

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:04:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238314.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_SRR6238314 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238314.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:04:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238314.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,286,916
Mapped reads	2,787,323 / 84.8%
Unmapped reads	499,593 / 15.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,556 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	163,681 / 4.98%
Duplication rate	4.36%
Clipped reads	1,614,586 / 49.12%

2.2. ACGT Content

Number/percentage of A's	48,135,633 / 27.05%
Number/percentage of C's	33,154,747 / 18.63%
Number/percentage of T's	55,547,167 / 31.21%
Number/percentage of G's	41,076,595 / 23.08%
Number/percentage of N's	46,374 / 0.03%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0575

Standard Deviation	0.5385
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2.4. Mapping Quality

Mean Mapping Quality	43.64
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2.5. Mismatches and indels

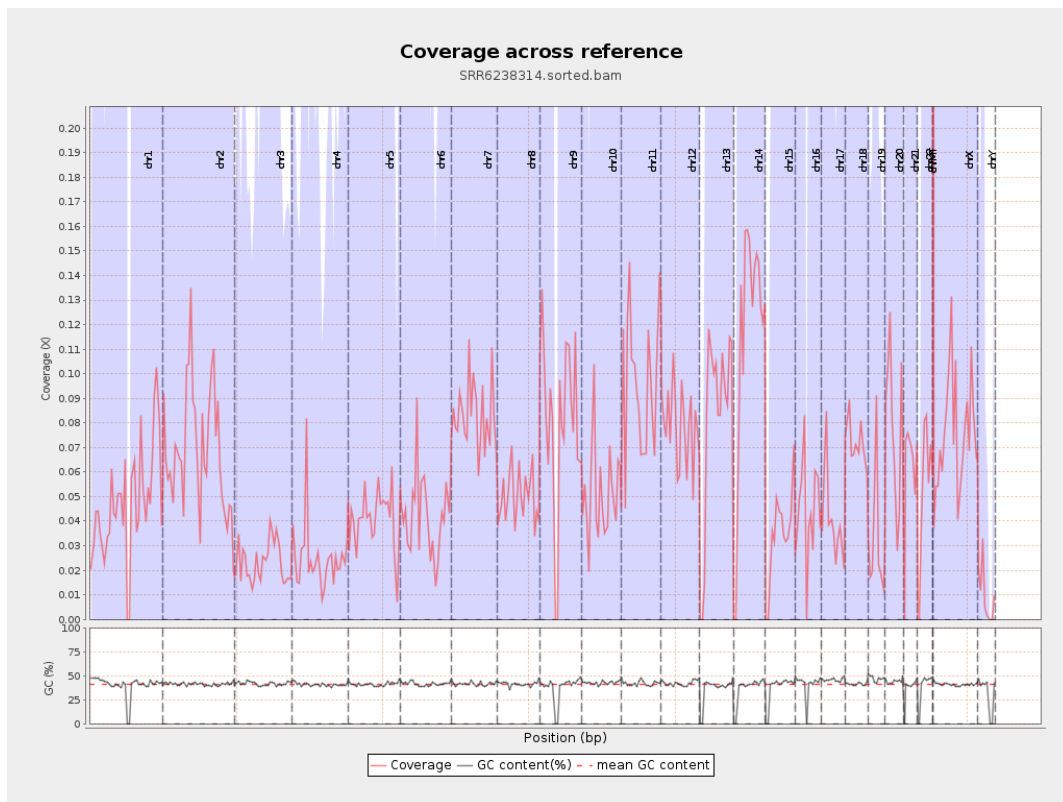
General error rate	0.93%
Mismatches	1,632,314
Insertions	13,915
Mapped reads with at least one insertion	0.49%
Deletions	62,828
Mapped reads with at least one deletion	2.23%
Homopolymer indels	43.62%

