

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:34:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238305.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_SRR6238305 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238305.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:34:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238305.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,481,371
Mapped reads	1,328,414 / 89.67%
Unmapped reads	152,957 / 10.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,941 / 1.41%
Read min/max/mean length	30 / 76 / 76.5
Duplicated reads (estimated)	102,934 / 6.95%
Duplication rate	6.32%
Clipped reads	683,919 / 46.17%

2.2. ACGT Content

Number/percentage of A's	24,267,346 / 27.84%
Number/percentage of C's	16,484,392 / 18.91%
Number/percentage of T's	27,178,653 / 31.18%
Number/percentage of G's	19,202,988 / 22.03%
Number/percentage of N's	21,239 / 0.02%
GC Percentage	40.95%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2815
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2.4. Mapping Quality

Mean Mapping Quality	43.06
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2.5. Mismatches and indels

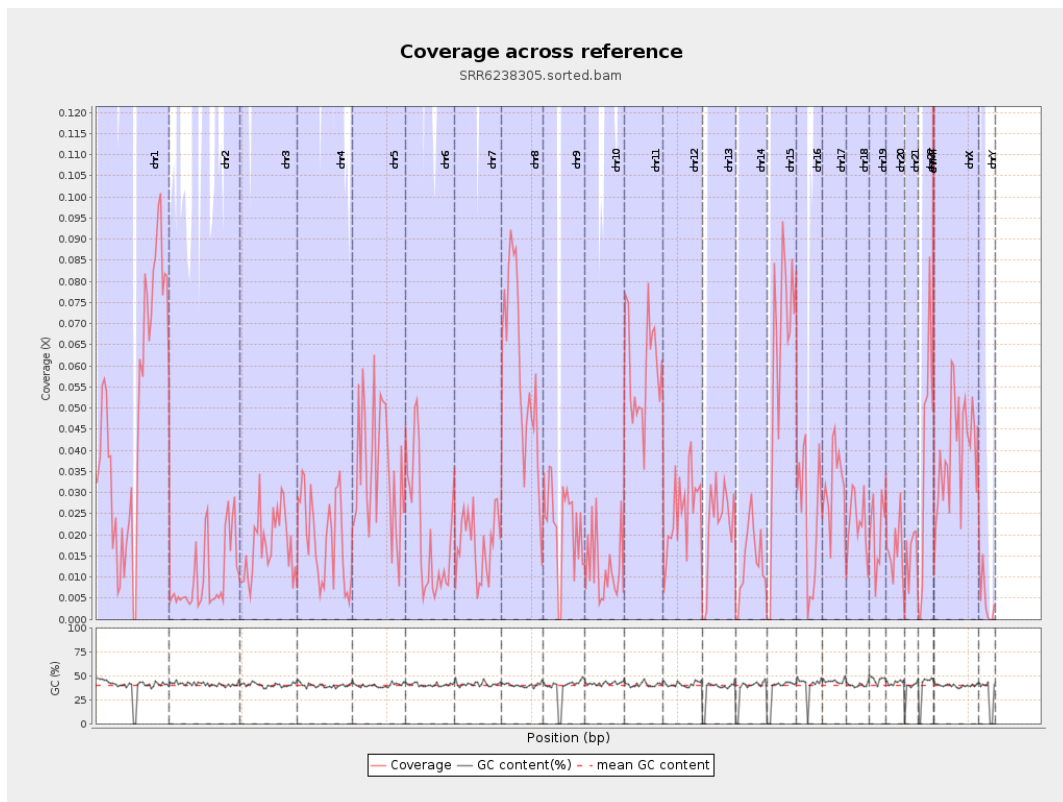
General error rate	0.82%
Mismatches	705,455
Insertions	6,570
Mapped reads with at least one insertion	0.49%
Deletions	23,863
Mapped reads with at least one deletion	1.77%
Homopolymer indels	46.15%

