Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:40:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238537.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_SRR6238537 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238537.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:40:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238537.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,973,832
Mapped reads	5,434,723 / 90.98%
Unmapped reads	539,109 / 9.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,570 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,757,778 / 29.42%
Duplication rate	20.28%
Clipped reads	3,335,762 / 55.84%

2.2. ACGT Content

Number/percentage of A's	84,017,015 / 24.85%
Number/percentage of C's	60,351,061 / 17.85%
Number/percentage of T's	112,638,732 / 33.31%
Number/percentage of G's	81,116,498 / 23.99%
Number/percentage of N's	23,874 / 0.01%
GC Percentage	41.84%

2.3. Coverage

Mean	0.1093

Standard Deviation	1.4648

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Mismatches and indels

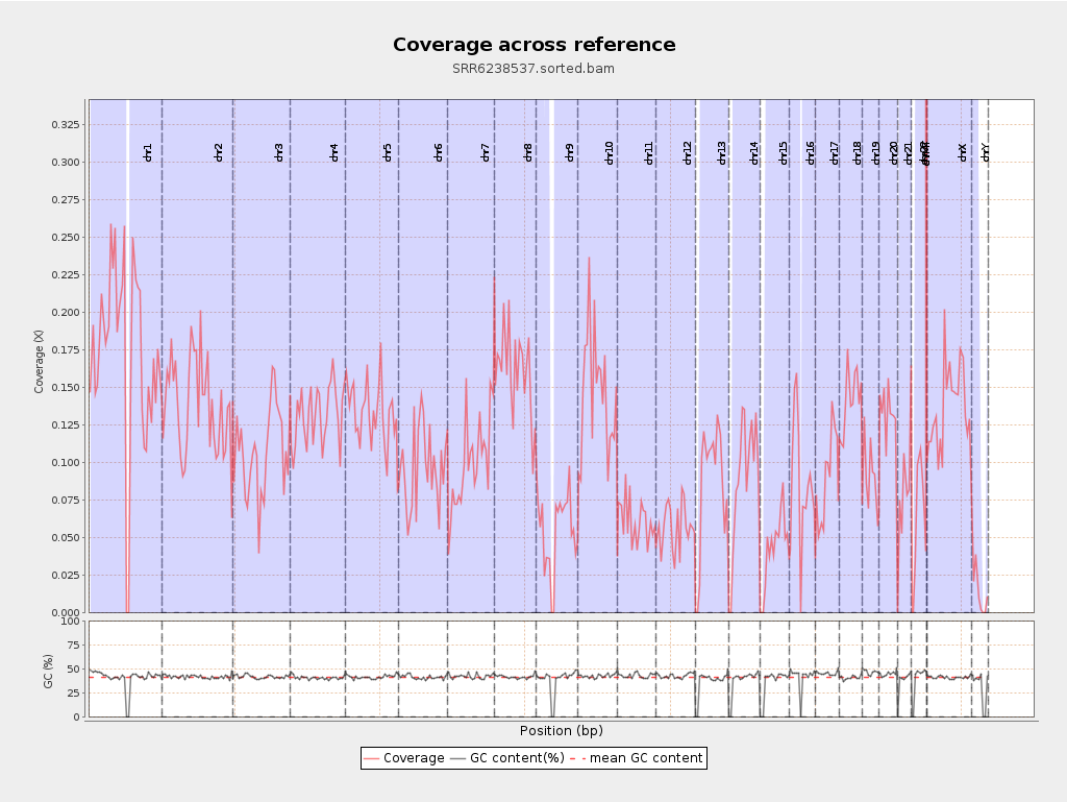
General error rate	0.58%
Mismatches	1,907,111
Insertions	21,482
Mapped reads with at least one insertion	0.39%
Deletions	98,653
Mapped reads with at least one deletion	1.8%
Homopolymer indels	42.45%

