

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 00:42:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506120.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_SRR1506120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 00:42:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,613,885
Mapped reads	6,304,046 / 73.18%
Unmapped reads	2,309,839 / 26.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	88,563 / 1.03%
Read min/max/mean length	30 / 94 / 94.37
Duplicated reads (estimated)	1,143,500 / 13.28%
Duplication rate	12.97%
Clipped reads	4,319,776 / 50.15%

2.2. ACGT Content

Number/percentage of A's	127,531,593 / 26.52%
Number/percentage of C's	92,200,153 / 19.18%
Number/percentage of T's	138,296,655 / 28.76%
Number/percentage of G's	122,697,091 / 25.52%
Number/percentage of N's	78,467 / 0.02%
GC Percentage	44.7%

2.3. Coverage

Mean	0.1554

Standard Deviation	1.1089
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2.4. Mapping Quality

Mean Mapping Quality	46.7
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2.5. Mismatches and indels

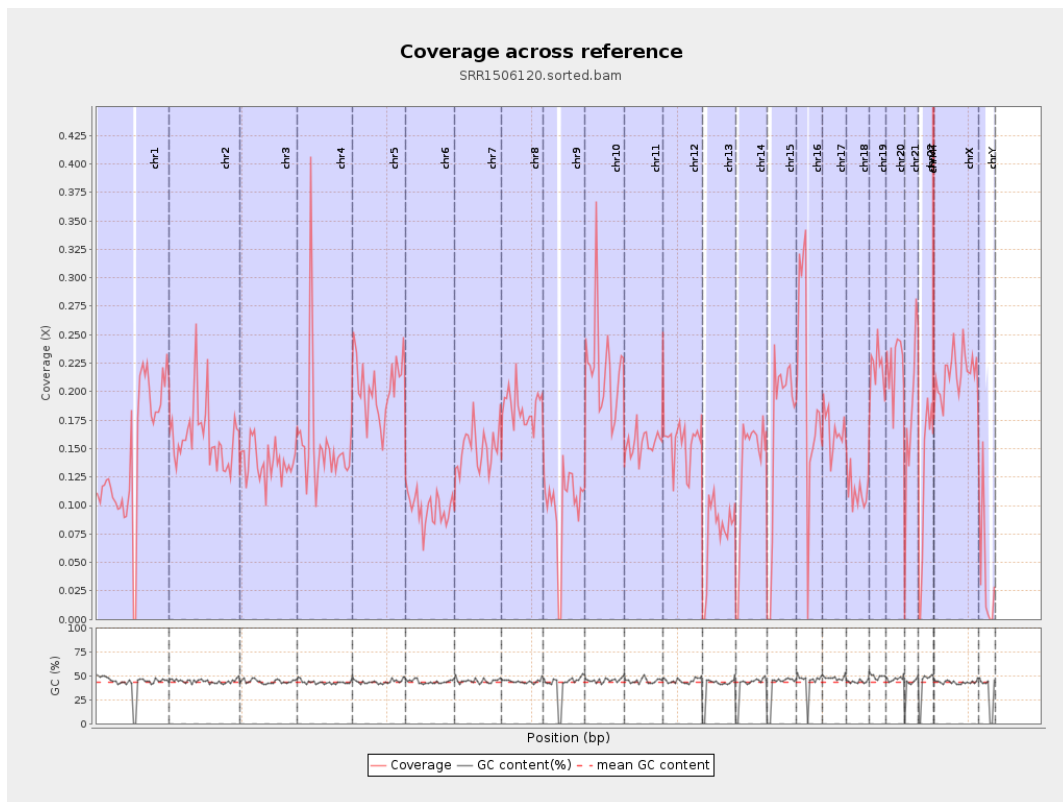
General error rate	0.87%
Mismatches	4,080,119
Insertions	41,015
Mapped reads with at least one insertion	0.63%
Deletions	94,869
Mapped reads with at least one deletion	1.47%
Homopolymer indels	40.45%

