

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 00:12:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514749.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_SRR5514749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514749.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 00:12:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	64,795,530
Mapped reads	59,654,413 / 92.07%
Unmapped reads	5,141,117 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,260,520 / 12.75%
Read min/max/mean length	30 / 100 / 104.47
Duplicated reads (estimated)	46,471,326 / 71.72%
Duplication rate	44.23%
Clipped reads	29,530,873 / 45.58%

2.2. ACGT Content

Number/percentage of A's	1,741,836,236 / 30.98%
Number/percentage of C's	1,057,294,169 / 18.81%
Number/percentage of T's	1,720,662,070 / 30.6%
Number/percentage of G's	1,102,213,221 / 19.6%
Number/percentage of N's	390,613 / 0.01%
GC Percentage	38.41%

2.3. Coverage

Mean	1.8175

Standard Deviation	102.9656
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2.4. Mapping Quality

Mean Mapping Quality	46.04
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2.5. Mismatches and indels

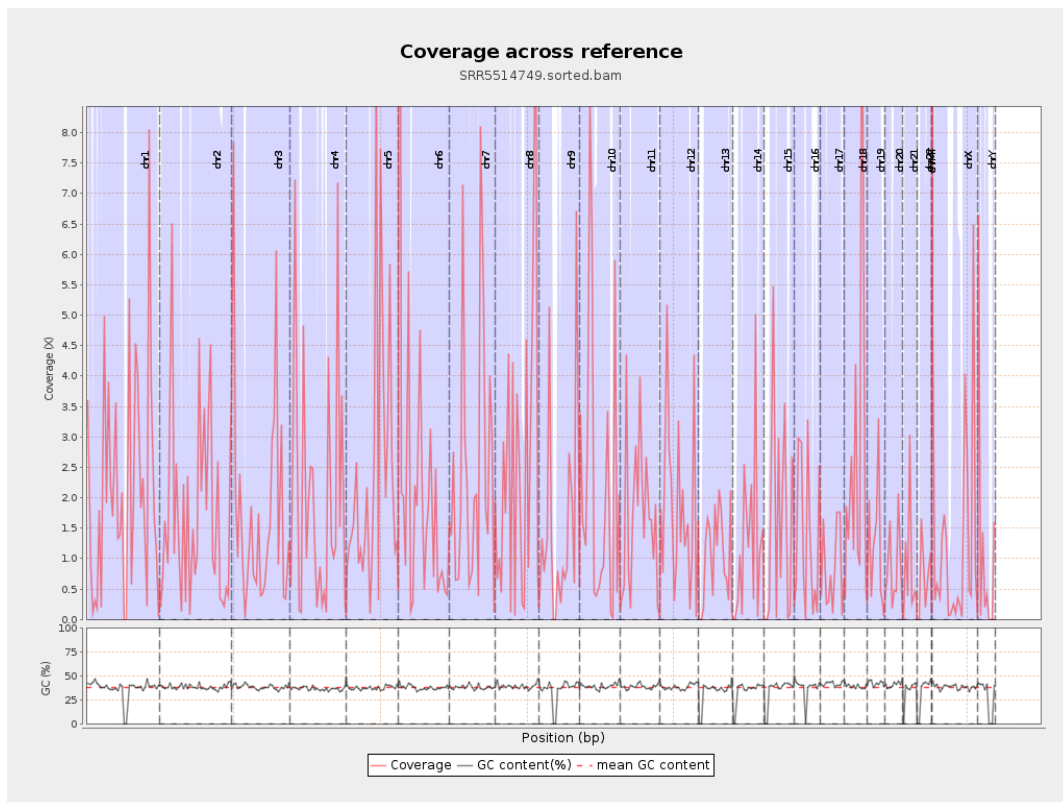
General error rate	0.65%
Mismatches	30,322,181
Insertions	3,968,927
Mapped reads with at least one insertion	6.38%
Deletions	1,426,959
Mapped reads with at least one deletion	2.25%
Homopolymer indels	54.99%

