

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:04:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237814.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_SRR6237814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237814.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:04:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,164,011
Mapped reads	2,034,986 / 94.04%
Unmapped reads	129,025 / 5.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,730 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	83,964 / 3.88%
Duplication rate	2.98%
Clipped reads	572,287 / 26.45%

2.2. ACGT Content

Number/percentage of A's	44,949,351 / 30.78%
Number/percentage of C's	28,524,609 / 19.53%
Number/percentage of T's	43,514,785 / 29.8%
Number/percentage of G's	28,805,886 / 19.72%
Number/percentage of N's	243,956 / 0.17%
GC Percentage	39.26%

2.3. Coverage

Mean	0.0472

Standard Deviation	0.5526
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2.4. Mapping Quality

Mean Mapping Quality	48.12
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2.5. Mismatches and indels

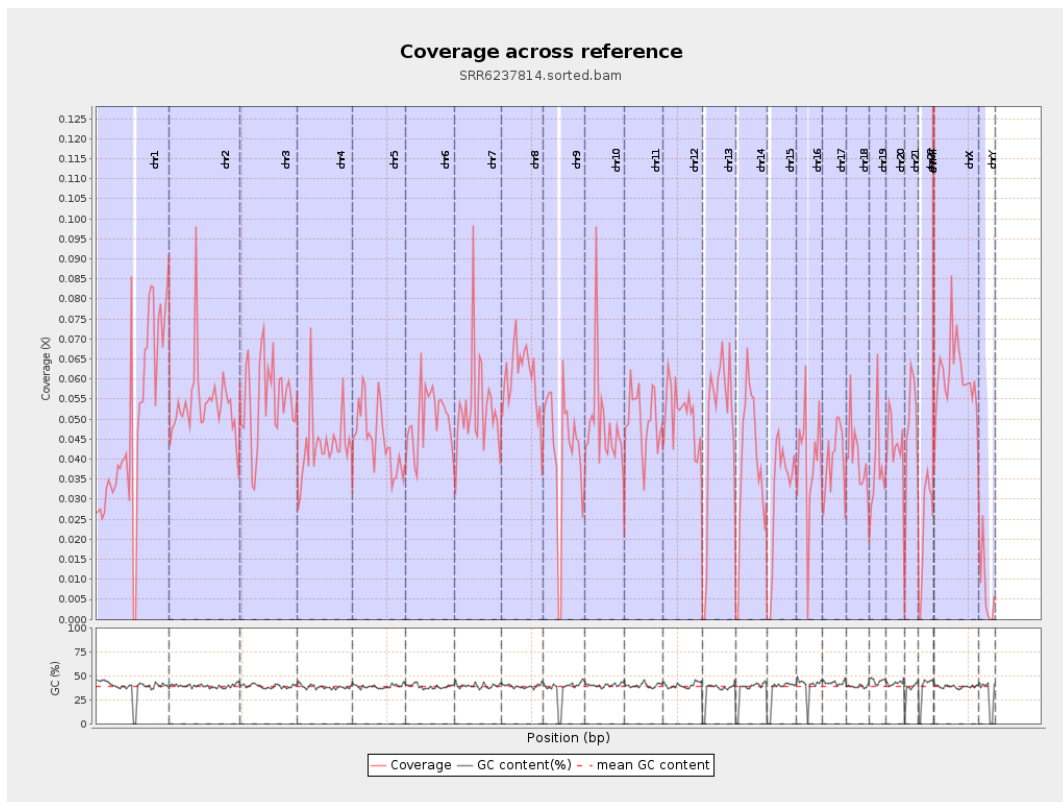
General error rate	0.93%
Mismatches	1,338,217
Insertions	11,278
Mapped reads with at least one insertion	0.55%
Deletions	50,608
Mapped reads with at least one deletion	2.45%
Homopolymer indels	44.1%

