

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:07:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238295.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_SRR6238295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238295.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:07:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,728,981
Mapped reads	2,487,918 / 91.17%
Unmapped reads	241,063 / 8.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,209 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	96,309 / 3.53%
Duplication rate	2.85%
Clipped reads	1,357,857 / 49.76%

2.2. ACGT Content

Number/percentage of A's	42,556,647 / 26.43%
Number/percentage of C's	30,003,638 / 18.64%
Number/percentage of T's	49,971,420 / 31.04%
Number/percentage of G's	38,434,306 / 23.87%
Number/percentage of N's	36,238 / 0.02%
GC Percentage	42.51%

2.3. Coverage

Mean	0.052

Standard Deviation	0.4226
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2.4. Mapping Quality

Mean Mapping Quality	44.28
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2.5. Mismatches and indels

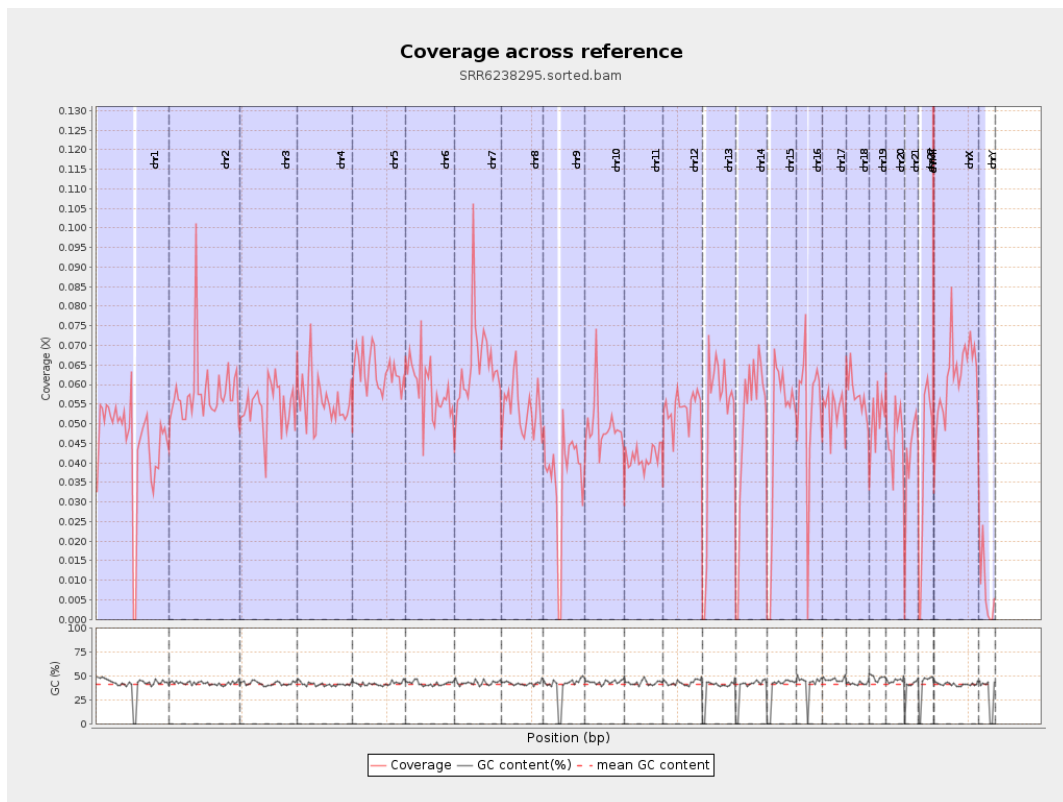
General error rate	0.86%
Mismatches	1,355,953
Insertions	12,426
Mapped reads with at least one insertion	0.5%
Deletions	49,980
Mapped reads with at least one deletion	1.99%
Homopolymer indels	44.82%

