

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:01:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013292.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_SRR6013292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013292.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:01:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,336,721
Mapped reads	2,064,758 / 88.36%
Unmapped reads	271,963 / 11.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,677 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	90,013 / 3.85%
Duplication rate	3.77%
Clipped reads	909,149 / 38.91%

2.2. ACGT Content

Number/percentage of A's	39,291,456 / 28.38%
Number/percentage of C's	25,492,900 / 18.41%
Number/percentage of T's	44,029,342 / 31.8%
Number/percentage of G's	29,593,250 / 21.38%
Number/percentage of N's	29,886 / 0.02%
GC Percentage	39.79%

2.3. Coverage

Mean	0.0447

Standard Deviation	0.3096
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2.4. Mapping Quality

Mean Mapping Quality	42.78
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2.5. Mismatches and indels

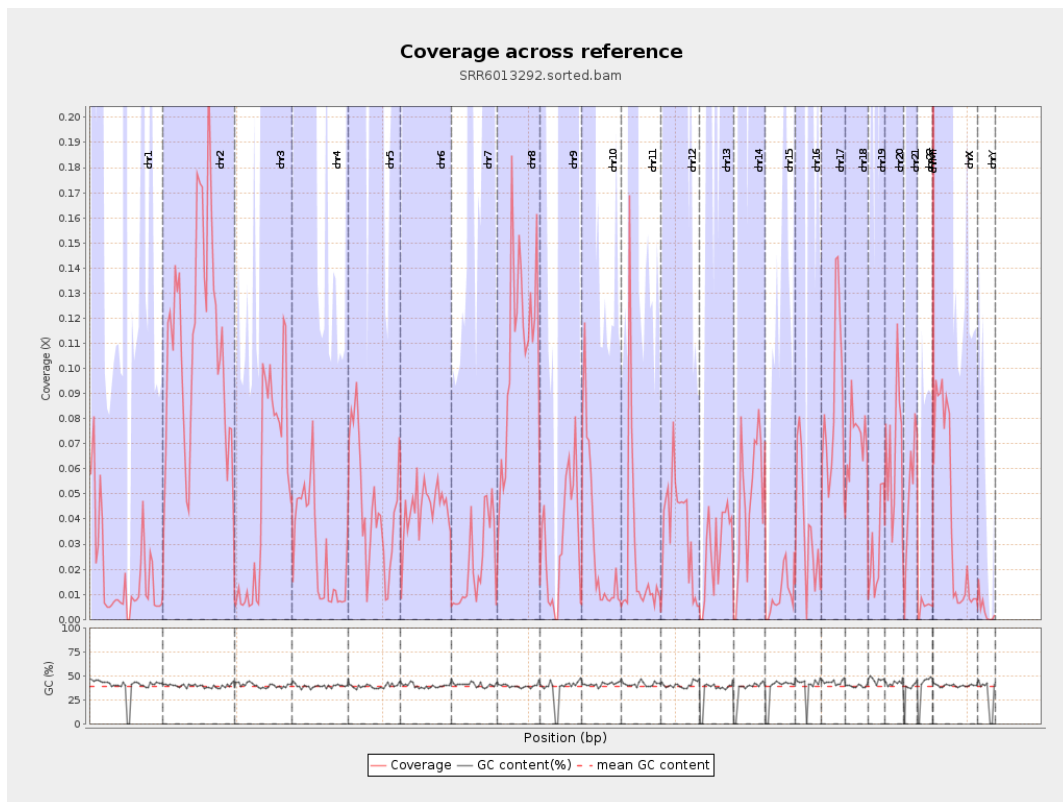
General error rate	0.79%
Mismatches	1,075,628
Insertions	9,550
Mapped reads with at least one insertion	0.46%
Deletions	31,746
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.38%

