

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:25:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237288.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_SRR6237288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237288.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:25:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,050,779
Mapped reads	1,899,976 / 92.65%
Unmapped reads	150,803 / 7.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,360 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	333,537 / 16.26%
Duplication rate	14.49%
Clipped reads	1,190,835 / 58.07%

2.2. ACGT Content

Number/percentage of A's	30,034,344 / 25.44%
Number/percentage of C's	20,434,077 / 17.31%
Number/percentage of T's	39,311,320 / 33.3%
Number/percentage of G's	28,249,367 / 23.93%
Number/percentage of N's	12,499 / 0.01%
GC Percentage	41.24%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.472
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	45.03
----------------------	-------

2.5. Mismatches and indels

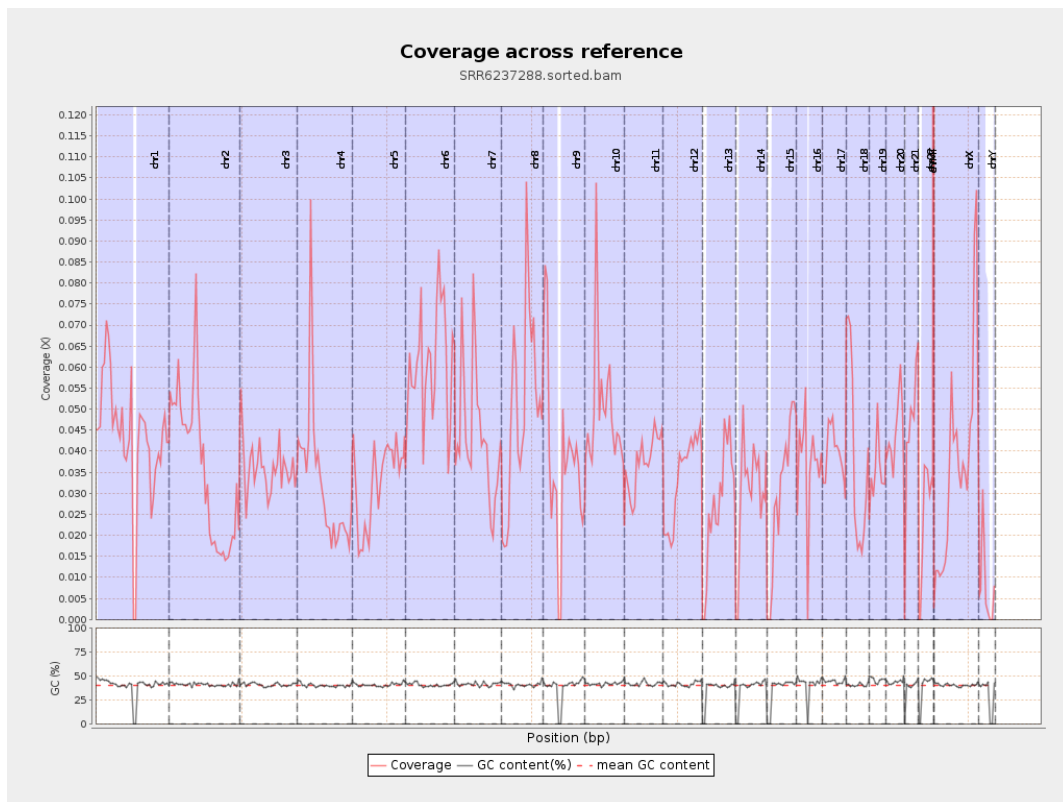
General error rate	0.68%
Mismatches	775,472
Insertions	9,326
Mapped reads with at least one insertion	0.49%
Deletions	42,924
Mapped reads with at least one deletion	2.23%
Homopolymer indels	42.3%