2.6. Chromosome stats

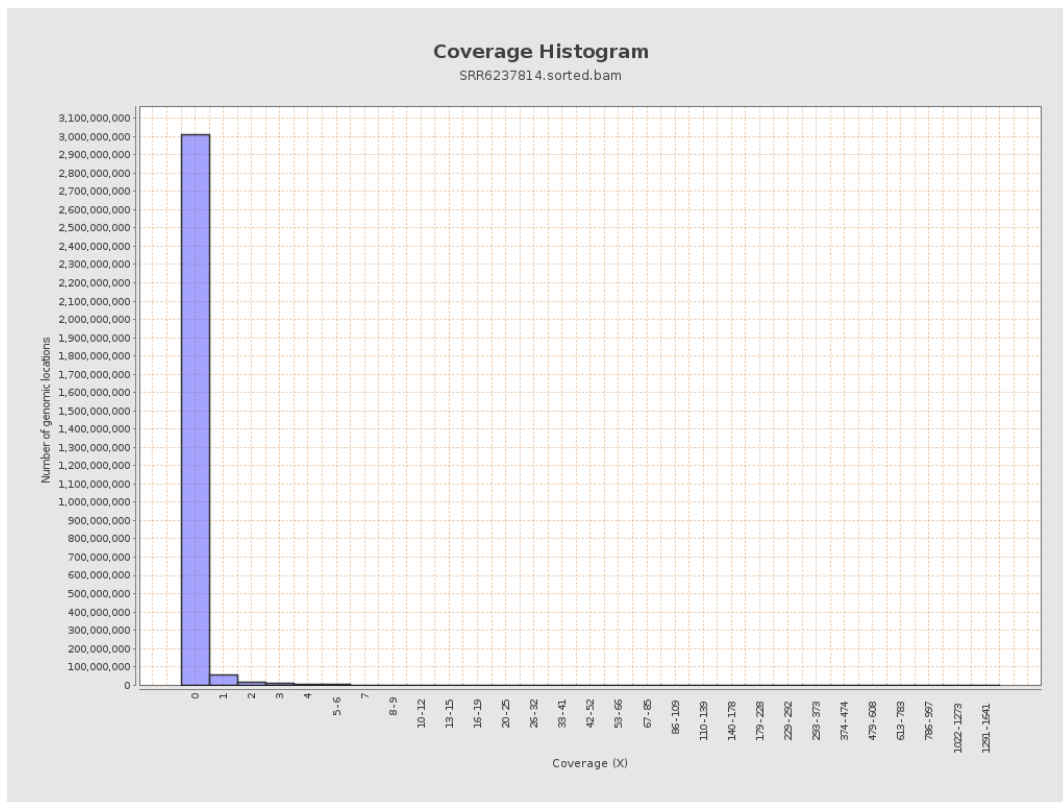
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12185385	0.0489	1.1284
chr2	243199373	13066970	0.0537	0.5183
chr3	198022430	10943490	0.0553	0.3754
chr4	191154276	8287469	0.0434	0.3606
chr5	180915260	8186934	0.0453	0.3375
chr6	171115067	8537613	0.0499	0.3921
chr7	159138663	8444116	0.0531	0.7121

chr8	146364022	8784257	0.06	0.596
chr9	141213431	5968434	0.0423	0.4698
chr10	135534747	6599500	0.0487	0.5347
chr11	135006516	6690205	0.0496	0.4902
chr12	133851895	6816623	0.0509	0.3608
chr13	115169878	5522085	0.0479	0.3461
chr14	107349540	4143587	0.0386	0.3296
chr15	102531392	3222874	0.0314	0.2765
chr16	90354753	3596391	0.0398	0.3606
chr17	81195210	3200553	0.0394	0.3701
chr18	78077248	3166773	0.0406	0.8784
chr19	59128983	2248249	0.038	0.6603
chr20	63025520	2786455	0.0442	0.3412
chr21	48129895	2245121	0.0466	0.3758
chr22	51304566	1179369	0.023	0.2341
chrMT	16571	490810	29.6186	20.6582
chrX	155270560	9378117	0.0604	0.4142
chrY	59373566	437601	0.0074	0.2258

