

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 01:10:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514751.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_SRR5514751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514751.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 01:10:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	69,133,902
Mapped reads	65,721,440 / 95.06%
Unmapped reads	3,412,462 / 4.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,239,711 / 14.81%
Read min/max/mean length	30 / 100 / 105.25
Duplicated reads (estimated)	53,642,425 / 77.59%
Duplication rate	44.56%
Clipped reads	34,766,827 / 50.29%

2.2. ACGT Content

Number/percentage of A's	1,905,557,181 / 30.67%
Number/percentage of C's	1,186,383,125 / 19.1%
Number/percentage of T's	1,884,800,404 / 30.34%
Number/percentage of G's	1,234,945,319 / 19.88%
Number/percentage of N's	425,218 / 0.01%
GC Percentage	38.98%

2.3. Coverage

Mean	2.0087

Standard Deviation	171.3396
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2.4. Mapping Quality

Mean Mapping Quality	44.25
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2.5. Mismatches and indels

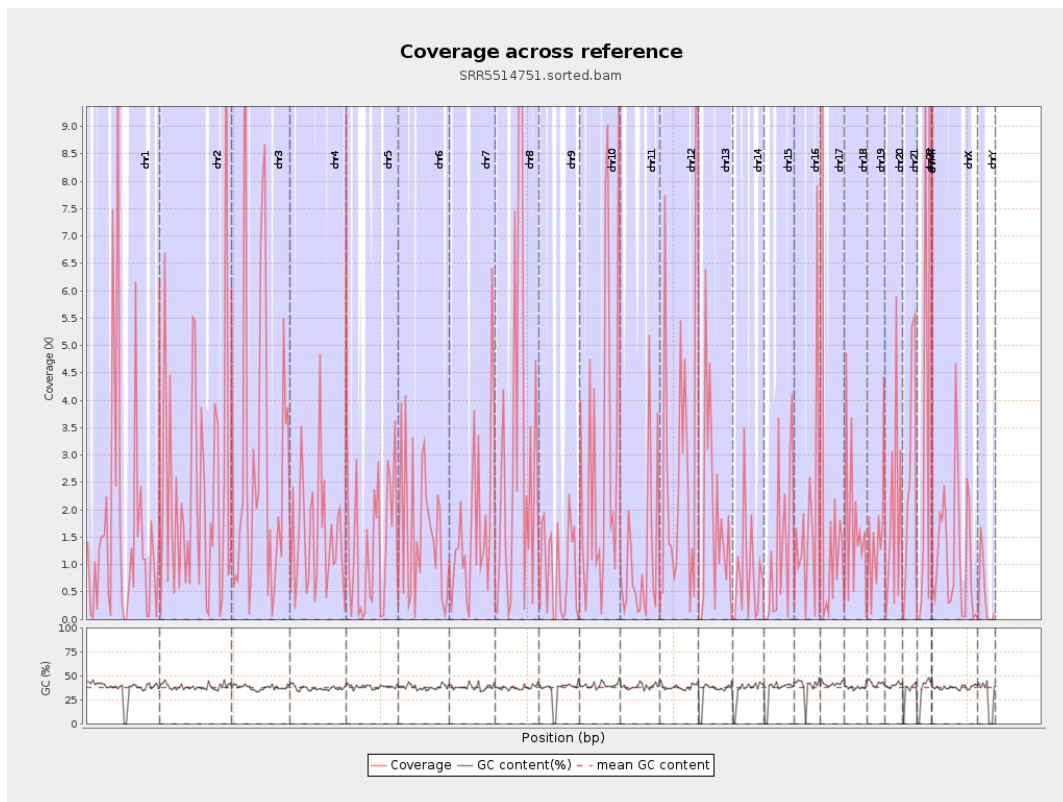
General error rate	0.71%
Mismatches	36,390,494
Insertions	4,760,095
Mapped reads with at least one insertion	6.86%
Deletions	2,168,502
Mapped reads with at least one deletion	3.11%
Homopolymer indels	45.03%

