

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:05:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237833.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_SRR6237833 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237833.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:05:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237833.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,561,422
Mapped reads	1,307,270 / 83.72%
Unmapped reads	254,152 / 16.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,463 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	269,138 / 17.24%
Duplication rate	13.05%
Clipped reads	641,732 / 41.1%

2.2. ACGT Content

Number/percentage of A's	23,518,248 / 27.47%
Number/percentage of C's	15,806,784 / 18.46%
Number/percentage of T's	27,038,618 / 31.58%
Number/percentage of G's	19,107,082 / 22.32%
Number/percentage of N's	136,896 / 0.16%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.4204
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2.4. Mapping Quality

Mean Mapping Quality	45.23
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2.5. Mismatches and indels

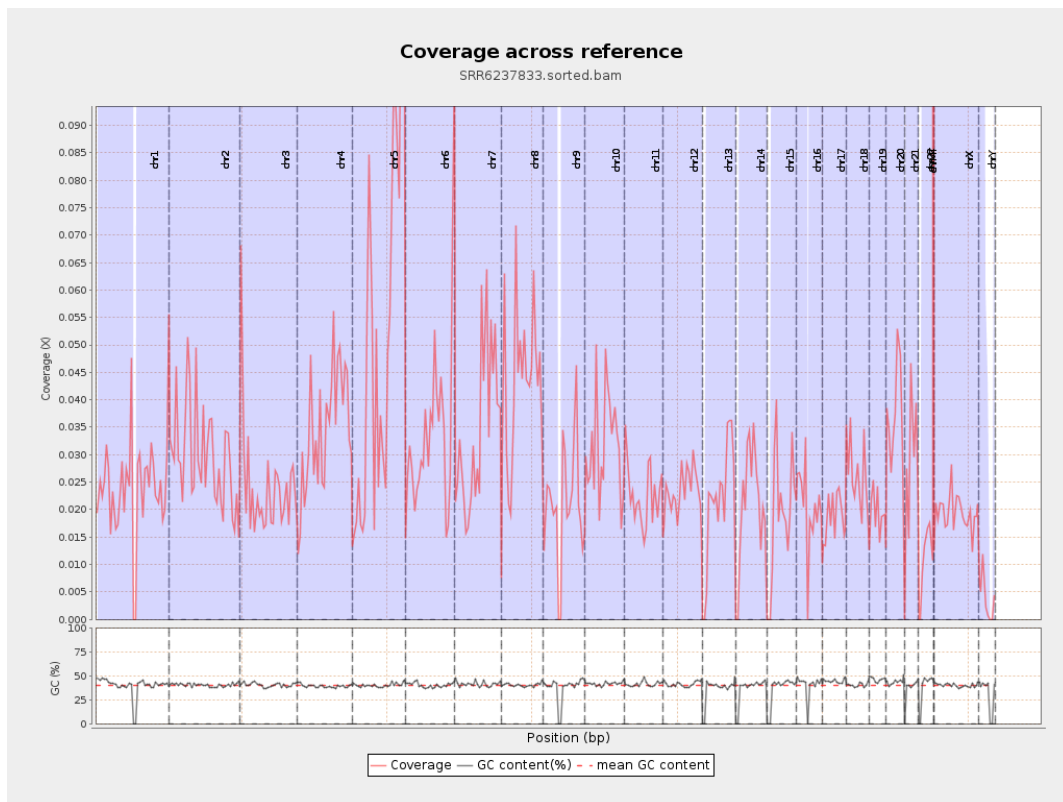
General error rate	0.85%
Mismatches	720,048
Insertions	5,657
Mapped reads with at least one insertion	0.43%
Deletions	21,125
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.95%

