

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 17:43:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514754.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_SRR5514754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 17:43:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,616,975
Mapped reads	56,439,751 / 94.67%
Unmapped reads	3,177,224 / 5.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,583,800 / 12.72%
Read min/max/mean length	30 / 100 / 104.3
Duplicated reads (estimated)	42,274,438 / 70.91%
Duplication rate	44.53%
Clipped reads	25,350,365 / 42.52%

2.2. ACGT Content

Number/percentage of A's	1,697,381,904 / 31.4%
Number/percentage of C's	1,007,719,902 / 18.64%
Number/percentage of T's	1,664,562,296 / 30.79%
Number/percentage of G's	1,035,646,833 / 19.16%
Number/percentage of N's	371,663 / 0.01%
GC Percentage	37.8%

2.3. Coverage

Mean	1.7471

Standard Deviation	39.665
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2.4. Mapping Quality

Mean Mapping Quality	44.81
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2.5. Mismatches and indels

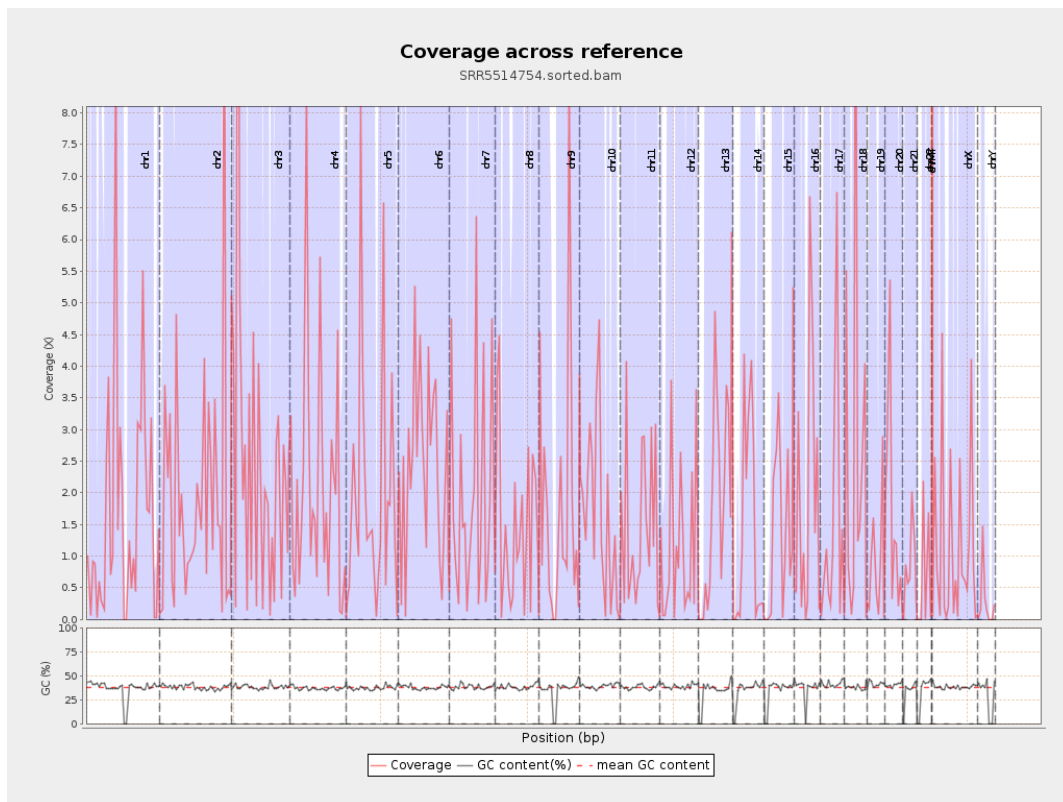
General error rate	0.56%
Mismatches	25,309,925
Insertions	3,463,207
Mapped reads with at least one insertion	5.91%
Deletions	1,086,684
Mapped reads with at least one deletion	1.83%
Homopolymer indels	58.22%

