

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:00:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013334.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_SRR6013334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013334.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:00:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,494,097
Mapped reads	564,274 / 37.77%
Unmapped reads	929,823 / 62.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,455 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	104,618 / 7%
Duplication rate	13.02%
Clipped reads	333,933 / 22.35%

2.2. ACGT Content

Number/percentage of A's	9,639,129 / 26.98%
Number/percentage of C's	6,687,808 / 18.72%
Number/percentage of T's	11,232,370 / 31.43%
Number/percentage of G's	8,169,072 / 22.86%
Number/percentage of N's	4,229 / 0.01%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0116

Standard Deviation	0.2268
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2.4. Mapping Quality

Mean Mapping Quality	43.68
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2.5. Mismatches and indels

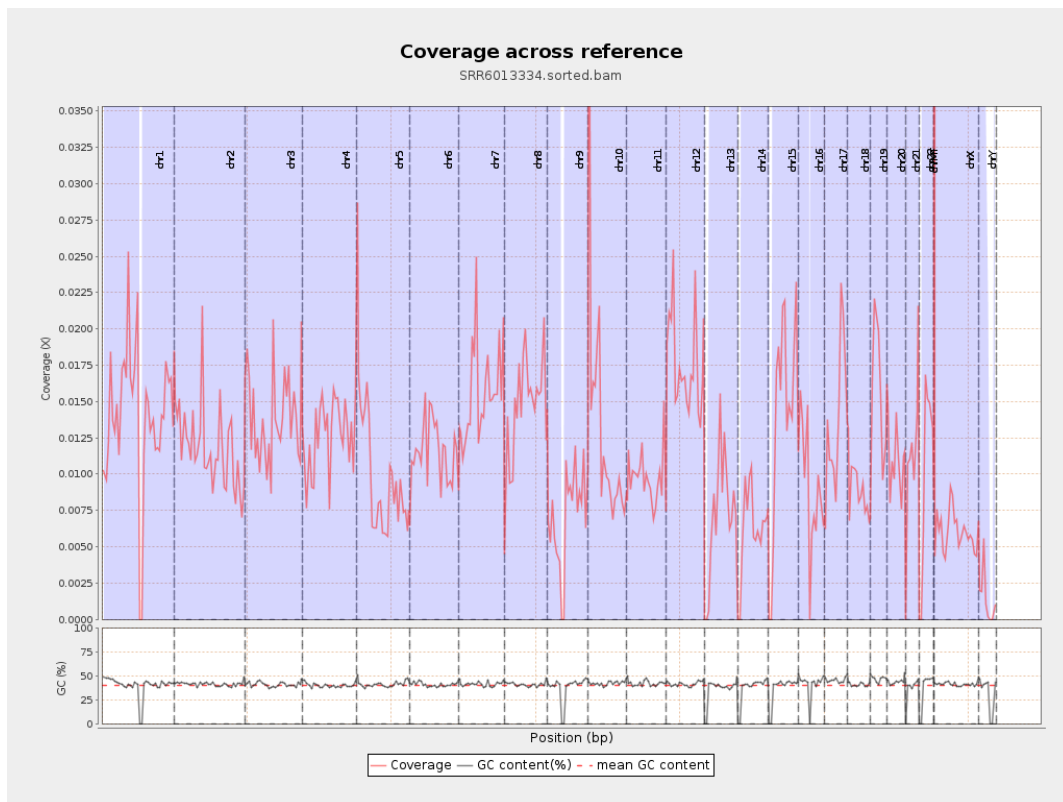
General error rate	0.94%
Mismatches	329,089
Insertions	2,803
Mapped reads with at least one insertion	0.49%
Deletions	14,832
Mapped reads with at least one deletion	2.59%
Homopolymer indels	42.6%

