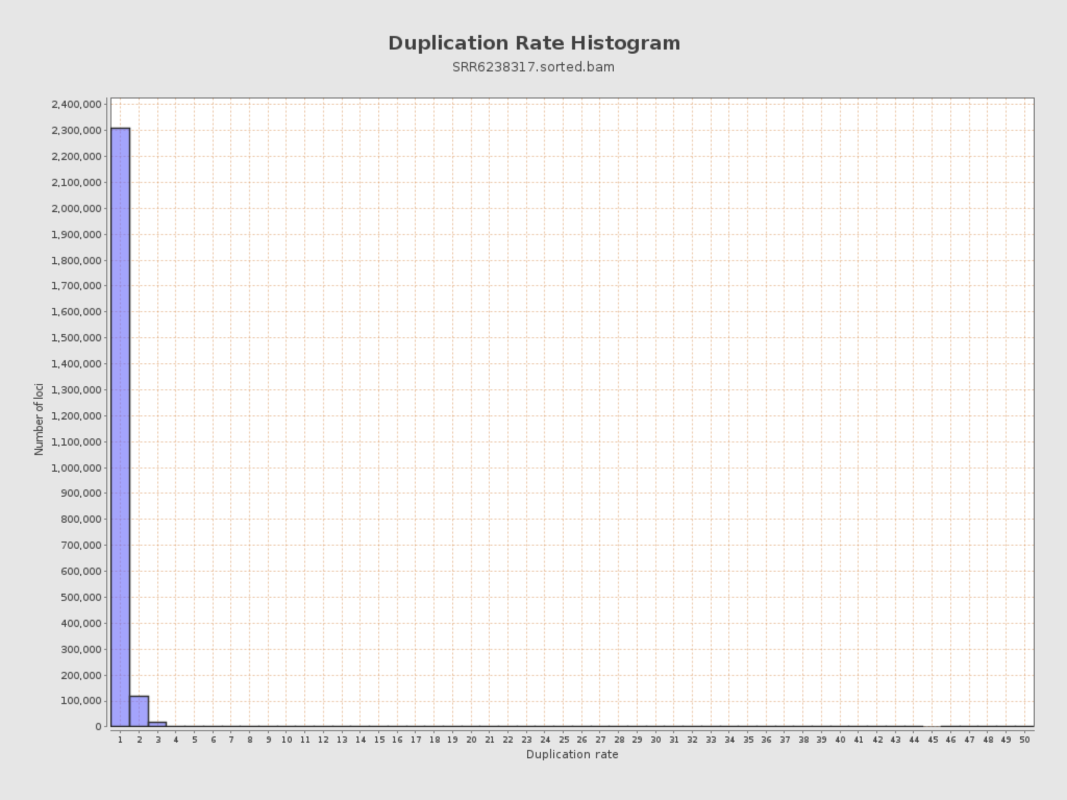
5. Results : Coverage Histogram (0-50X)



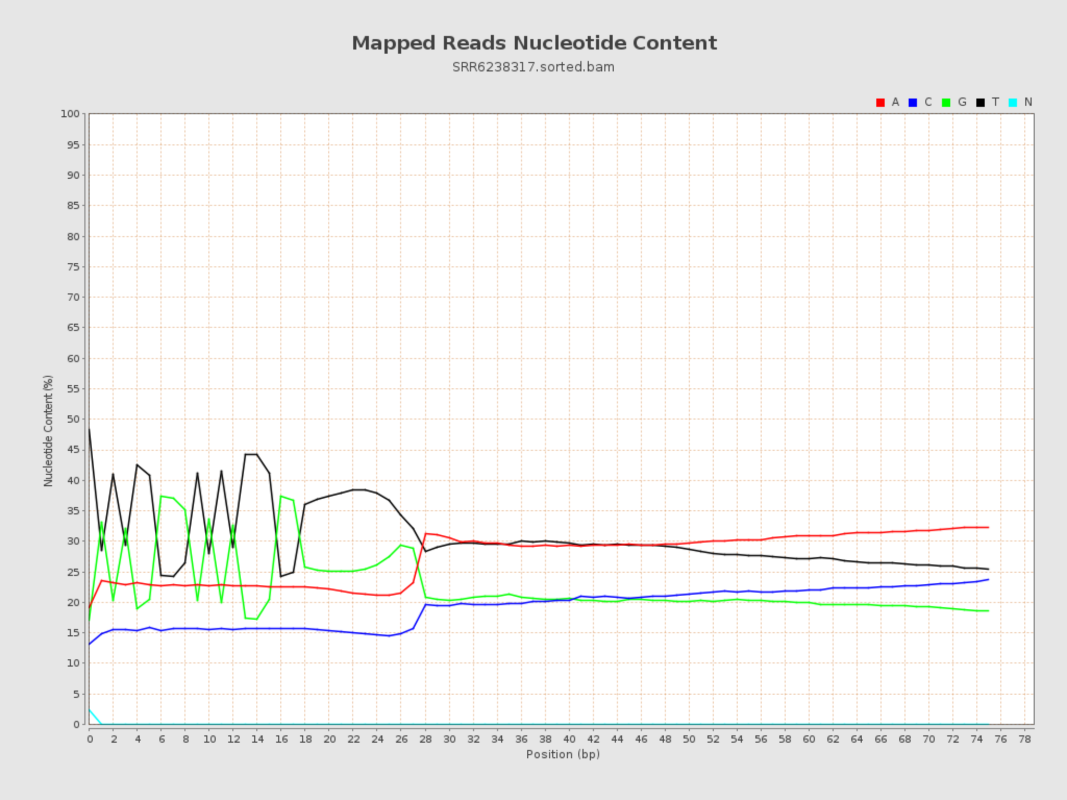
