

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:47:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238327.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_SRR6238327 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238327.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:47:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238327.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,853,262
Mapped reads	1,668,221 / 90.02%
Unmapped reads	185,041 / 9.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,077 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	52,878 / 2.85%
Duplication rate	1.89%
Clipped reads	768,803 / 41.48%

2.2. ACGT Content

Number/percentage of A's	31,802,255 / 28.67%
Number/percentage of C's	21,106,031 / 19.03%
Number/percentage of T's	33,464,650 / 30.17%
Number/percentage of G's	24,530,166 / 22.11%
Number/percentage of N's	35,125 / 0.03%
GC Percentage	41.14%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.4402
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2.4. Mapping Quality

Mean Mapping Quality	43.28
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2.5. Mismatches and indels

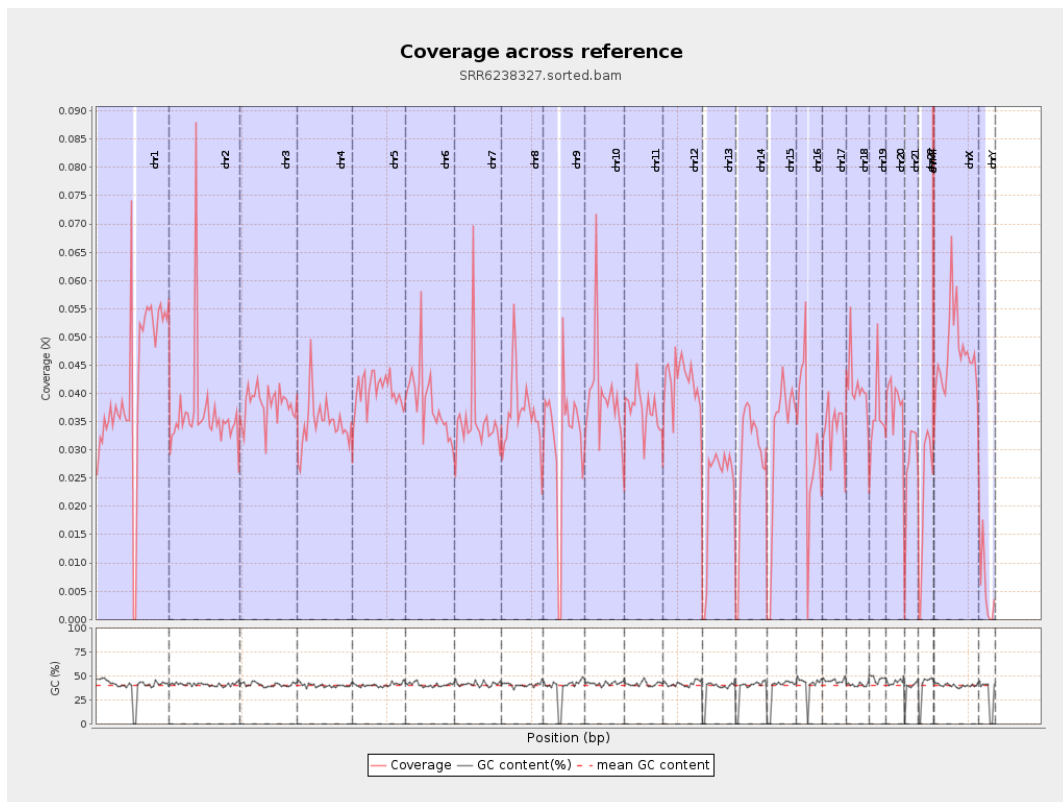
General error rate	0.91%
Mismatches	993,036
Insertions	9,118
Mapped reads with at least one insertion	0.54%
Deletions	31,738
Mapped reads with at least one deletion	1.88%
Homopolymer indels	45.41%

