

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:16:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013318.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_SRR6013318 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013318.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:16:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013318.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,542,484
Mapped reads	1,111,877 / 72.08%
Unmapped reads	430,607 / 27.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,888 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	168,635 / 10.93%
Duplication rate	11.39%
Clipped reads	600,308 / 38.92%

2.2. ACGT Content

Number/percentage of A's	19,554,035 / 27.35%
Number/percentage of C's	12,786,490 / 17.88%
Number/percentage of T's	23,221,960 / 32.48%
Number/percentage of G's	15,932,993 / 22.28%
Number/percentage of N's	8,260 / 0.01%
GC Percentage	40.17%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.3012
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2.4. Mapping Quality

Mean Mapping Quality	45.49
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2.5. Mismatches and indels

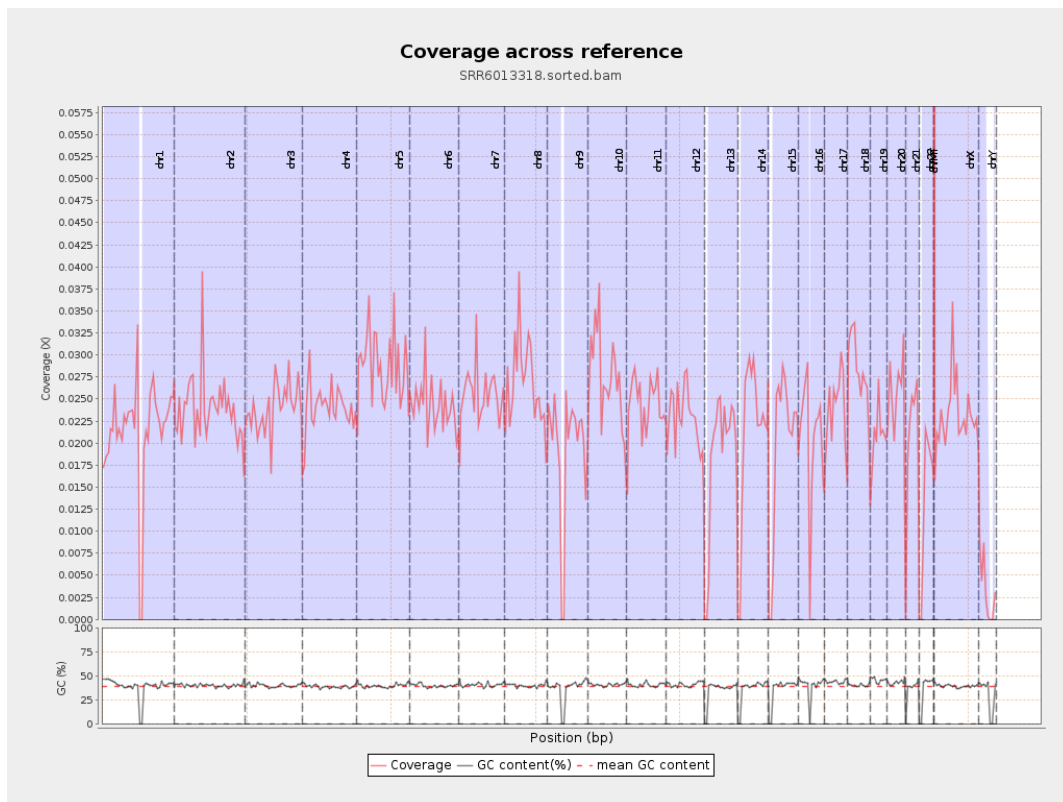
General error rate	0.81%
Mismatches	568,784
Insertions	5,273
Mapped reads with at least one insertion	0.47%
Deletions	20,519
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.05%