2.6. Chromosome stats

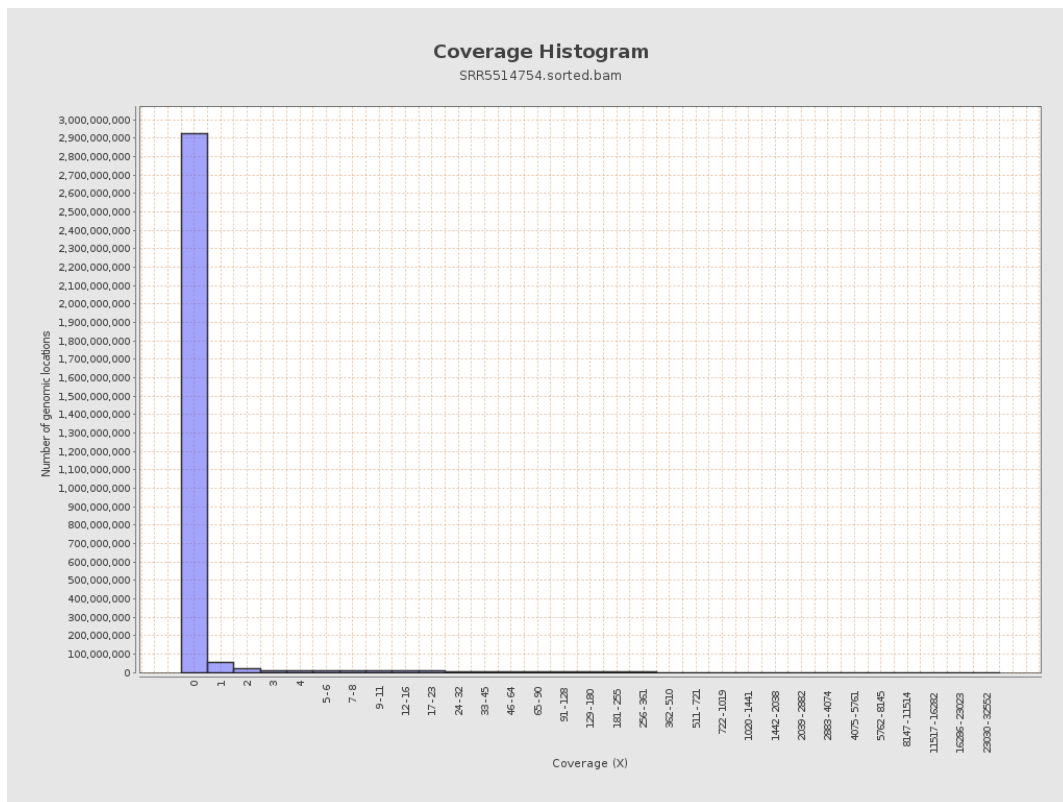
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	415225341	1.6659	29.125
chr2	243199373	467702008	1.9231	38.7477
chr3	198022430	501898157	2.5346	35.899
chr4	191154276	396147978	2.0724	42.4293
chr5	180915260	349755754	1.9333	27.7587
chr6	171115067	421072881	2.4608	31.8664
chr7	159138663	305895585	1.9222	52.7488

chr8	146364022	214165126	1.4632	41.1833
chr9	141213431	229118943	1.6225	36.5729
chr10	135534747	222693162	1.6431	26.009
chr11	135006516	198867052	1.473	23.75
chr12	133851895	150913976	1.1275	18.1819
chr13	115169878	215400145	1.8703	42.8993
chr14	107349540	143301803	1.3349	23.7214
chr15	102531392	141159357	1.3767	29.8015
chr16	90354753	162919753	1.8031	29.5248
chr17	81195210	120362512	1.4824	33.8313
chr18	78077248	215928810	2.7656	33.1955
chr19	59128983	55834921	0.9443	16.6045
chr20	63025520	102294387	1.6231	28.2053
chr21	48129895	41539516	0.8631	25.6879
chr22	51304566	30764242	0.5996	21.5304
chrMT	16571	113579616	6,854.1196	6,350.1676
chrX	155270560	173939214	1.1202	24.5877
chrY	59373566	18065463	0.3043	9.7476