2.6. Chromosome stats

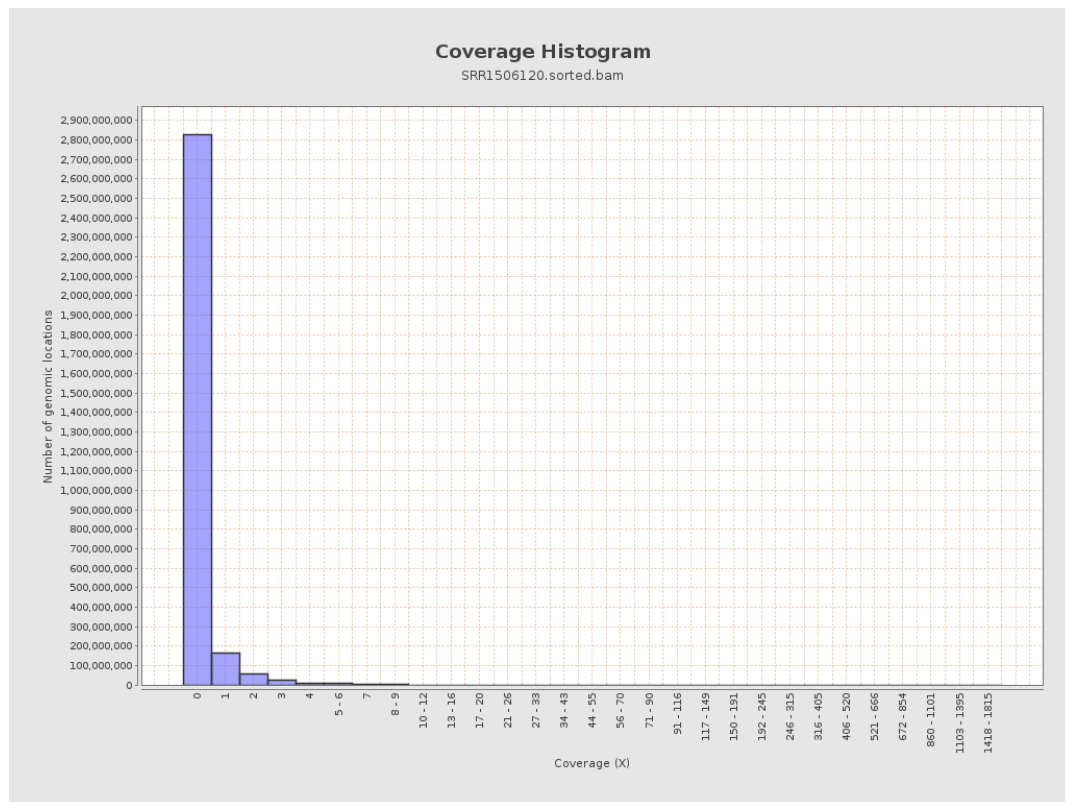
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	36034640	0.1446	1.7707
chr2	243199373	39202640	0.1612	1.2917
chr3	198022430	27348698	0.1381	0.6141
chr4	191154276	29165718	0.1526	1.2178
chr5	180915260	36734520	0.203	0.8122
chr6	171115067	16677646	0.0975	0.559
chr7	159138663	23951938	0.1505	1.0551

chr8	146364022	27309210	0.1866	1.1335
chr9	141213431	13951268	0.0988	0.9526
chr10	135534747	29845306	0.2202	1.5689
chr11	135006516	20908470	0.1549	1.1125
chr12	133851895	20654793	0.1543	0.7216
chr13	115169878	8664026	0.0752	0.449
chr14	107349540	14341888	0.1336	0.6747
chr15	102531392	17304398	0.1688	0.71
chr16	90354753	18606186	0.2059	1.04
chr17	81195210	13500383	0.1663	0.8595
chr18	78077248	8772045	0.1124	1.7262
chr19	59128983	13039128	0.2205	1.3909
chr20	63025520	14133018	0.2242	0.943
chr21	48129895	8757540	0.182	1.1301
chr22	51304566	6228729	0.1214	0.6877
chrMT	16571	117070	7.0648	6.2664
chrX	155270560	33543937	0.216	0.8739
chrY	59373566	2209665	0.0372	1.4719