2.6. Chromosome stats

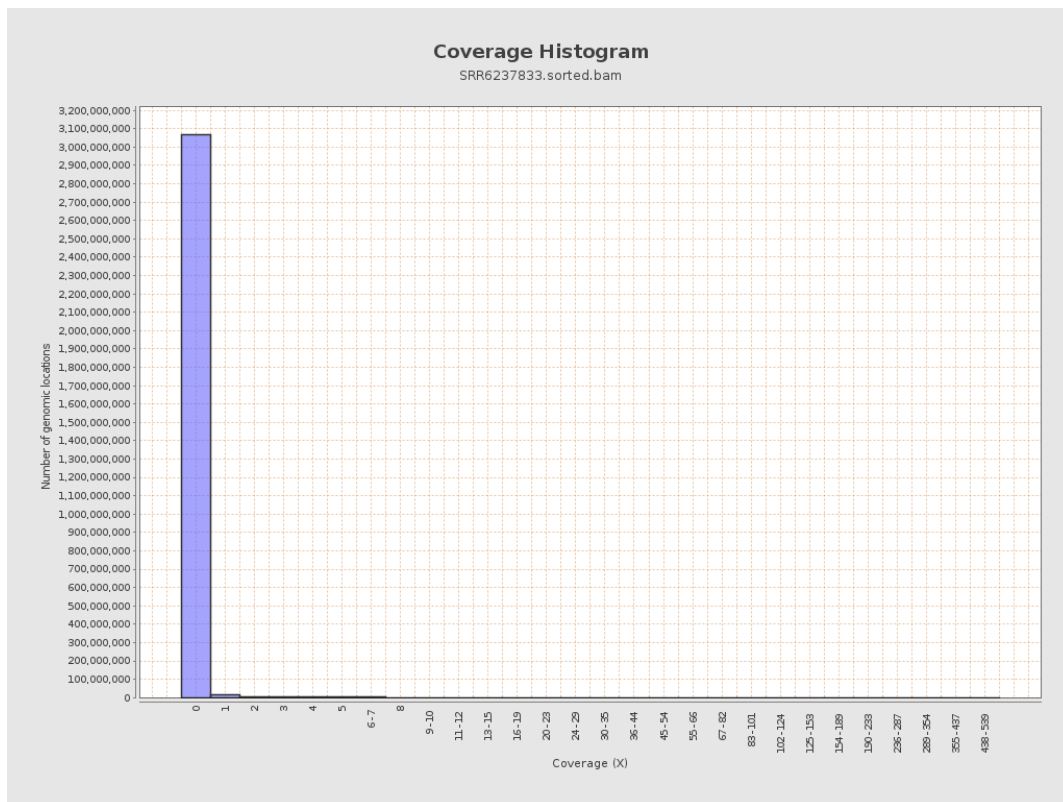
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5888411	0.0236	0.5377
chr2	243199373	7239588	0.0298	0.4774
chr3	198022430	4758176	0.024	0.3488
chr4	191154276	6590883	0.0345	0.4192
chr5	180915260	9306608	0.0514	0.5352
chr6	171115067	5718436	0.0334	0.431
chr7	159138663	5499074	0.0346	0.4488

chr8	146364022	6445428	0.044	0.5474
chr9	141213431	3018393	0.0214	0.3593
chr10	135534747	4309625	0.0318	0.4622
chr11	135006516	3063590	0.0227	0.357
chr12	133851895	3140196	0.0235	0.3411
chr13	115169878	2477975	0.0215	0.3313
chr14	107349540	2229208	0.0208	0.3303
chr15	102531392	1988821	0.0194	0.312
chr16	90354753	1830661	0.0203	0.3279
chr17	81195210	1509759	0.0186	0.3145
chr18	78077248	2043900	0.0262	0.5244
chr19	59128983	1148863	0.0194	0.4091
chr20	63025520	2310867	0.0367	0.4563
chr21	48129895	1326955	0.0276	0.3706
chr22	51304566	557138	0.0109	0.2198
chrMT	16571	35699	2.1543	3.5733
chrX	155270560	2985597	0.0192	0.3171
chrY	59373566	221097	0.0037	0.1136