2.6. Chromosome stats

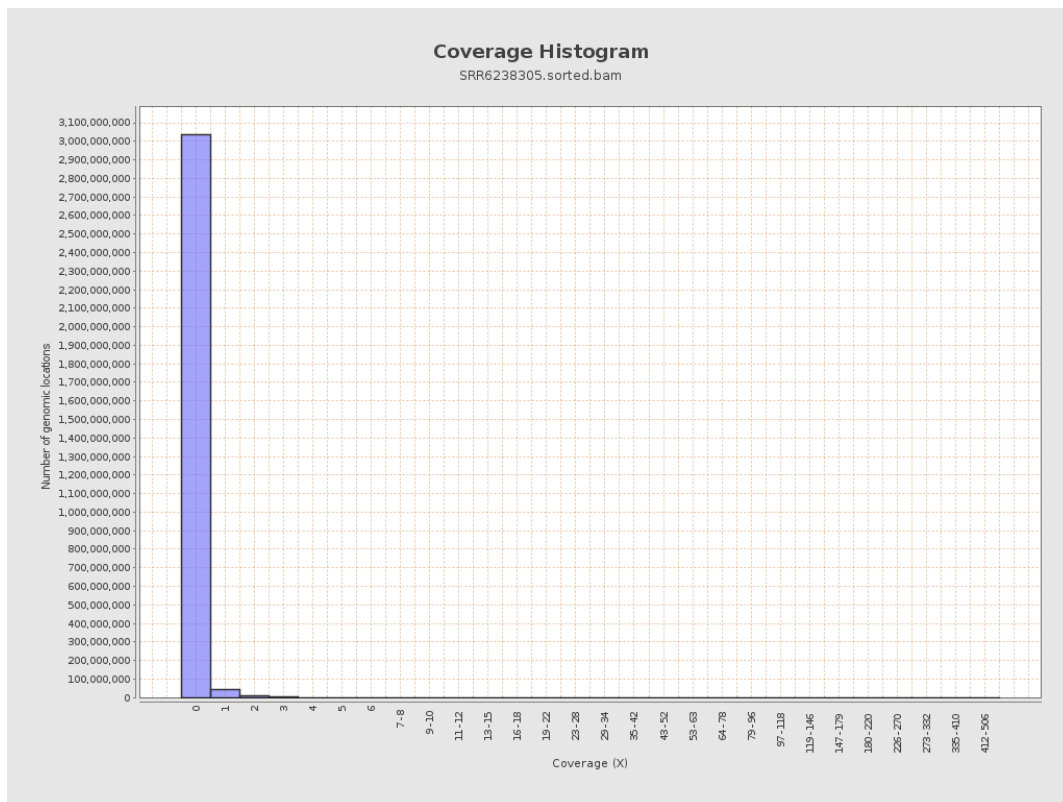
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11975716	0.048	0.3266
chr2	243199373	2485909	0.0102	0.2496
chr3	198022430	3492343	0.0176	0.1774
chr4	191154276	3640207	0.019	0.1973
chr5	180915260	6482538	0.0358	0.2538
chr6	171115067	3494340	0.0204	0.2007
chr7	159138663	2857395	0.018	0.2717

chr8	146364022	8449923	0.0577	0.4792
chr9	141213431	3123486	0.0221	0.2773
chr10	135534747	1662212	0.0123	0.218
chr11	135006516	7938099	0.0588	0.4699
chr12	133851895	3409966	0.0255	0.2187
chr13	115169878	2516306	0.0218	0.1948
chr14	107349540	1524931	0.0142	0.1869
chr15	102531392	6180188	0.0603	0.3247
chr16	90354753	2186969	0.0242	0.2281
chr17	81195210	2604626	0.0321	0.26
chr18	78077248	1799730	0.0231	0.4651
chr19	59128983	1224515	0.0207	0.2708
chr20	63025520	1002733	0.0159	0.1704
chr21	48129895	672905	0.014	0.183
chr22	51304566	2064286	0.0402	0.2651
chrMT	16571	7778	0.4694	0.9695
chrX	155270560	6130650	0.0395	0.2829
chrY	59373566	267769	0.0045	0.1803