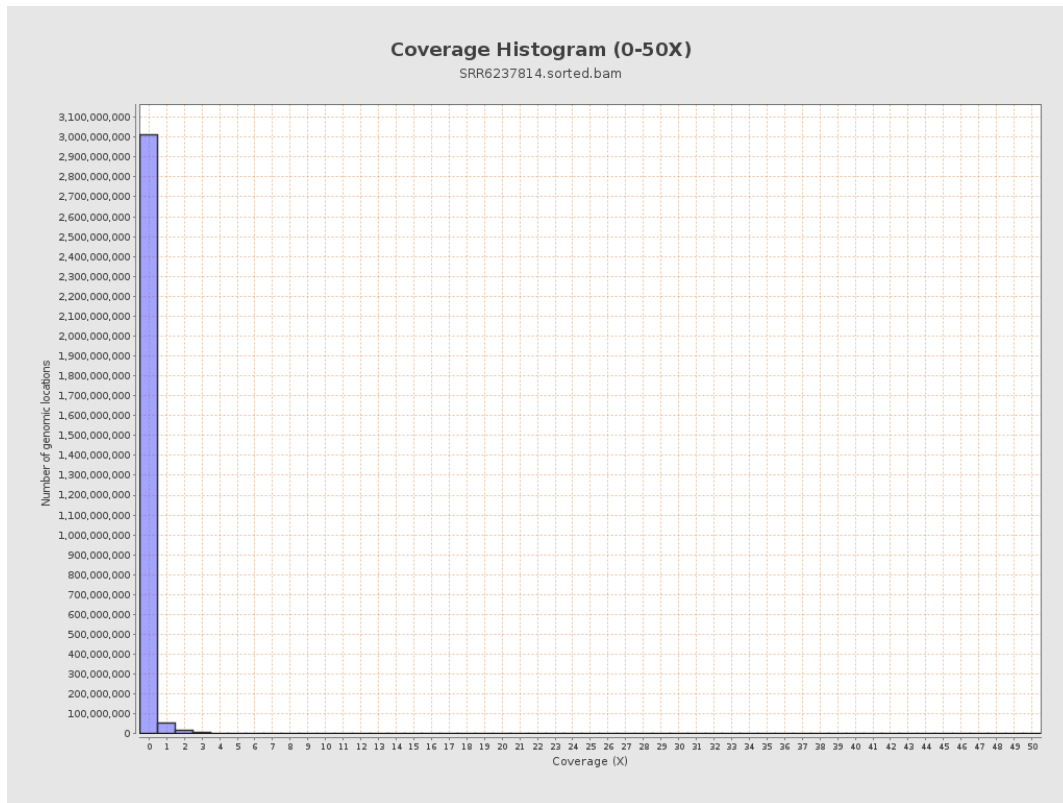
3. Results : Coverage across reference



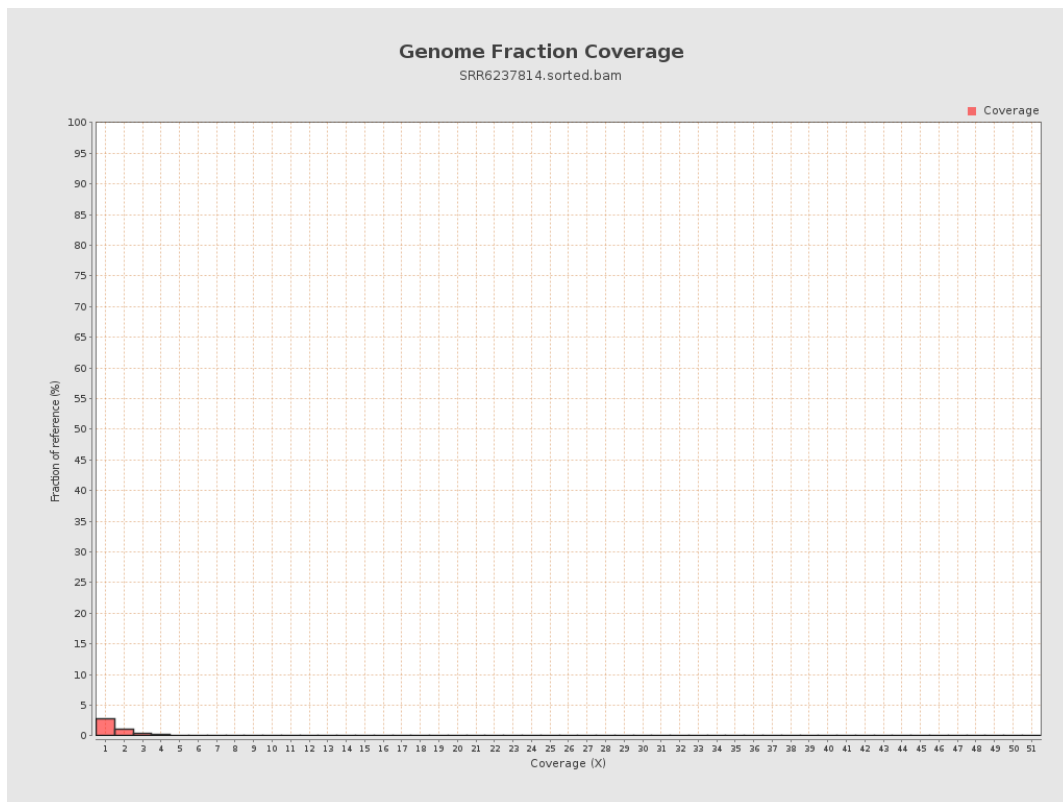
