

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:33:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238065.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_SRR6238065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:33:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,187,258
Mapped reads	1,998,678 / 91.38%
Unmapped reads	188,580 / 8.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,237 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	69,071 / 3.16%
Duplication rate	2.29%
Clipped reads	840,581 / 38.43%

2.2. ACGT Content

Number/percentage of A's	35,691,523 / 26.72%
Number/percentage of C's	25,572,416 / 19.14%
Number/percentage of T's	41,109,883 / 30.77%
Number/percentage of G's	31,207,495 / 23.36%
Number/percentage of N's	17,221 / 0.01%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.439
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2.4. Mapping Quality

Mean Mapping Quality	44.18
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2.5. Mismatches and indels

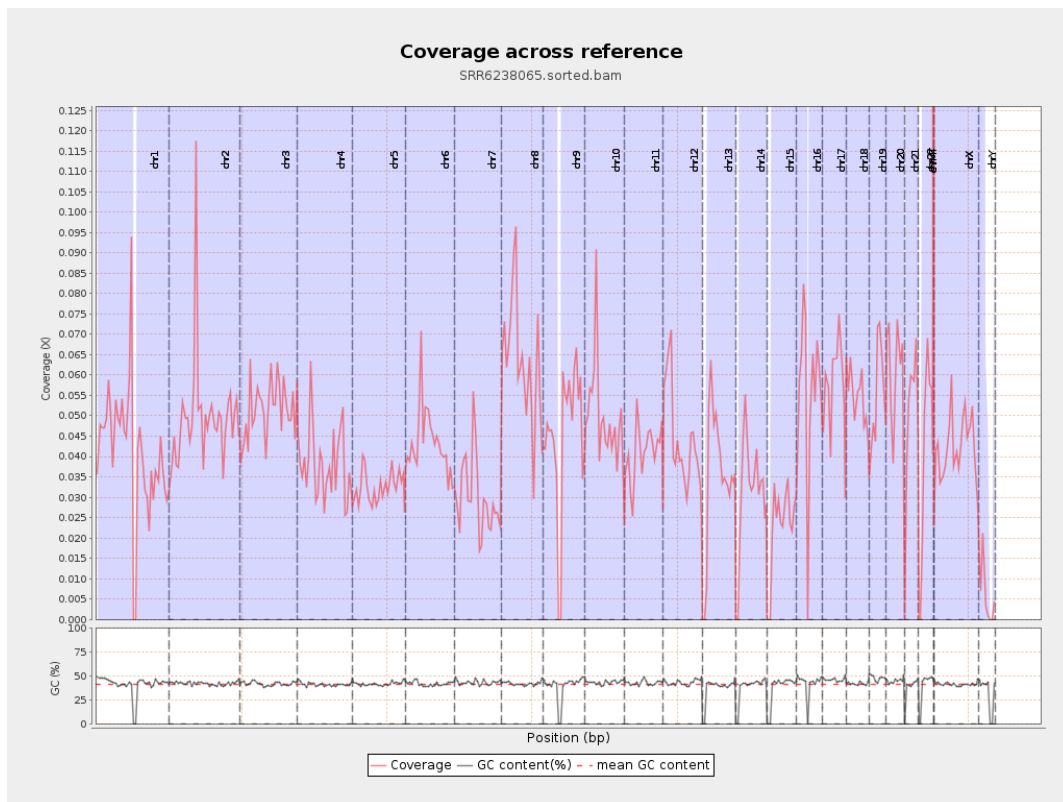
General error rate	0.79%
Mismatches	1,034,936
Insertions	9,782
Mapped reads with at least one insertion	0.48%
Deletions	38,252
Mapped reads with at least one deletion	1.89%
Homopolymer indels	45.26%