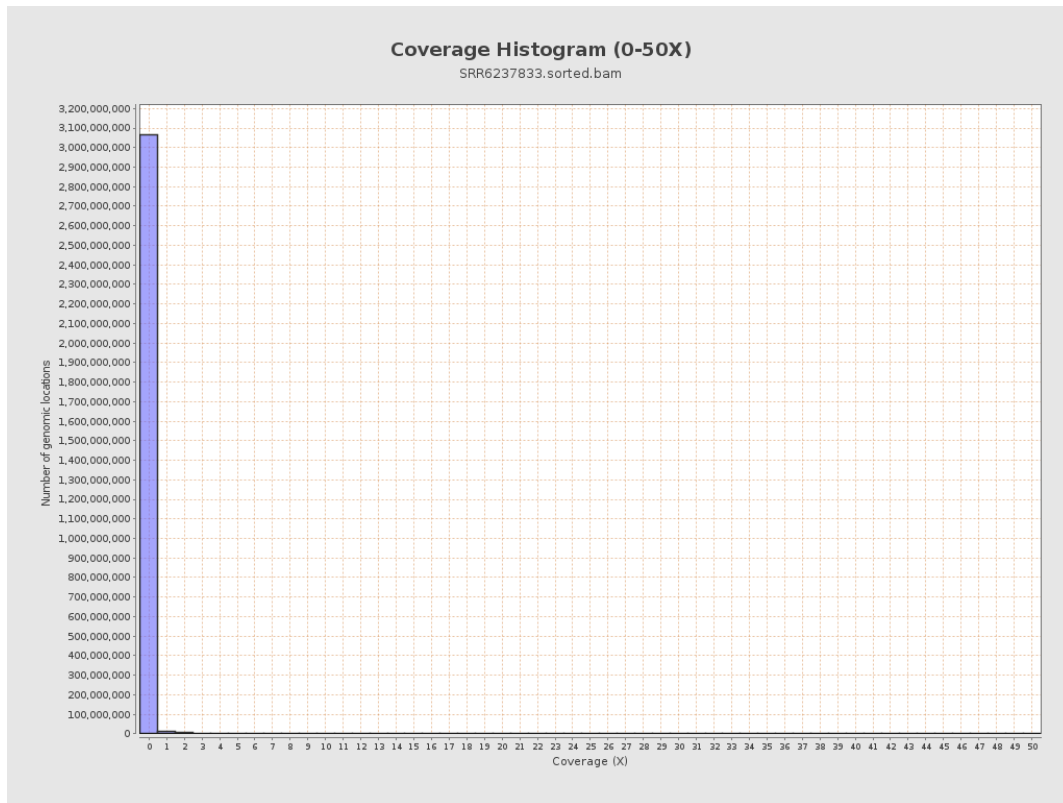
3. Results : Coverage across reference



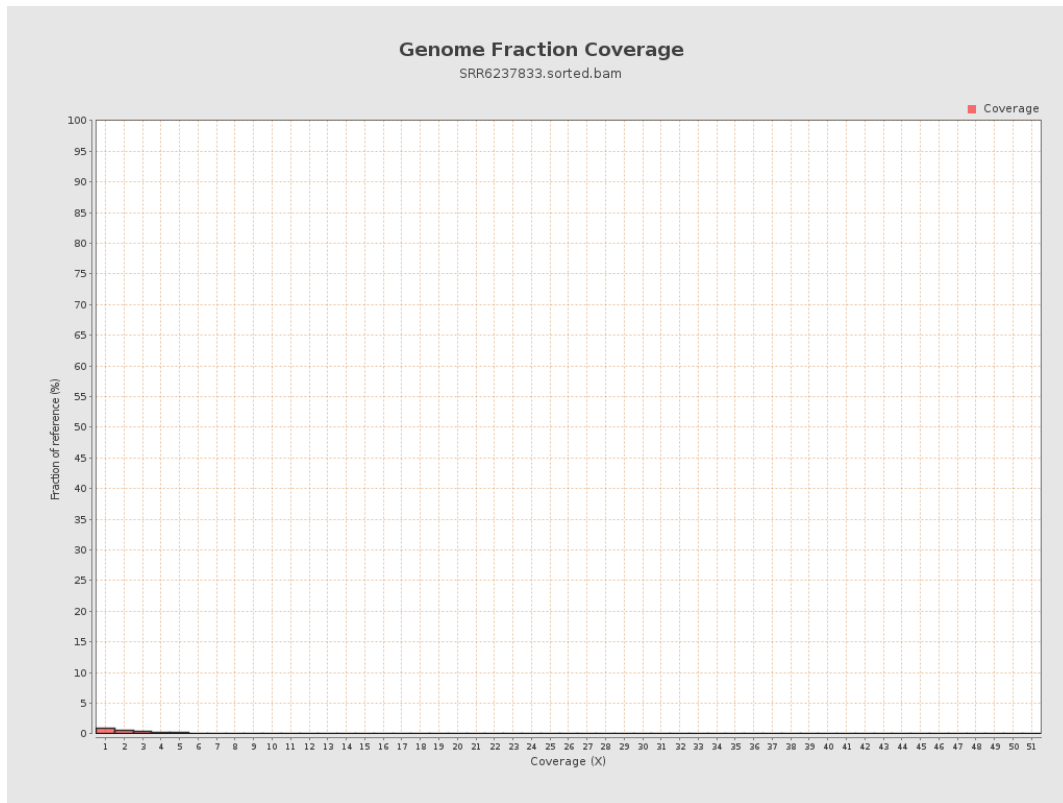