2.6. Chromosome stats

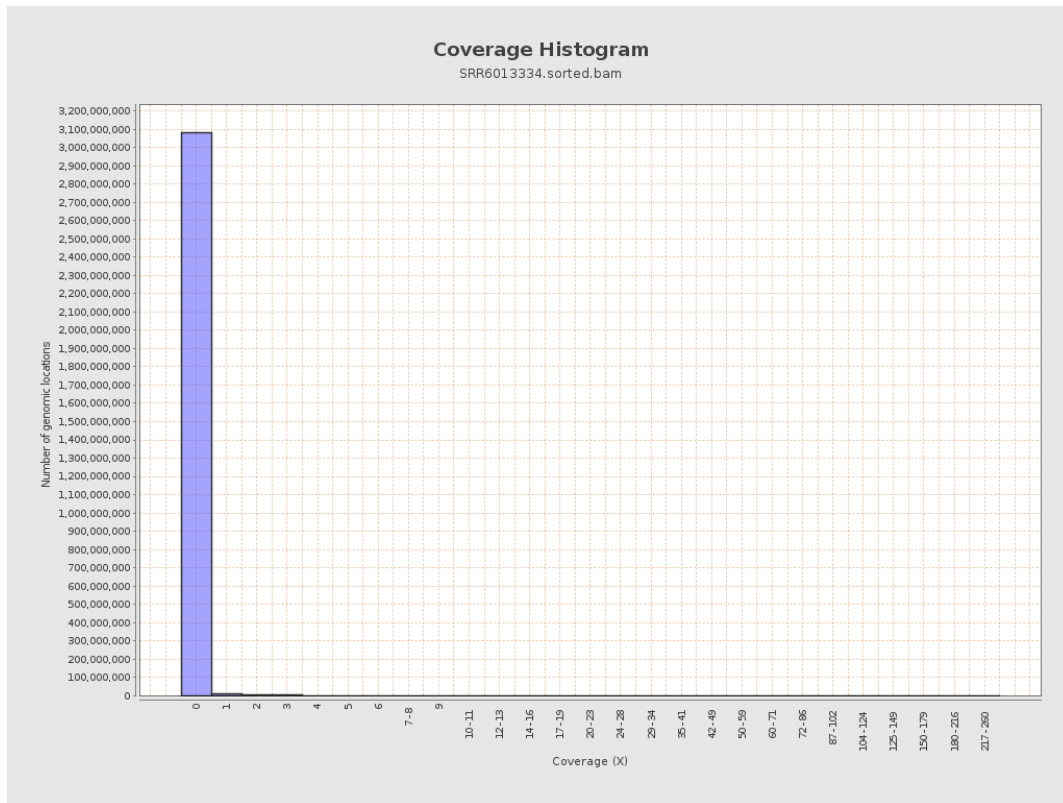
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3499449	0.014	0.2866
chr2	243199373	2858379	0.0118	0.2484
chr3	198022430	2722738	0.0137	0.2299
chr4	191154276	2421410	0.0127	0.2277
chr5	180915260	1725595	0.0095	0.2069
chr6	171115067	1969902	0.0115	0.2145
chr7	159138663	2517207	0.0158	0.2748

chr8	146364022	2165381	0.0148	0.2442
chr9	141213431	996523	0.0071	0.1653
chr10	135534747	1823916	0.0135	0.2446
chr11	135006516	1329130	0.0098	0.2091
chr12	133851895	2349813	0.0176	0.2578
chr13	115169878	831217	0.0072	0.1626
chr14	107349540	668524	0.0062	0.1578
chr15	102531392	1474783	0.0144	0.2355
chr16	90354753	819303	0.0091	0.1885
chr17	81195210	1117333	0.0138	0.253
chr18	78077248	692231	0.0089	0.2359
chr19	59128983	957130	0.0162	0.2753
chr20	63025520	686309	0.0109	0.2287
chr21	48129895	552946	0.0115	0.2138
chr22	51304566	529048	0.0103	0.2056
chrMT	16571	24847	1.4994	2.6826
chrX	155270560	939169	0.006	0.1504
chrY	59373566	86020	0.0014	0.0625