2.6. Chromosome stats

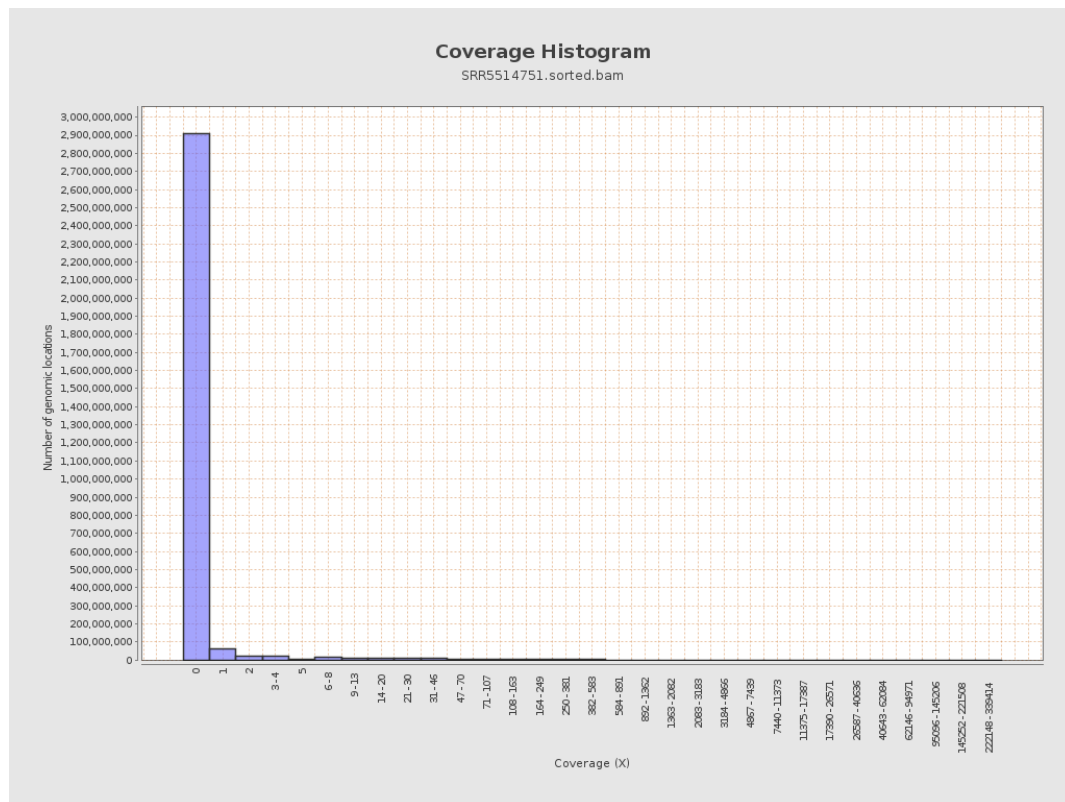
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	408589049	1.6393	36.4665
chr2	243199373	564988597	2.3231	88.0899
chr3	198022430	589501336	2.9769	41.2508
chr4	191154276	290041388	1.5173	27.9244
chr5	180915260	246754725	1.3639	26.4434
chr6	171115067	277763697	1.6233	25.241
chr7	159138663	275769939	1.7329	41.8518

chr8	146364022	442255843	3.0216	40.3015
chr9	141213431	120036137	0.85	19.6163
chr10	135534747	402169580	2.9673	139.0448
chr11	135006516	148574085	1.1005	27.1504
chr12	133851895	395653374	2.9559	55.8792
chr13	115169878	204785698	1.7781	145.2125
chr14	107349540	89542982	0.8341	17.9142
chr15	102531392	136828340	1.3345	25.9638
chr16	90354753	150242564	1.6628	28.1601
chr17	81195210	399489259	4.9201	861.7539
chr18	78077248	136602674	1.7496	24.6611
chr19	59128983	80362432	1.3591	47.2139
chr20	63025520	112781402	1.7895	27.128
chr21	48129895	130495097	2.7113	65.1913
chr22	51304566	281271386	5.4824	611.6398
chrMT	16571	110458564	6,665.7754	6,738.9443
chrX	155270560	195322207	1.2579	36.1222
chrY	59373566	28070527	0.4728	15.5446

