

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 09:37:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514720.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_SRR5514720 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514720.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 09:37:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514720.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	184,682,202
Mapped reads	173,706,600 / 94.06%
Unmapped reads	10,975,602 / 5.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,162,713 / 5.5%
Read min/max/mean length	30 / 100 / 100.96
Duplicated reads (estimated)	167,688,757 / 90.8%
Duplication rate	52.34%
Clipped reads	53,988,592 / 29.23%

2.2. ACGT Content

Number/percentage of A's	4,315,618,934 / 26.95%
Number/percentage of C's	3,570,835,133 / 22.3%
Number/percentage of T's	4,338,648,543 / 27.1%
Number/percentage of G's	3,591,492,762 / 22.43%
Number/percentage of N's	195,655,138 / 1.22%
GC Percentage	44.73%

2.3. Coverage

Mean	5.1772

Standard Deviation	322.4512
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2.4. Mapping Quality

Mean Mapping Quality	47.97
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2.5. Mismatches and indels

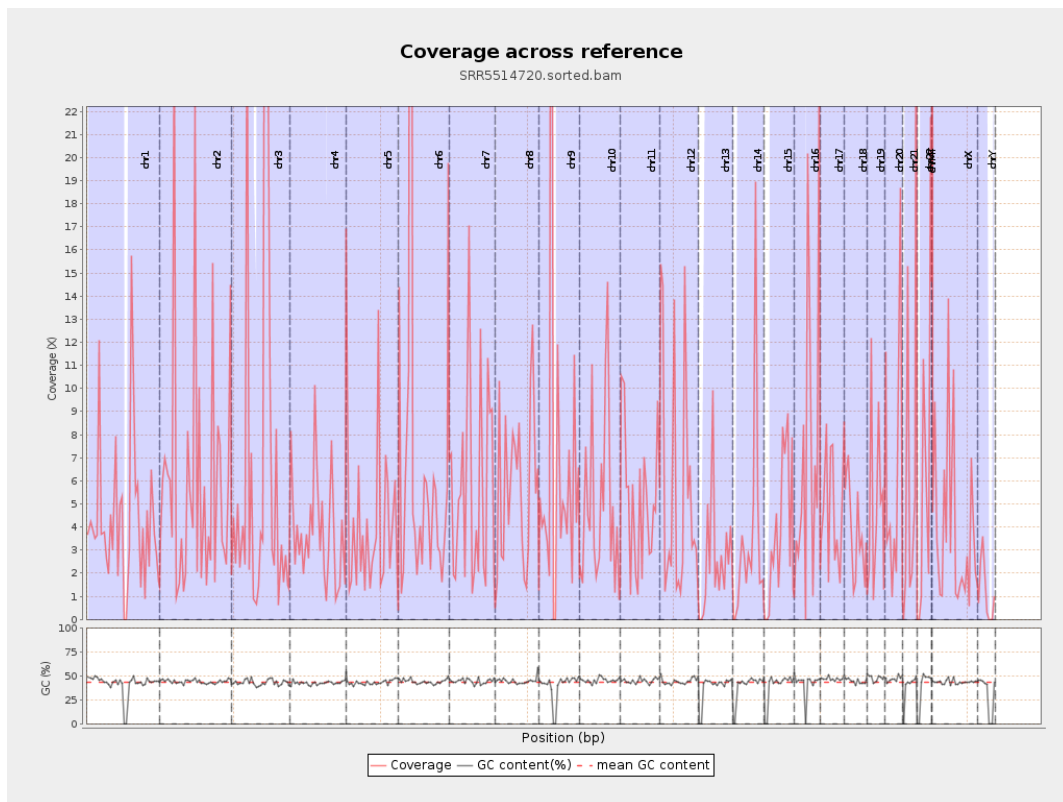
General error rate	1.08%
Mismatches	158,215,578
Insertions	8,385,902
Mapped reads with at least one insertion	4.58%
Deletions	6,040,932
Mapped reads with at least one deletion	3.19%
Homopolymer indels	37.7%