4. Results : Coverage Histogram



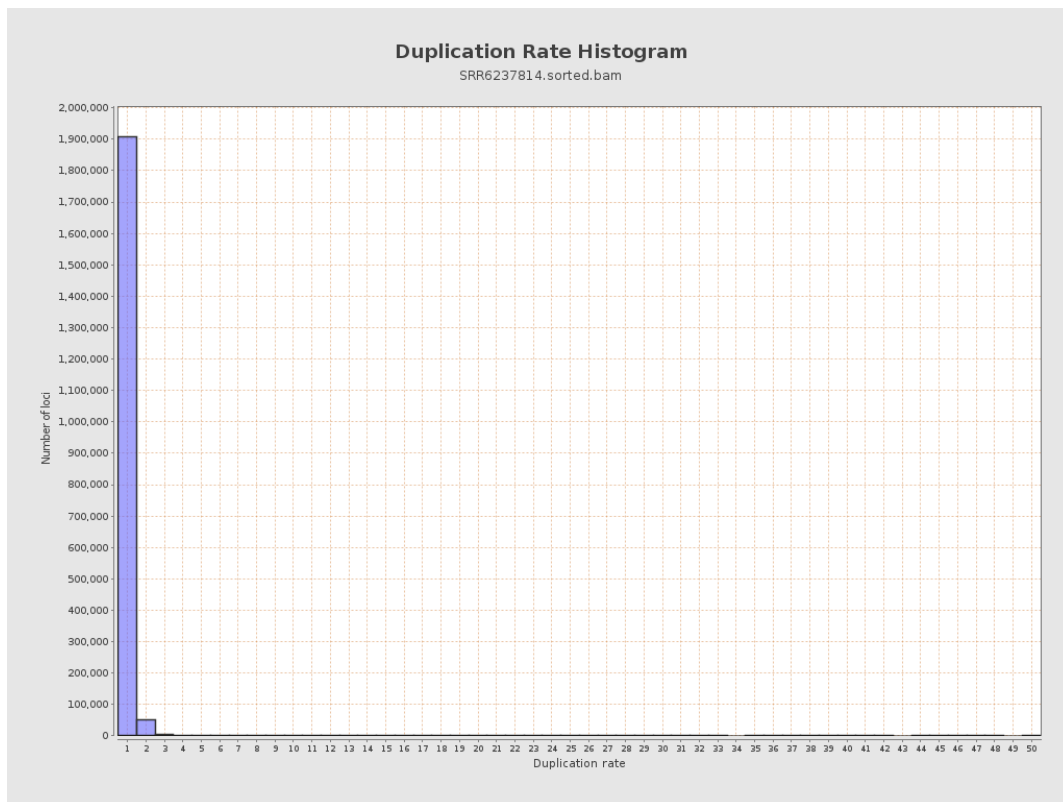
5. Results : Coverage Histogram (0-50X)