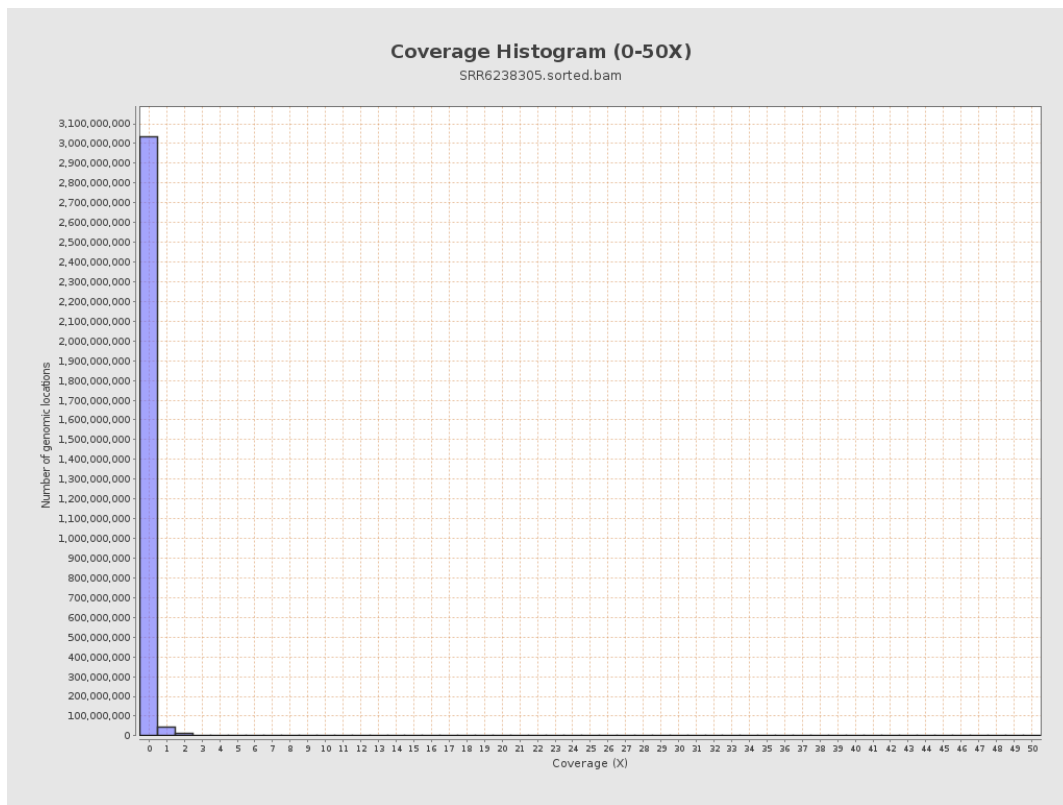
3. Results : Coverage across reference



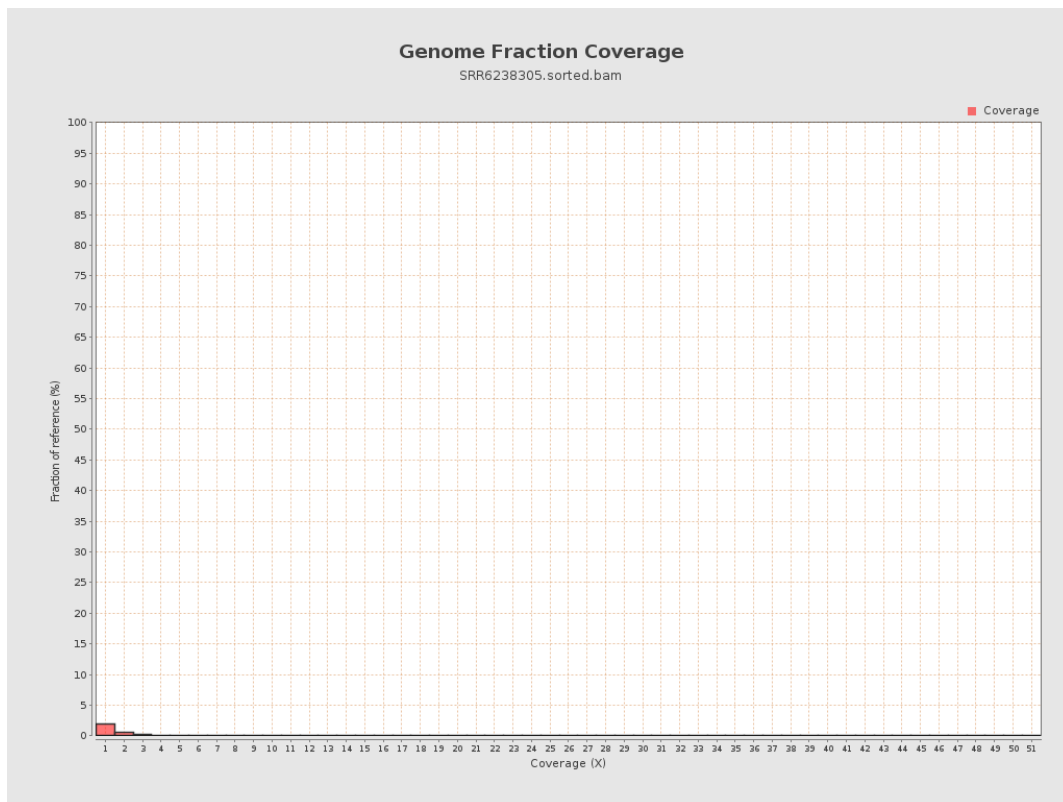