2.6. Chromosome stats

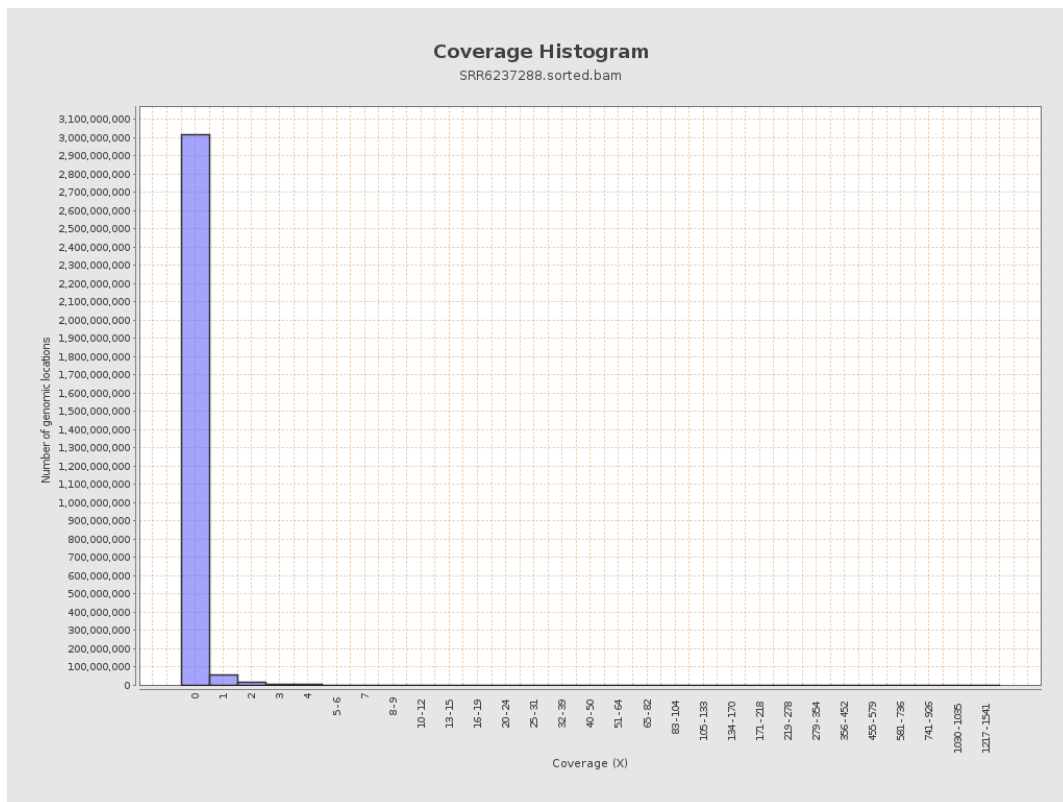
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10851576	0.0435	0.5765
chr2	243199373	8708168	0.0358	0.8118
chr3	198022430	7167695	0.0362	0.266
chr4	191154276	6157410	0.0322	0.3782
chr5	180915260	5857902	0.0324	0.2539
chr6	171115067	10316054	0.0603	0.4387
chr7	159138663	7001950	0.044	0.5168

chr8	146364022	7185922	0.0491	0.8702
chr9	141213431	5206845	0.0369	0.3742
chr10	135534747	6712739	0.0495	0.5615
chr11	135006516	5010058	0.0371	0.3135
chr12	133851895	4508461	0.0337	0.2674
chr13	115169878	3138220	0.0272	0.2548
chr14	107349540	3158591	0.0294	0.2524
chr15	102531392	3104847	0.0303	0.2583
chr16	90354753	3325770	0.0368	0.2982
chr17	81195210	3194685	0.0393	0.3175
chr18	78077248	2967950	0.038	0.714
chr19	59128983	2106741	0.0356	0.4343
chr20	63025520	2803230	0.0445	0.3148
chr21	48129895	2214150	0.046	0.3507
chr22	51304566	1230604	0.024	0.2116
chrMT	16571	13689	0.8261	1.138
chrX	155270560	5747387	0.037	0.2985
chrY	59373566	425722	0.0072	0.2922