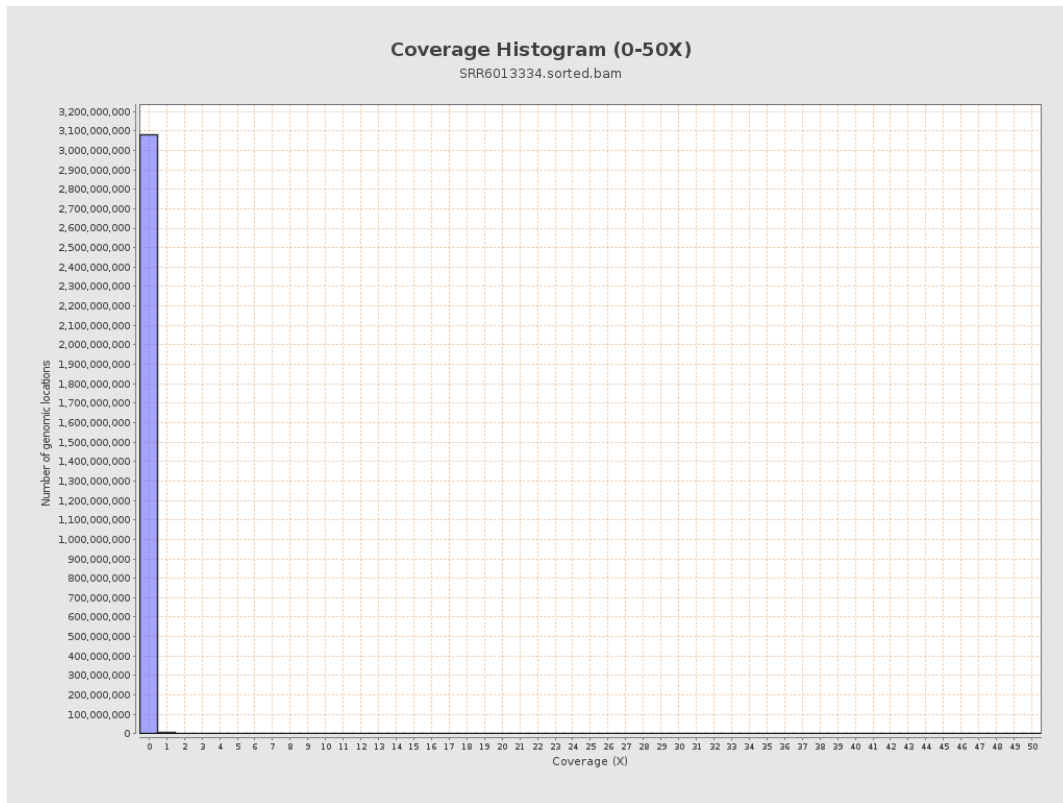
3. Results : Coverage across reference



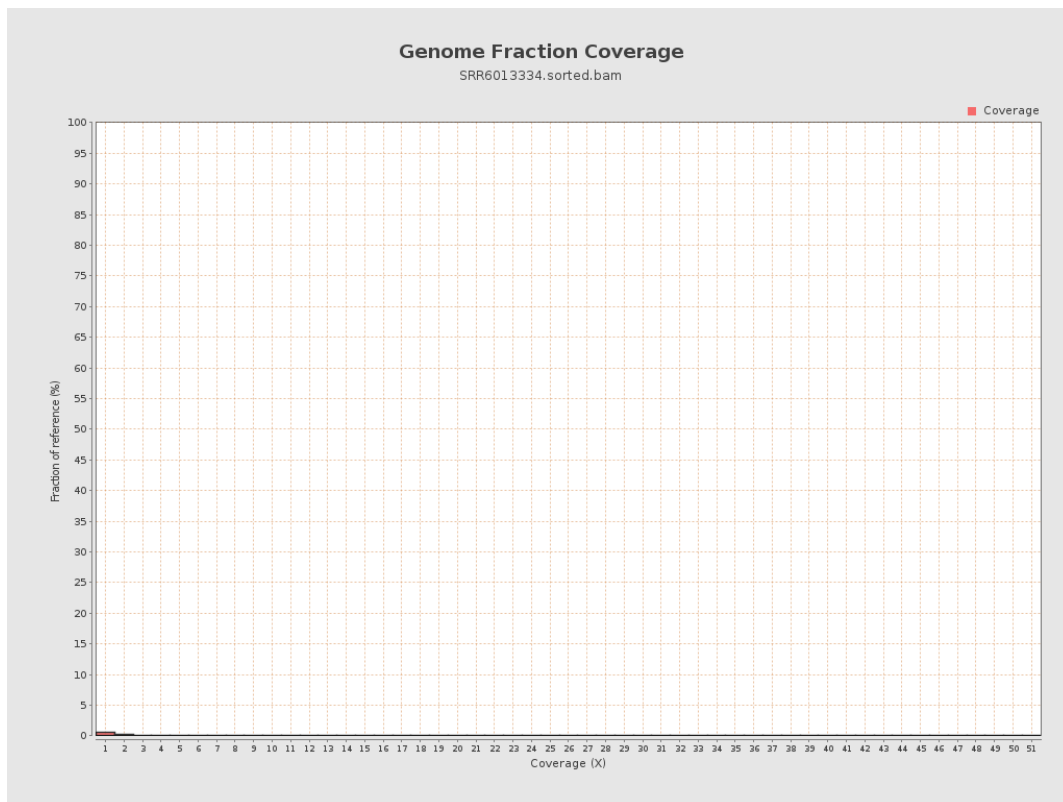