4. Results : Coverage Histogram



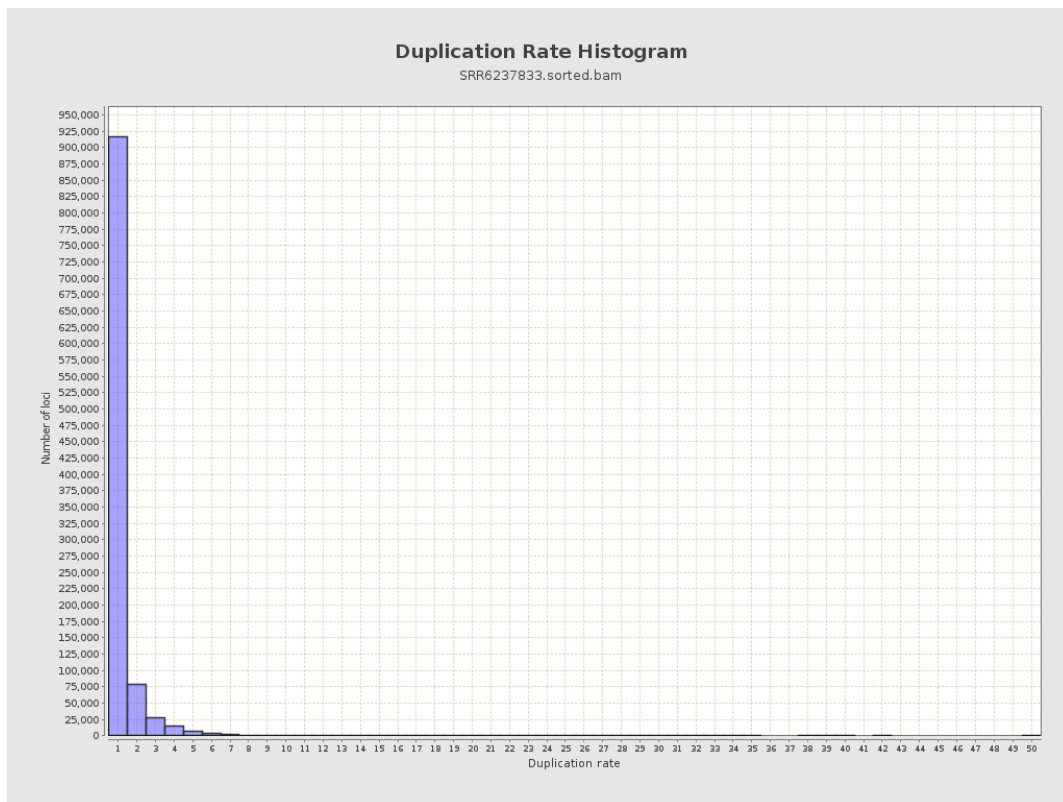
5. Results : Coverage Histogram (0-50X)