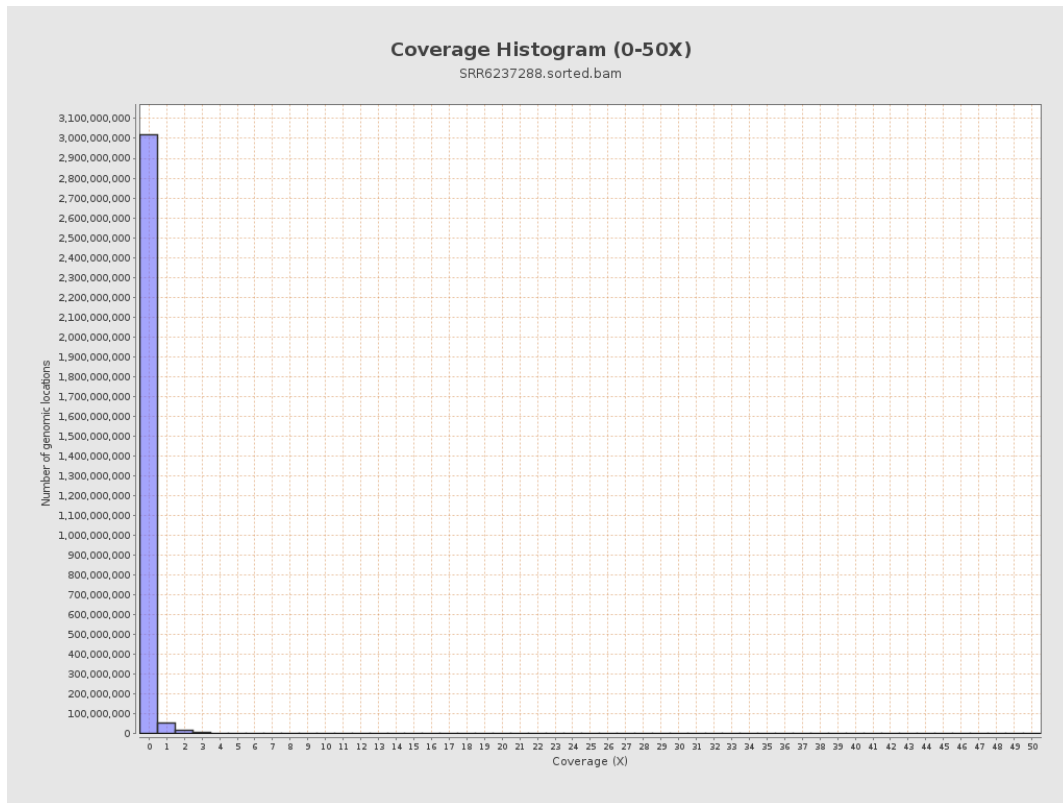
3. Results : Coverage across reference



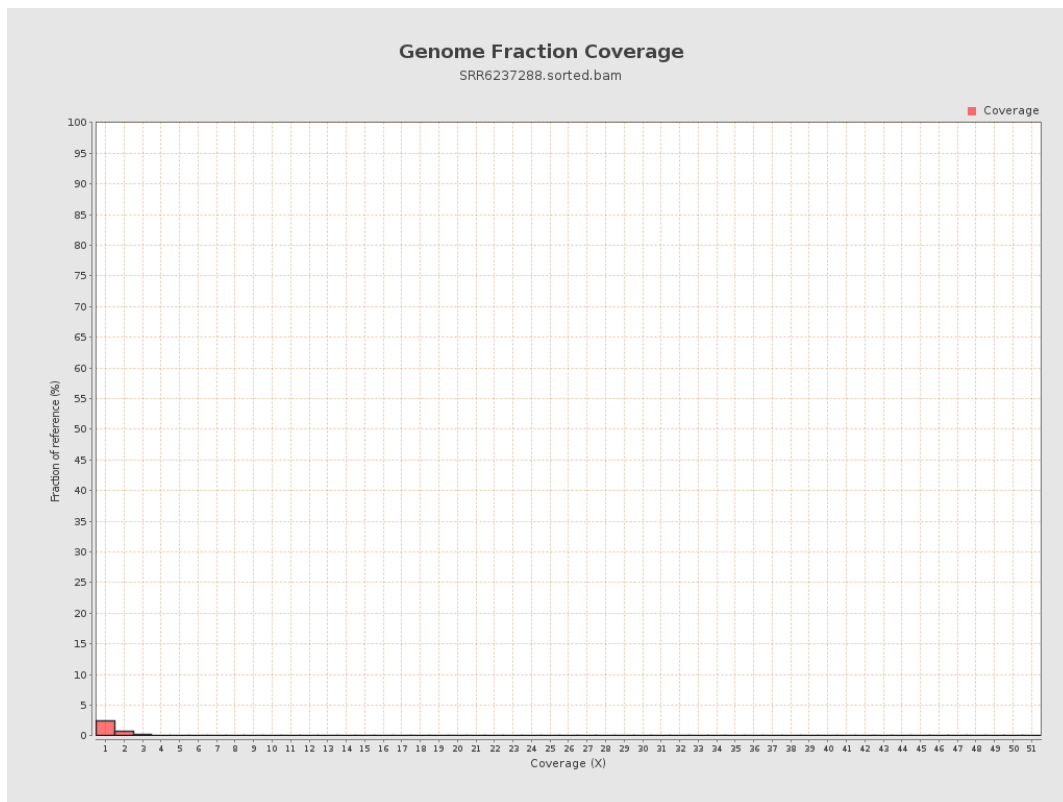
