

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 22:34:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514702.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_SRR5514702 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514702.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 22:34:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514702.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,235,843
Mapped reads	48,829,934 / 99.18%
Unmapped reads	405,909 / 0.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,445,136 / 7%
Read min/max/mean length	30 / 100 / 100.56
Duplicated reads (estimated)	40,193,270 / 81.63%
Duplication rate	44.17%
Clipped reads	15,322,382 / 31.12%

2.2. ACGT Content

Number/percentage of A's	1,320,091,926 / 28.64%
Number/percentage of C's	982,667,429 / 21.32%
Number/percentage of T's	1,307,951,538 / 28.38%
Number/percentage of G's	994,673,337 / 21.58%
Number/percentage of N's	3,738,991 / 0.08%
GC Percentage	42.9%

2.3. Coverage

Mean	1.4923

Standard Deviation	278.7715
--------------------	----------

2.4. Mapping Quality

Mean Mapping Quality	49.64
----------------------	-------

2.5. Mismatches and indels

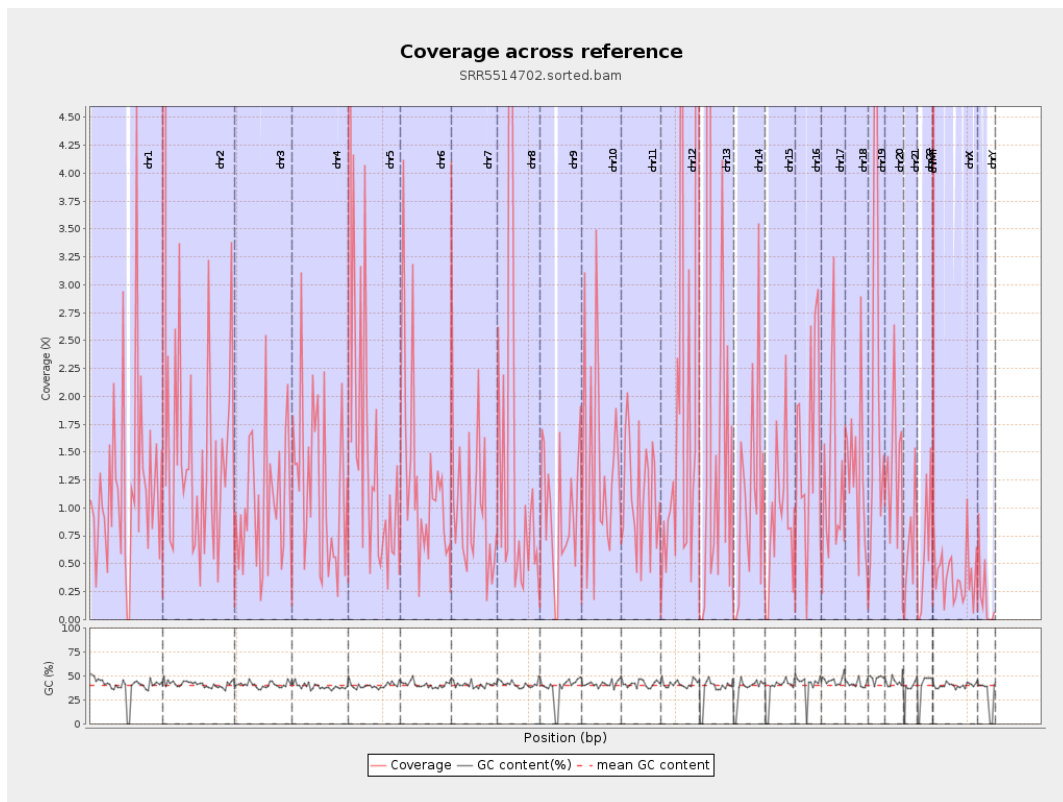
General error rate	1.11%
Mismatches	43,937,744
Insertions	3,140,794
Mapped reads with at least one insertion	5.97%
Deletions	3,162,051
Mapped reads with at least one deletion	5.85%
Homopolymer indels	26.19%