2.6. Chromosome stats

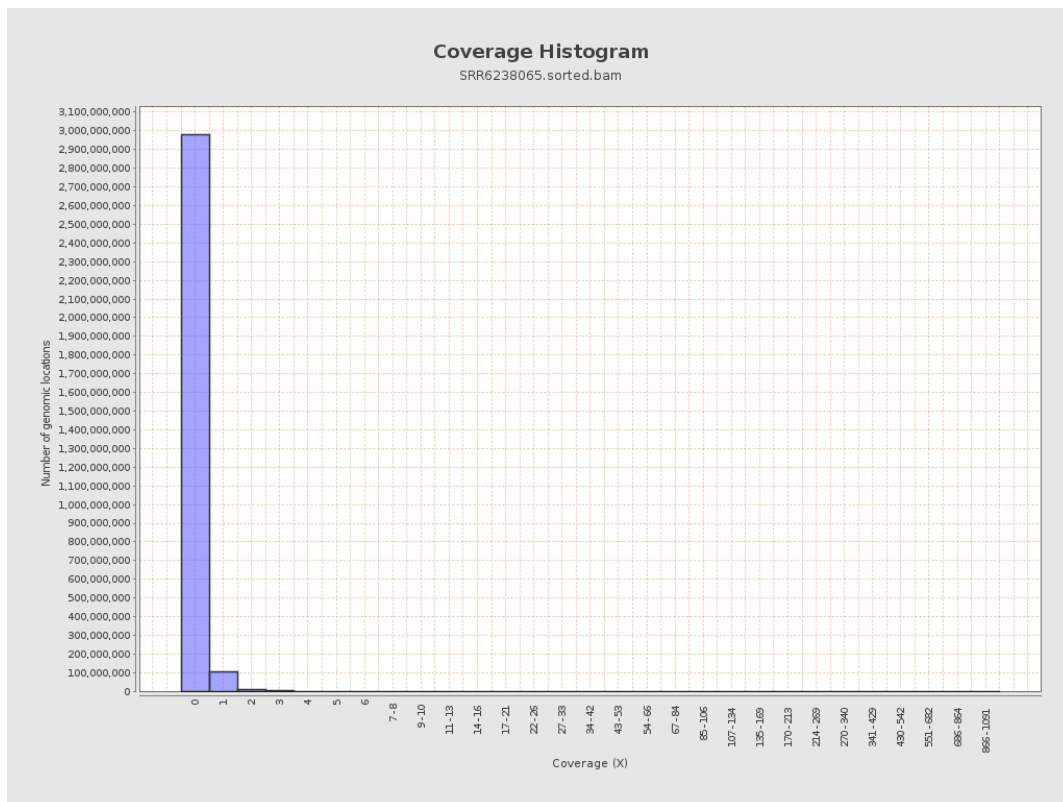
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10226660	0.041	0.9355
chr2	243199373	12028002	0.0495	0.5889
chr3	198022430	10154277	0.0513	0.2532
chr4	191154276	7191248	0.0376	0.2461
chr5	180915260	5900008	0.0326	0.2046
chr6	171115067	7394223	0.0432	0.3006
chr7	159138663	4810304	0.0302	0.3432

chr8	146364022	9230283	0.0631	0.503
chr9	141213431	6405550	0.0454	0.4359
chr10	135534747	6750594	0.0498	0.4148
chr11	135006516	5520382	0.0409	0.3473
chr12	133851895	5894622	0.044	0.2389
chr13	115169878	4005162	0.0348	0.2052
chr14	107349540	3350364	0.0312	0.229
chr15	102531392	2366870	0.0231	0.1733
chr16	90354753	5093140	0.0564	0.3002
chr17	81195210	4645282	0.0572	0.2966
chr18	78077248	4295609	0.055	0.7467
chr19	59128983	3270346	0.0553	0.5786
chr20	63025520	3787595	0.0601	0.2854
chr21	48129895	2379986	0.0494	0.2795
chr22	51304566	2039408	0.0398	0.2227
chrMT	16571	15245	0.92	1.109
chrX	155270560	6558163	0.0422	0.2686
chrY	59373566	353205	0.0059	0.1747