4. Results : Coverage Histogram



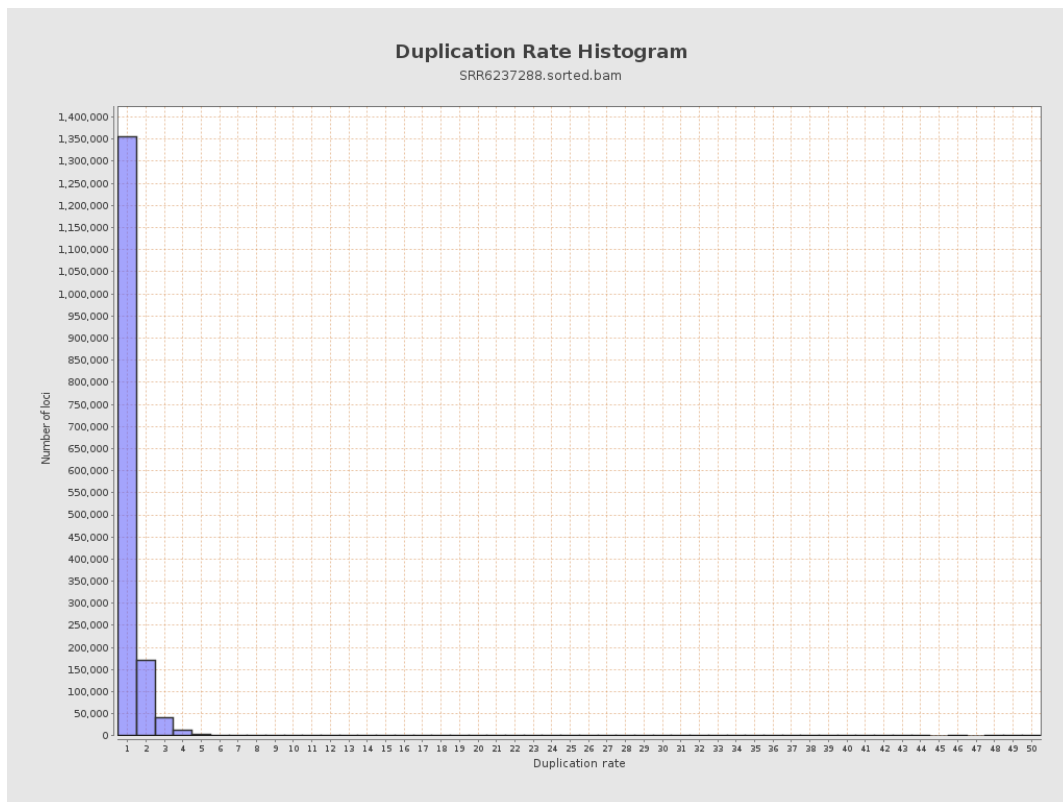
5. Results : Coverage Histogram (0-50X)