2.6. Chromosome stats

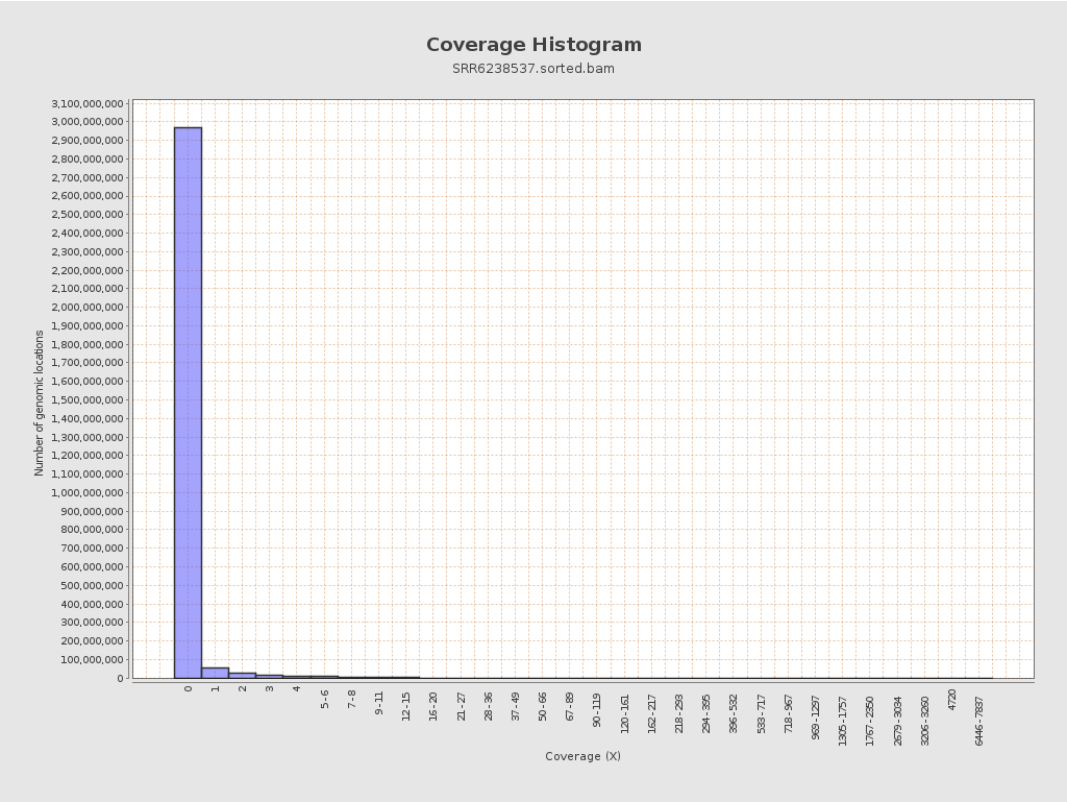
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	42989852	0.1725	2.1086
chr2	243199373	33433522	0.1375	3.4919
chr3	198022430	21331263	0.1077	0.7748
chr4	191154276	25119447	0.1314	0.8118
chr5	180915260	24005124	0.1327	0.8301
chr6	171115067	16452096	0.0961	1.339
chr7	159138663	15783170	0.0992	1.1956

chr8	146364022	23331799	0.1594	1.0769
chr9	141213431	7599695	0.0538	0.6162
chr10	135534747	19789675	0.146	1.3021
chr11	135006516	8195571	0.0607	0.5867
chr12	133851895	7652307	0.0572	0.5362
chr13	115169878	9660761	0.0839	0.9433
chr14	107349540	9633348	0.0897	0.6848
chr15	102531392	4414697	0.0431	0.7769
chr16	90354753	7951132	0.088	0.7417
chr17	81195210	7350617	0.0905	0.6769
chr18	78077248	11028145	0.1412	2.4896
chr19	59128983	5329276	0.0901	1.4686
chr20	63025520	8268108	0.1312	0.8385
chr21	48129895	3856833	0.0801	0.6559
chr22	51304566	3117010	0.0608	0.5581
chrMT	16571	59252	3.5756	4.267
chrX	155270560	21069443	0.1357	0.8465
chrY	59373566	892282	0.015	0.5302