2.6. Chromosome stats

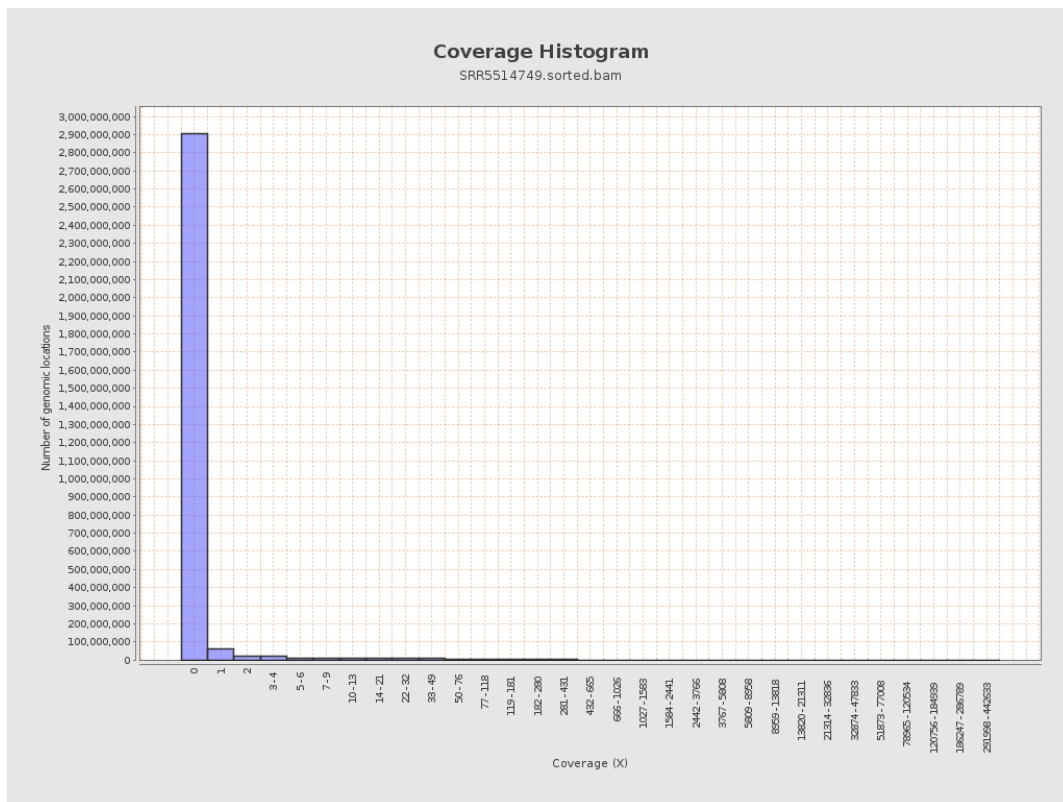
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	519152716	2.0829	34.0788
chr2	243199373	422627734	1.7378	57.2039
chr3	198022430	346043369	1.7475	111.9908
chr4	191154276	386791665	2.0235	32.1623
chr5	180915260	427534282	2.3632	34.813
chr6	171115067	397997046	2.3259	374.7366
chr7	159138663	387529927	2.4352	39.1951

chr8	146364022	365782719	2.4991	42.1849
chr9	141213431	221743730	1.5703	78.9479
chr10	135534747	312204649	2.3035	66.6878
chr11	135006516	226564502	1.6782	29.8219
chr12	133851895	250401480	1.8707	33.6944
chr13	115169878	123453257	1.0719	19.9085
chr14	107349540	133510798	1.2437	27.0989
chr15	102531392	166136110	1.6203	24.5184
chr16	90354753	119886665	1.3268	24.9244
chr17	81195210	63124670	0.7774	16.5935
chr18	78077248	206158515	2.6404	59.2419
chr19	59128983	71778097	1.2139	31.1667
chr20	63025520	53020958	0.8413	20.1207
chr21	48129895	44150143	0.9173	24.2403
chr22	51304566	37318019	0.7274	105.0764
chrMT	16571	85282378	5,146.4835	5,302.3557
chrX	155270560	195088932	1.2564	44.5355
chrY	59373566	63132472	1.0633	44.1833