6. Results : Genome Fraction Coverage



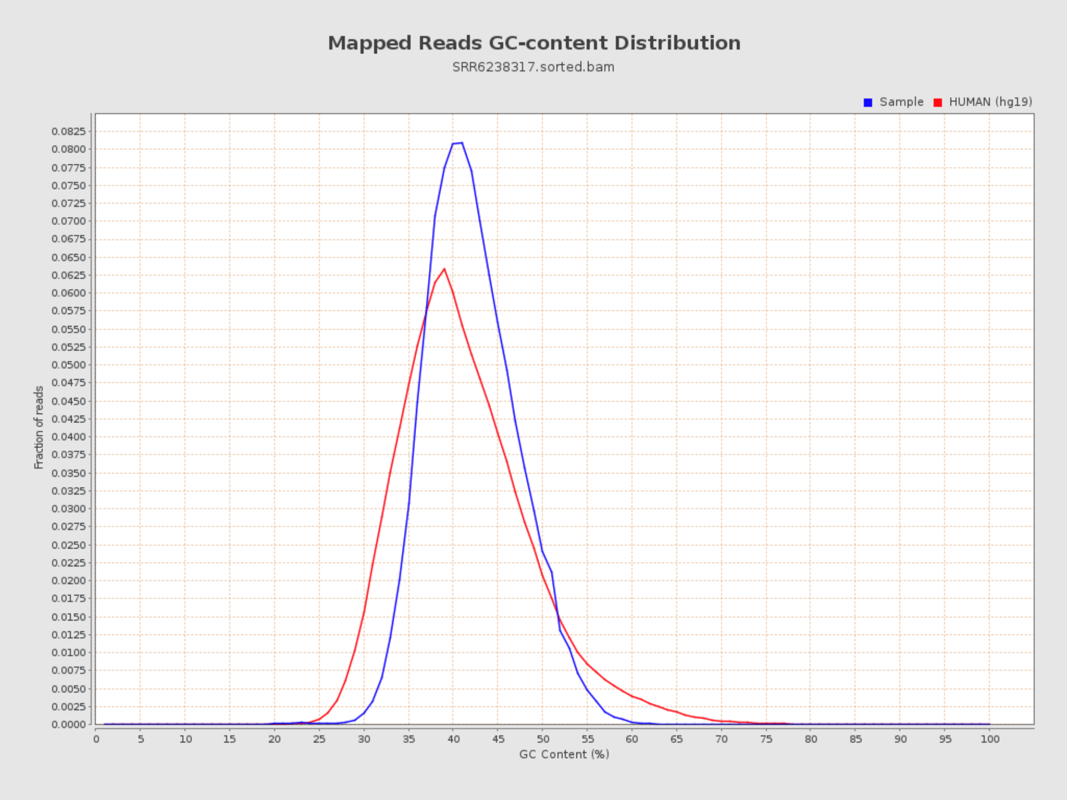
7. Results : Duplication Rate Histogram