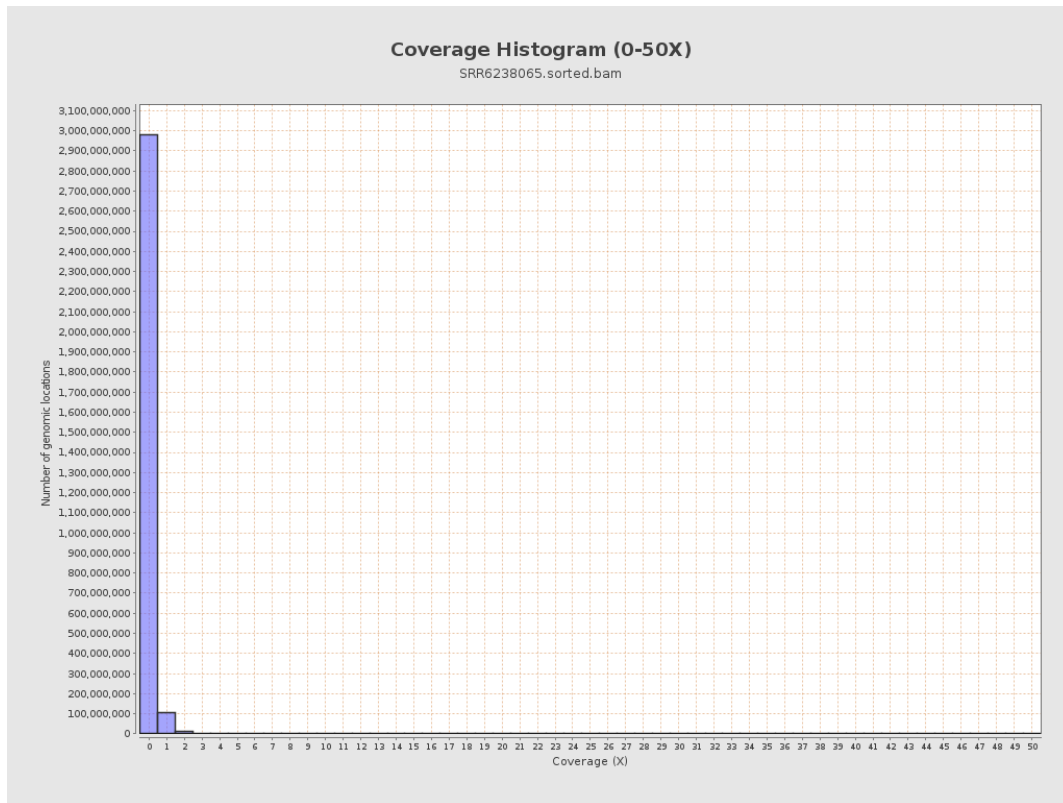
3. Results : Coverage across reference



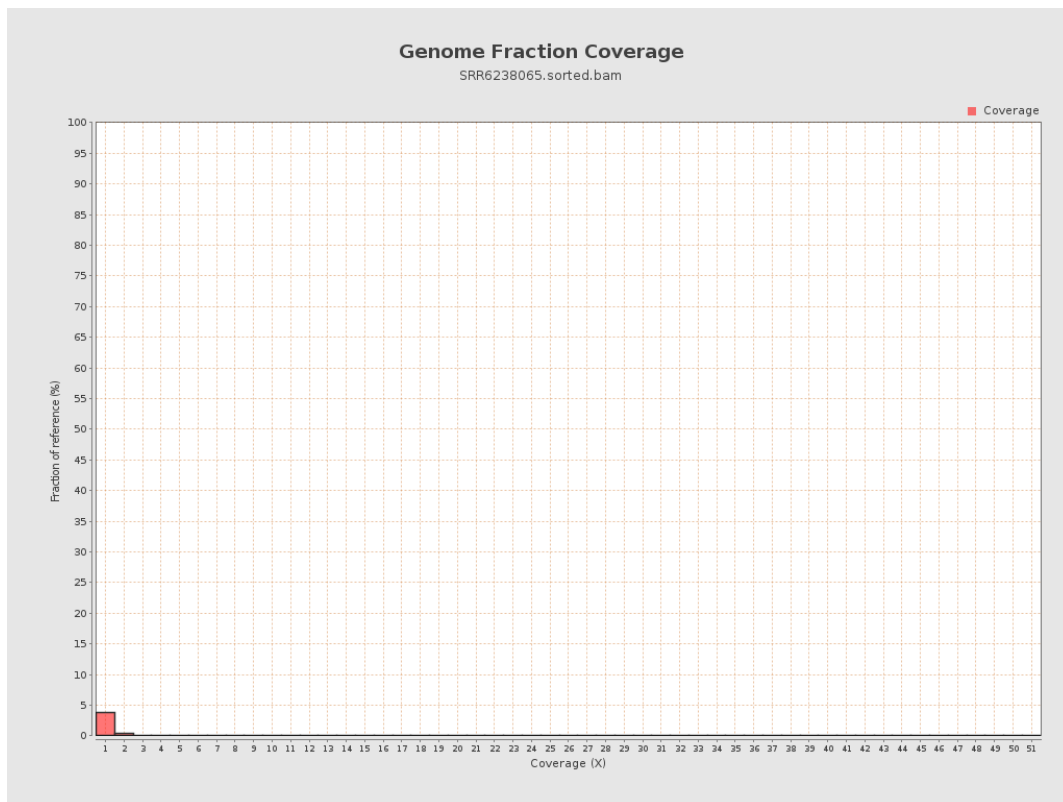