4. Results : Coverage Histogram



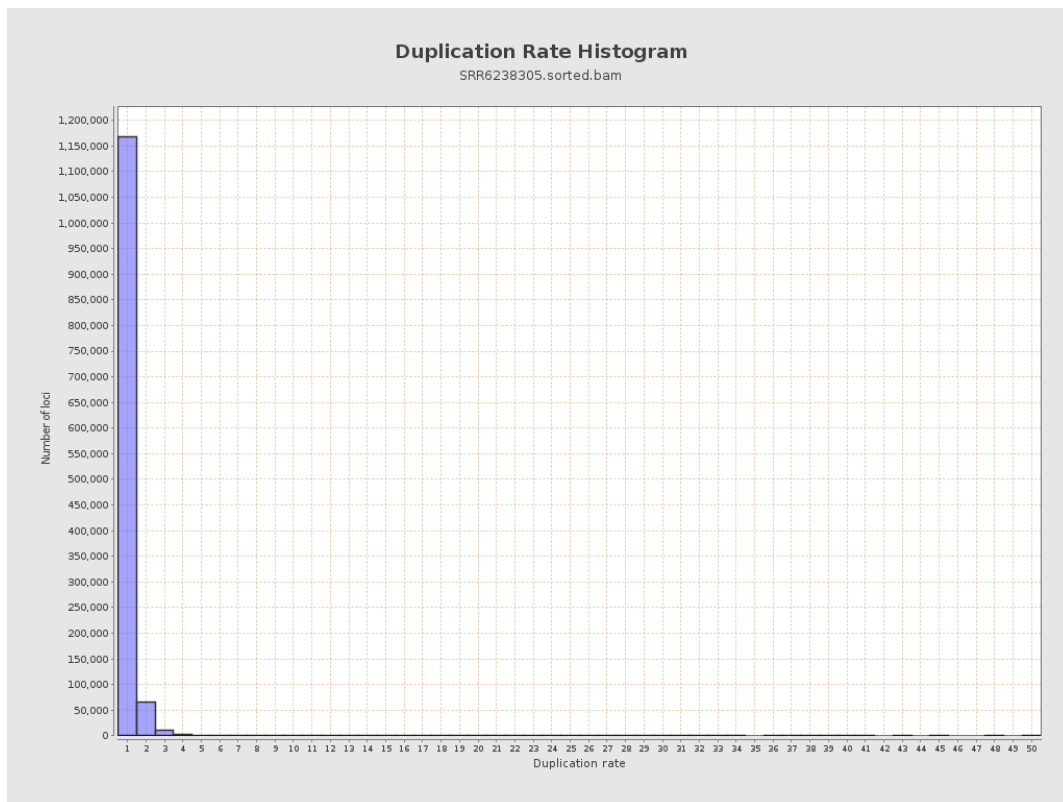
5. Results : Coverage Histogram (0-50X)