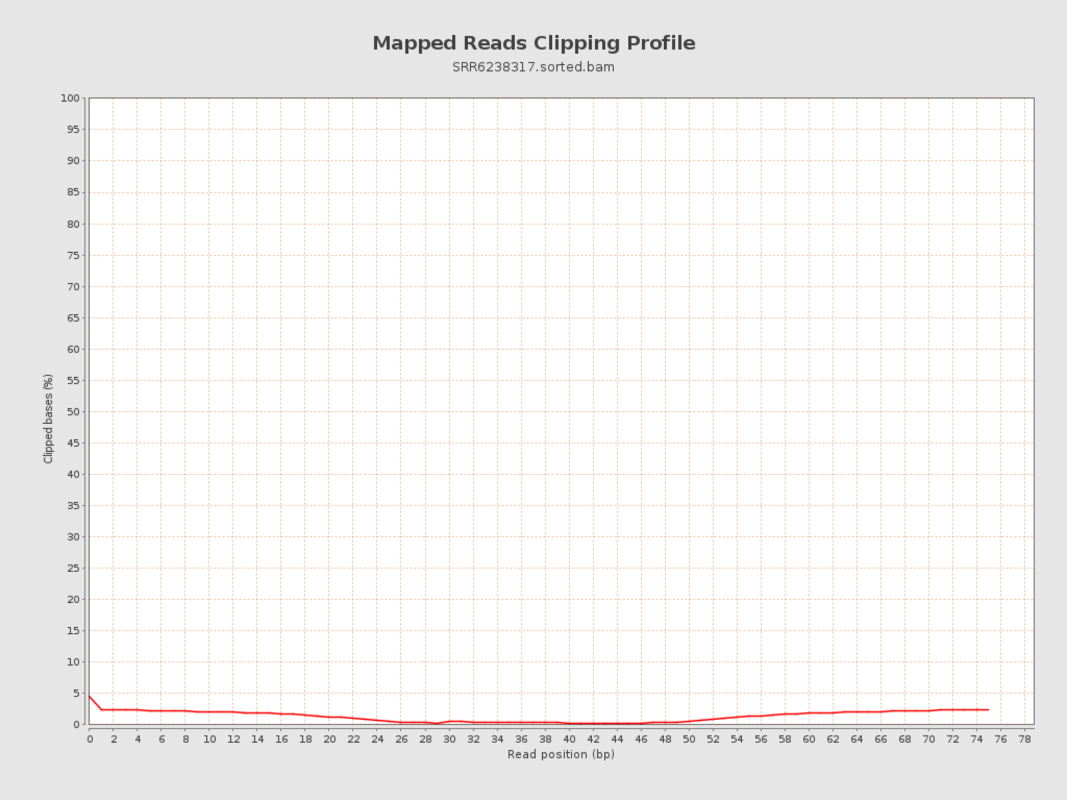
8. Results : Mapped Reads Nucleotide Content



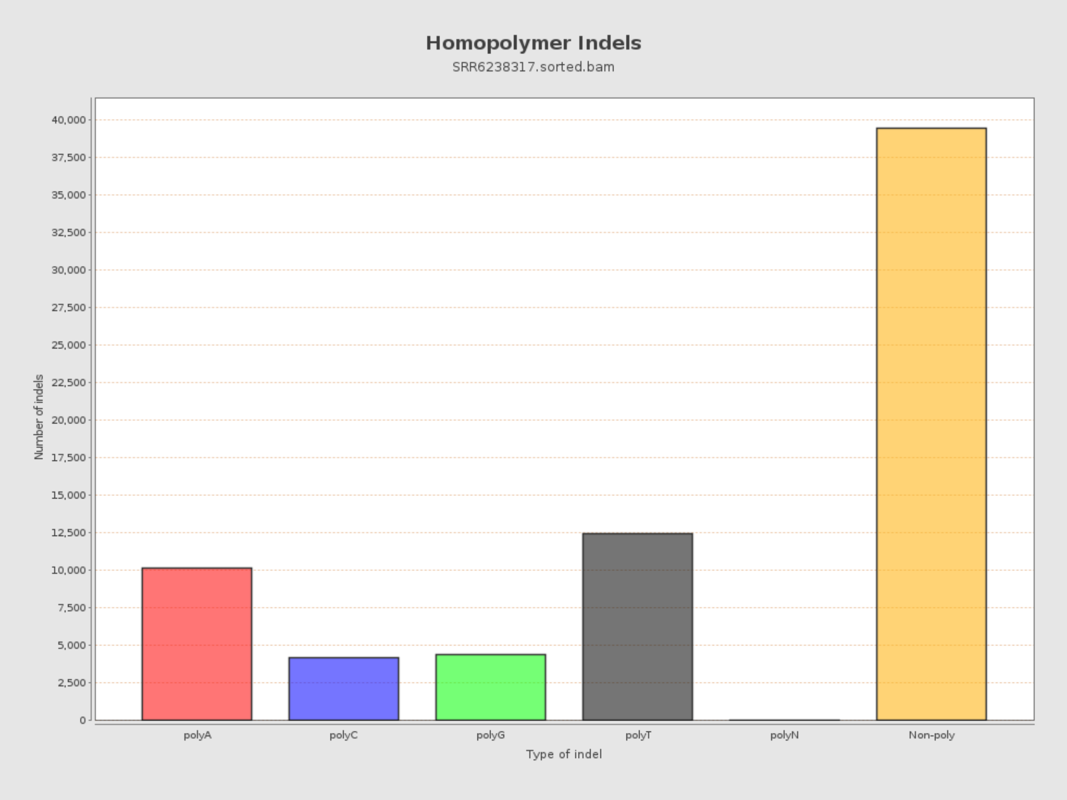
