

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:47:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237847.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_SRR6237847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237847.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:47:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,332,505
Mapped reads	2,971,238 / 89.16%
Unmapped reads	361,267 / 10.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,778 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	104,411 / 3.13%
Duplication rate	2.16%
Clipped reads	1,517,066 / 45.52%

2.2. ACGT Content

Number/percentage of A's	53,857,583 / 27.86%
Number/percentage of C's	38,170,251 / 19.74%
Number/percentage of T's	57,333,942 / 29.66%
Number/percentage of G's	43,781,151 / 22.65%
Number/percentage of N's	180,259 / 0.09%
GC Percentage	42.39%

2.3. Coverage

Mean	0.0625

Standard Deviation	0.6613
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2.4. Mapping Quality

Mean Mapping Quality	43.31
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2.5. Mismatches and indels

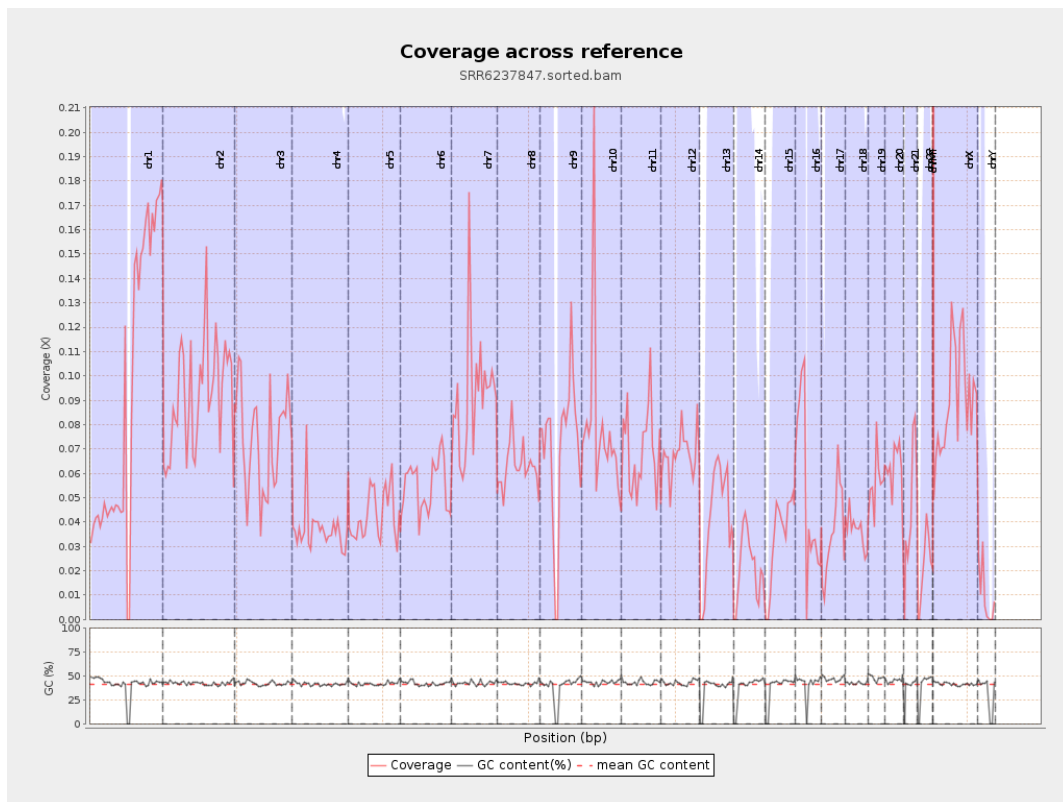
General error rate	0.84%
Mismatches	1,595,930
Insertions	15,773
Mapped reads with at least one insertion	0.53%
Deletions	61,580
Mapped reads with at least one deletion	2.05%
Homopolymer indels	43.91%