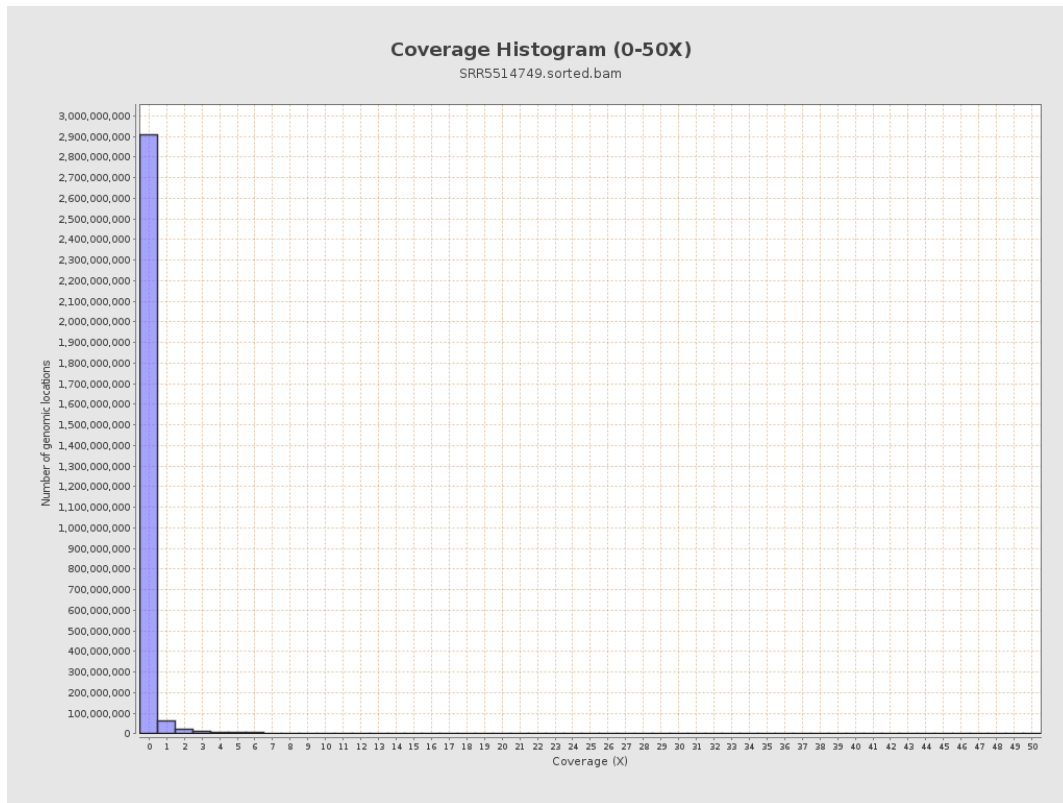
3. Results : Coverage across reference



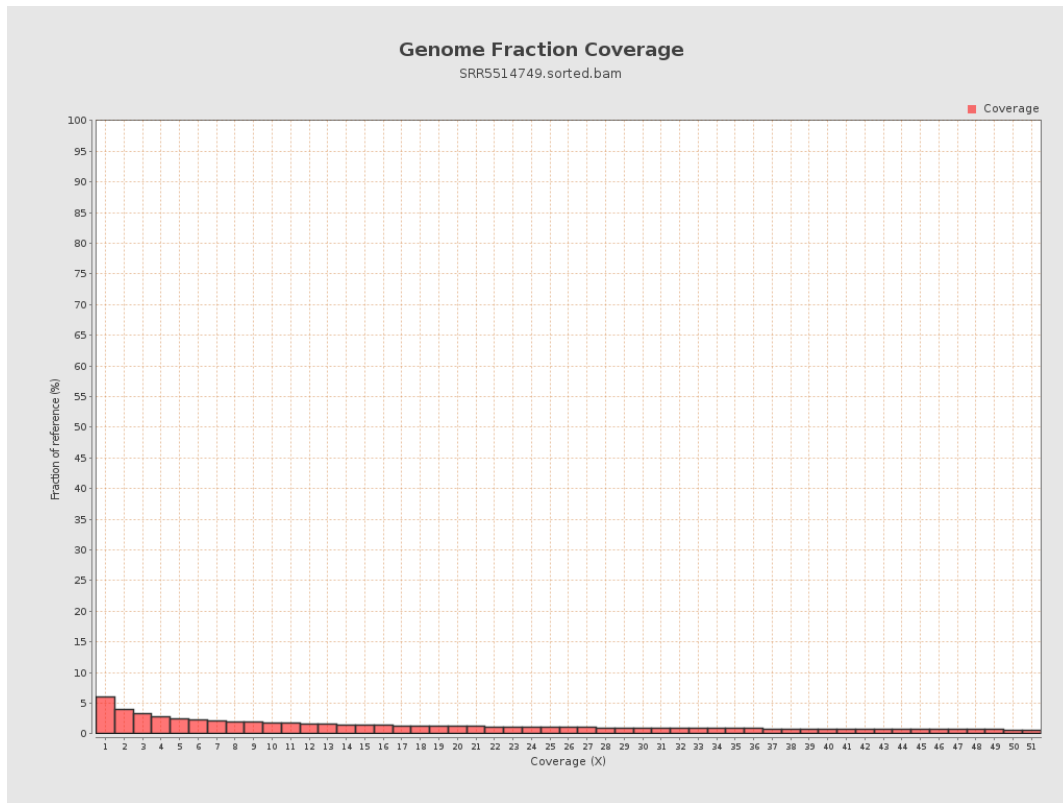