2.6. Chromosome stats

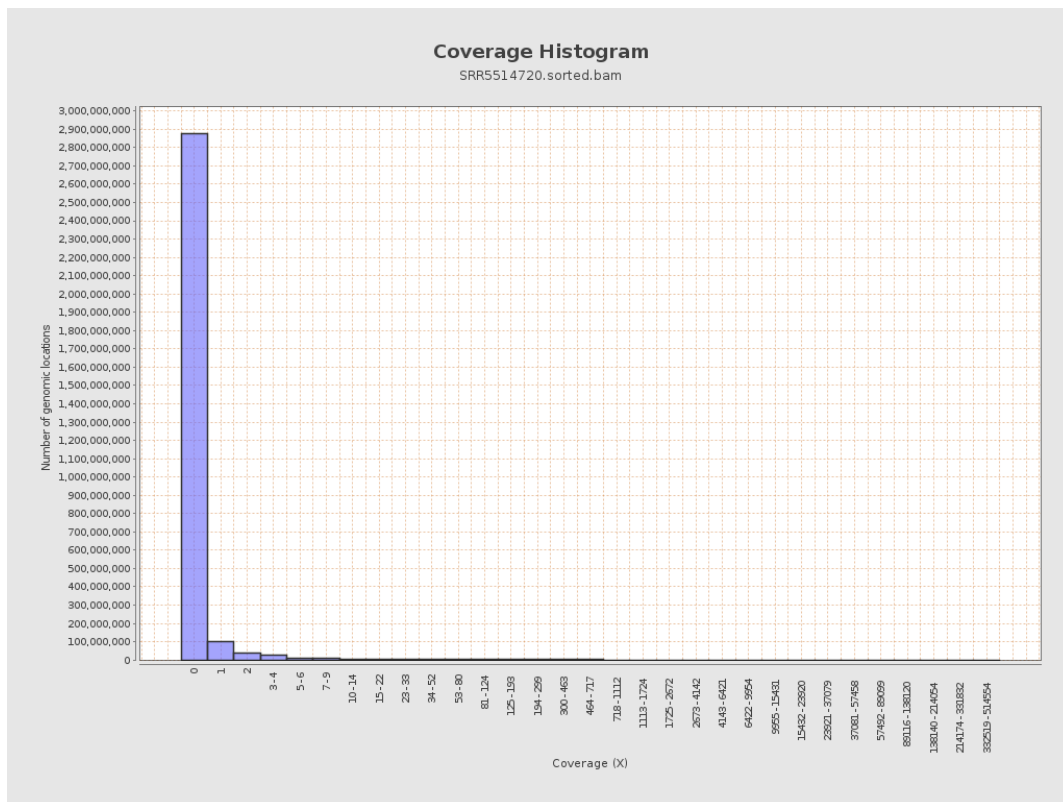
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1078907155	4.3286	180.278
chr2	243199373	1482778117	6.097	443.116
chr3	198022430	1267496744	6.4008	186.8759
chr4	191154276	719197571	3.7624	161.5512
chr5	180915260	724931805	4.007	152.6543
chr6	171115067	1324599272	7.741	330.5039
chr7	159138663	915167938	5.7508	303.7799

chr8	146364022	860663971	5.8803	225.0946
chr9	141213431	984558148	6.9721	738.6511
chr10	135534747	683760995	5.0449	185.0989
chr11	135006516	689890718	5.1101	229.9705
chr12	133851895	732414412	5.4718	259.7376
chr13	115169878	297393302	2.5822	145.573
chr14	107349540	377659076	3.518	132.122
chr15	102531392	388680316	3.7908	189.1855
chr16	90354753	691758377	7.656	582.1853
chr17	81195210	390020468	4.8035	178.3736
chr18	78077248	295310778	3.7823	135.2257
chr19	59128983	310546345	5.252	457.1594
chr20	63025520	401283554	6.367	274.1194
chr21	48129895	353101026	7.3364	574.9987
chr22	51304566	364214153	7.0991	703.2058
chrMT	16571	2252071	135.9044	228.029
chrX	155270560	613536710	3.9514	245.5427
chrY	59373566	76961268	1.2962	121.8158