2.6. Chromosome stats

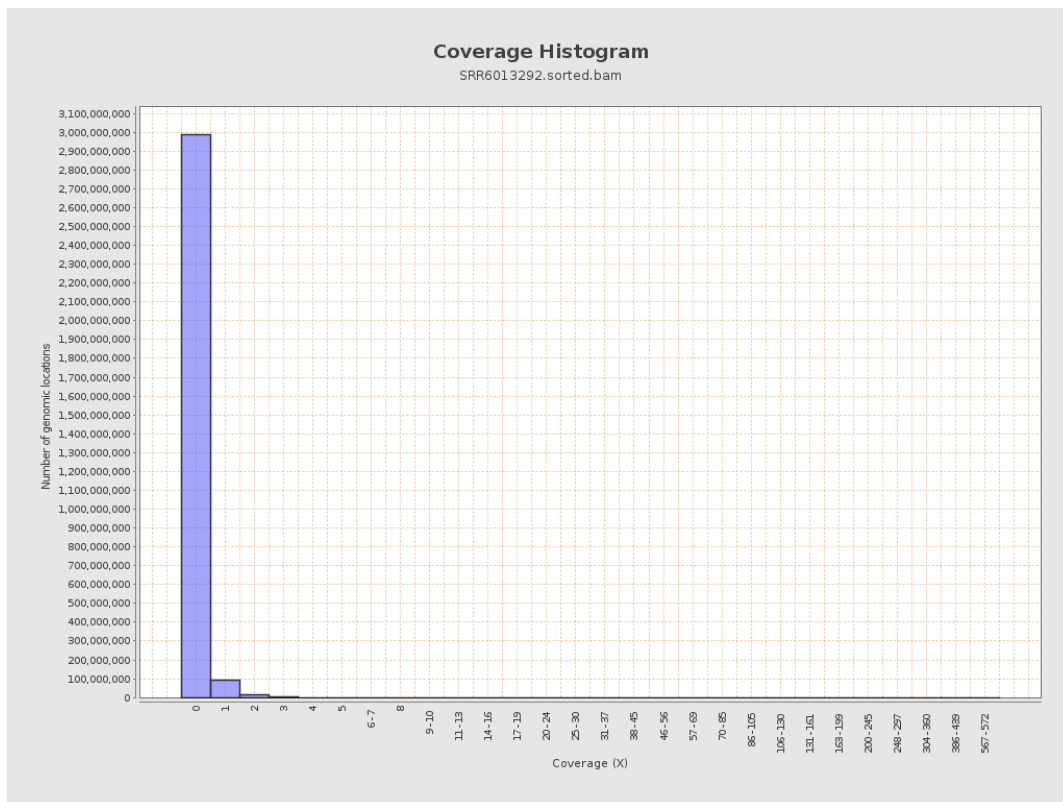
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4327871	0.0174	0.2656
chr2	243199373	26959341	0.1109	0.5034
chr3	198022430	9835055	0.0497	0.2676
chr4	191154276	5282818	0.0276	0.1997
chr5	180915260	8274848	0.0457	0.255
chr6	171115067	7602718	0.0444	0.3157
chr7	159138663	3403972	0.0214	0.1945

chr8	146364022	15744567	0.1076	0.6
chr9	141213431	4481160	0.0317	0.258
chr10	135534747	4182258	0.0309	0.2708
chr11	135006516	3192477	0.0236	0.2265
chr12	133851895	4784924	0.0357	0.2241
chr13	115169878	3264495	0.0283	0.1987
chr14	107349540	5129289	0.0478	0.2656
chr15	102531392	1007142	0.0098	0.1196
chr16	90354753	3210034	0.0355	0.2323
chr17	81195210	7211570	0.0888	0.3749
chr18	78077248	5584617	0.0715	0.4607
chr19	59128983	1637848	0.0277	0.2608
chr20	63025520	4279406	0.0679	0.3154
chr21	48129895	2389744	0.0497	0.266
chr22	51304566	254748	0.005	0.0784
chrMT	16571	19199	1.1586	1.2681
chrX	155270560	6221585	0.0401	0.2749
chrY	59373566	209629	0.0035	0.0718