2.6. Chromosome stats

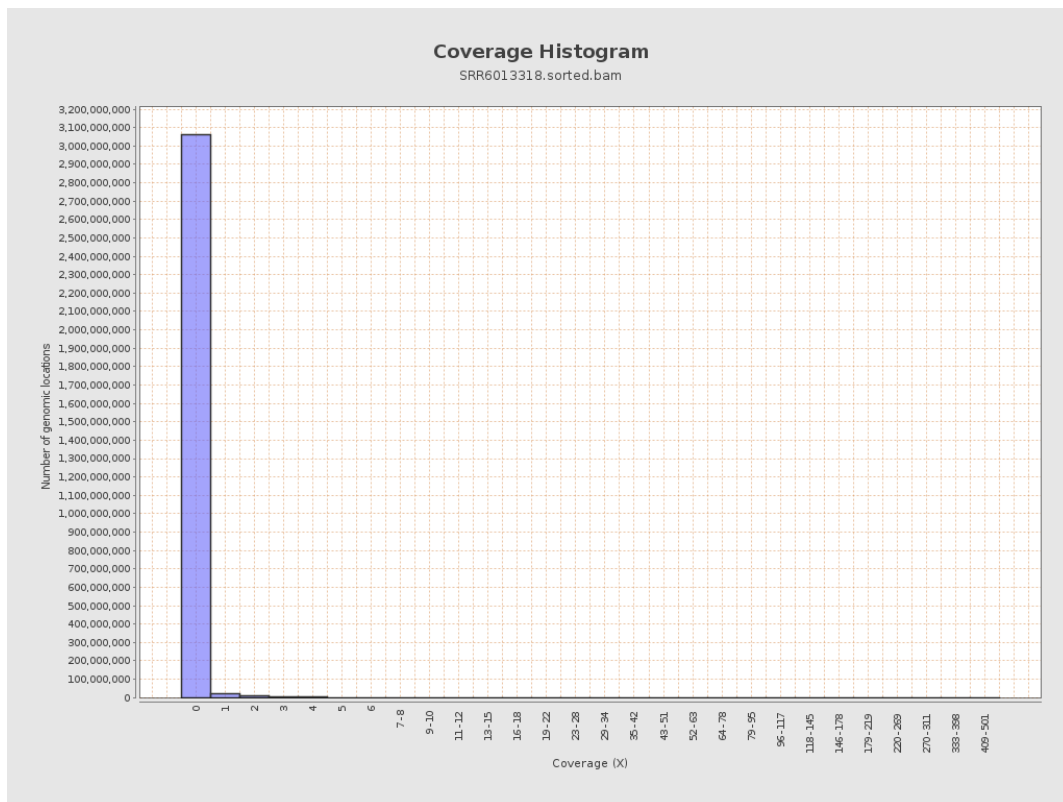
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5325442	0.0214	0.3632
chr2	243199373	5814404	0.0239	0.3622
chr3	198022430	4760312	0.024	0.2727
chr4	191154276	4560018	0.0239	0.2679
chr5	180915260	5261561	0.0291	0.3057
chr6	171115067	4152019	0.0243	0.2884
chr7	159138663	4059842	0.0255	0.3226

chr8	146364022	3932666	0.0269	0.3796
chr9	141213431	2719515	0.0193	0.2557
chr10	135534747	3725022	0.0275	0.3313
chr11	135006516	3317009	0.0246	0.2972
chr12	133851895	3048008	0.0228	0.2639
chr13	115169878	2121151	0.0184	0.2415
chr14	107349540	2298290	0.0214	0.2598
chr15	102531392	2034458	0.0198	0.2481
chr16	90354753	1820341	0.0201	0.2435
chr17	81195210	1937356	0.0239	0.2813
chr18	78077248	2226302	0.0285	0.4136
chr19	59128983	1237031	0.0209	0.2994
chr20	63025520	1605265	0.0255	0.2869
chr21	48129895	1000258	0.0208	0.2492
chr22	51304566	713033	0.0139	0.2119
chrMT	16571	66644	4.0217	5.6855
chrX	155270560	3610676	0.0233	0.2662
chrY	59373566	193158	0.0033	0.0868