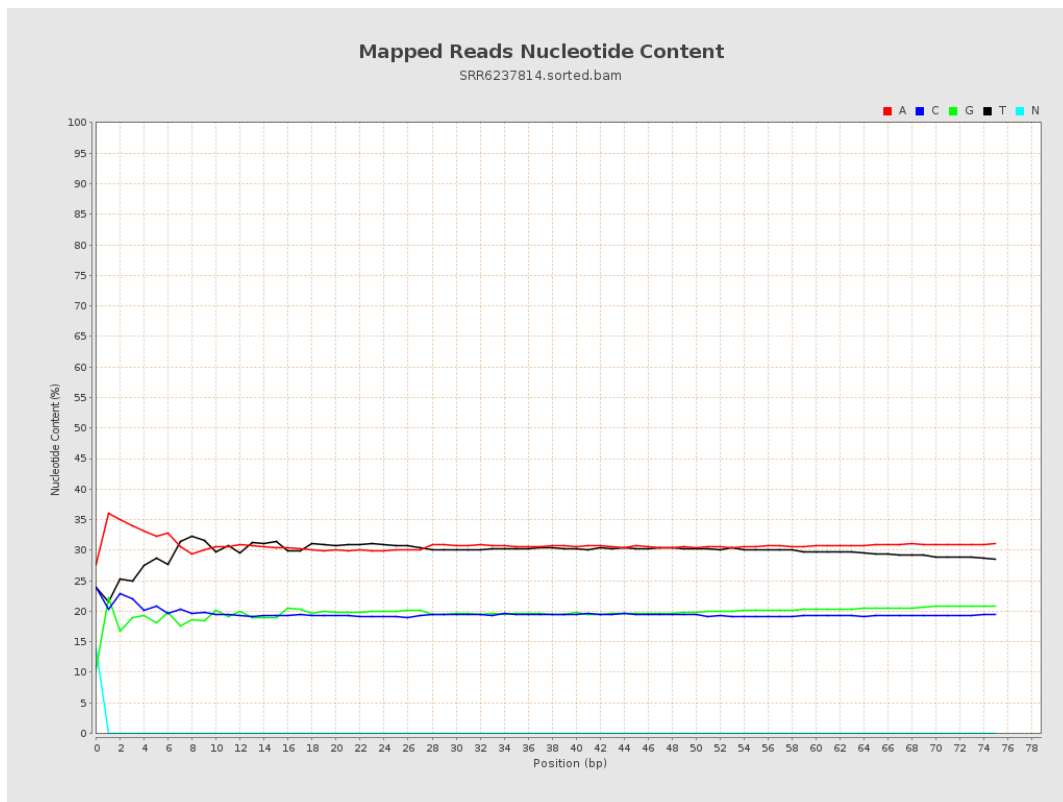
6. Results : Genome Fraction Coverage



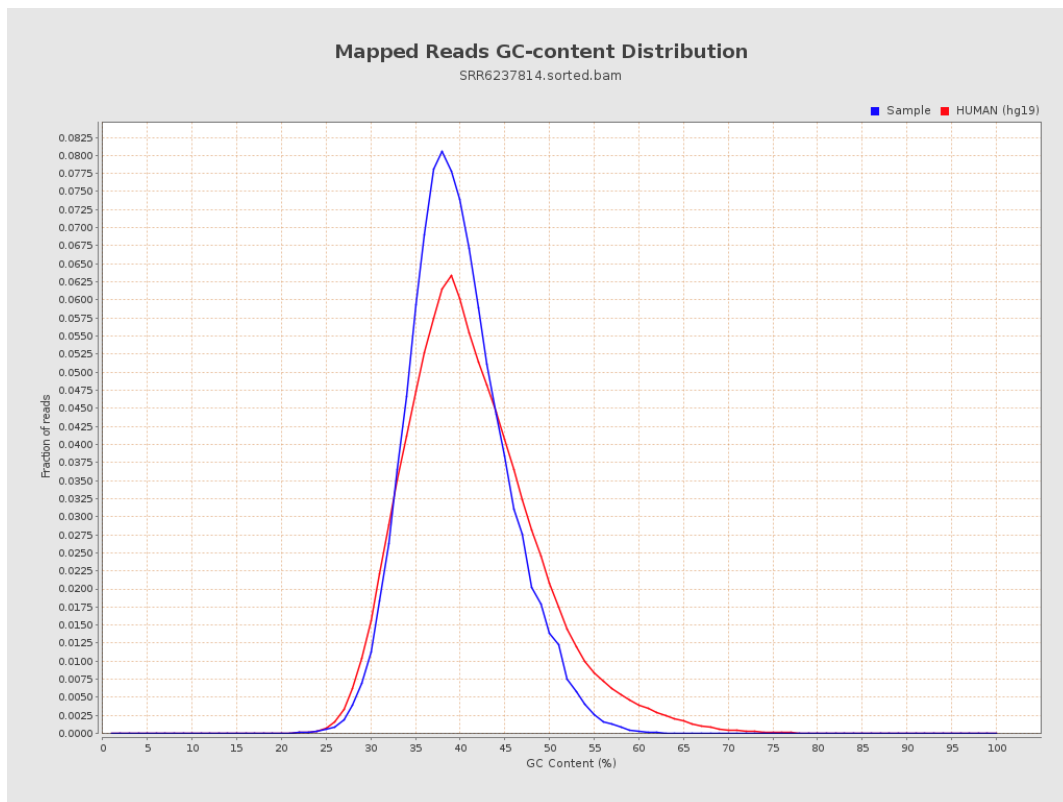