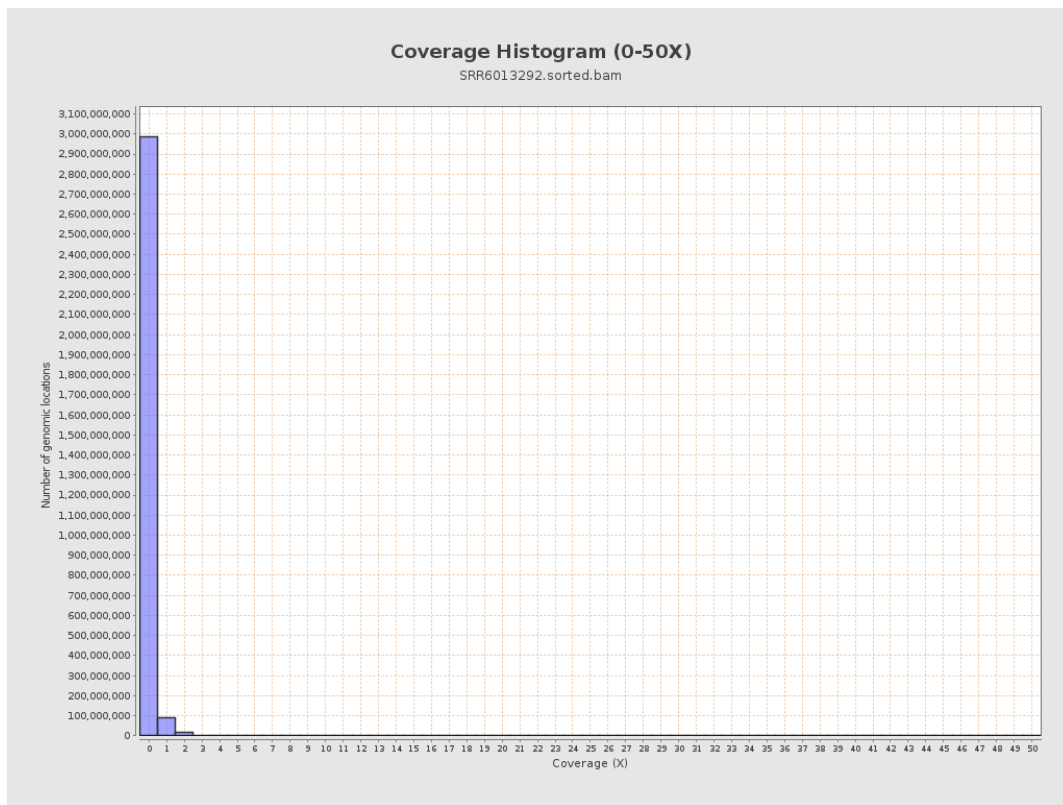
3. Results : Coverage across reference



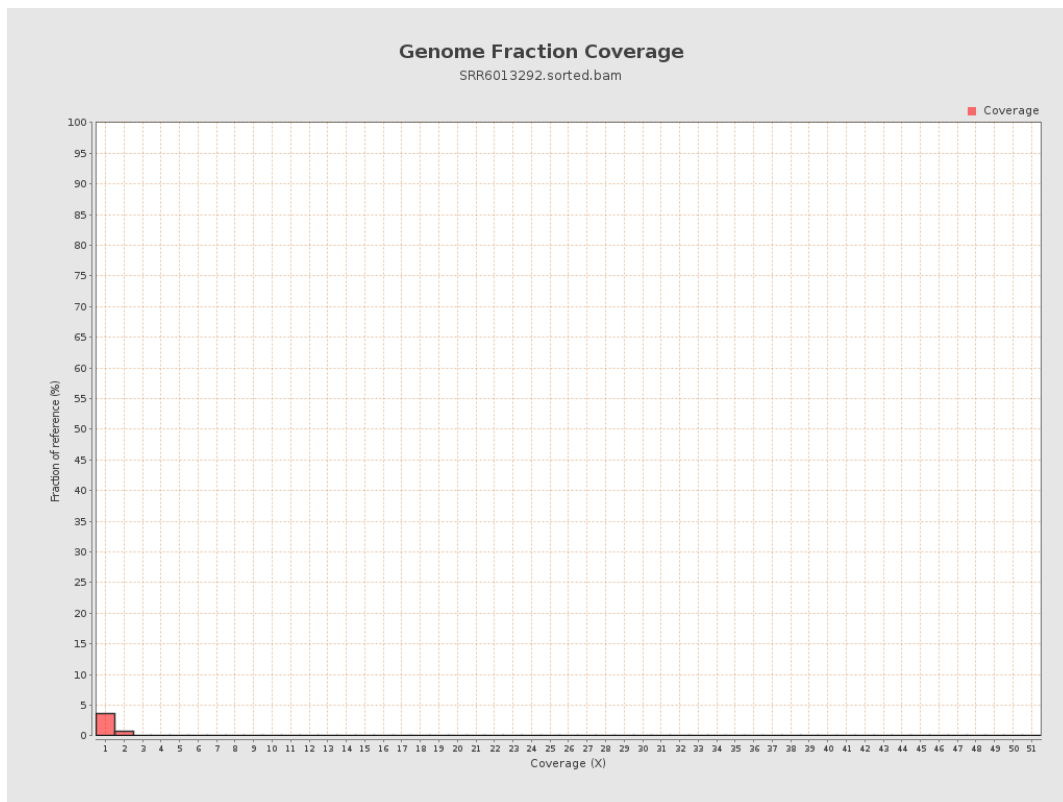