2.6. Chromosome stats

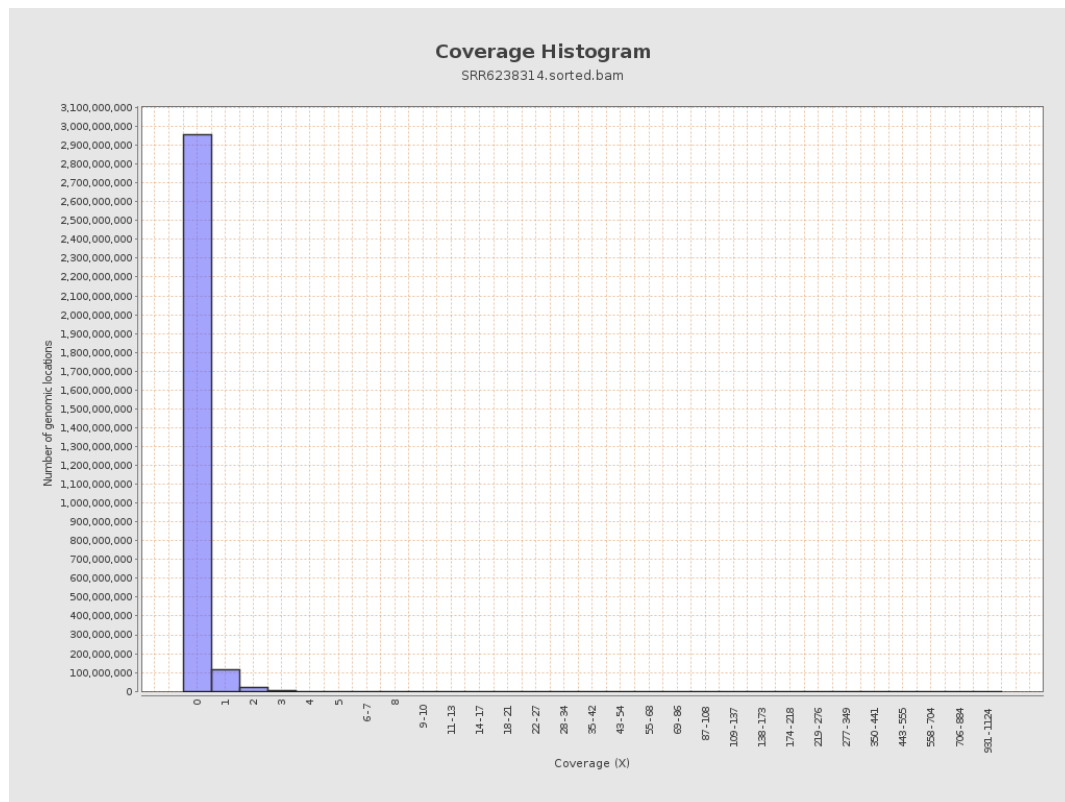
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11708790	0.047	0.8359
chr2	243199373	16916165	0.0696	0.6935
chr3	198022430	4616589	0.0233	0.1844
chr4	191154276	4708231	0.0246	0.2588
chr5	180915260	7450511	0.0412	0.2487
chr6	171115067	7152373	0.0418	0.4226
chr7	159138663	13154758	0.0827	0.7511

chr8	146364022	7344835	0.0502	0.7354
chr9	141213431	11353375	0.0804	0.5399
chr10	135534747	6865422	0.0507	0.4648
chr11	135006516	12866795	0.0953	0.5453
chr12	133851895	10550494	0.0788	0.354
chr13	115169878	9501931	0.0825	0.3482
chr14	107349540	12504298	0.1165	0.4673
chr15	102531392	3512375	0.0343	0.2311
chr16	90354753	3930372	0.0435	0.3308
chr17	81195210	3330408	0.041	0.3604
chr18	78077248	5663048	0.0725	1.1877
chr19	59128983	1953957	0.033	0.5787
chr20	63025520	5010348	0.0795	0.3748
chr21	48129895	2963883	0.0616	0.3519
chr22	51304566	2662042	0.0519	0.2764
chrMT	16571	21863	1.3194	1.5591
chrX	155270560	11751733	0.0757	0.4565
chrY	59373566	571184	0.0096	0.2191