2.6. Chromosome stats

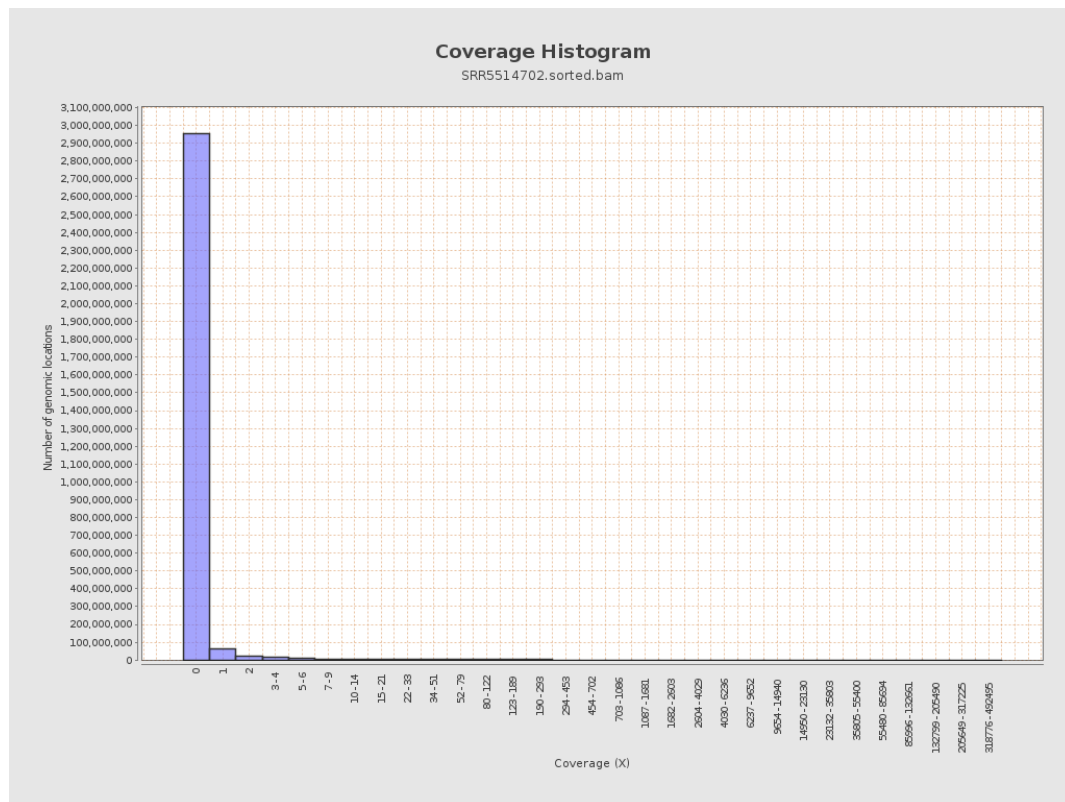
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	294257825	1.1806	32.3746
chr2	243199373	854596856	3.514	754.2855
chr3	198022430	198866489	1.0043	27.9833
chr4	191154276	226782096	1.1864	31.0489
chr5	180915260	335655627	1.8553	133.0337
chr6	171115067	216739641	1.2666	38.5899
chr7	159138663	161785863	1.0166	32.4067

chr8	146364022	216336858	1.4781	147.7355
chr9	141213431	133163922	0.943	27.1508
chr10	135534747	189175582	1.3958	30.4811
chr11	135006516	154262815	1.1426	21.8777
chr12	133851895	359391471	2.685	380.6751
chr13	115169878	369435969	3.2077	793.7949
chr14	107349540	117466100	1.0942	28.6531
chr15	102531392	91809773	0.8954	39.7937
chr16	90354753	134350641	1.4869	40.4685
chr17	81195210	99562469	1.2262	25.8222
chr18	78077248	105266037	1.3482	24.368
chr19	59128983	135878321	2.298	175.245
chr20	63025520	86265318	1.3687	29.2087
chr21	48129895	31725184	0.6592	19.1768
chr22	51304566	31630008	0.6165	33.5677
chrMT	16571	1900936	114.7146	167.6279
chrX	155270560	61414240	0.3955	20.9666
chrY	59373566	12058020	0.2031	15.5517

