

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:37:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238520.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_SRR6238520 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238520.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:37:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238520.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,470,432
Mapped reads	1,315,883 / 89.49%
Unmapped reads	154,549 / 10.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,469 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	351,618 / 23.91%
Duplication rate	18.43%
Clipped reads	804,065 / 54.68%

2.2. ACGT Content

Number/percentage of A's	20,481,004 / 25.12%
Number/percentage of C's	14,059,044 / 17.24%
Number/percentage of T's	27,801,443 / 34.1%
Number/percentage of G's	19,192,820 / 23.54%
Number/percentage of N's	5,504 / 0.01%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.3991
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2.4. Mapping Quality

Mean Mapping Quality	44.14
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2.5. Mismatches and indels

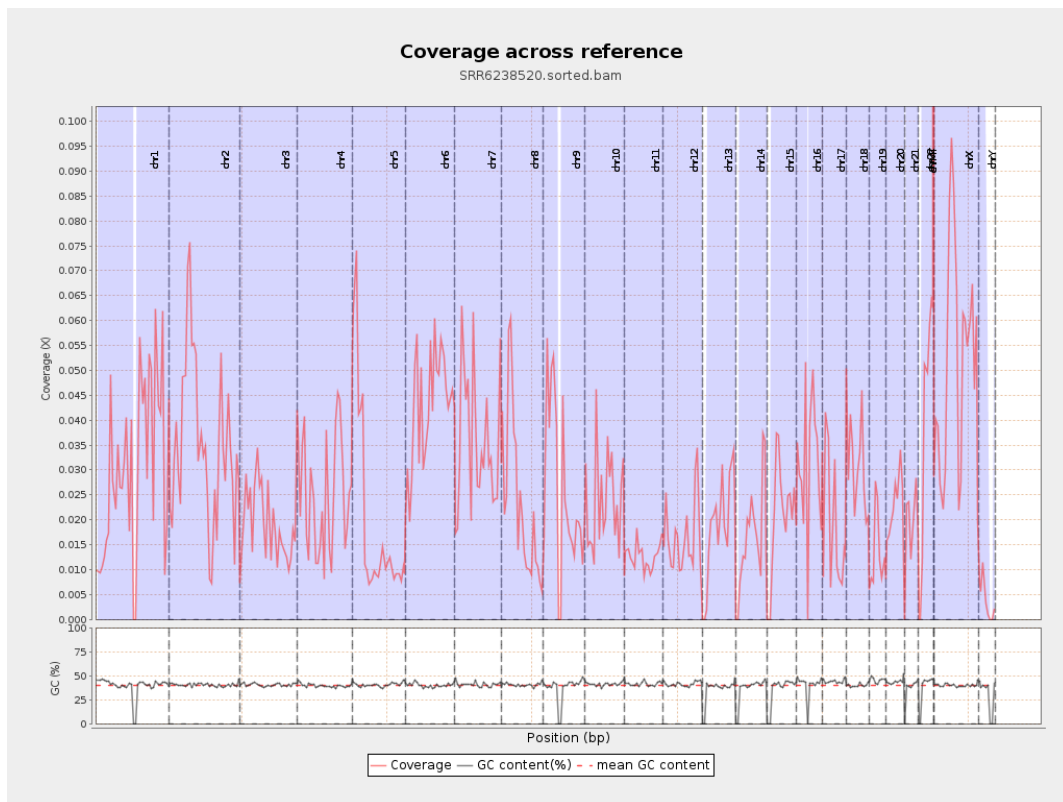
General error rate	0.57%
Mismatches	456,041
Insertions	5,385
Mapped reads with at least one insertion	0.41%
Deletions	20,223
Mapped reads with at least one deletion	1.52%
Homopolymer indels	43.59%