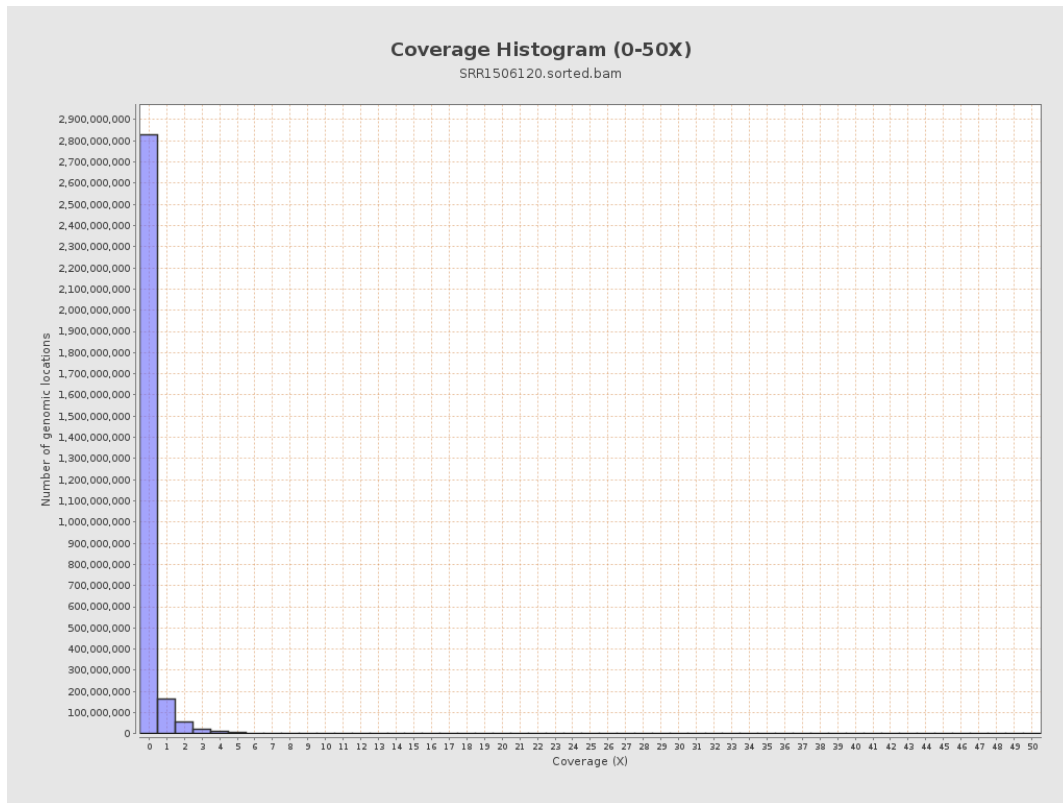
3. Results : Coverage across reference



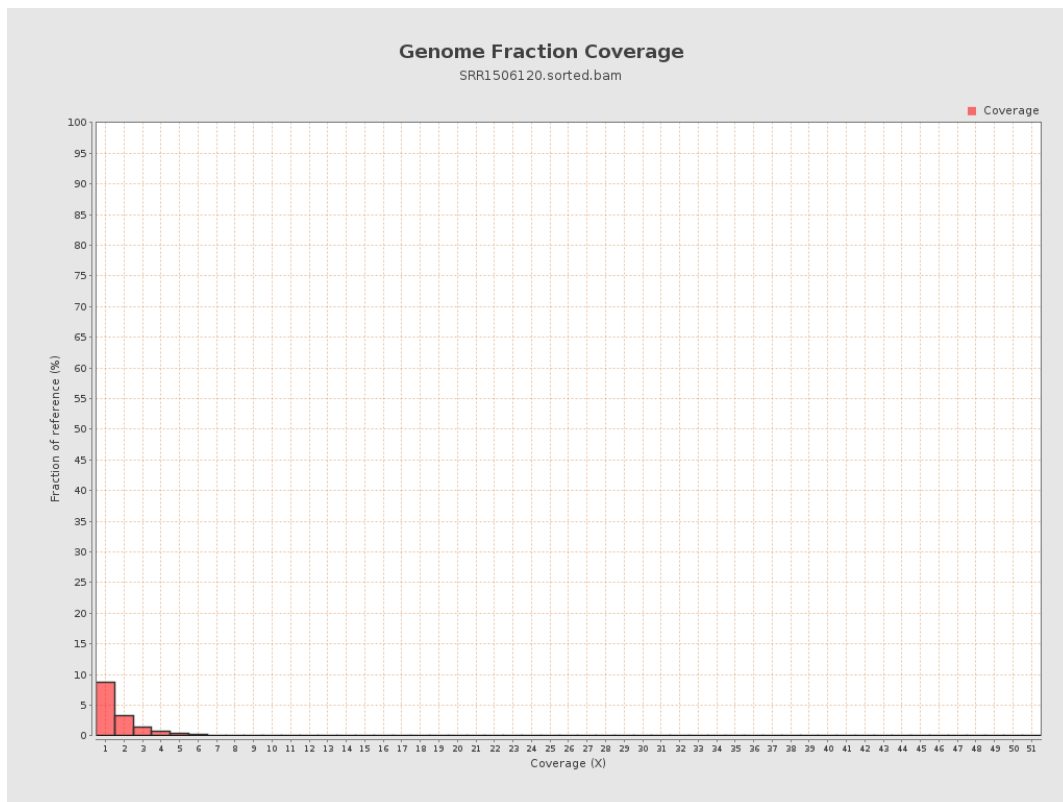
4. Results : Coverage Histogram



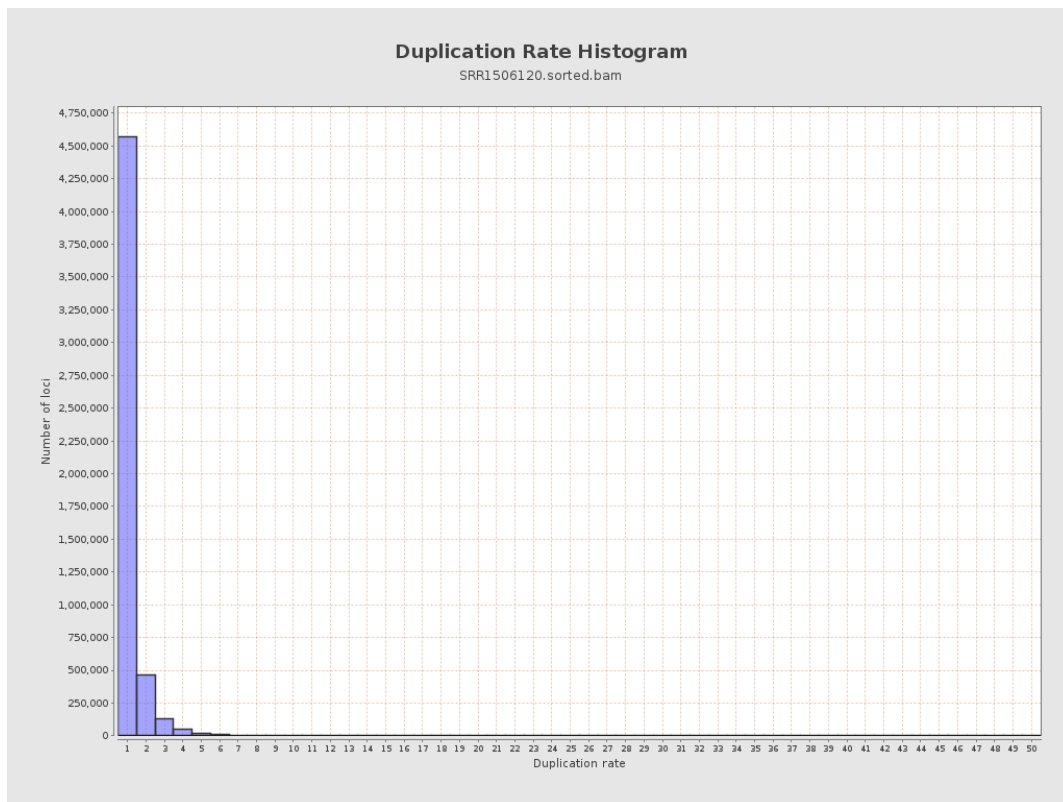
5. Results : Coverage Histogram (0-50X)



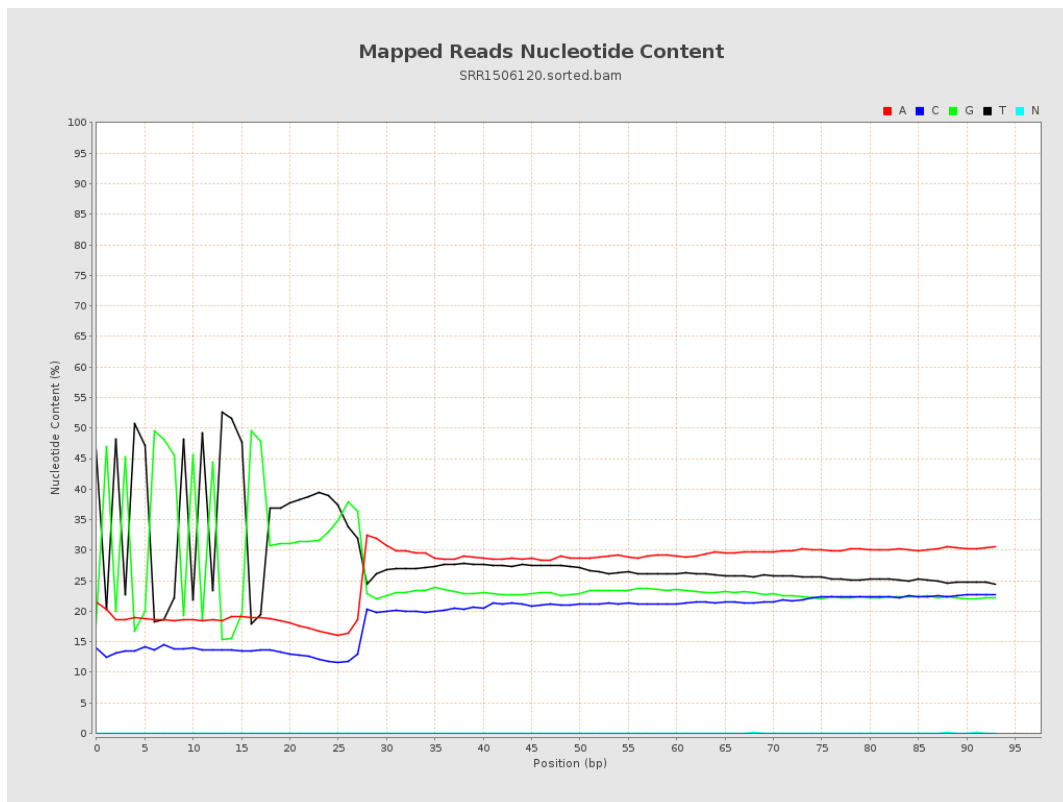
6. Results : Genome Fraction Coverage



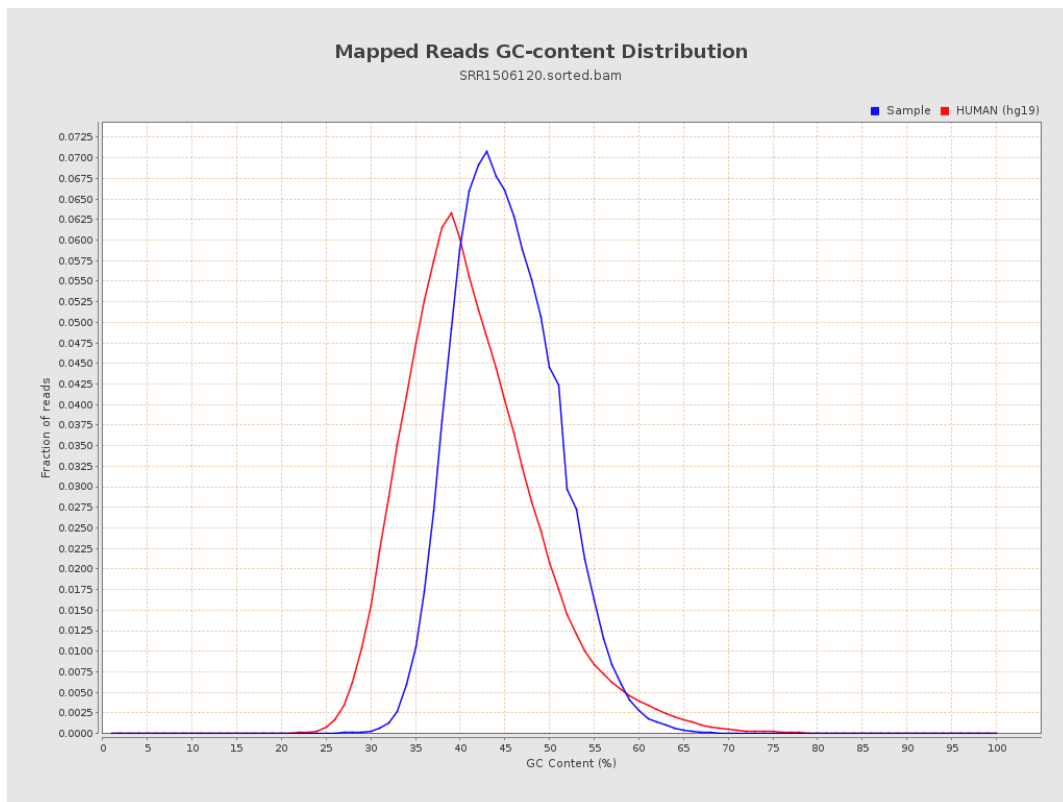