2.6. Chromosome stats

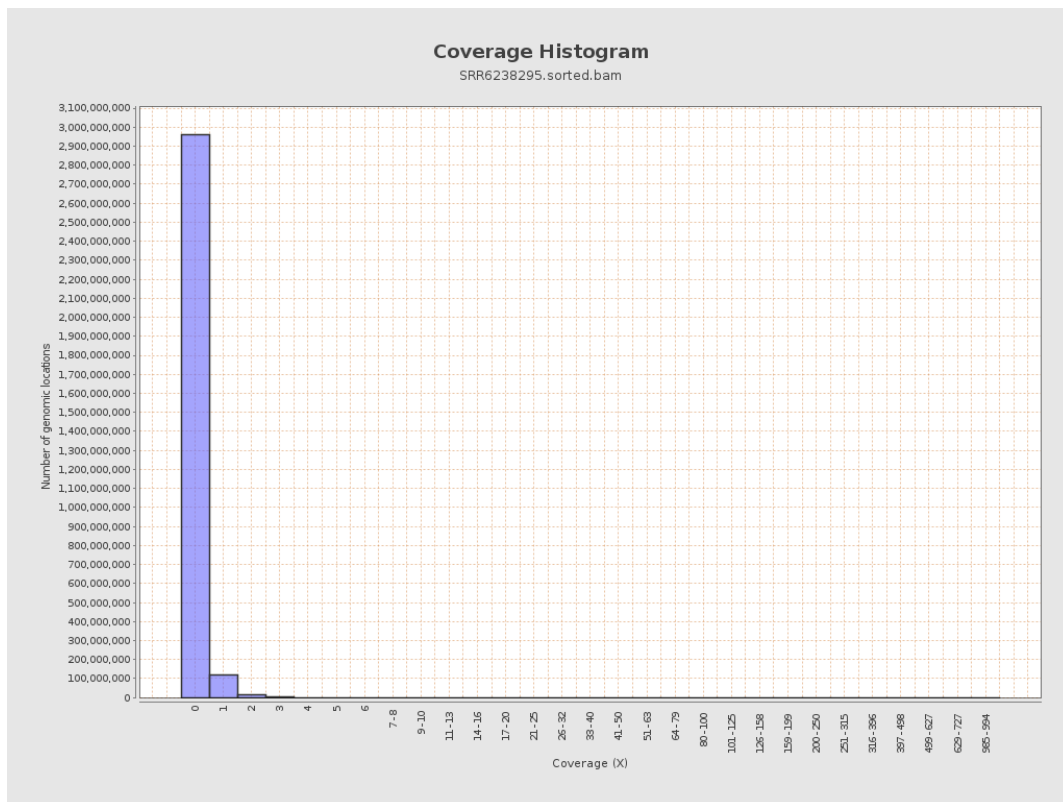
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11227703	0.045	0.6096
chr2	243199373	14112635	0.058	0.6032
chr3	198022430	10769774	0.0544	0.2632
chr4	191154276	10634143	0.0556	0.2999
chr5	180915260	11440355	0.0632	0.2876
chr6	171115067	10043665	0.0587	0.3516
chr7	159138663	10459608	0.0657	0.6931

chr8	146364022	7895413	0.0539	0.4961
chr9	141213431	5089756	0.036	0.3886
chr10	135534747	6681972	0.0493	0.3881
chr11	135006516	5570529	0.0413	0.3301
chr12	133851895	7215769	0.0539	0.2693
chr13	115169878	5837467	0.0507	0.255
chr14	107349540	5423189	0.0505	0.2919
chr15	102531392	4970448	0.0485	0.2696
chr16	90354753	4906499	0.0543	0.3001
chr17	81195210	4330168	0.0533	0.2967
chr18	78077248	4496123	0.0576	0.7531
chr19	59128983	3042929	0.0515	0.4557
chr20	63025520	2918068	0.0463	0.2631
chr21	48129895	1982026	0.0412	0.2656
chr22	51304566	2013367	0.0392	0.2253
chrMT	16571	6815	0.4113	0.7741
chrX	155270560	9572654	0.0617	0.3324
chrY	59373566	444508	0.0075	0.192

