

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:23:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238083.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_SRR6238083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238083.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:23:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,274,380
Mapped reads	1,810,688 / 79.61%
Unmapped reads	463,692 / 20.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,339 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	204,025 / 8.97%
Duplication rate	8.3%
Clipped reads	1,108,574 / 48.74%

2.2. ACGT Content

Number/percentage of A's	28,891,733 / 25.63%
Number/percentage of C's	19,239,225 / 17.07%
Number/percentage of T's	36,940,046 / 32.77%
Number/percentage of G's	27,637,647 / 24.52%
Number/percentage of N's	5,117 / 0%
GC Percentage	41.59%

2.3. Coverage

Mean	0.0364

Standard Deviation	0.3701
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2.4. Mapping Quality

Mean Mapping Quality	44.55
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2.5. Mismatches and indels

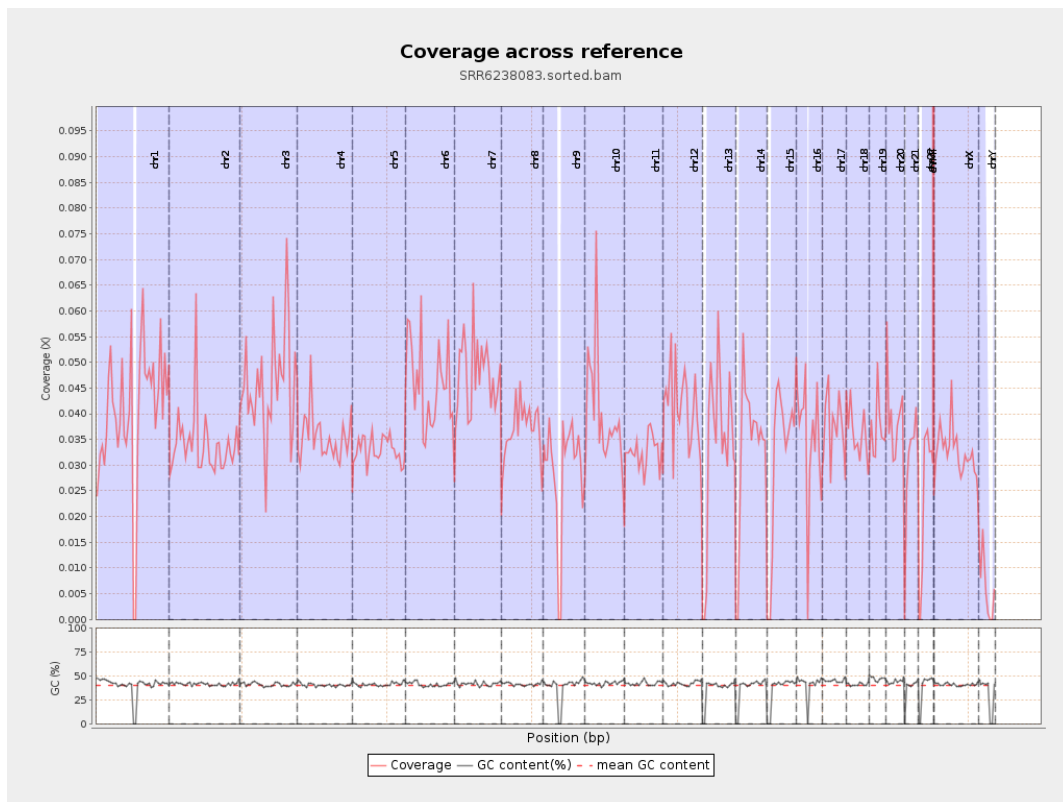
General error rate	0.79%
Mismatches	878,260
Insertions	9,717
Mapped reads with at least one insertion	0.53%
Deletions	36,859
Mapped reads with at least one deletion	2.01%
Homopolymer indels	48.51%