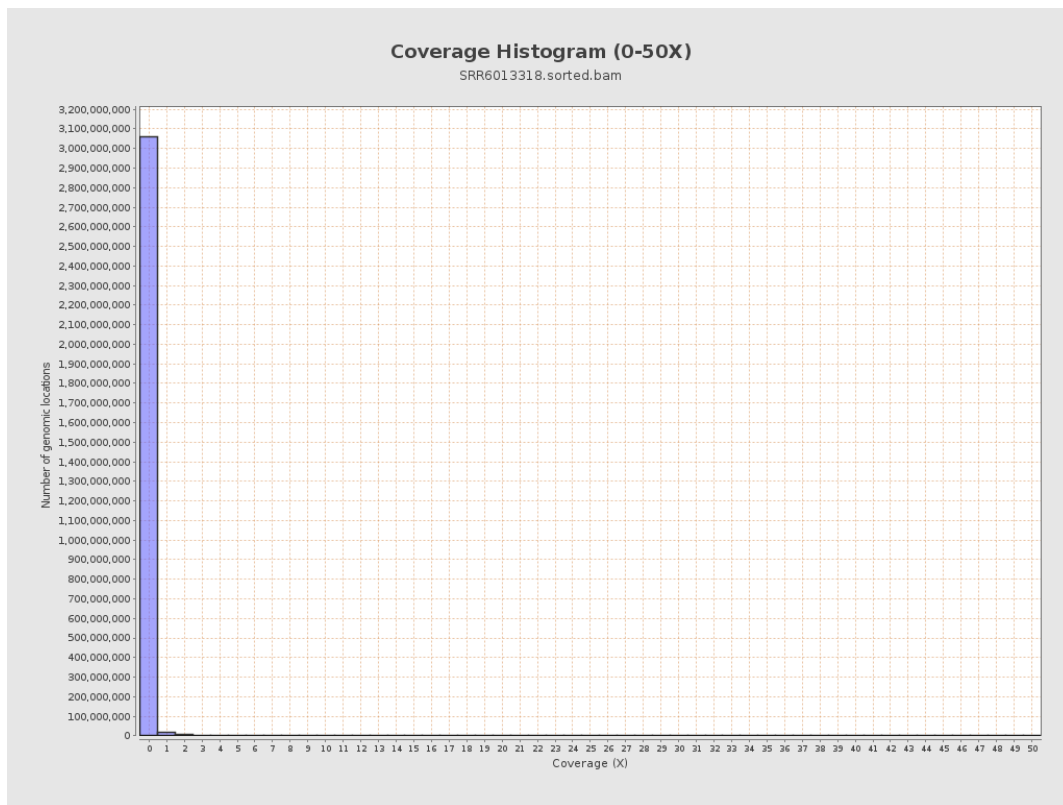
3. Results : Coverage across reference



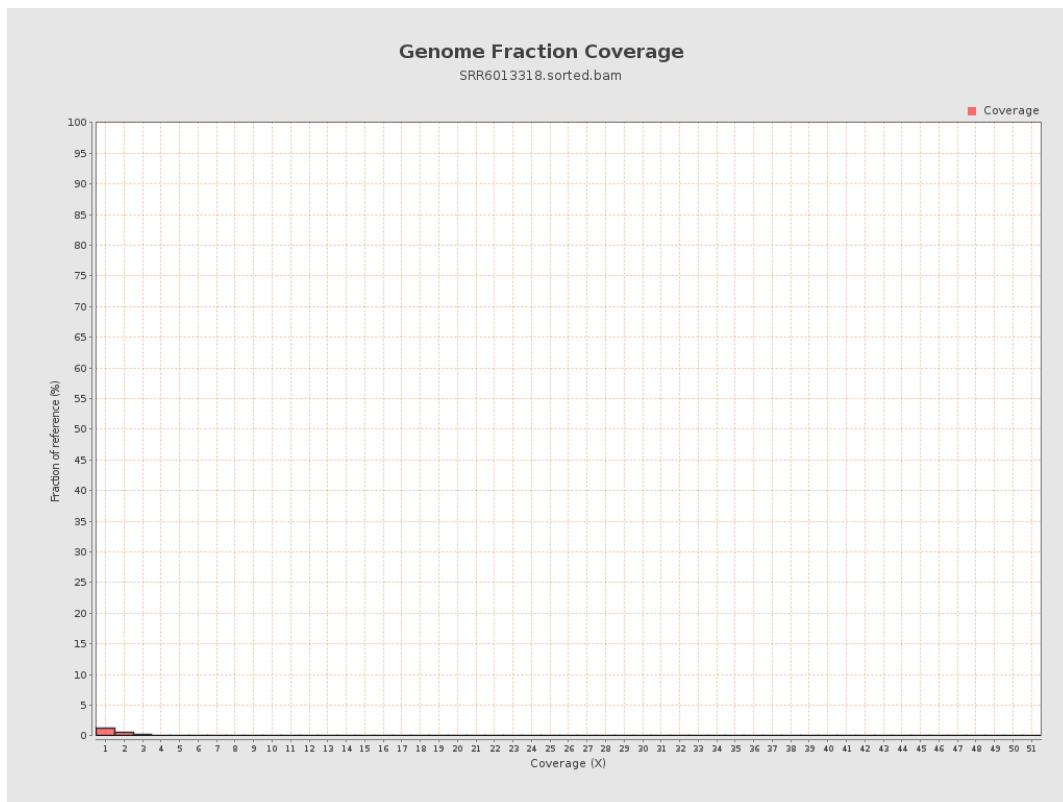