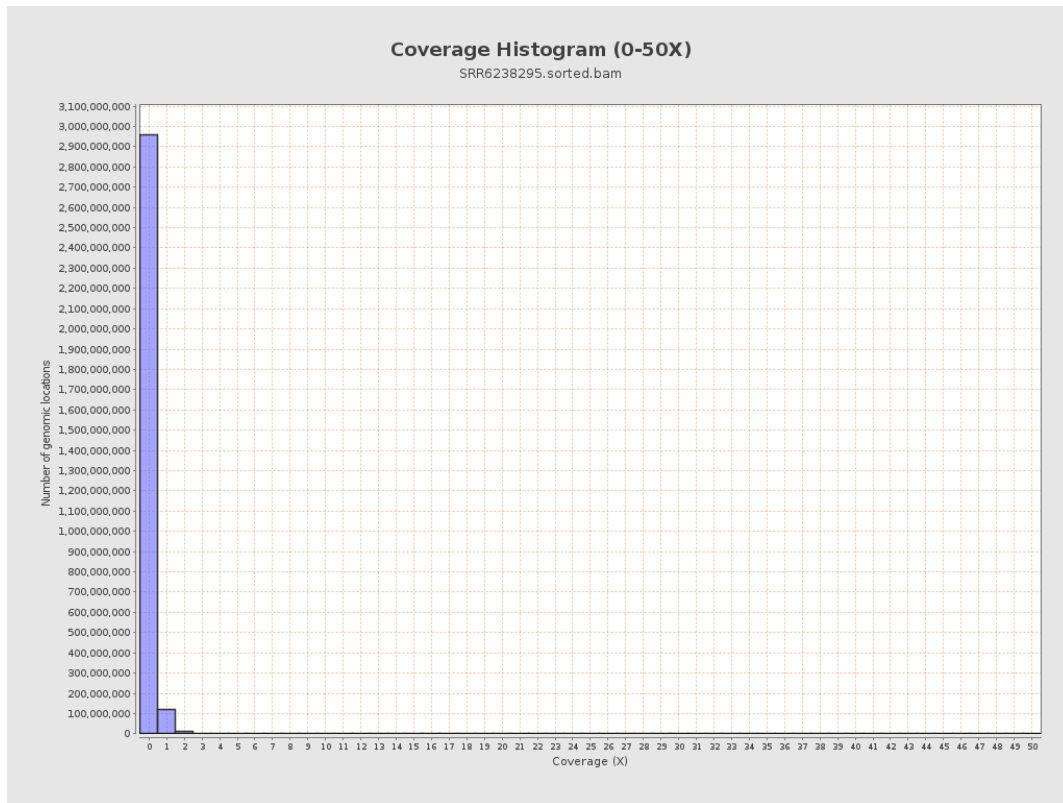
3. Results : Coverage across reference



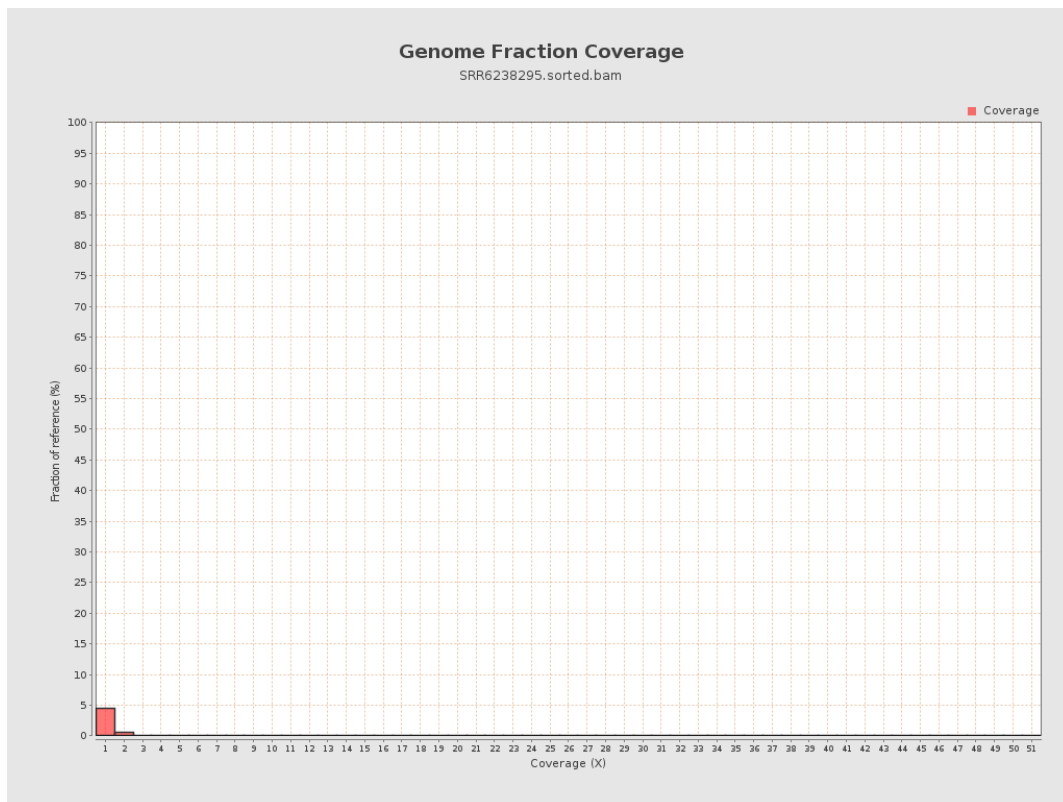
