

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:56:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238540.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_SRR6238540 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238540.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:56:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238540.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,509,900
Mapped reads	4,095,544 / 90.81%
Unmapped reads	414,356 / 9.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,680 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	375,438 / 8.32%
Duplication rate	7.29%
Clipped reads	2,539,473 / 56.31%

2.2. ACGT Content

Number/percentage of A's	63,157,428 / 24.95%
Number/percentage of C's	45,024,141 / 17.79%
Number/percentage of T's	82,844,039 / 32.73%
Number/percentage of G's	62,084,645 / 24.53%
Number/percentage of N's	17,343 / 0.01%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0818

Standard Deviation	0.799
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2.4. Mapping Quality

Mean Mapping Quality	42.84
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2.5. Mismatches and indels

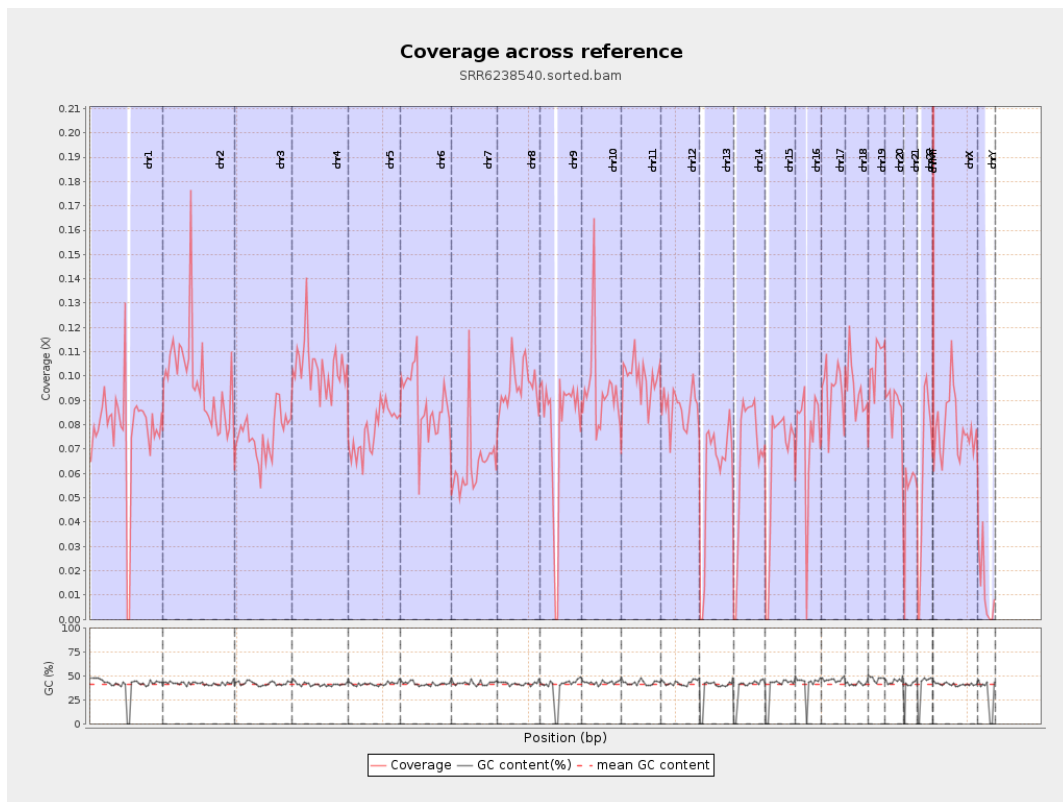
General error rate	0.59%
Mismatches	1,452,711
Insertions	19,022
Mapped reads with at least one insertion	0.46%
Deletions	62,842
Mapped reads with at least one deletion	1.52%
Homopolymer indels	43.02%