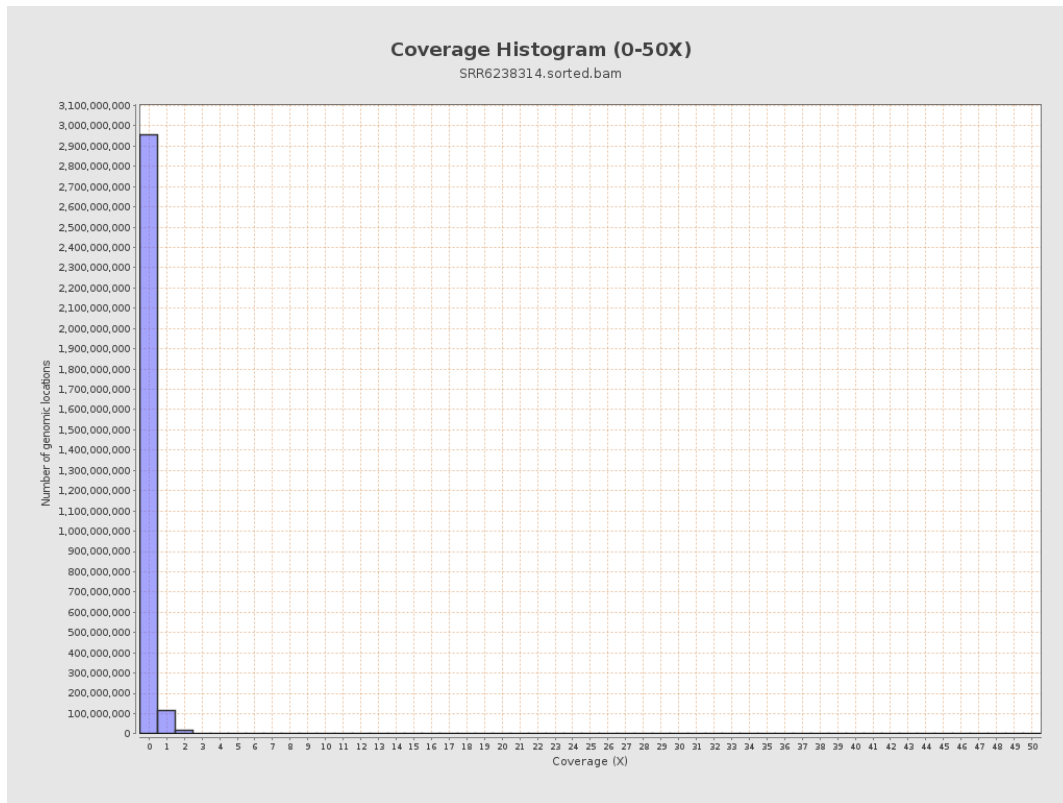
3. Results : Coverage across reference



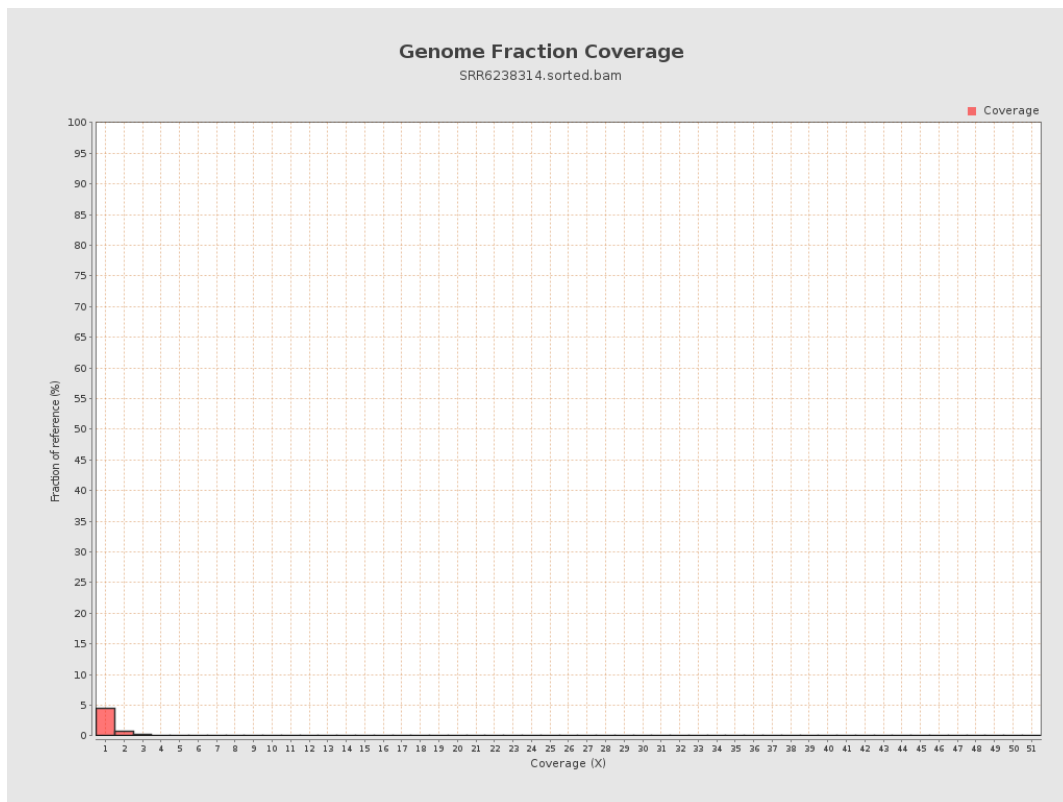