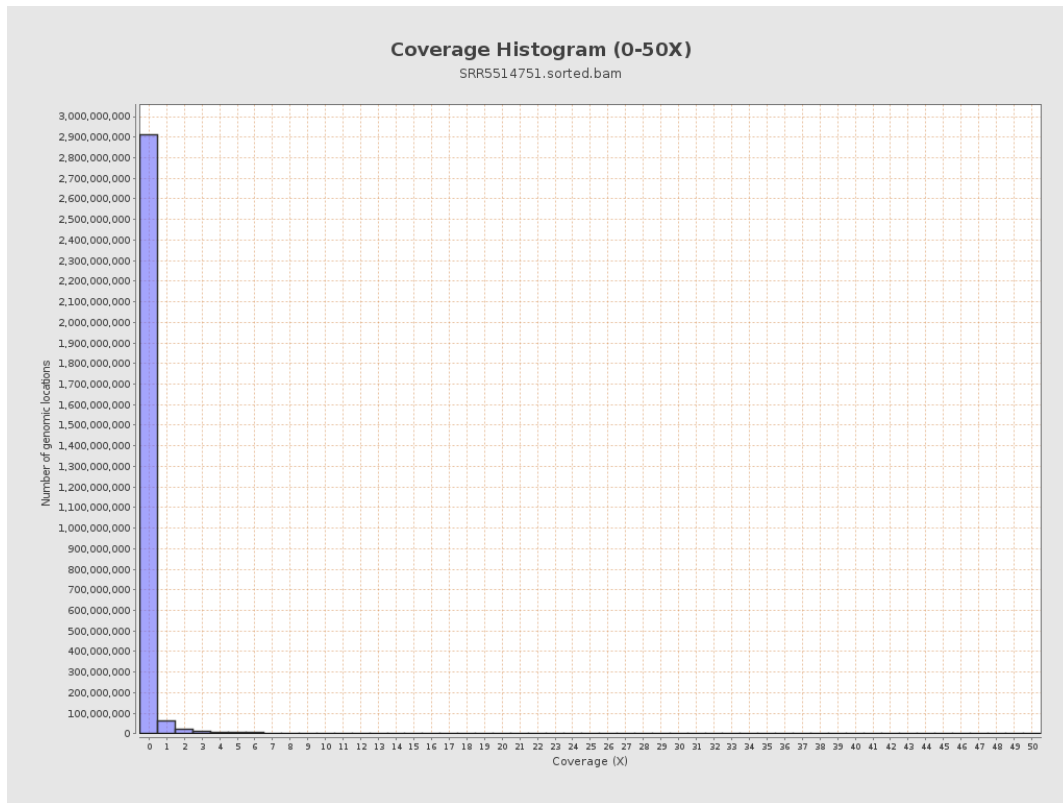
3. Results : Coverage across reference



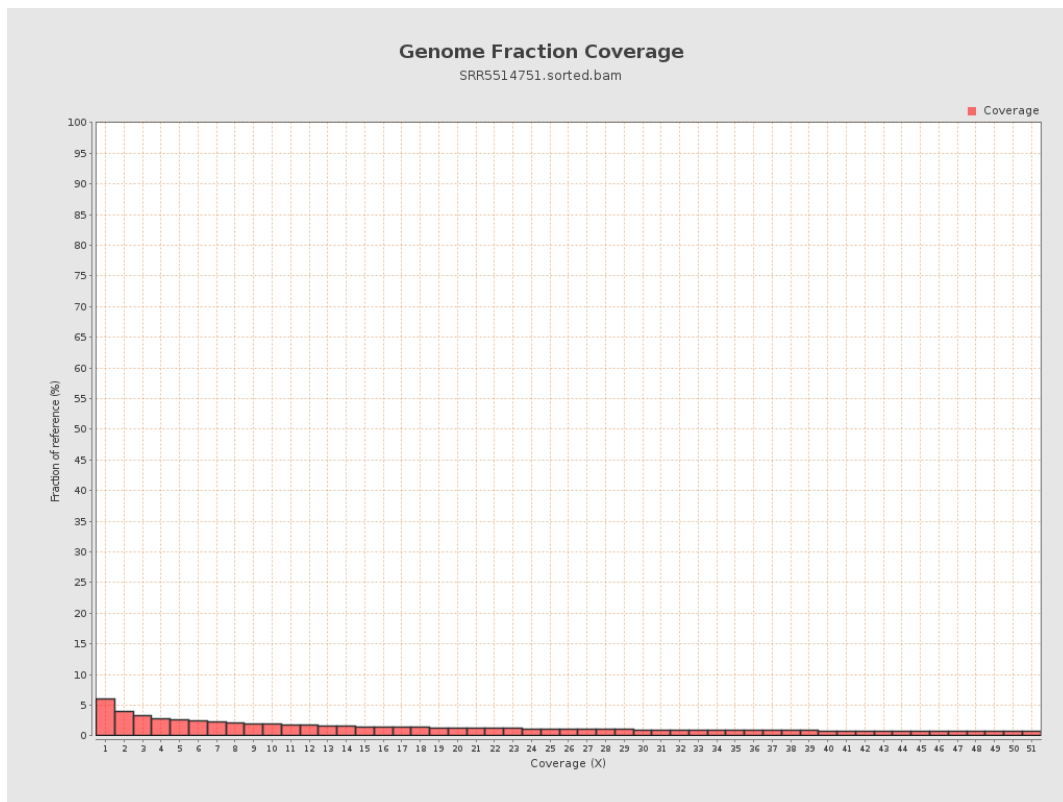