4. Results : Coverage Histogram



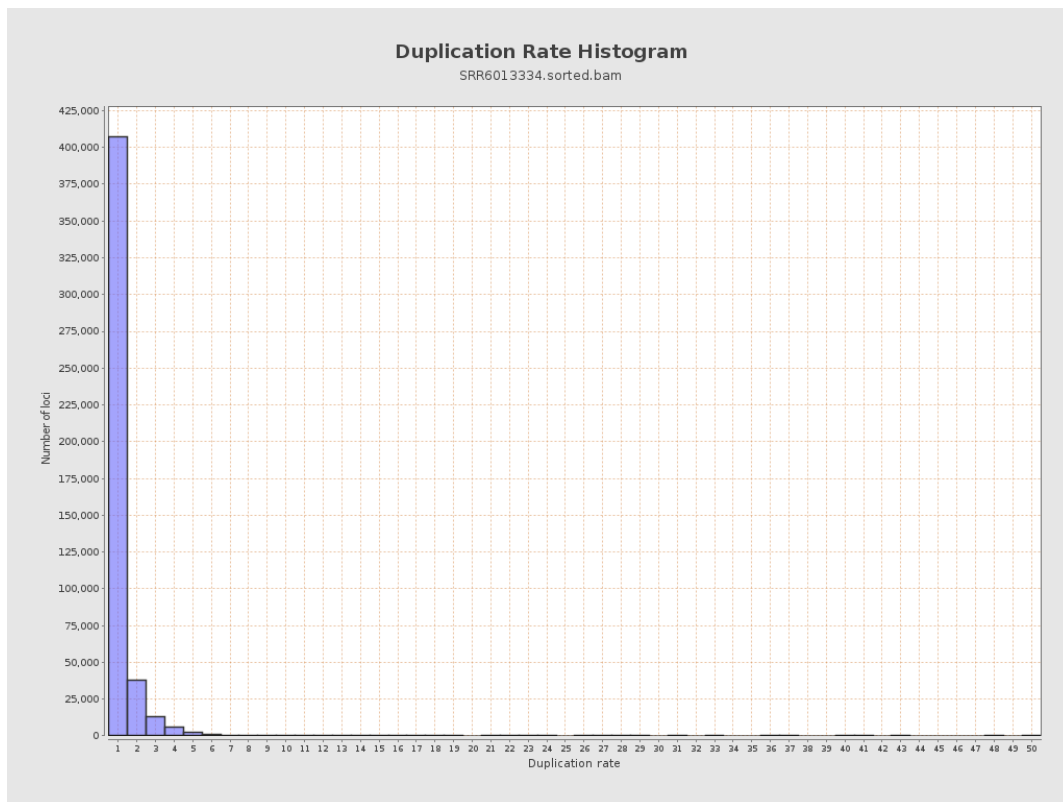
5. Results : Coverage Histogram (0-50X)