2.6. Chromosome stats

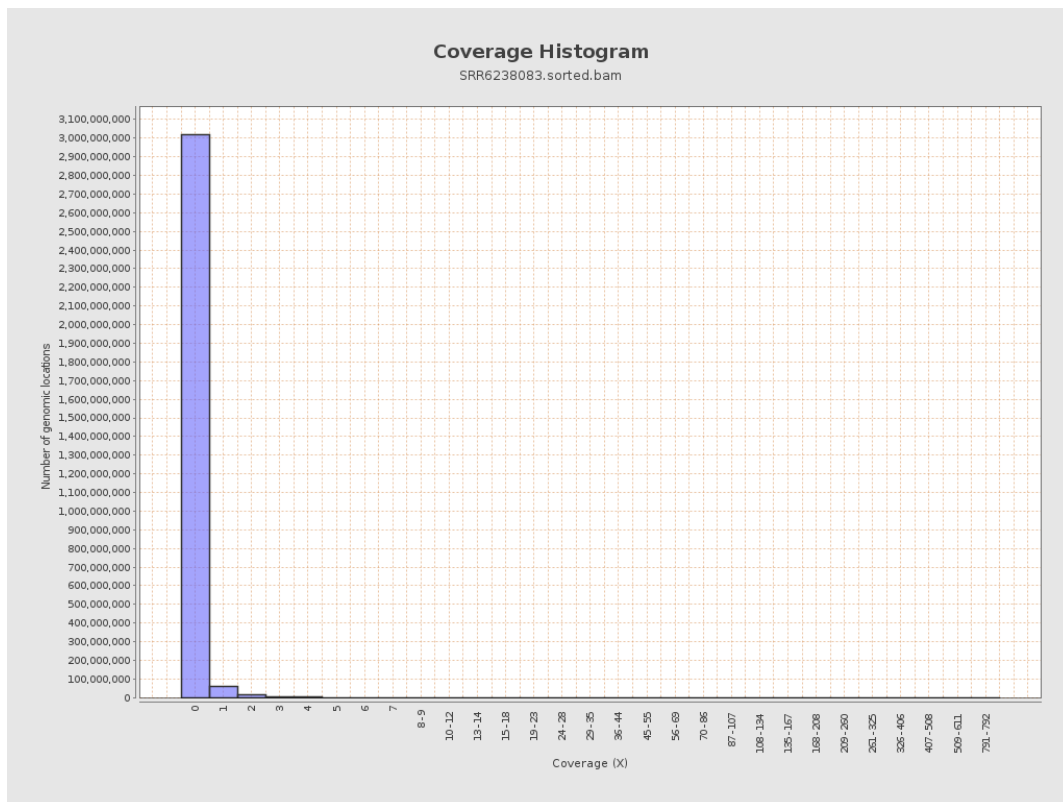
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10080773	0.0404	0.5556
chr2	243199373	8305904	0.0342	0.4808
chr3	198022430	9018008	0.0455	0.319
chr4	191154276	6758353	0.0354	0.2768
chr5	180915260	5951162	0.0329	0.2521
chr6	171115067	7794650	0.0456	0.3414
chr7	159138663	7663416	0.0482	0.5098

chr8	146364022	5406708	0.0369	0.3569
chr9	141213431	4064878	0.0288	0.3318
chr10	135534747	5407522	0.0399	0.4464
chr11	135006516	4377529	0.0324	0.2883
chr12	133851895	5492958	0.041	0.3096
chr13	115169878	3894345	0.0338	0.2723
chr14	107349540	3587032	0.0334	0.2645
chr15	102531392	3302806	0.0322	0.2614
chr16	90354753	3097815	0.0343	0.2736
chr17	81195210	3001187	0.037	0.2887
chr18	78077248	2842090	0.0364	0.6093
chr19	59128983	2191583	0.0371	0.3886
chr20	63025520	2430185	0.0386	0.2811
chr21	48129895	1459668	0.0303	0.2506
chr22	51304566	1202972	0.0234	0.217
chrMT	16571	54851	3.3101	3.0762
chrX	155270560	5028661	0.0324	0.2724
chrY	59373566	358158	0.006	0.1363