4. Results : Coverage Histogram



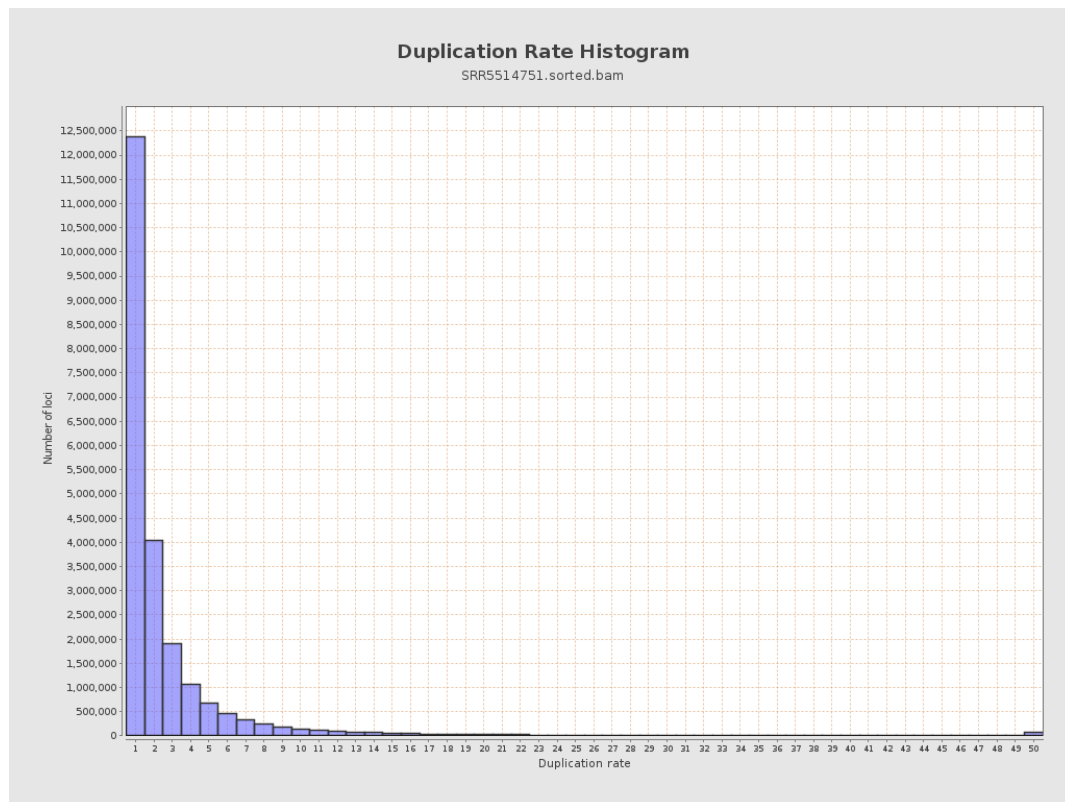
5. Results : Coverage Histogram (0-50X)