2.6. Chromosome stats

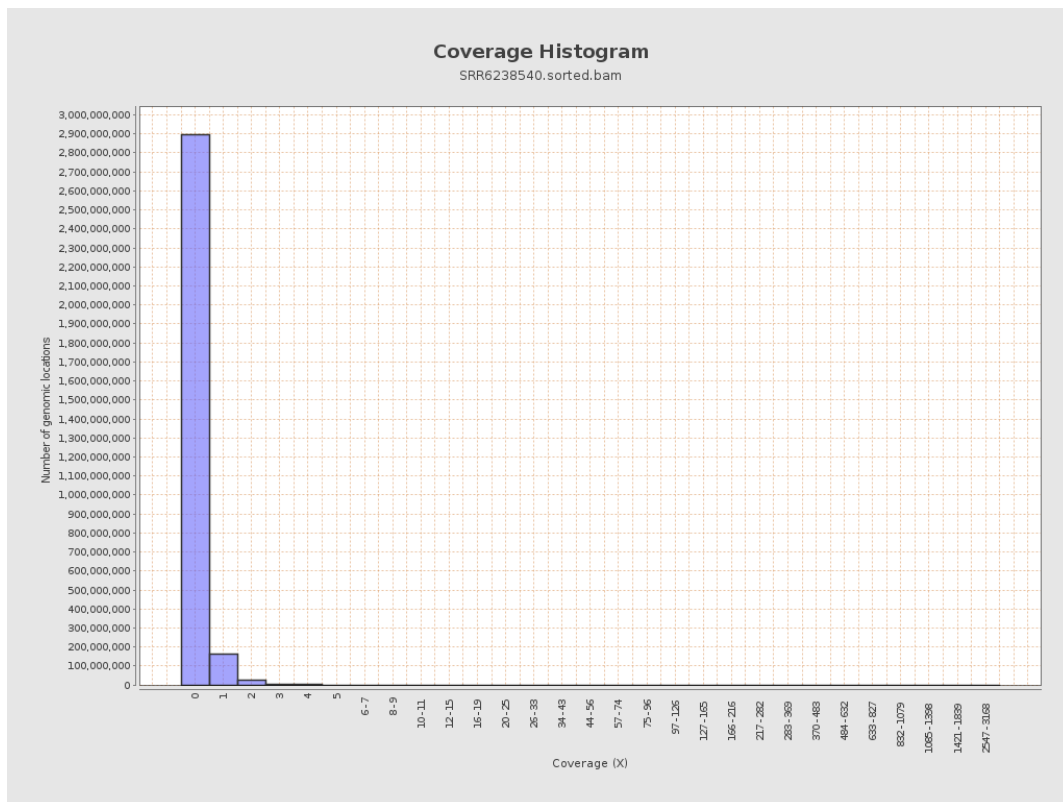
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19290799	0.0774	1.2346
chr2	243199373	23780789	0.0978	1.5831
chr3	198022430	14981888	0.0757	0.3531
chr4	191154276	19862906	0.1039	0.4613
chr5	180915260	14071975	0.0778	0.3595
chr6	171115067	15182333	0.0887	0.6119
chr7	159138663	10146158	0.0638	0.8761

chr8	146364022	14028369	0.0958	0.7326
chr9	141213431	11137928	0.0789	0.7262
chr10	135534747	12735199	0.094	0.823
chr11	135006516	13333445	0.0988	0.7429
chr12	133851895	11674401	0.0872	0.4002
chr13	115169878	6896372	0.0599	0.3924
chr14	107349540	7263210	0.0677	0.4047
chr15	102531392	6574618	0.0641	0.4025
chr16	90354753	6630354	0.0734	0.462
chr17	81195210	7732284	0.0952	0.4554
chr18	78077248	7437411	0.0953	1.5284
chr19	59128983	6225042	0.1053	0.8326
chr20	63025520	5518743	0.0876	0.4015
chr21	48129895	2534314	0.0527	0.3617
chr22	51304566	3206312	0.0625	0.3087
chrMT	16571	73603	4.4417	3.5624
chrX	155270560	12196891	0.0786	0.4444
chrY	59373566	721959	0.0122	0.3307

