

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:46:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472813.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_SRR3472813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472813.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:46:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,931,969
Mapped reads	1,500,402 / 77.66%
Unmapped reads	431,567 / 22.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,266 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	50,843 / 2.63%
Duplication rate	2.55%
Clipped reads	867,818 / 44.92%

2.2. ACGT Content

Number/percentage of A's	25,405,520 / 26.73%
Number/percentage of C's	19,453,033 / 20.47%
Number/percentage of T's	27,680,976 / 29.12%
Number/percentage of G's	22,502,856 / 23.68%
Number/percentage of N's	1,925 / 0%
GC Percentage	44.14%

2.3. Coverage

Mean	0.0307

Standard Deviation	0.2549
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2.4. Mapping Quality

Mean Mapping Quality	43.03
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2.5. Mismatches and indels

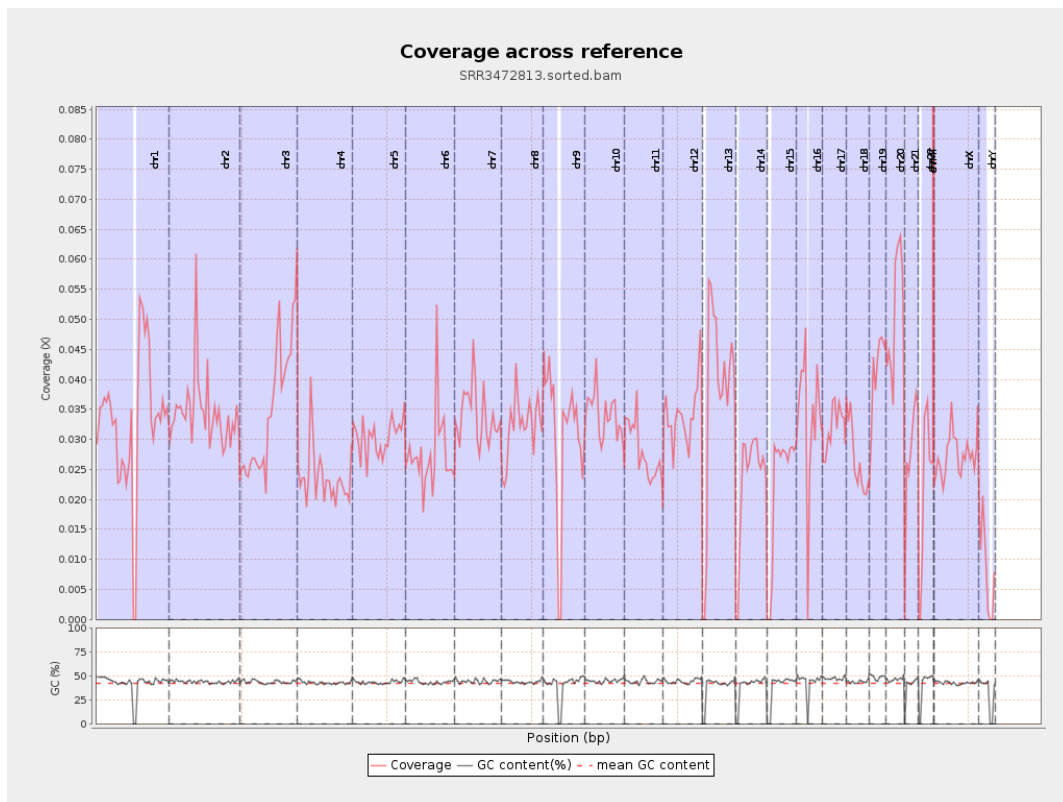
General error rate	0.88%
Mismatches	824,095
Insertions	7,399
Mapped reads with at least one insertion	0.49%
Deletions	22,791
Mapped reads with at least one deletion	1.5%
Homopolymer indels	44.03%