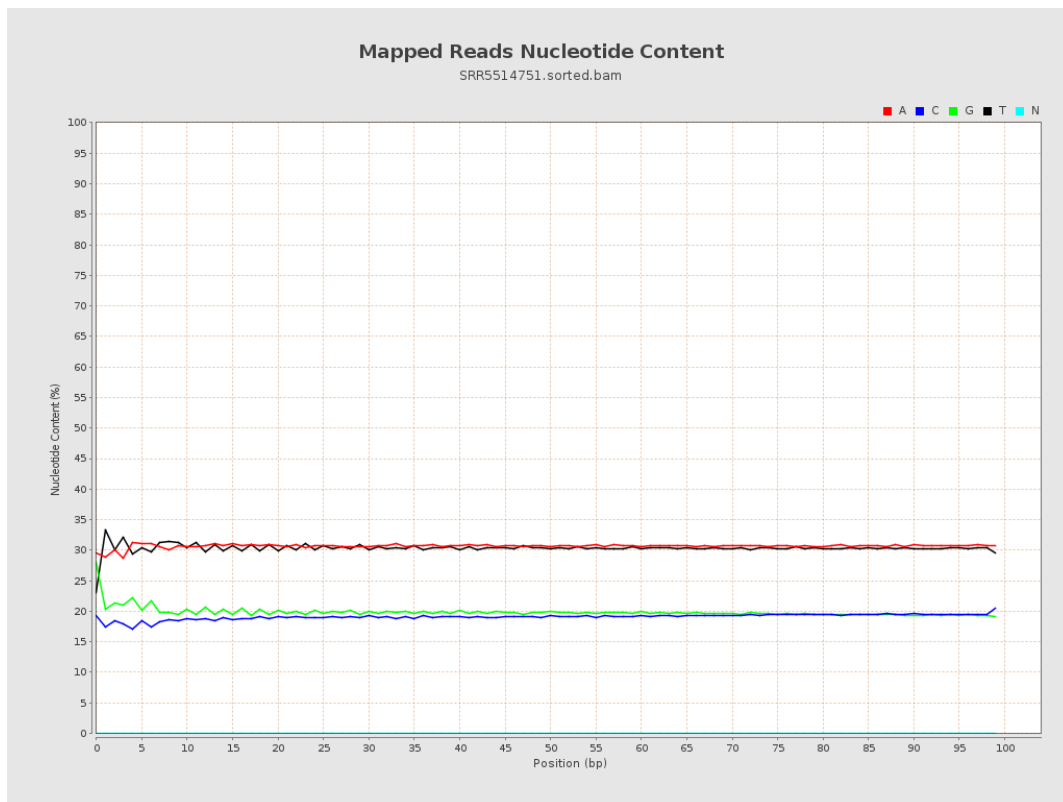
6. Results : Genome Fraction Coverage



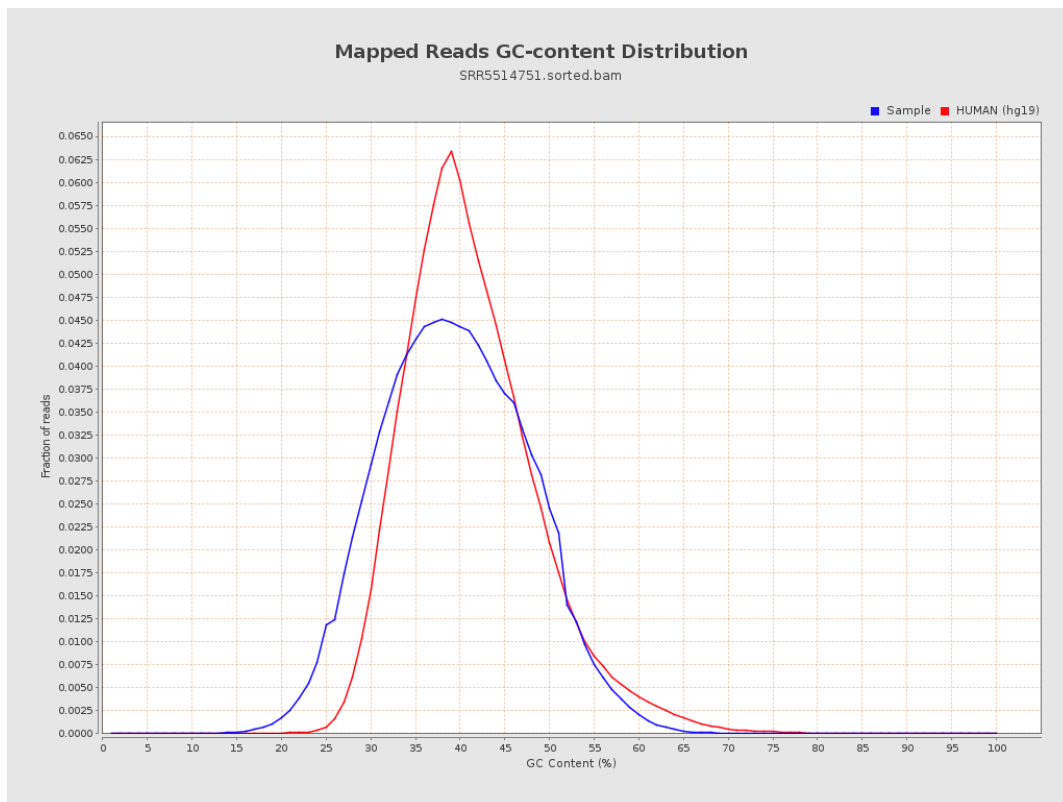
7. Results : Duplication Rate Histogram



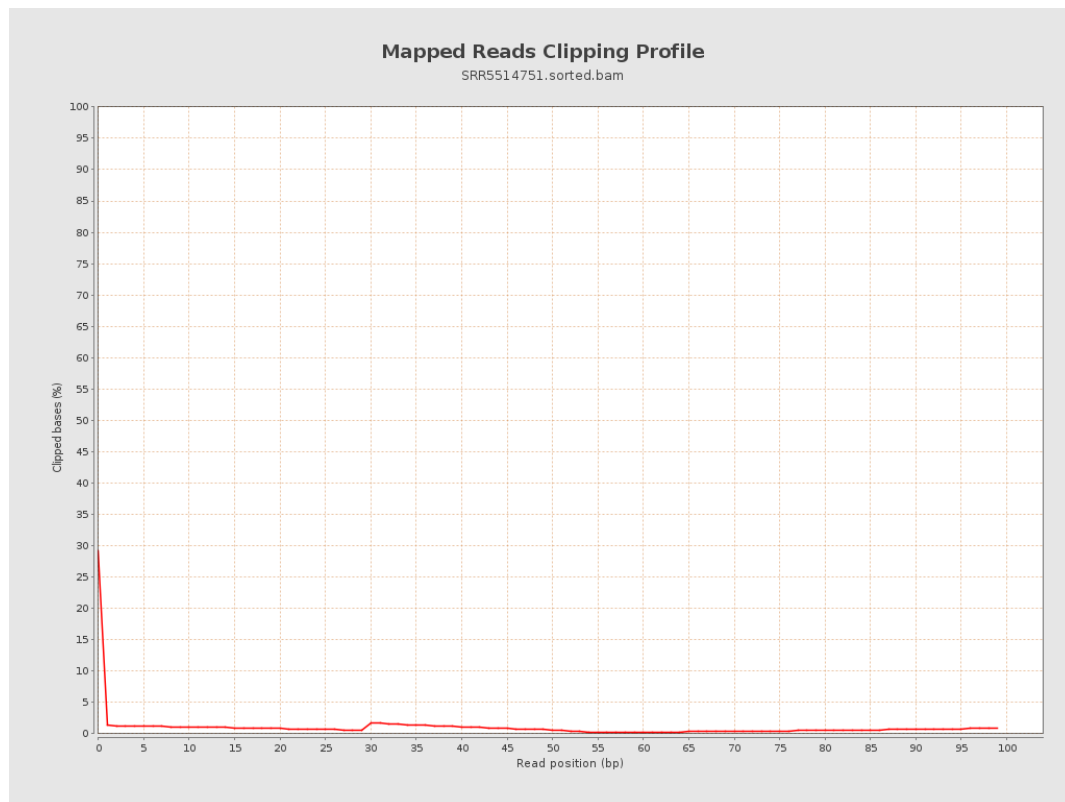
8. Results : Mapped Reads Nucleotide Content