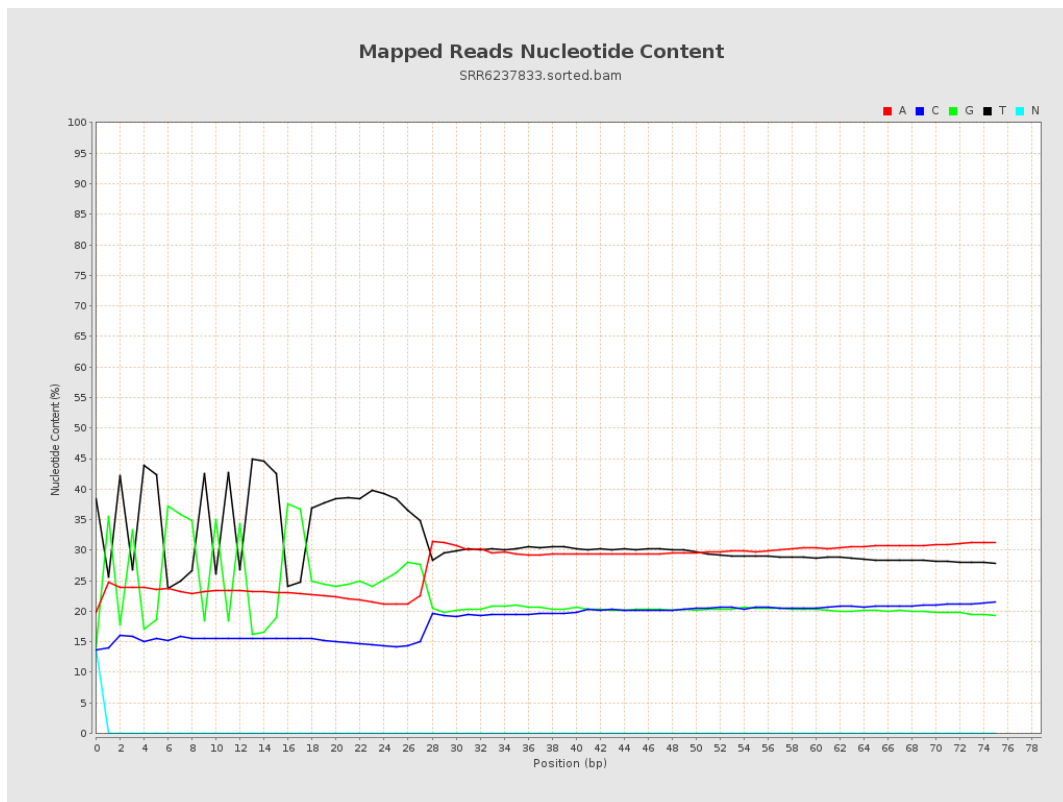
6. Results : Genome Fraction Coverage



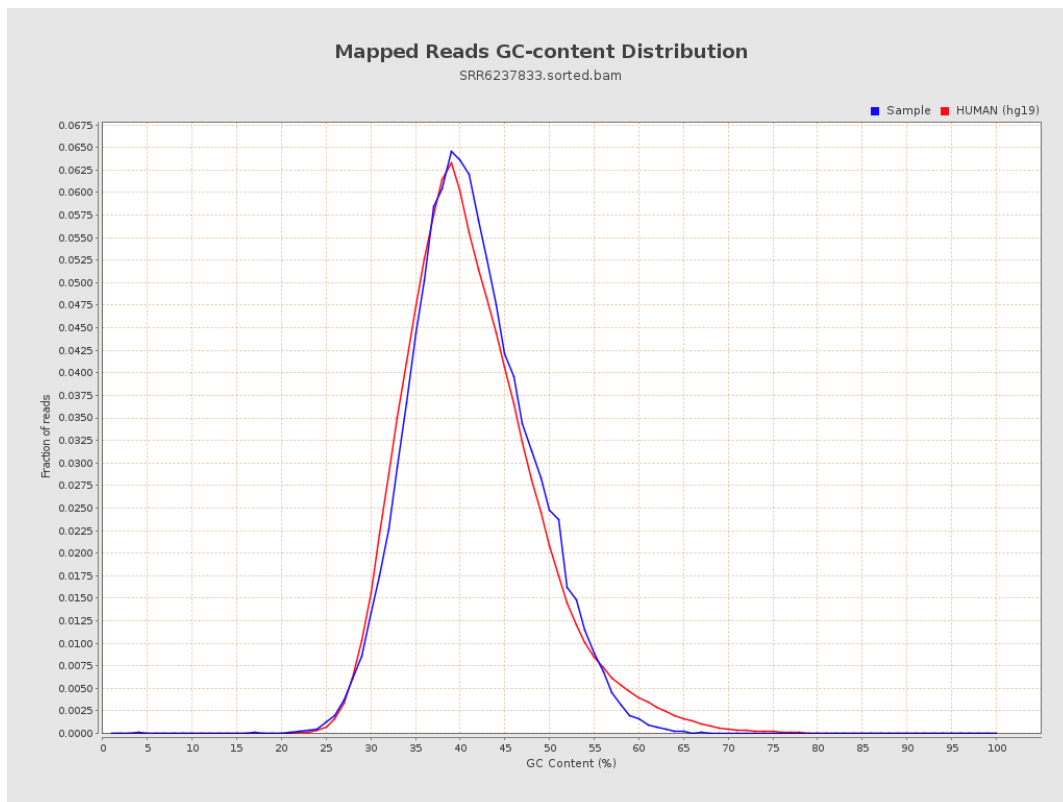