2.6. Chromosome stats

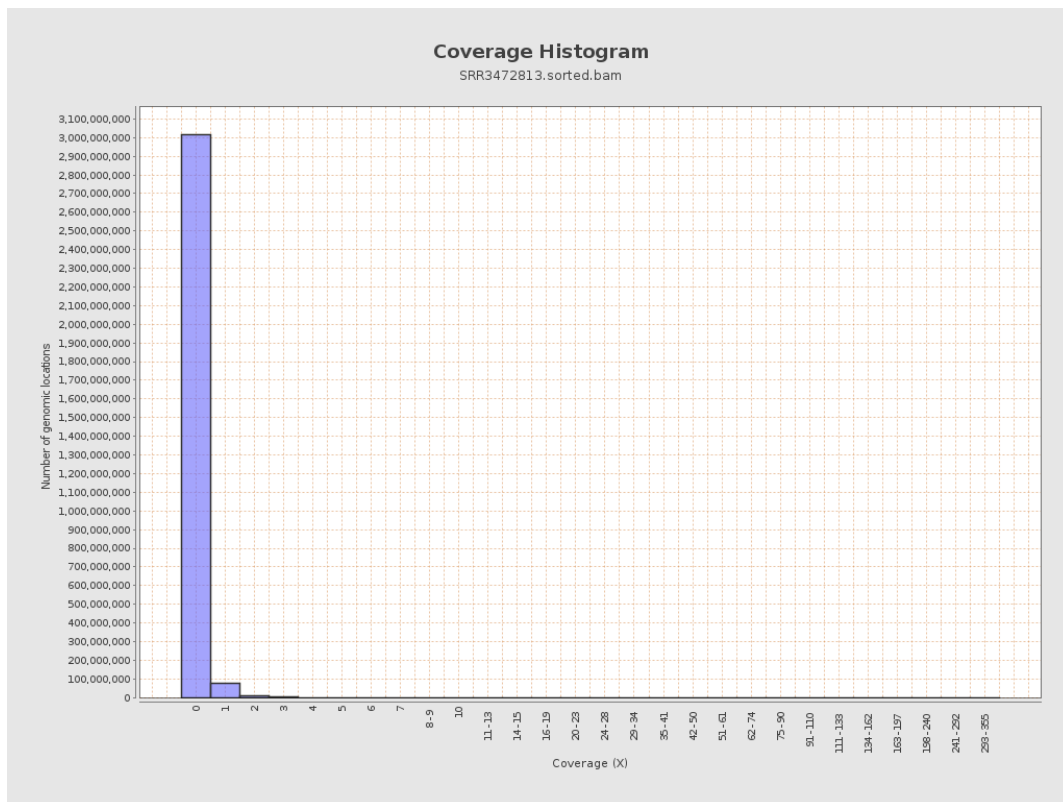
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8185411	0.0328	0.3274
chr2	243199373	8379923	0.0345	0.3453
chr3	198022430	6853599	0.0346	0.21
chr4	191154276	4485737	0.0235	0.1899
chr5	180915260	5492172	0.0304	0.1978
chr6	171115067	4684502	0.0274	0.2057
chr7	159138663	5405819	0.034	0.323

chr8	146364022	4698675	0.0321	0.2422
chr9	141213431	4300316	0.0305	0.2667
chr10	135534747	4616006	0.0341	0.2578
chr11	135006516	3759908	0.0278	0.2607
chr12	133851895	4567872	0.0341	0.2122
chr13	115169878	4299300	0.0373	0.2233
chr14	107349540	2468910	0.023	0.1876
chr15	102531392	2305251	0.0225	0.1849
chr16	90354753	3038201	0.0336	0.2235
chr17	81195210	2600855	0.032	0.2164
chr18	78077248	2087145	0.0267	0.4183
chr19	59128983	2441841	0.0413	0.2875
chr20	63025520	3211516	0.051	0.2623
chr21	48129895	1344772	0.0279	0.2084
chr22	51304566	1086328	0.0212	0.1695
chrMT	16571	68907	4.1583	3.5918
chrX	155270560	4226652	0.0272	0.2077
chrY	59373566	475553	0.008	0.1268