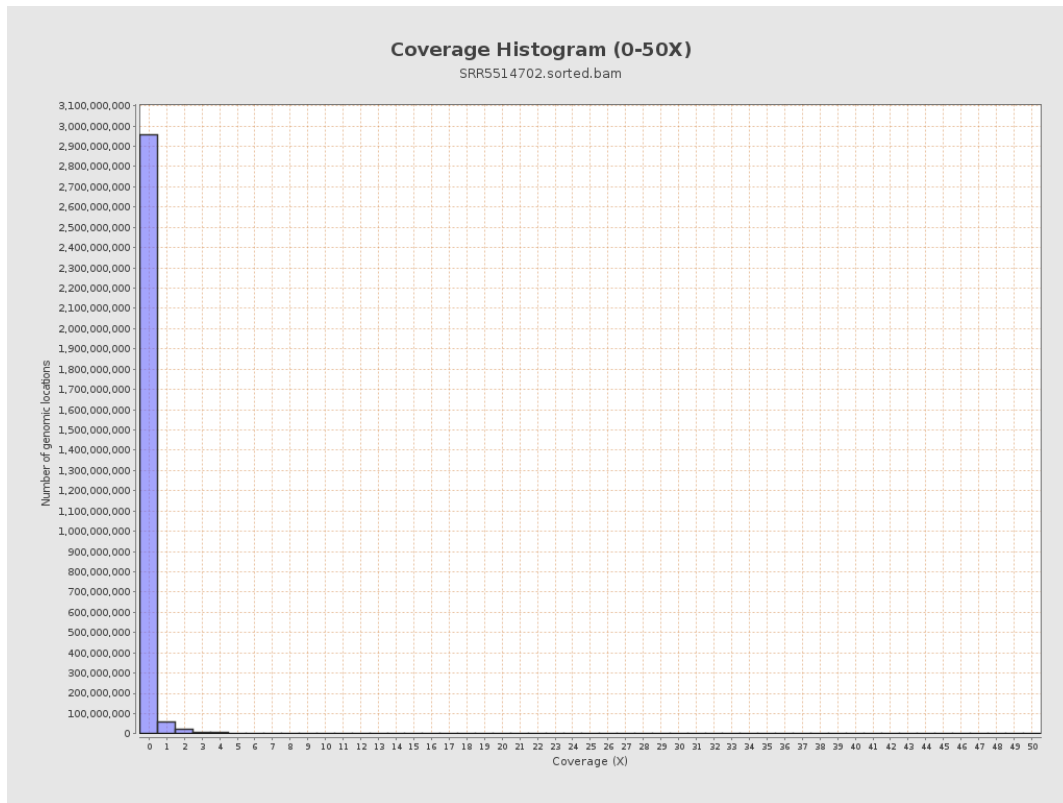
3. Results : Coverage across reference



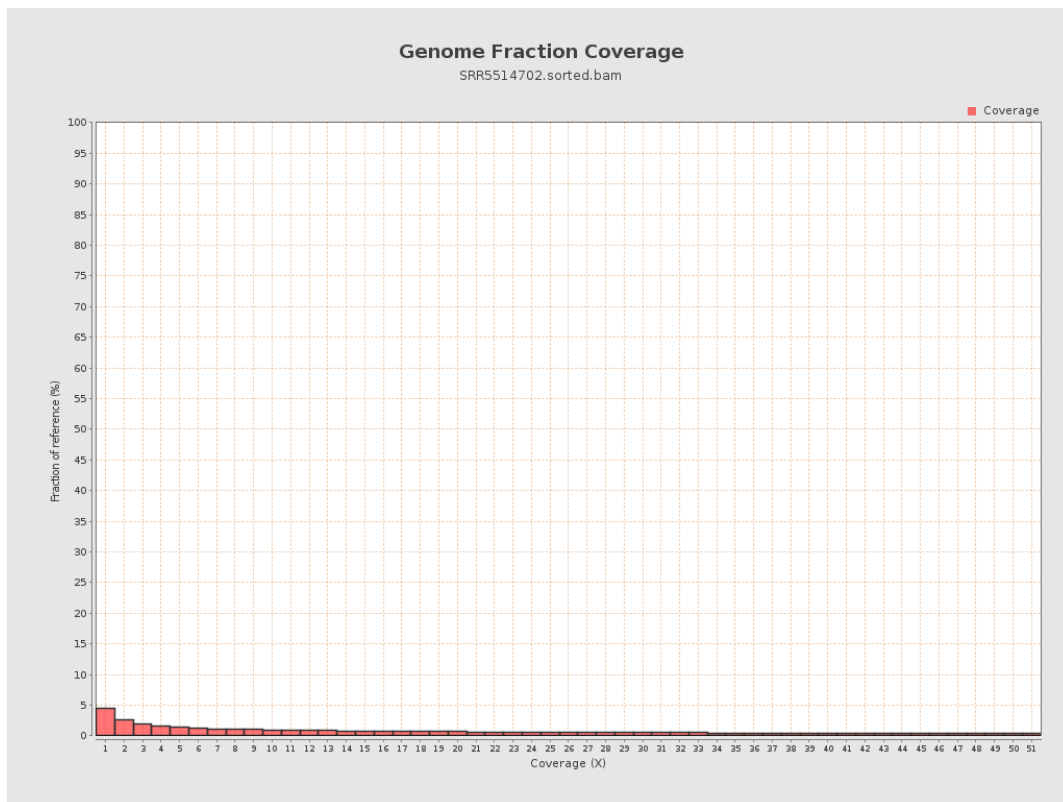