4. Results : Coverage Histogram



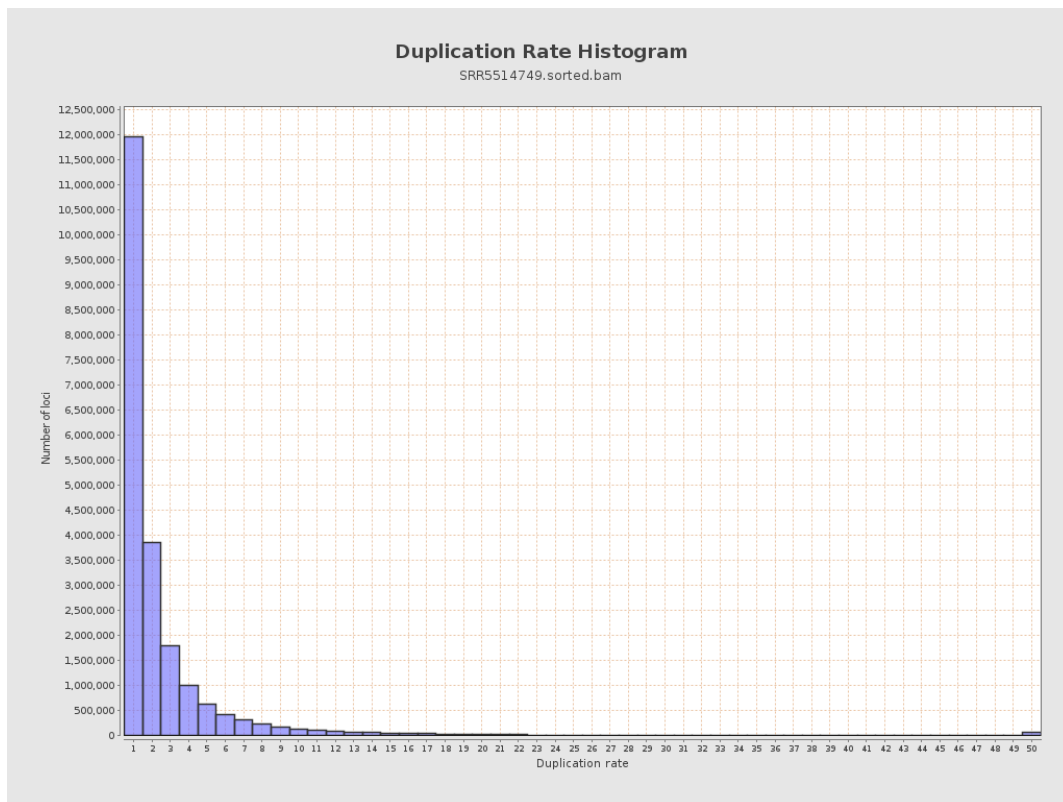
5. Results : Coverage Histogram (0-50X)



