

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:27:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013216.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_SRR6013216 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013216.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:27:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013216.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,518,738
Mapped reads	1,301,594 / 85.7%
Unmapped reads	217,144 / 14.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,888 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	160,339 / 10.56%
Duplication rate	9.65%
Clipped reads	695,645 / 45.8%

2.2. ACGT Content

Number/percentage of A's	22,898,756 / 27.33%
Number/percentage of C's	15,180,124 / 18.12%
Number/percentage of T's	26,935,194 / 32.14%
Number/percentage of G's	18,771,413 / 22.4%
Number/percentage of N's	9,076 / 0.01%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.3053
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2.4. Mapping Quality

Mean Mapping Quality	45.41
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2.5. Mismatches and indels

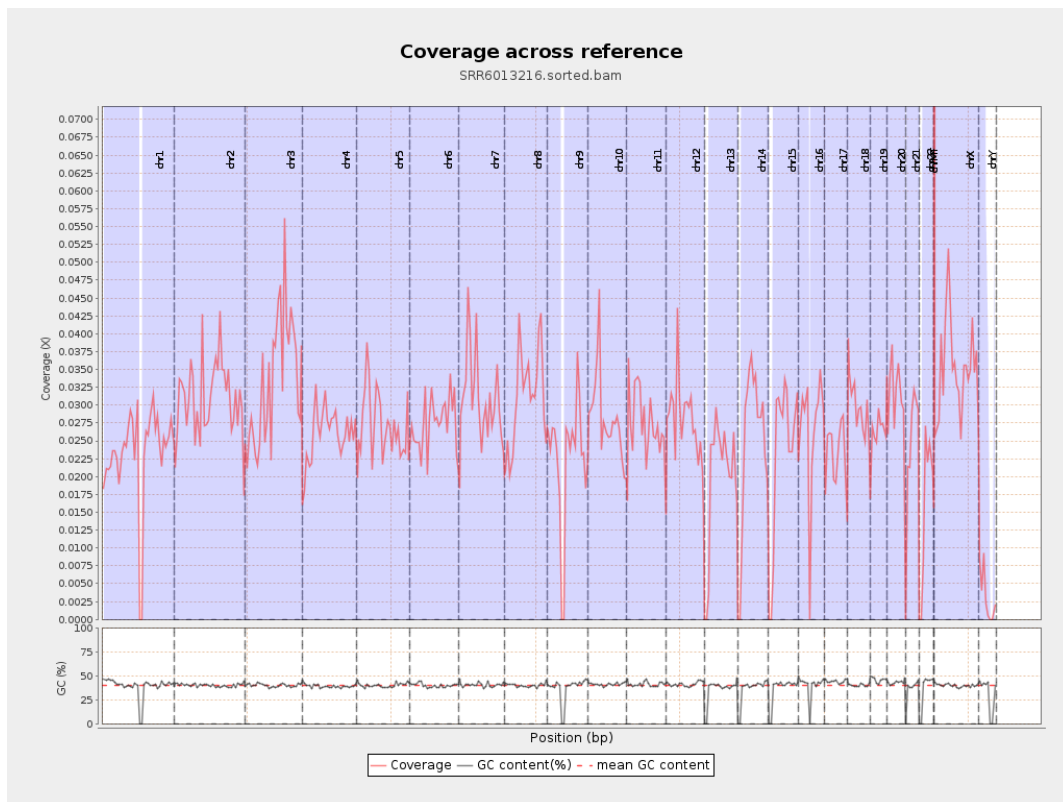
General error rate	0.81%
Mismatches	663,506
Insertions	6,038
Mapped reads with at least one insertion	0.46%
Deletions	25,049
Mapped reads with at least one deletion	1.9%
Homopolymer indels	48.12%