7. Results : Duplication Rate Histogram



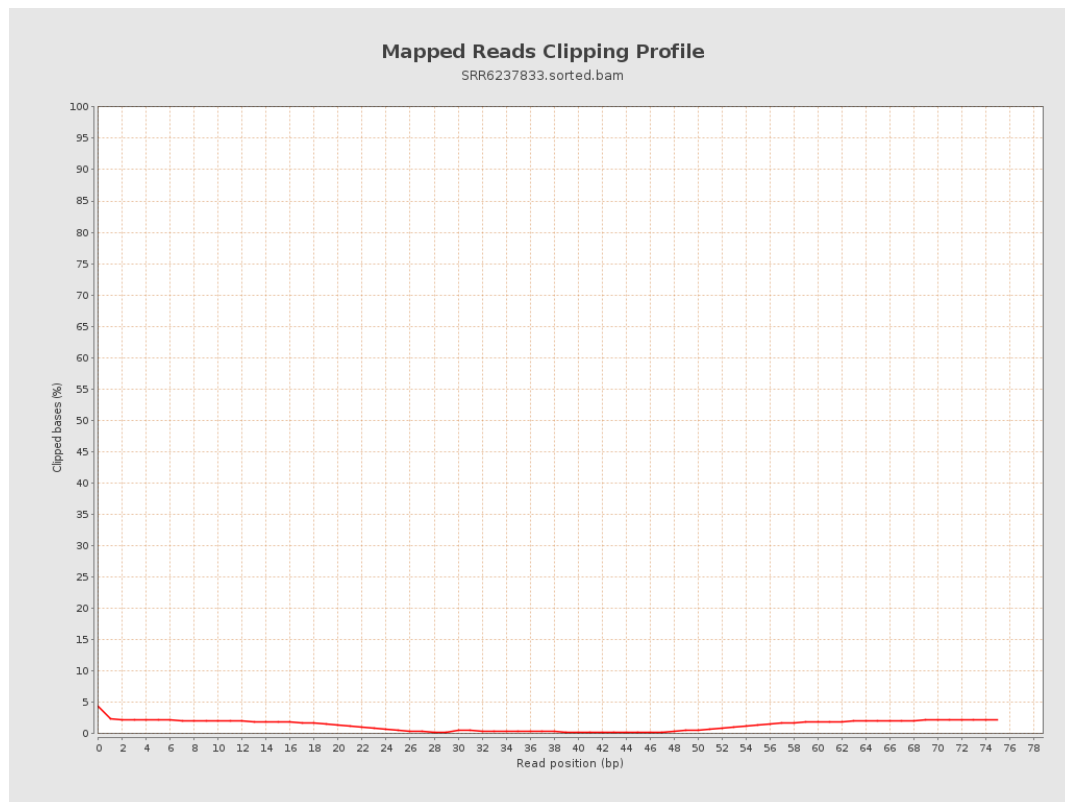
8. Results : Mapped Reads Nucleotide Content