4. Results : Coverage Histogram



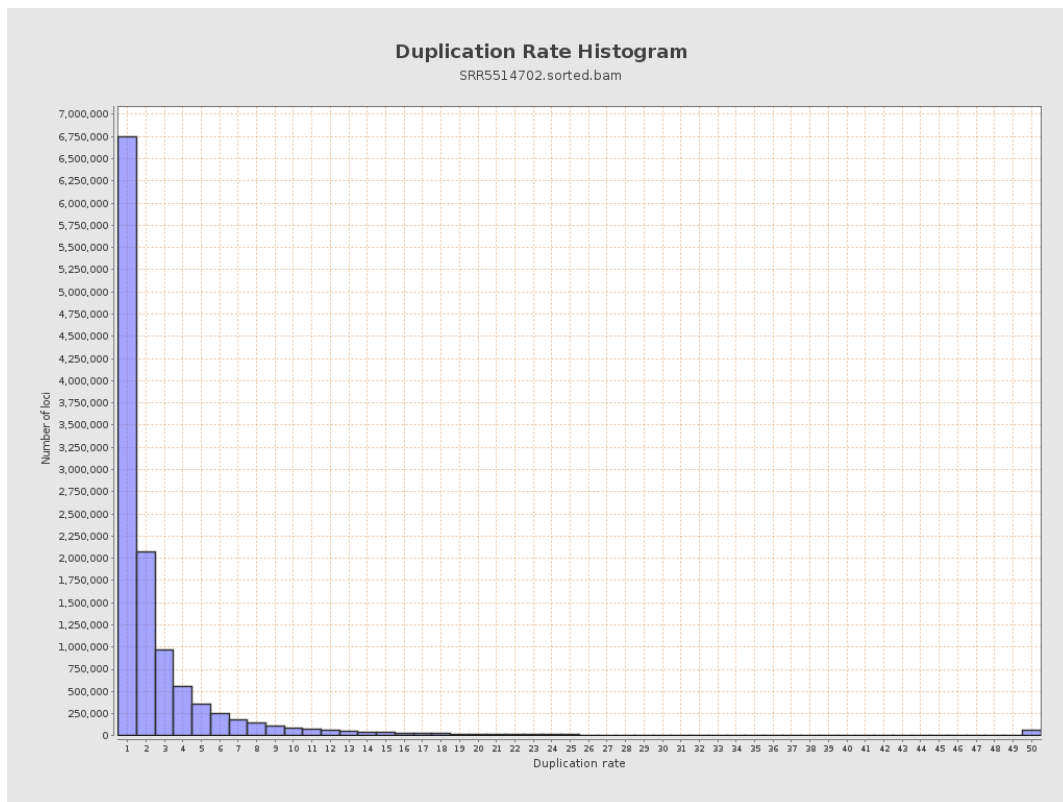
5. Results : Coverage Histogram (0-50X)



