

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:23:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237304.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_SRR6237304 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237304.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:23:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237304.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,970,419
Mapped reads	2,712,310 / 91.31%
Unmapped reads	258,109 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,054 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	741,513 / 24.96%
Duplication rate	19.25%
Clipped reads	1,663,265 / 55.99%

2.2. ACGT Content

Number/percentage of A's	43,238,586 / 25.47%
Number/percentage of C's	29,776,765 / 17.54%
Number/percentage of T's	56,167,668 / 33.09%
Number/percentage of G's	40,565,956 / 23.9%
Number/percentage of N's	17,792 / 0.01%
GC Percentage	41.43%

2.3. Coverage

Mean	0.0549

Standard Deviation	0.768
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2.4. Mapping Quality

Mean Mapping Quality	43.73
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2.5. Mismatches and indels

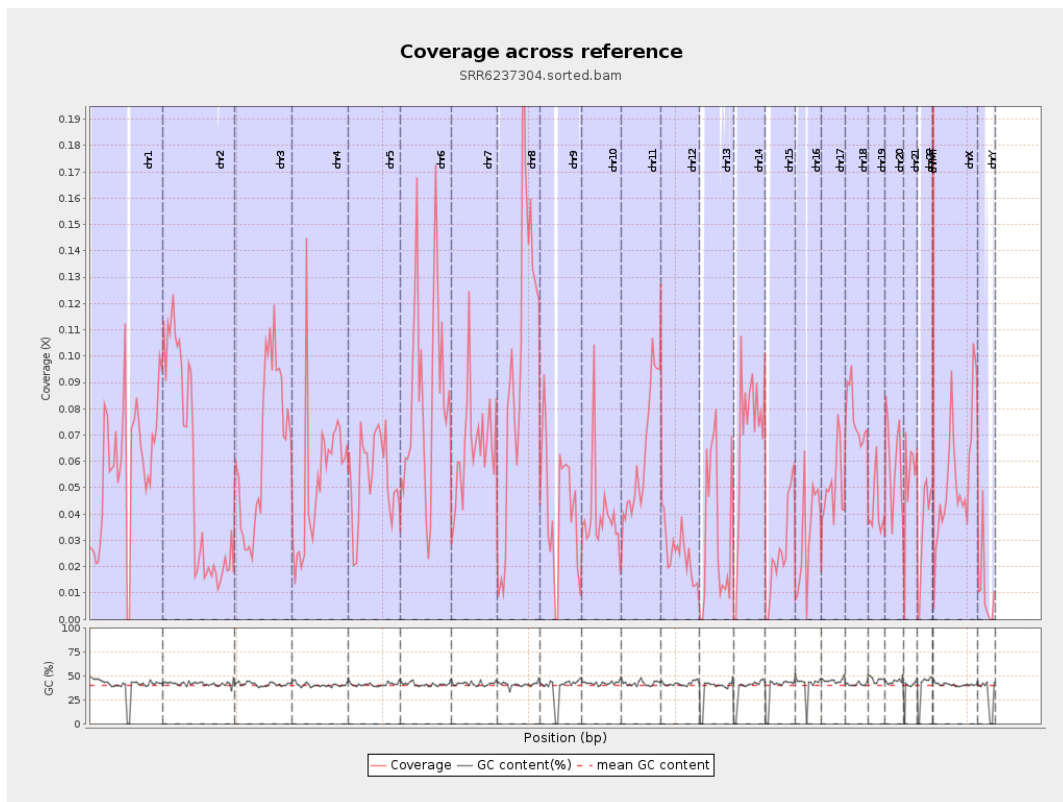
General error rate	0.62%
Mismatches	1,016,850
Insertions	13,507
Mapped reads with at least one insertion	0.49%
Deletions	42,692
Mapped reads with at least one deletion	1.56%
Homopolymer indels	42.78%