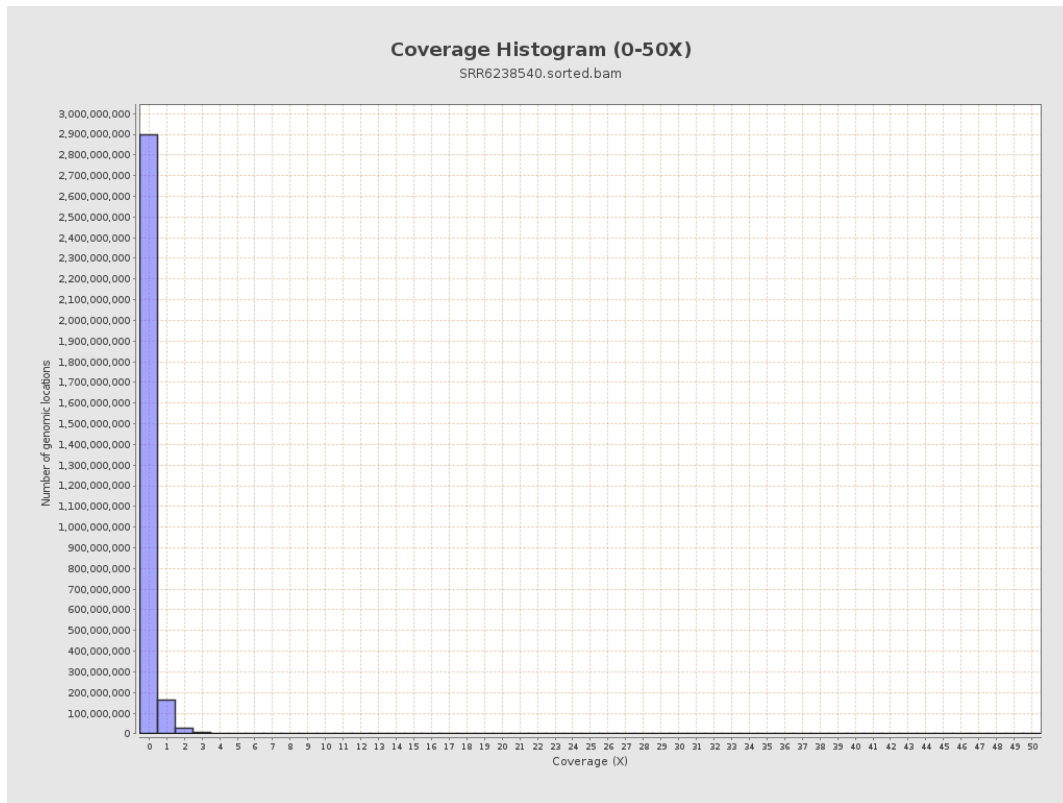
3. Results : Coverage across reference



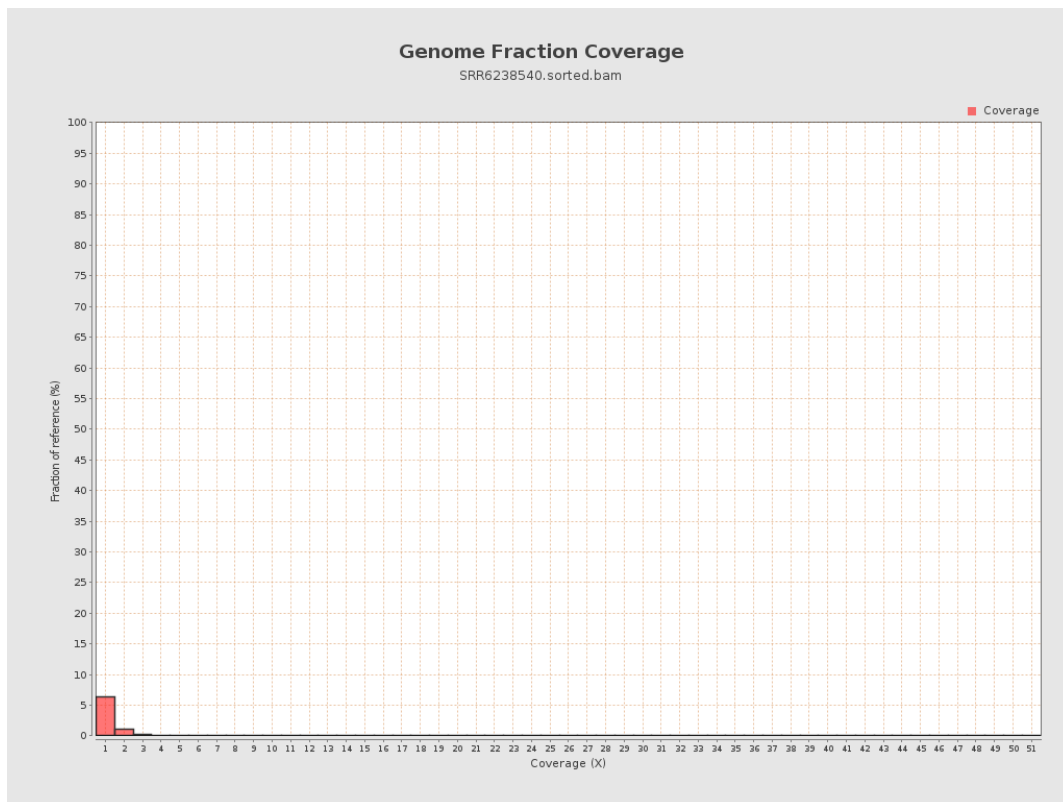