2.6. Chromosome stats

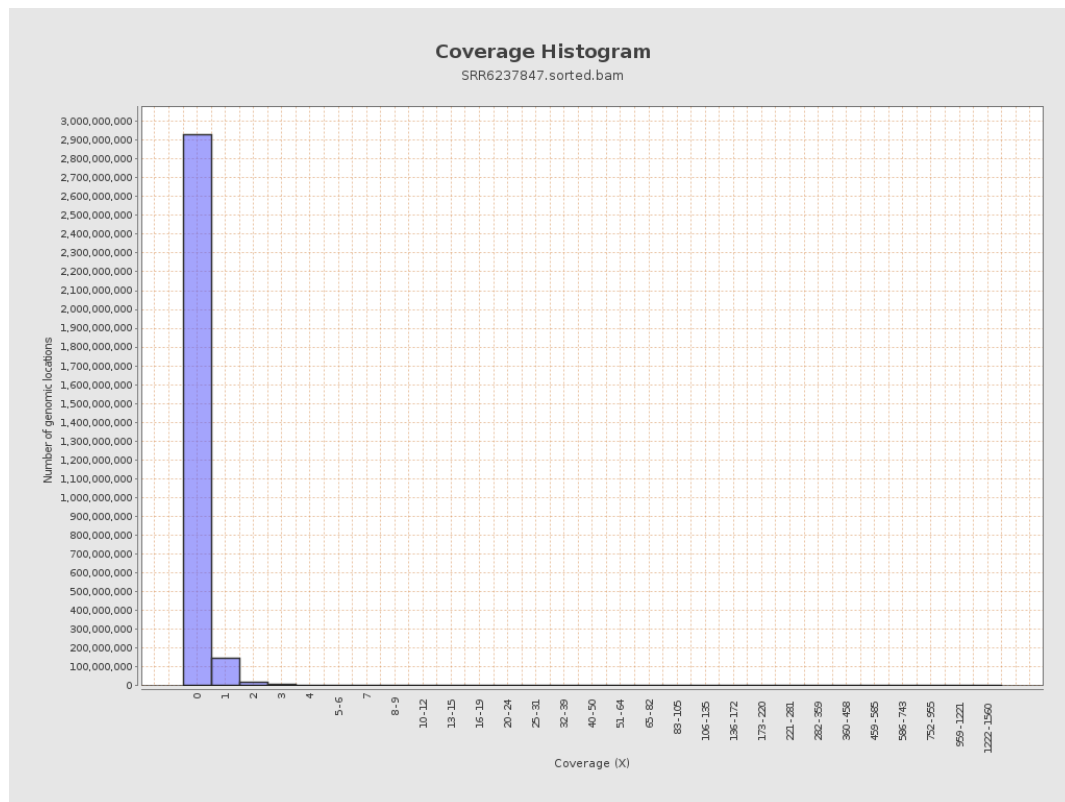
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22820424	0.0916	1.3604
chr2	243199373	22474310	0.0924	0.5592
chr3	198022430	14489078	0.0732	0.3835
chr4	191154276	7074836	0.037	0.2937
chr5	180915260	7808280	0.0432	0.2339
chr6	171115067	9430006	0.0551	0.323
chr7	159138663	14686498	0.0923	1.3684

chr8	146364022	9191082	0.0628	0.4232
chr9	141213431	10095031	0.0715	0.4706
chr10	135534747	10574172	0.078	1.2405
chr11	135006516	9408820	0.0697	0.364
chr12	133851895	9106935	0.068	0.3015
chr13	115169878	4774235	0.0415	0.224
chr14	107349540	2347770	0.0219	0.2388
chr15	102531392	3405348	0.0332	0.2012
chr16	90354753	4656662	0.0515	0.3526
chr17	81195210	2944297	0.0363	0.2564
chr18	78077248	2861057	0.0366	0.6142
chr19	59128983	3357684	0.0568	0.8769
chr20	63025520	3929500	0.0623	0.2889
chr21	48129895	2261311	0.047	0.3096
chr22	51304566	1127806	0.022	0.1674
chrMT	16571	110651	6.6774	4.2644
chrX	155270560	13924123	0.0897	0.3929
chrY	59373566	567930	0.0096	0.2479