2.6. Chromosome stats

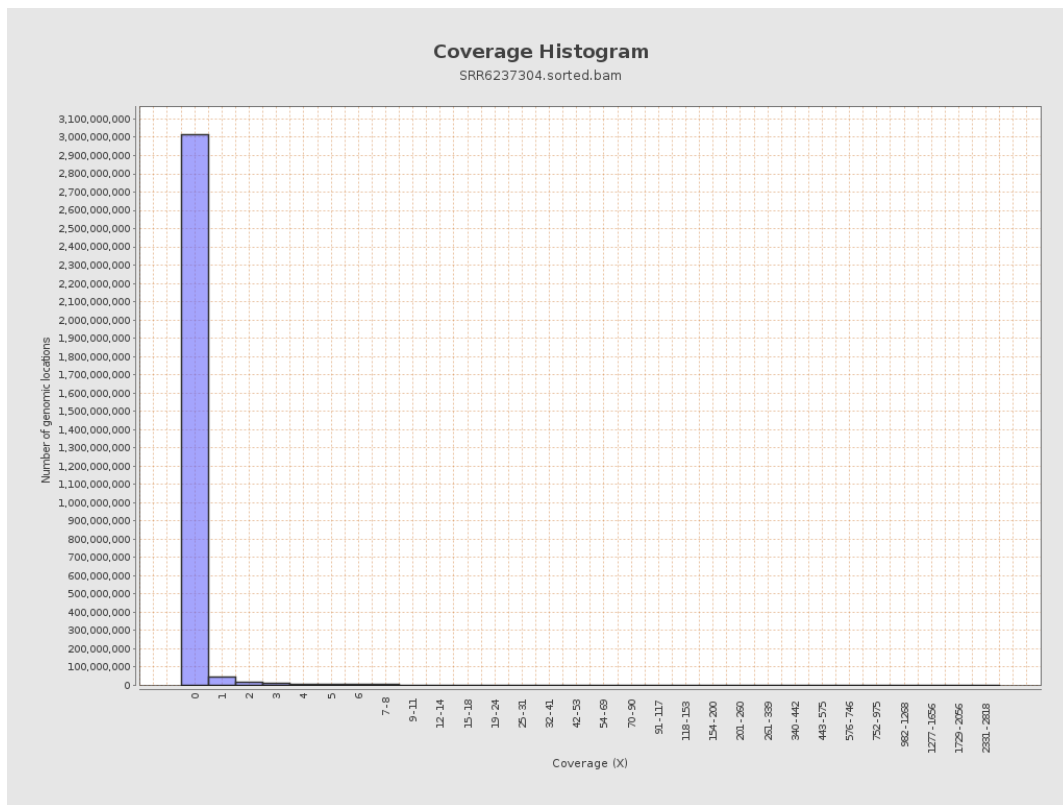
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14568533	0.0584	0.9958
chr2	243199373	13160391	0.0541	1.4082
chr3	198022430	12813303	0.0647	0.4609
chr4	191154276	10220307	0.0535	0.6144
chr5	180915260	9813432	0.0542	0.4181
chr6	171115067	14544420	0.085	0.8236
chr7	159138663	10453617	0.0657	0.8993

chr8	146364022	14351858	0.0981	1.4111
chr9	141213431	6103107	0.0432	0.4699
chr10	135534747	5333478	0.0394	0.7185
chr11	135006516	8532469	0.0632	0.5297
chr12	133851895	3383968	0.0253	0.2911
chr13	115169878	3850975	0.0334	0.3784
chr14	107349540	7362084	0.0686	0.476
chr15	102531392	2675423	0.0261	0.3117
chr16	90354753	2837134	0.0314	0.3594
chr17	81195210	4136021	0.0509	0.4472
chr18	78077248	6005780	0.0769	1.0359
chr19	59128983	2500550	0.0423	0.6381
chr20	63025520	3751058	0.0595	0.4686
chr21	48129895	2616239	0.0544	0.5047
chr22	51304566	1782944	0.0348	0.3326
chrMT	16571	20017	1.208	2.0186
chrX	155270560	8355675	0.0538	0.4537
chrY	59373566	668921	0.0113	0.4631