7. Results : Duplication Rate Histogram



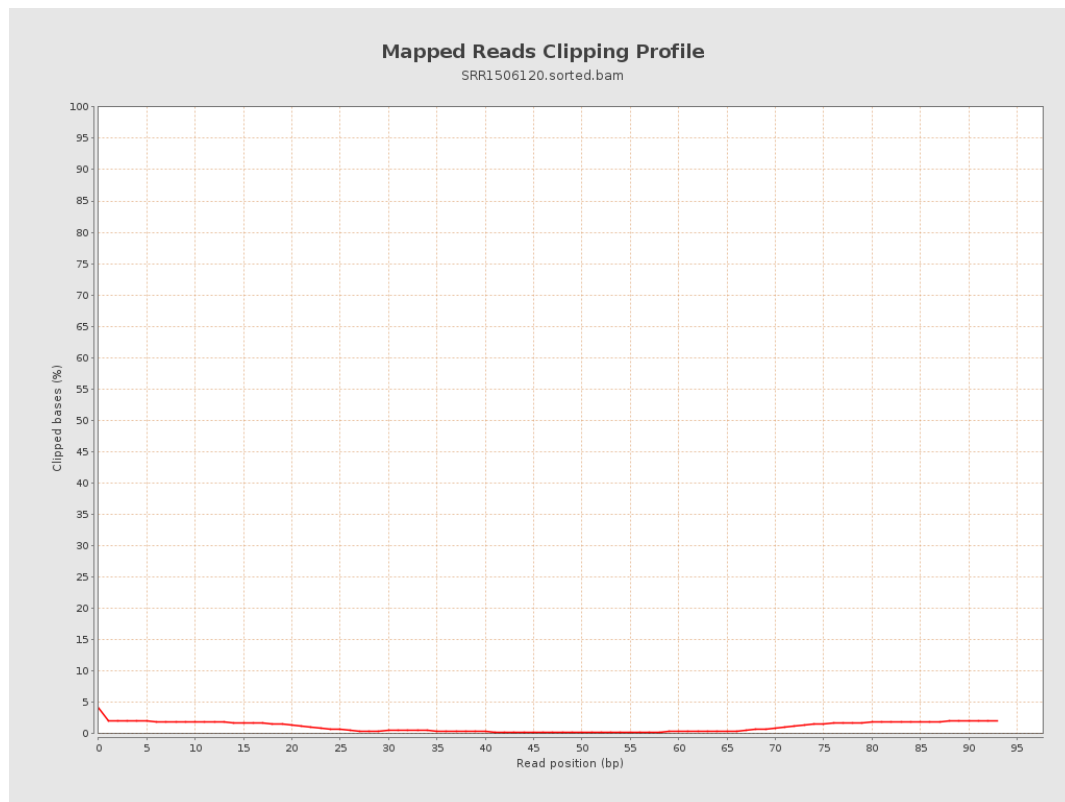
8. Results : Mapped Reads Nucleotide Content