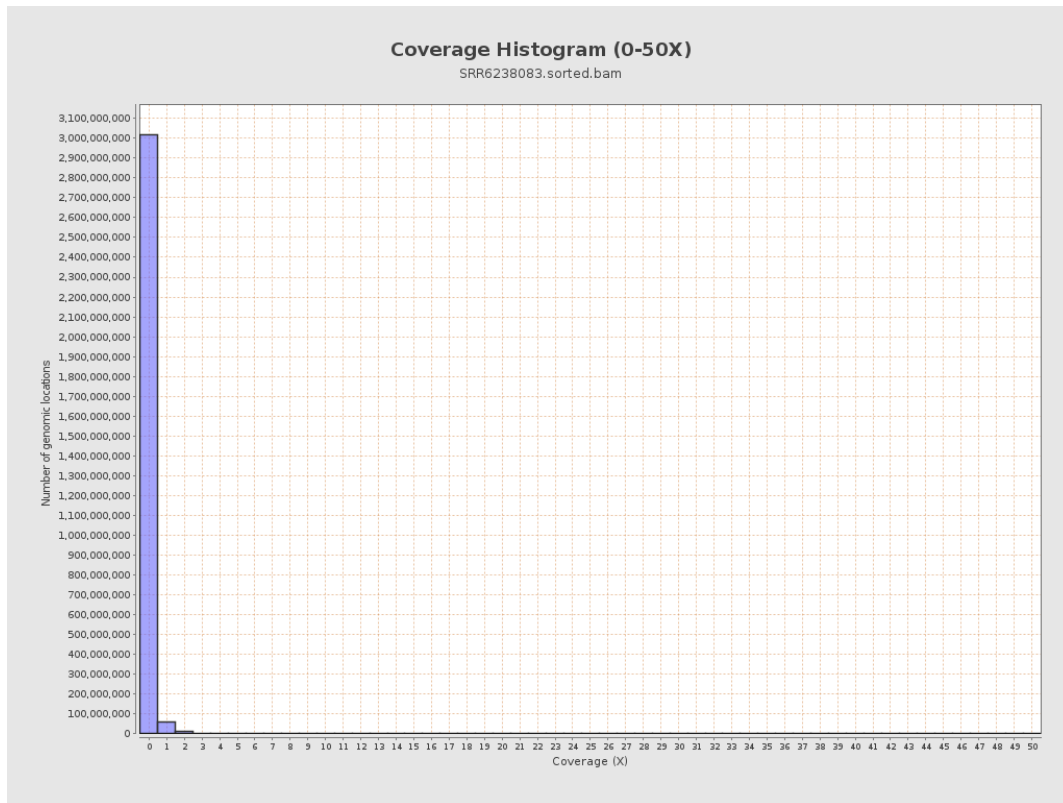
3. Results : Coverage across reference



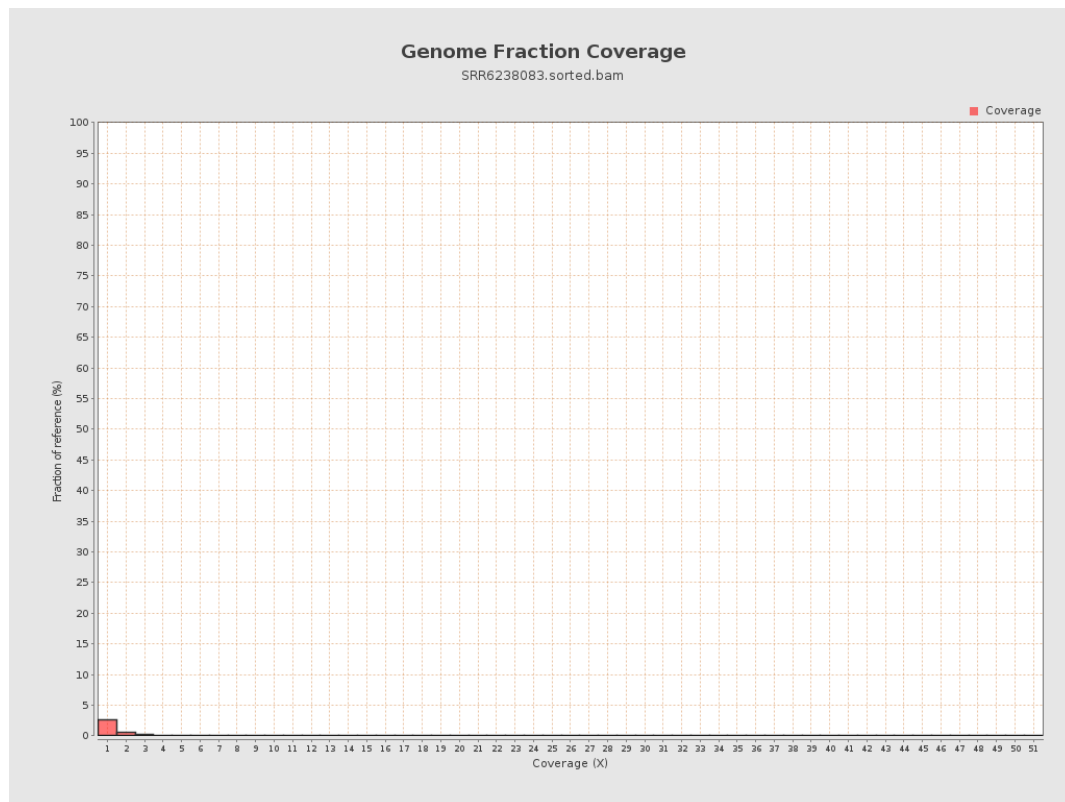
