

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 20:57:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514714.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_SRR5514714 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514714.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 20:57:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514714.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	118,573,124
Mapped reads	117,841,307 / 99.38%
Unmapped reads	731,817 / 0.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,087,399 / 4.29%
Read min/max/mean length	30 / 100 / 99.54
Duplicated reads (estimated)	78,312,981 / 66.05%
Duplication rate	45.24%
Clipped reads	20,345,096 / 17.16%

2.2. ACGT Content

Number/percentage of A's	3,318,568,166 / 29.23%
Number/percentage of C's	2,363,420,784 / 20.81%
Number/percentage of T's	3,272,214,868 / 28.82%
Number/percentage of G's	2,397,112,618 / 21.11%
Number/percentage of N's	3,372,510 / 0.03%
GC Percentage	41.93%

2.3. Coverage

Mean	3.67

Standard Deviation	79.8582
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2.4. Mapping Quality

Mean Mapping Quality	48.94
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2.5. Mismatches and indels

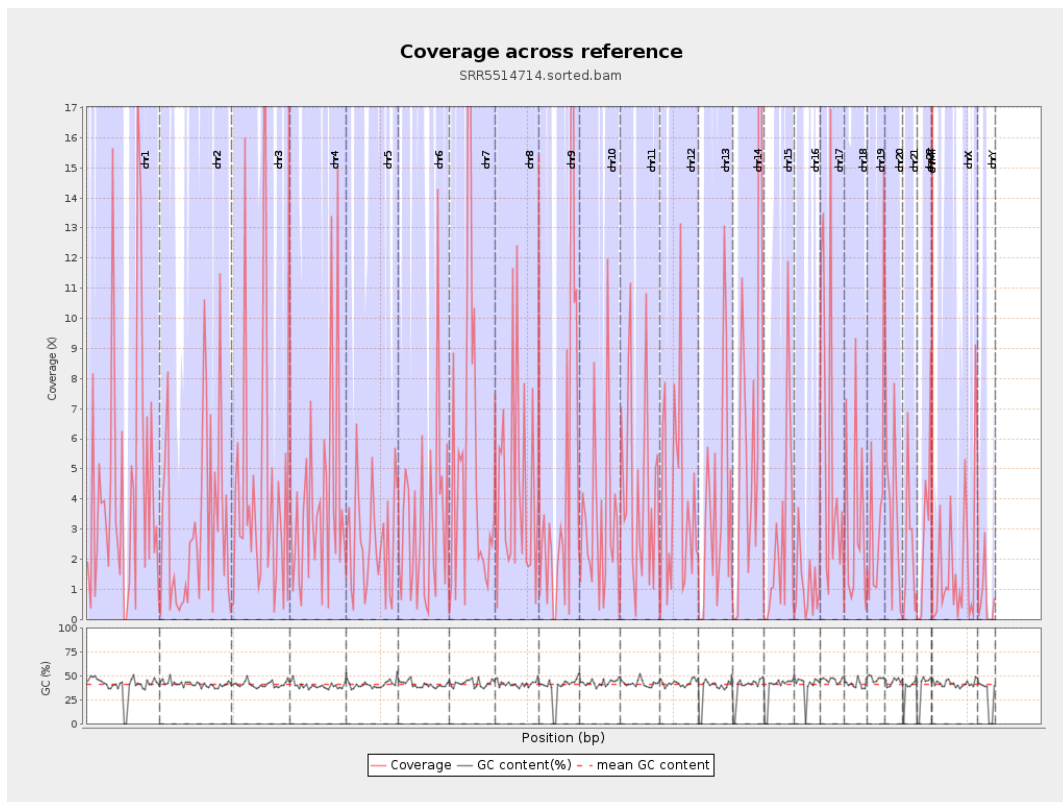
General error rate	0.61%
Mismatches	63,305,800
Insertions	3,361,753
Mapped reads with at least one insertion	2.77%
Deletions	3,239,577
Mapped reads with at least one deletion	2.66%
Homopolymer indels	44.78%