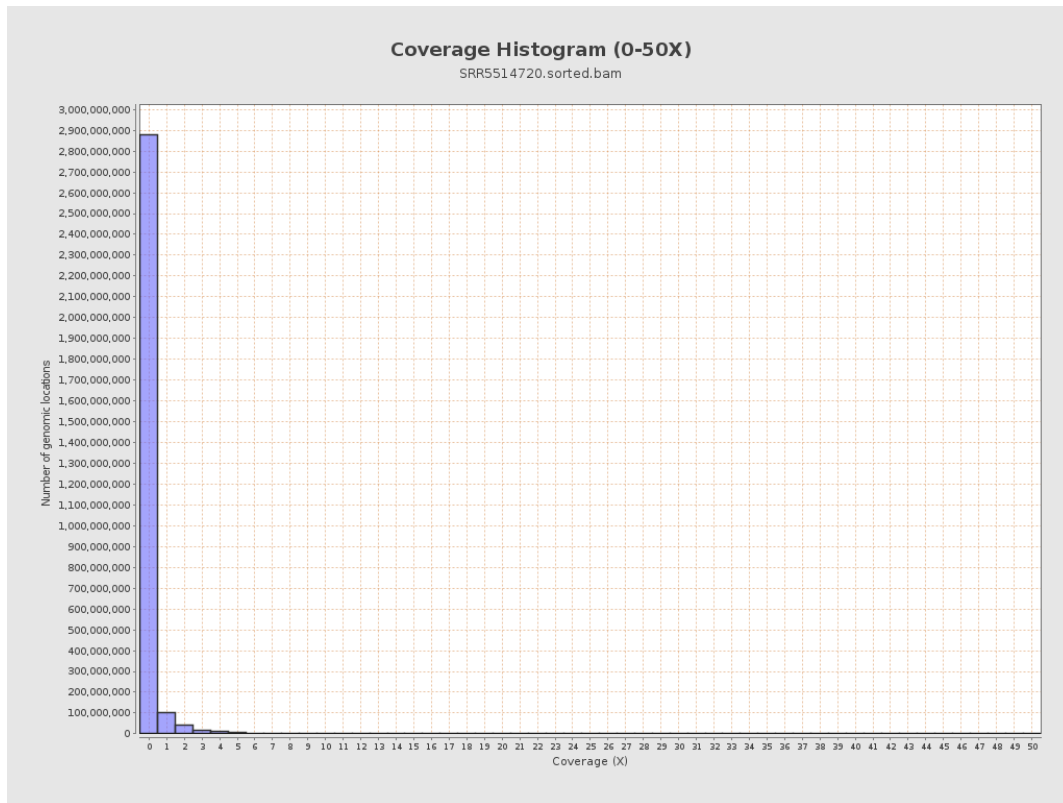
3. Results : Coverage across reference



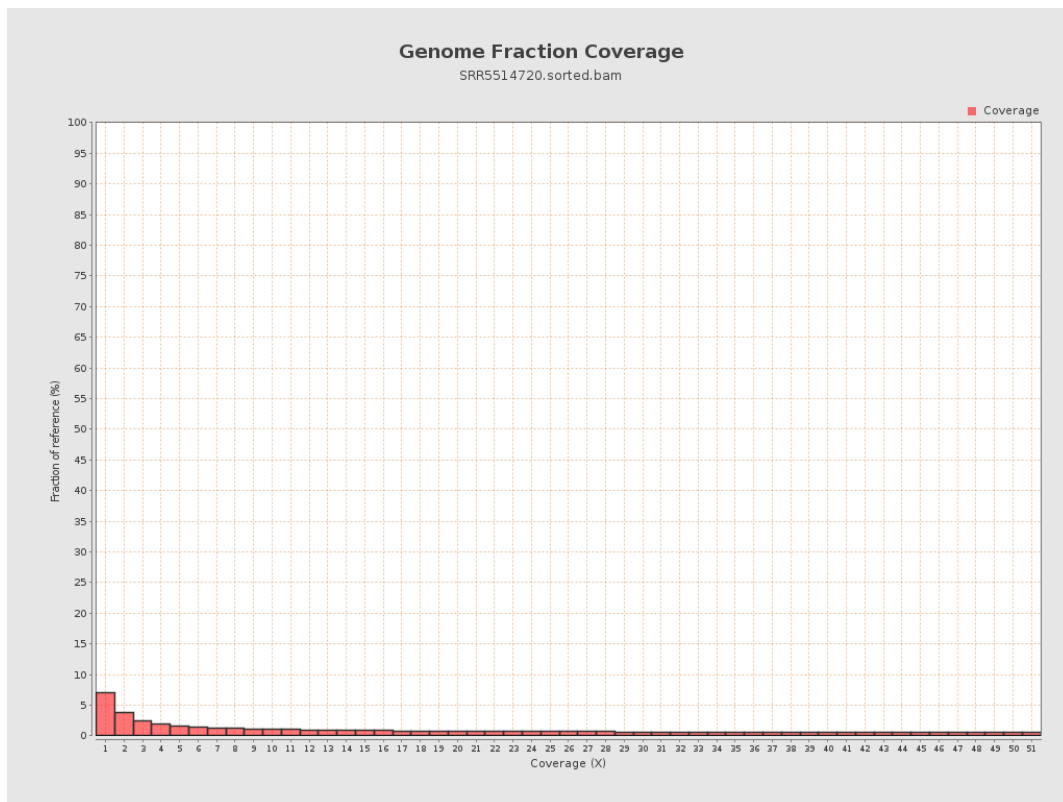