4. Results : Coverage Histogram



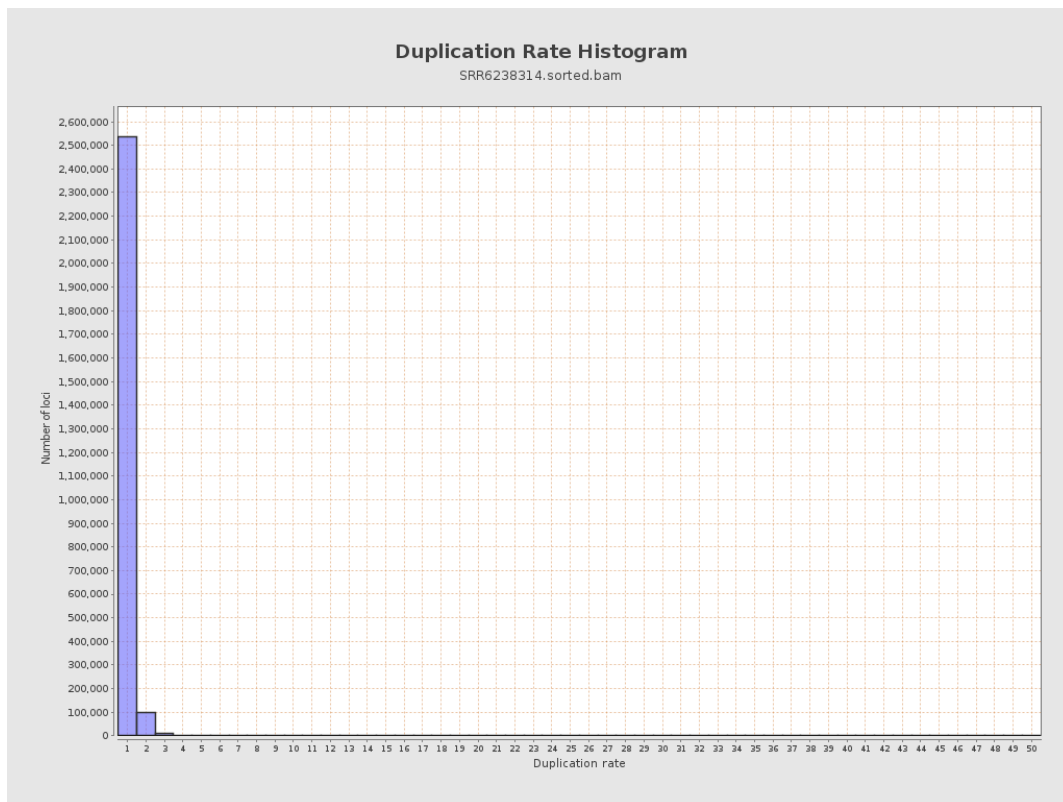
5. Results : Coverage Histogram (0-50X)