2.6. Chromosome stats

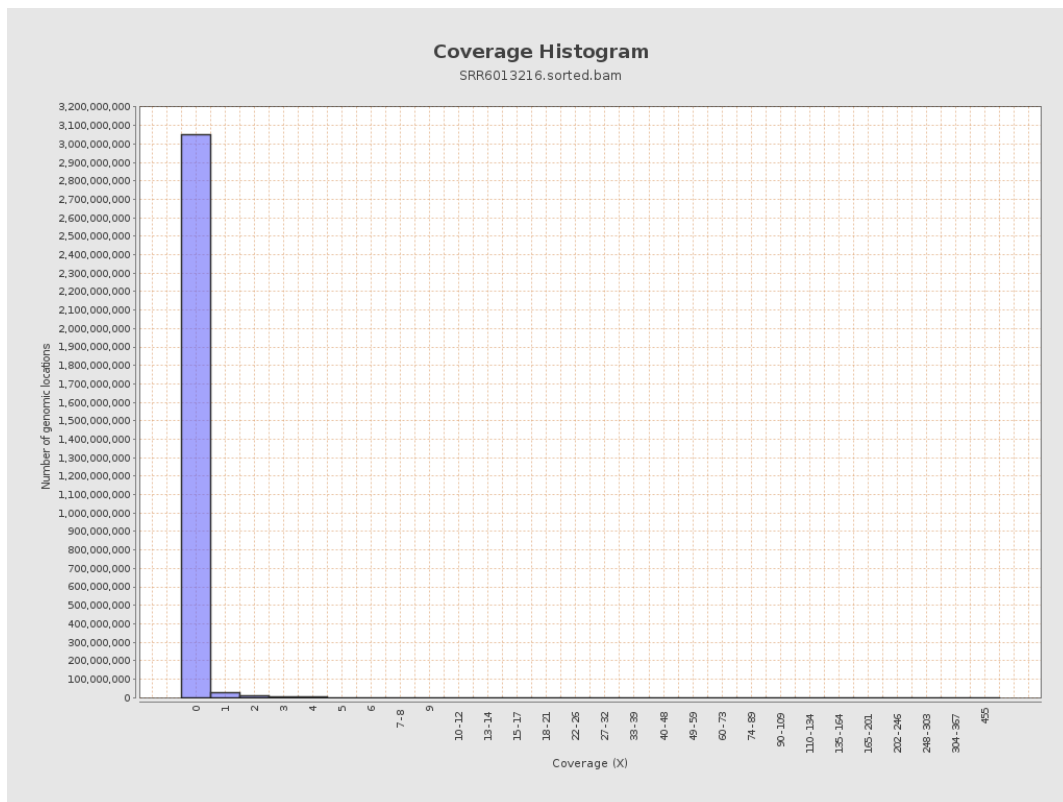
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5809576	0.0233	0.3731
chr2	243199373	7553023	0.0311	0.3766
chr3	198022430	6579777	0.0332	0.286
chr4	191154276	4971800	0.026	0.2637
chr5	180915260	4967020	0.0275	0.2665
chr6	171115067	4685357	0.0274	0.2867
chr7	159138663	4913357	0.0309	0.3747

chr8	146364022	4573037	0.0312	0.3488
chr9	141213431	3186793	0.0226	0.2701
chr10	135534747	3832781	0.0283	0.3082
chr11	135006516	3726953	0.0276	0.296
chr12	133851895	3764197	0.0281	0.2752
chr13	115169878	2280497	0.0198	0.2323
chr14	107349540	2666728	0.0248	0.2574
chr15	102531392	2393091	0.0233	0.2431
chr16	90354753	2372007	0.0263	0.2605
chr17	81195210	1881620	0.0232	0.2504
chr18	78077248	2328062	0.0298	0.3996
chr19	59128983	1571134	0.0266	0.3187
chr20	63025520	1964283	0.0312	0.2842
chr21	48129895	1182204	0.0246	0.2601
chr22	51304566	828269	0.0161	0.1985
chrMT	16571	162897	9.8302	11.3929
chrX	155270560	5459471	0.0352	0.3
chrY	59373566	185912	0.0031	0.0873