4. Results : Coverage Histogram



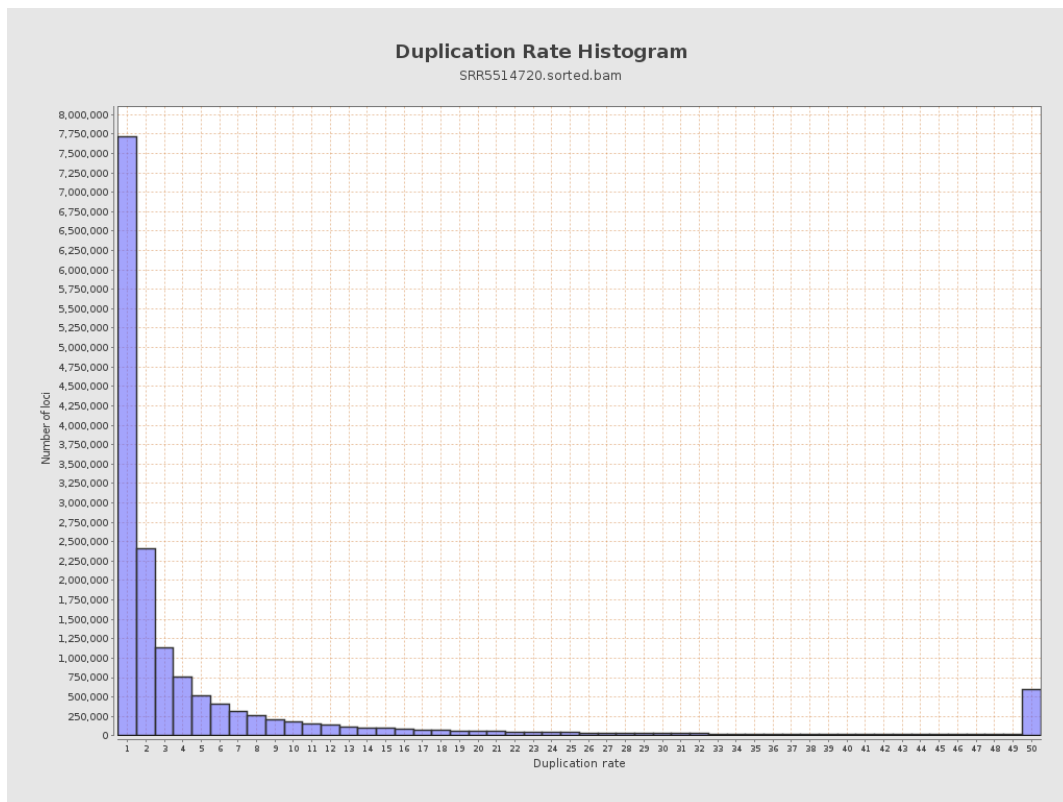
5. Results : Coverage Histogram (0-50X)