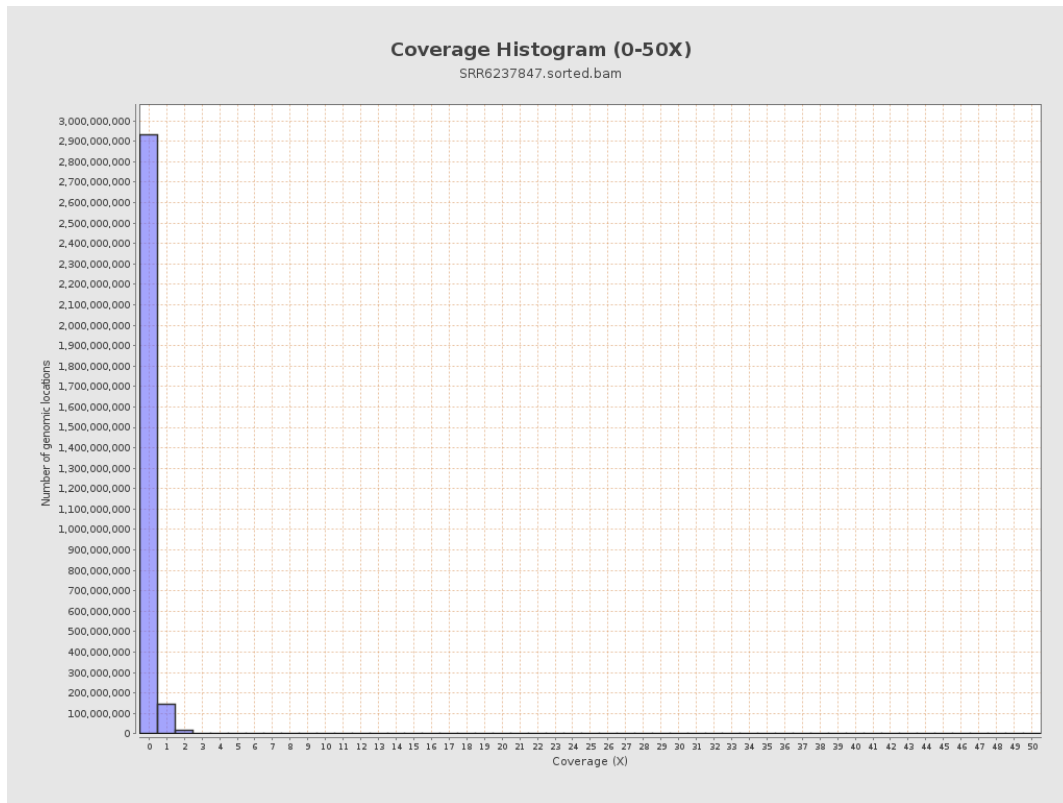
3. Results : Coverage across reference



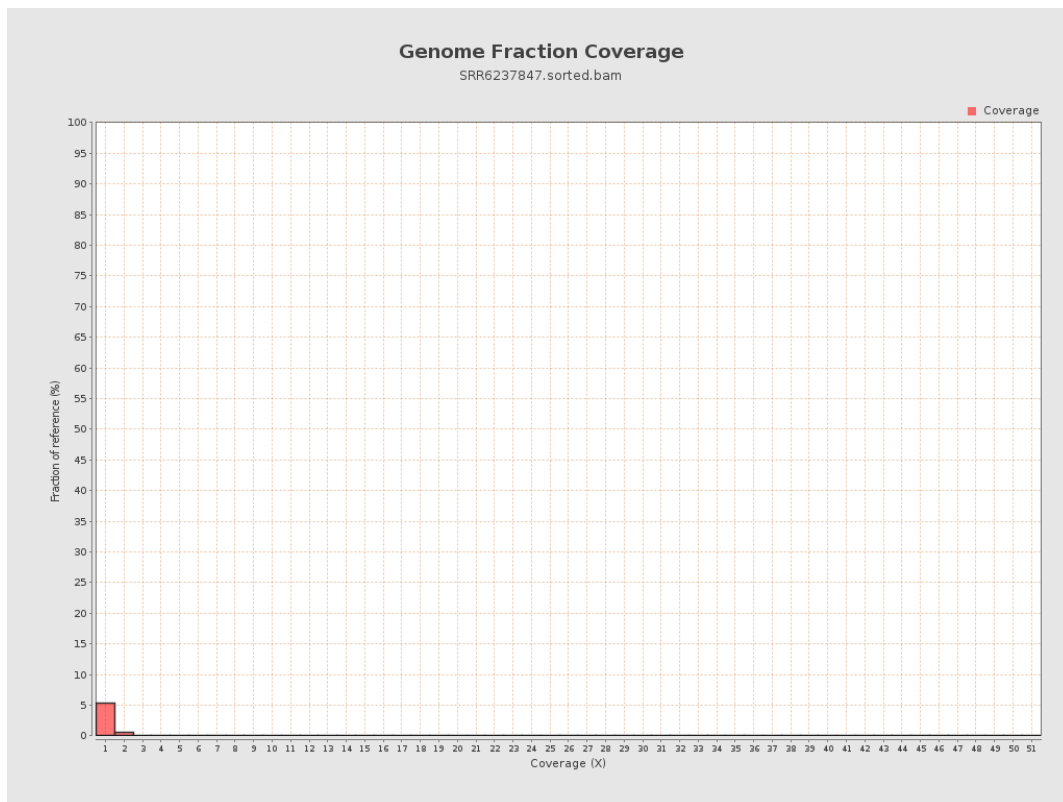