9. Results : Mapped Reads GC-content Distribution



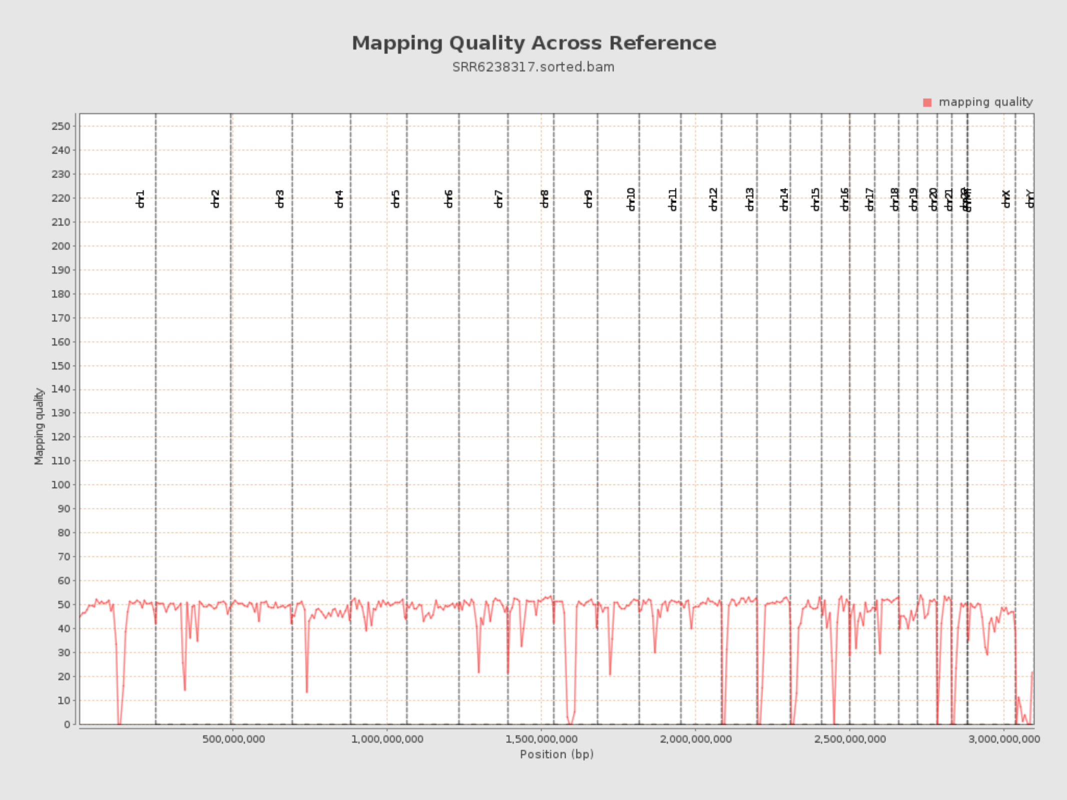
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram