

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:15:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083620.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_SRR3083620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083620.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:15:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,841,763
Mapped reads	1,642,344 / 89.17%
Unmapped reads	199,419 / 10.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,684 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	79,181 / 4.3%
Duplication rate	4.09%
Clipped reads	783,908 / 42.56%

2.2. ACGT Content

Number/percentage of A's	28,616,737 / 26.45%
Number/percentage of C's	20,393,147 / 18.85%
Number/percentage of T's	33,841,869 / 31.28%
Number/percentage of G's	25,344,049 / 23.42%
Number/percentage of N's	5,192 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.035

Standard Deviation	0.2952
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2.4. Mapping Quality

Mean Mapping Quality	45.19
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2.5. Mismatches and indels

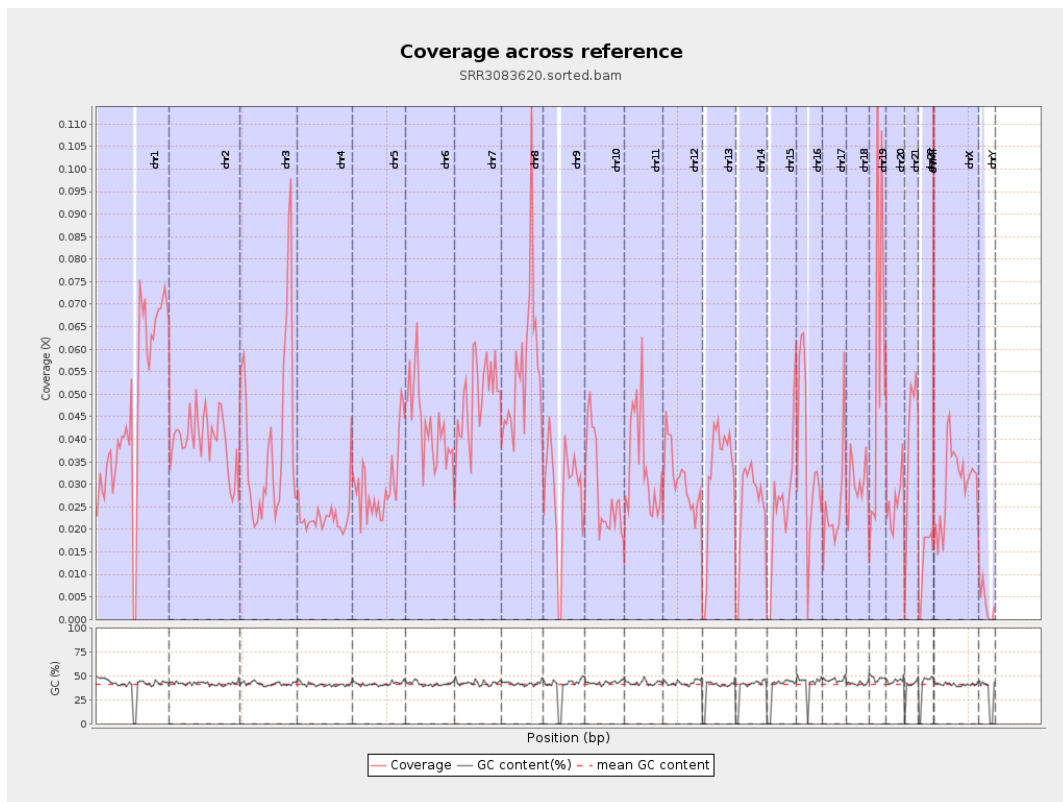
General error rate	0.71%
Mismatches	755,171
Insertions	7,775
Mapped reads with at least one insertion	0.47%
Deletions	23,782
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.54%