2.6. Chromosome stats

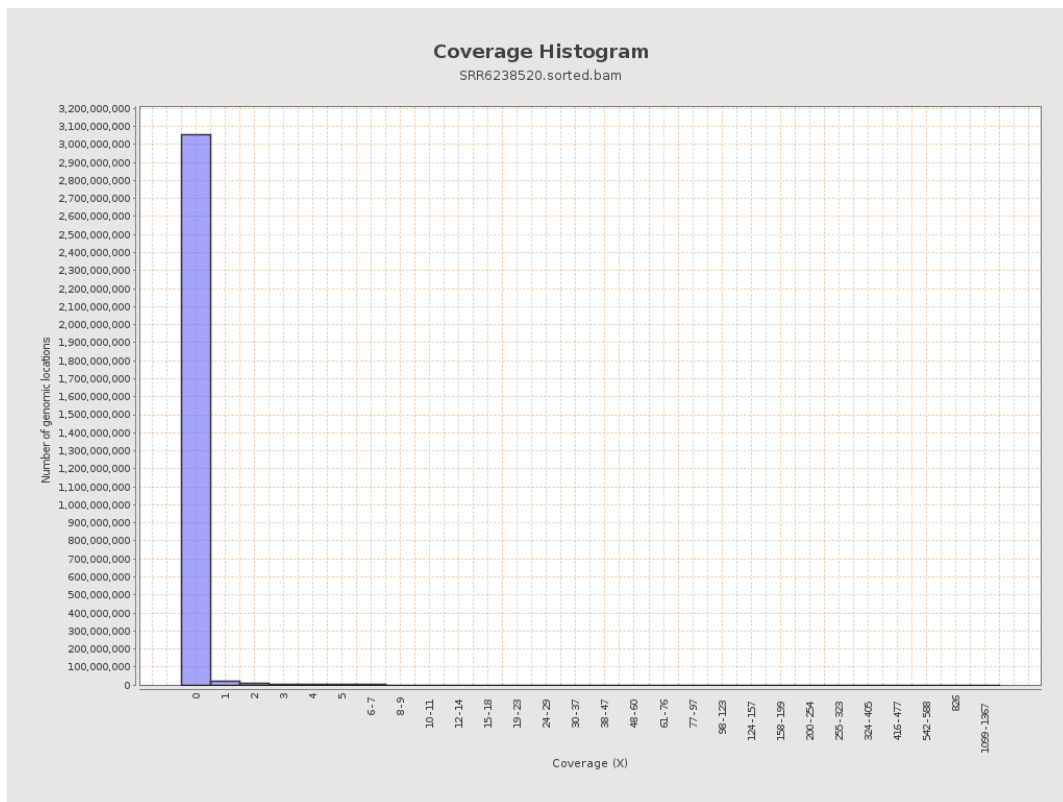
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7469853	0.03	0.4832
chr2	243199373	8590248	0.0353	0.7107
chr3	198022430	3775257	0.0191	0.2632
chr4	191154276	4678460	0.0245	0.2807
chr5	180915260	3486492	0.0193	0.2551
chr6	171115067	7351630	0.043	0.446
chr7	159138663	5747287	0.0361	0.477

chr8	146364022	3403518	0.0233	0.3258
chr9	141213431	3685668	0.0261	0.3883
chr10	135534747	3193577	0.0236	0.3811
chr11	135006516	1703635	0.0126	0.2022
chr12	133851895	2179791	0.0163	0.2358
chr13	115169878	2176996	0.0189	0.2837
chr14	107349540	1791091	0.0167	0.2413
chr15	102531392	2166877	0.0211	0.2953
chr16	90354753	2780688	0.0308	0.3343
chr17	81195210	1470875	0.0181	0.2369
chr18	78077248	2444019	0.0313	0.6673
chr19	59128983	815546	0.0138	0.3432
chr20	63025520	1444615	0.0229	0.374
chr21	48129895	927778	0.0193	0.2638
chr22	51304566	1962190	0.0382	0.3673
chrMT	16571	70661	4.2641	4.2438
chrX	155270560	8039237	0.0518	0.4391
chrY	59373566	218370	0.0037	0.1314