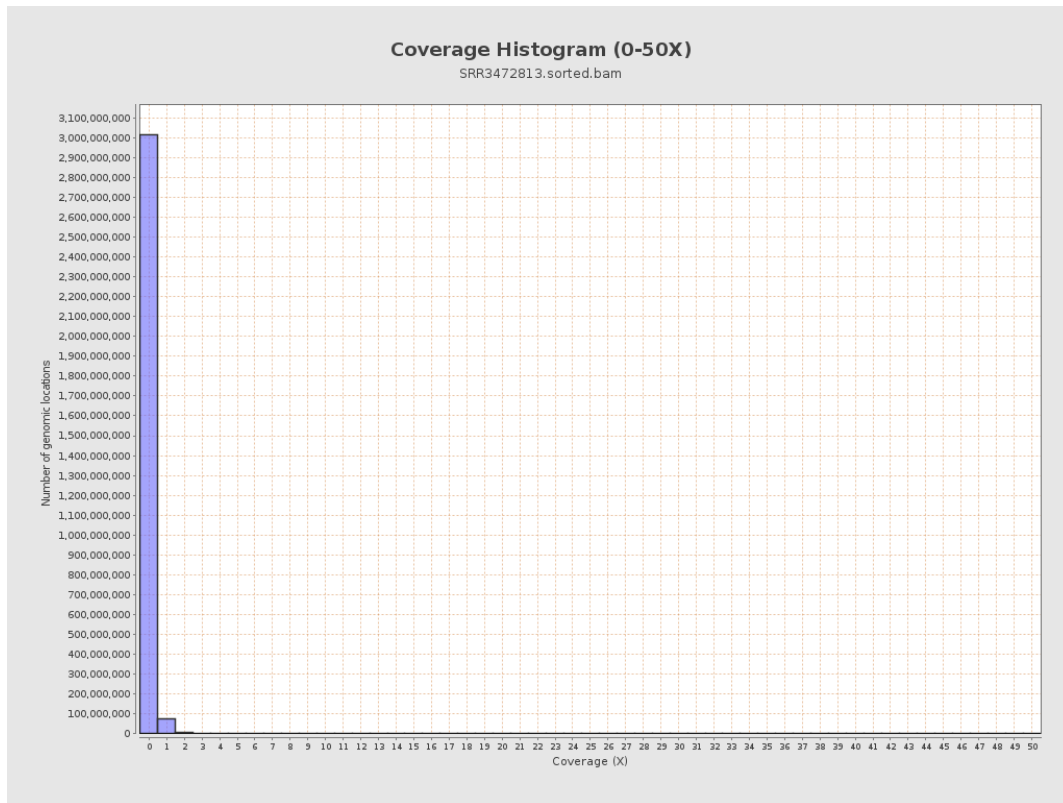
3. Results : Coverage across reference



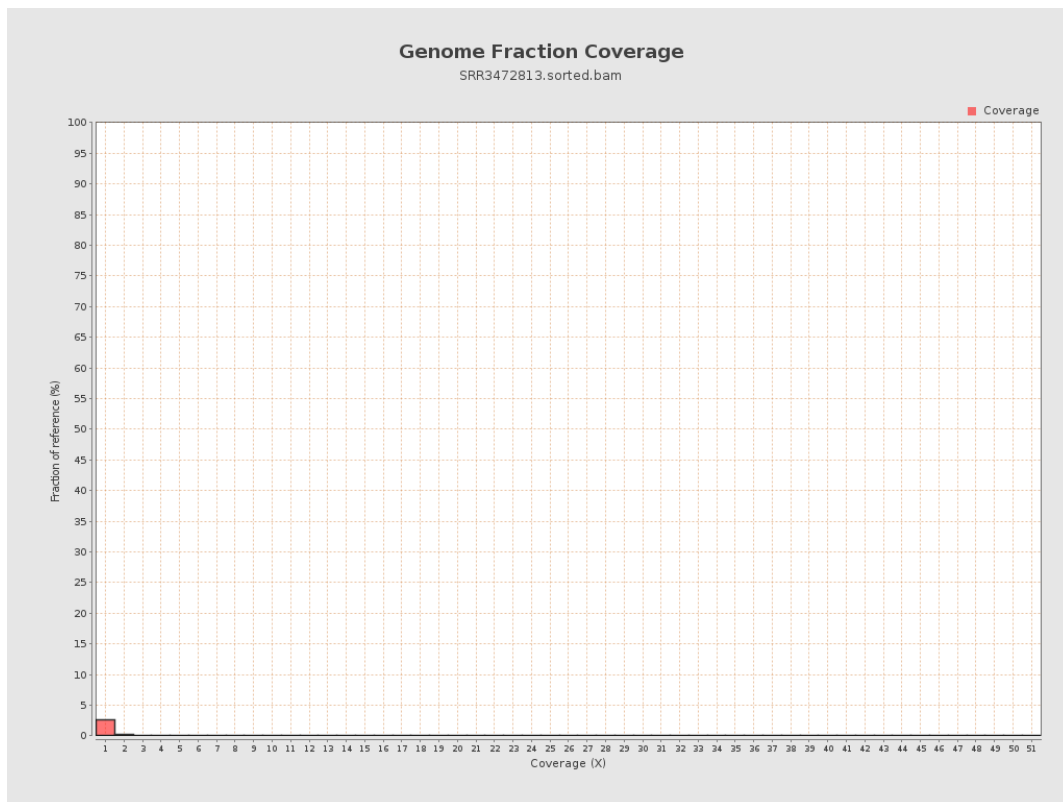