4. Results : Coverage Histogram



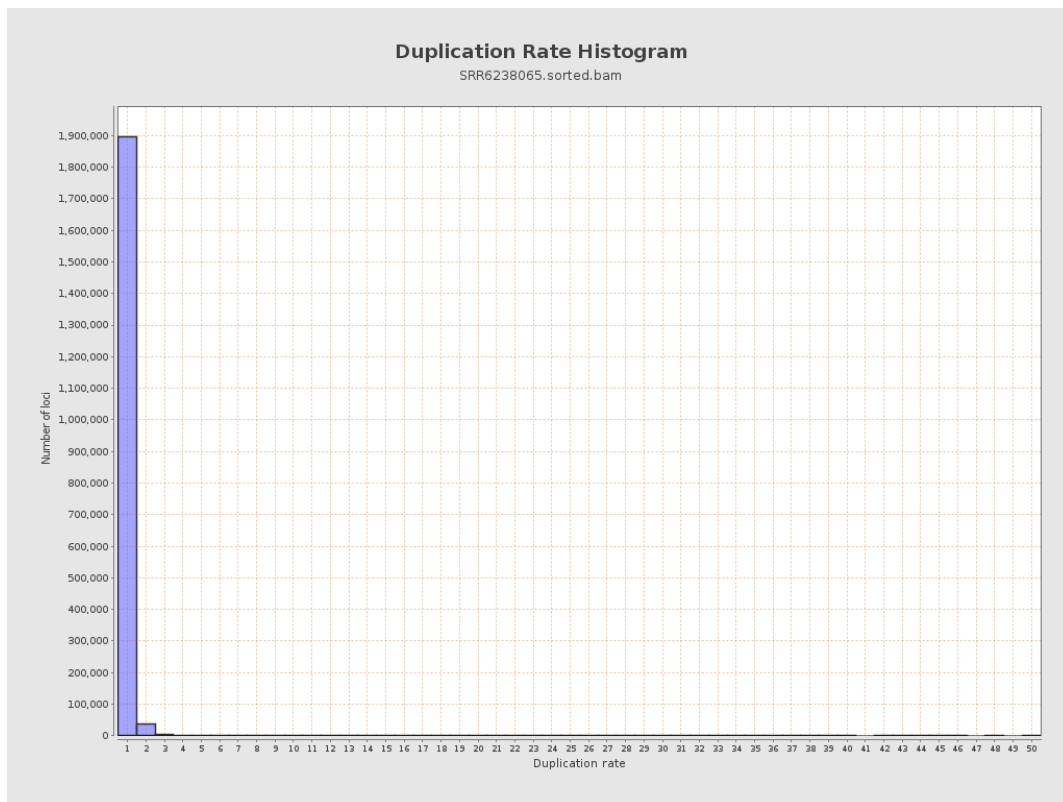
5. Results : Coverage Histogram (0-50X)