4. Results : Coverage Histogram



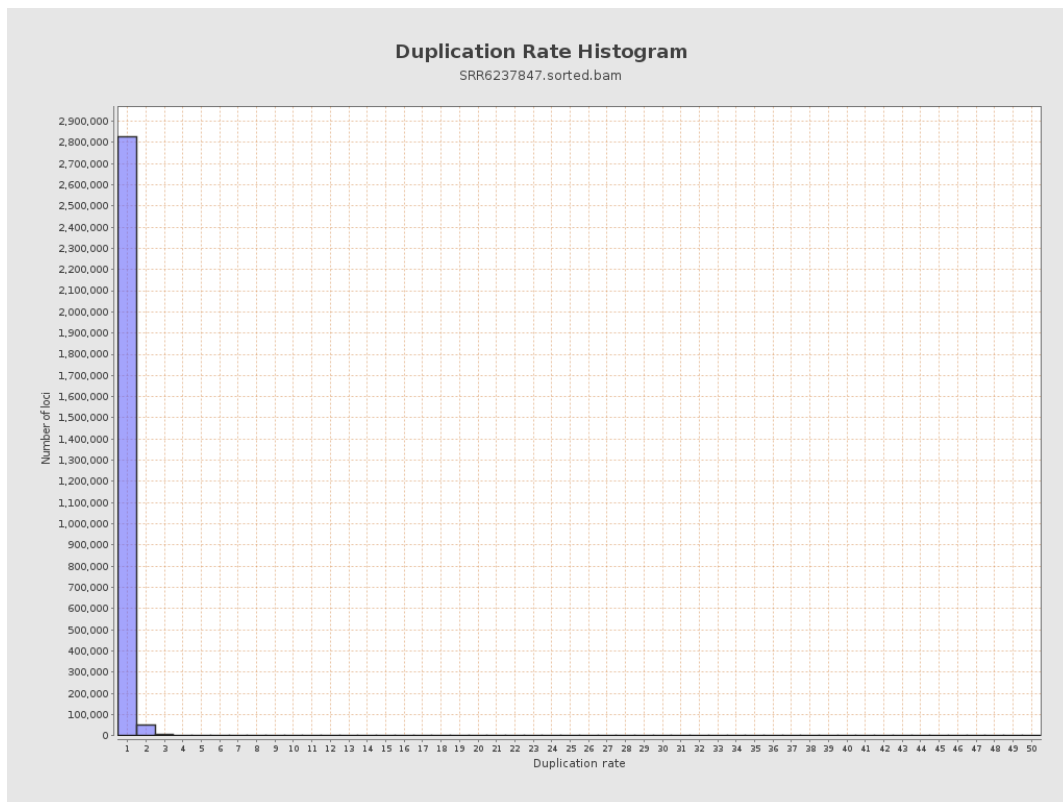
5. Results : Coverage Histogram (0-50X)