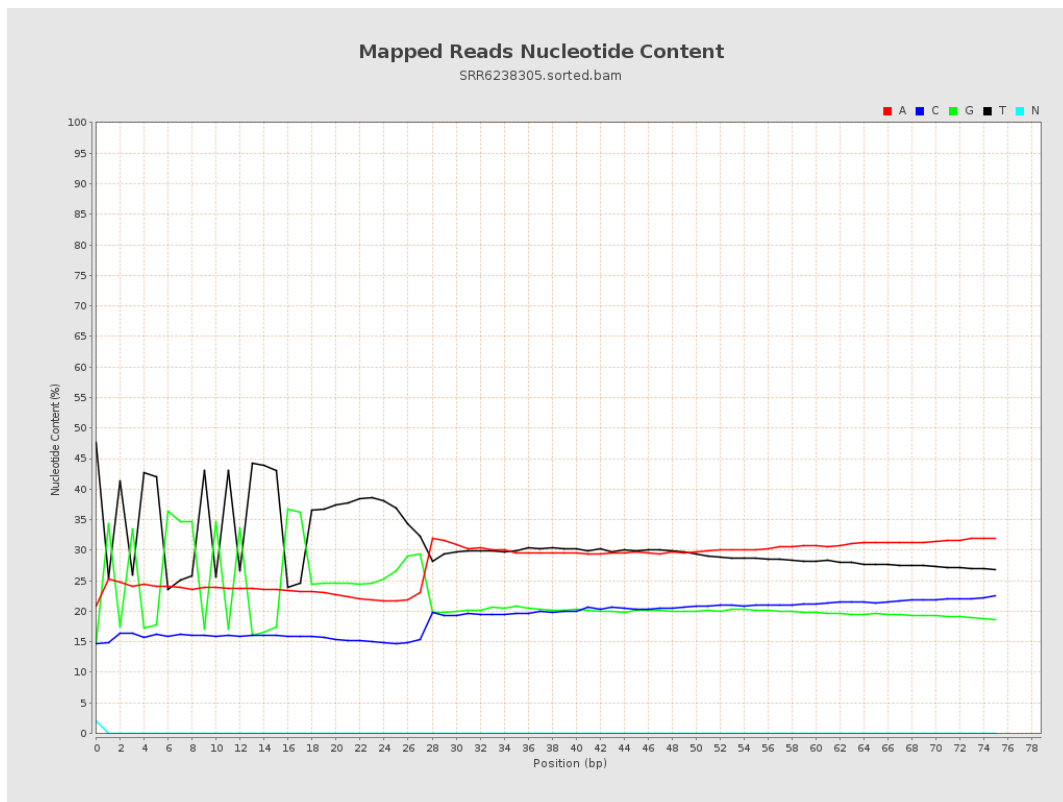
6. Results : Genome Fraction Coverage



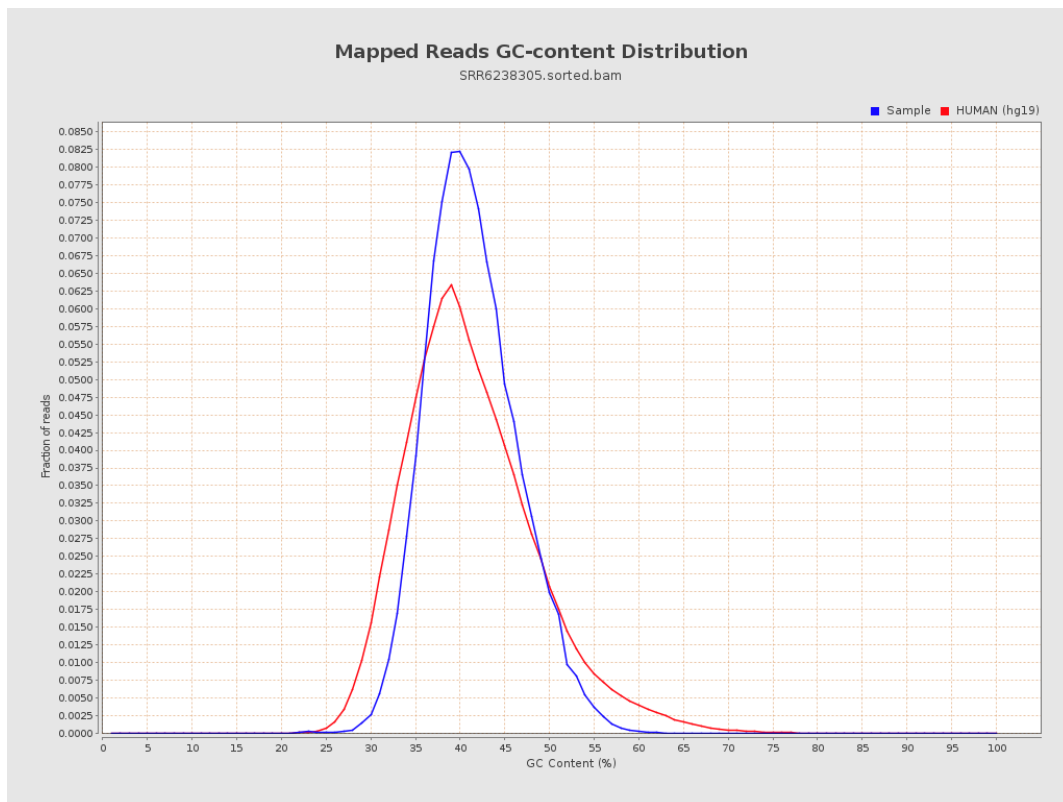
