

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:31:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237822.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_SRR6237822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237822.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:31:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,518,574
Mapped reads	2,309,920 / 91.72%
Unmapped reads	208,654 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,630 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	246,323 / 9.78%
Duplication rate	8.23%
Clipped reads	607,020 / 24.1%

2.2. ACGT Content

Number/percentage of A's	48,158,960 / 29.37%
Number/percentage of C's	31,397,056 / 19.15%
Number/percentage of T's	50,407,240 / 30.74%
Number/percentage of G's	33,717,505 / 20.56%
Number/percentage of N's	297,466 / 0.18%
GC Percentage	39.71%

2.3. Coverage

Mean	0.053

Standard Deviation	0.7656
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2.4. Mapping Quality

Mean Mapping Quality	47.02
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2.5. Mismatches and indels

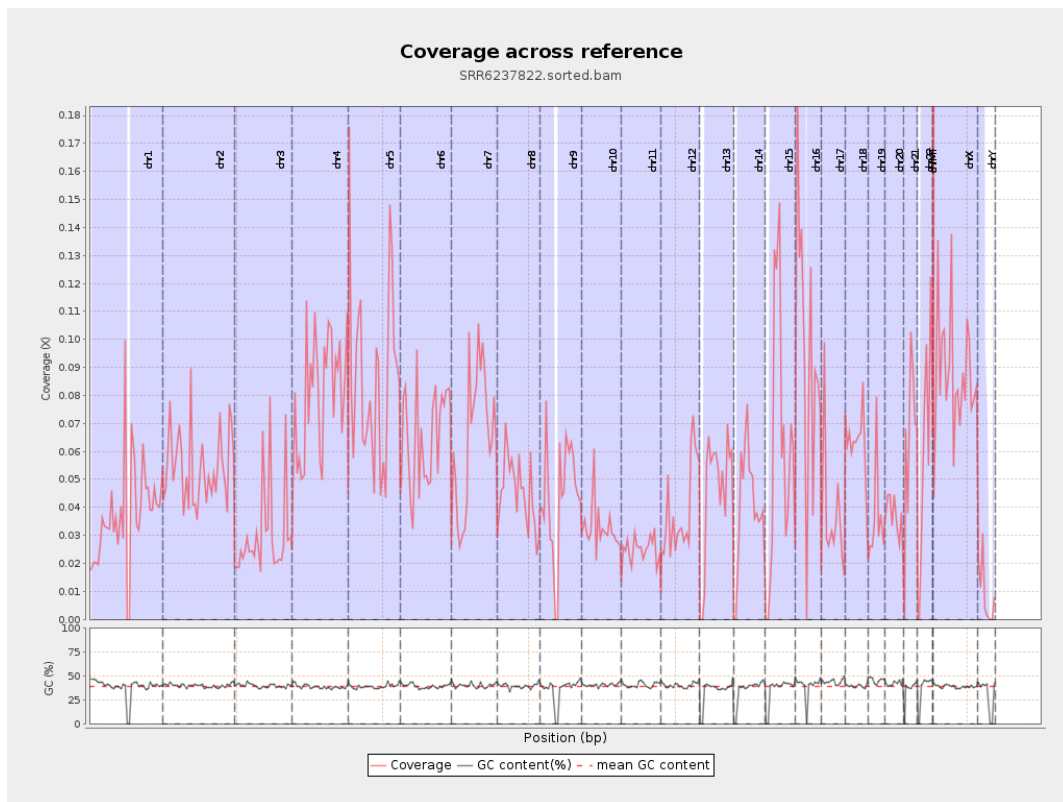
General error rate	0.88%
Mismatches	1,423,857
Insertions	12,366
Mapped reads with at least one insertion	0.53%
Deletions	47,274
Mapped reads with at least one deletion	2.02%
Homopolymer indels	46.01%