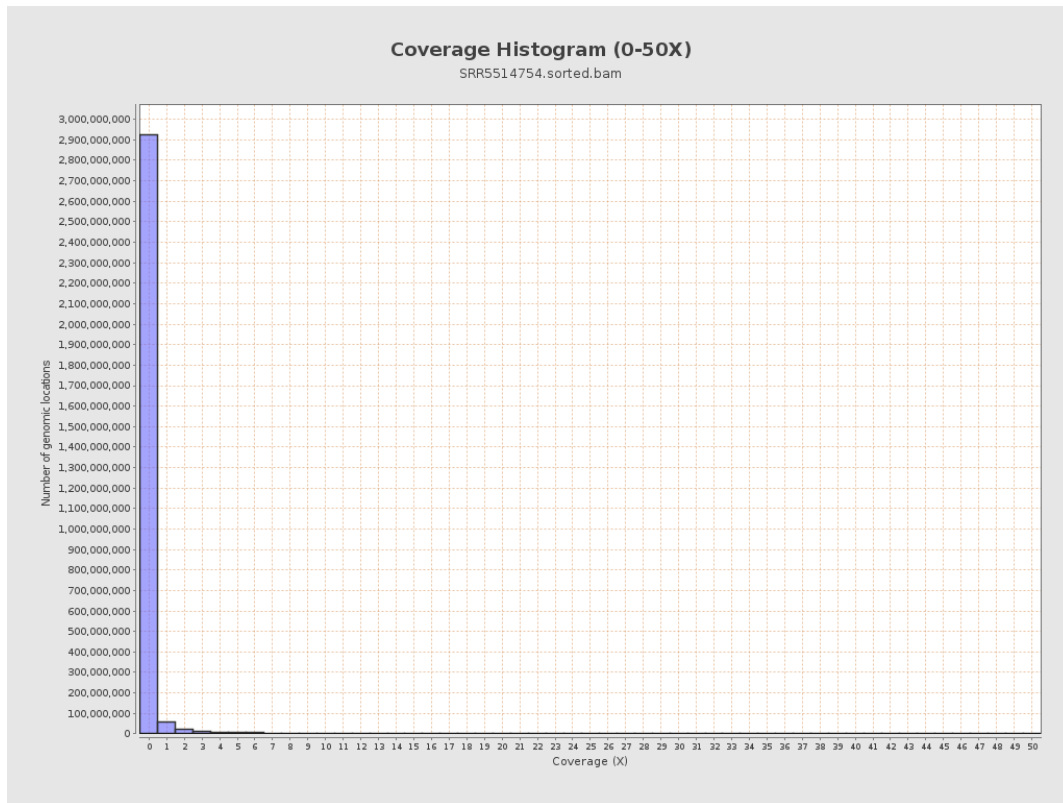
3. Results : Coverage across reference



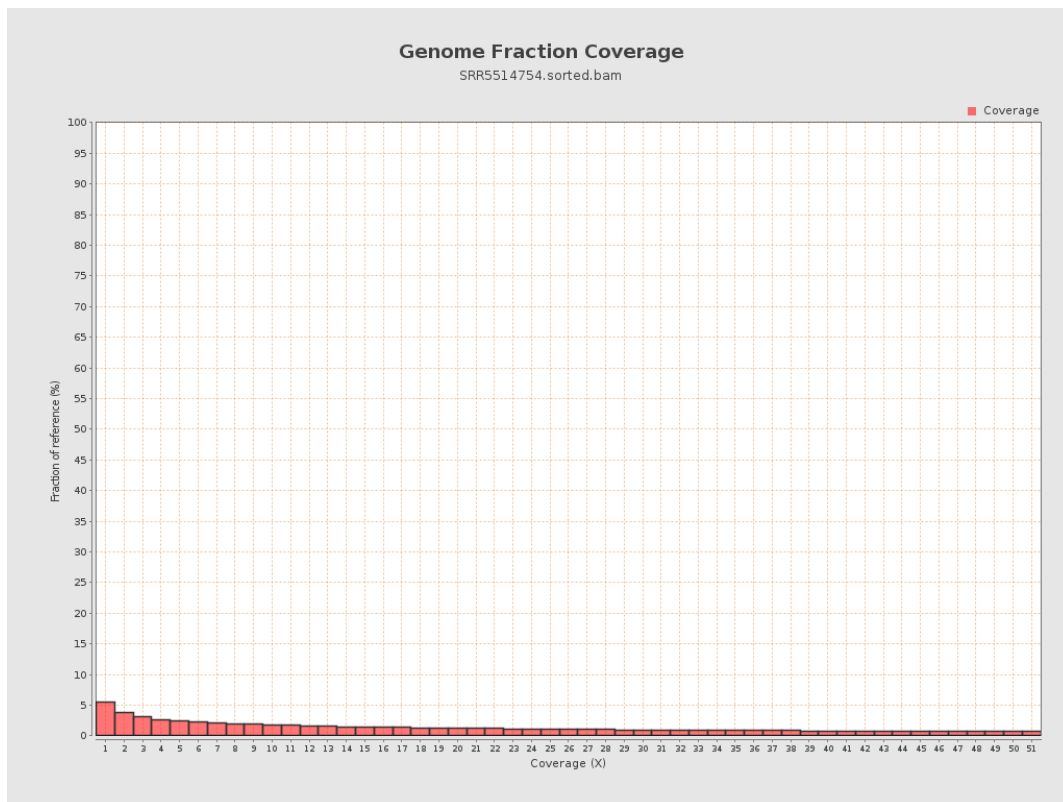