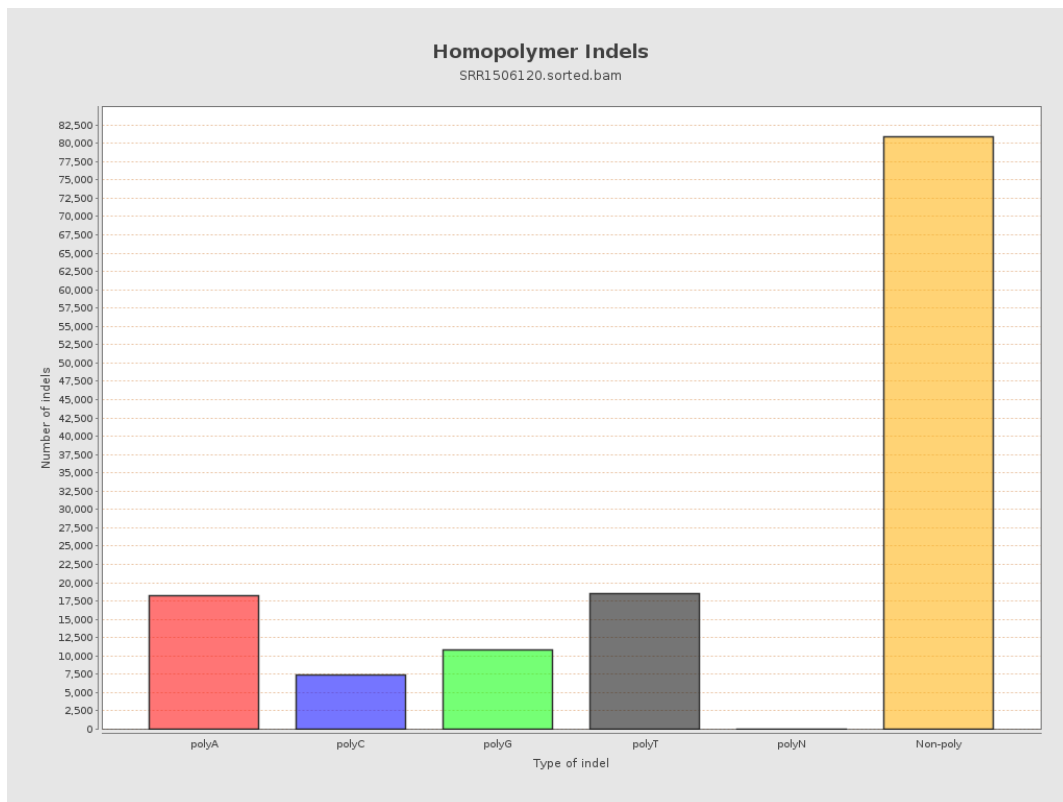
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