2.6. Chromosome stats

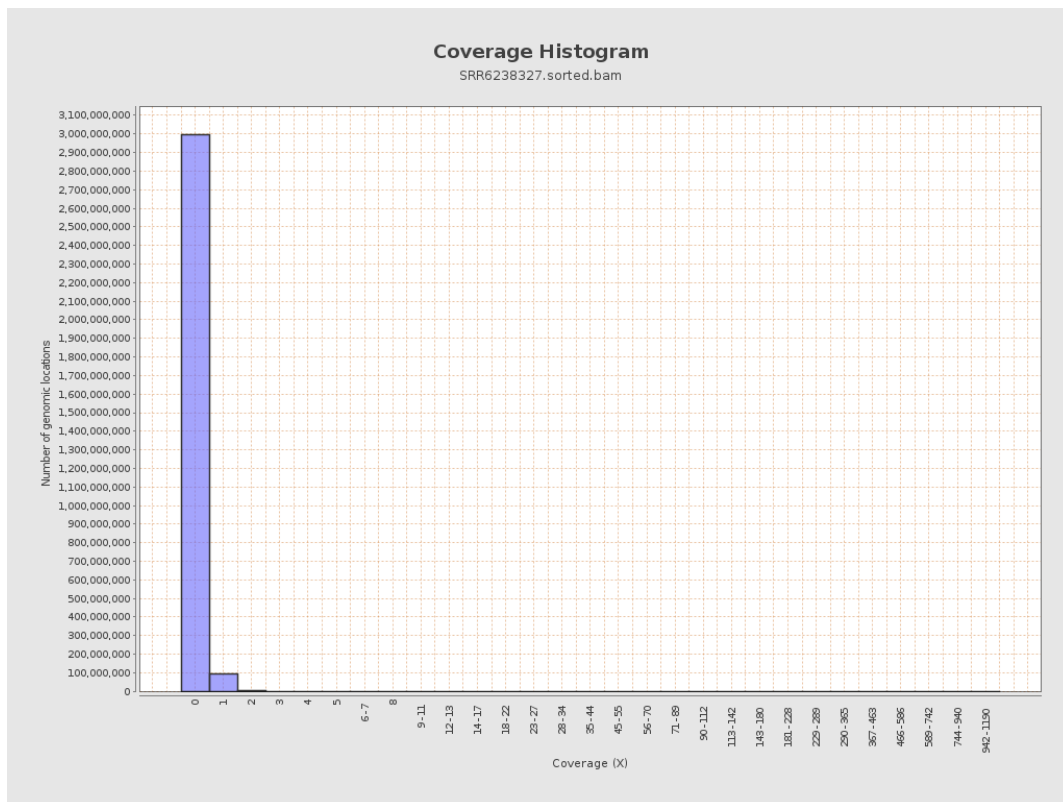
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10348974	0.0415	0.9182
chr2	243199373	8871205	0.0365	0.4534
chr3	198022430	7536874	0.0381	0.2096
chr4	191154276	6619283	0.0346	0.2231
chr5	180915260	7320862	0.0405	0.2208
chr6	171115067	6512415	0.0381	0.2675
chr7	159138663	5605479	0.0352	0.5381

chr8	146364022	5319973	0.0363	0.7482
chr9	141213431	4531144	0.0321	0.4094
chr10	135534747	5350798	0.0395	0.3818
chr11	135006516	4964692	0.0368	0.3476
chr12	133851895	5636050	0.0421	0.2288
chr13	115169878	2626758	0.0228	0.1601
chr14	107349540	3030461	0.0282	0.2349
chr15	102531392	3209021	0.0313	0.194
chr16	90354753	2863291	0.0317	0.2276
chr17	81195210	2720289	0.0335	0.2306
chr18	78077248	3239061	0.0415	0.7482
chr19	59128983	2128847	0.036	0.5758
chr20	63025520	2425684	0.0385	0.2209
chr21	48129895	1312339	0.0273	0.2222
chr22	51304566	1115075	0.0217	0.1561
chrMT	16571	104961	6.334	4.7076
chrX	155270560	7274020	0.0468	0.2704
chrY	59373566	325643	0.0055	0.1502