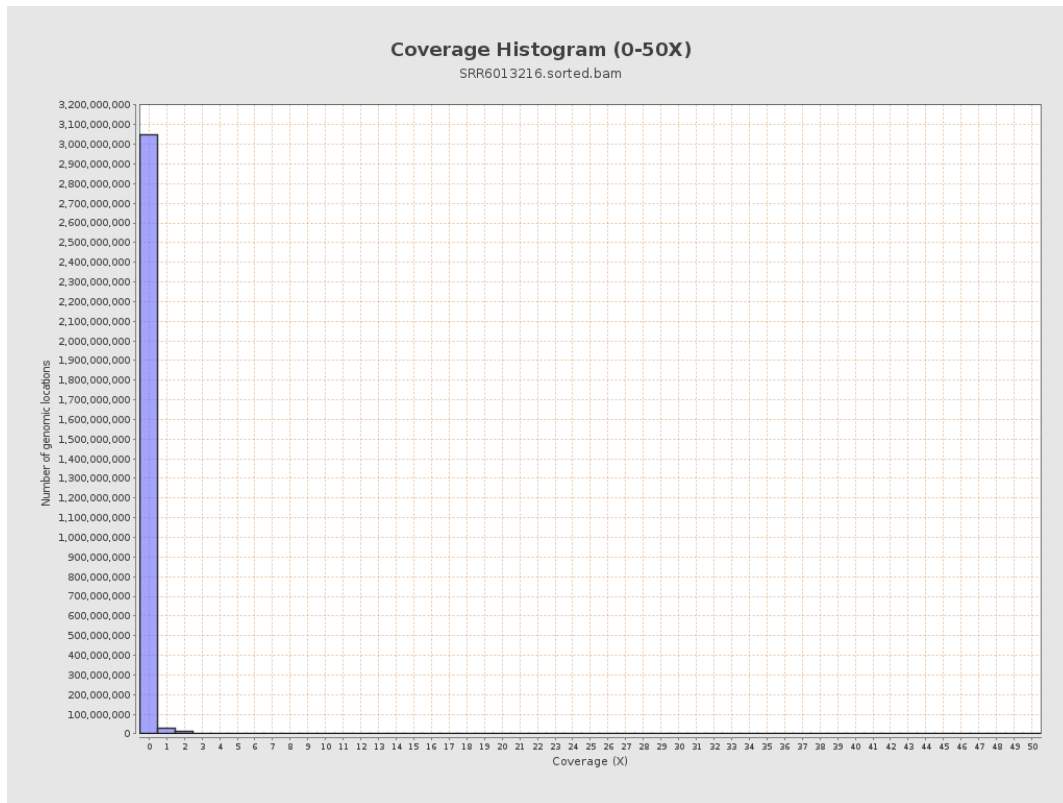
3. Results : Coverage across reference



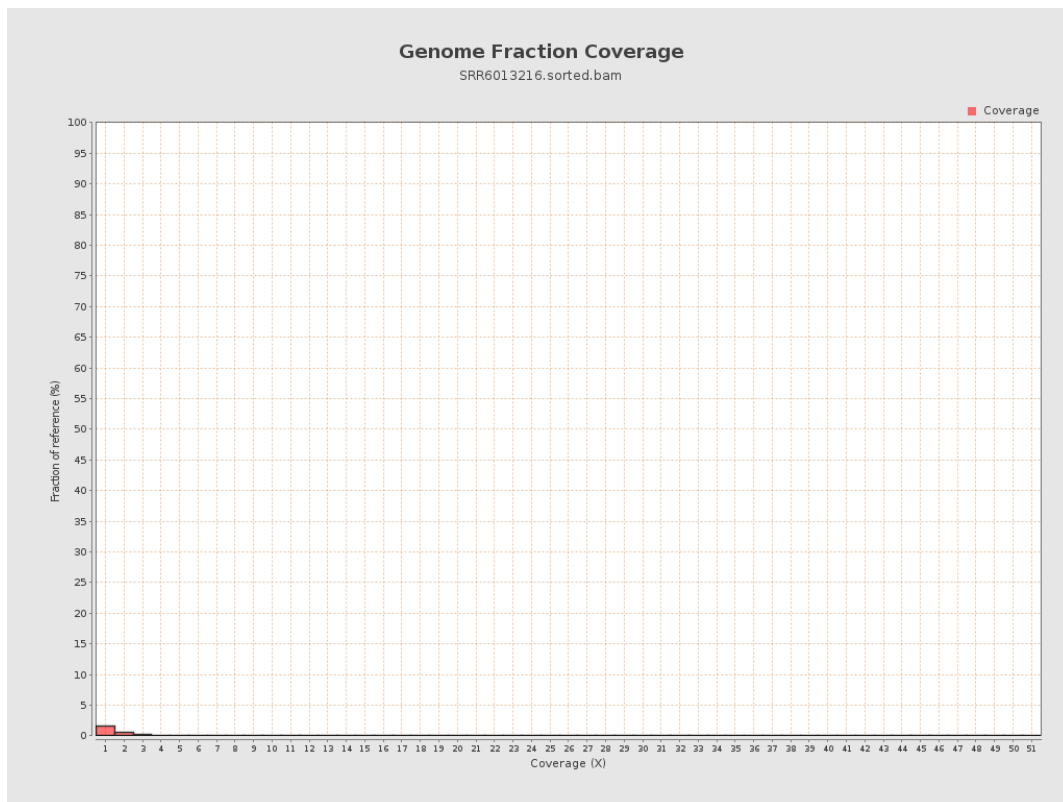