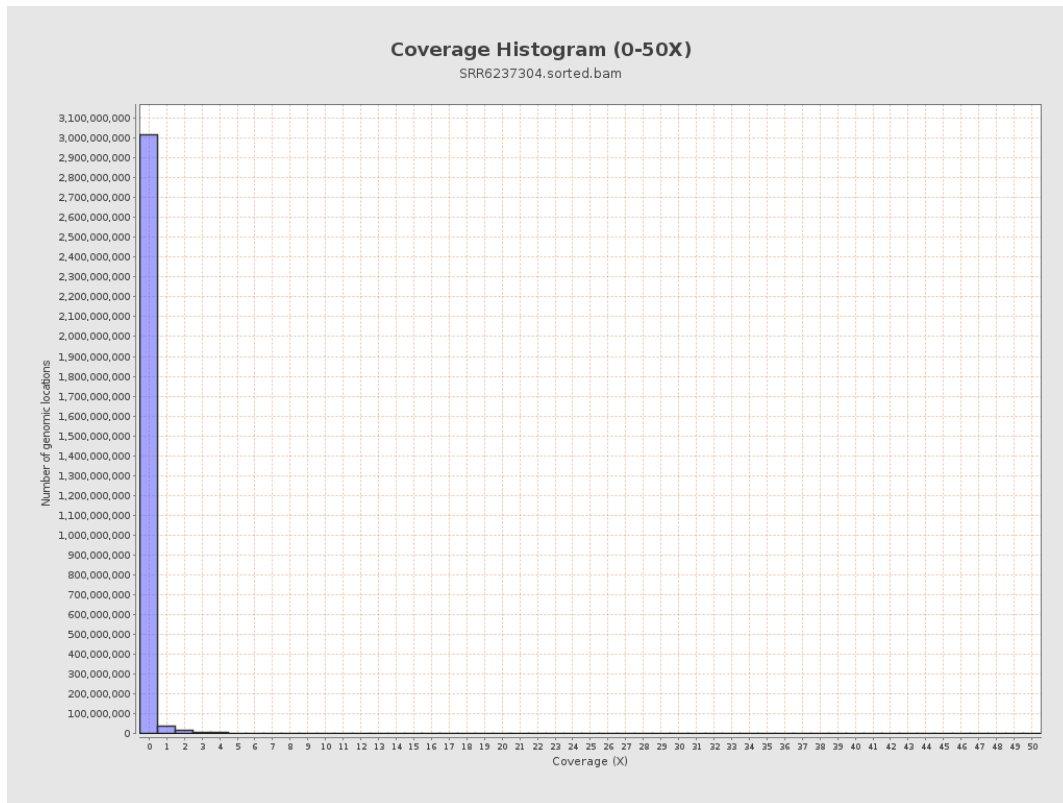
3. Results : Coverage across reference



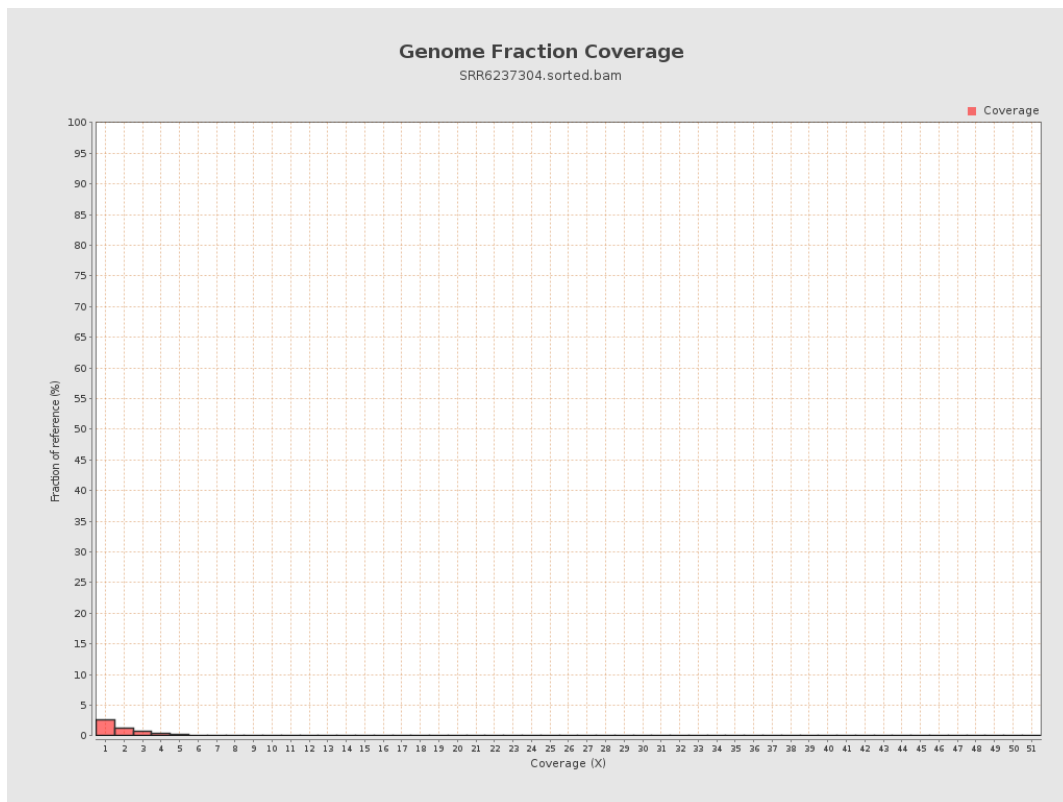