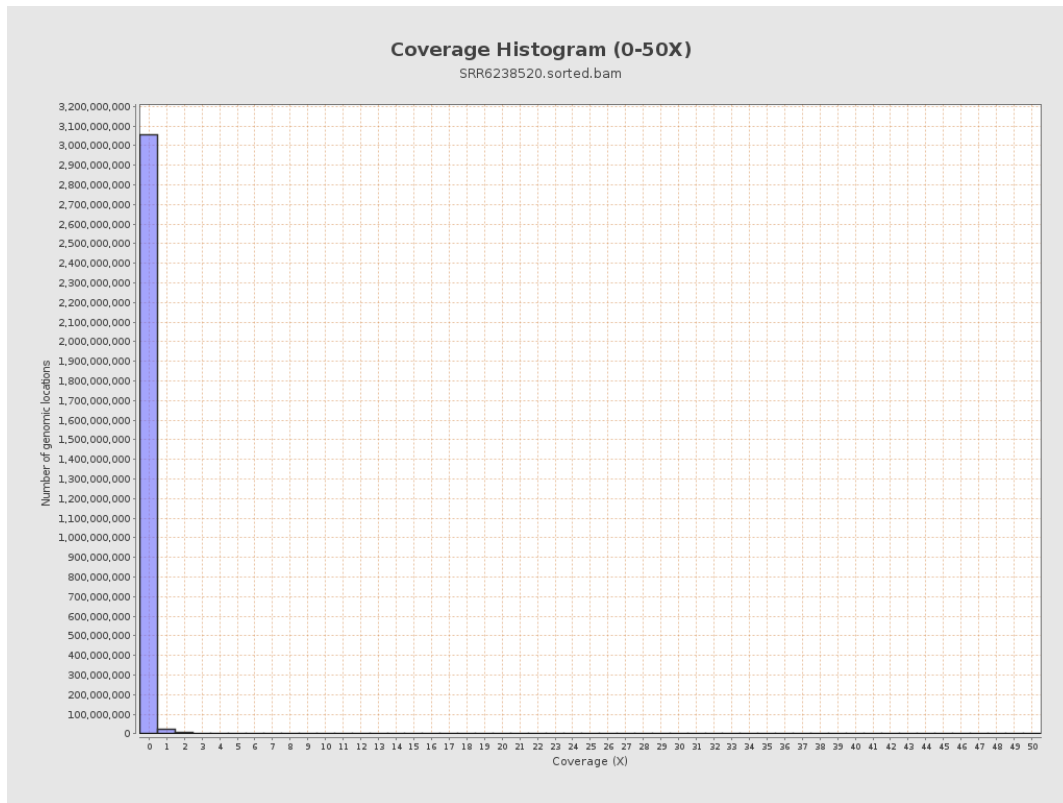
3. Results : Coverage across reference



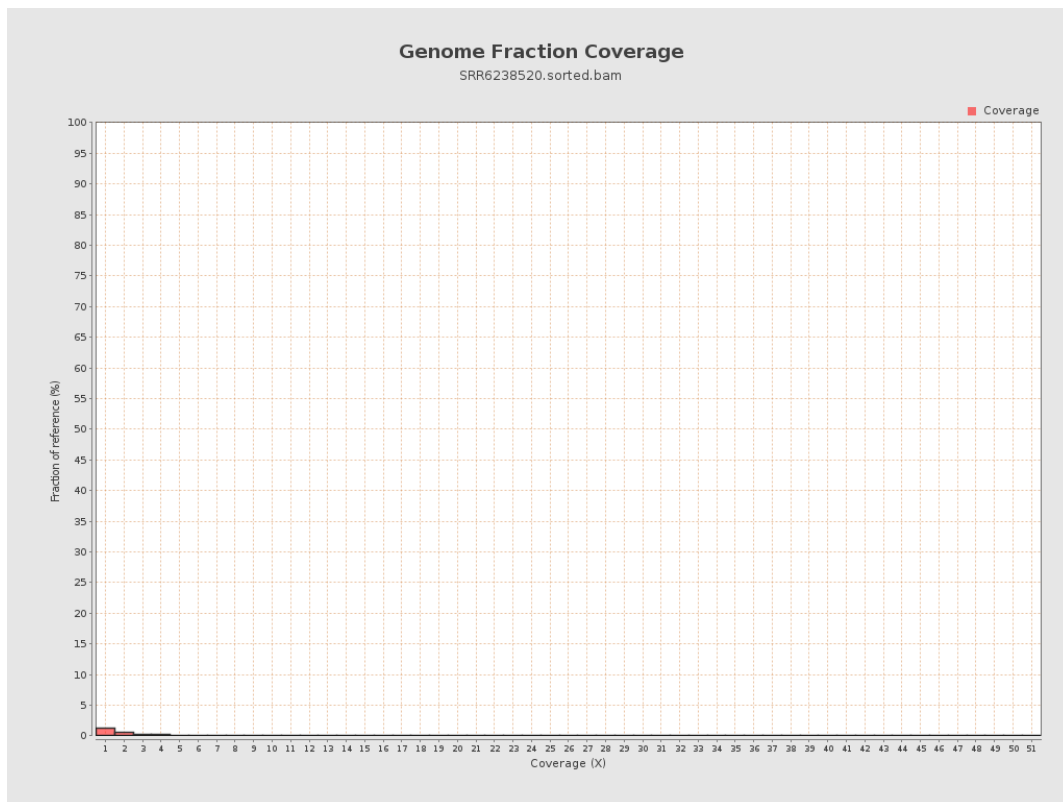