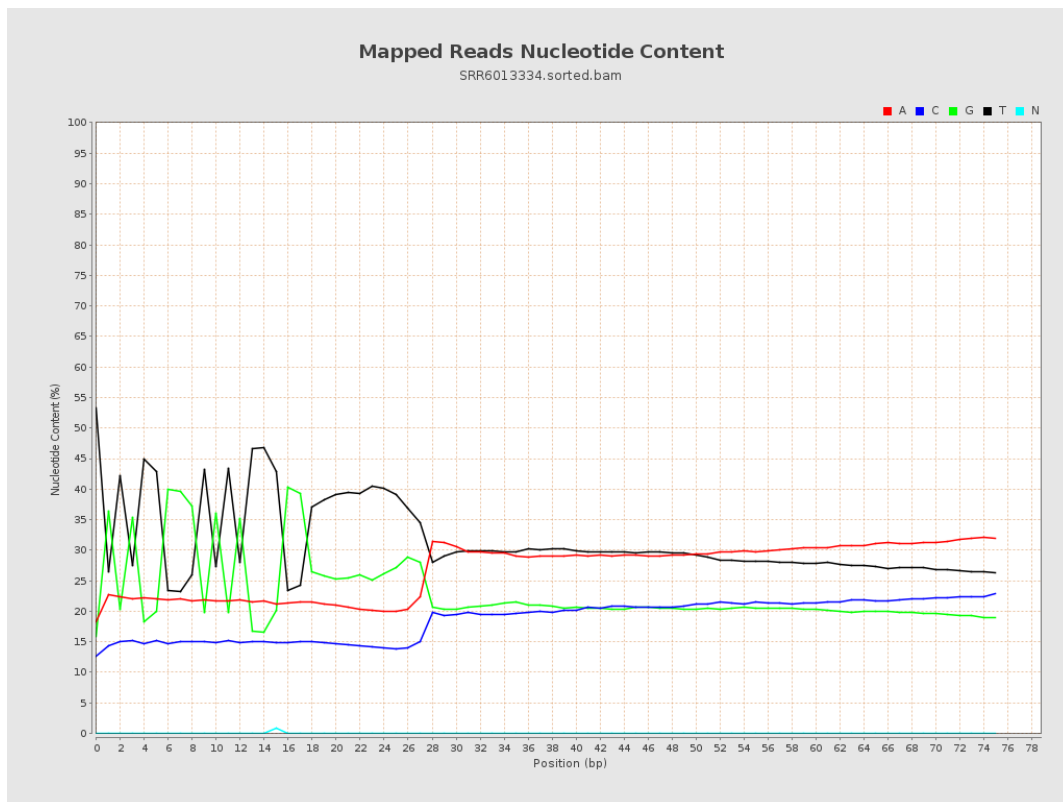
6. Results : Genome Fraction Coverage



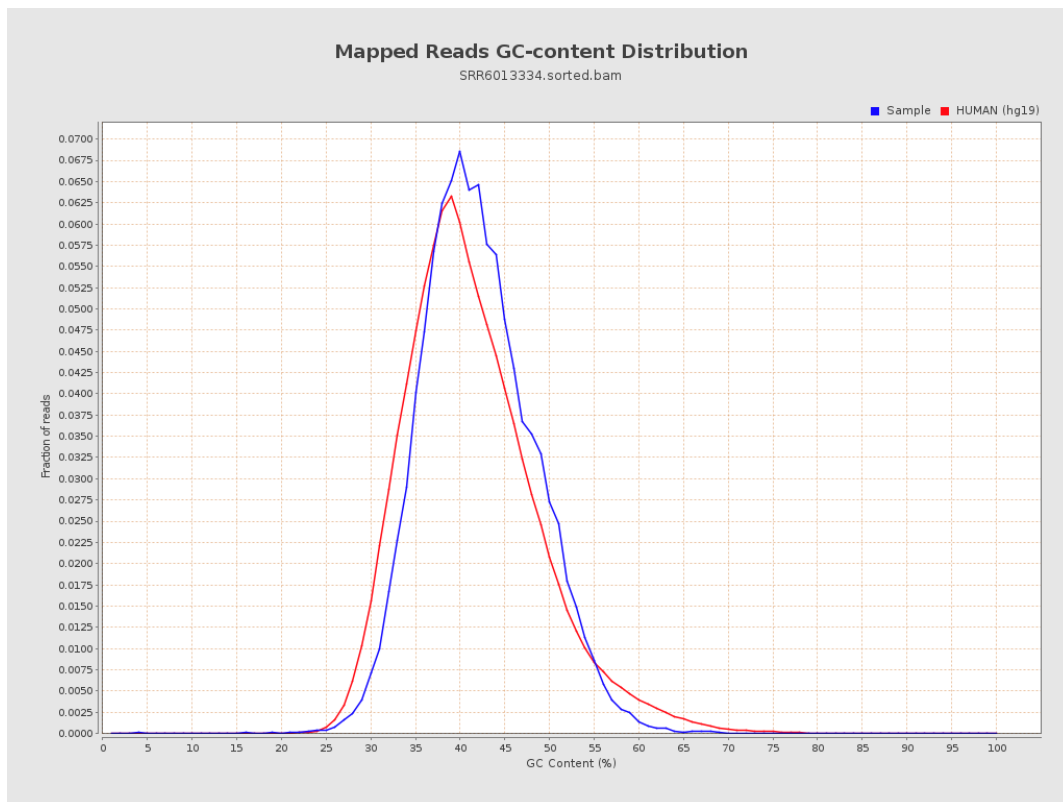