2.6. Chromosome stats

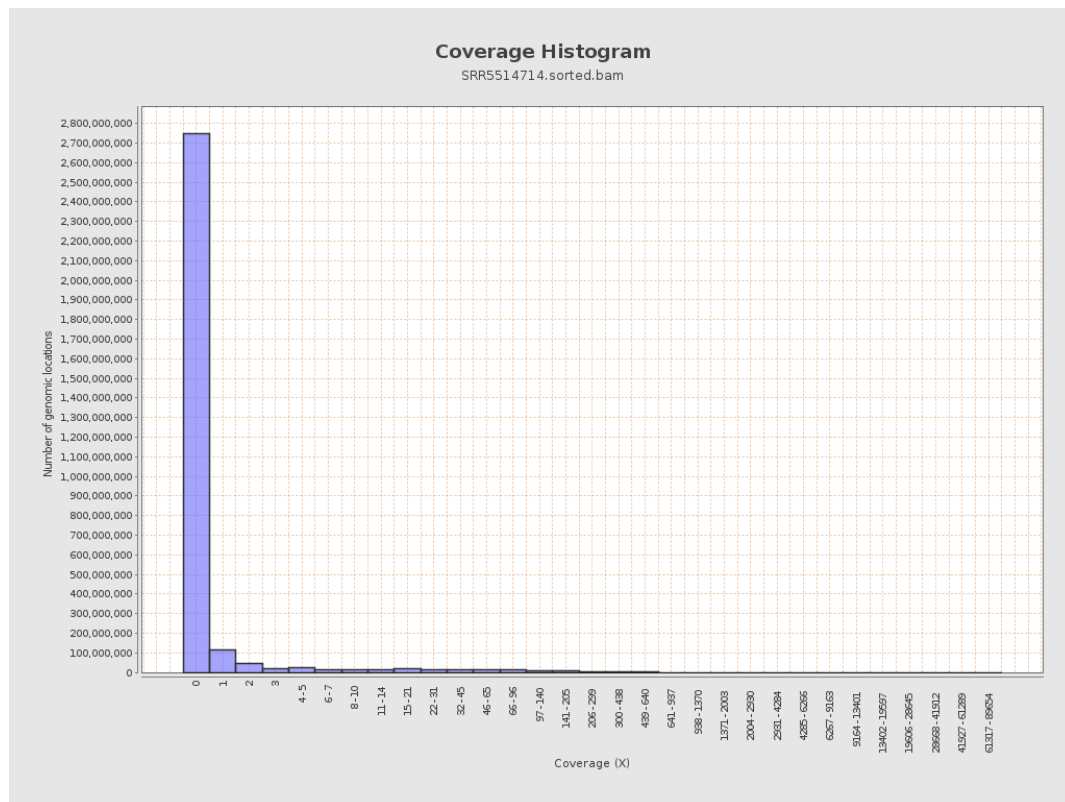
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1066958006	4.2807	34.7666
chr2	243199373	740379992	3.0443	60.442
chr3	198022430	861835367	4.3522	44.6632
chr4	191154276	738705953	3.8644	32.8421
chr5	180915260	484515518	2.6781	31.4384
chr6	171115067	545853559	3.19	28.2796
chr7	159138663	811735152	5.1008	39.232

chr8	146364022	644885840	4.406	43.8204
chr9	141213431	664128245	4.703	157.9481
chr10	135534747	439947142	3.246	54.7713
chr11	135006516	602902013	4.4657	43.5566
chr12	133851895	532430186	3.9778	37.4606
chr13	115169878	426508885	3.7033	44.9451
chr14	107349540	711125252	6.6244	210.8441
chr15	102531392	277437914	2.7059	29.8607
chr16	90354753	98868577	1.0942	15.9496
chr17	81195210	459596294	5.6604	216.1938
chr18	78077248	253639688	3.2486	33.6374
chr19	59128983	184431605	3.1191	37.2212
chr20	63025520	231119783	3.6671	43.6794
chr21	48129895	115526079	2.4003	23.2788
chr22	51304566	150148272	2.9266	93.5735
chrMT	16571	6563181	396.0643	211.5548
chrX	155270560	271632803	1.7494	139.8503
chrY	59373566	40242403	0.6778	13.9572