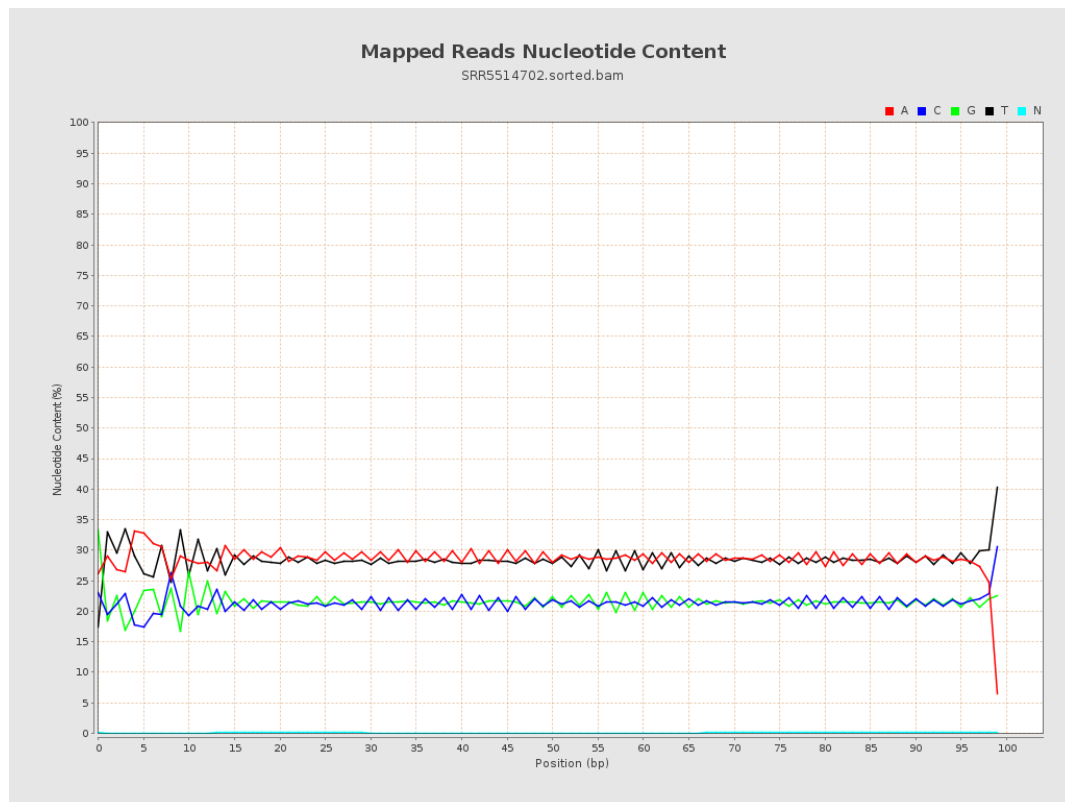
6. Results : Genome Fraction Coverage



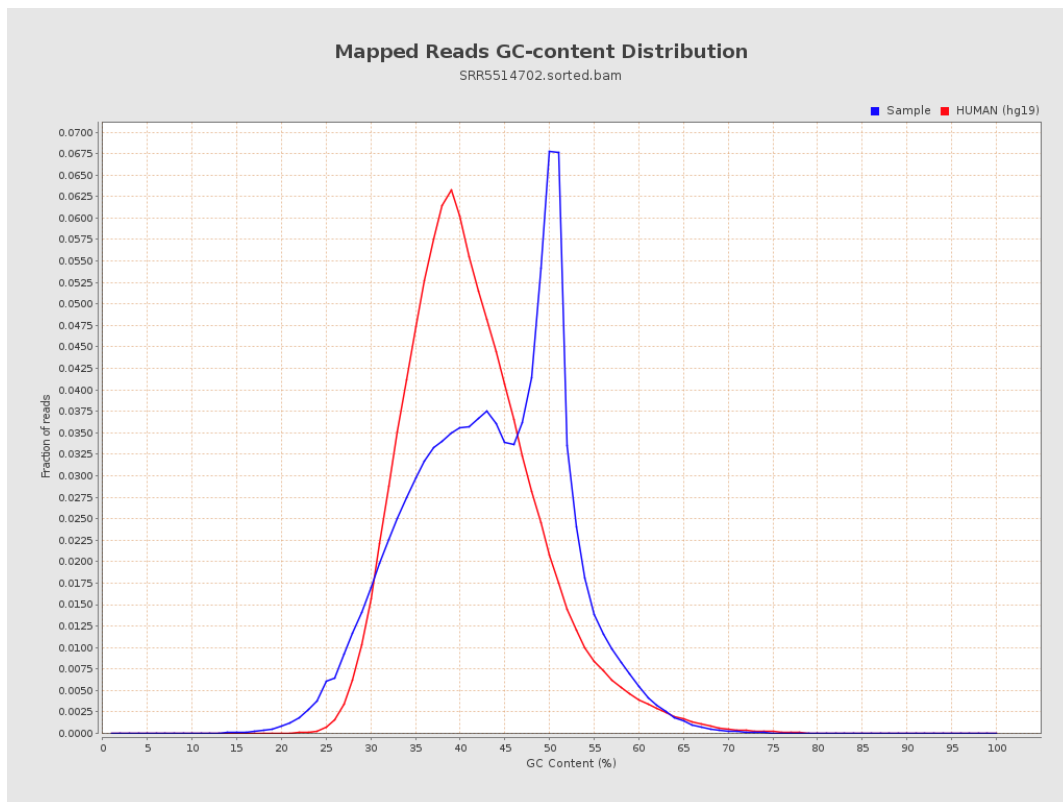