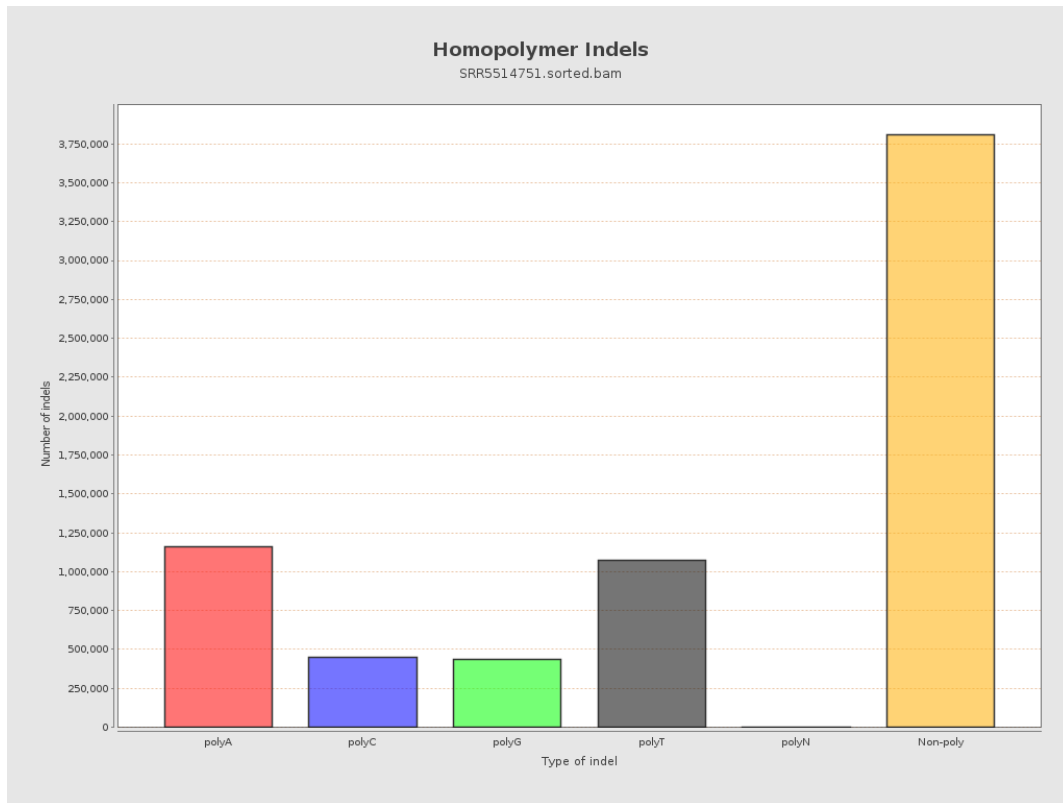
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