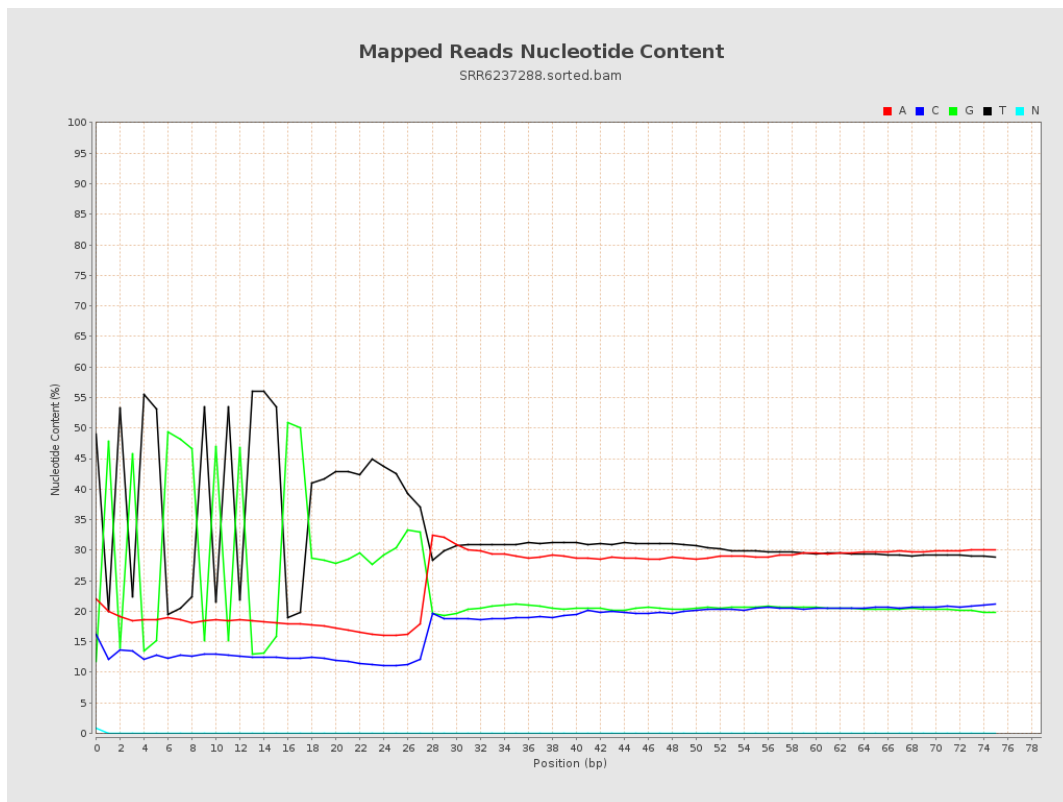
6. Results : Genome Fraction Coverage



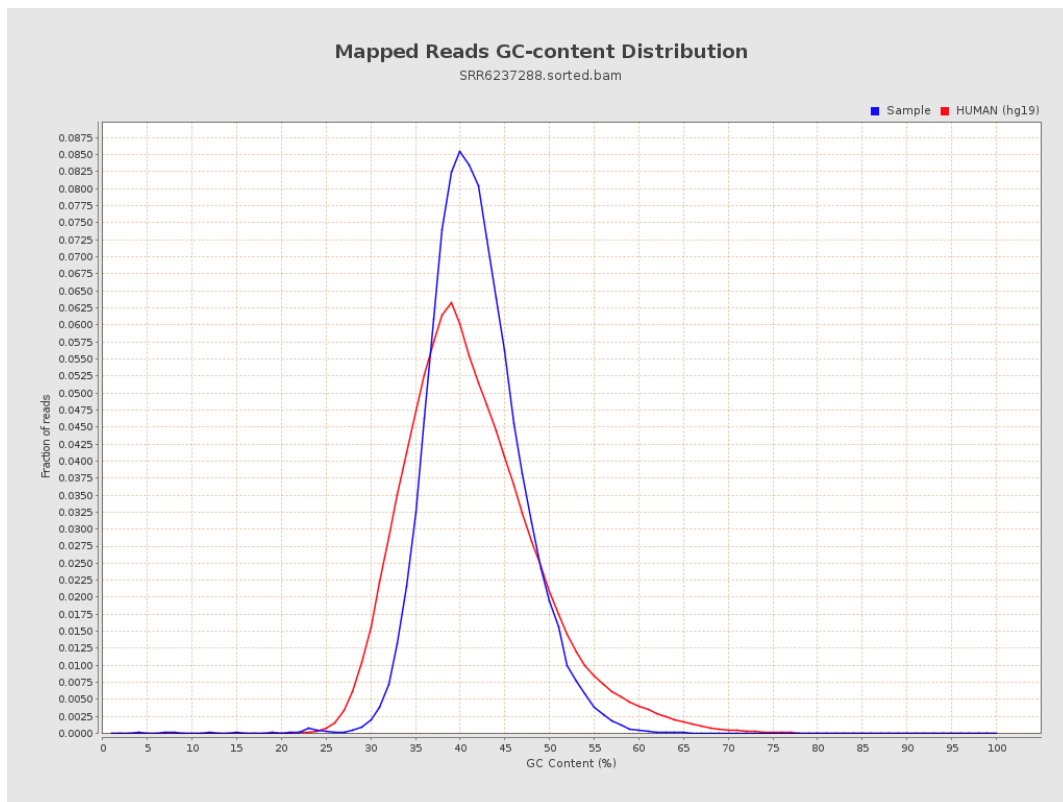