7. Results : Duplication Rate Histogram



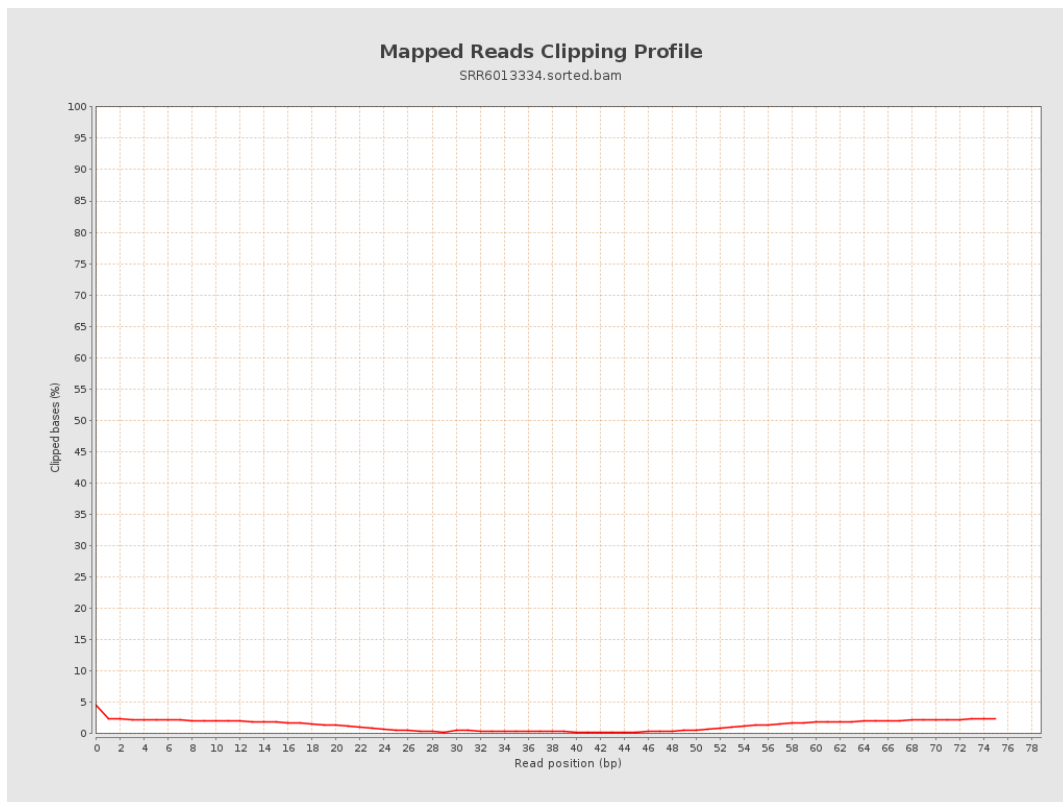
8. Results : Mapped Reads Nucleotide Content