4. Results : Coverage Histogram



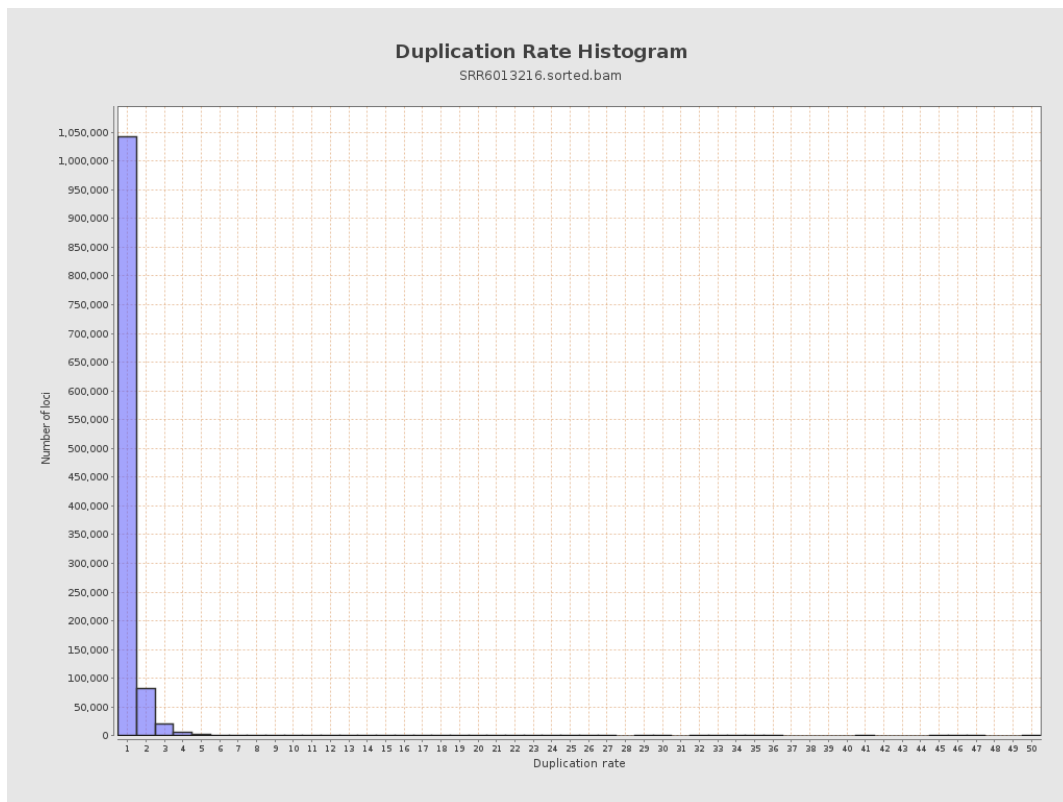
5. Results : Coverage Histogram (0-50X)