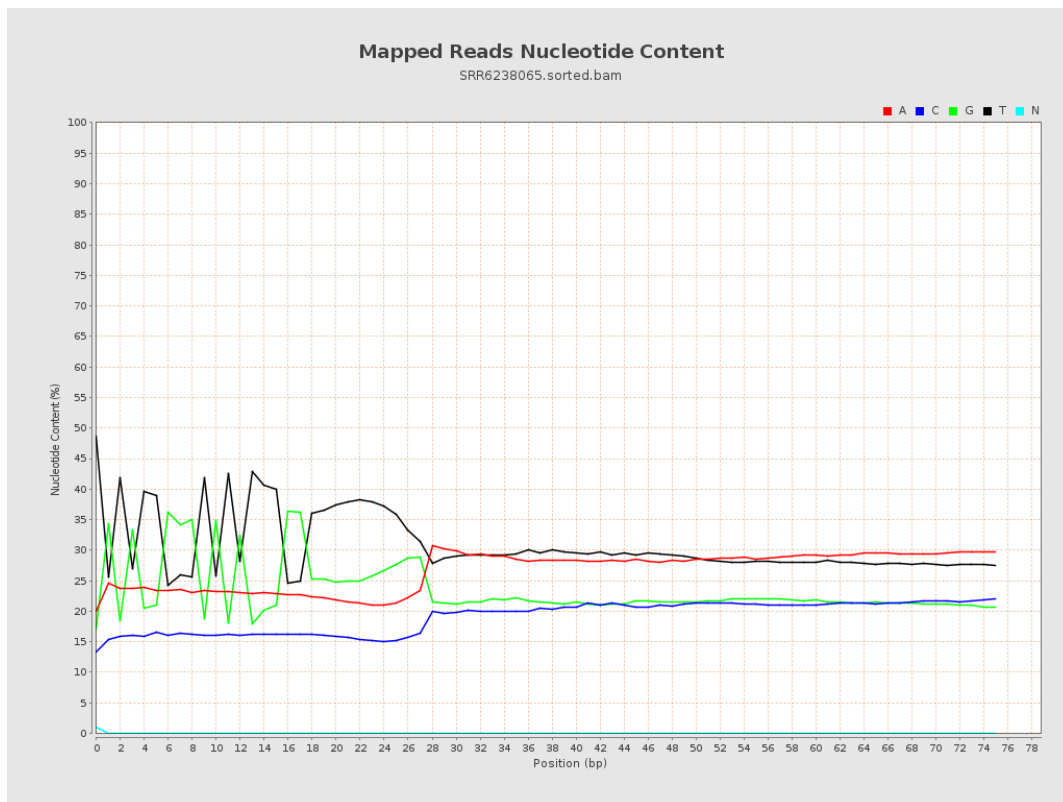
6. Results : Genome Fraction Coverage



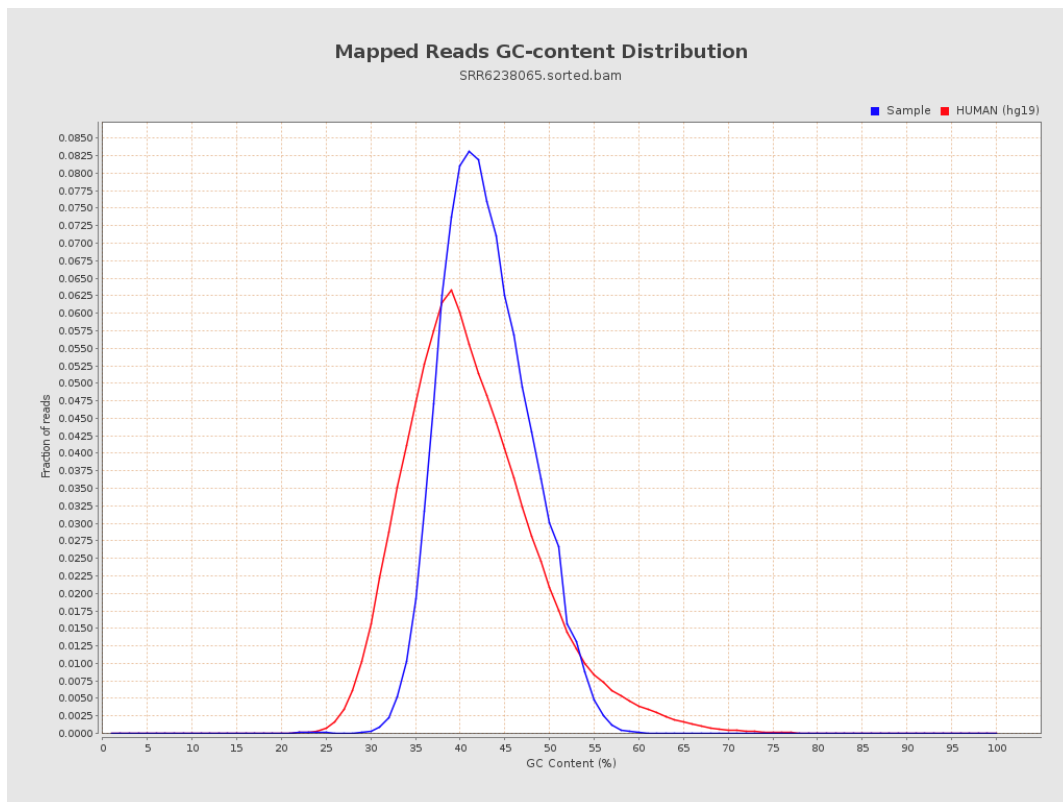