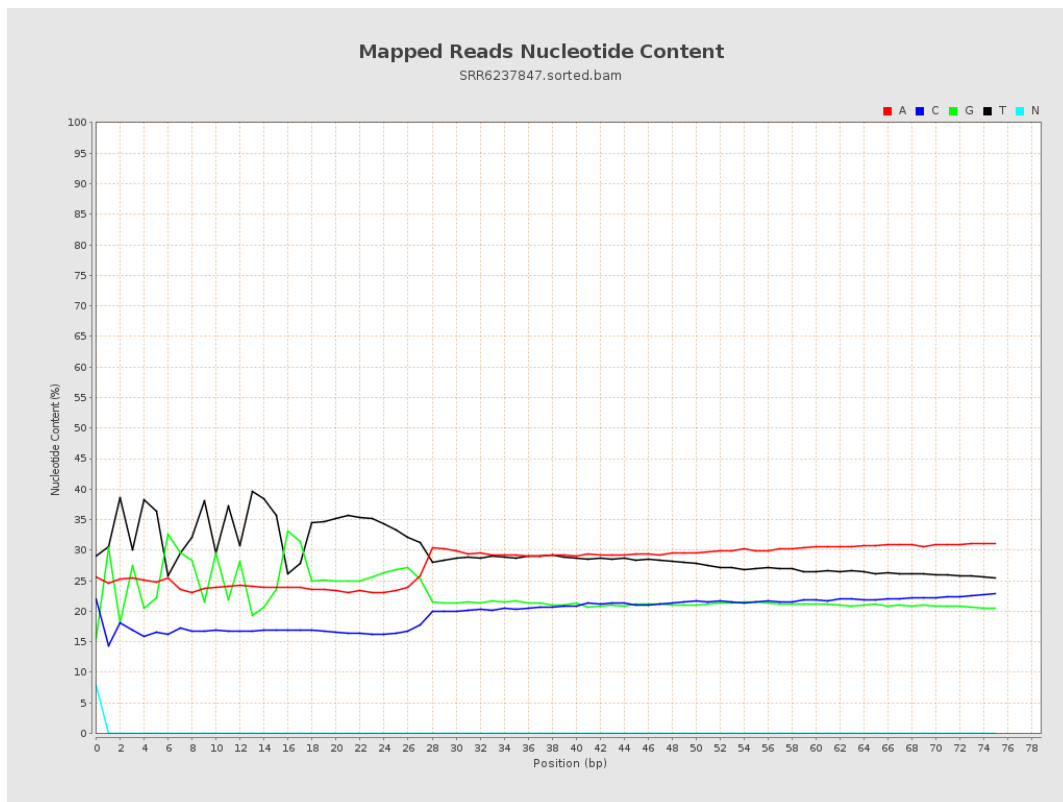
6. Results : Genome Fraction Coverage



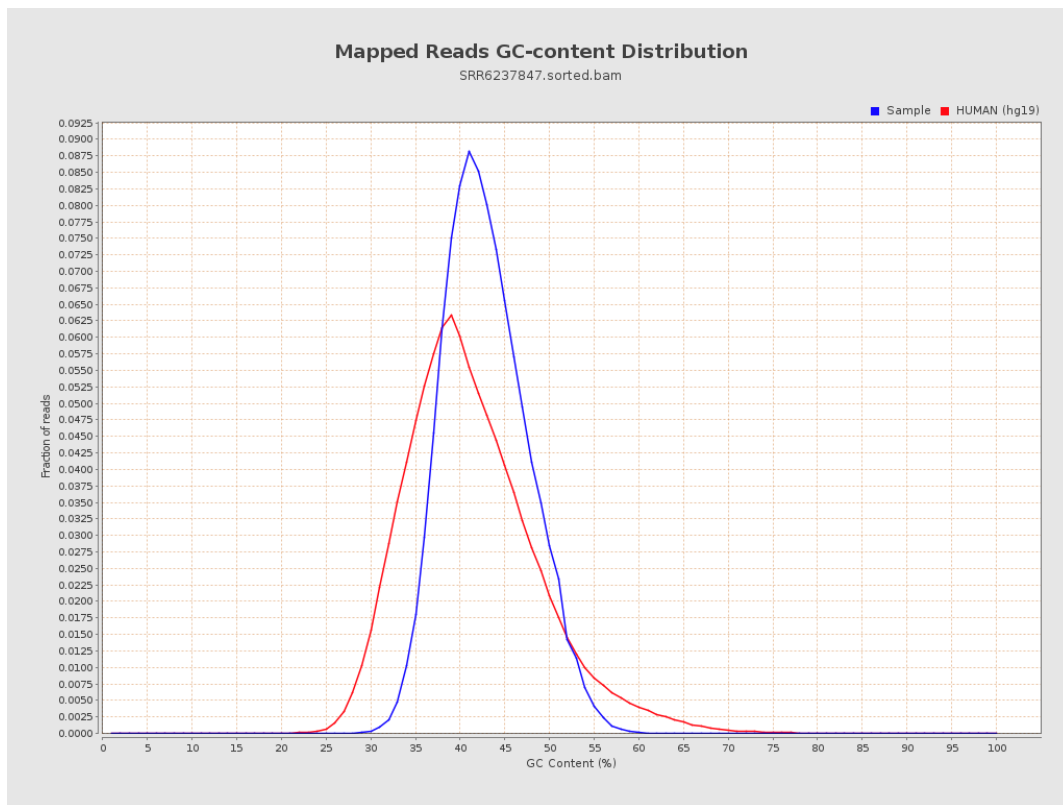