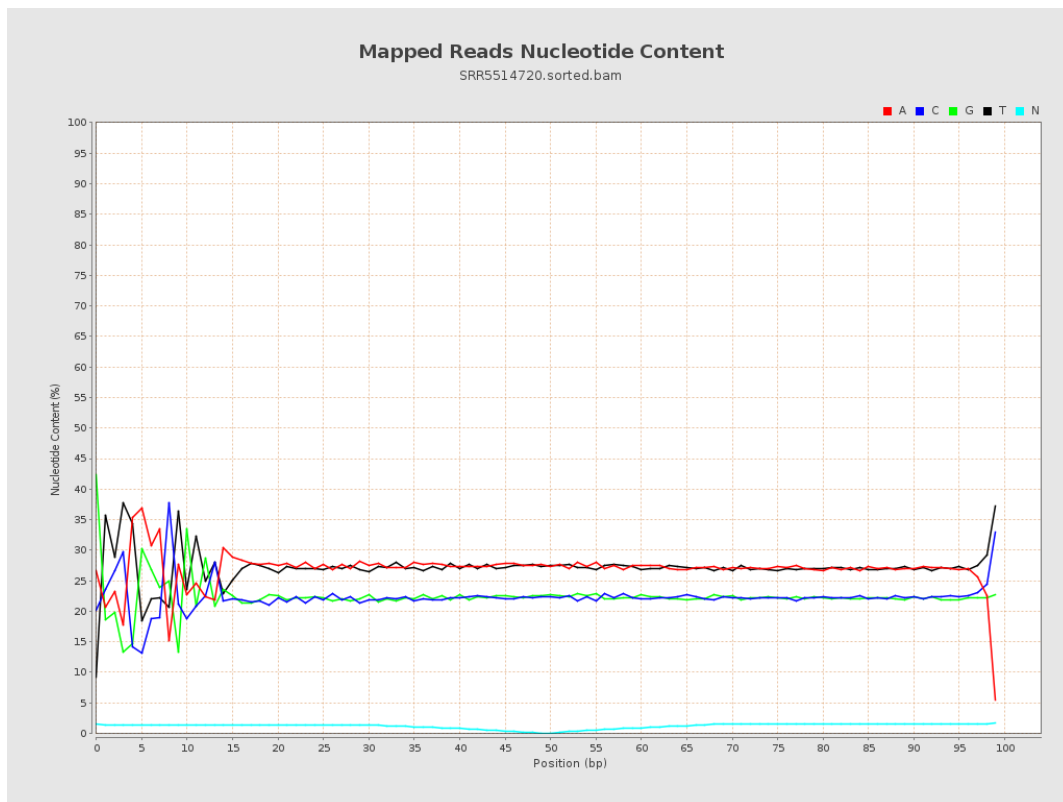
6. Results : Genome Fraction Coverage



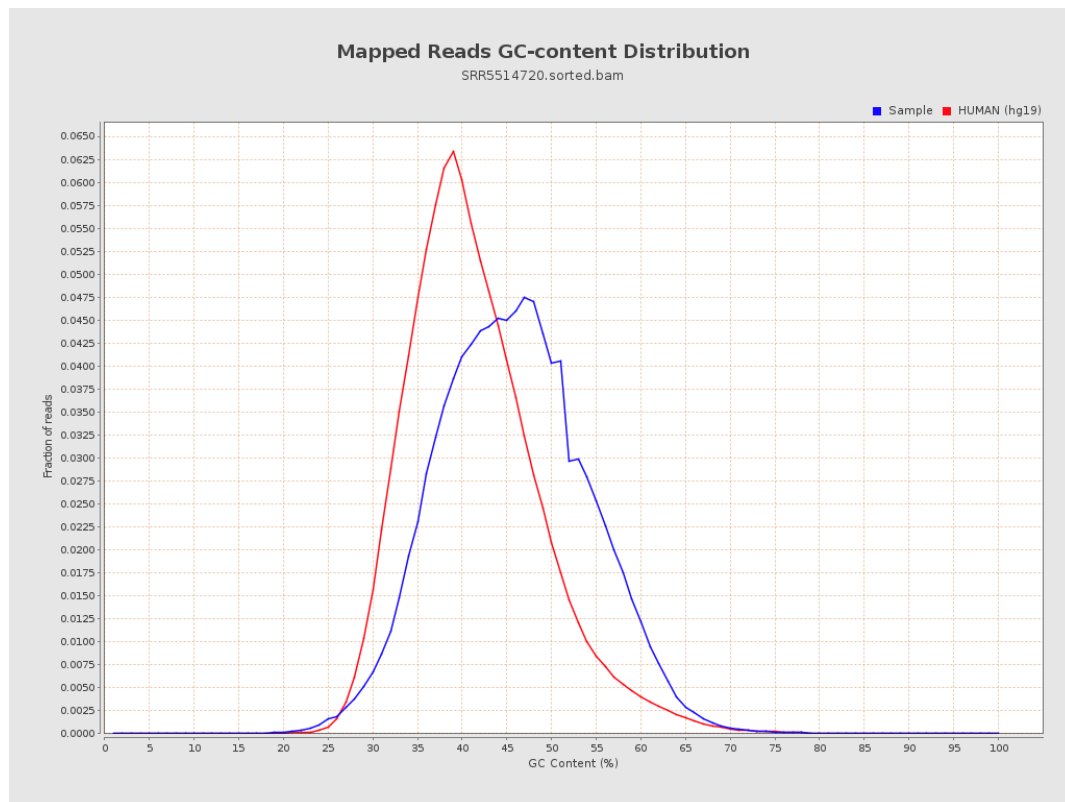