7. Results : Duplication Rate Histogram



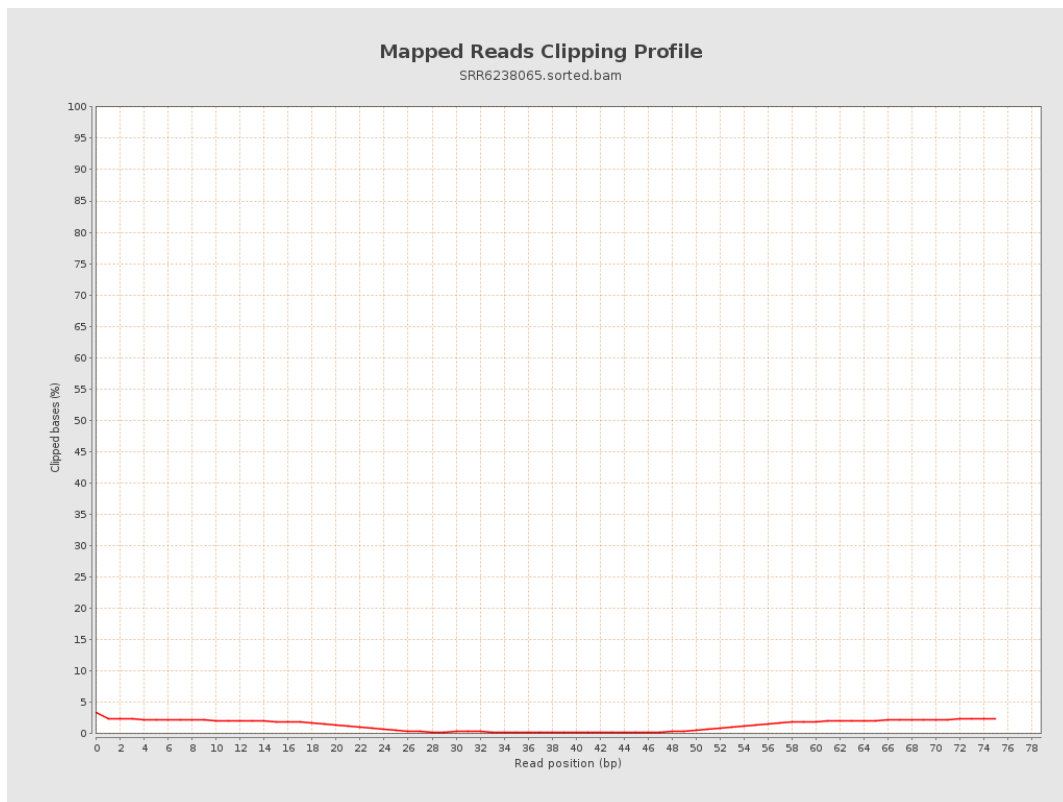
8. Results : Mapped Reads Nucleotide Content