4. Results : Coverage Histogram



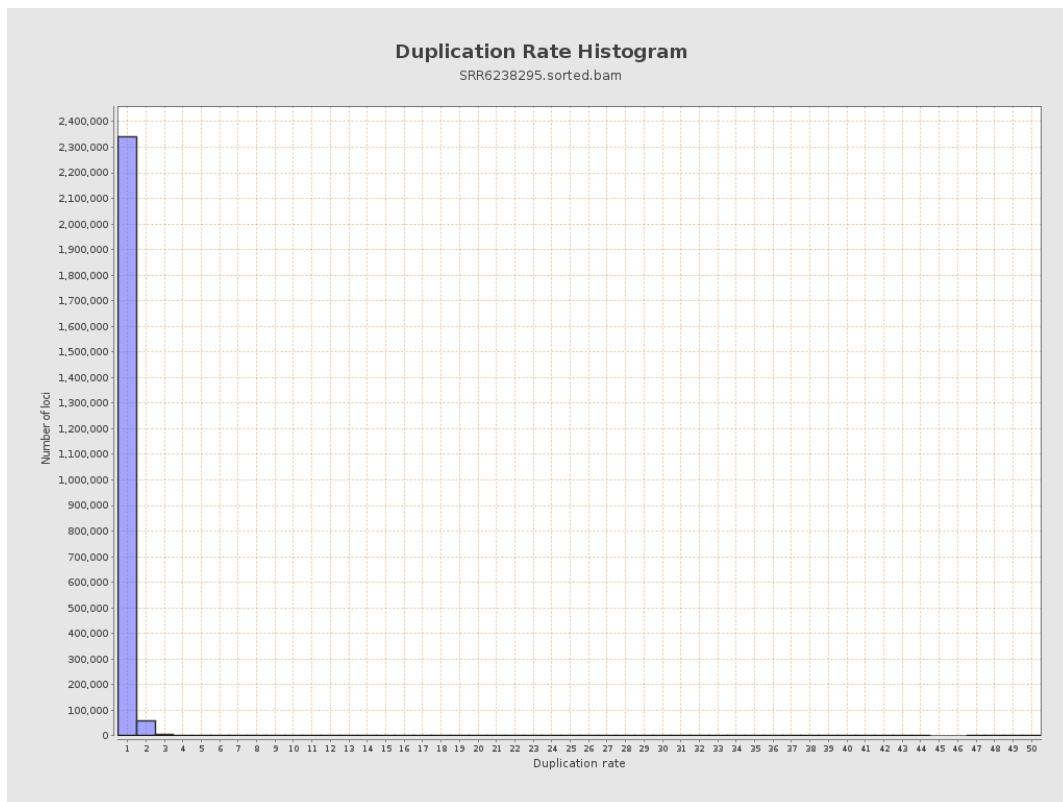
5. Results : Coverage Histogram (0-50X)