7. Results : Duplication Rate Histogram



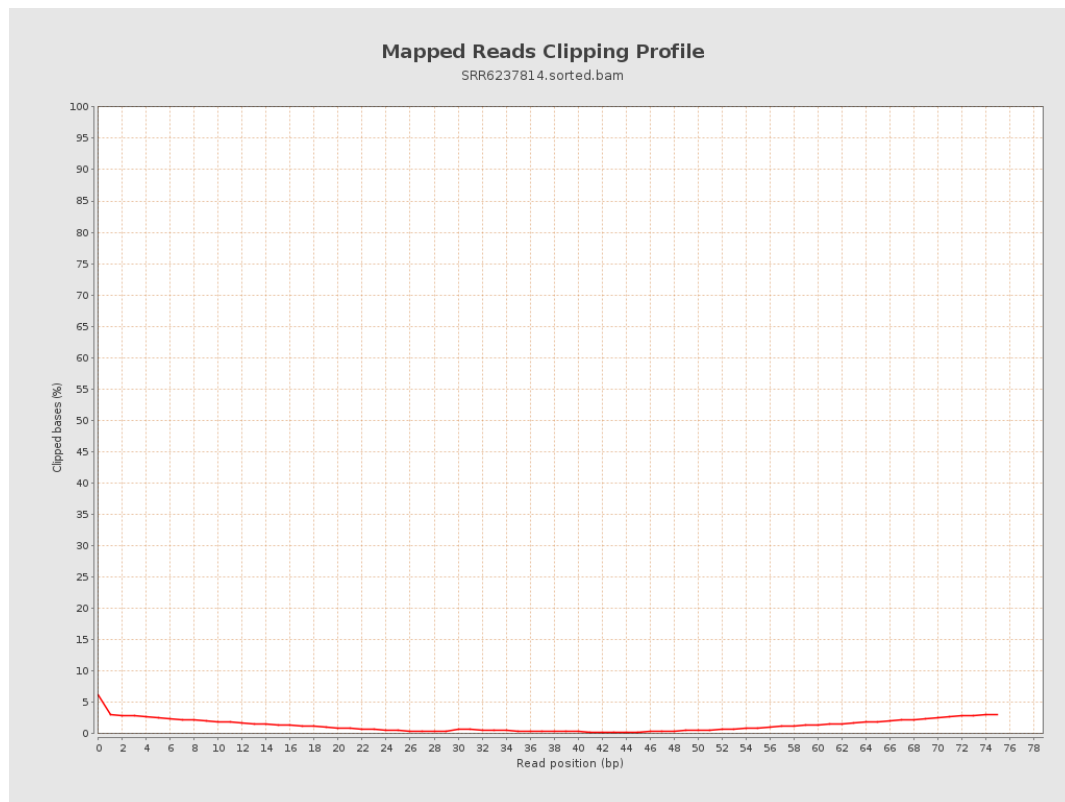
8. Results : Mapped Reads Nucleotide Content