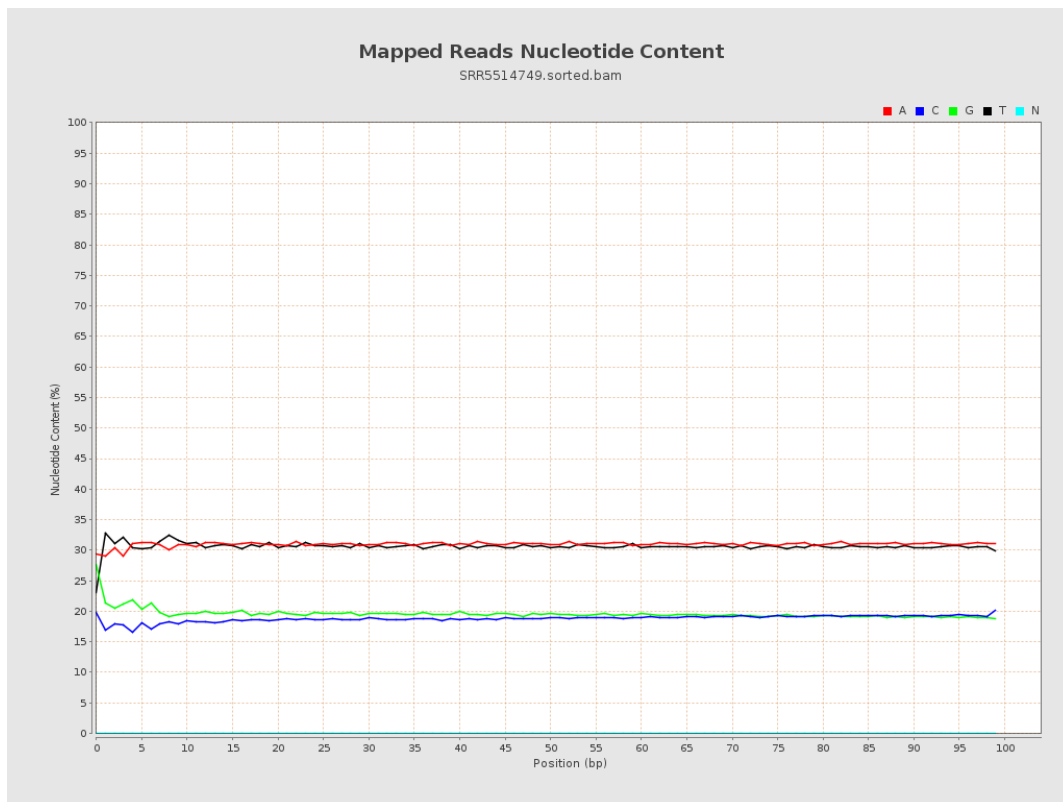
6. Results : Genome Fraction Coverage



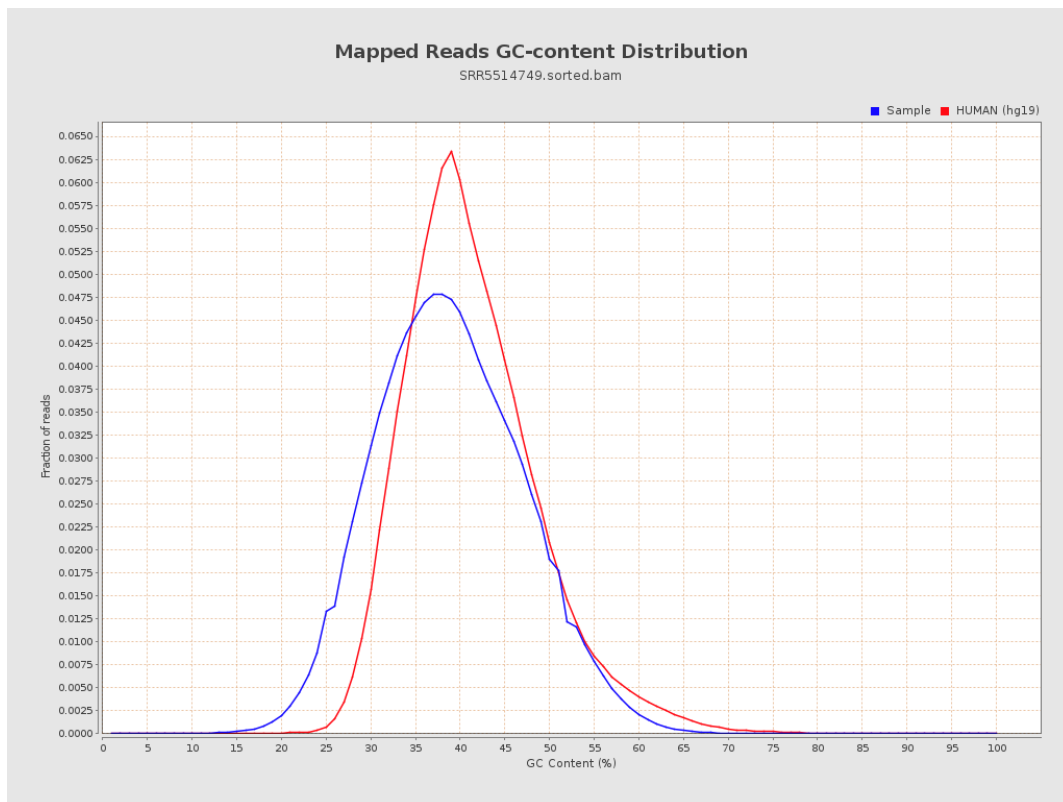