4. Results : Coverage Histogram



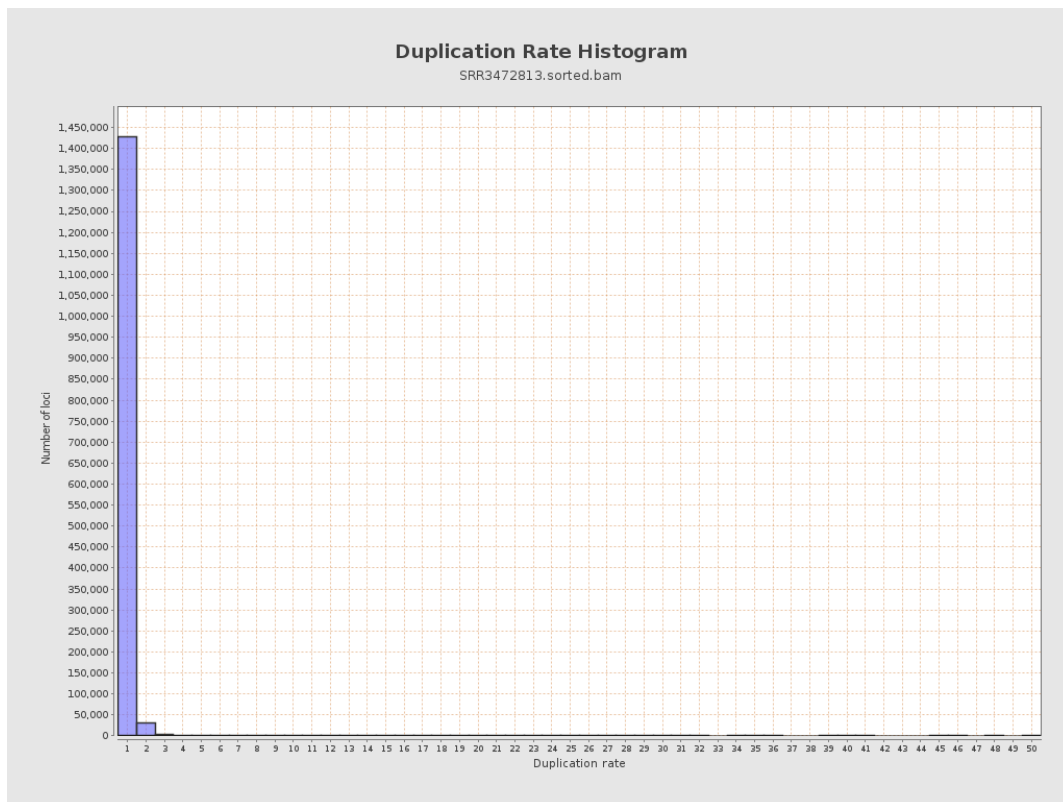
5. Results : Coverage Histogram (0-50X)