4. Results : Coverage Histogram



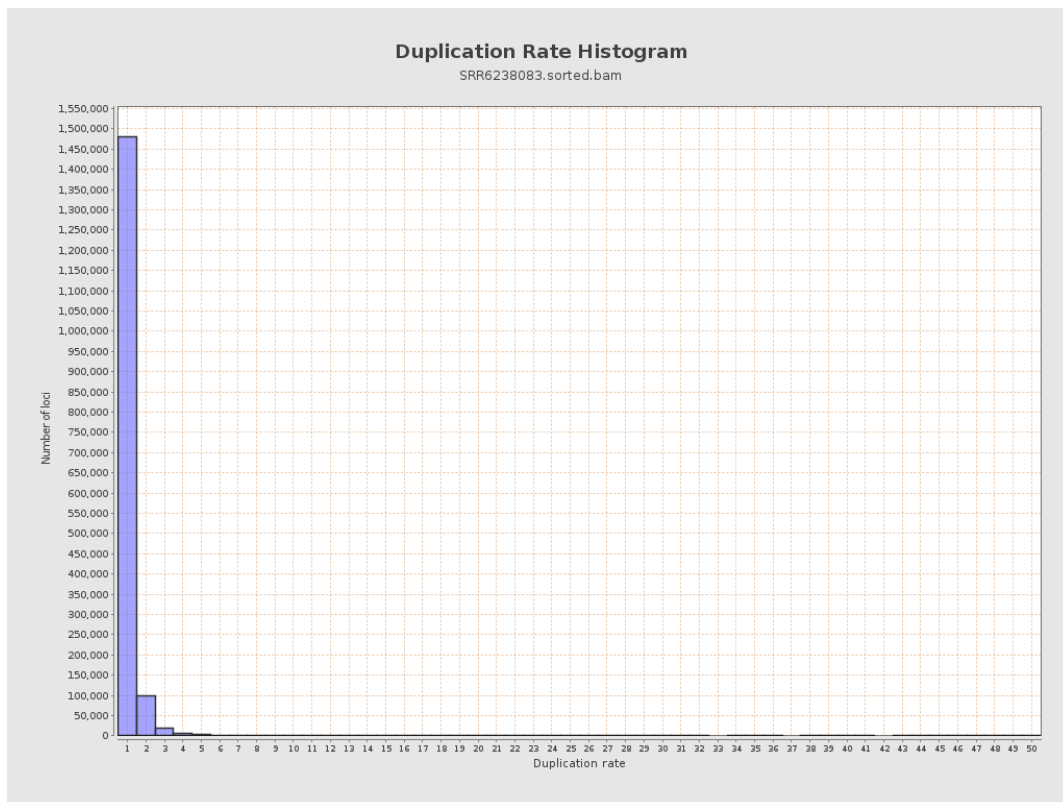
5. Results : Coverage Histogram (0-50X)