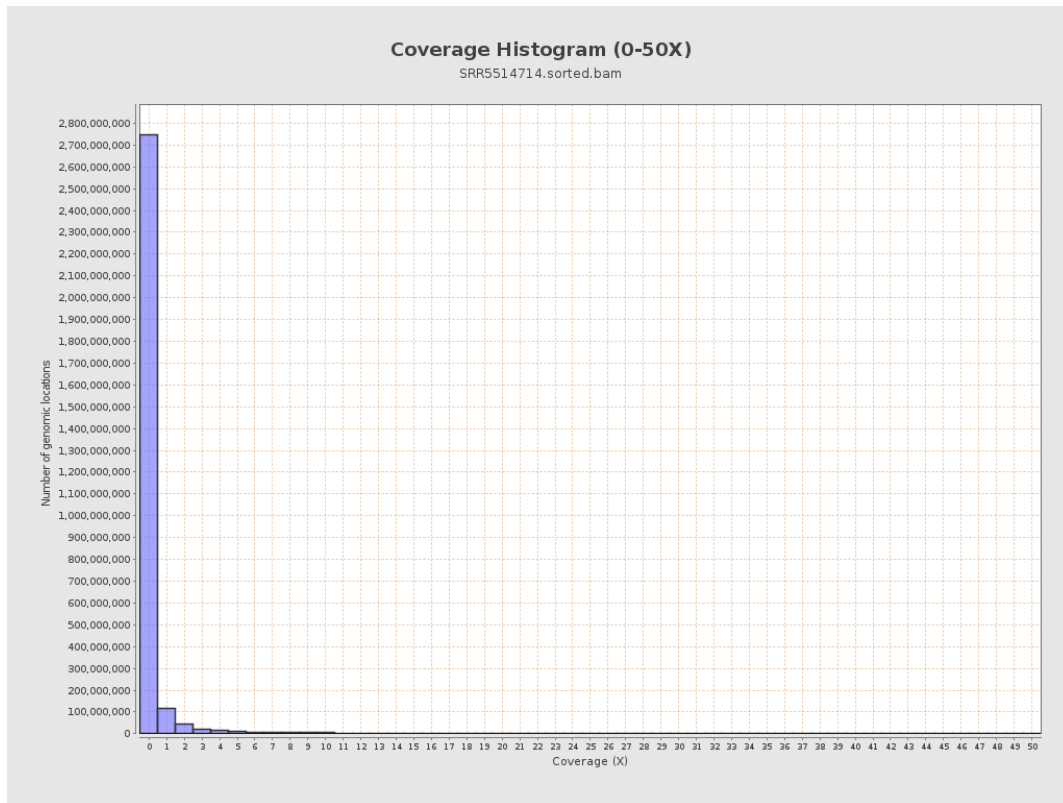
3. Results : Coverage across reference



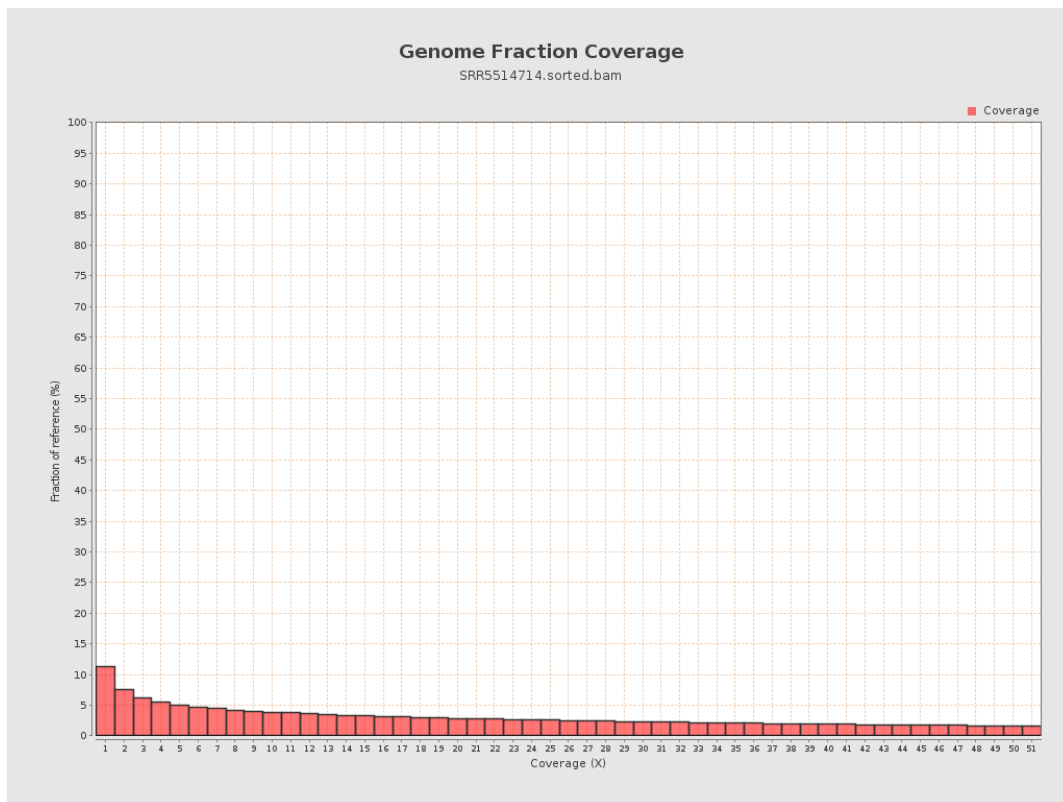