7. Results : Duplication Rate Histogram



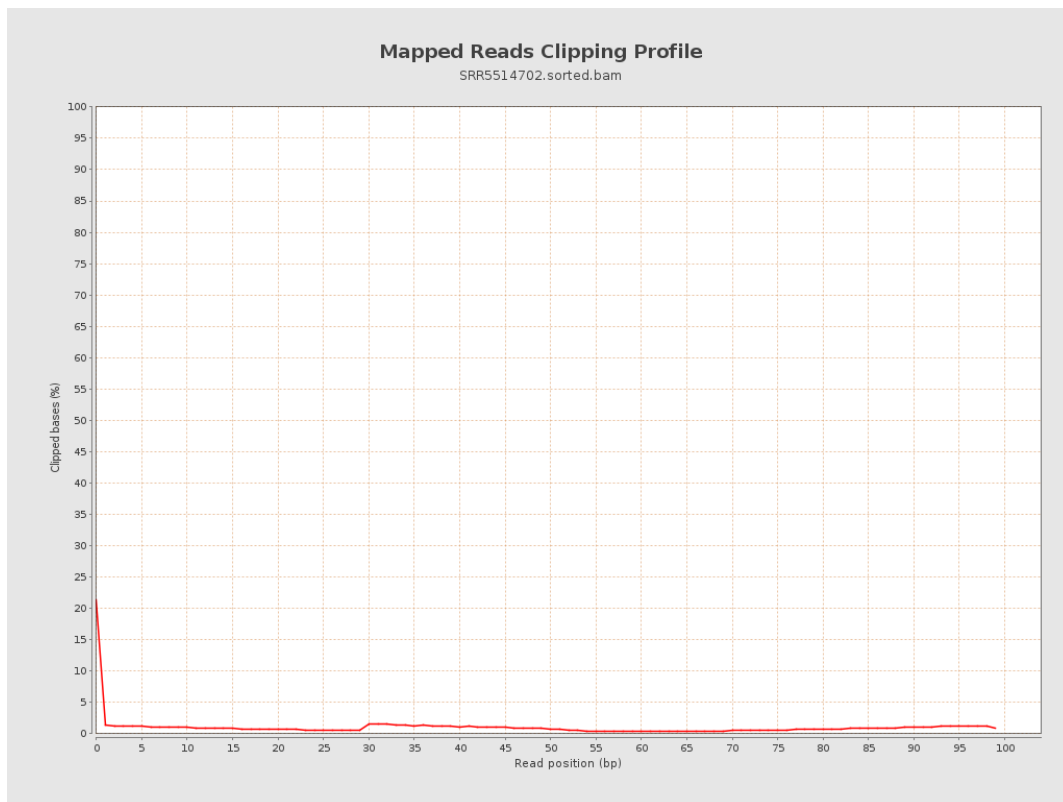
8. Results : Mapped Reads Nucleotide Content