2.6. Chromosome stats

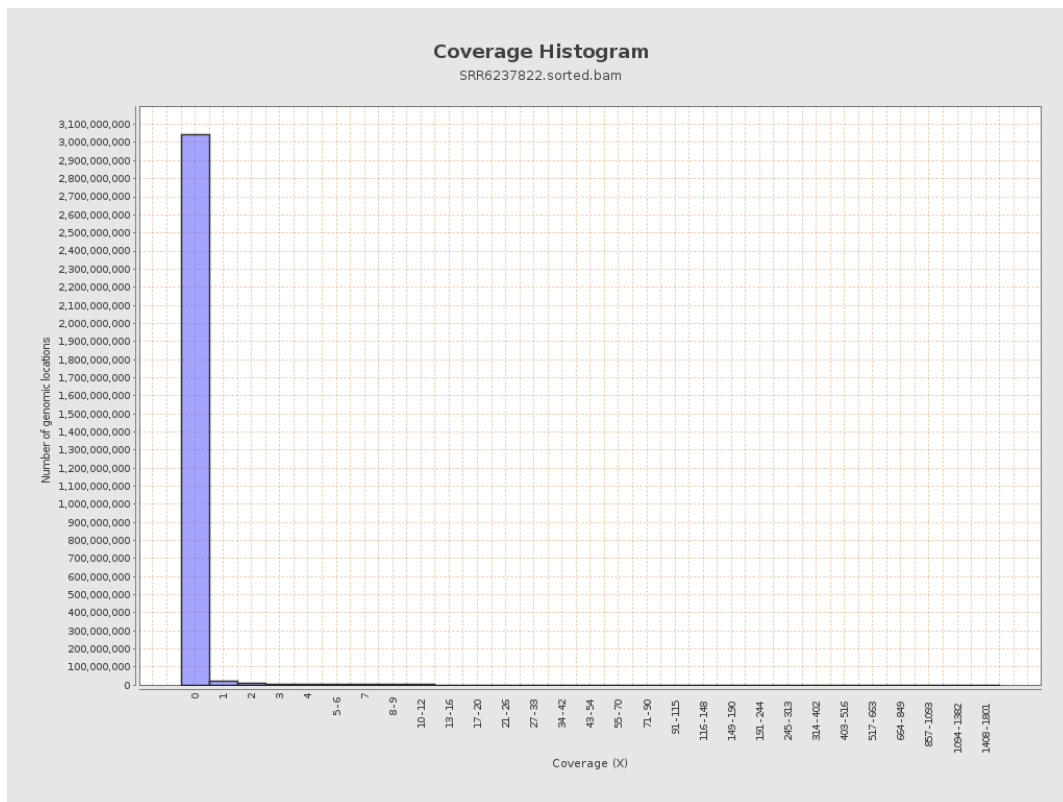
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9325484	0.0374	1.4271
chr2	243199373	13264786	0.0545	0.6824
chr3	198022430	5976245	0.0302	0.4293
chr4	191154276	15450356	0.0808	0.7634
chr5	180915260	15596344	0.0862	0.7475
chr6	171115067	11150618	0.0652	0.6644
chr7	159138663	10370462	0.0652	0.8411

chr8	146364022	6684033	0.0457	0.8522
chr9	141213431	6198456	0.0439	0.6278
chr10	135534747	4405332	0.0325	0.5019
chr11	135006516	3396578	0.0252	0.4273
chr12	133851895	5215374	0.039	0.4917
chr13	115169878	5324620	0.0462	0.532
chr14	107349540	4427806	0.0412	0.5167
chr15	102531392	6106037	0.0596	0.643
chr16	90354753	8238922	0.0912	0.8077
chr17	81195210	3090250	0.0381	0.5156
chr18	78077248	4975017	0.0637	0.9925
chr19	59128983	2152776	0.0364	1.1908
chr20	63025520	2343742	0.0372	0.4849
chr21	48129895	3188244	0.0662	0.691
chr22	51304566	3064716	0.0597	0.6504
chrMT	16571	41057	2.4776	3.8495
chrX	155270560	13538831	0.0872	0.779
chrY	59373566	536041	0.009	0.2342