4. Results : Coverage Histogram



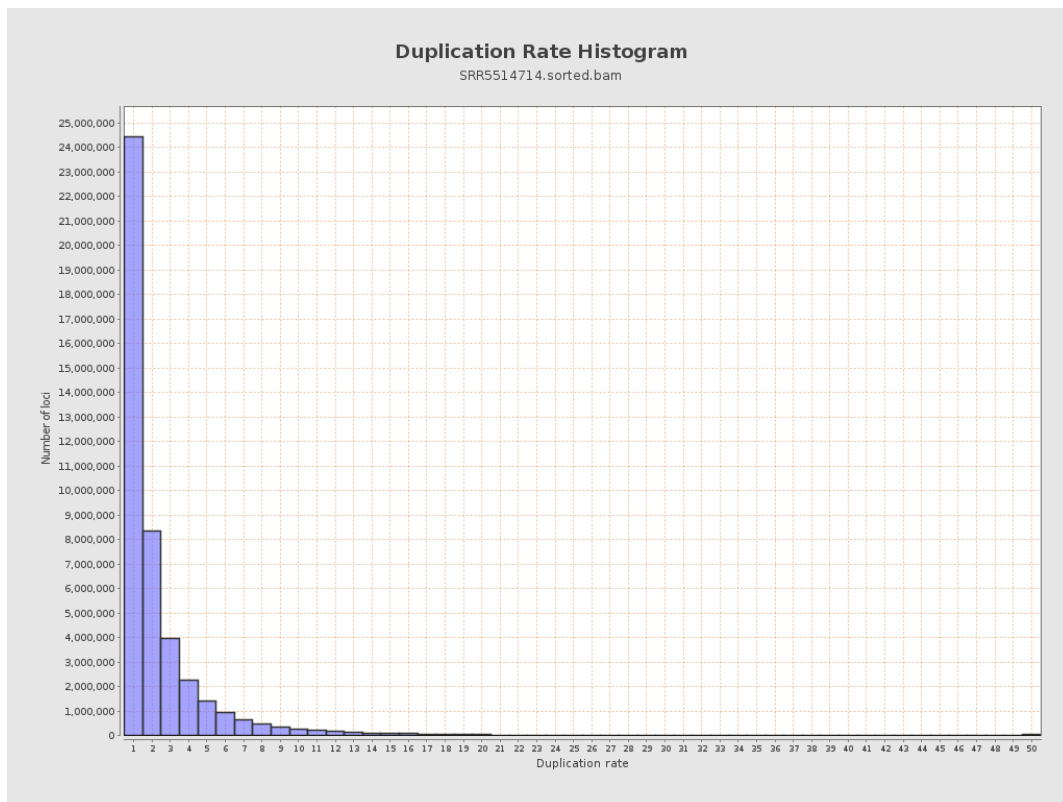
5. Results : Coverage Histogram (0-50X)