2.6. Chromosome stats

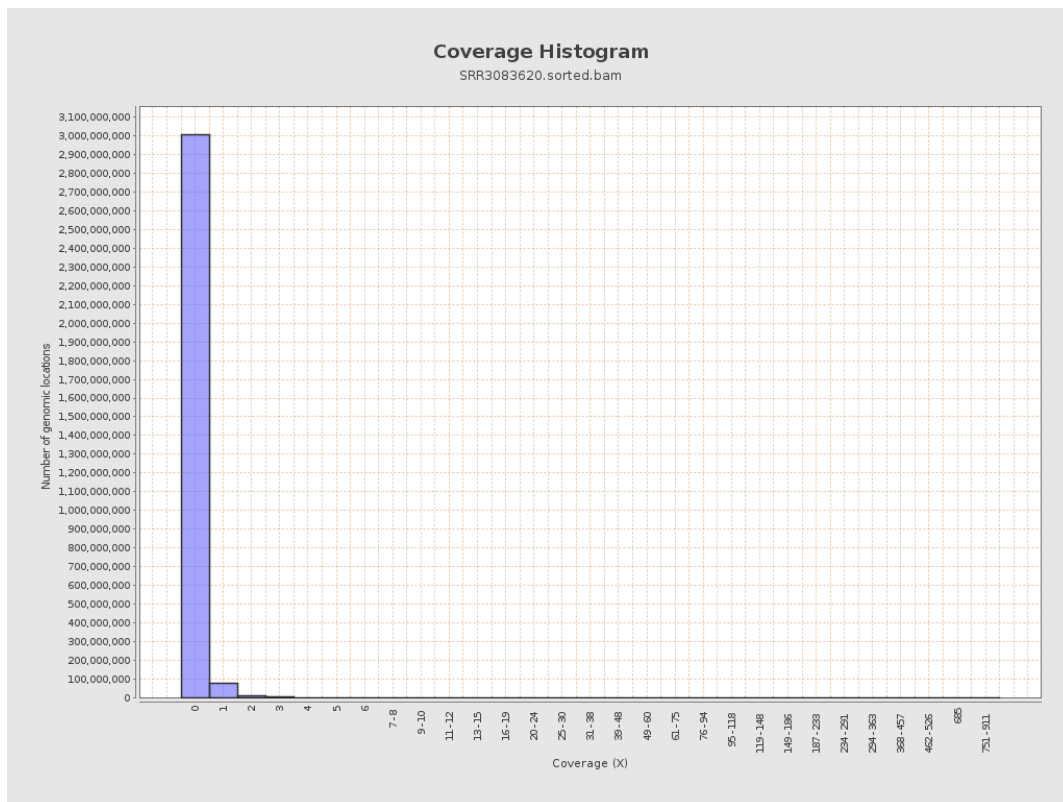
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11650776	0.0467	0.5034
chr2	243199373	9676958	0.0398	0.4564
chr3	198022430	7823857	0.0395	0.2321
chr4	191154276	4388522	0.023	0.1835
chr5	180915260	5452961	0.0301	0.2007
chr6	171115067	7355717	0.043	0.2721
chr7	159138663	7908284	0.0497	0.4028

chr8	146364022	8144147	0.0556	0.3095
chr9	141213431	4073437	0.0288	0.224
chr10	135534747	3926908	0.029	0.2328
chr11	135006516	4597848	0.0341	0.2473
chr12	133851895	4120477	0.0308	0.2035
chr13	115169878	3642115	0.0316	0.2079
chr14	107349540	2713777	0.0253	0.185
chr15	102531392	2582792	0.0252	0.1943
chr16	90354753	3278294	0.0363	0.225
chr17	81195210	2084628	0.0257	0.1942
chr18	78077248	2365242	0.0303	0.3298
chr19	59128983	3303895	0.0559	0.3821
chr20	63025520	1666535	0.0264	0.1938
chr21	48129895	1919332	0.0399	0.2352
chr22	51304566	680556	0.0133	0.1323
chrMT	16571	2899	0.1749	0.4393
chrX	155270560	4678323	0.0301	0.2116
chrY	59373566	201022	0.0034	0.0731

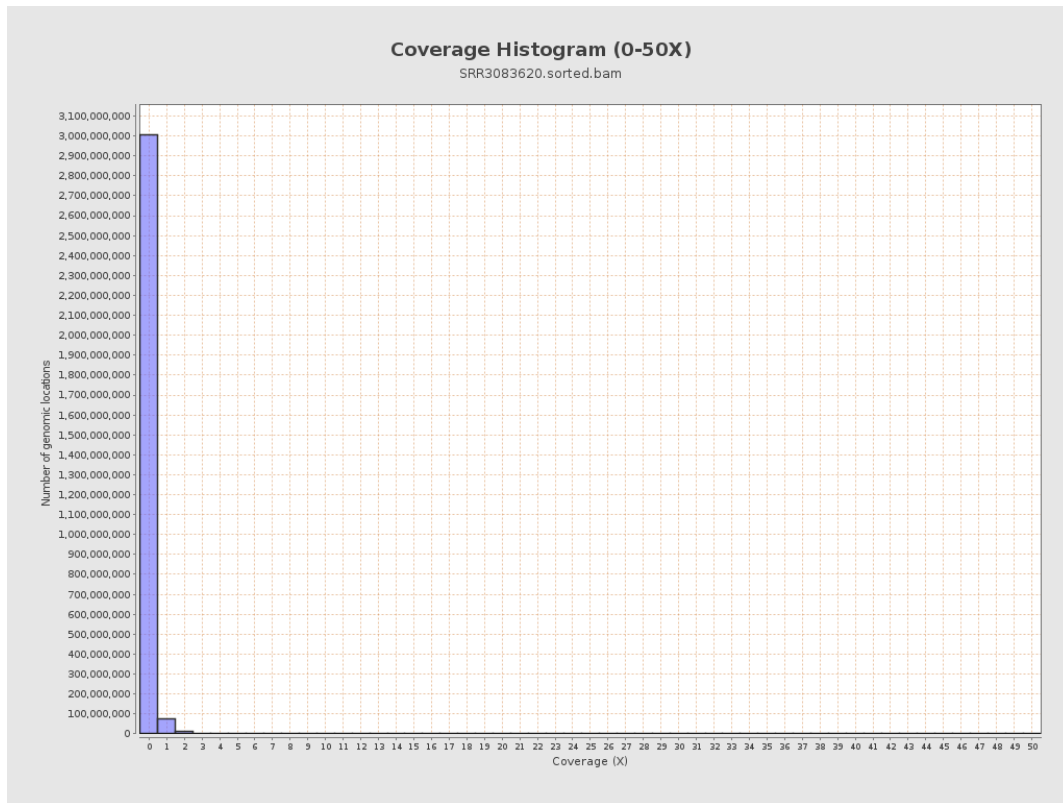
3. Results : Coverage across reference



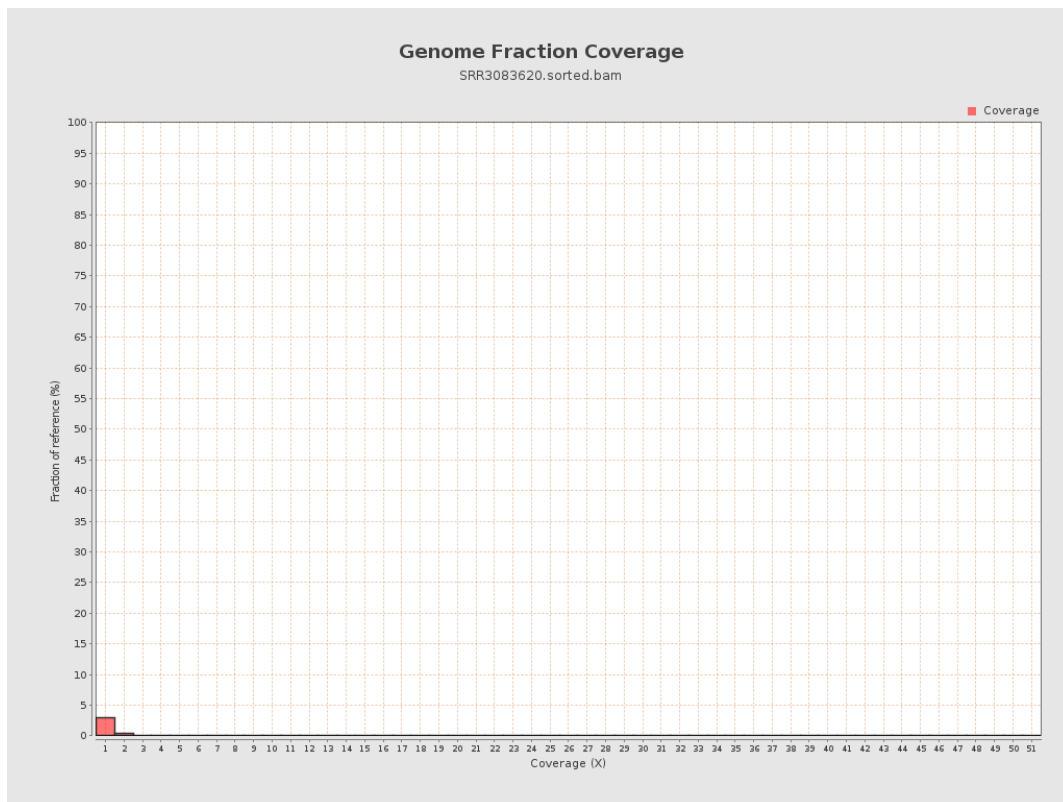
4. Results : Coverage Histogram



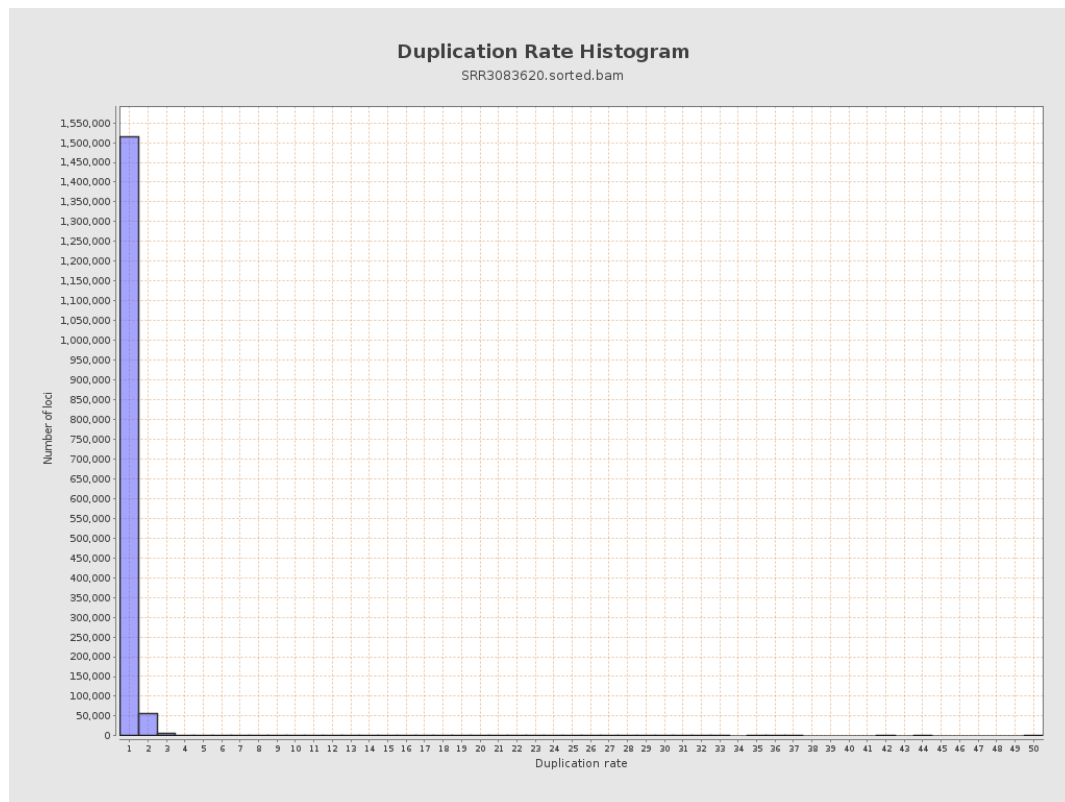
5. Results : Coverage Histogram (0-50X)



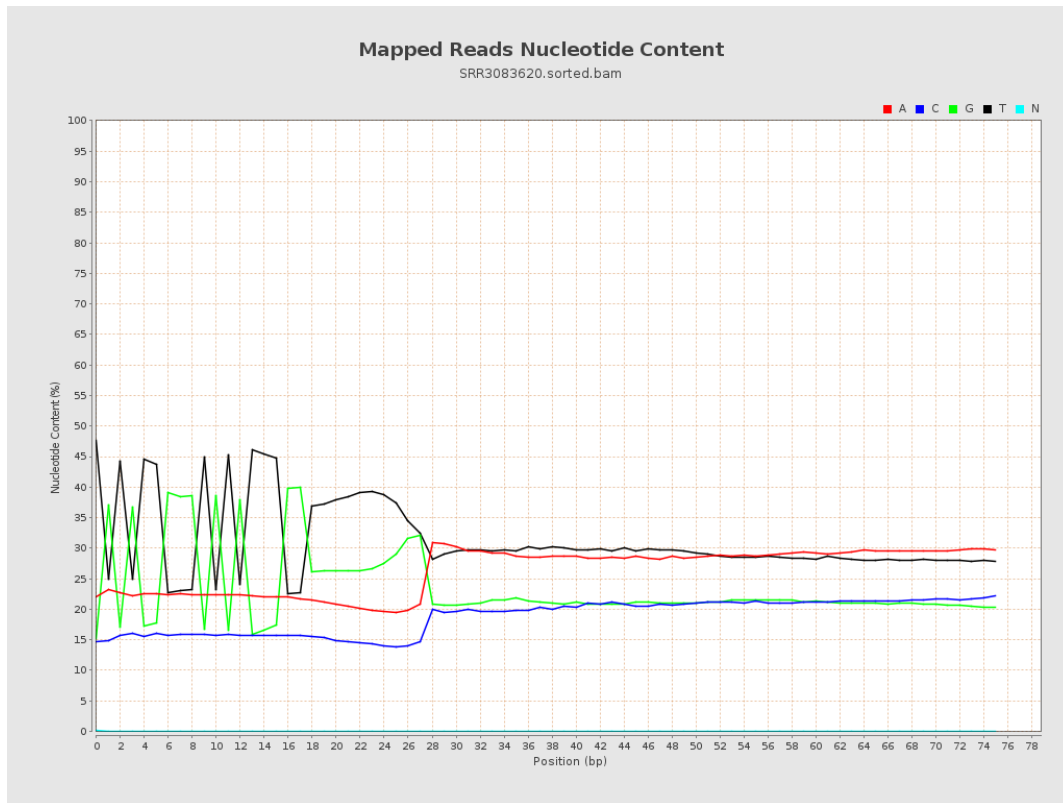
6. Results : Genome Fraction Coverage



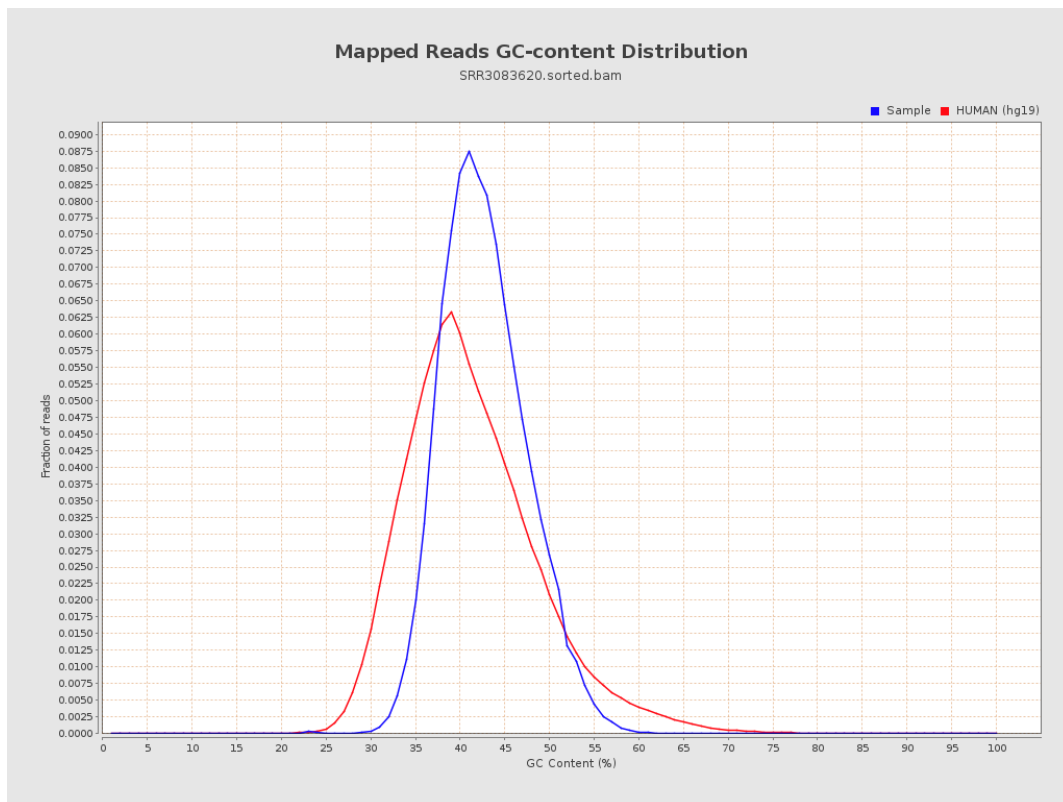
7. Results : Duplication Rate Histogram



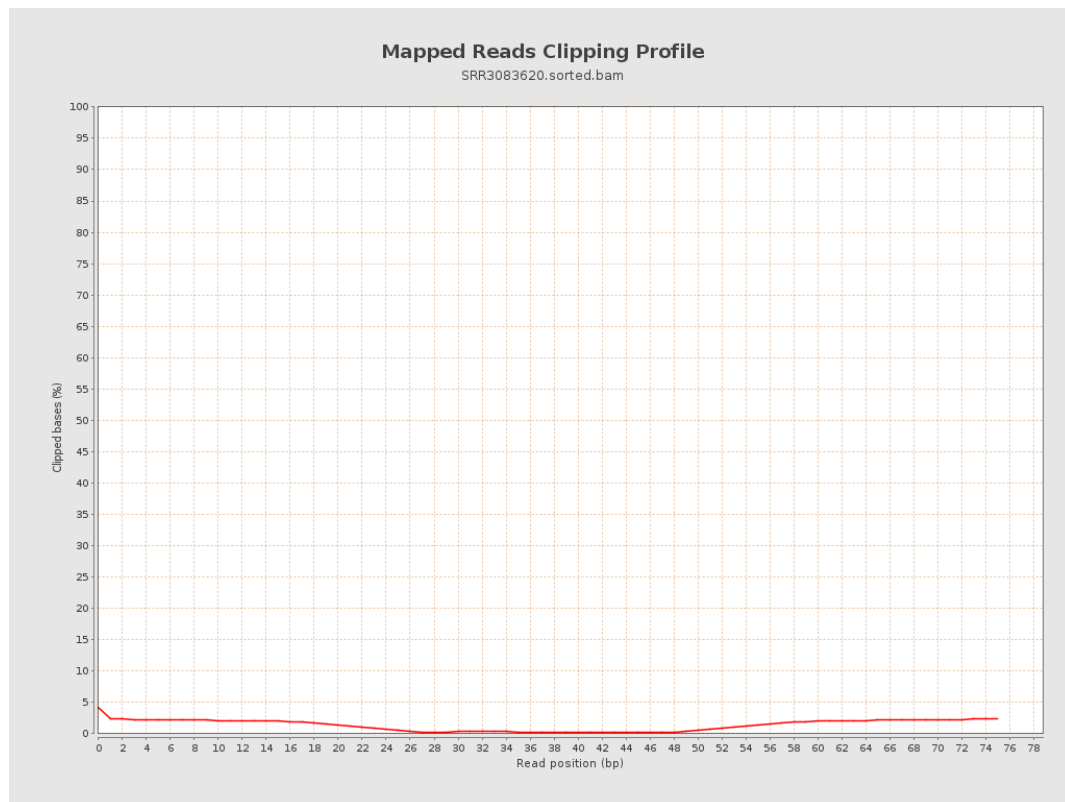
8. Results : Mapped Reads Nucleotide Content



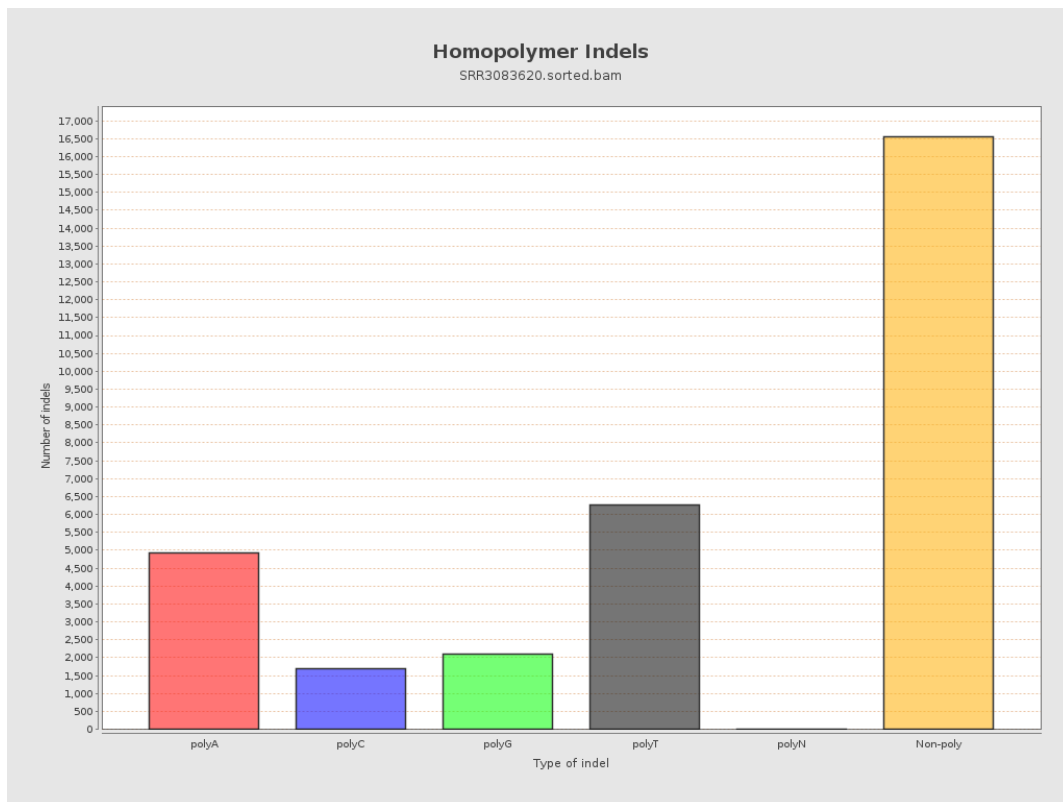
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