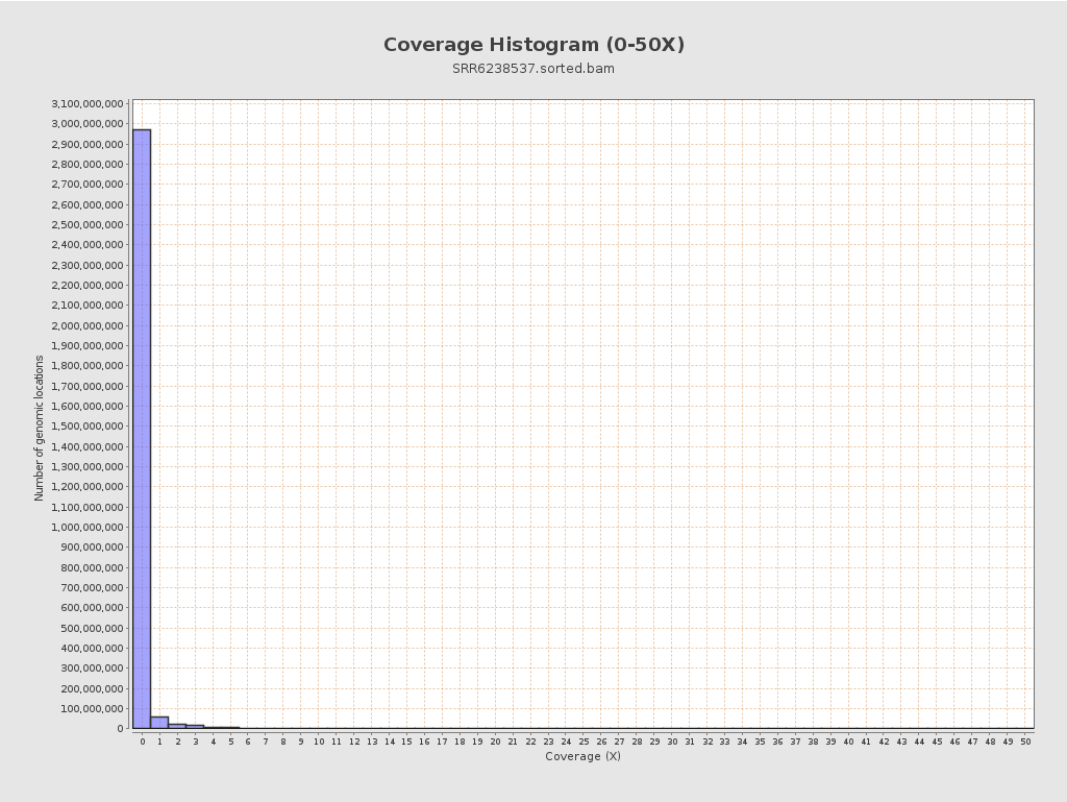
3. Results : Coverage across reference



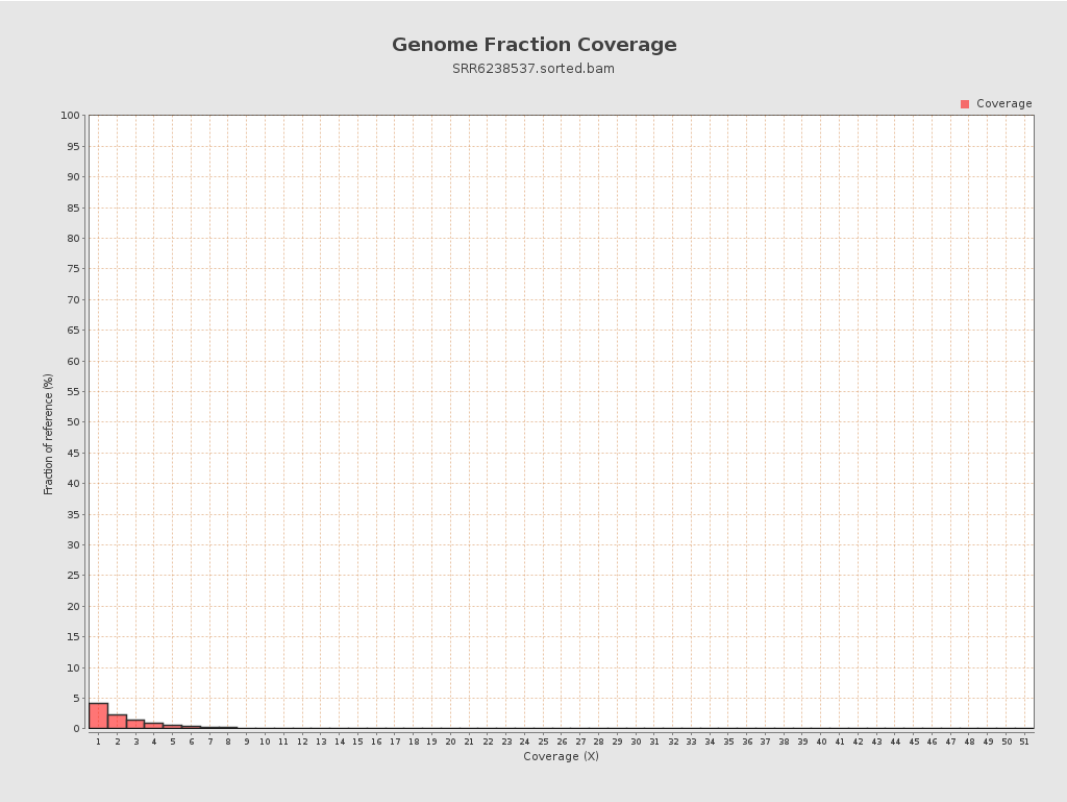