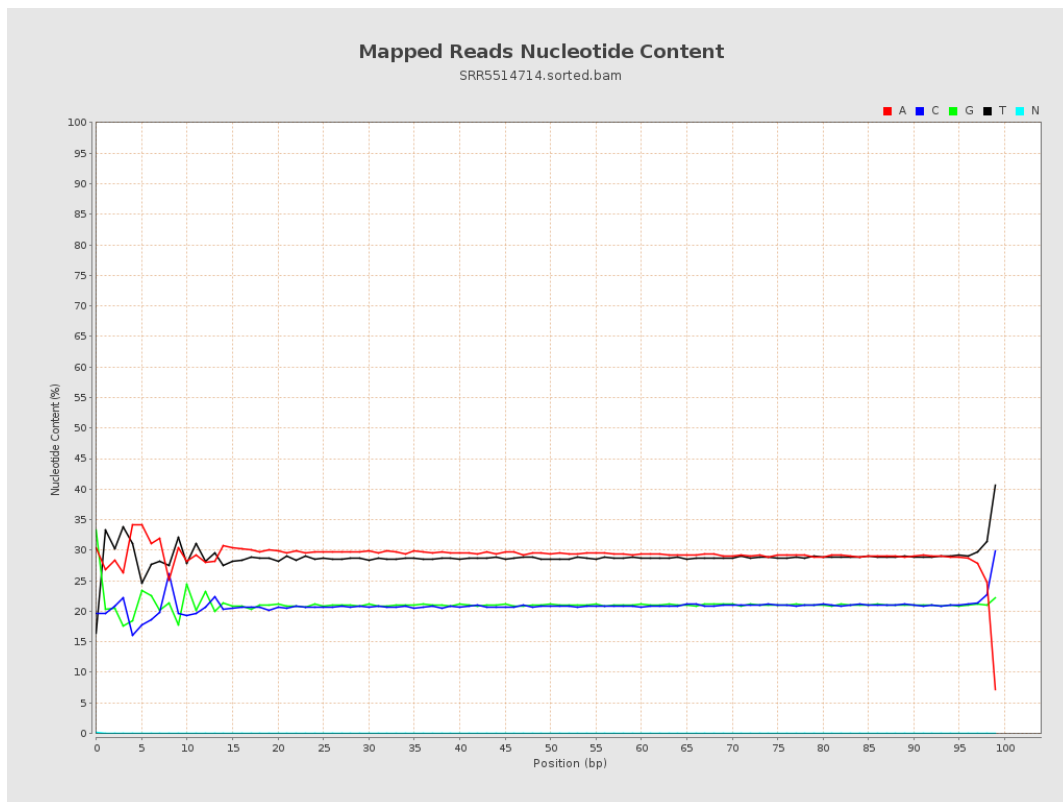
6. Results : Genome Fraction Coverage



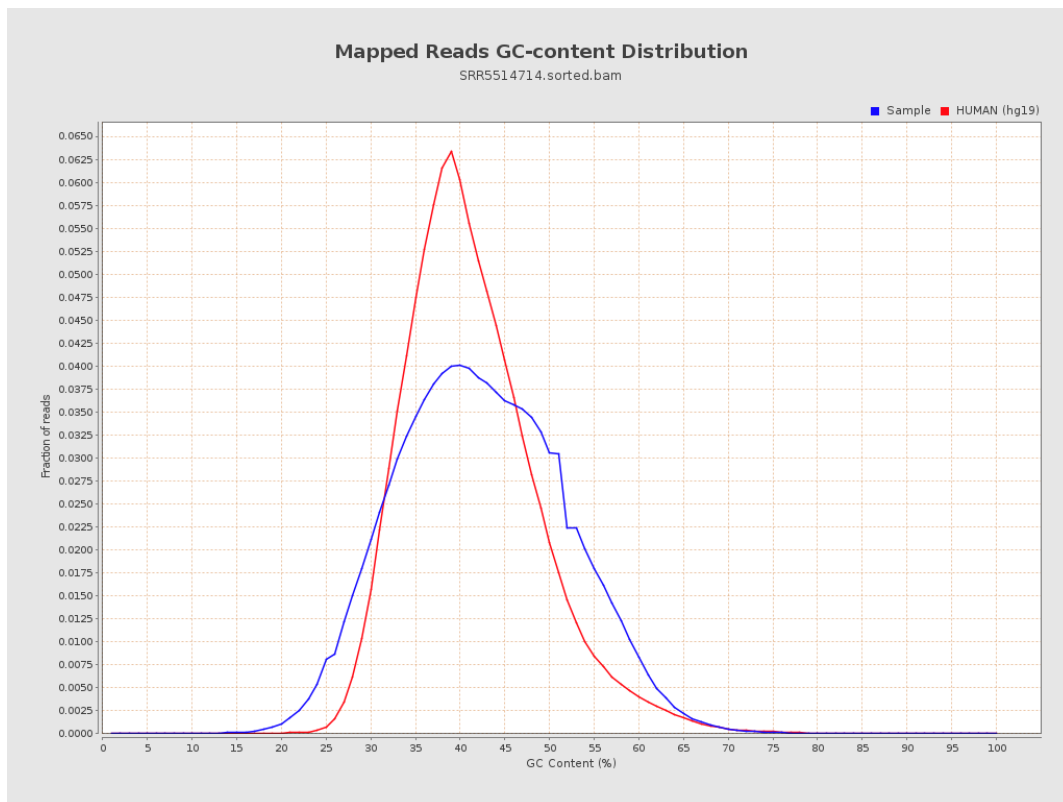