4. Results : Coverage Histogram



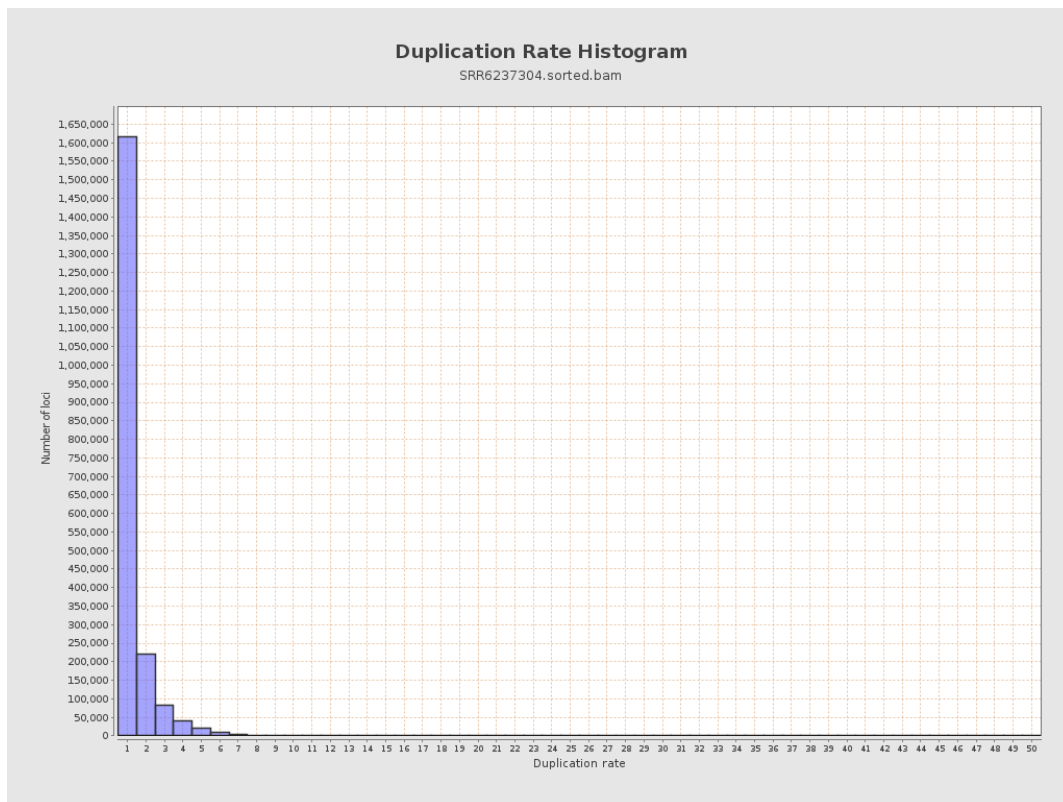
5. Results : Coverage Histogram (0-50X)