7. Results : Duplication Rate Histogram



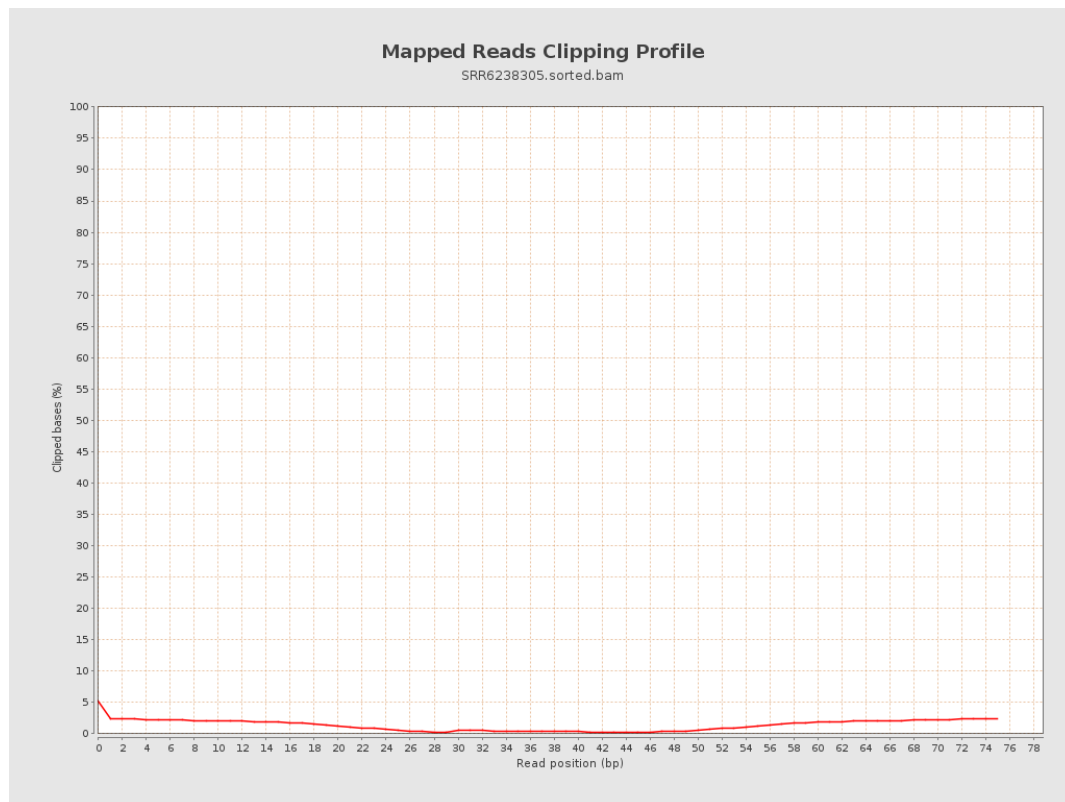
8. Results : Mapped Reads Nucleotide Content