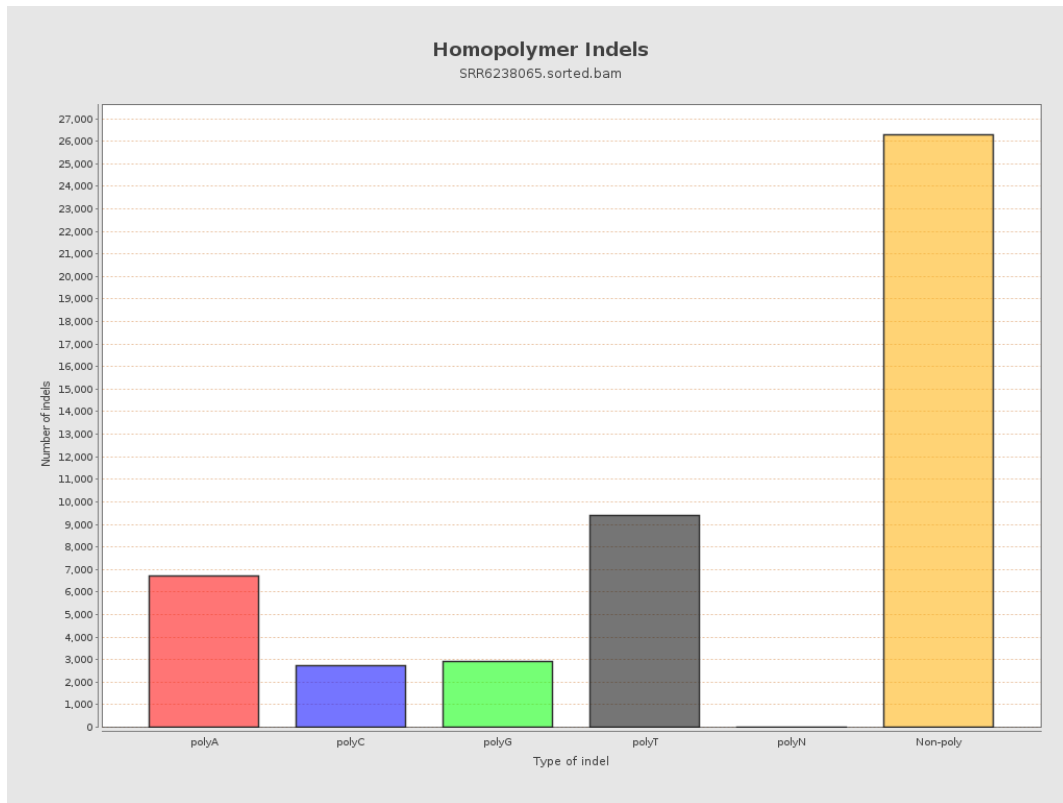
9. Results : Mapped Reads GC-content Distribution



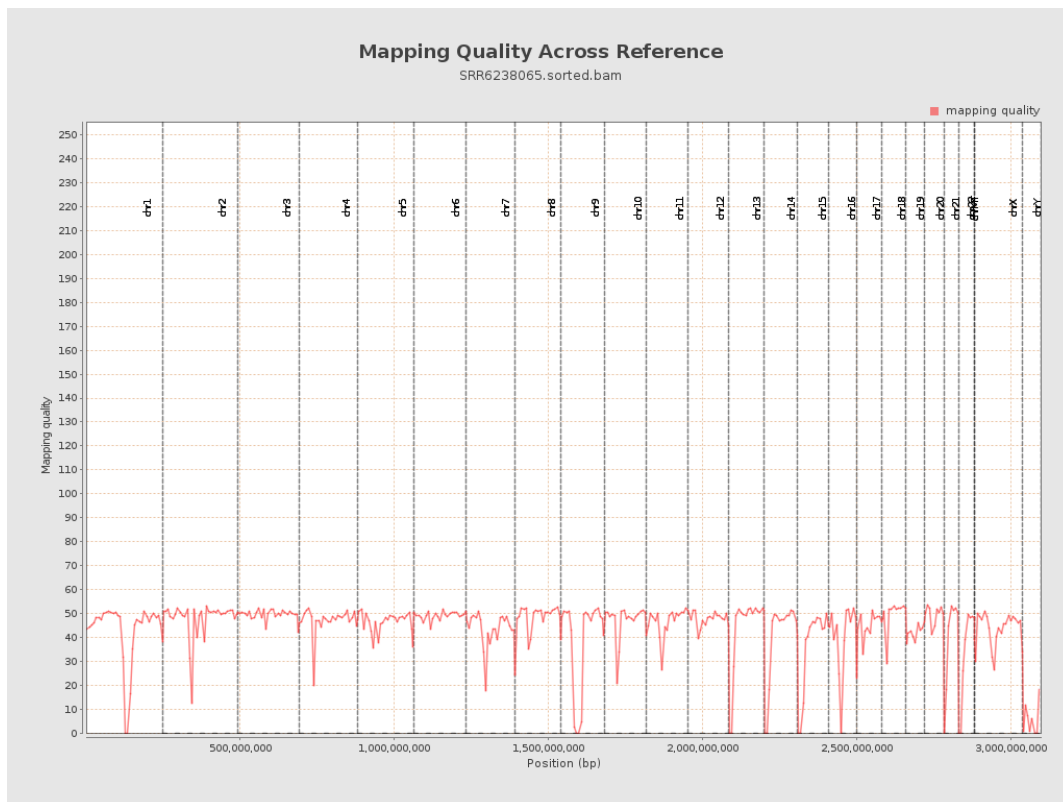
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