4. Results : Coverage Histogram



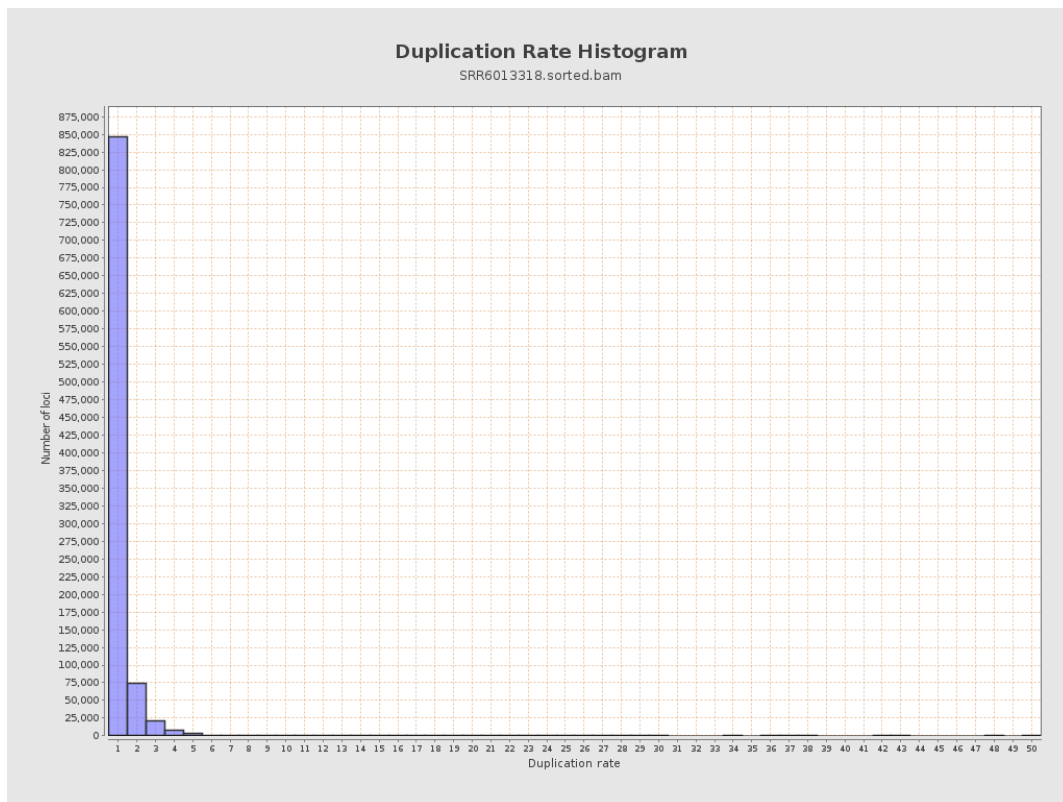
5. Results : Coverage Histogram (0-50X)