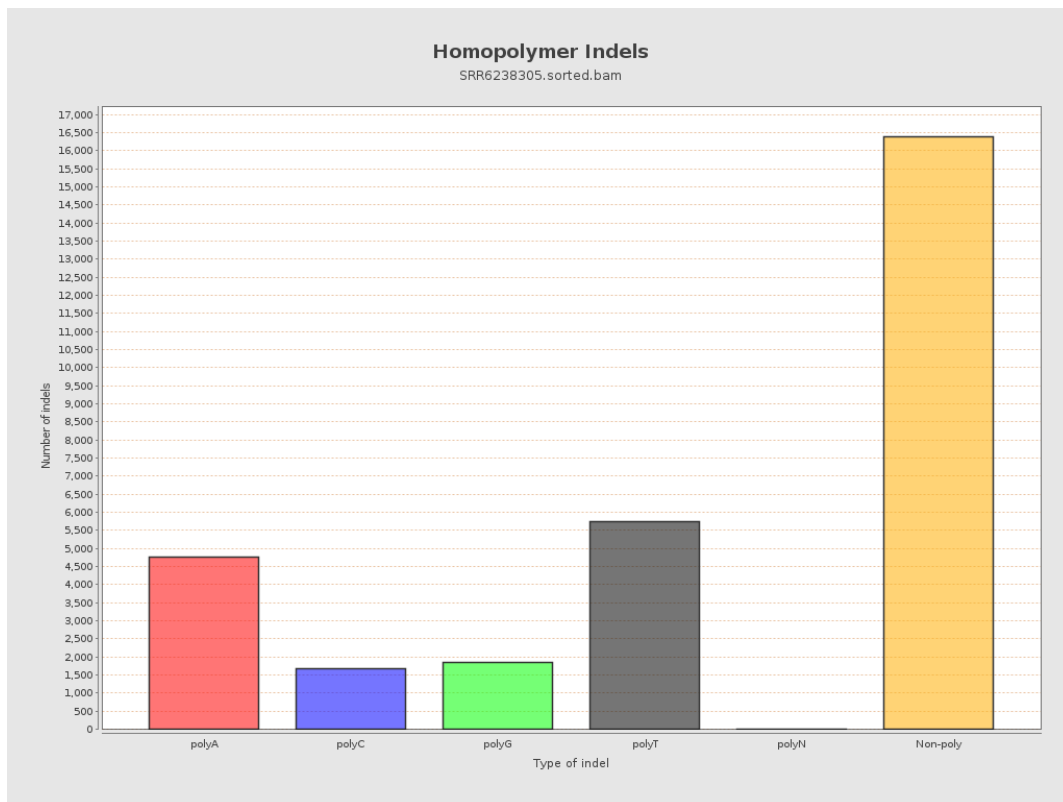
9. Results : Mapped Reads GC-content Distribution



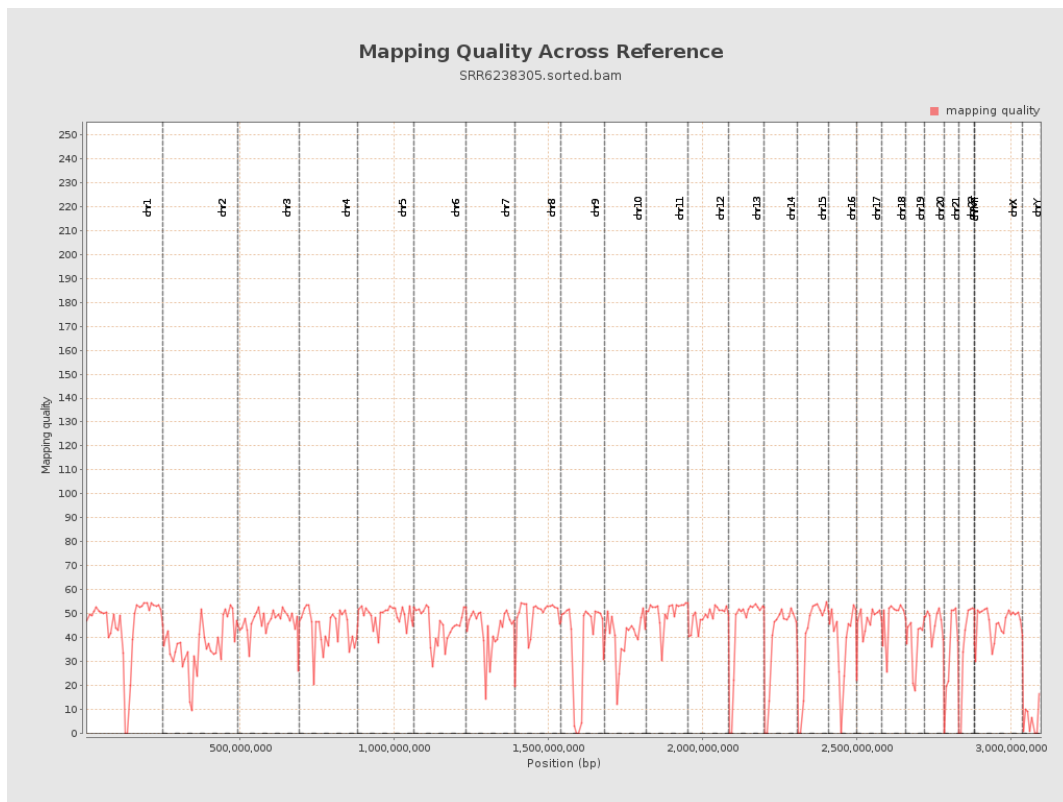
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