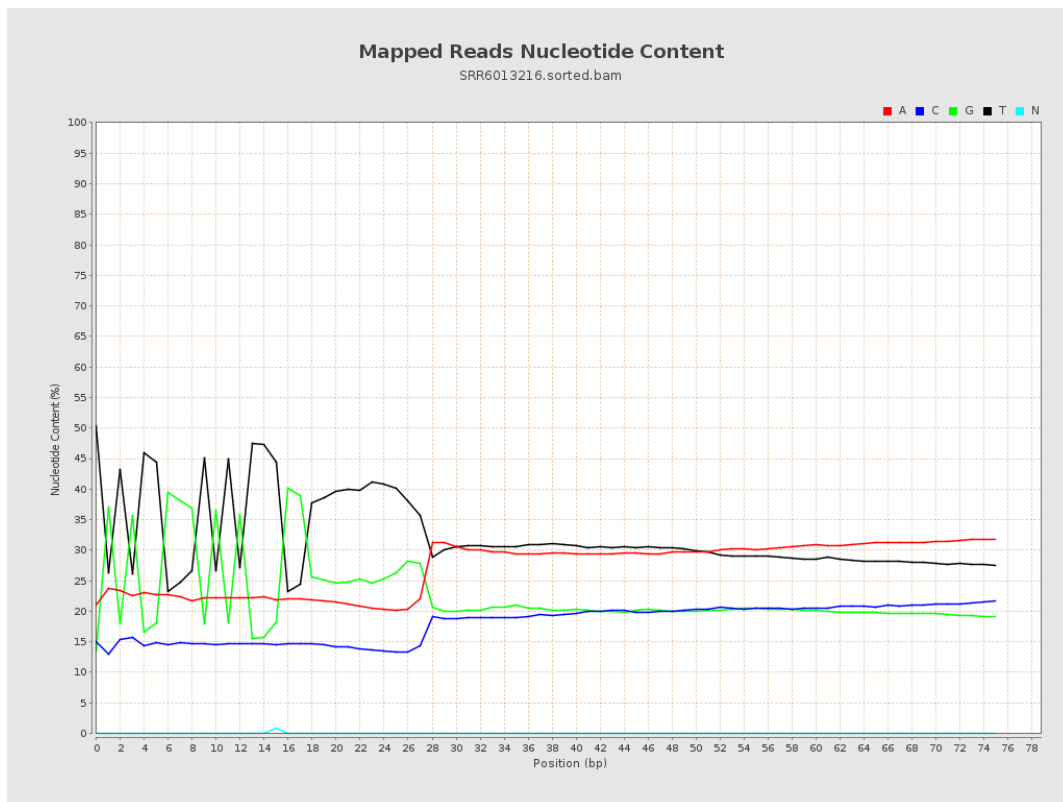
6. Results : Genome Fraction Coverage



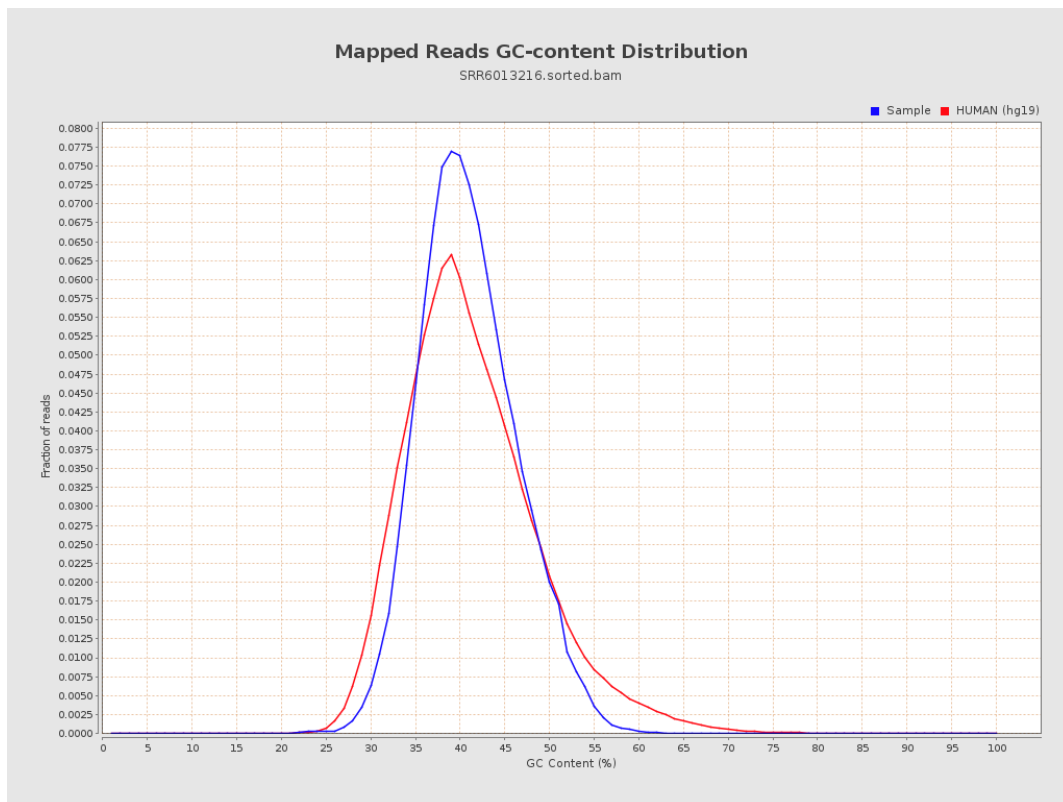