7. Results : Duplication Rate Histogram



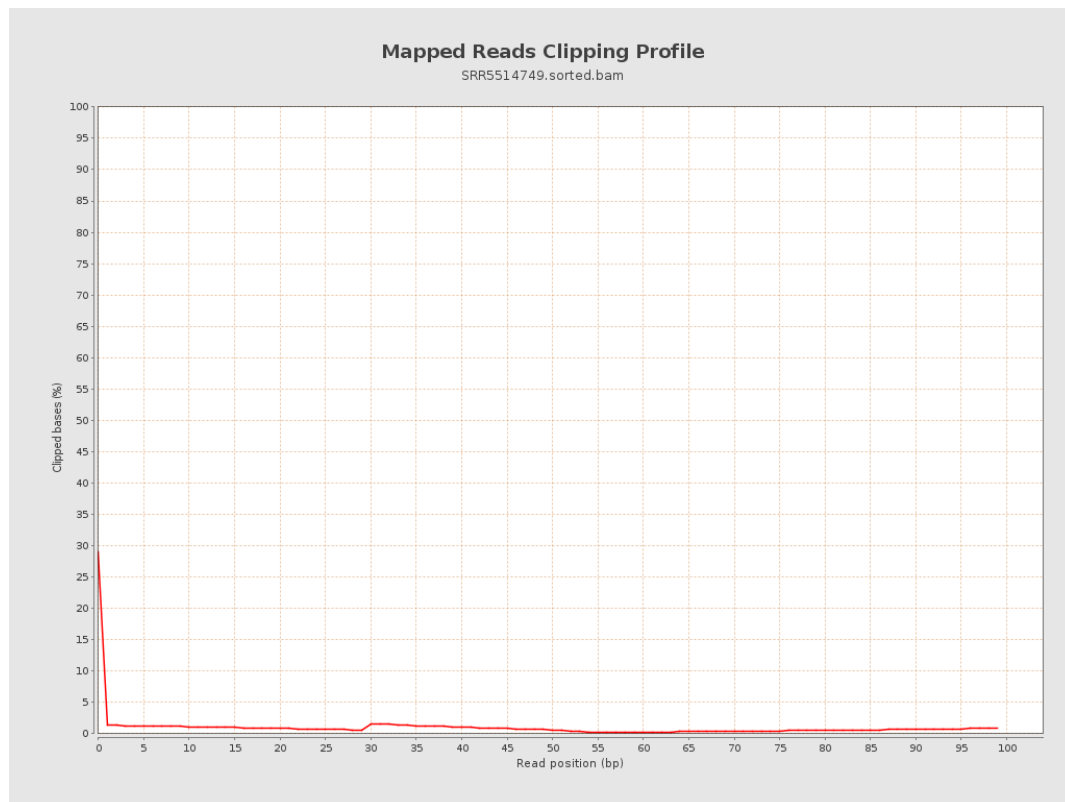
8. Results : Mapped Reads Nucleotide Content