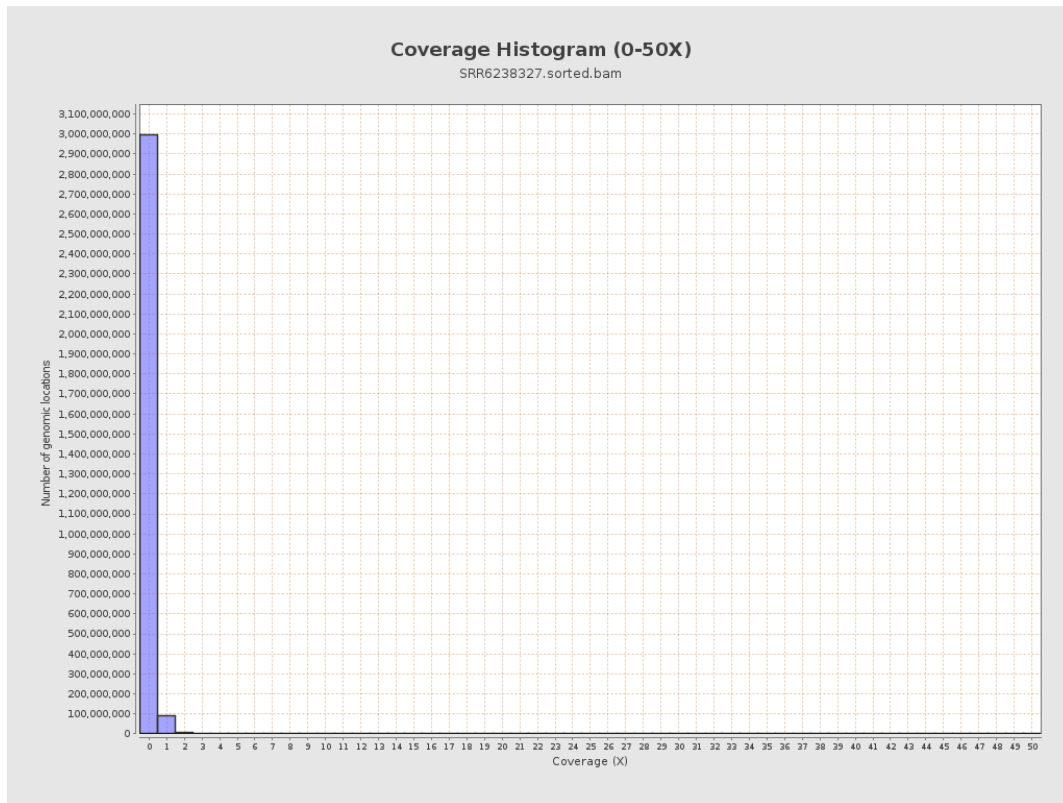
3. Results : Coverage across reference



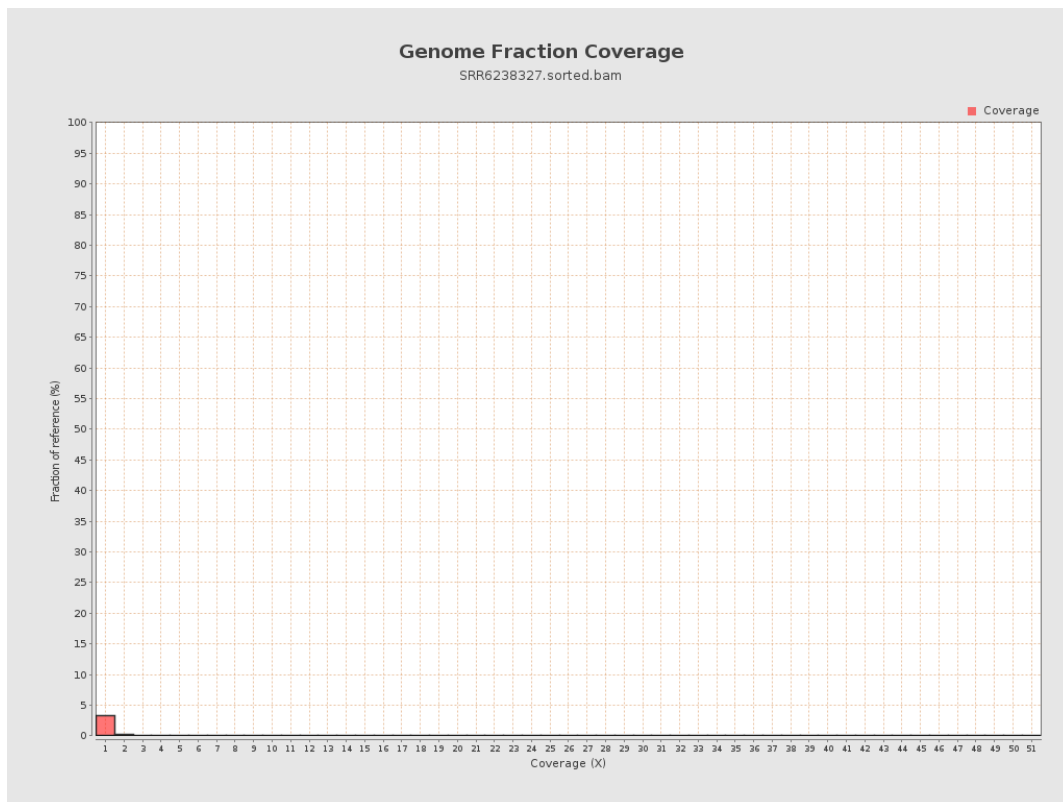