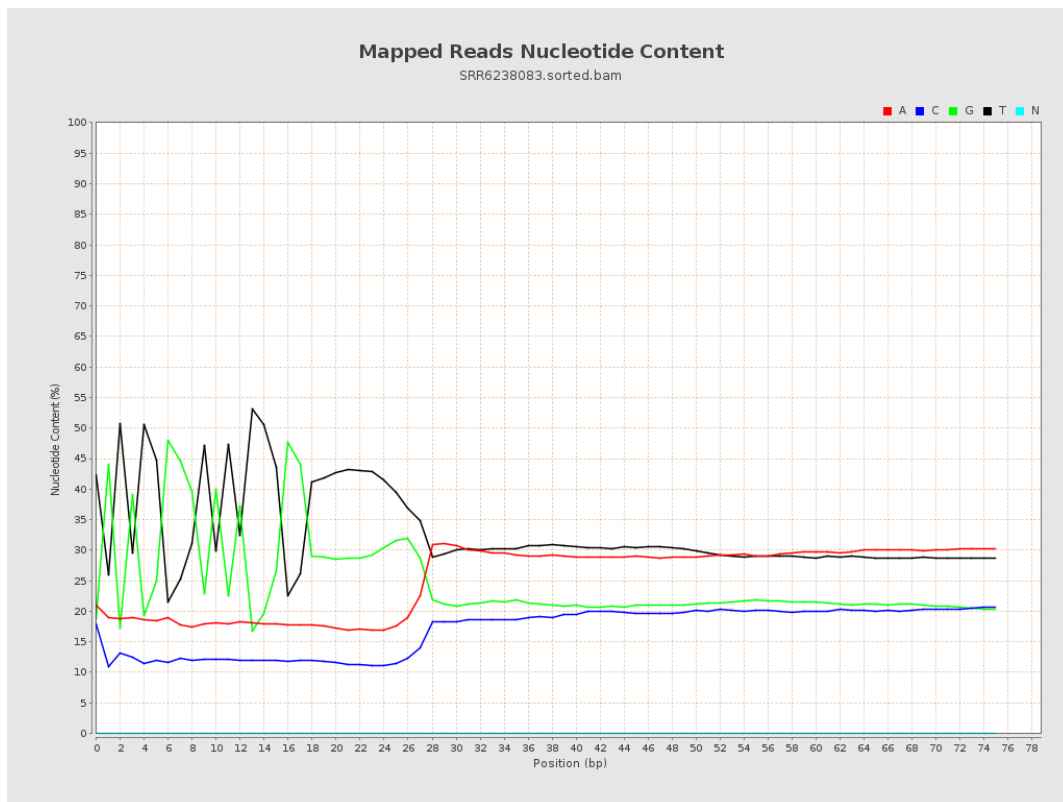
6. Results : Genome Fraction Coverage



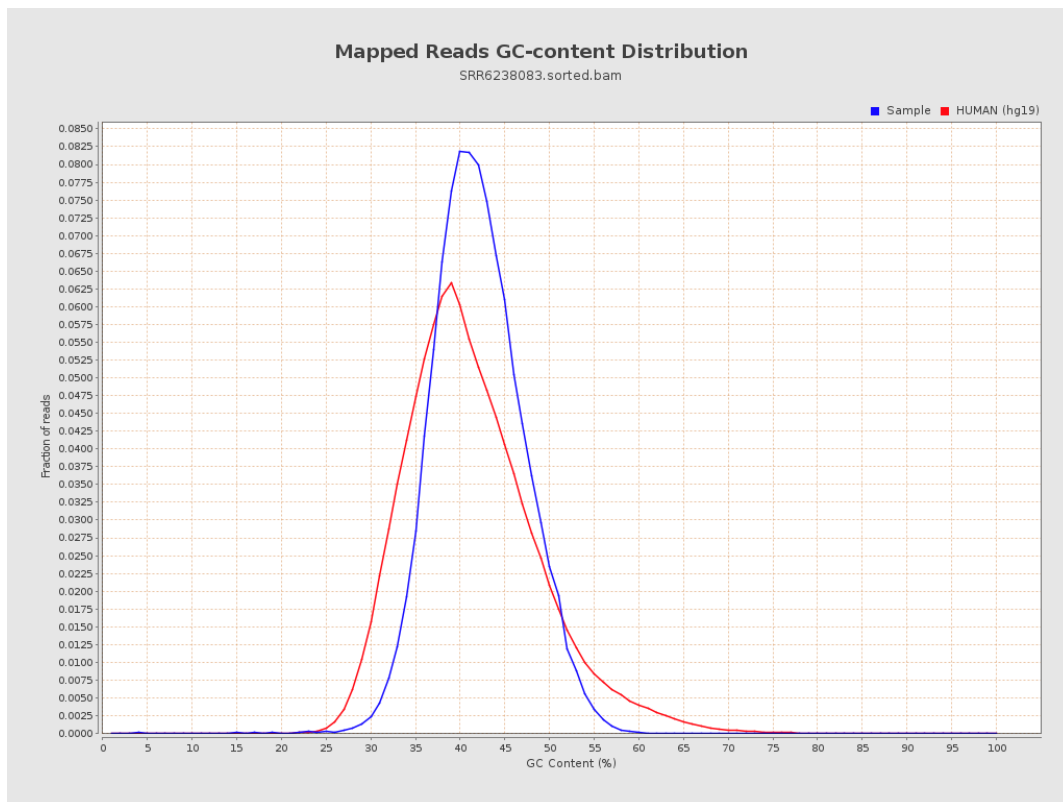