4. Results : Coverage Histogram



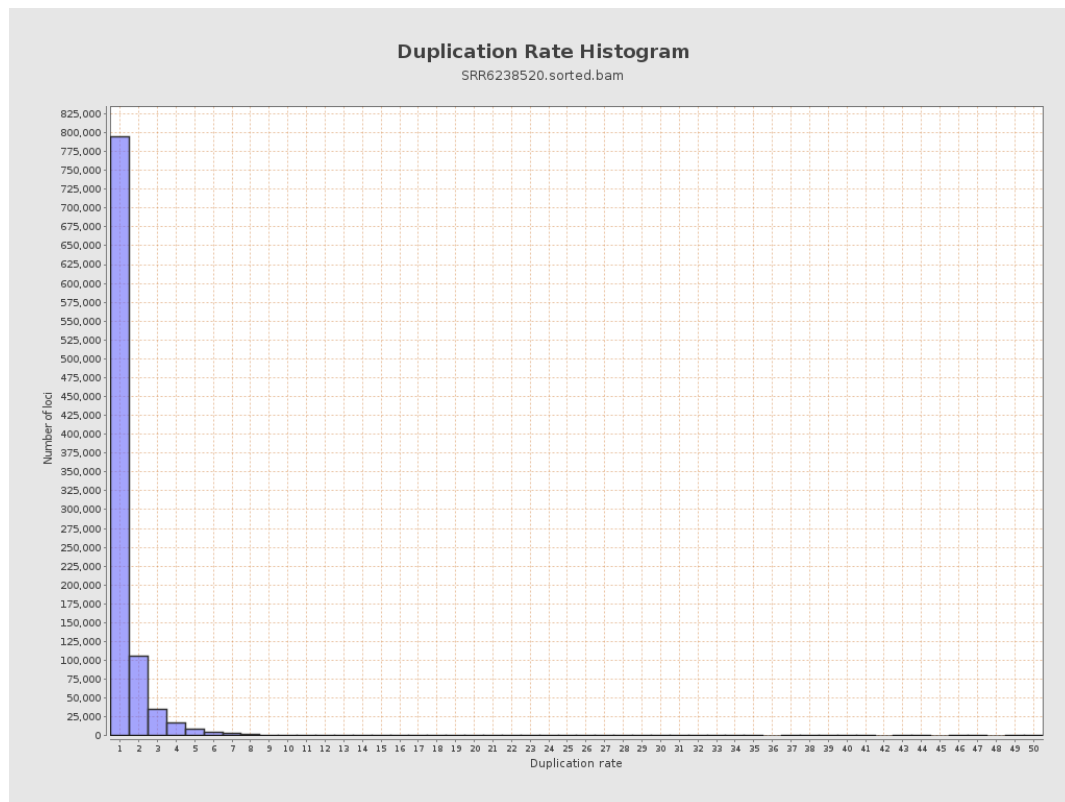
5. Results : Coverage Histogram (0-50X)