7. Results : Duplication Rate Histogram



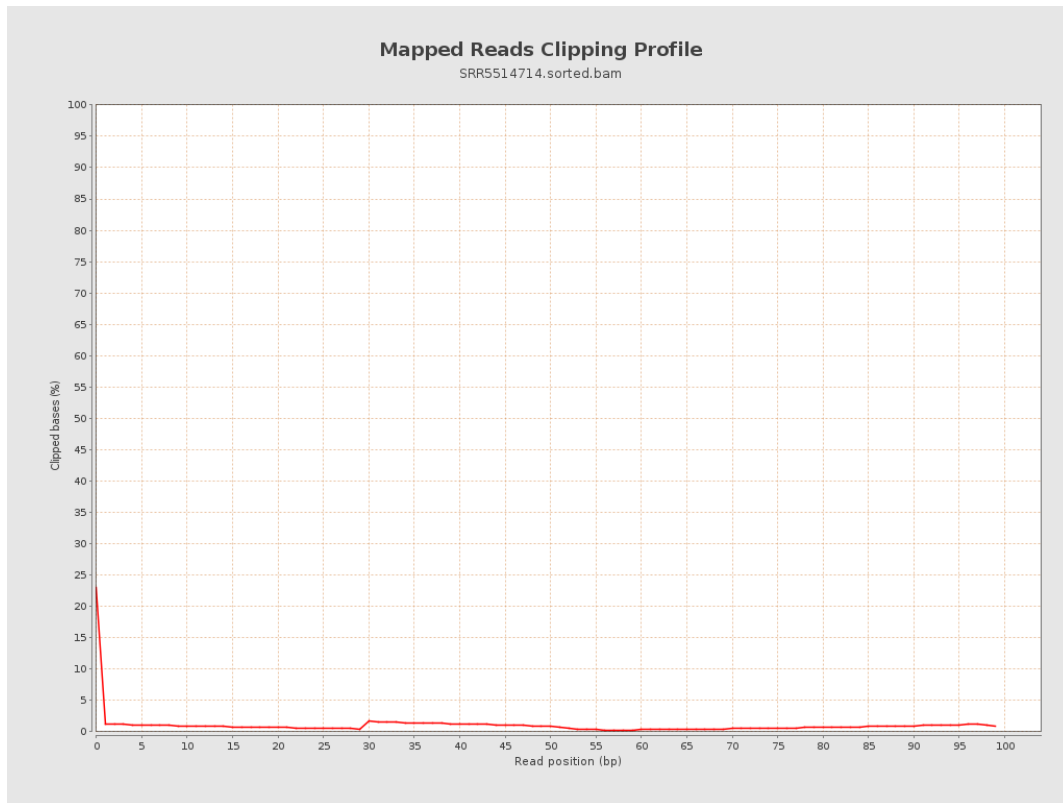
8. Results : Mapped Reads Nucleotide Content