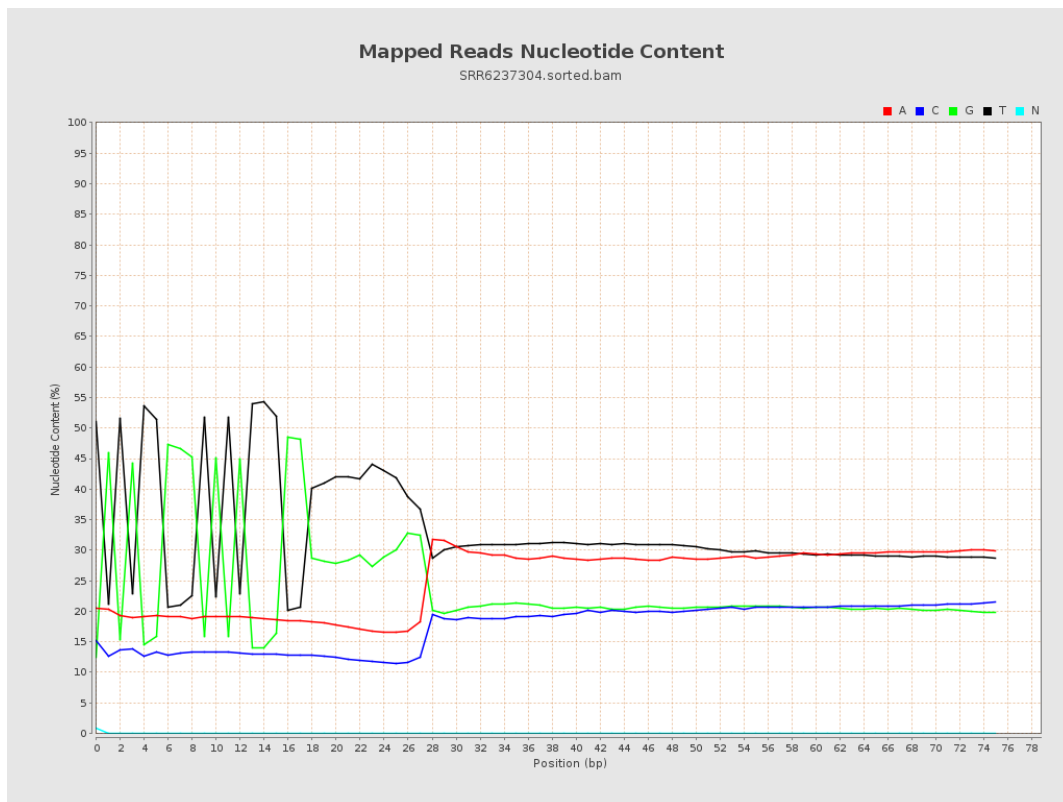
6. Results : Genome Fraction Coverage



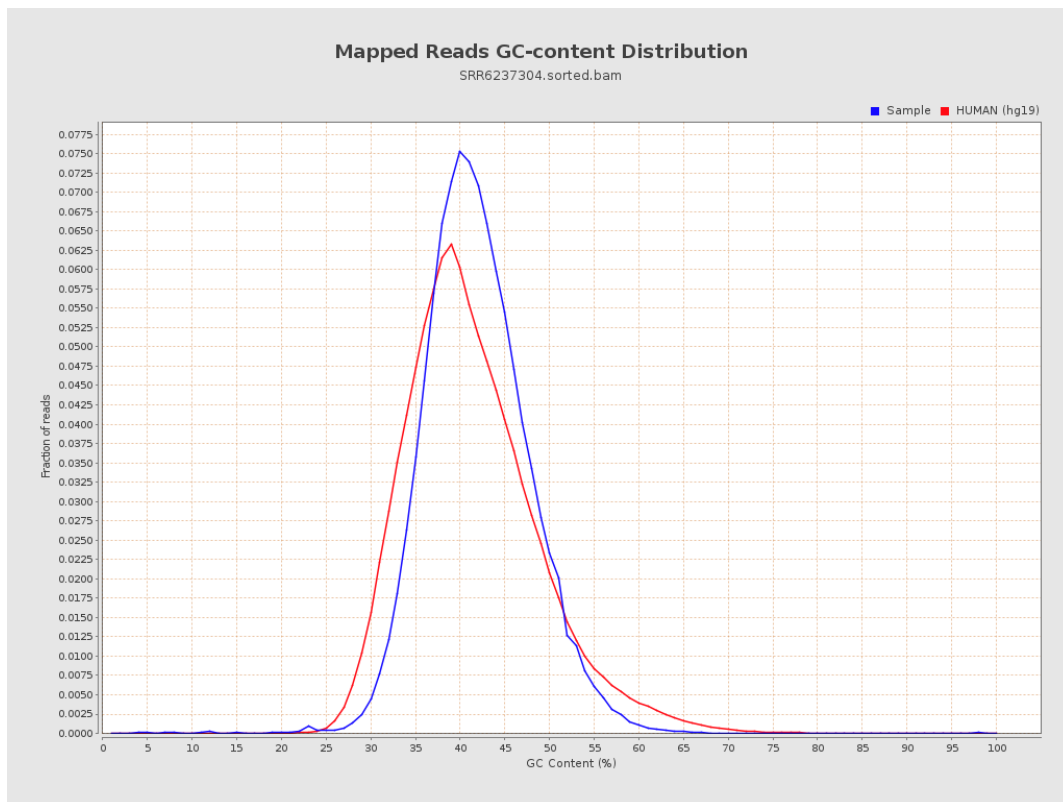