4. Results : Coverage Histogram



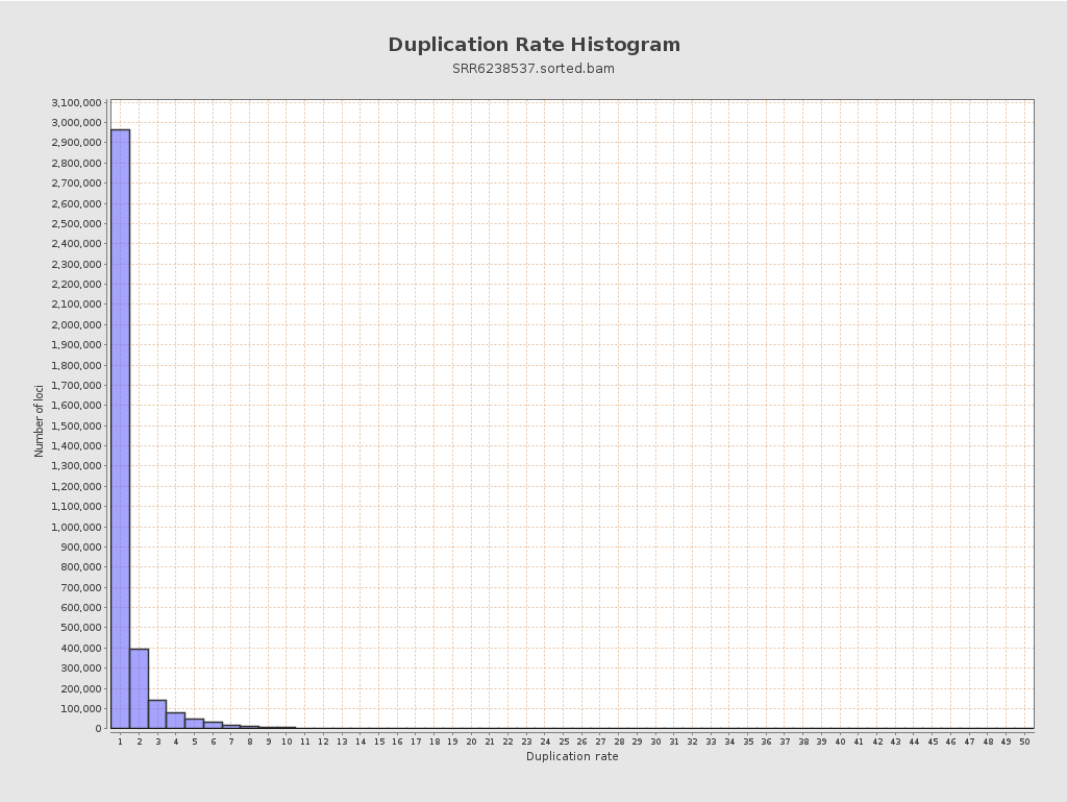
5. Results : Coverage Histogram (0-50X)