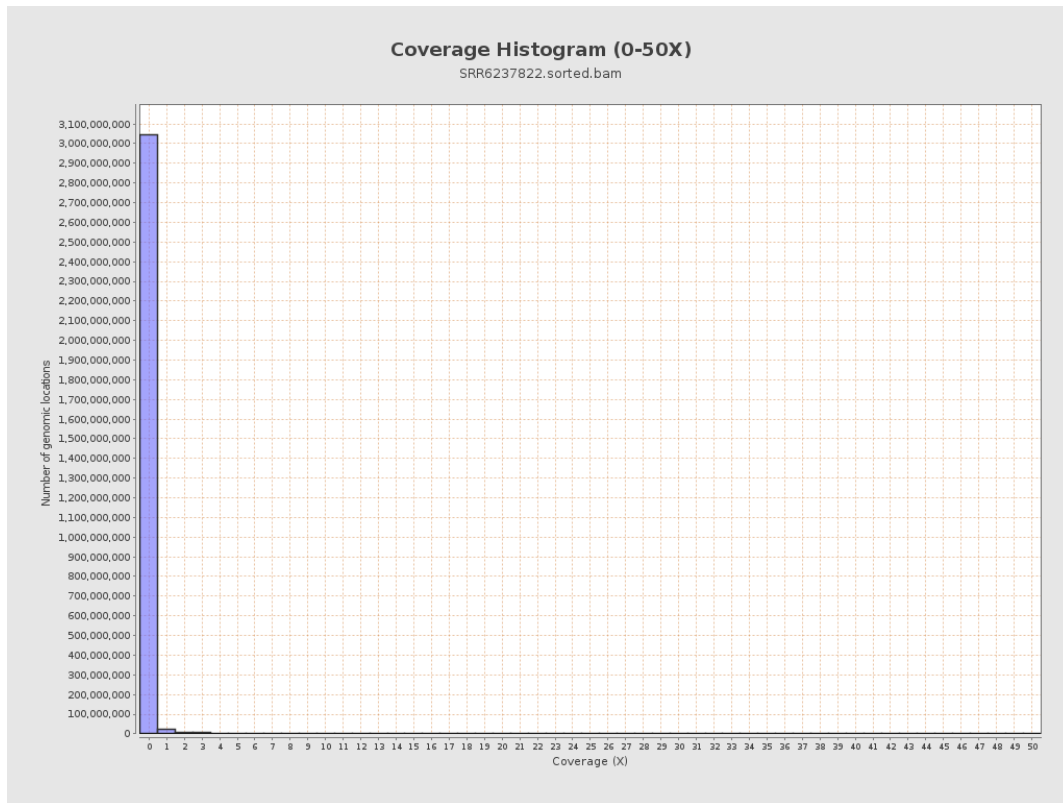
3. Results : Coverage across reference



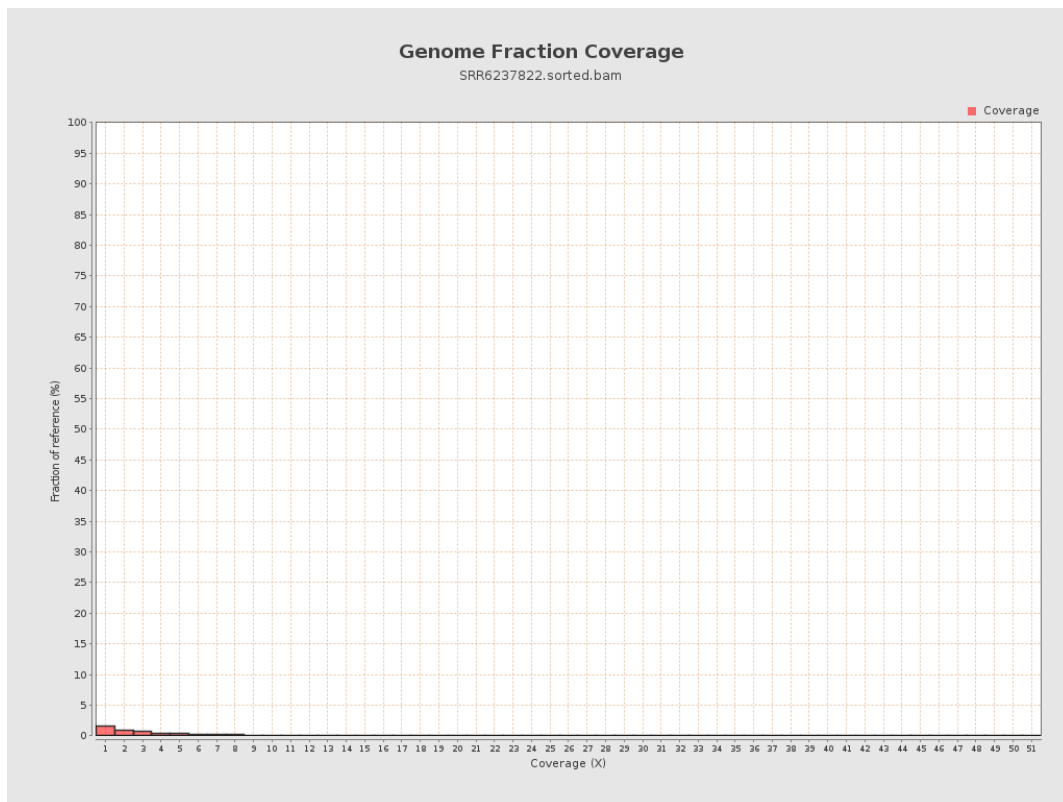