7. Results : Duplication Rate Histogram



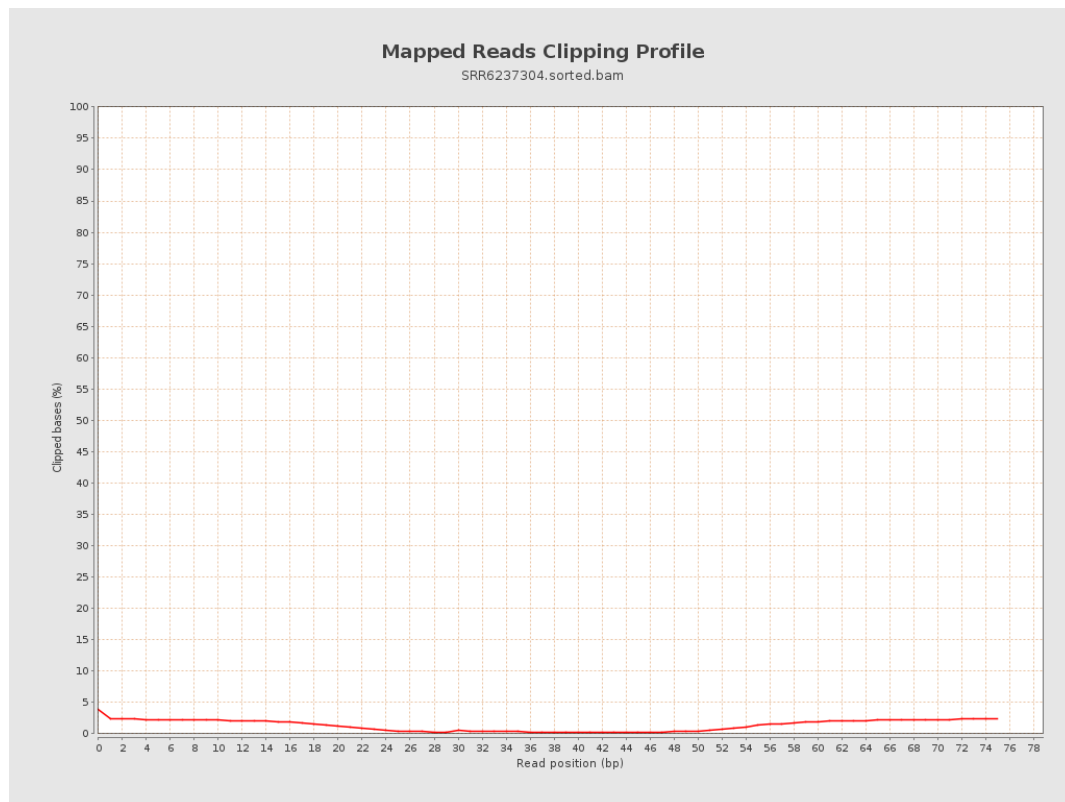
8. Results : Mapped Reads Nucleotide Content