7. Results : Duplication Rate Histogram



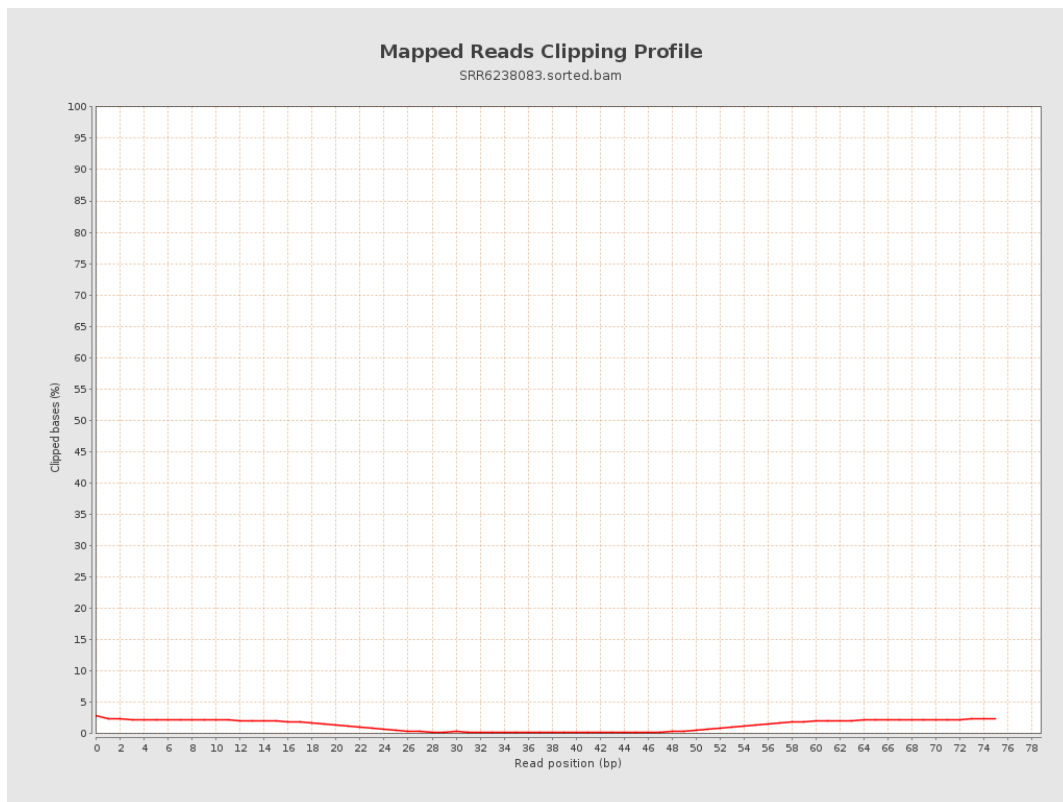
8. Results : Mapped Reads Nucleotide Content