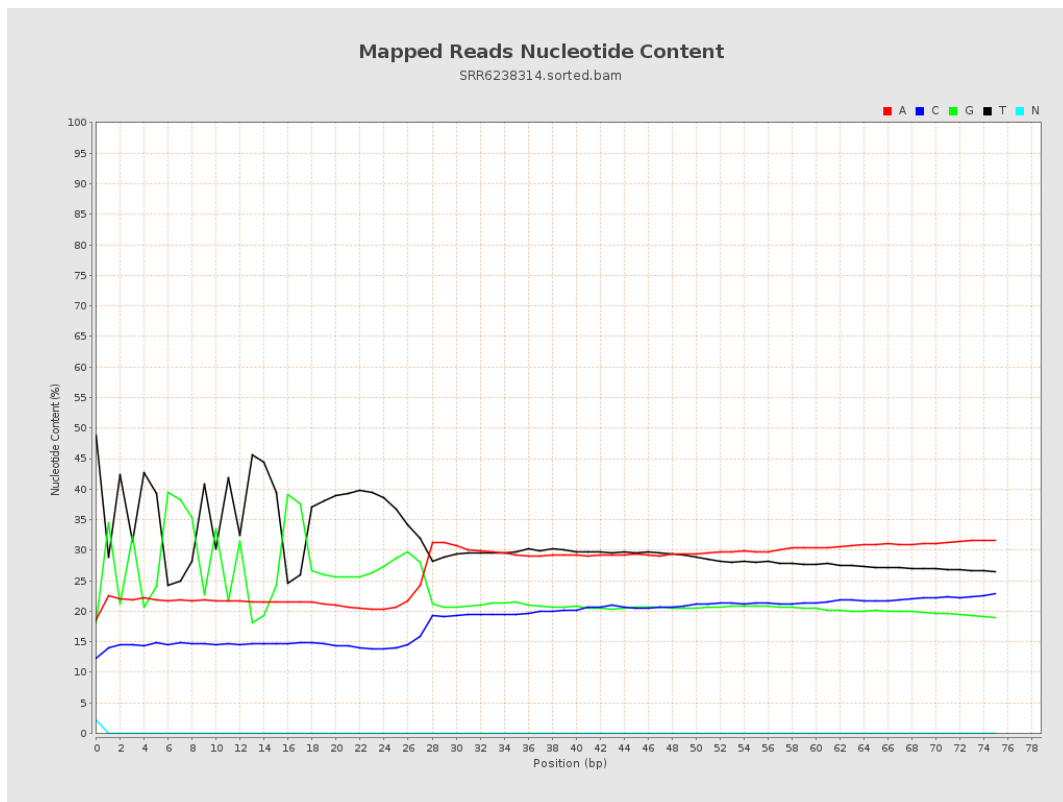
6. Results : Genome Fraction Coverage



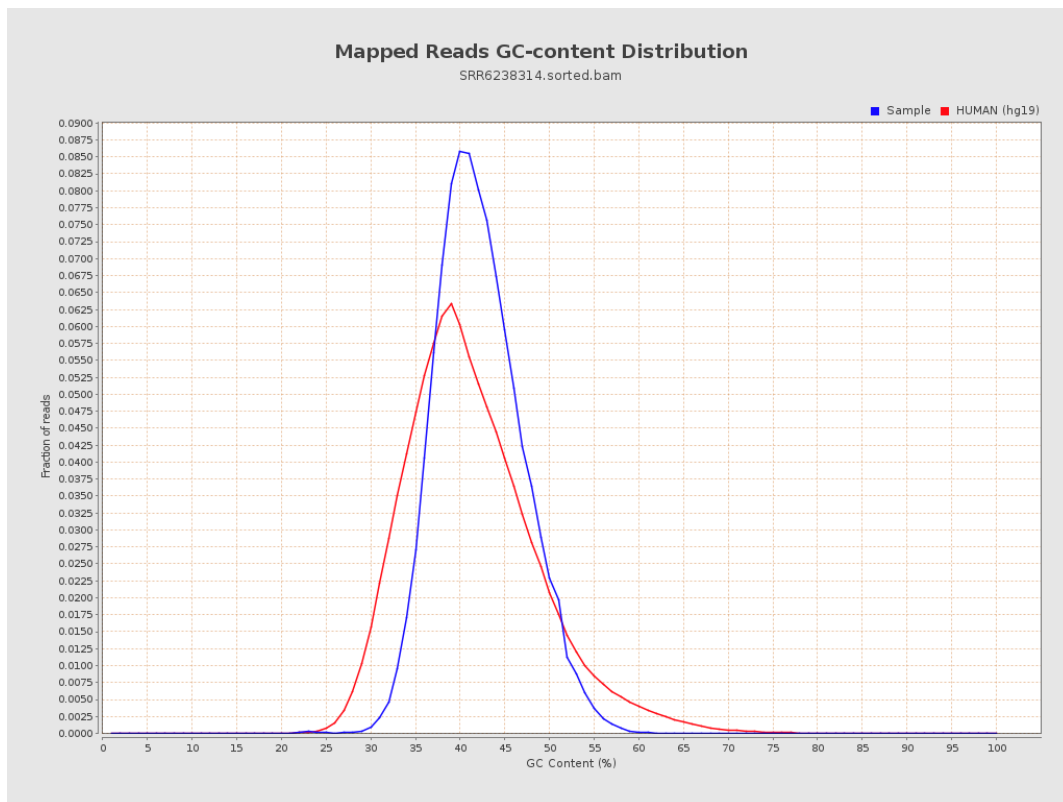