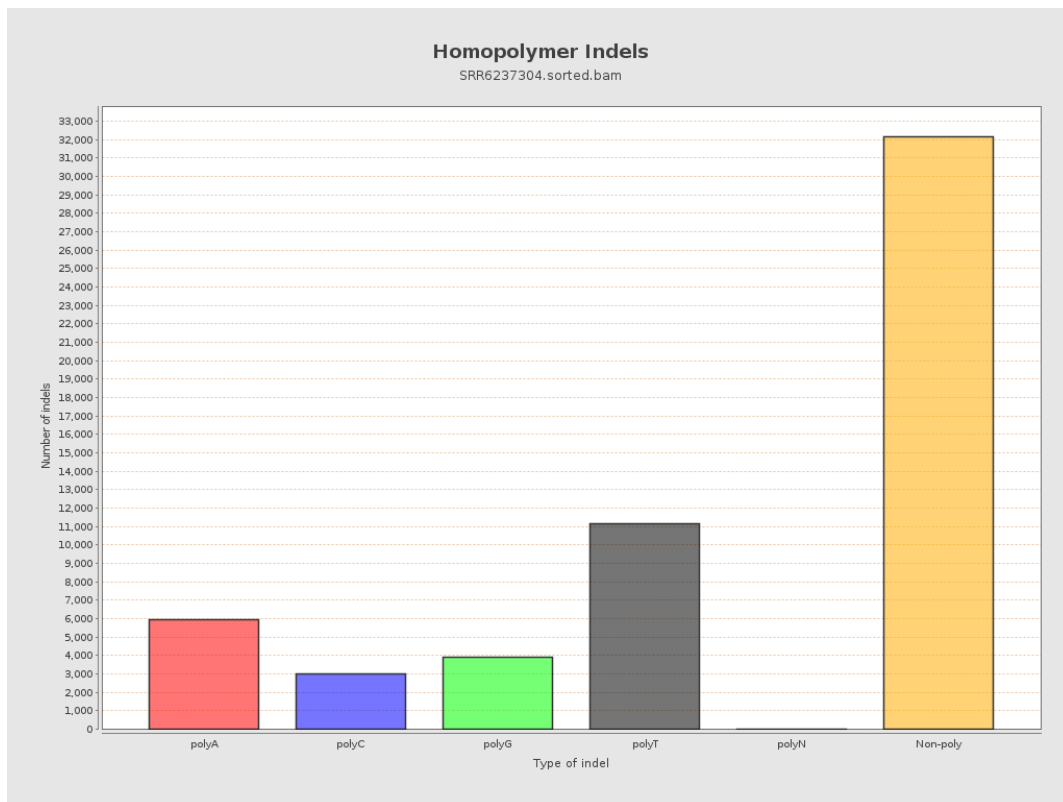
9. Results : Mapped Reads GC-content Distribution



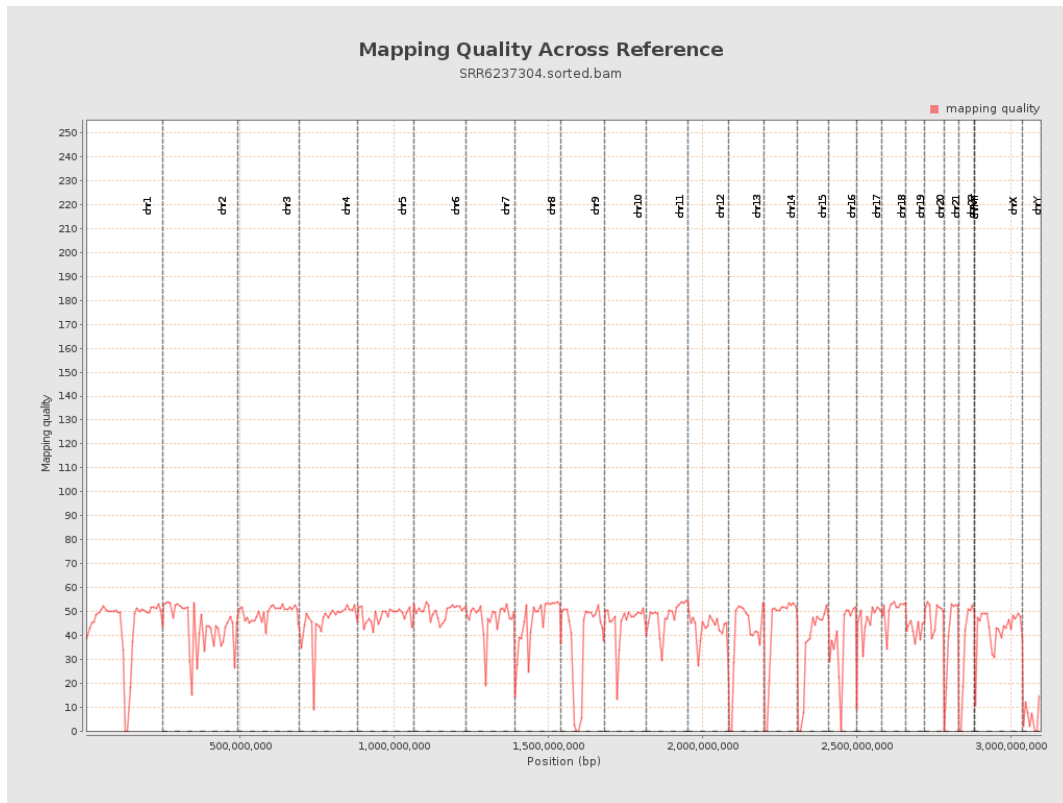
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