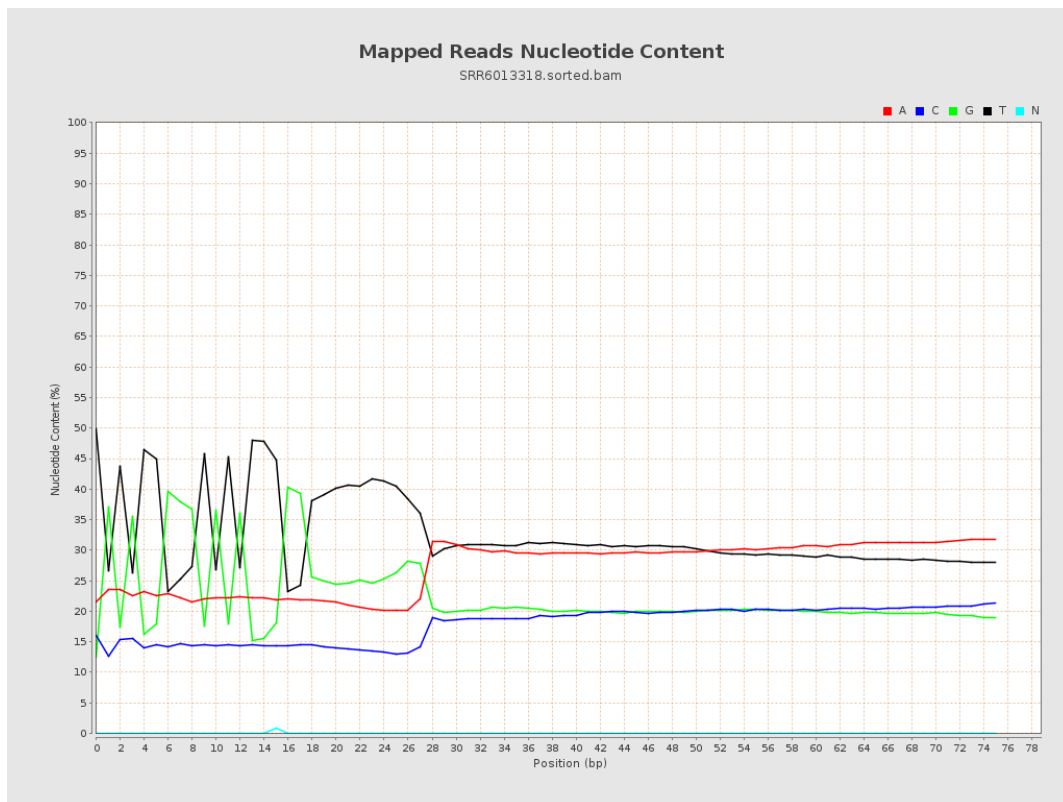
6. Results : Genome Fraction Coverage



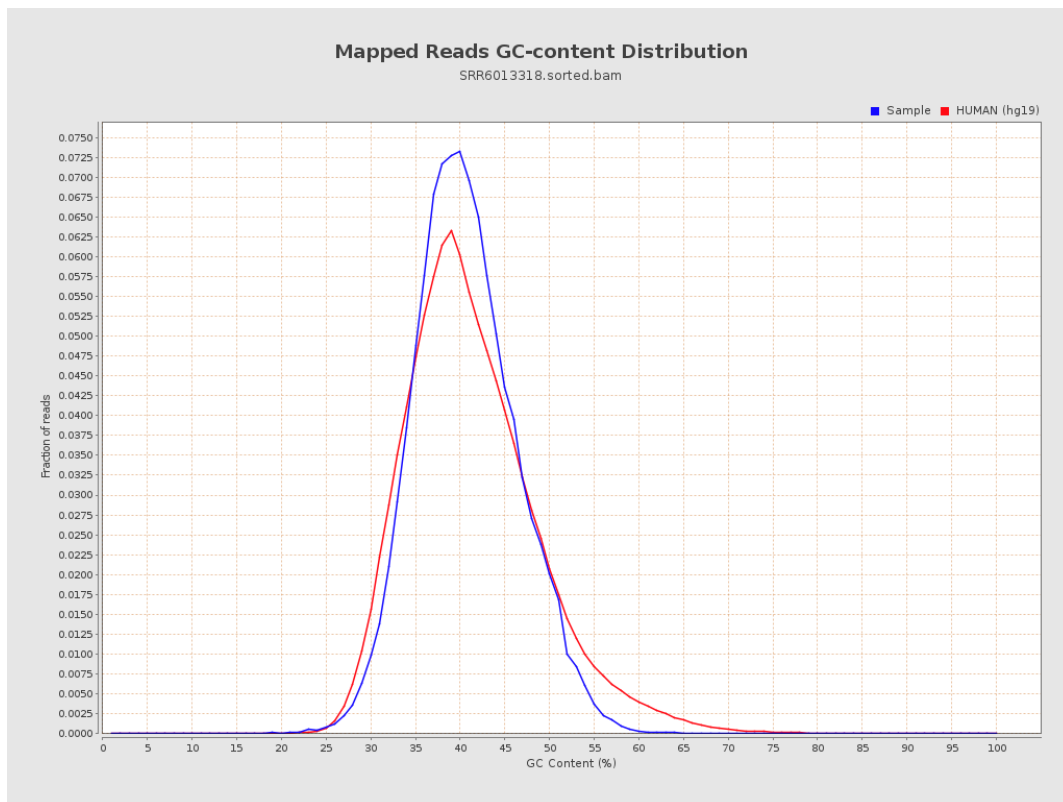