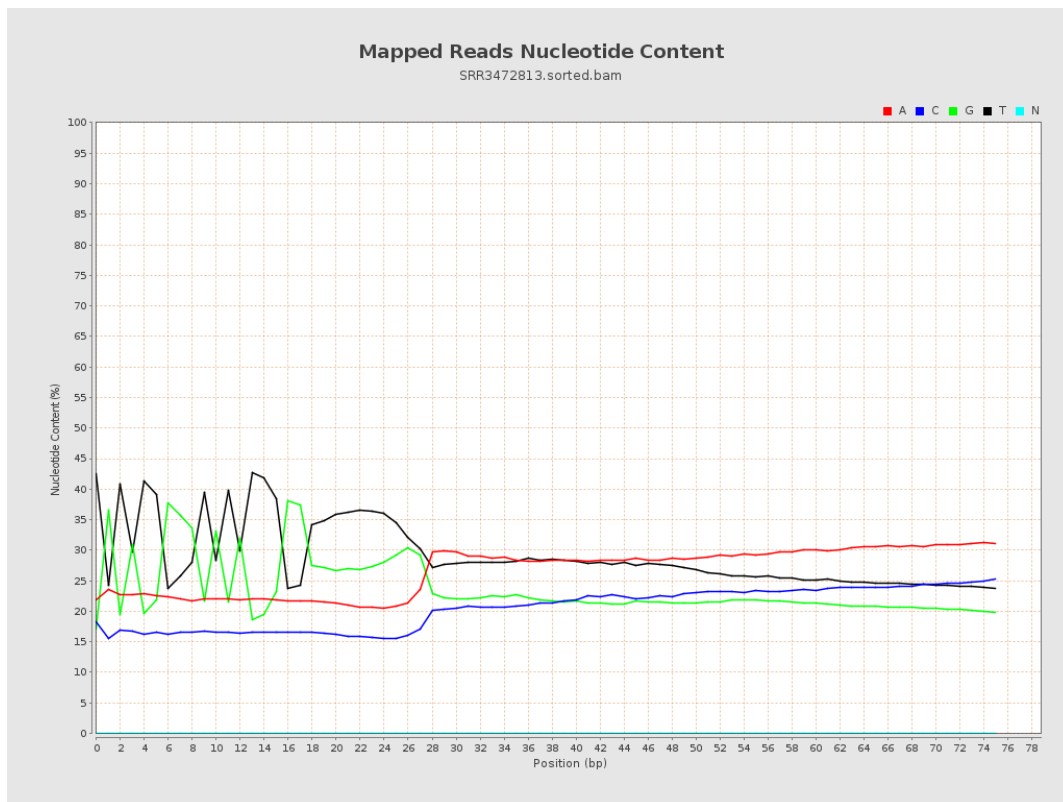
6. Results : Genome Fraction Coverage



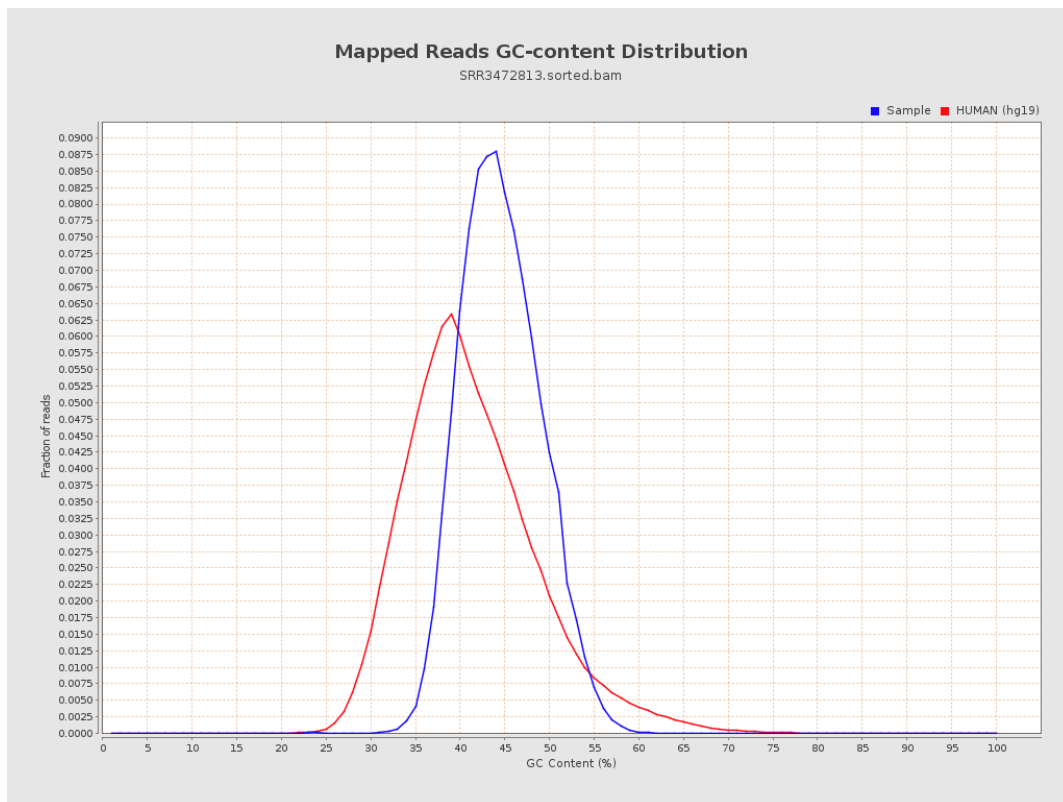