4. Results : Coverage Histogram



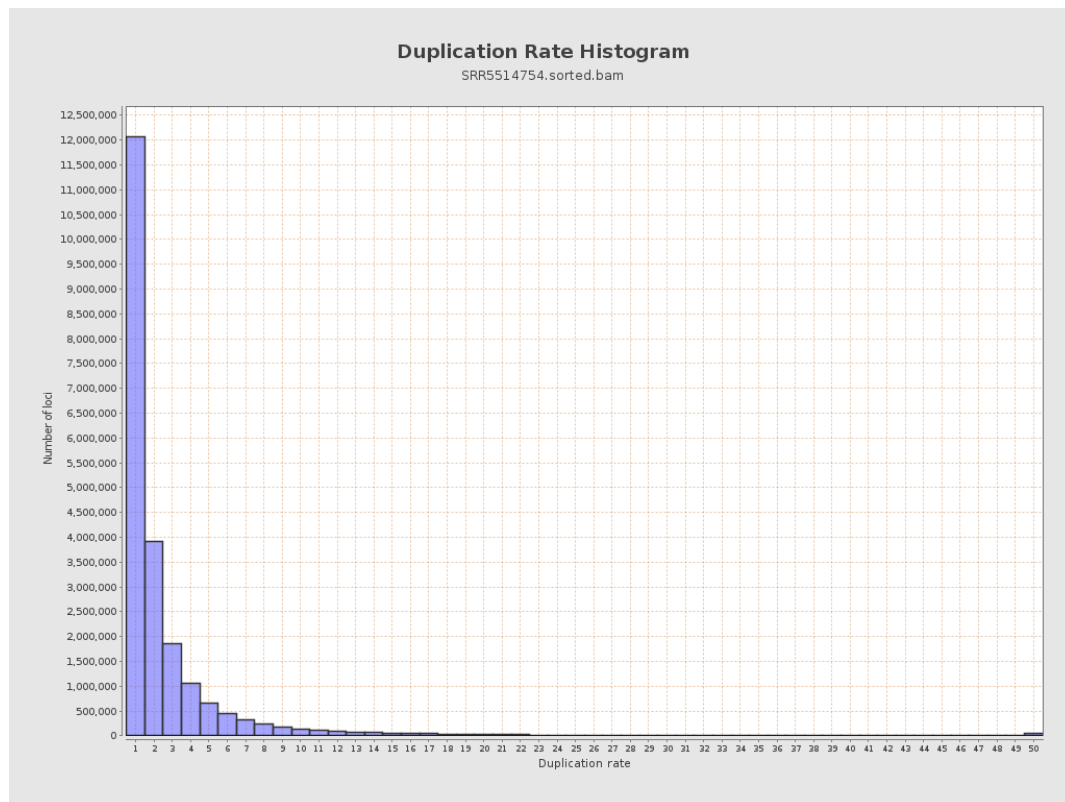
5. Results : Coverage Histogram (0-50X)