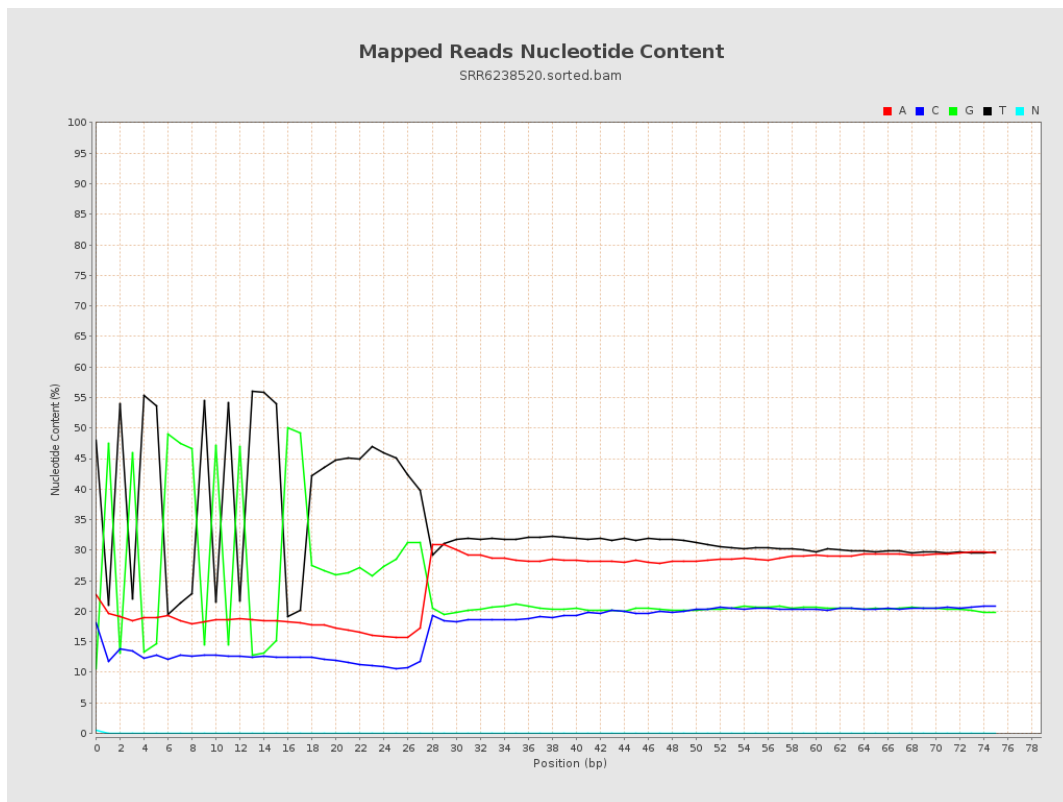
6. Results : Genome Fraction Coverage



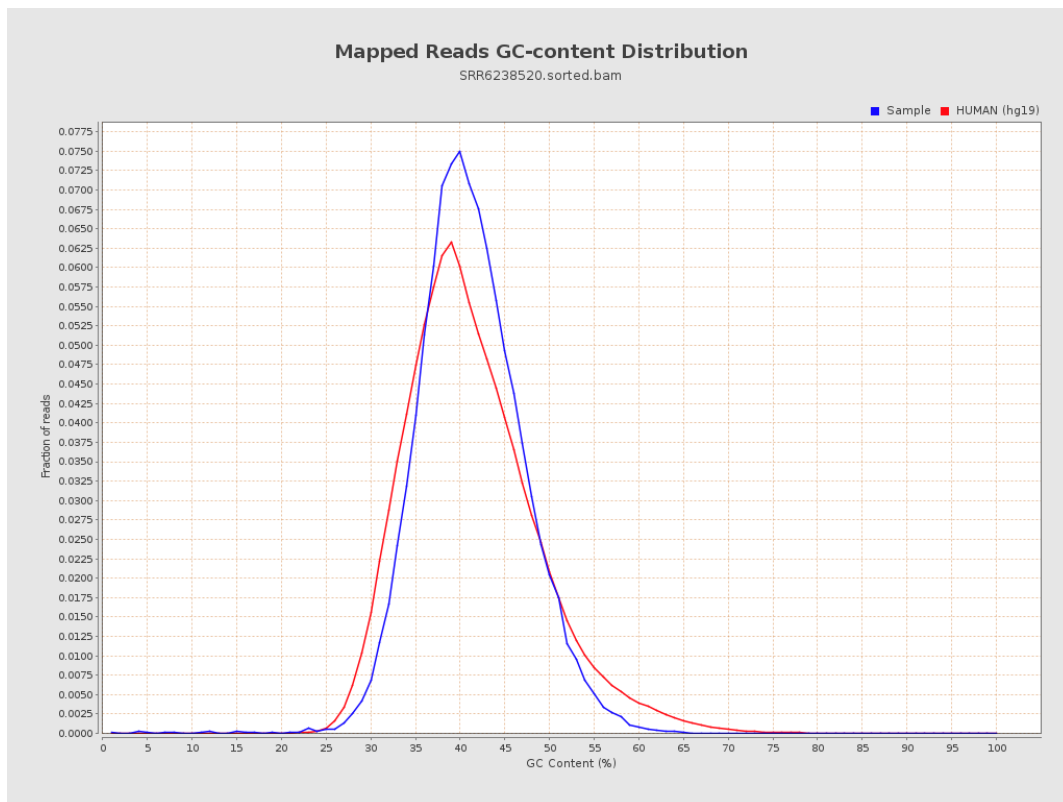