4. Results : Coverage Histogram



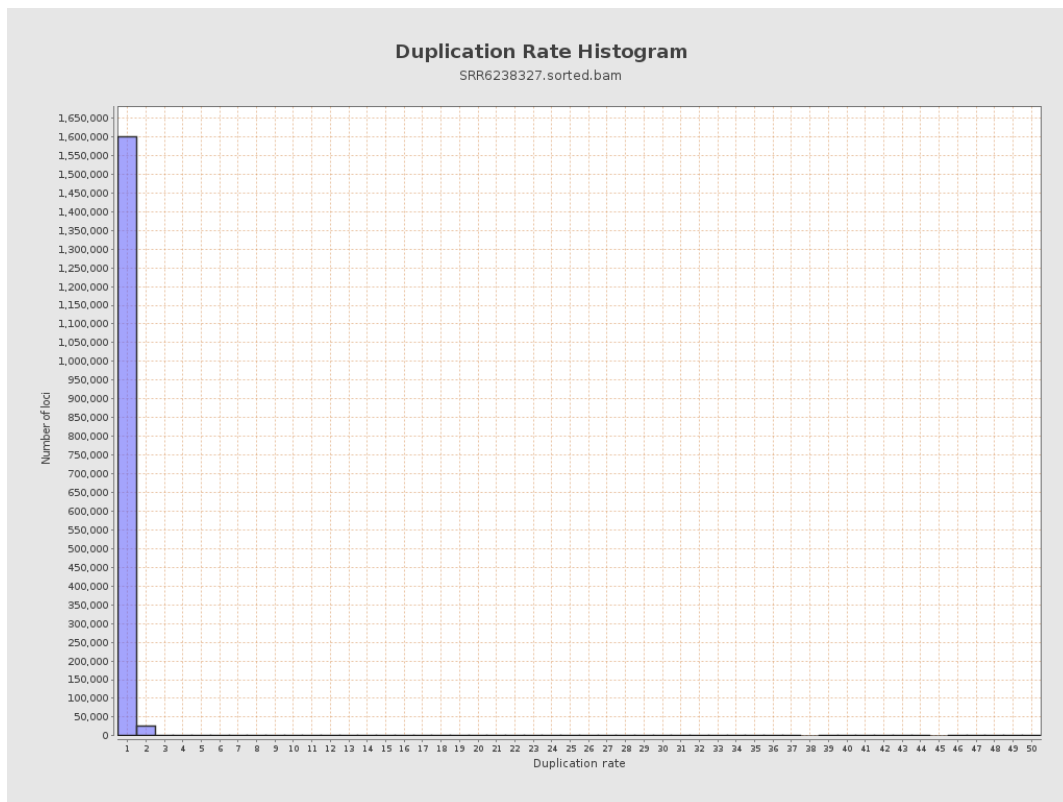
5. Results : Coverage Histogram (0-50X)