4. Results : Coverage Histogram



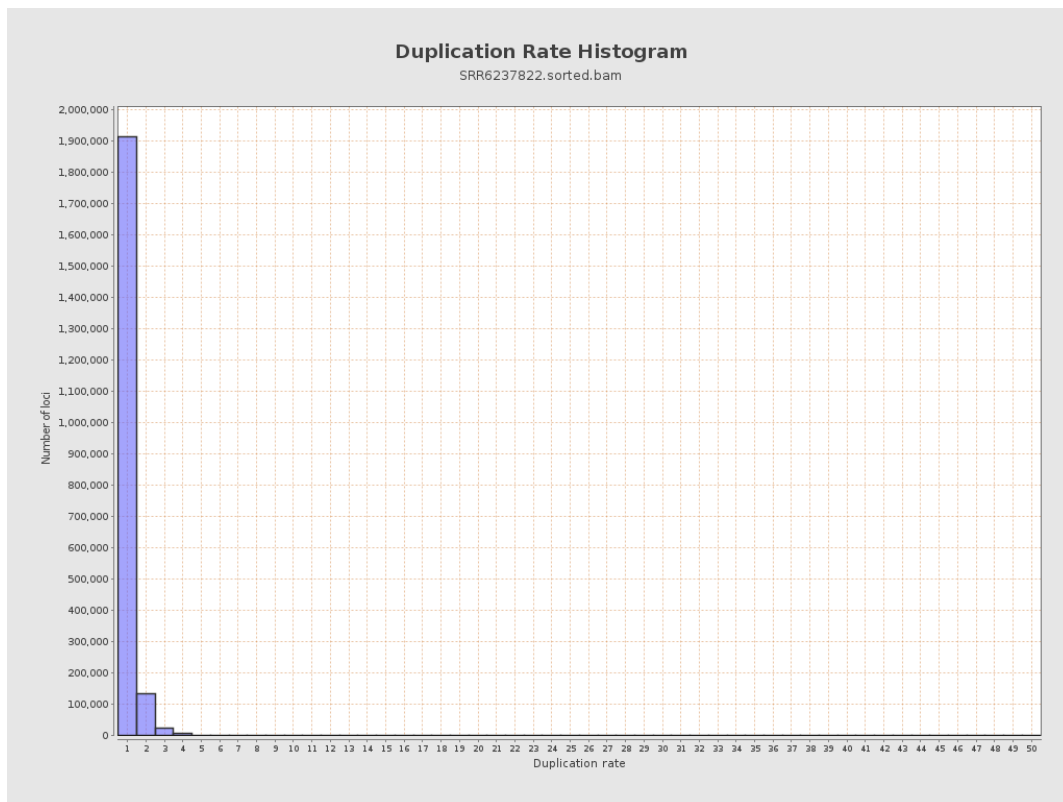
5. Results : Coverage Histogram (0-50X)