7. Results : Duplication Rate Histogram



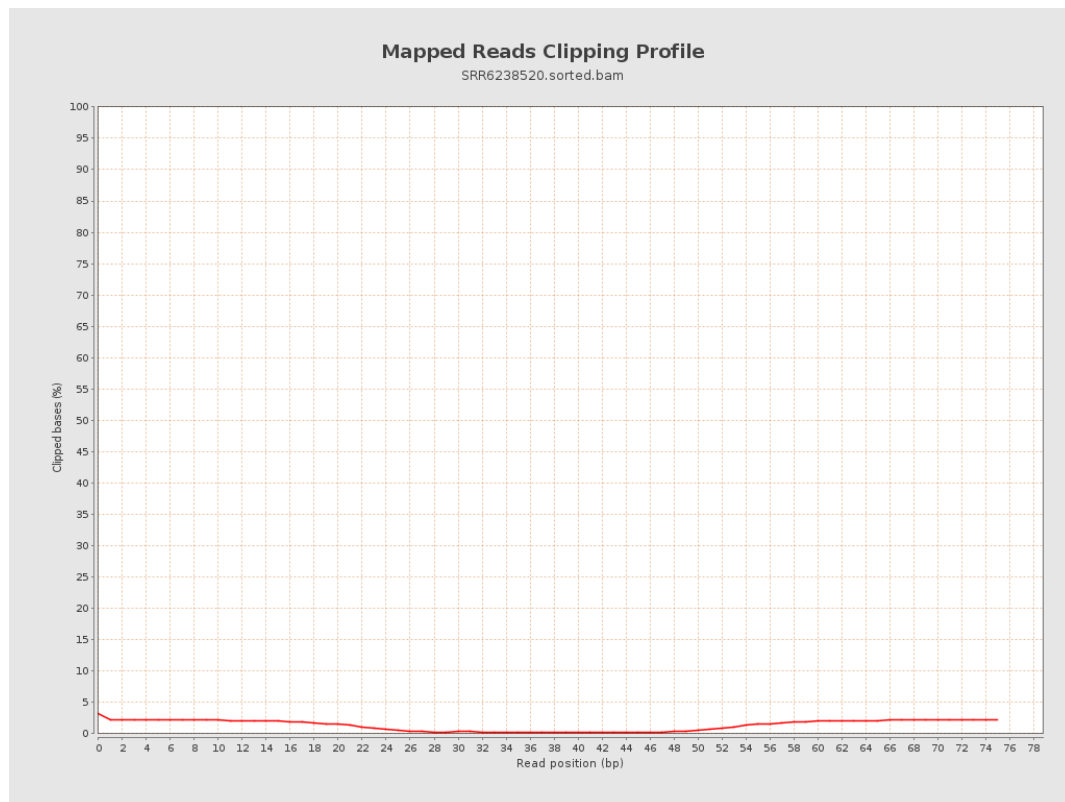
8. Results : Mapped Reads Nucleotide Content