4. Results : Coverage Histogram



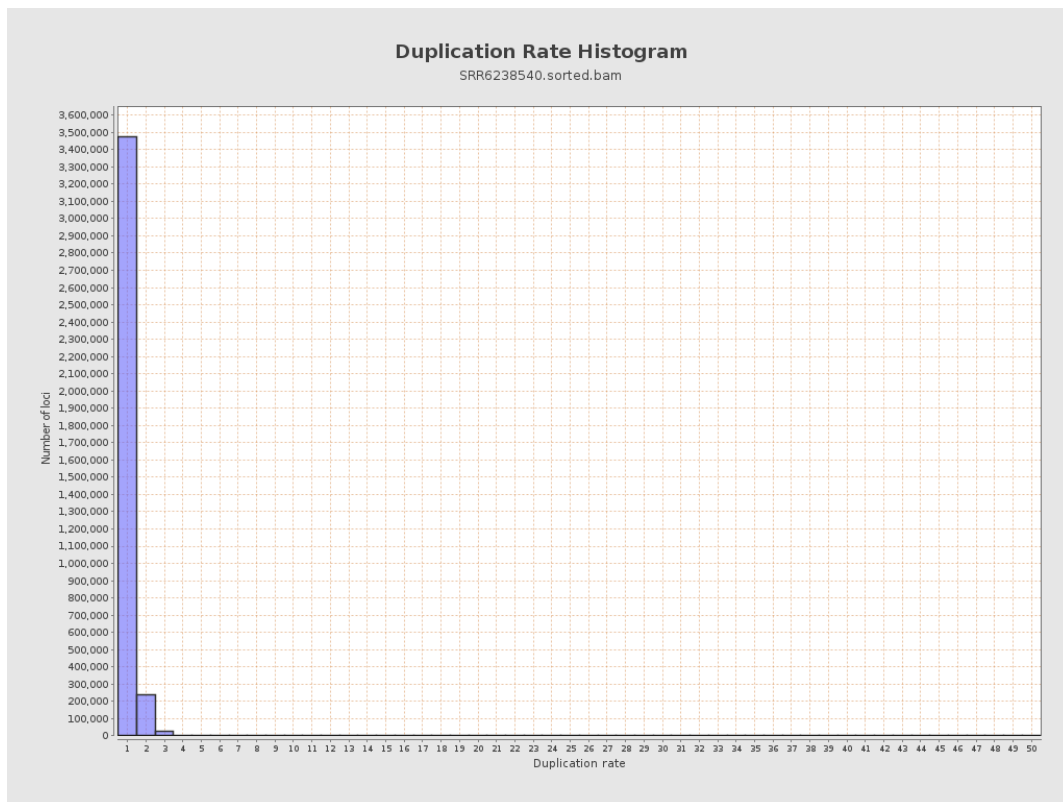
5. Results : Coverage Histogram (0-50X)