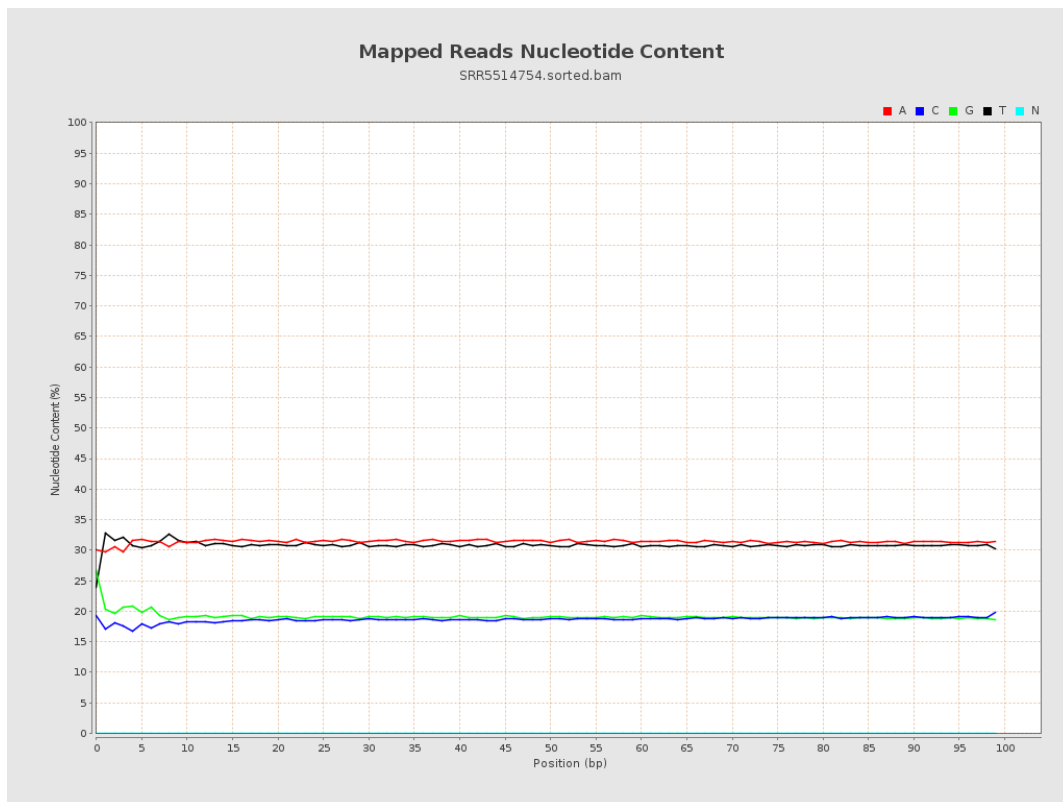
6. Results : Genome Fraction Coverage



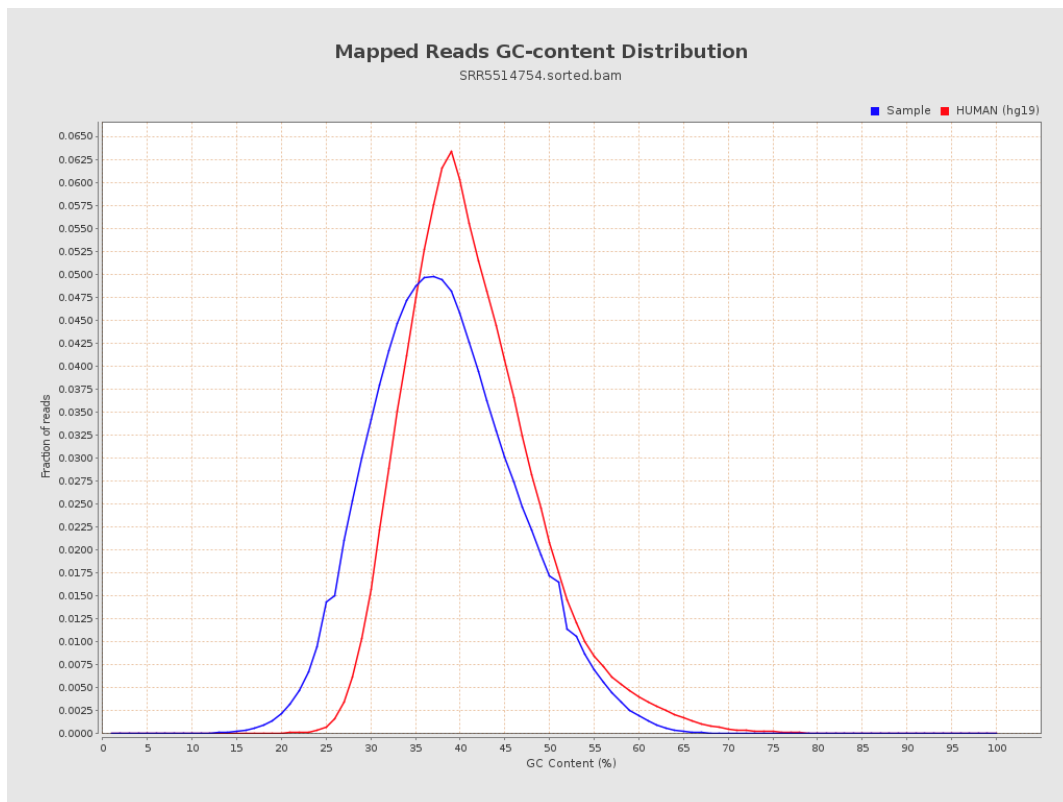