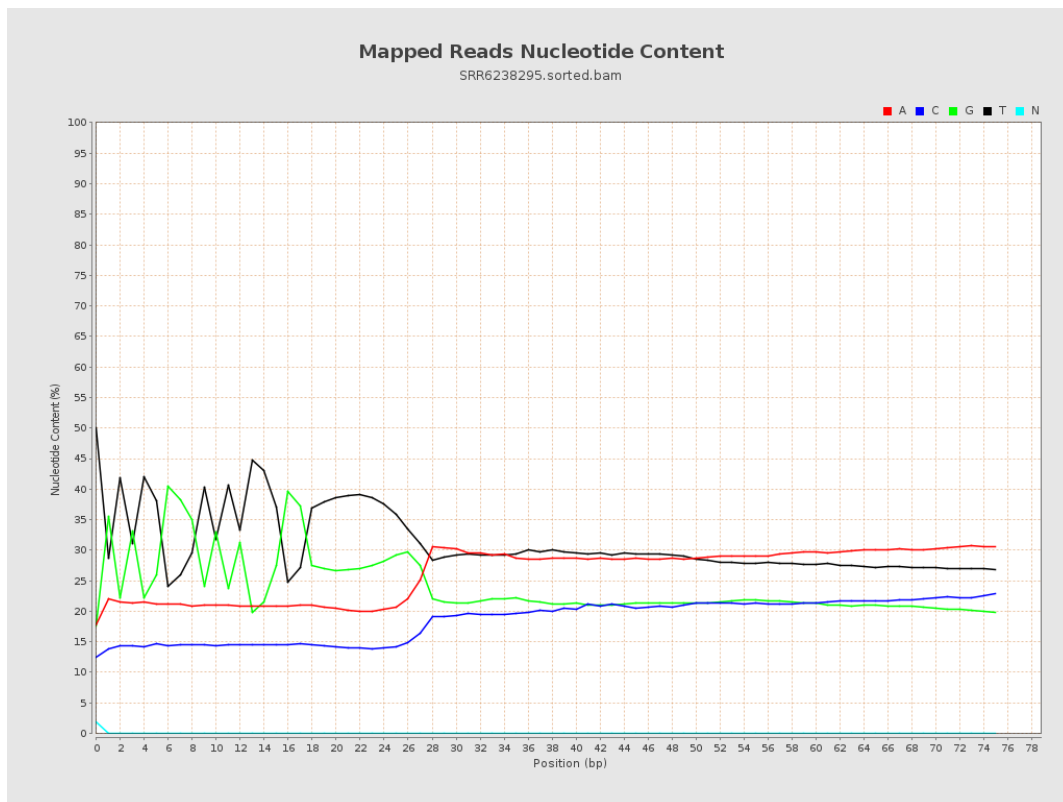
6. Results : Genome Fraction Coverage



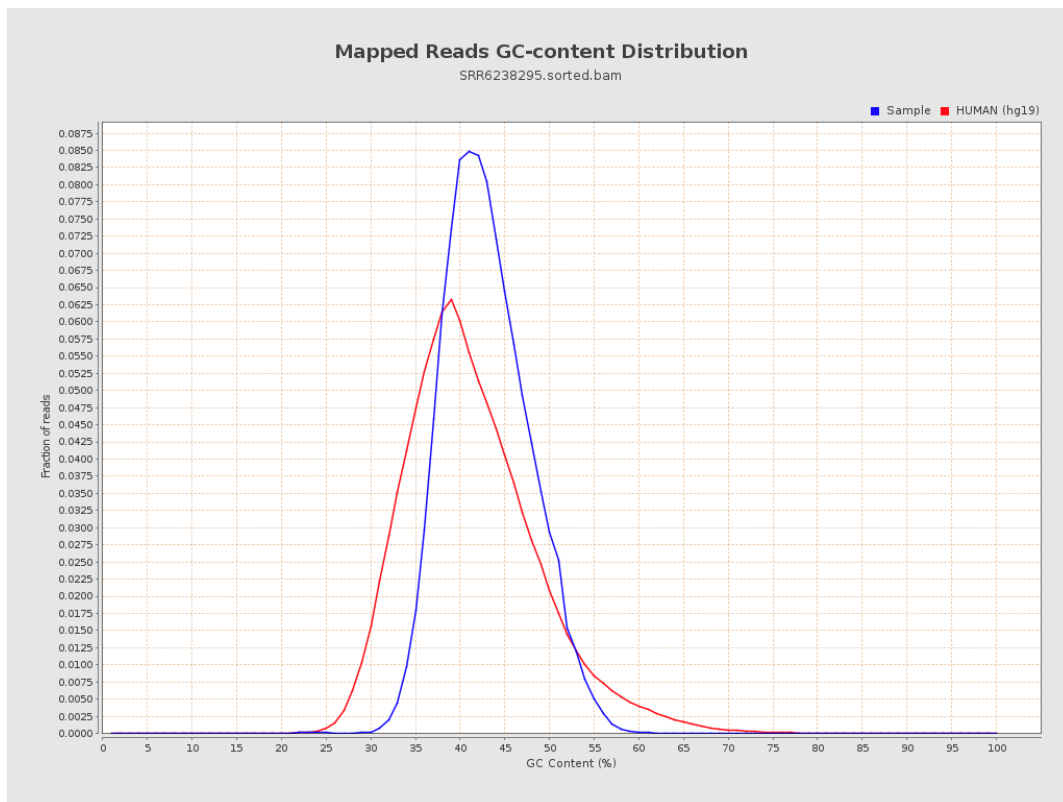