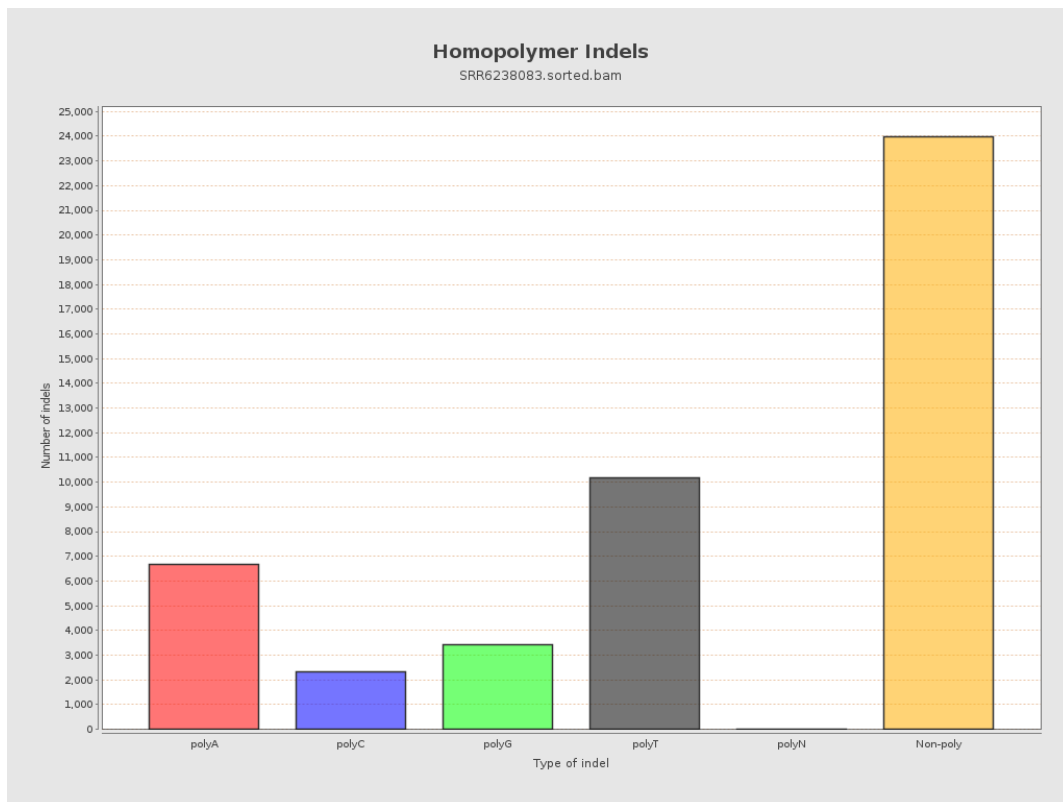
9. Results : Mapped Reads GC-content Distribution



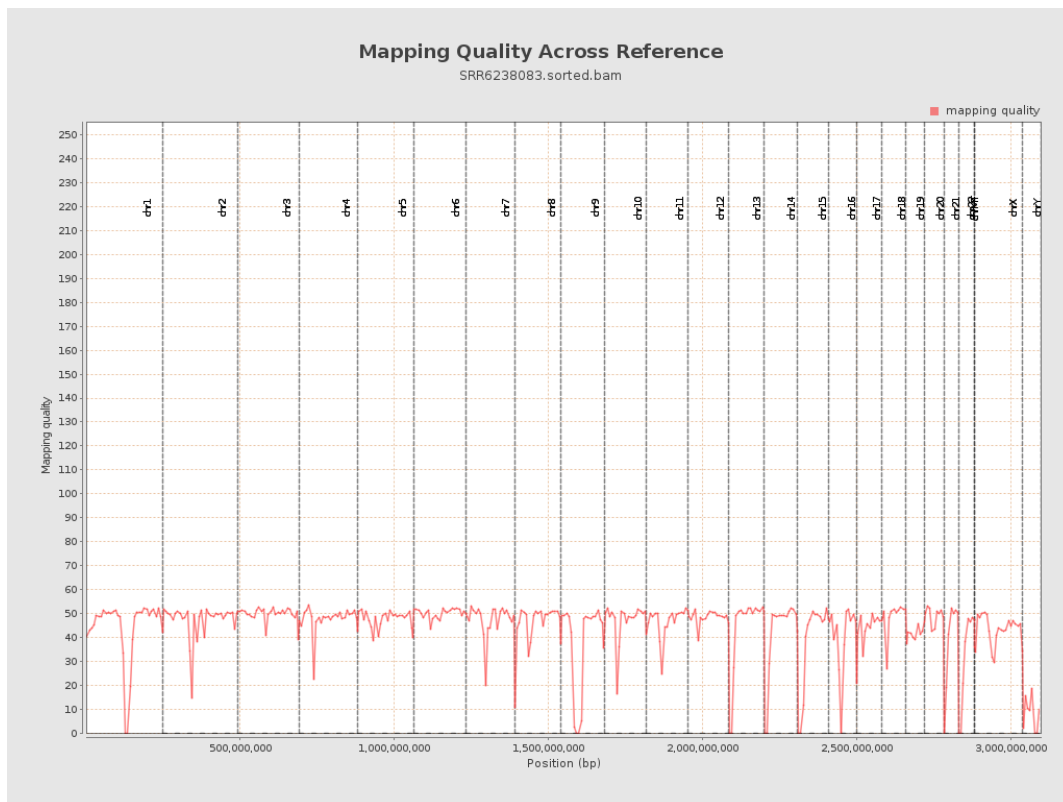
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