7. Results : Duplication Rate Histogram



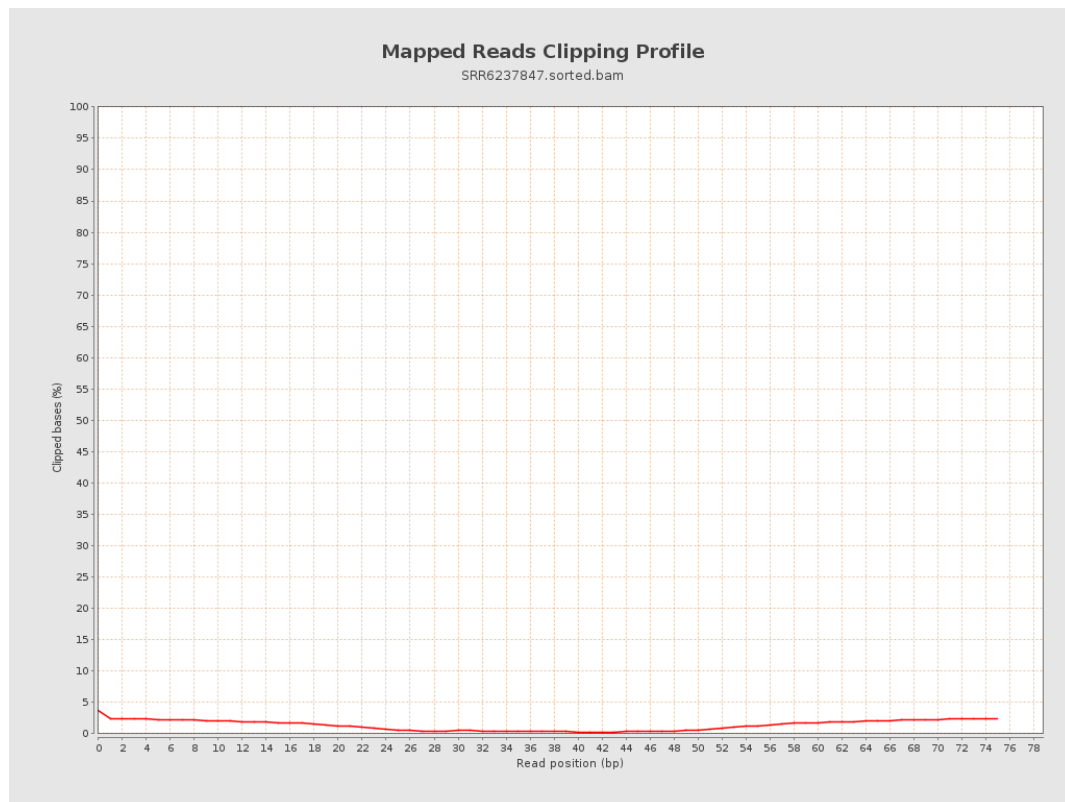
8. Results : Mapped Reads Nucleotide Content