7. Results : Duplication Rate Histogram



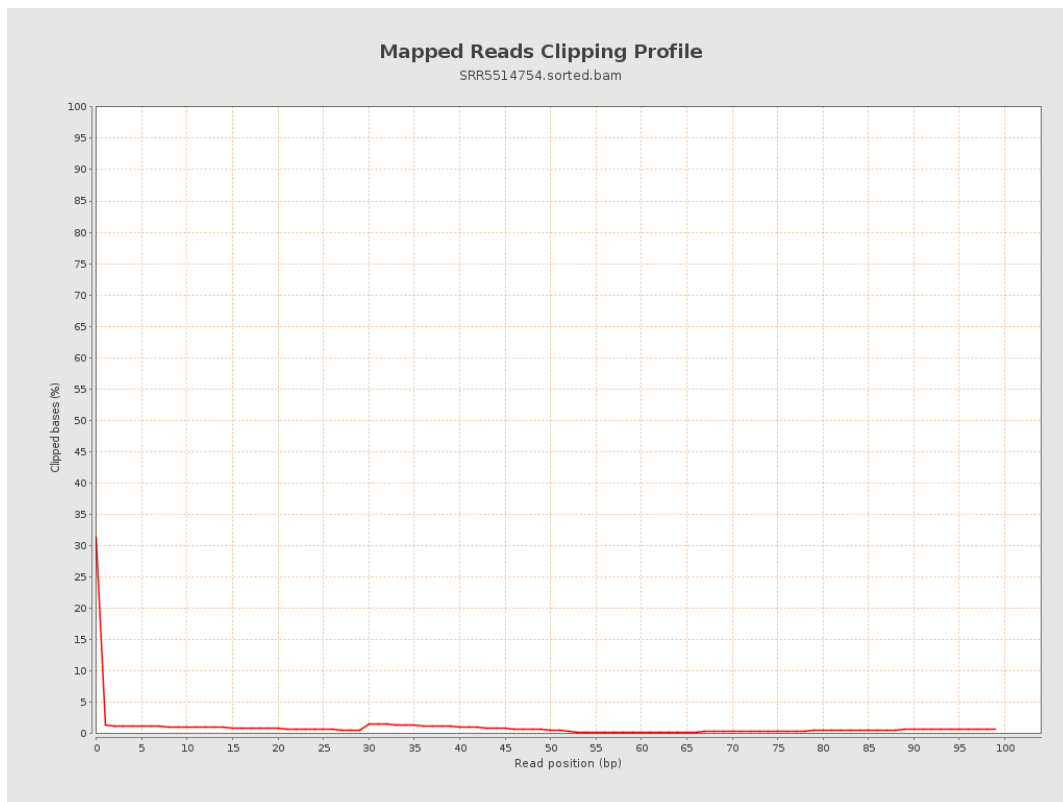
8. Results : Mapped Reads Nucleotide Content