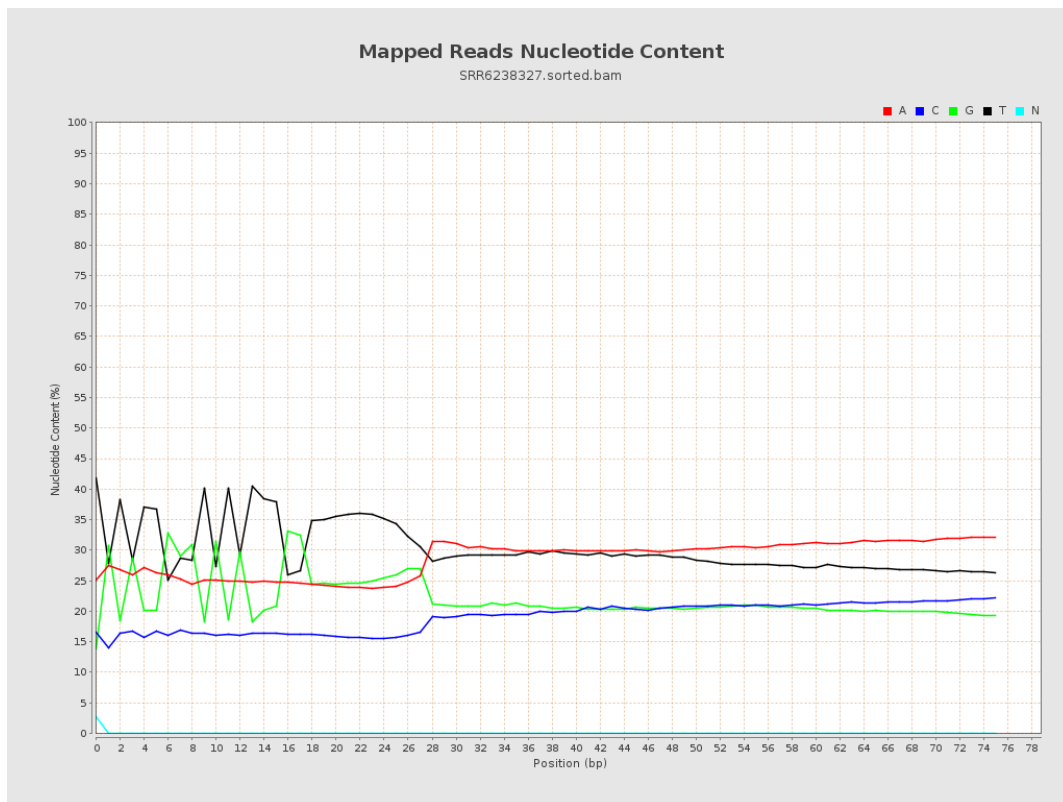
6. Results : Genome Fraction Coverage



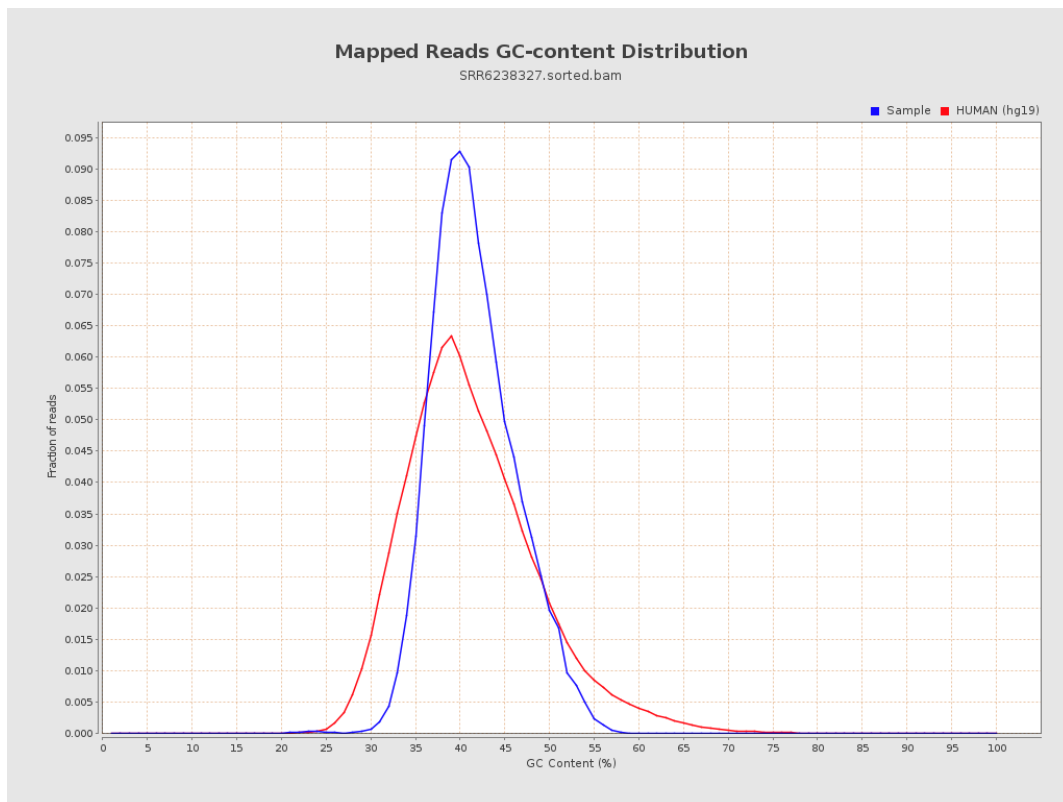