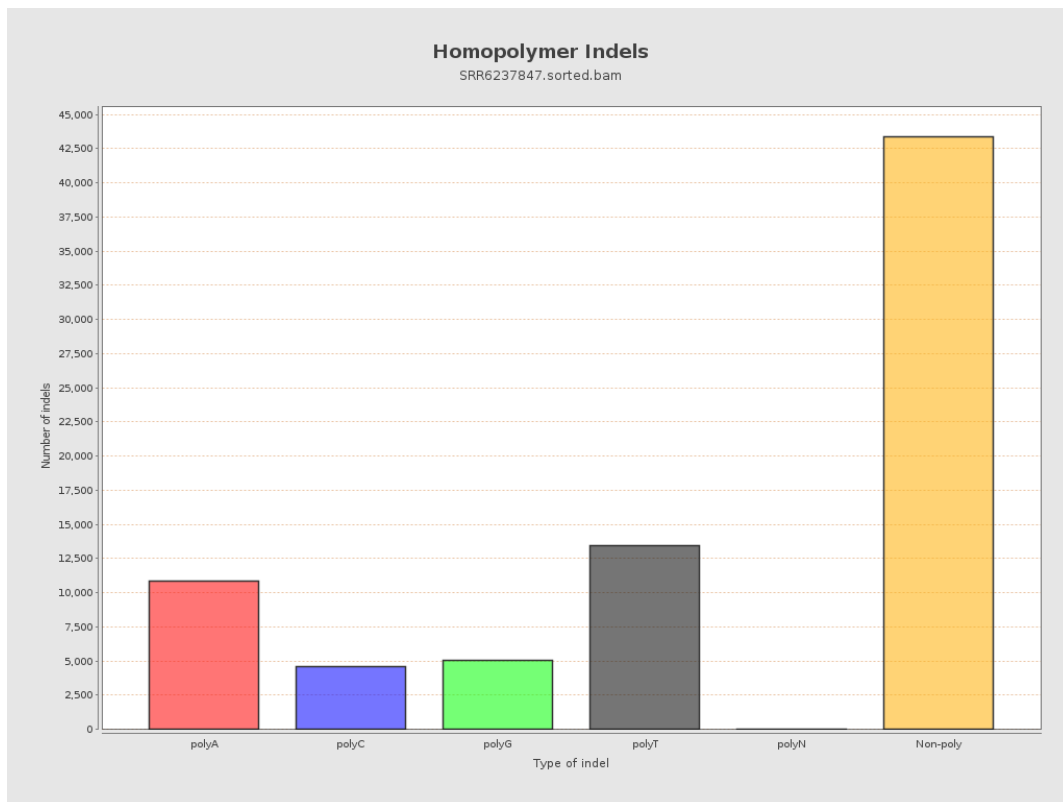
9. Results : Mapped Reads GC-content Distribution



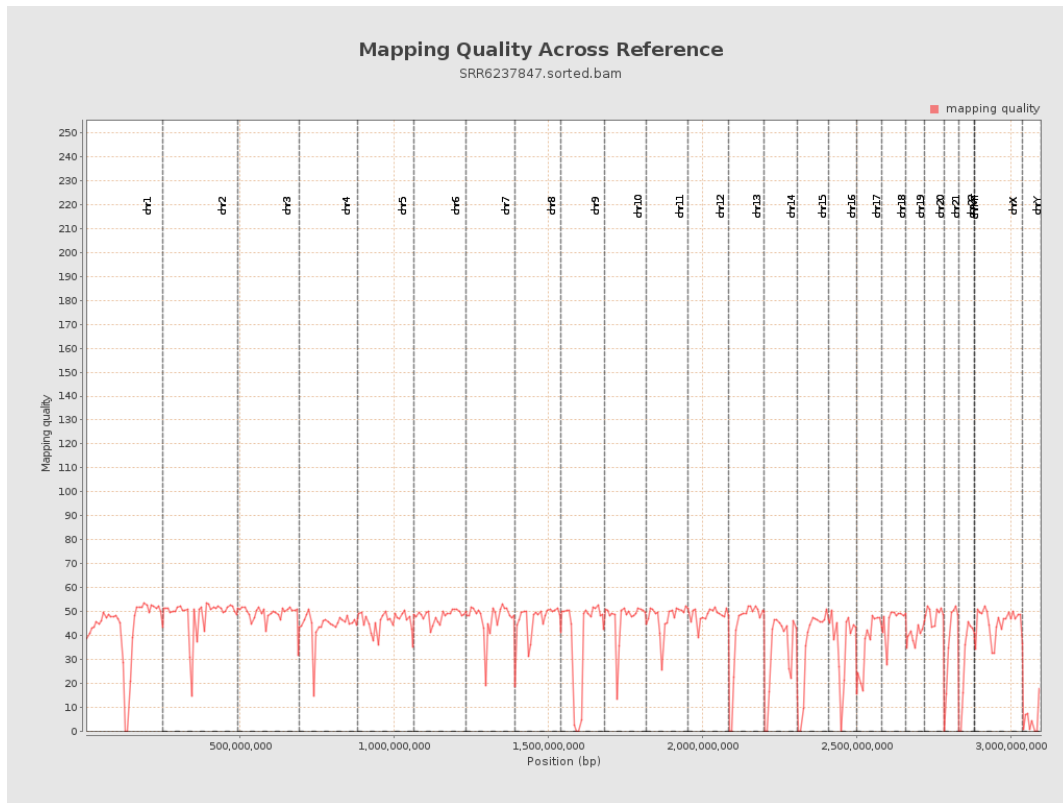
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