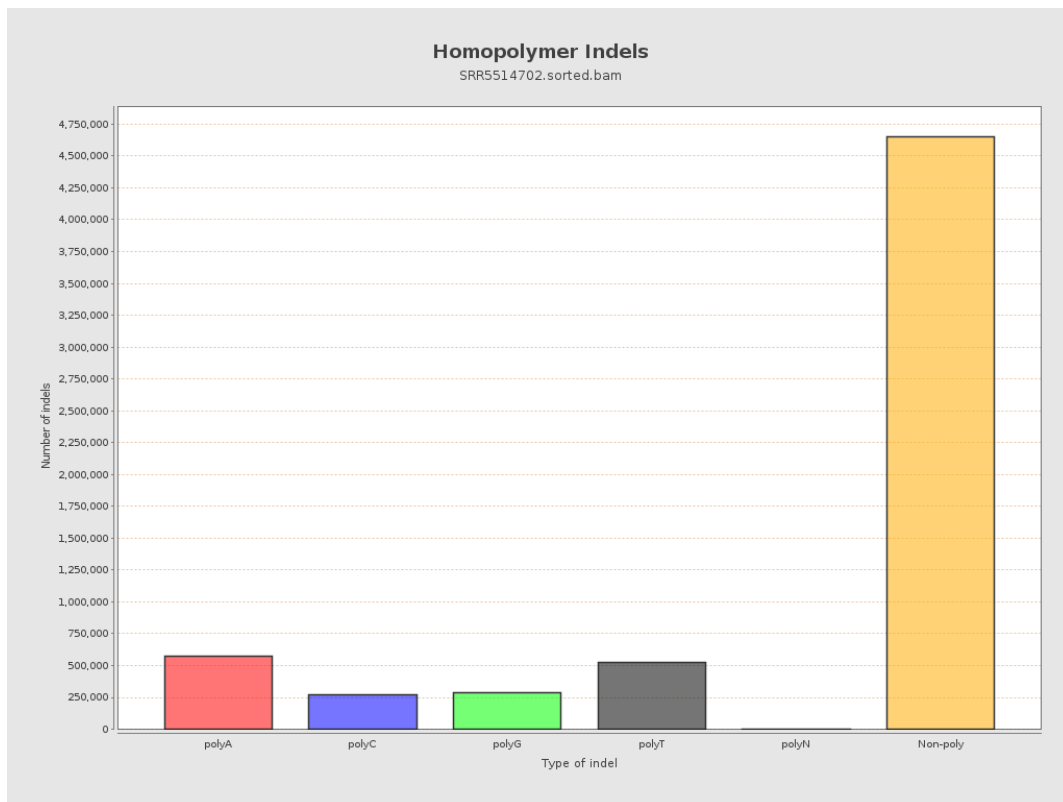
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