7. Results : Duplication Rate Histogram



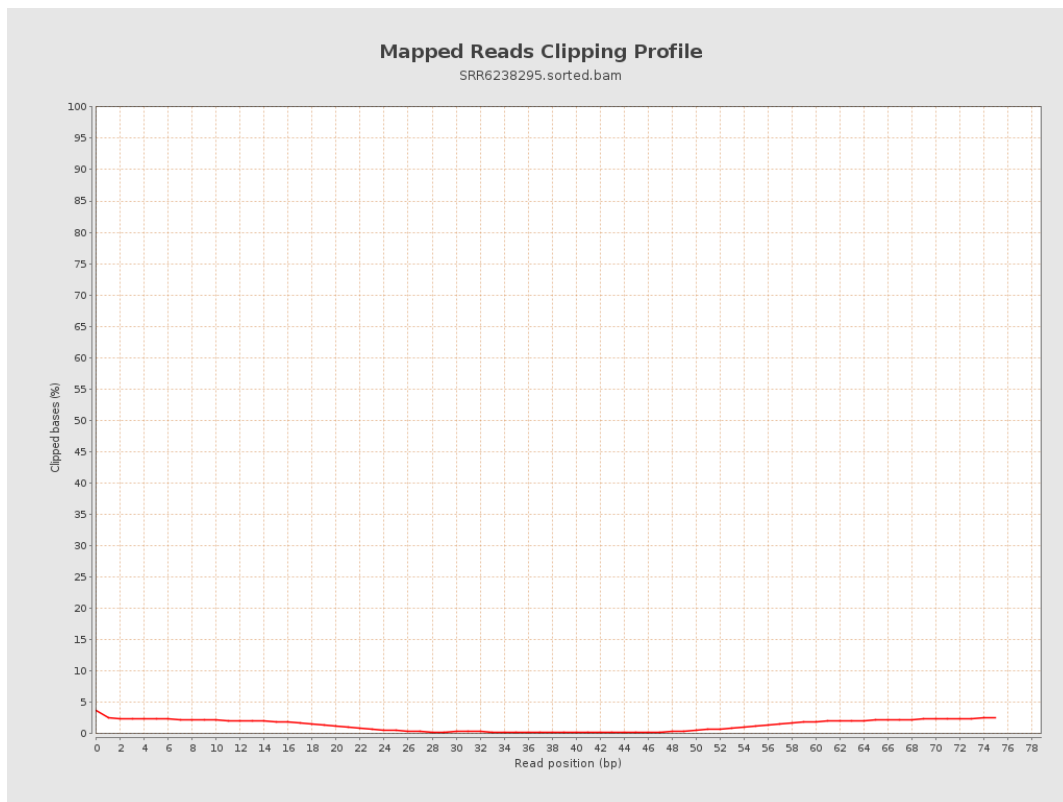
8. Results : Mapped Reads Nucleotide Content