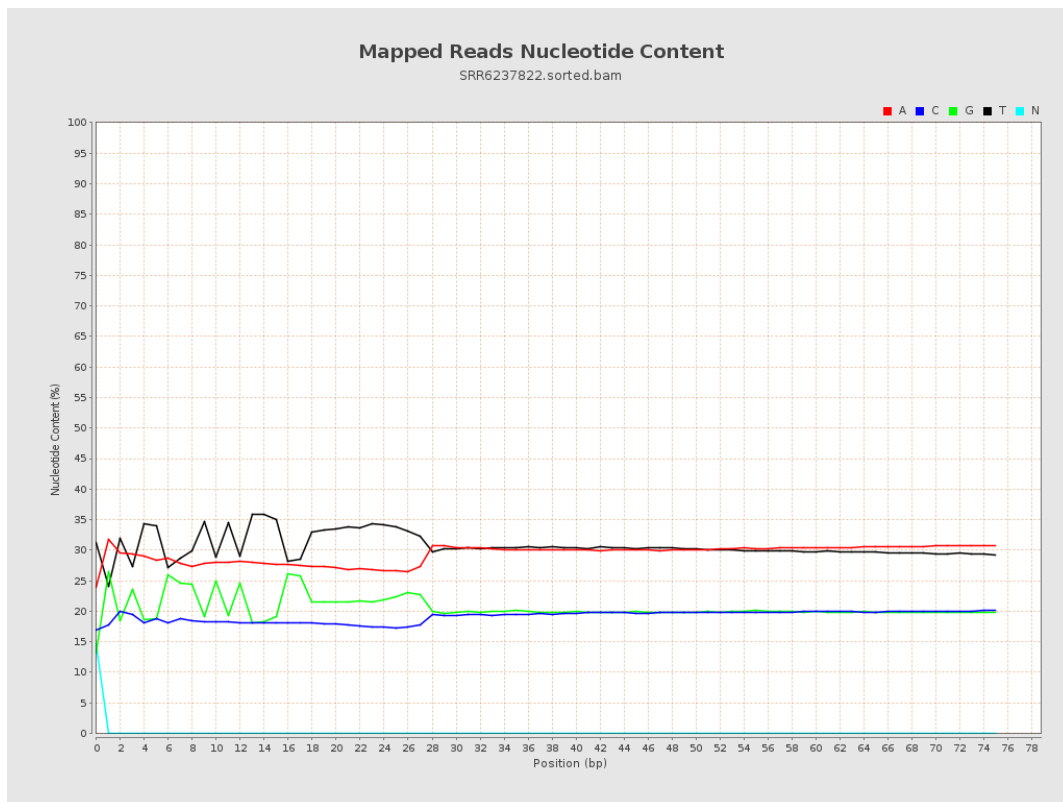
6. Results : Genome Fraction Coverage



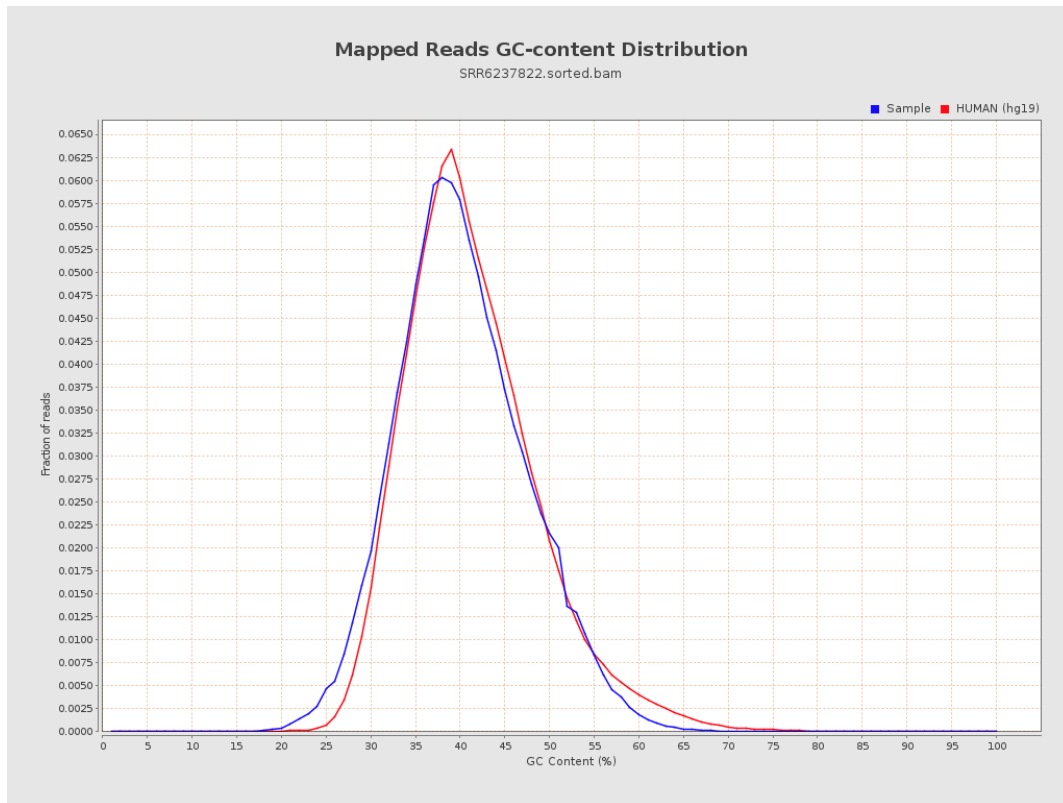