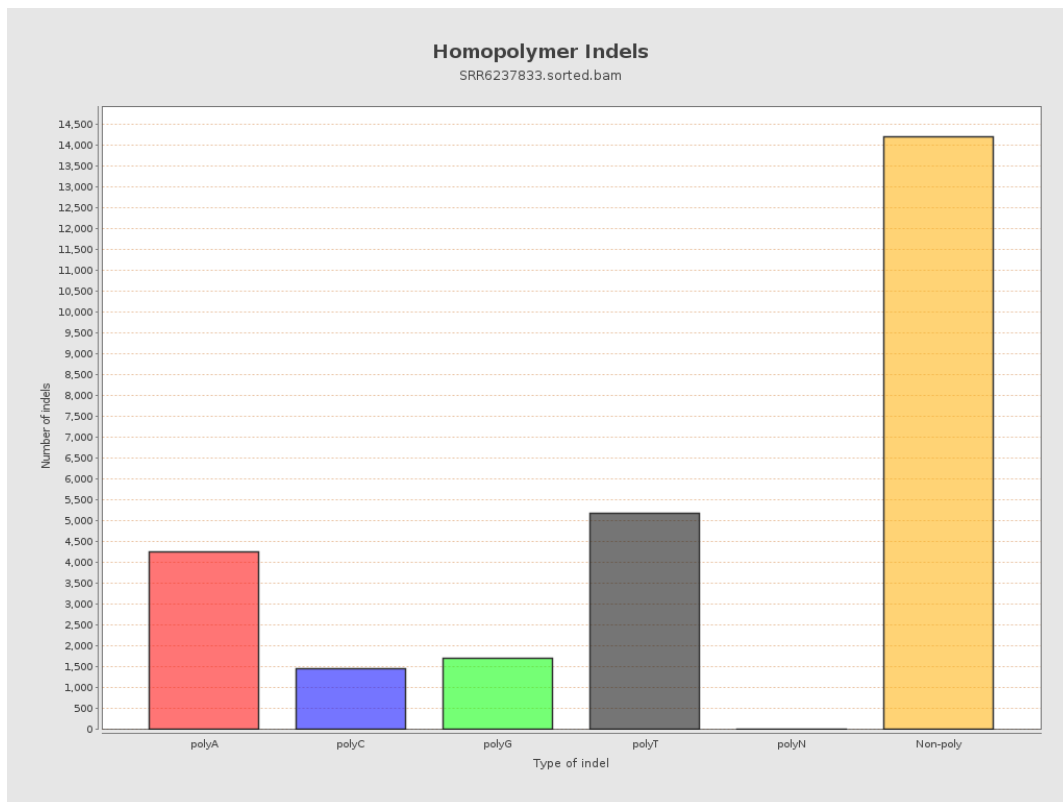
9. Results : Mapped Reads GC-content Distribution



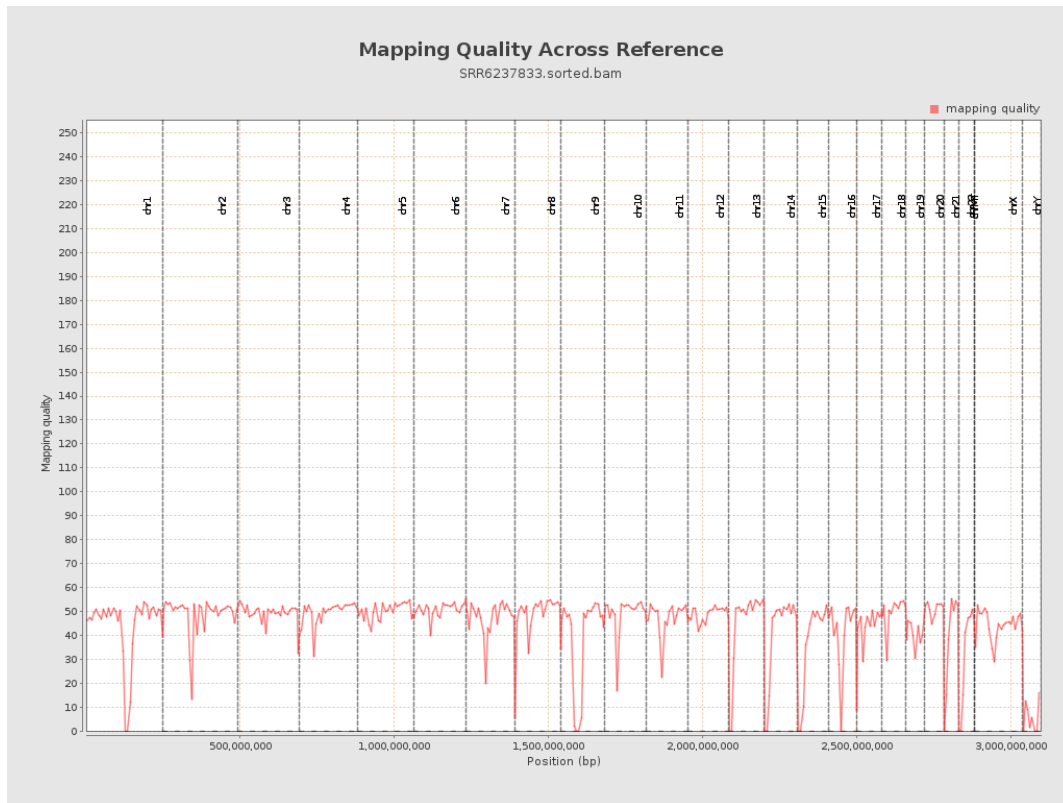
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