7. Results : Duplication Rate Histogram



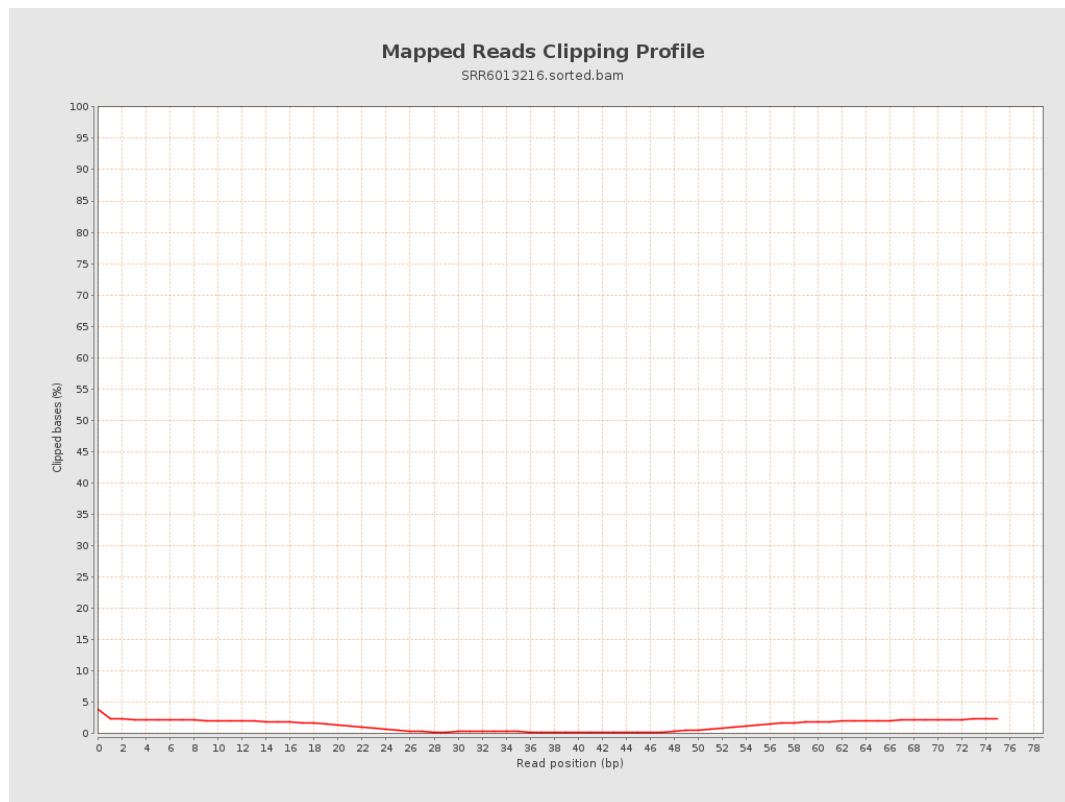
8. Results : Mapped Reads Nucleotide Content