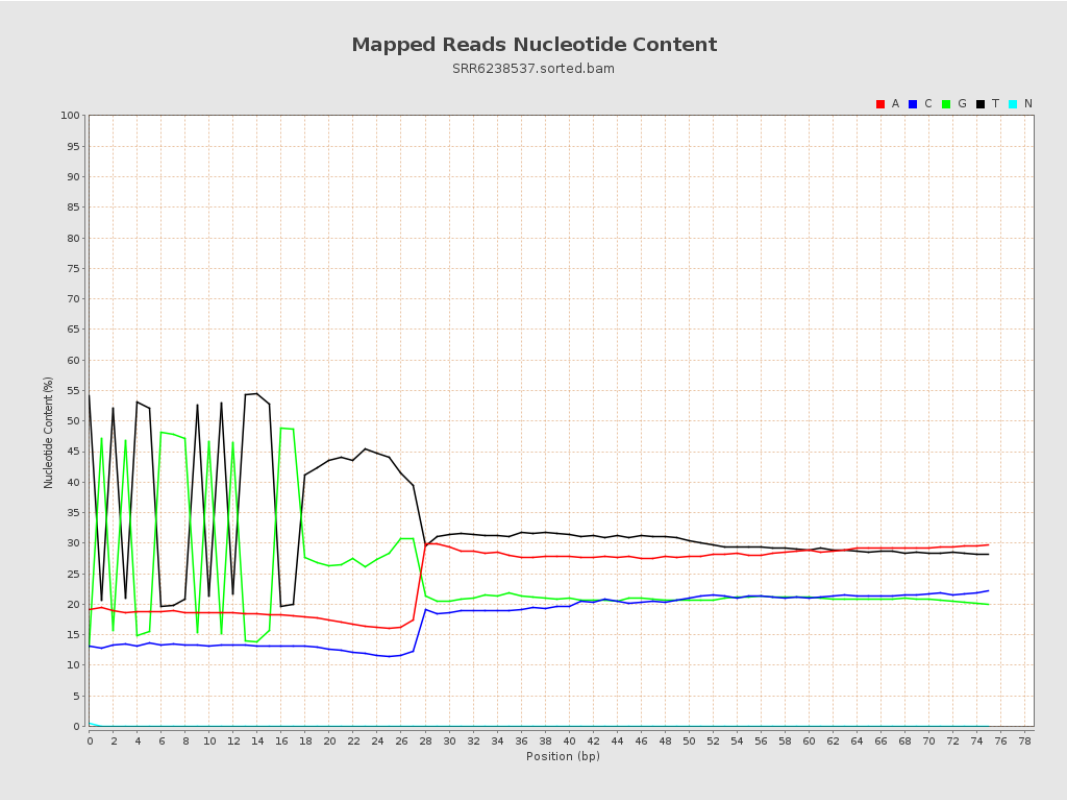
6. Results : Genome Fraction Coverage



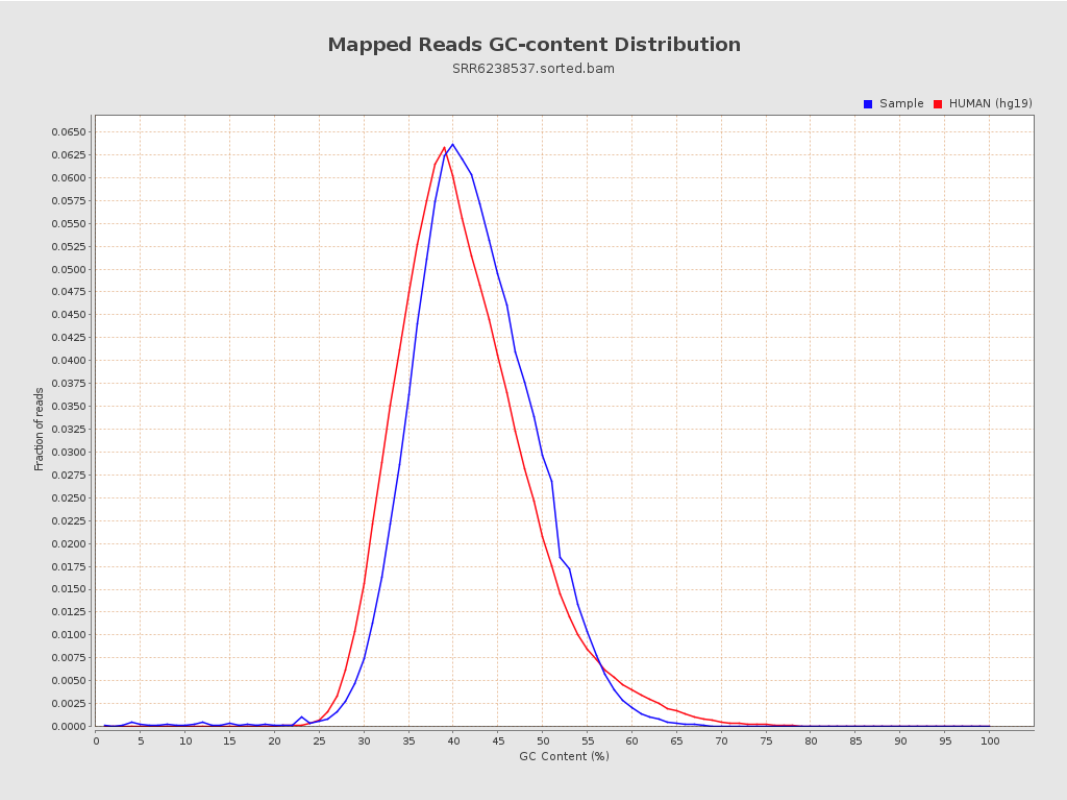