7. Results : Duplication Rate Histogram



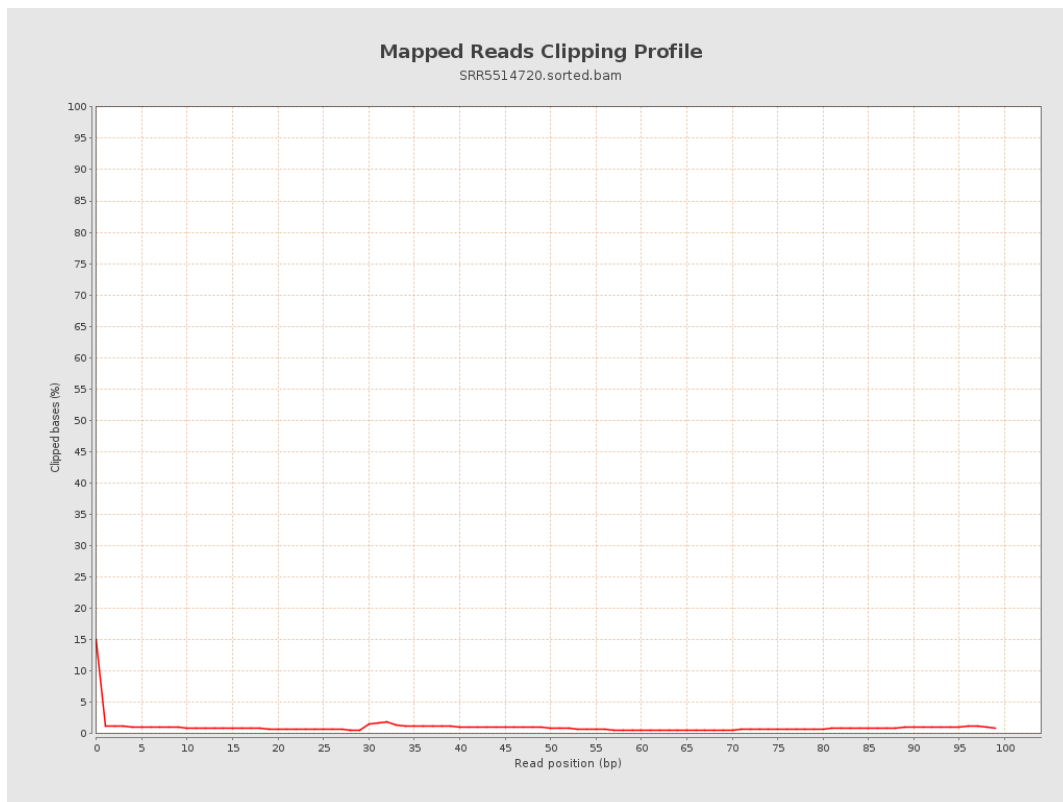
8. Results : Mapped Reads Nucleotide Content