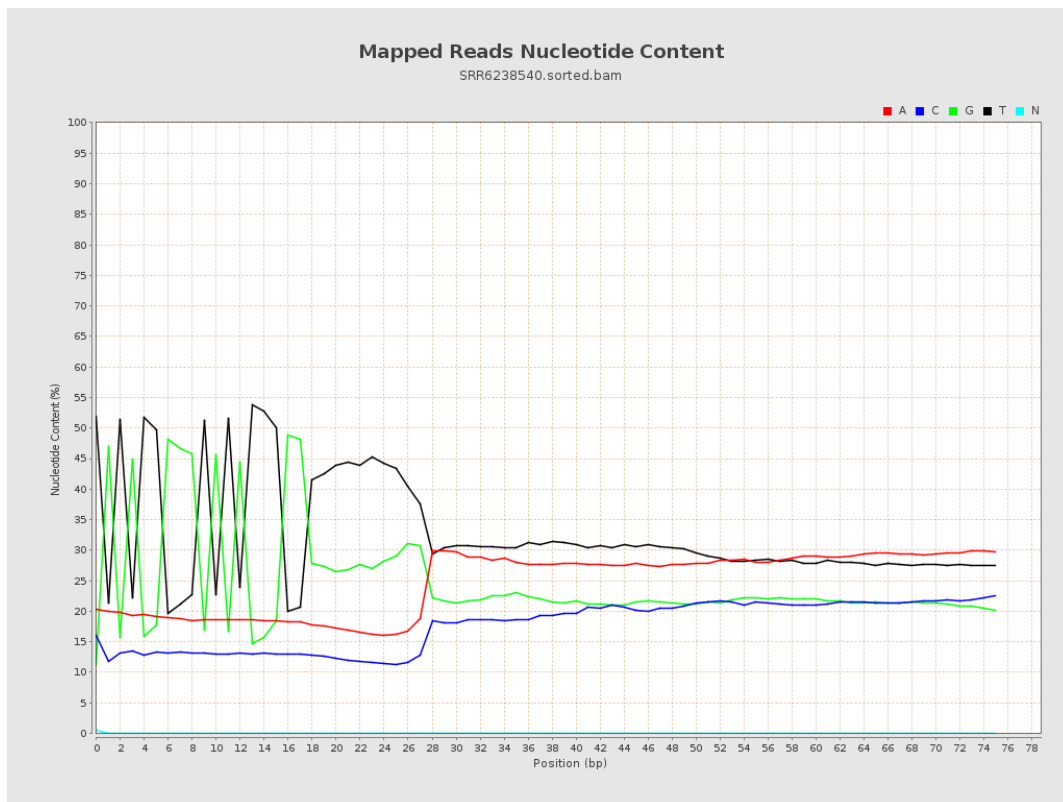
6. Results : Genome Fraction Coverage



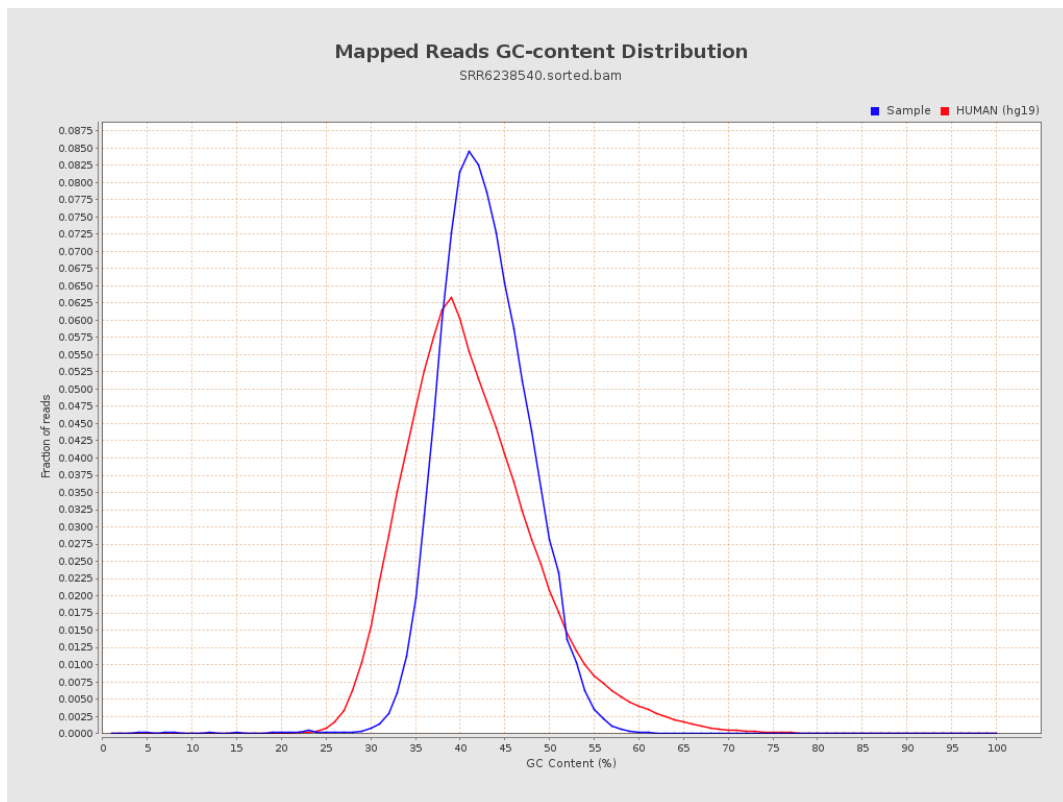