7. Results : Duplication Rate Histogram



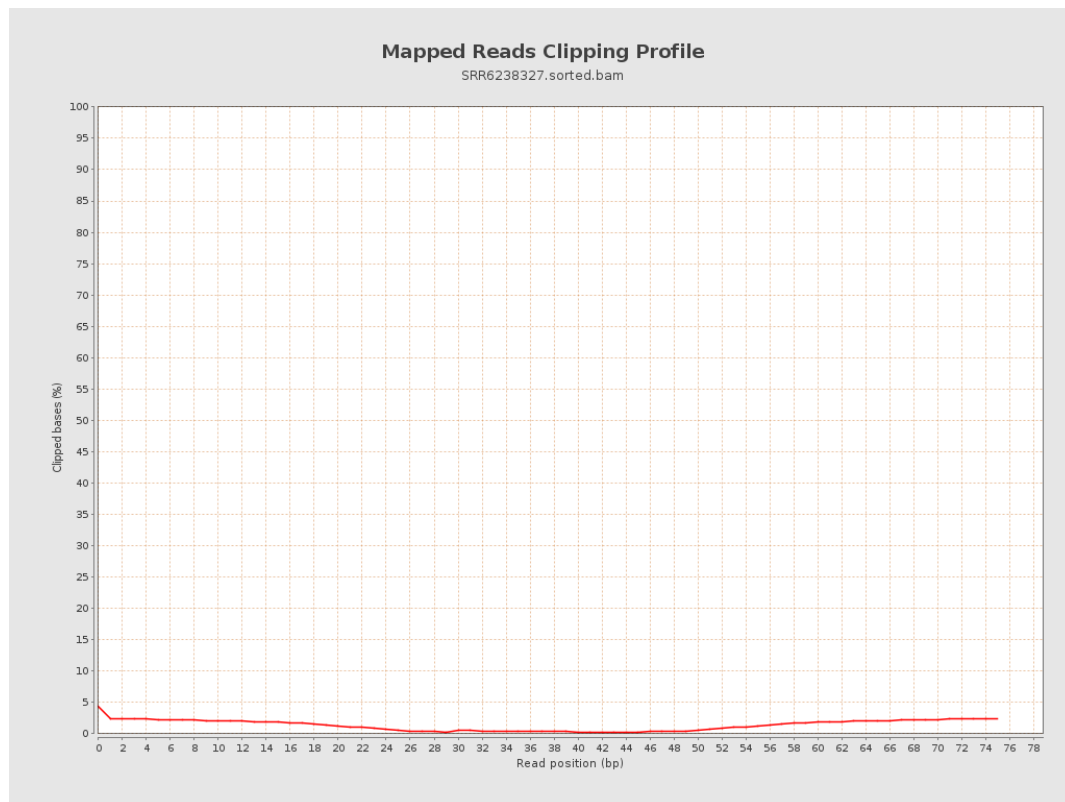
8. Results : Mapped Reads Nucleotide Content