7. Results : Duplication Rate Histogram



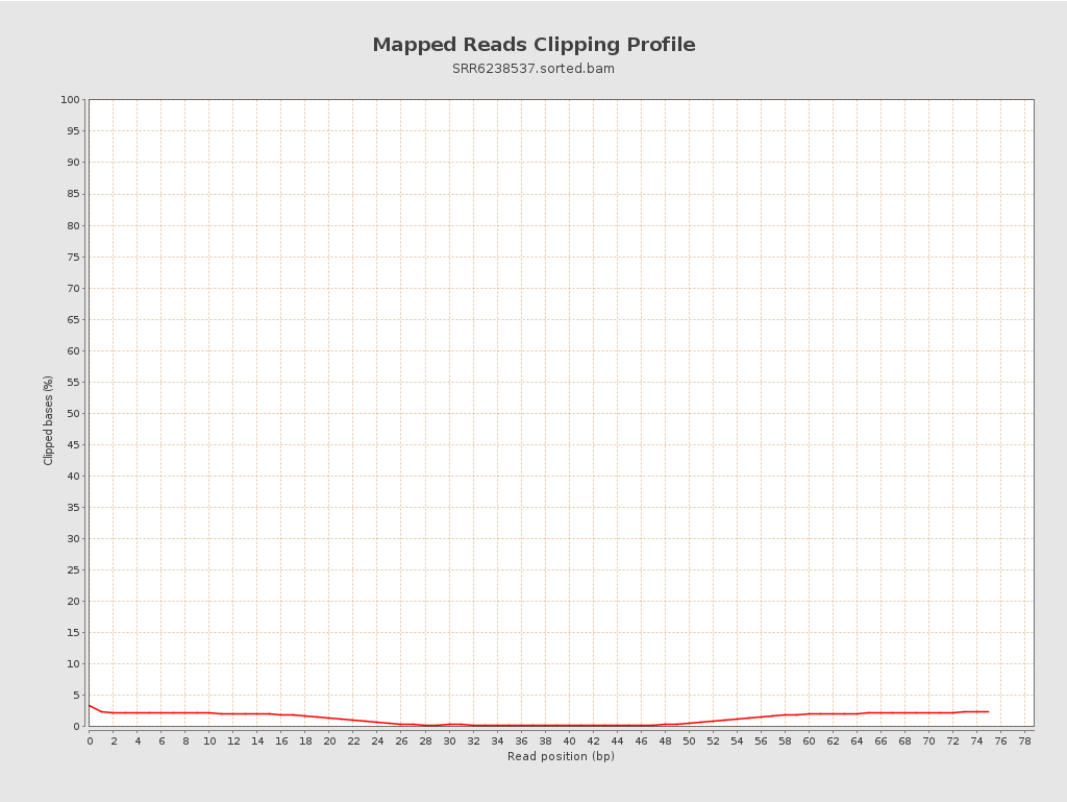
8. Results : Mapped Reads