7. Results : Duplication Rate Histogram



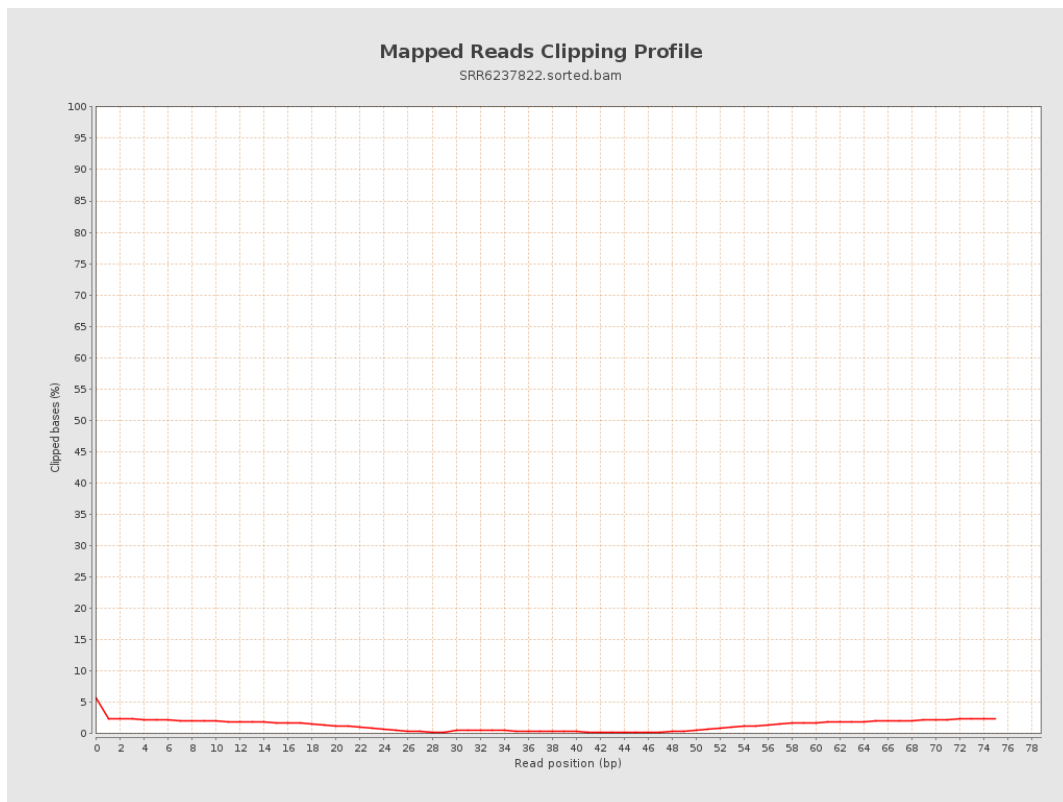
8. Results : Mapped Reads Nucleotide Content