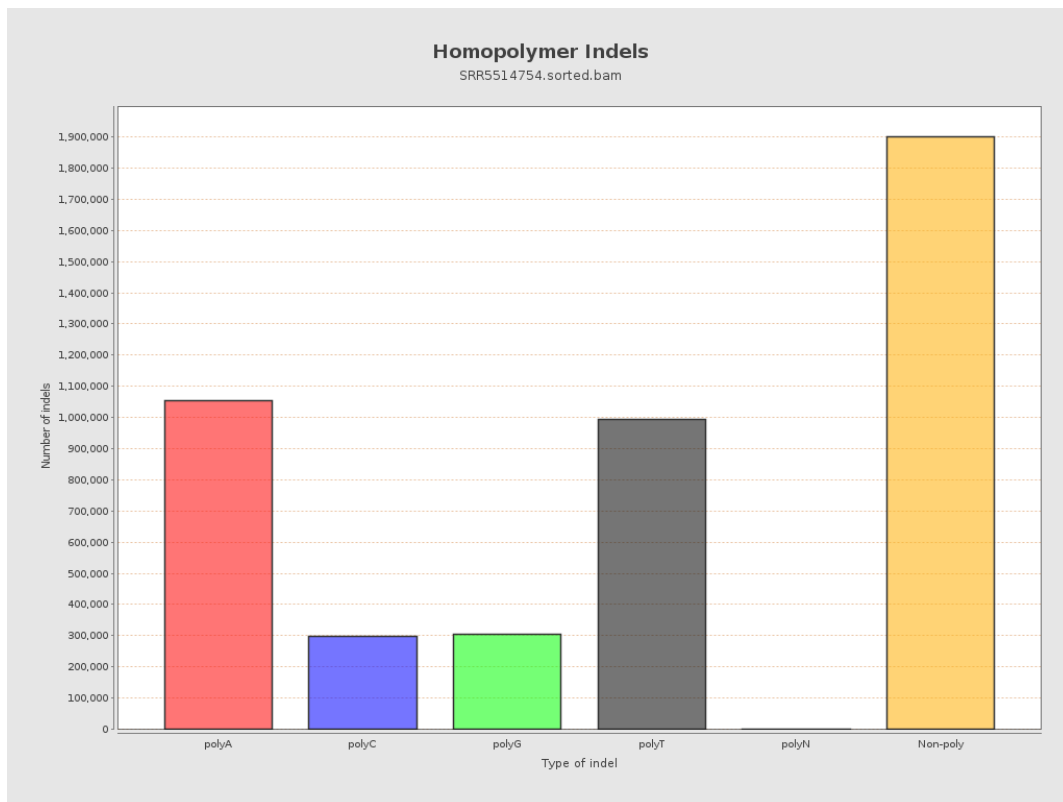
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