Nucleotide Content



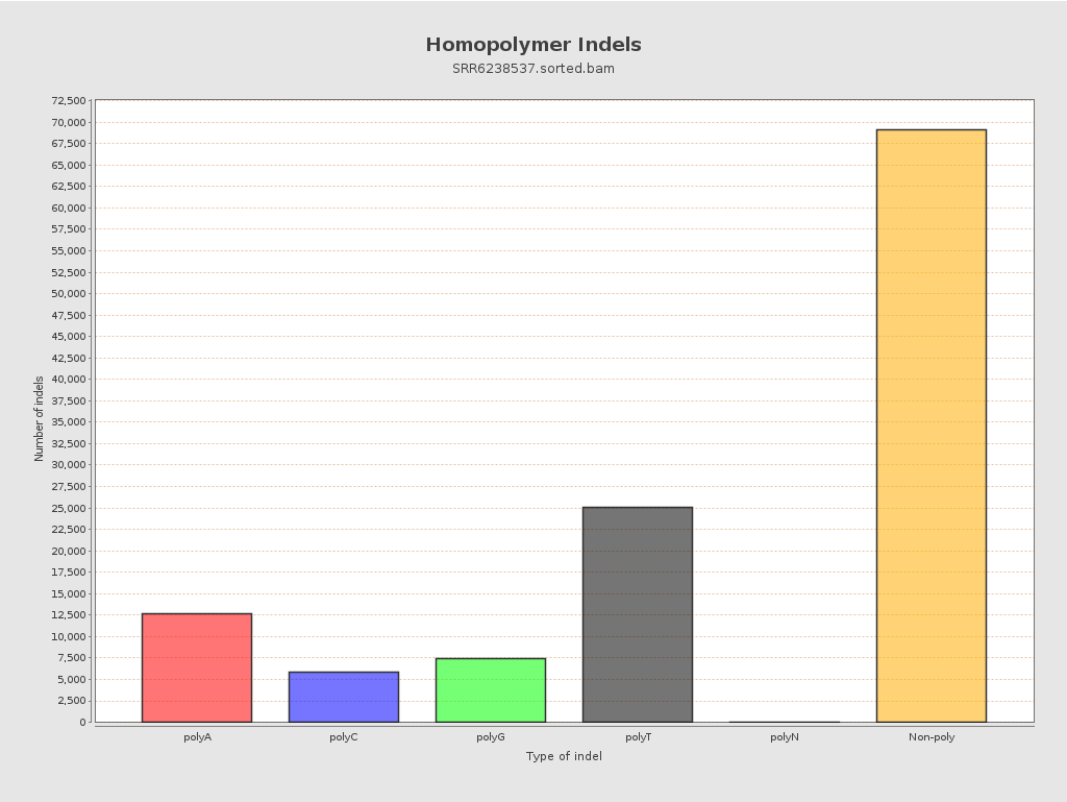
9. Results : Mapped Reads GC-content Distribution