7. Results : Duplication Rate Histogram



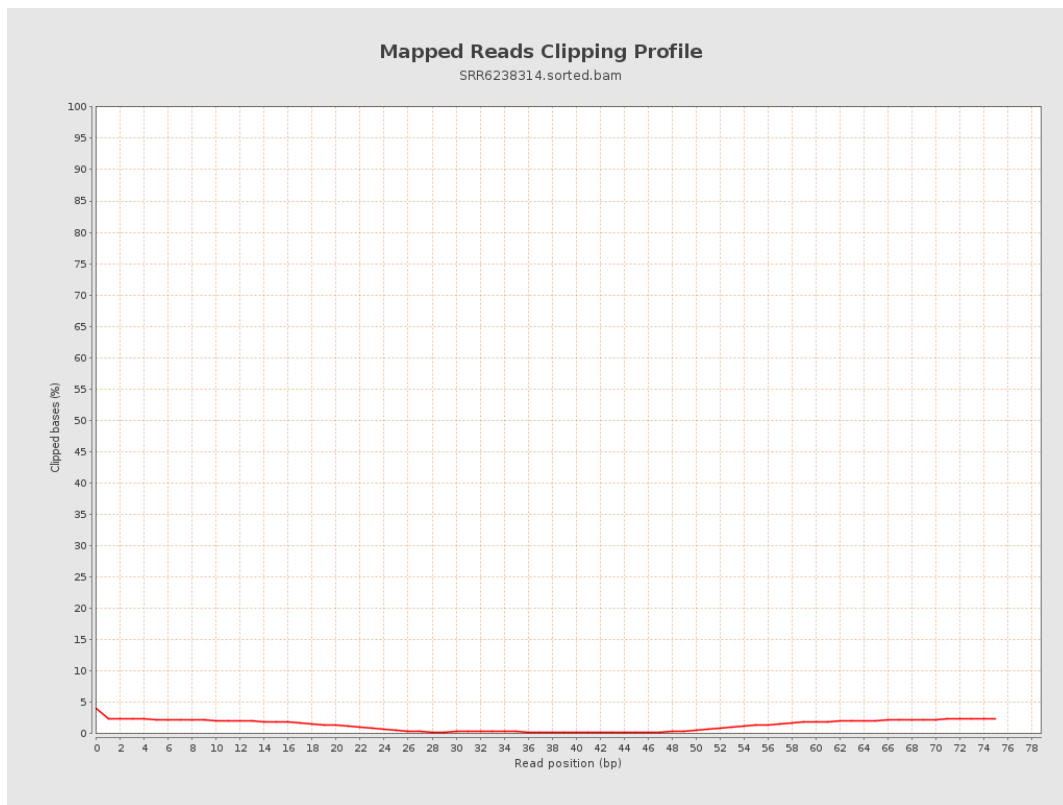
8. Results : Mapped Reads Nucleotide Content