7. Results : Duplication Rate Histogram



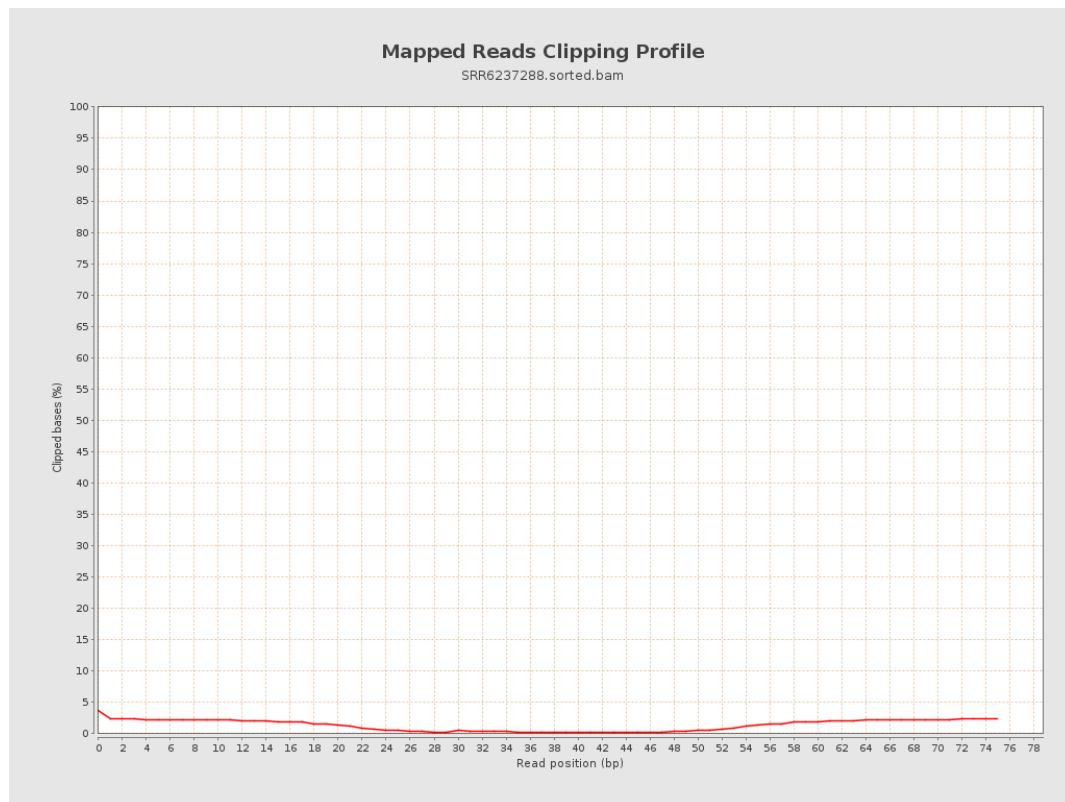
8. Results : Mapped Reads Nucleotide Content