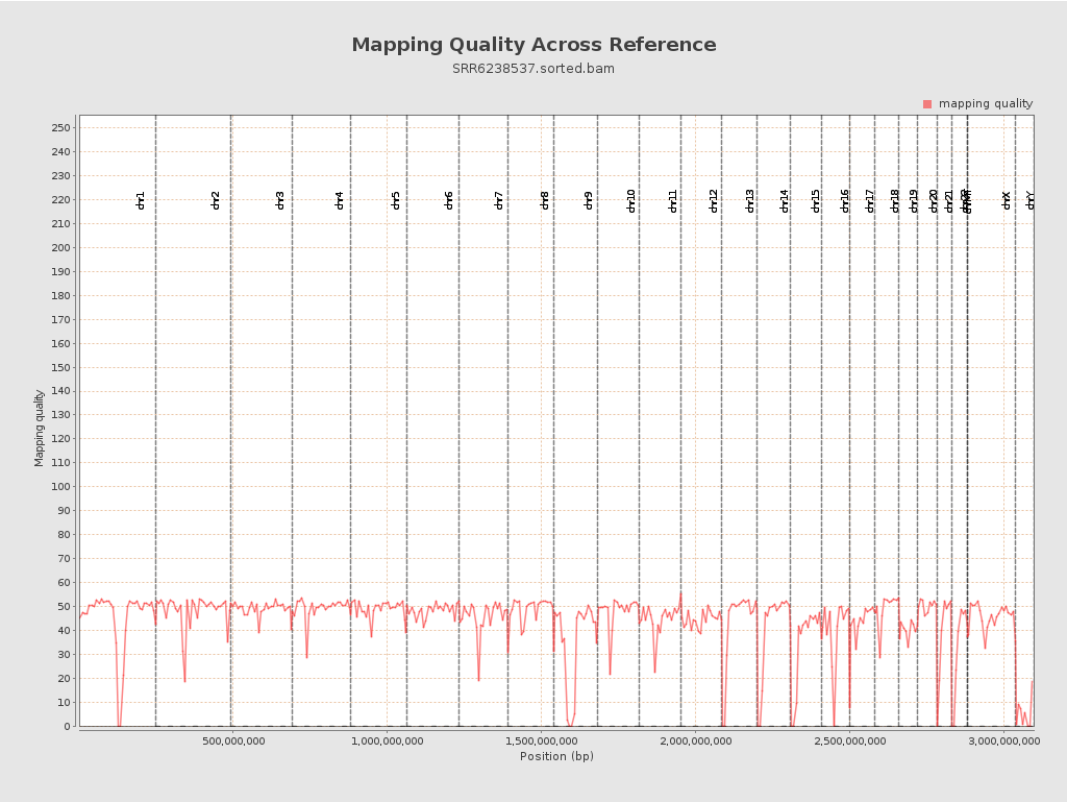
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram