

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:57:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004120.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_SRR6004120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:57:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,748,930
Mapped reads	2,284,333 / 83.1%
Unmapped reads	464,597 / 16.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,401 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	114,250 / 4.16%
Duplication rate	3.76%
Clipped reads	1,088,890 / 39.61%

2.2. ACGT Content

Number/percentage of A's	41,295,773 / 27.38%
Number/percentage of C's	26,731,613 / 17.72%
Number/percentage of T's	49,184,271 / 32.61%
Number/percentage of G's	33,609,412 / 22.28%
Number/percentage of N's	15,932 / 0.01%
GC Percentage	40%

2.3. Coverage

Mean	0.0487

Standard Deviation	0.5082
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2.4. Mapping Quality

Mean Mapping Quality	44.54
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2.5. Mismatches and indels

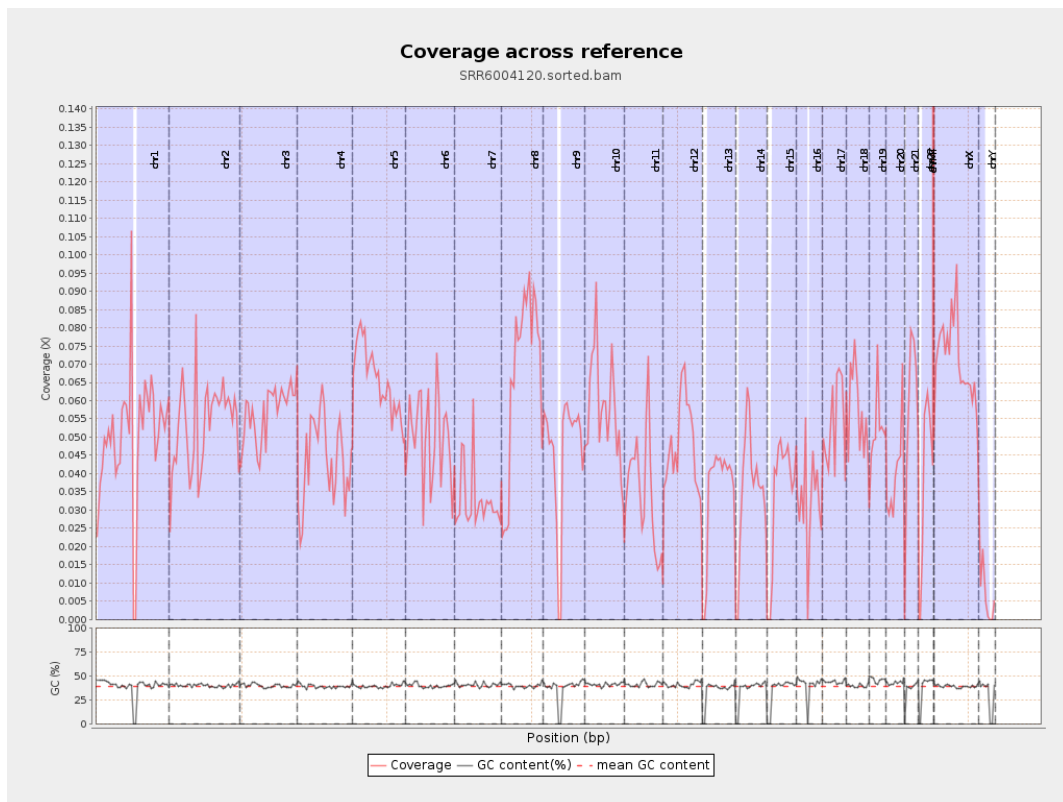
General error rate	0.98%
Mismatches	1,452,906
Insertions	13,793
Mapped reads with at least one insertion	0.6%
Deletions	42,253
Mapped reads with at least one deletion	1.83%
Homopolymer indels	47.46%

2.6. Chromosome stats

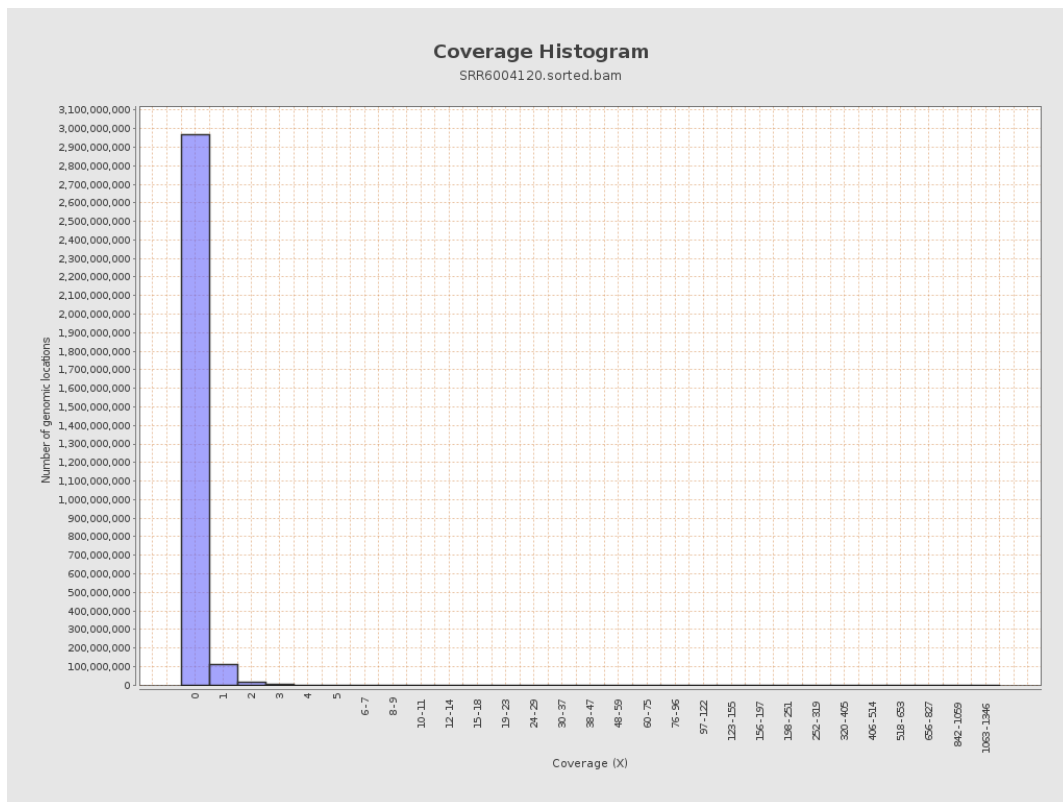
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12501466	0.0502	1.1606
chr2	243199373	12982372	0.0534	0.5608
chr3	198022430	11211342	0.0566	0.2748
chr4	191154276	8340370	0.0436	0.263
chr5	180915260	11872195	0.0656	0.2998
chr6	171115067	8476003	0.0495	0.2958
chr7	159138663	5208293	0.0327	0.4419

chr8	146364022	9835201	0.0672	0.637
chr9	141213431	6452221	0.0457	0.4392
chr10	135534747	7858857	0.058	0.4325
chr11	135006516	4772474	0.0353	0.3304
chr12	133851895	6428466	0.048	0.2604
chr13	115169878	3986173	0.0346	0.2119
chr14	107349540	3863979	0.036	0.2553
chr15	102531392	3556222	0.0347	0.222
chr16	90354753	2866347	0.0317	0.2679
chr17	81195210	4371722	0.0538	0.3039
chr18	78077248	4477271	0.0573	0.9228
chr19	59128983	3096978	0.0524	0.7195
chr20	63025520	2534680	0.0402	0.2509
chr21	48129895	2774829	0.0577	0.2977
chr22	51304566	1954474	0.0381	0.2205
chrMT	16571	76547	4.6193	3.4161
chrX	155270560	10988278	0.0708	0.3548
chrY	59373566	420947	0.0071	0.1494

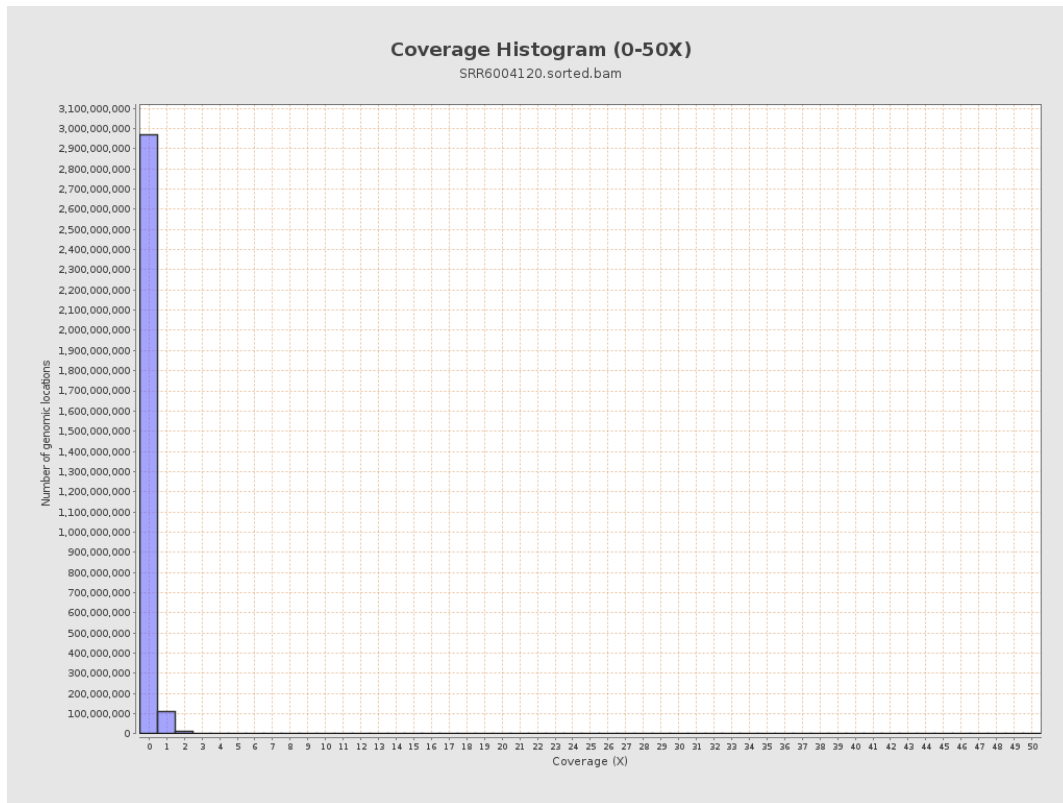
3. Results : Coverage across reference



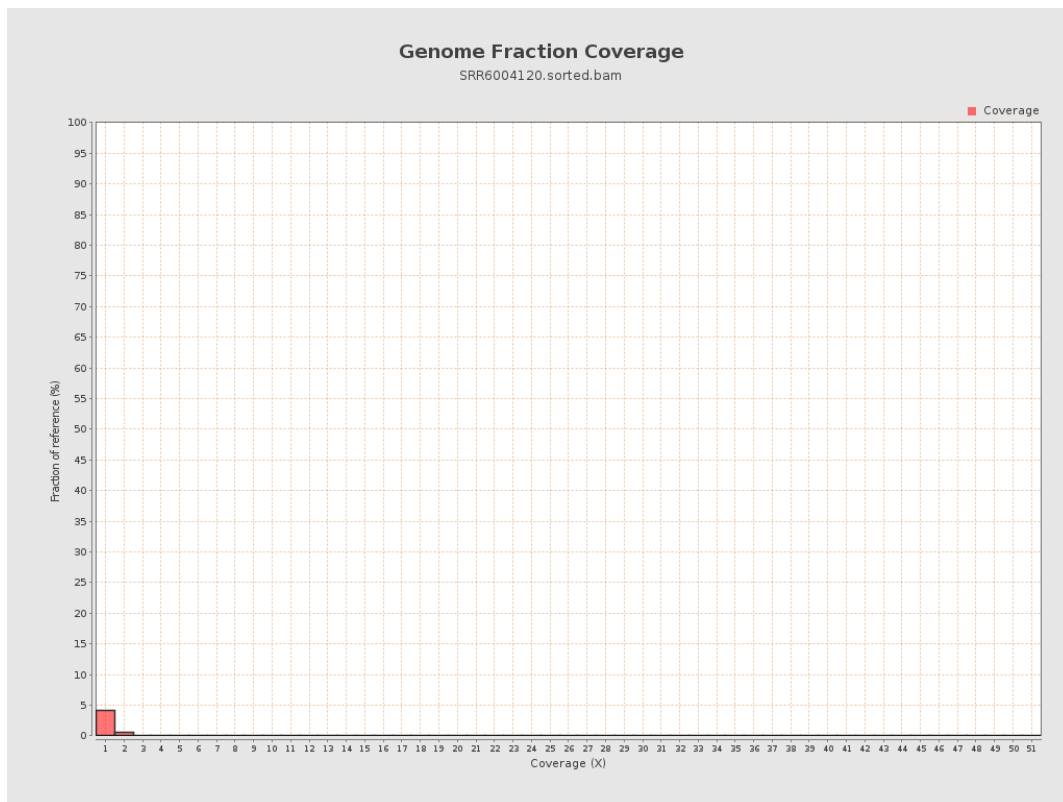
4. Results : Coverage Histogram



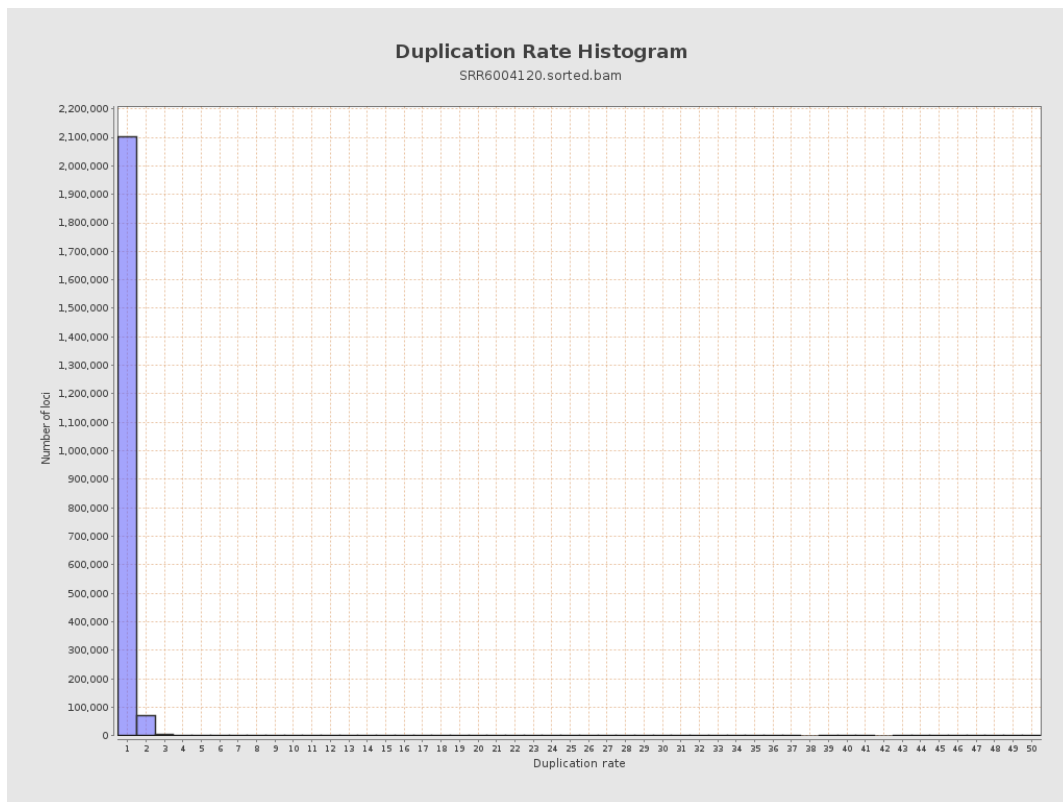
5. Results : Coverage Histogram (0-50X)



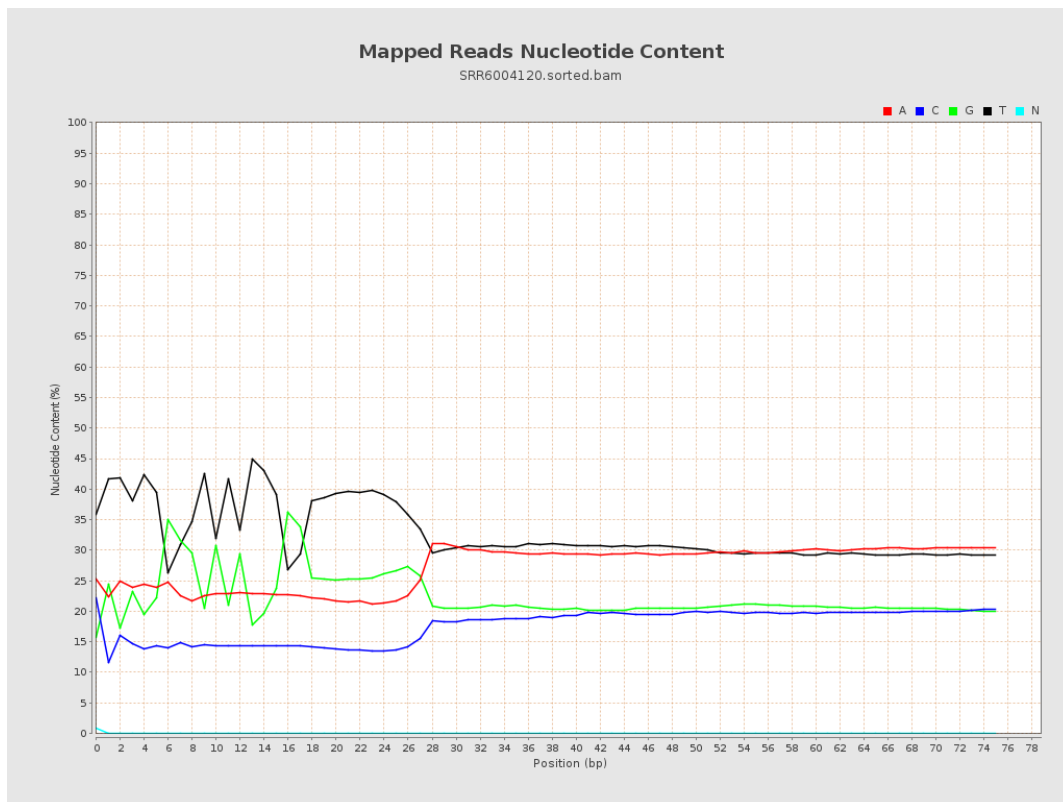
6. Results : Genome Fraction Coverage



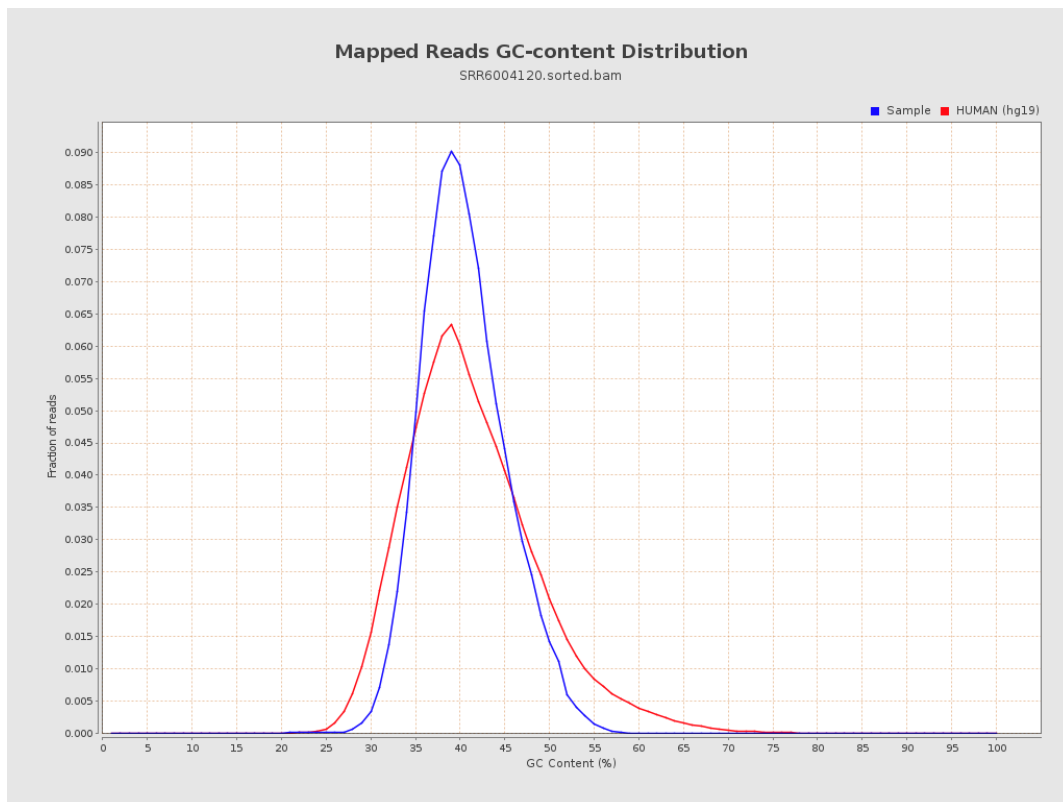
7. Results : Duplication Rate Histogram



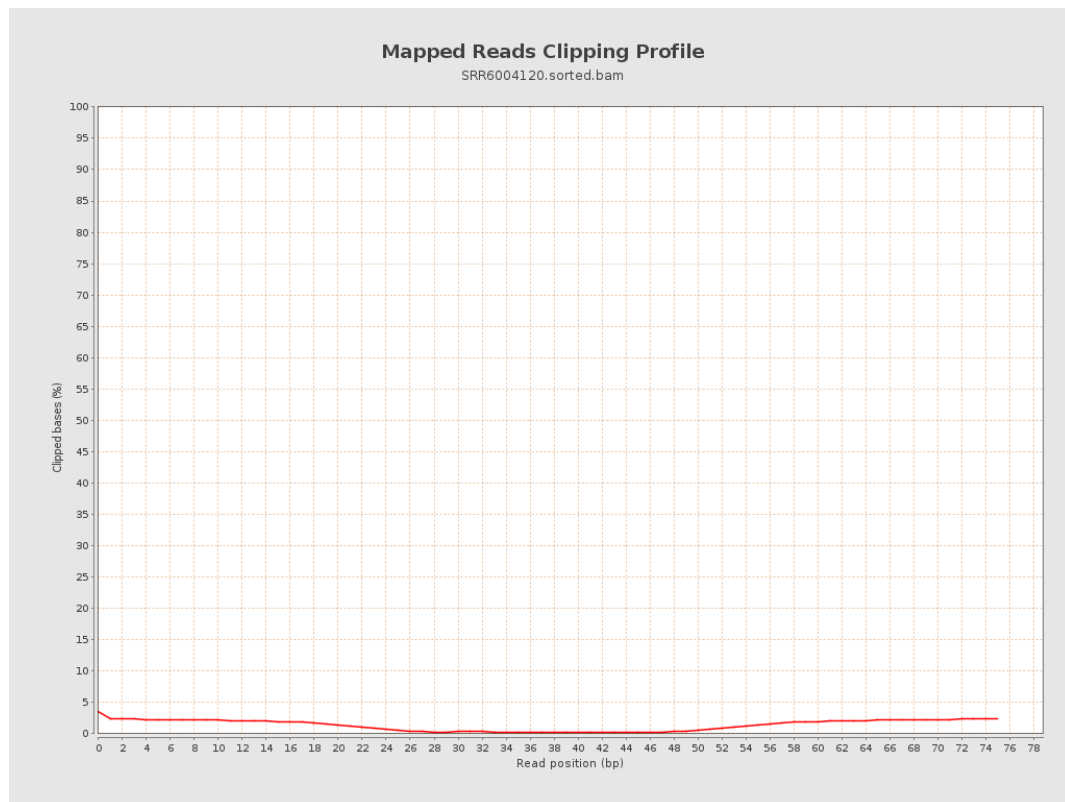
8. Results : Mapped Reads Nucleotide Content



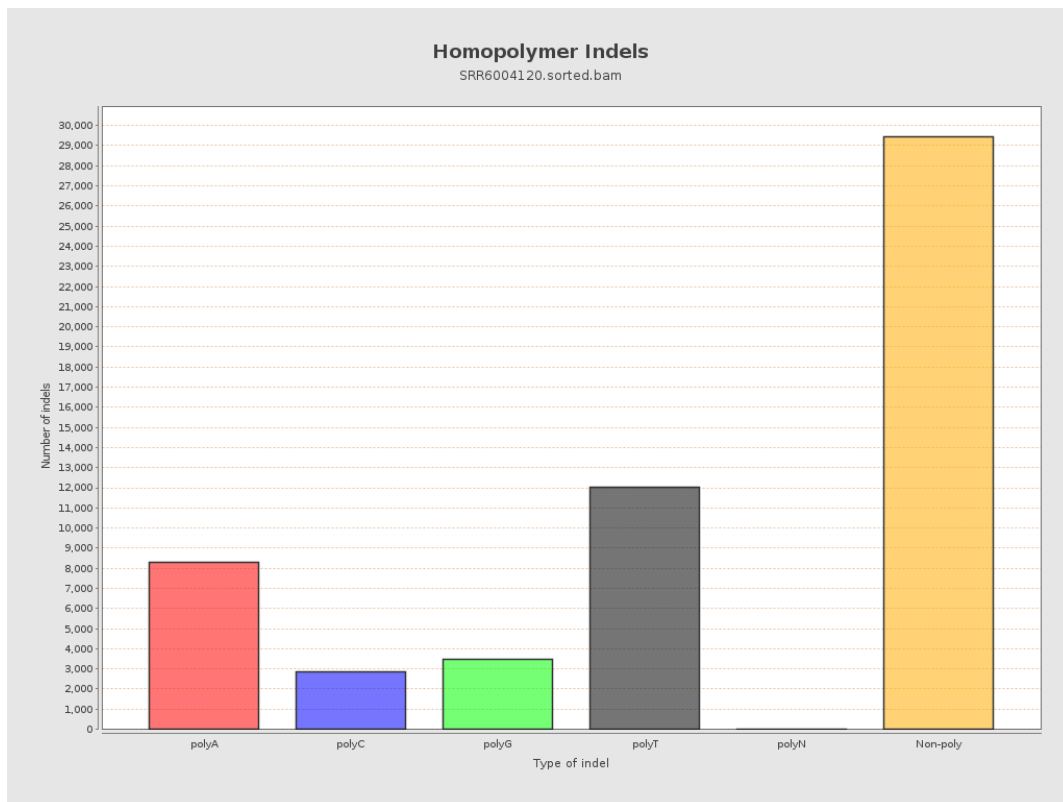
9. Results : Mapped Reads GC-content Distribution



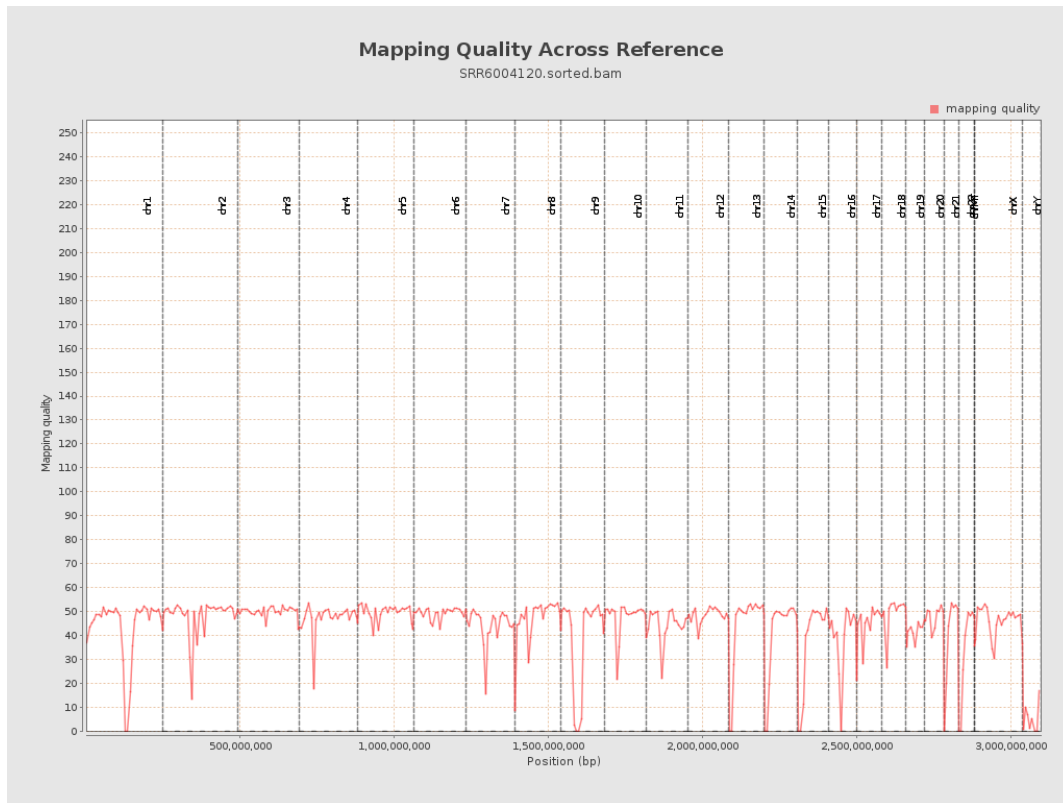
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