7. Results : Duplication Rate Histogram



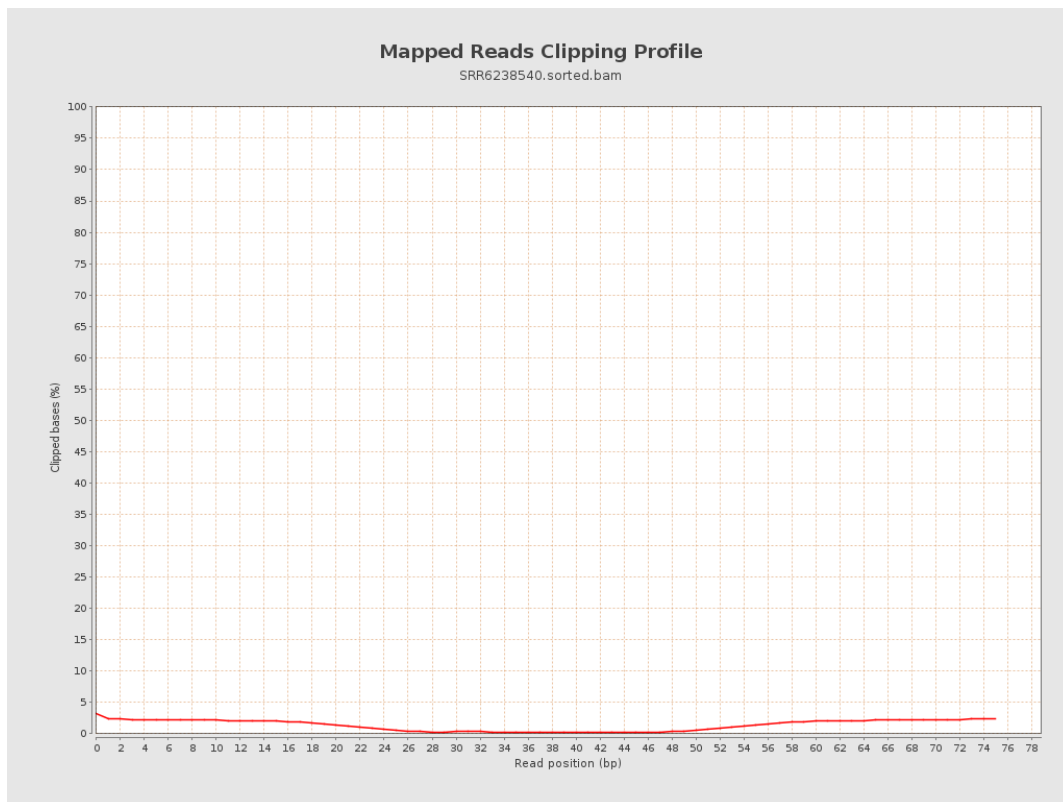
8. Results : Mapped Reads Nucleotide Content