7. Results : Duplication Rate Histogram



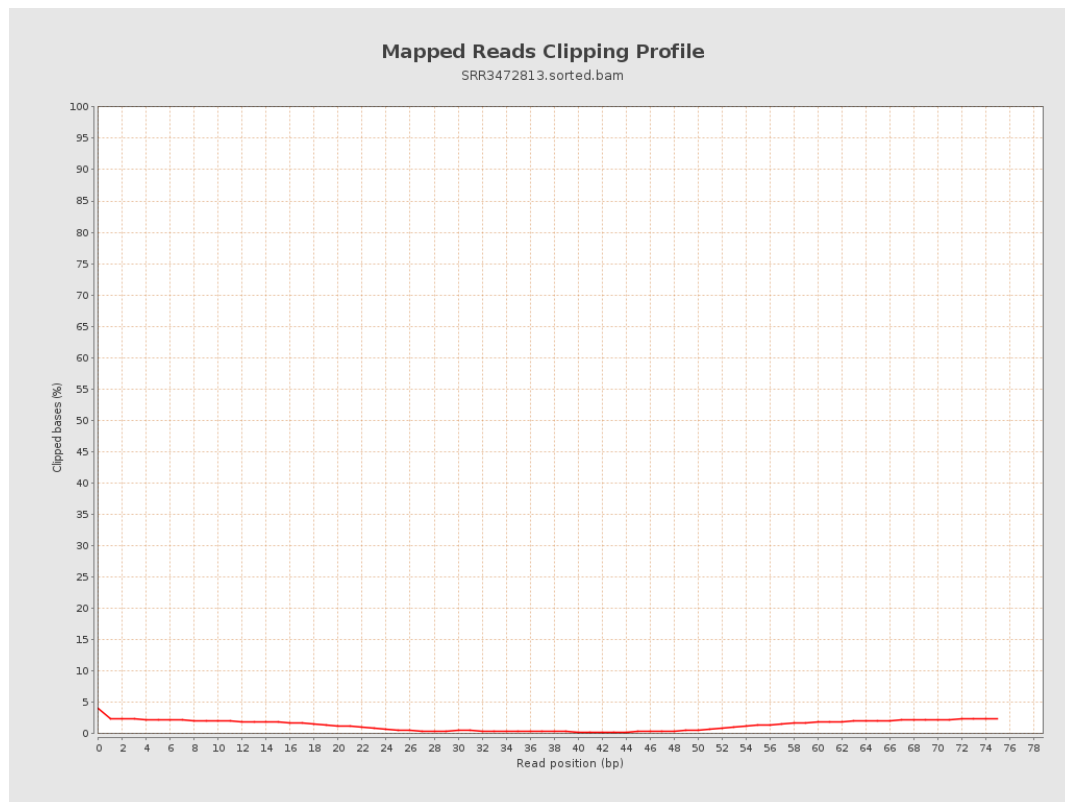
8. Results : Mapped Reads Nucleotide Content