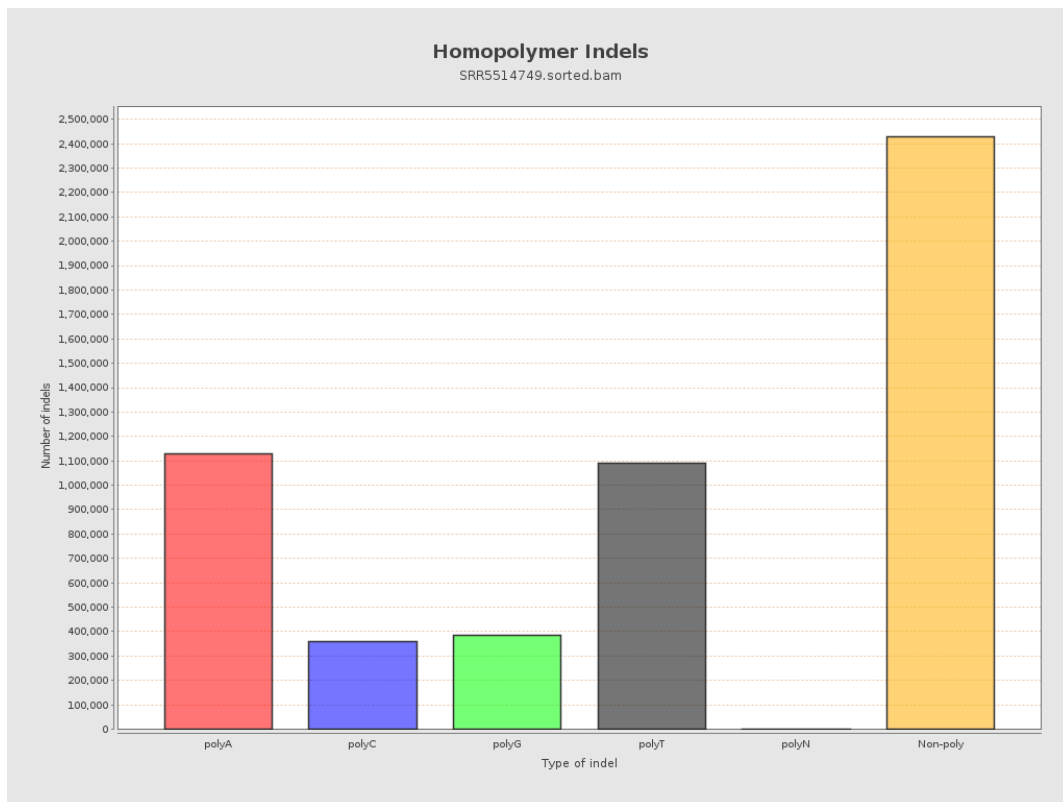
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