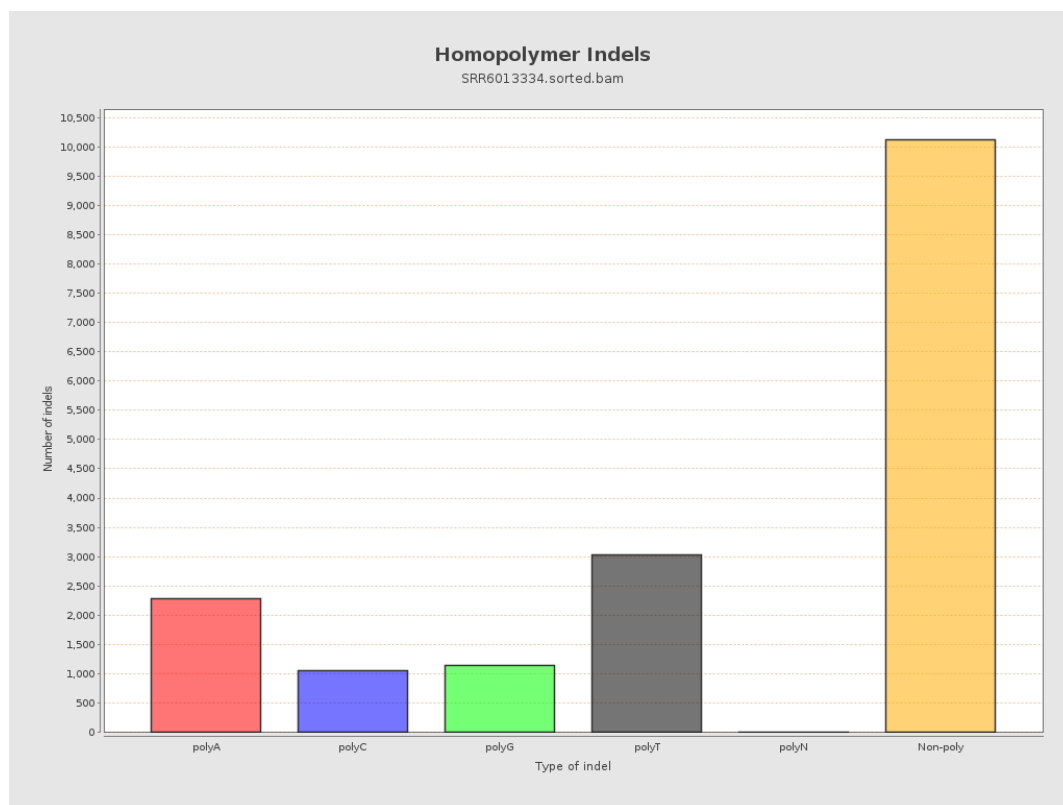
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