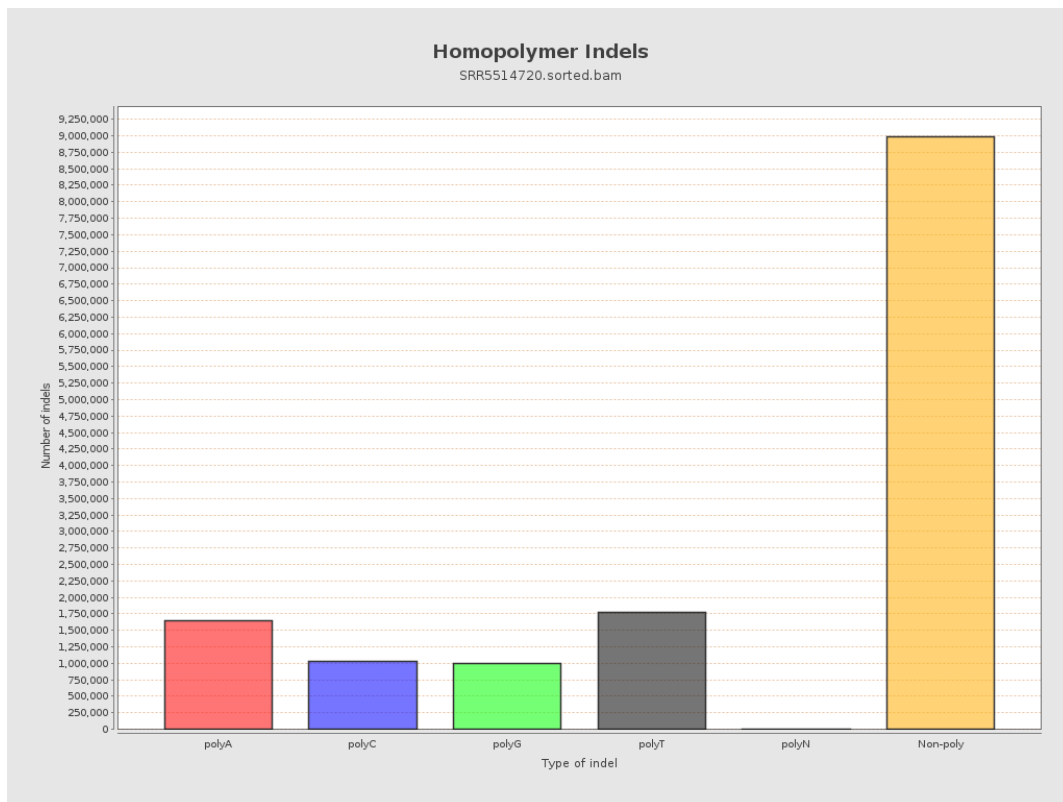
9. Results : Mapped Reads GC-content Distribution



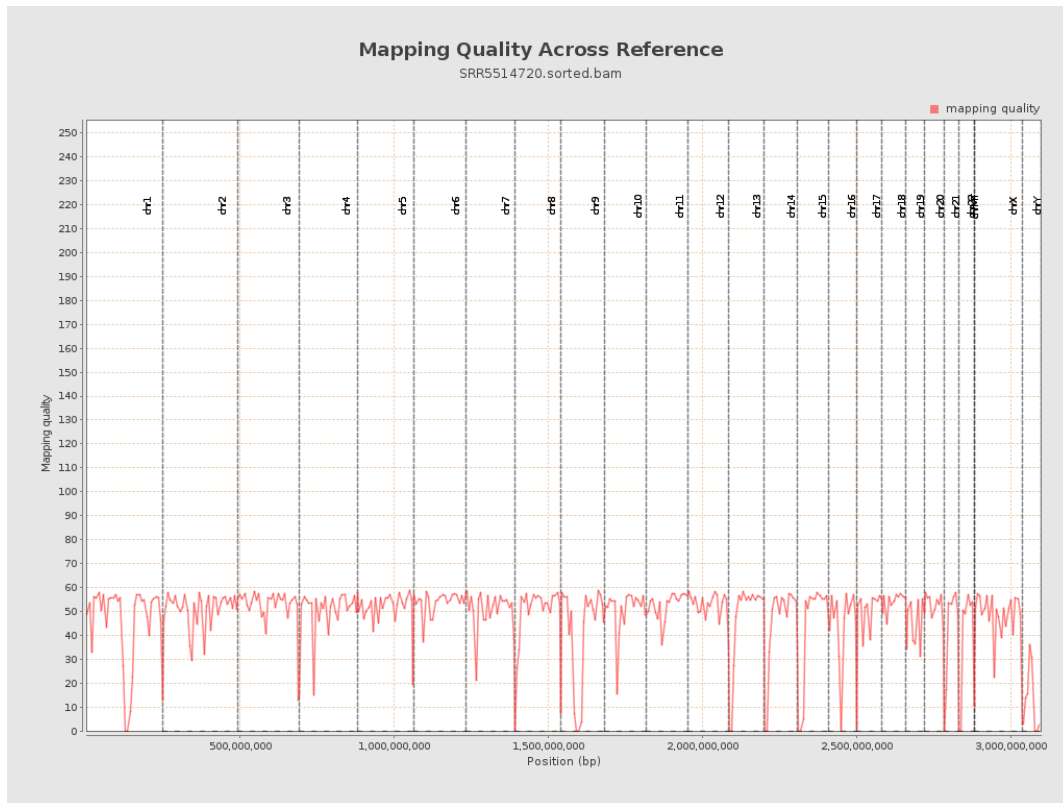
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