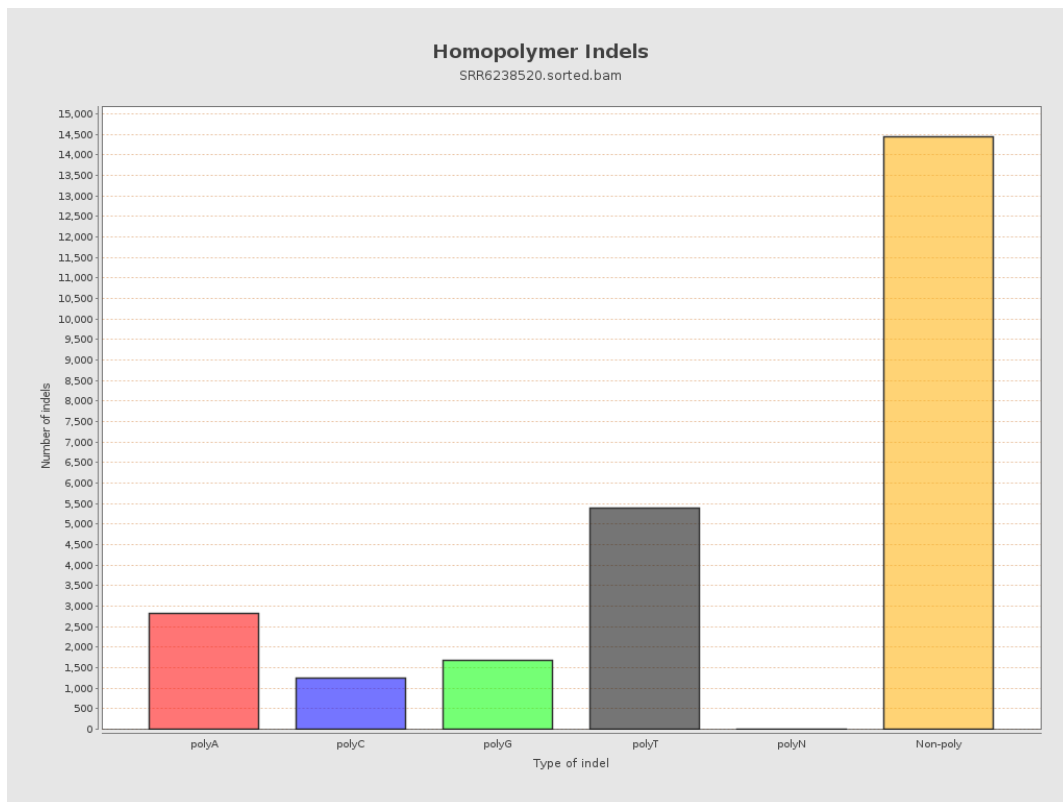
9. Results : Mapped Reads GC-content Distribution



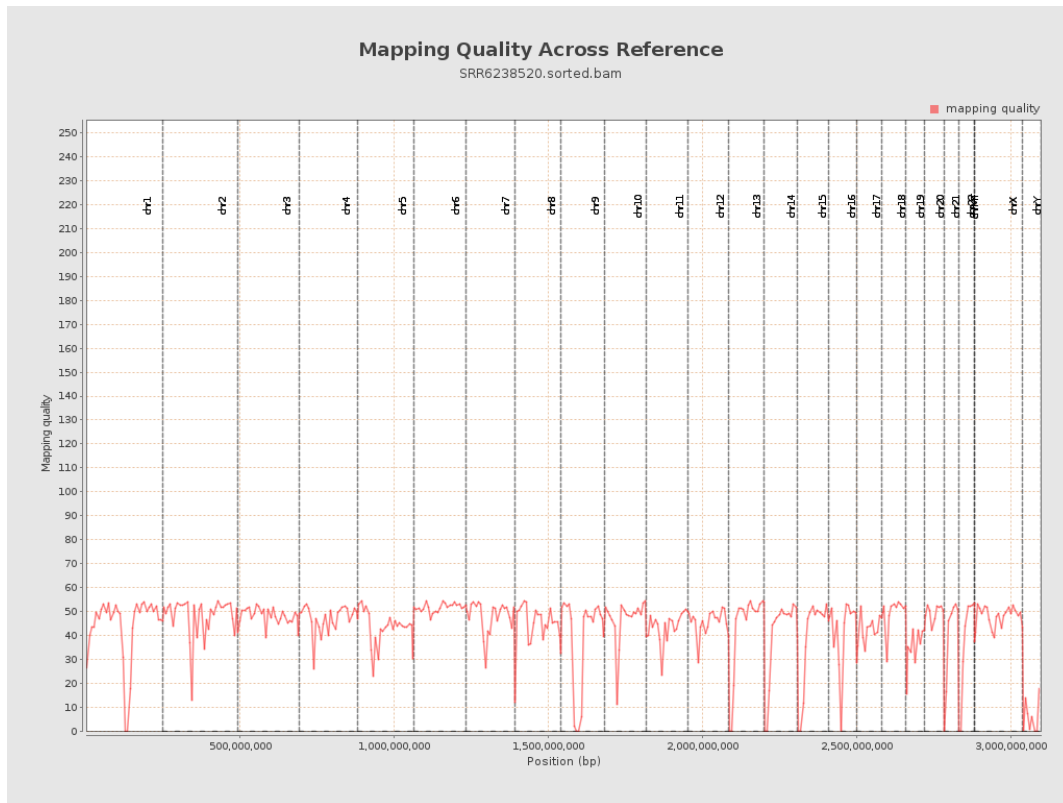
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