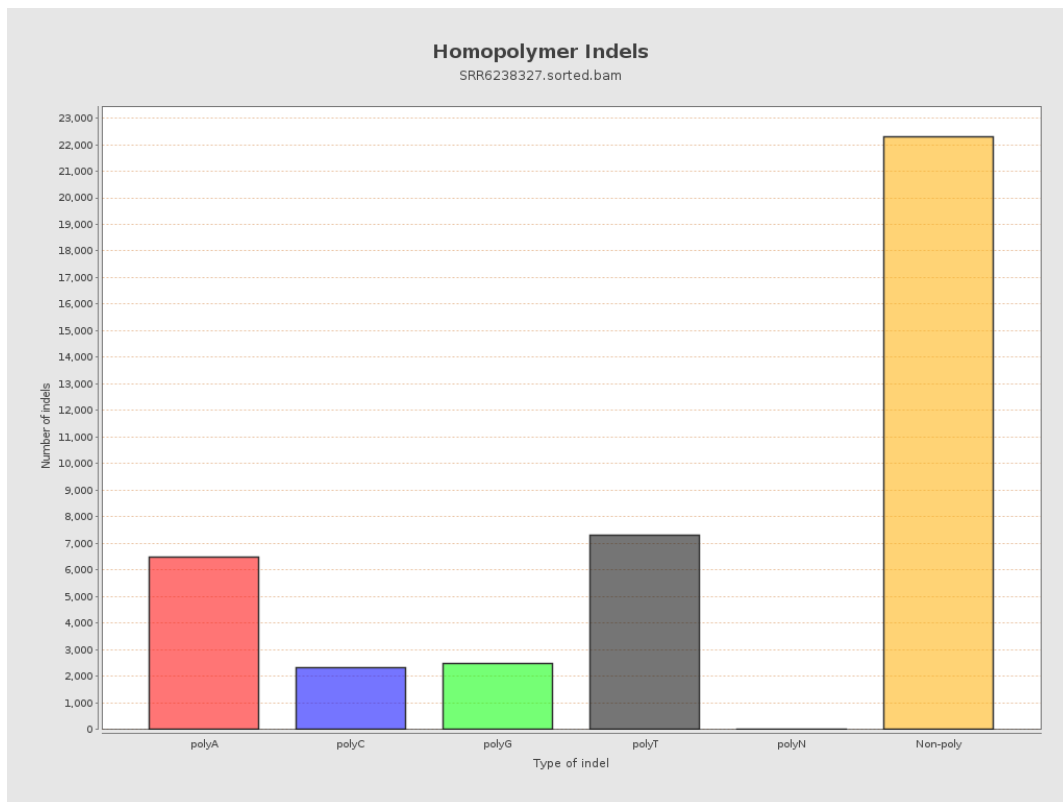
9. Results : Mapped Reads GC-content Distribution



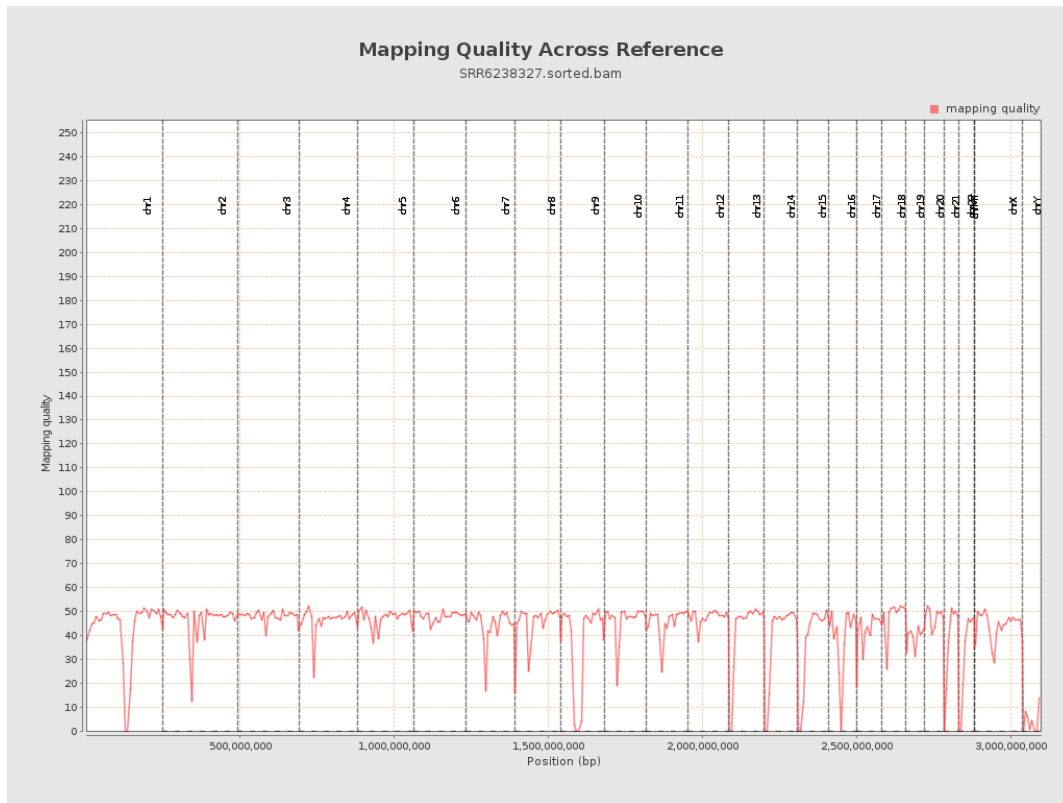
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