7. Results : Duplication Rate Histogram



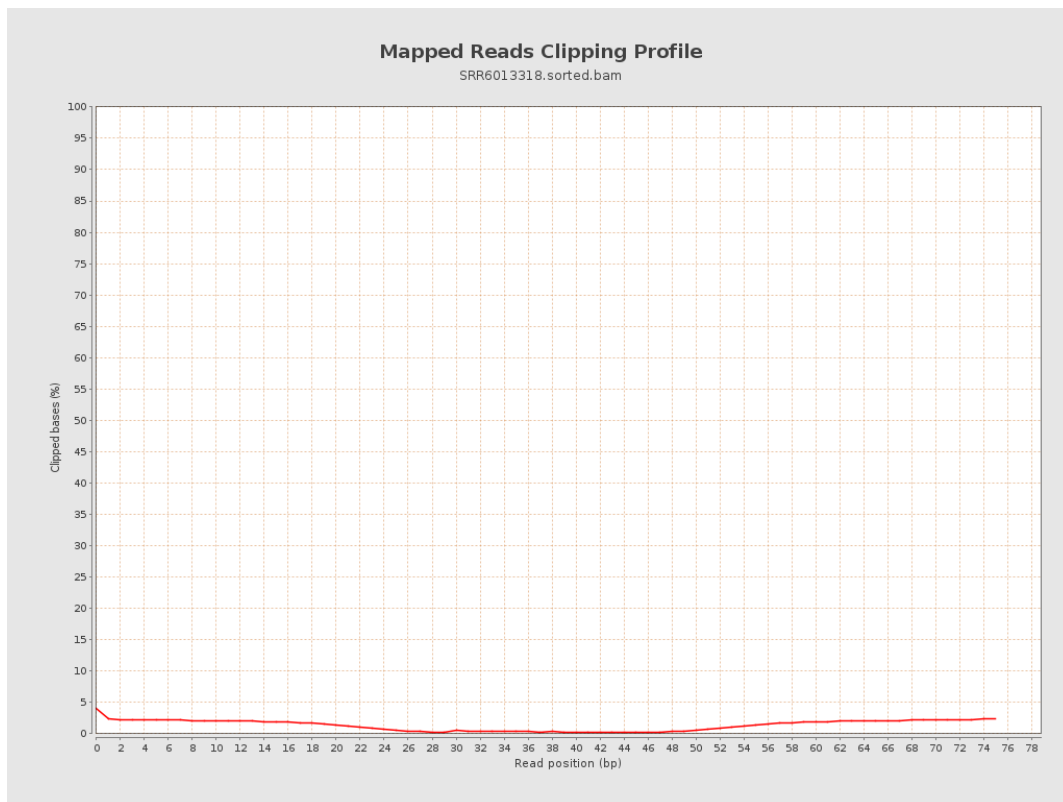
8. Results : Mapped Reads Nucleotide Content