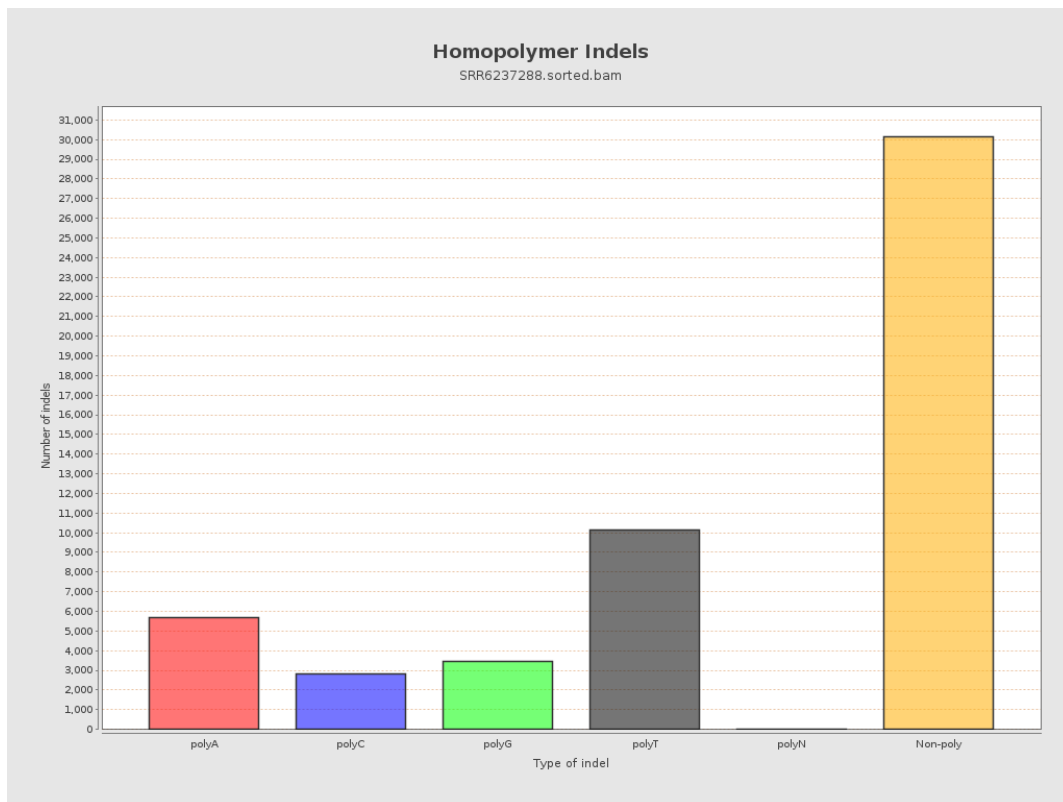
9. Results : Mapped Reads GC-content Distribution



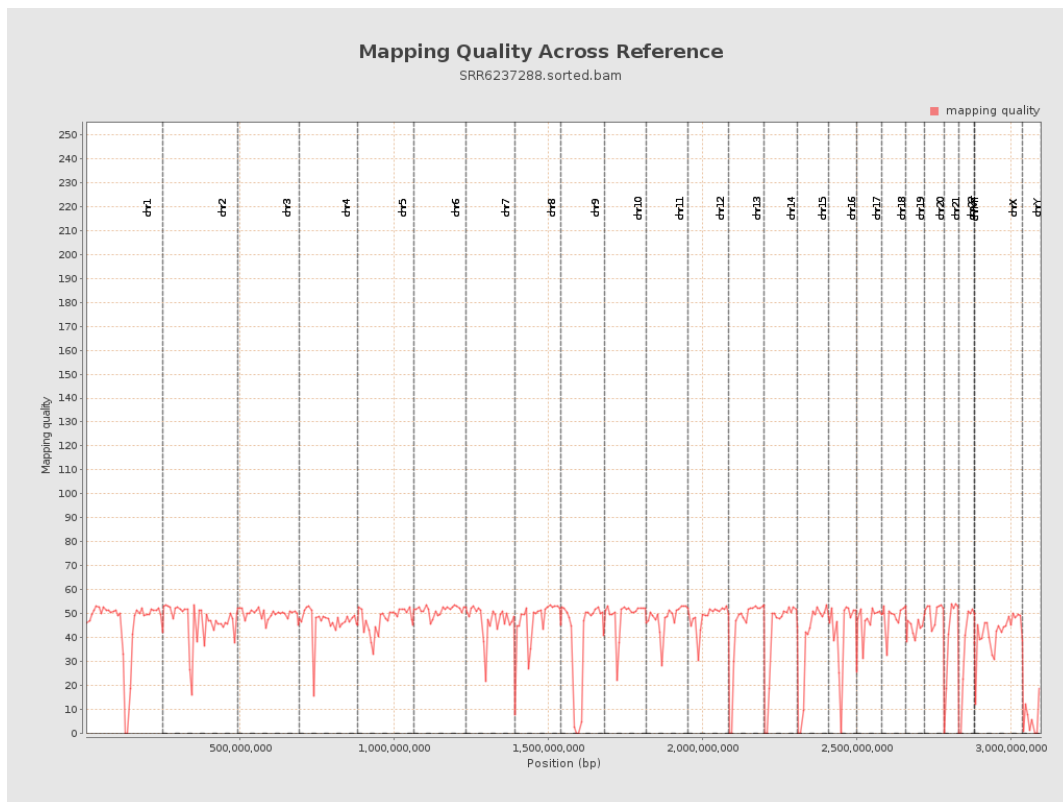
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