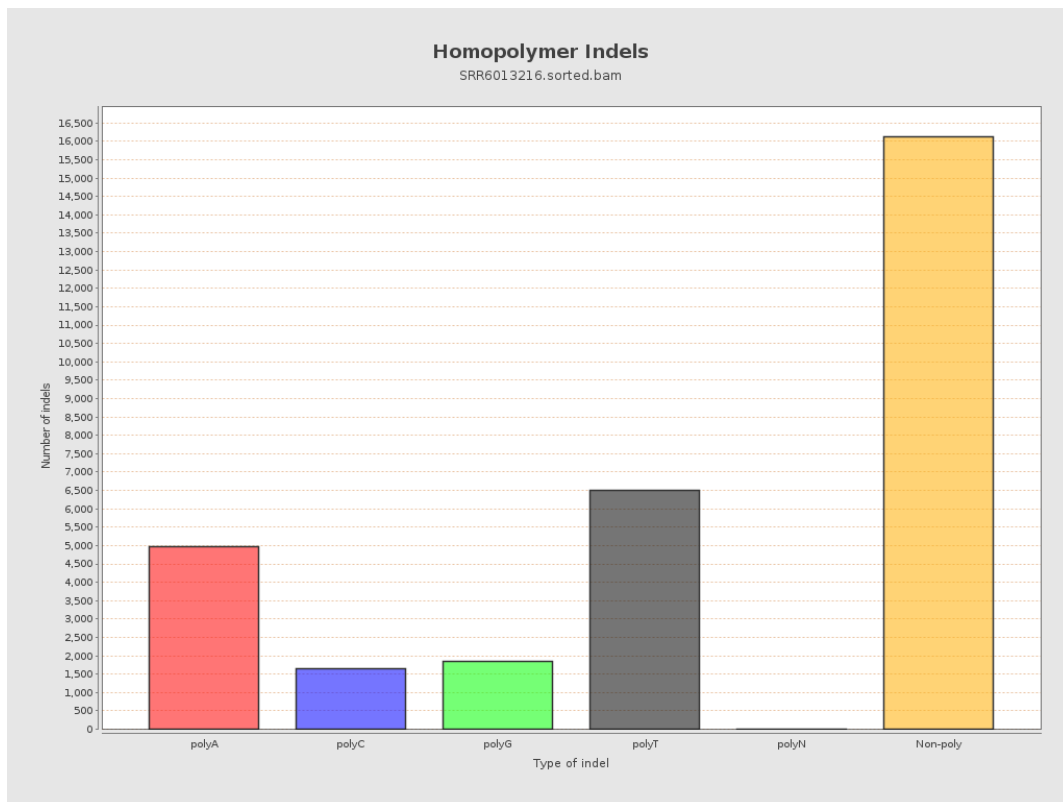
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