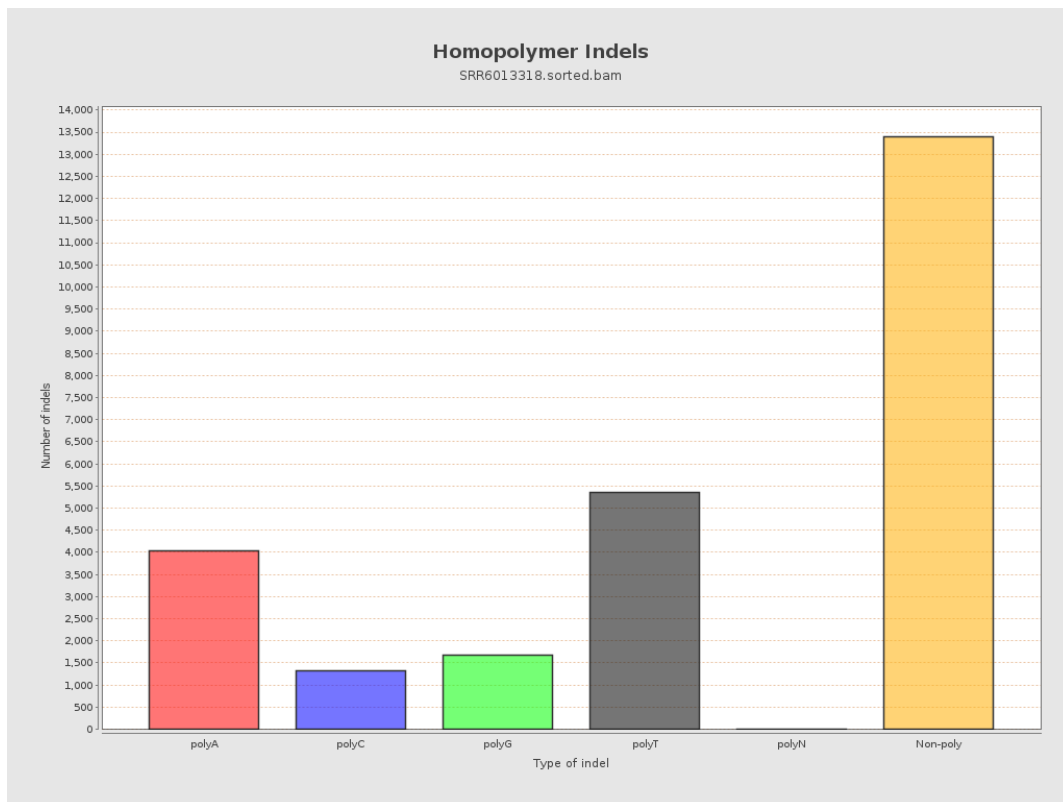
9. Results : Mapped Reads GC-content Distribution



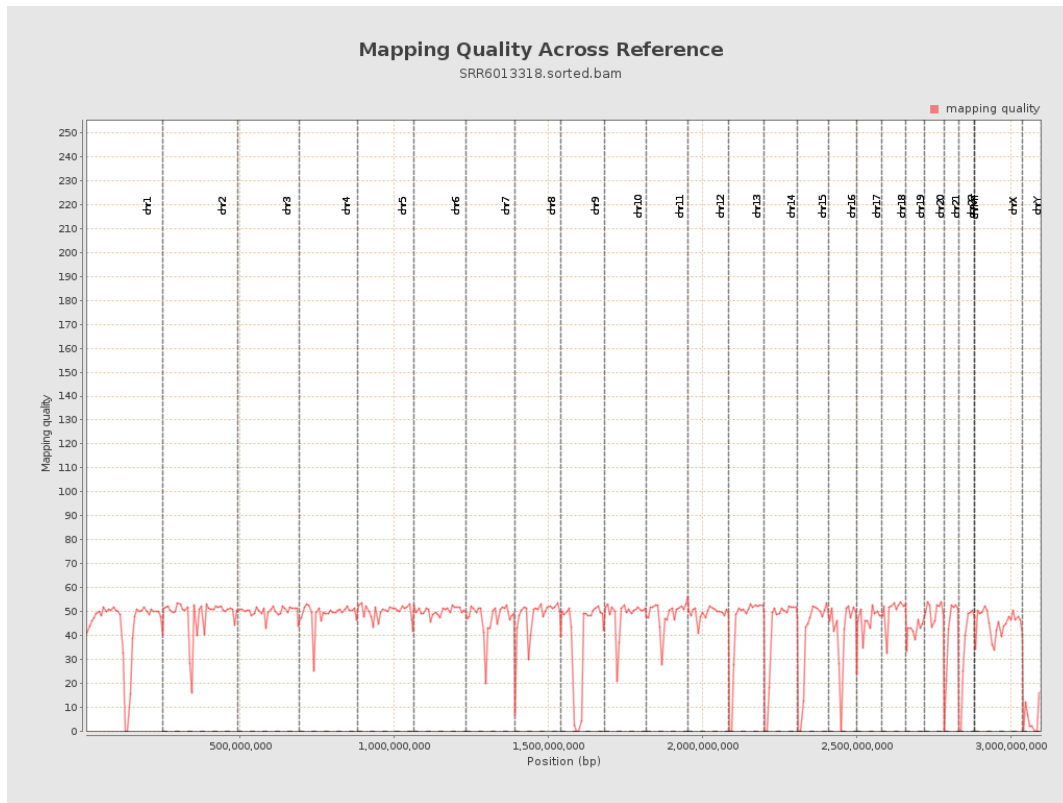
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