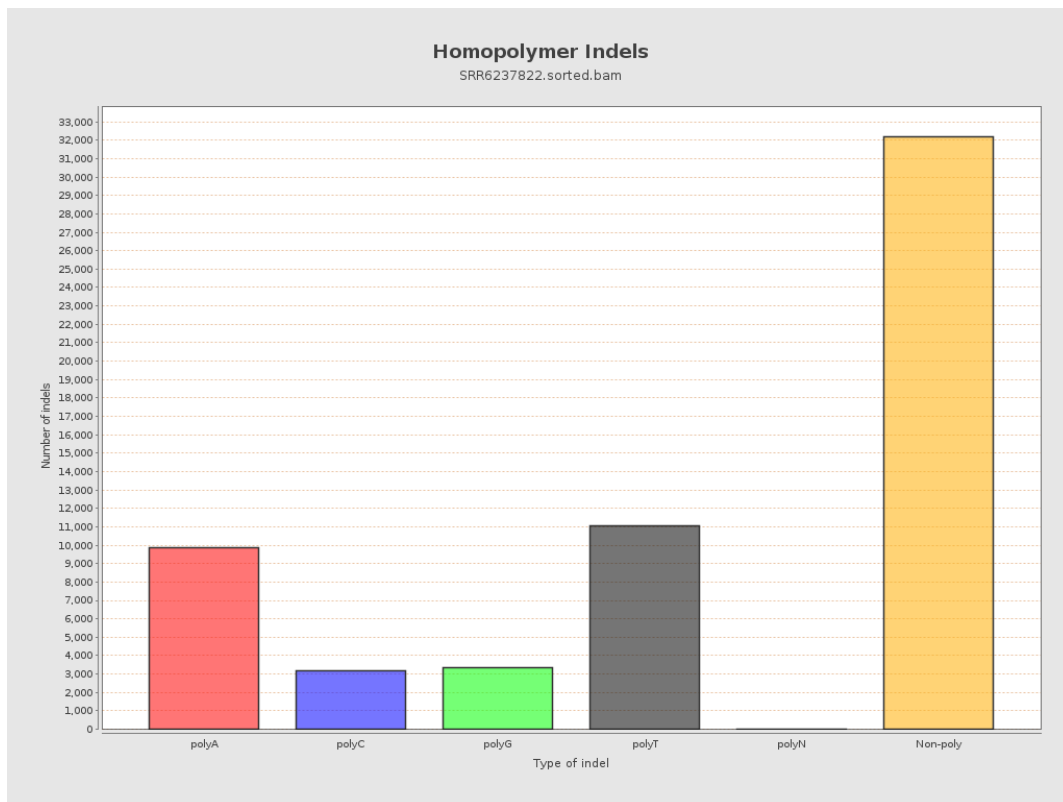
9. Results : Mapped Reads GC-content Distribution



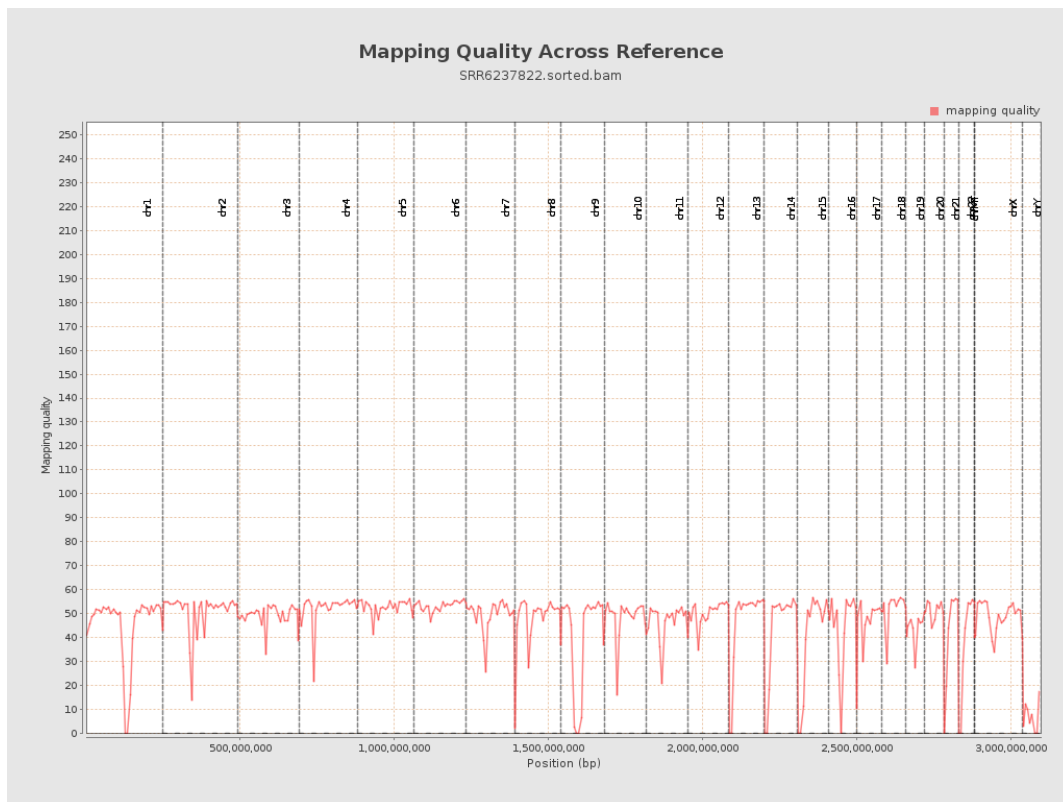
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