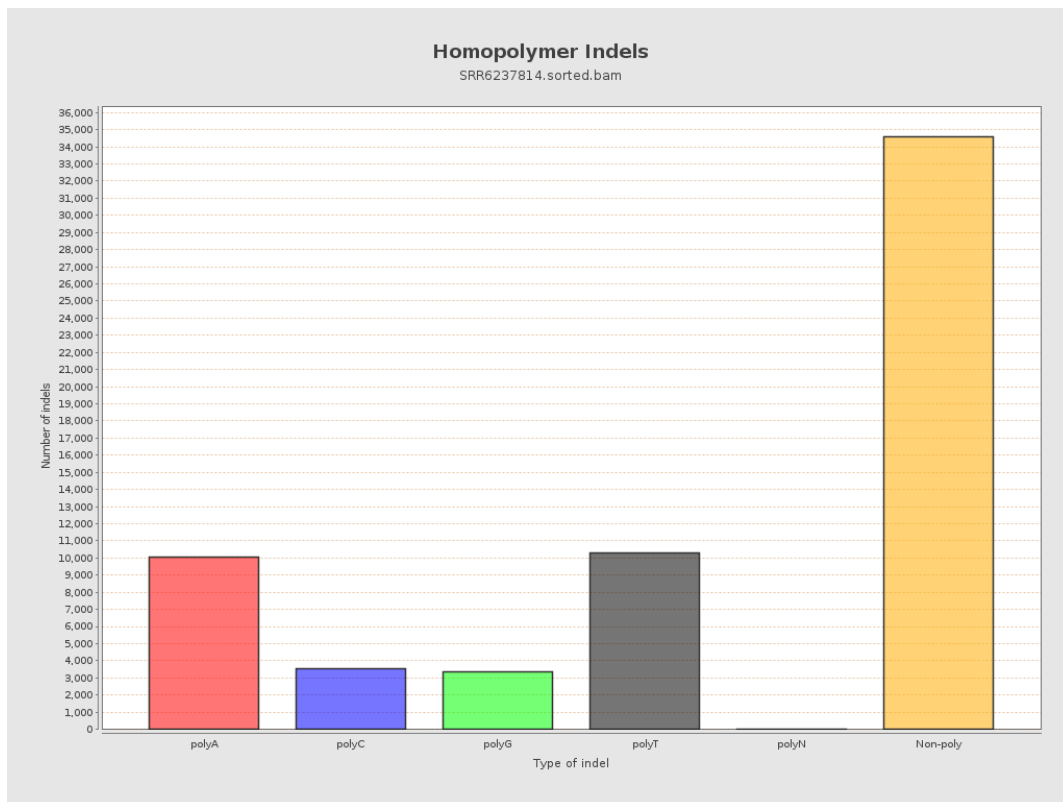
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