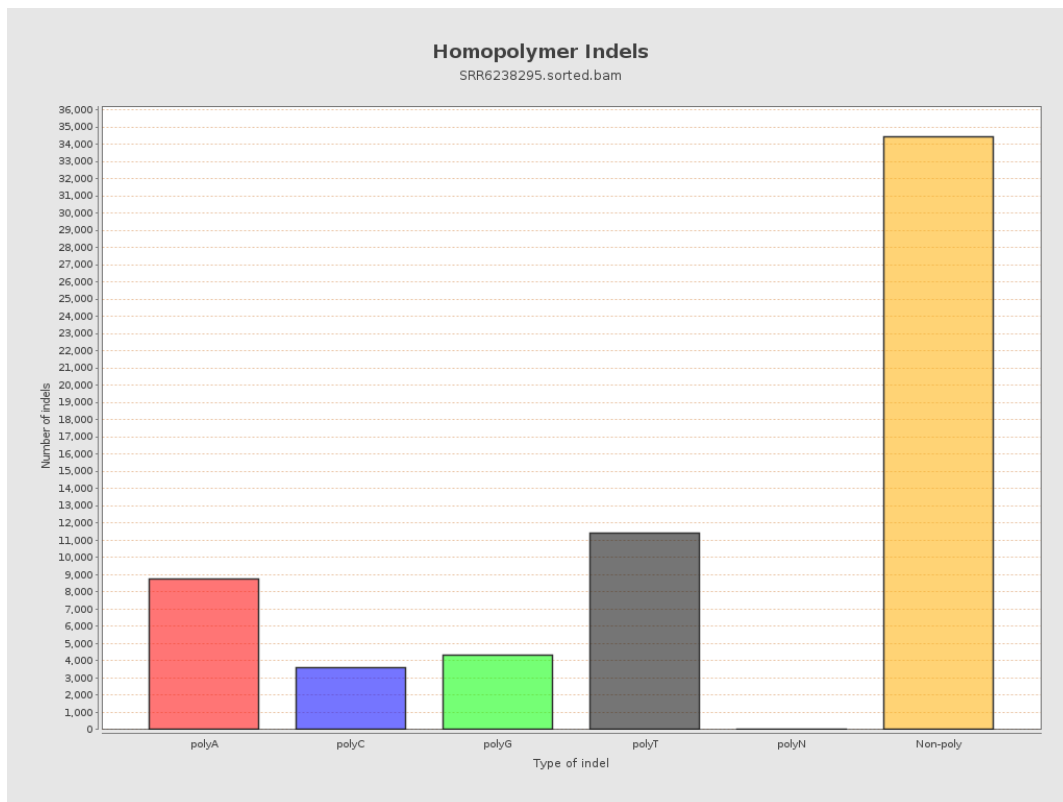
9. Results : Mapped Reads GC-content Distribution



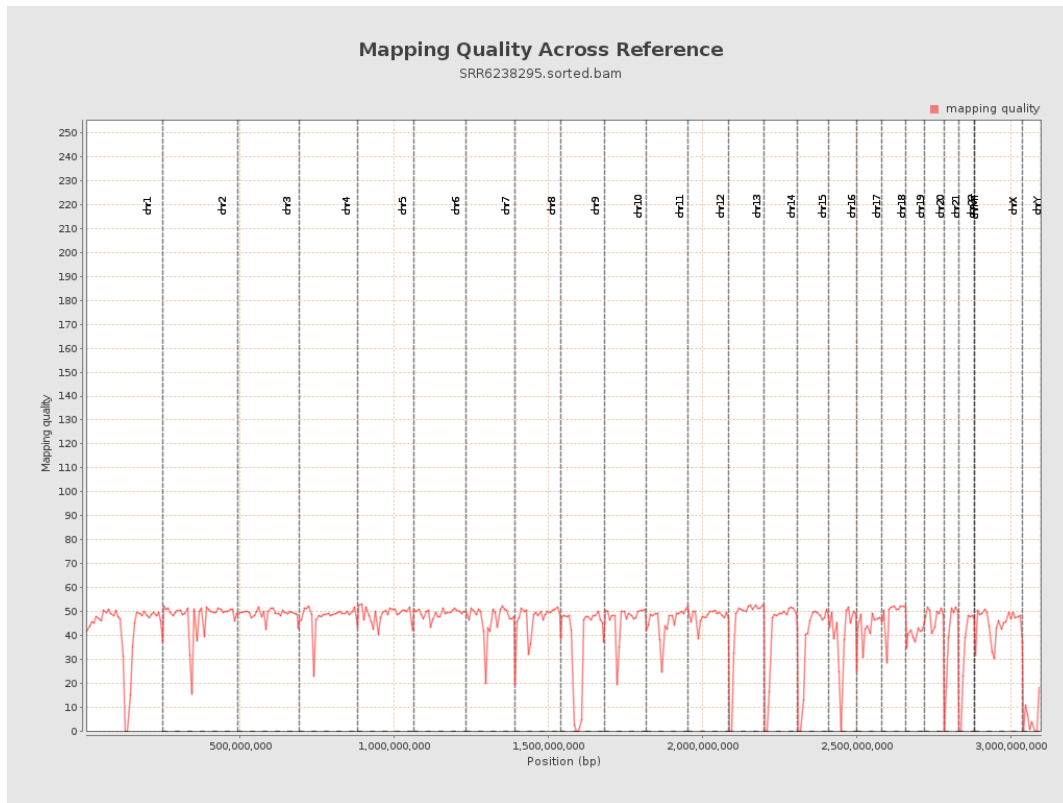
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