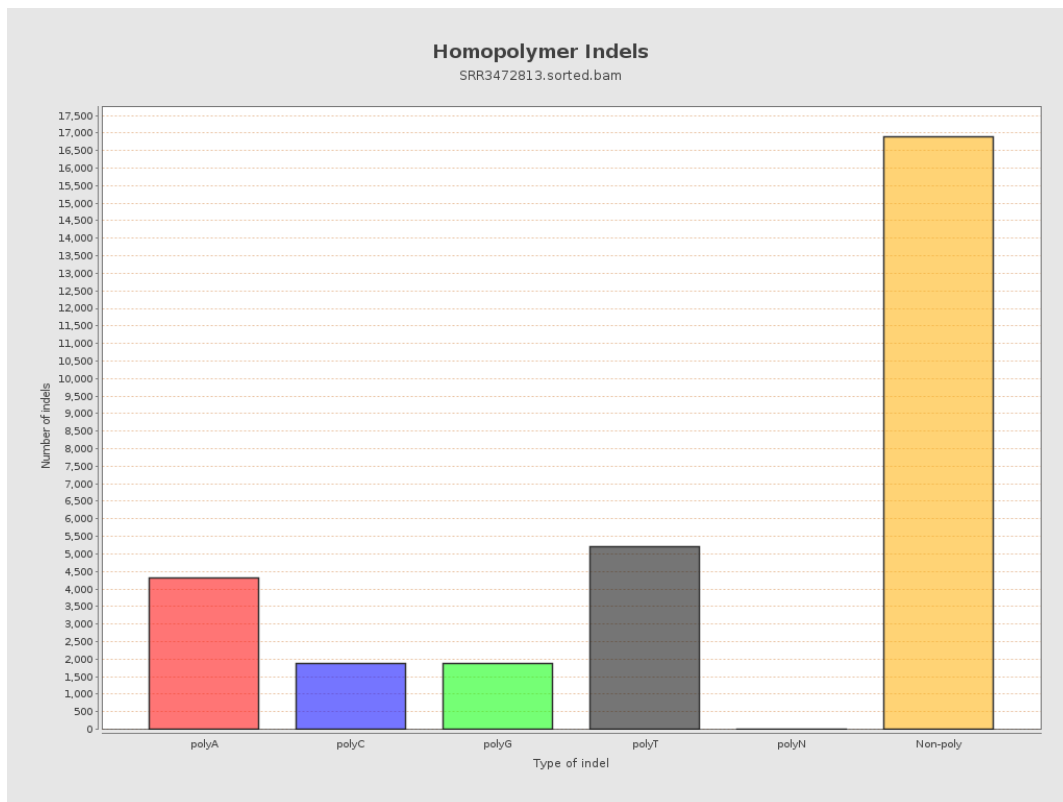
9. Results : Mapped Reads GC-content Distribution



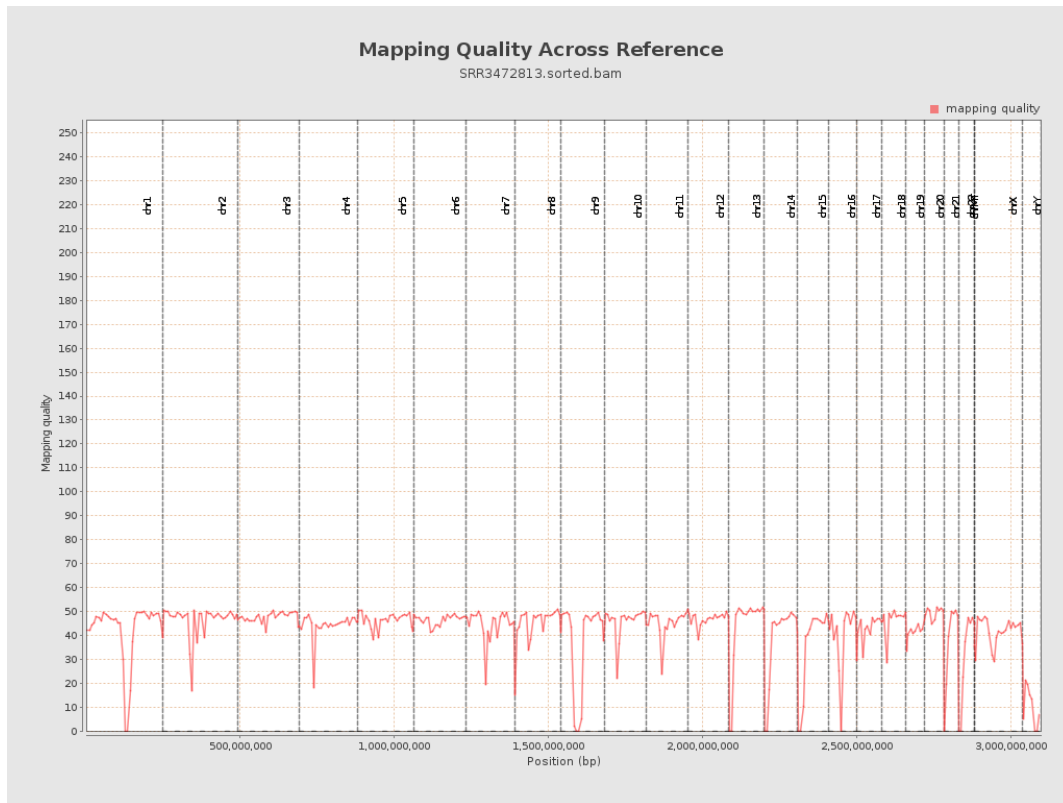
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