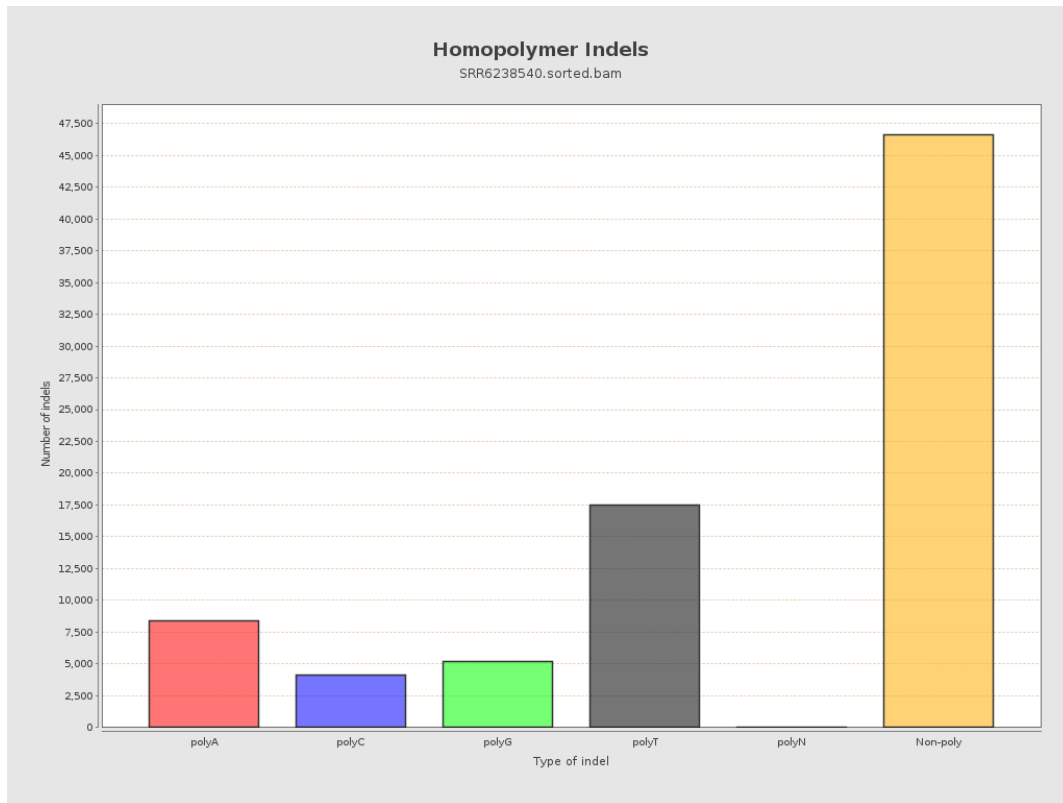
9. Results : Mapped Reads GC-content Distribution



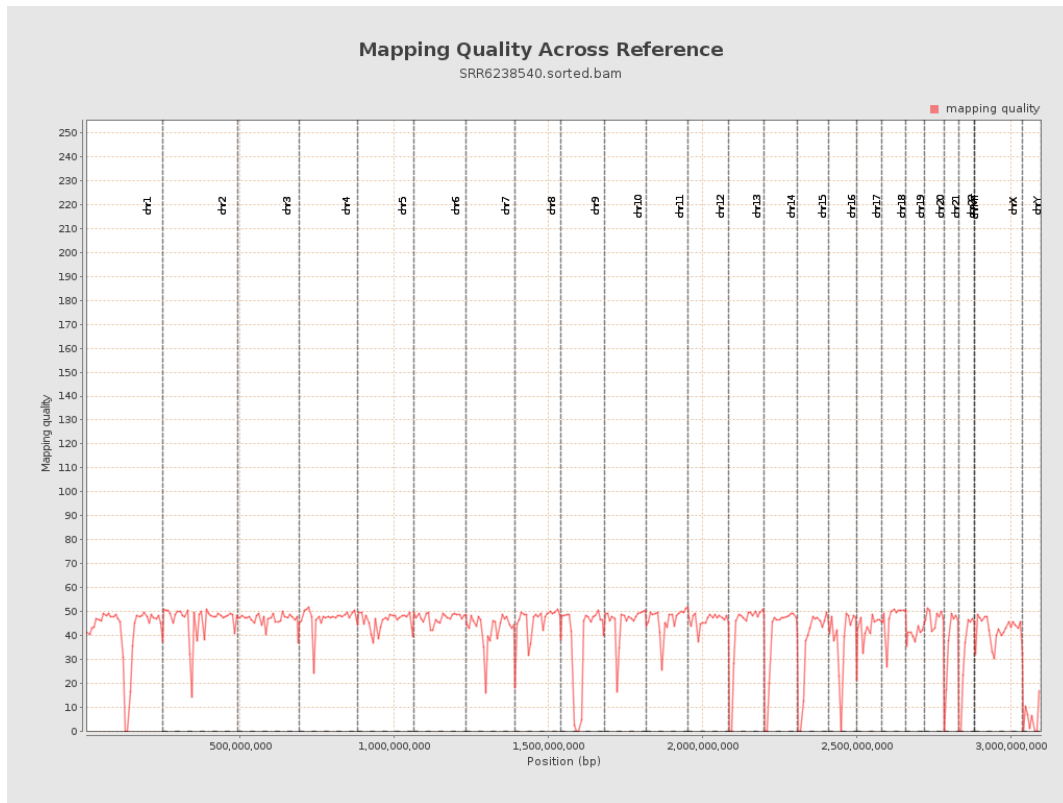
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