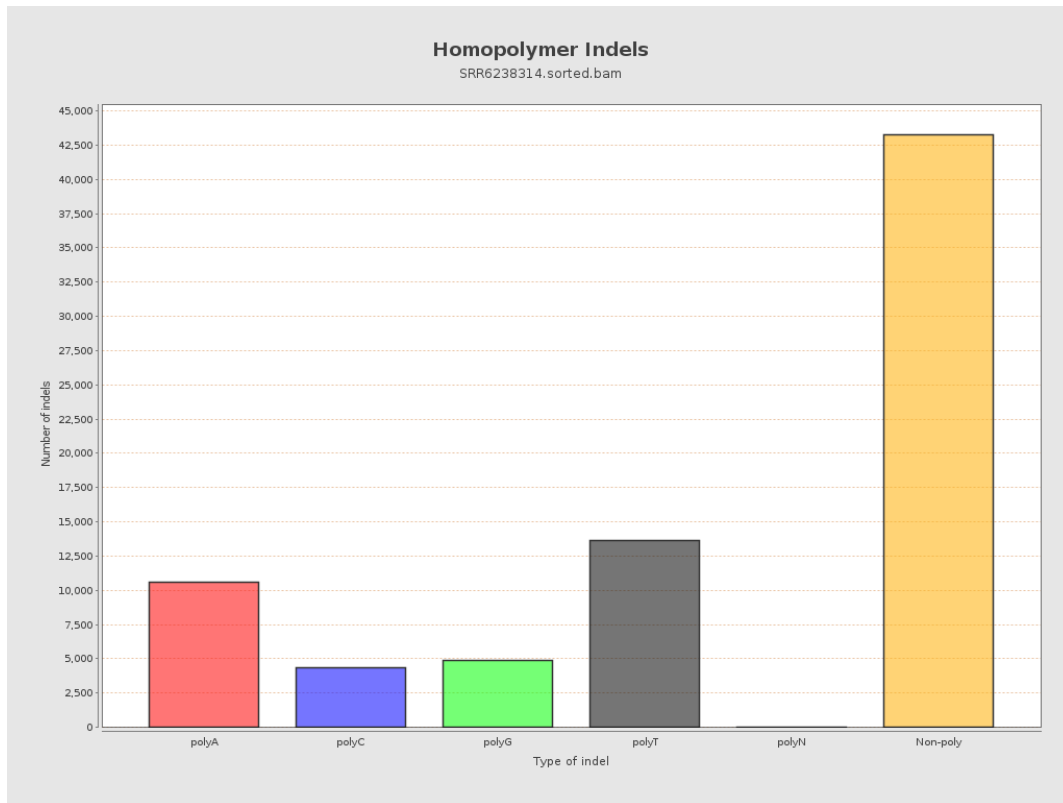
9. Results : Mapped Reads GC-content Distribution



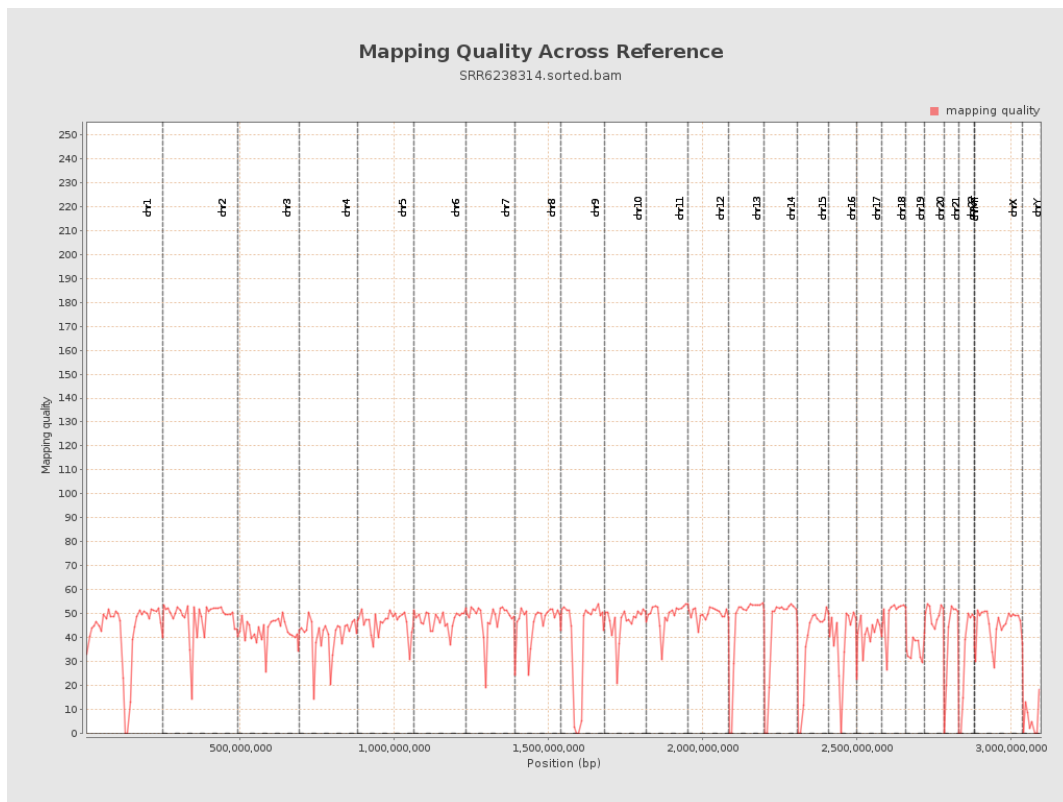
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