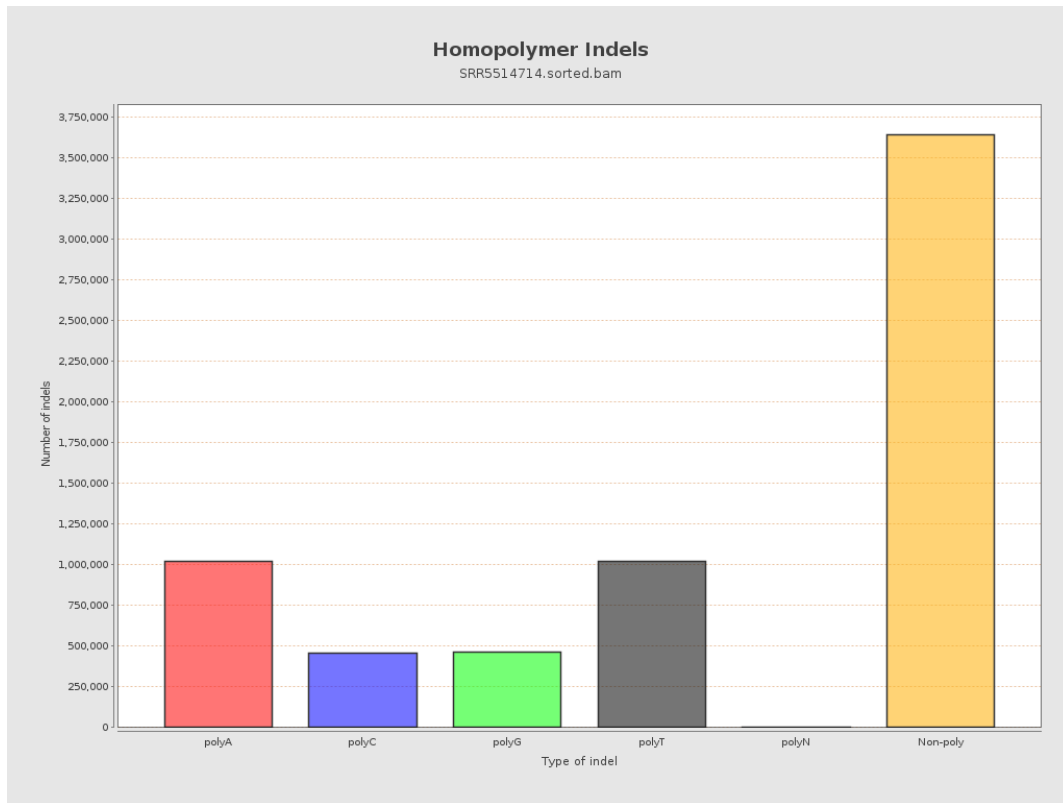
9. Results : Mapped Reads GC-content Distribution



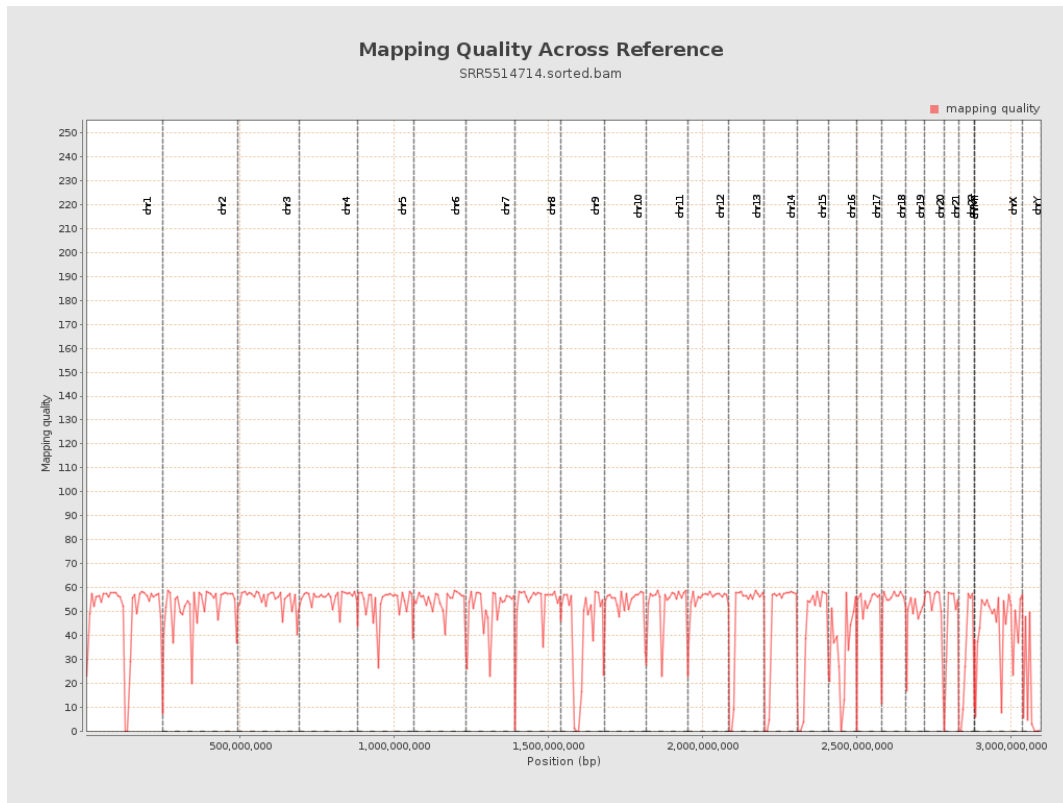
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