4. Results : Coverage Histogram



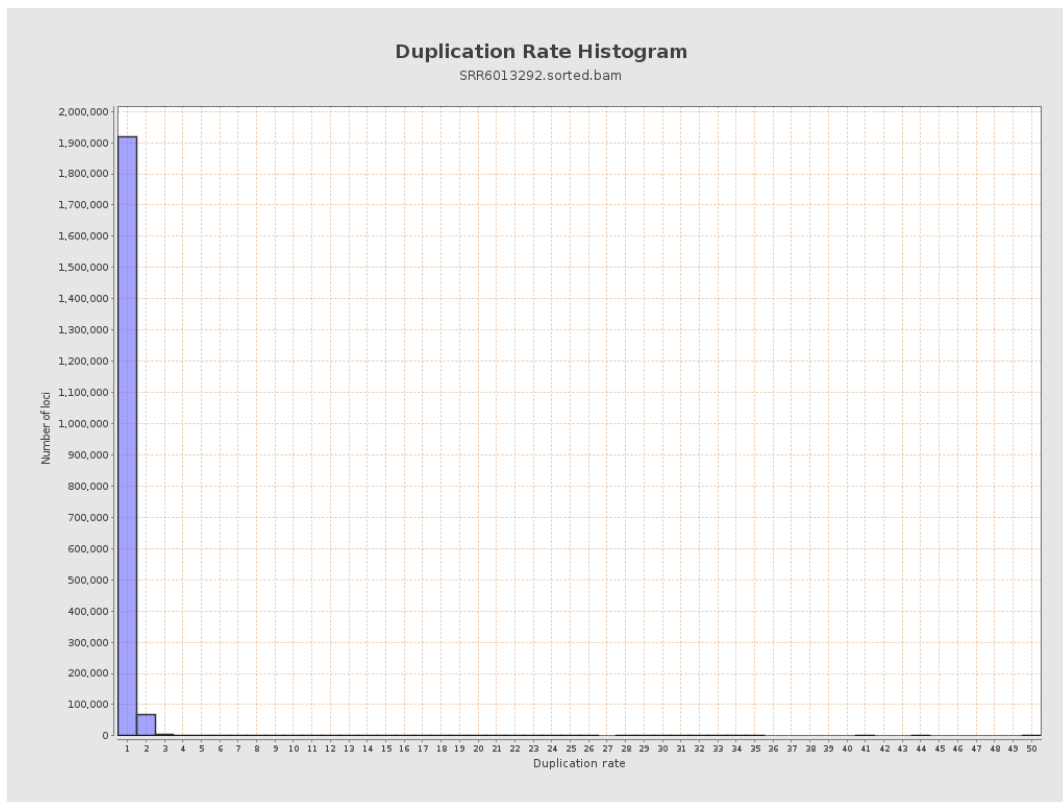
5. Results : Coverage Histogram (0-50X)



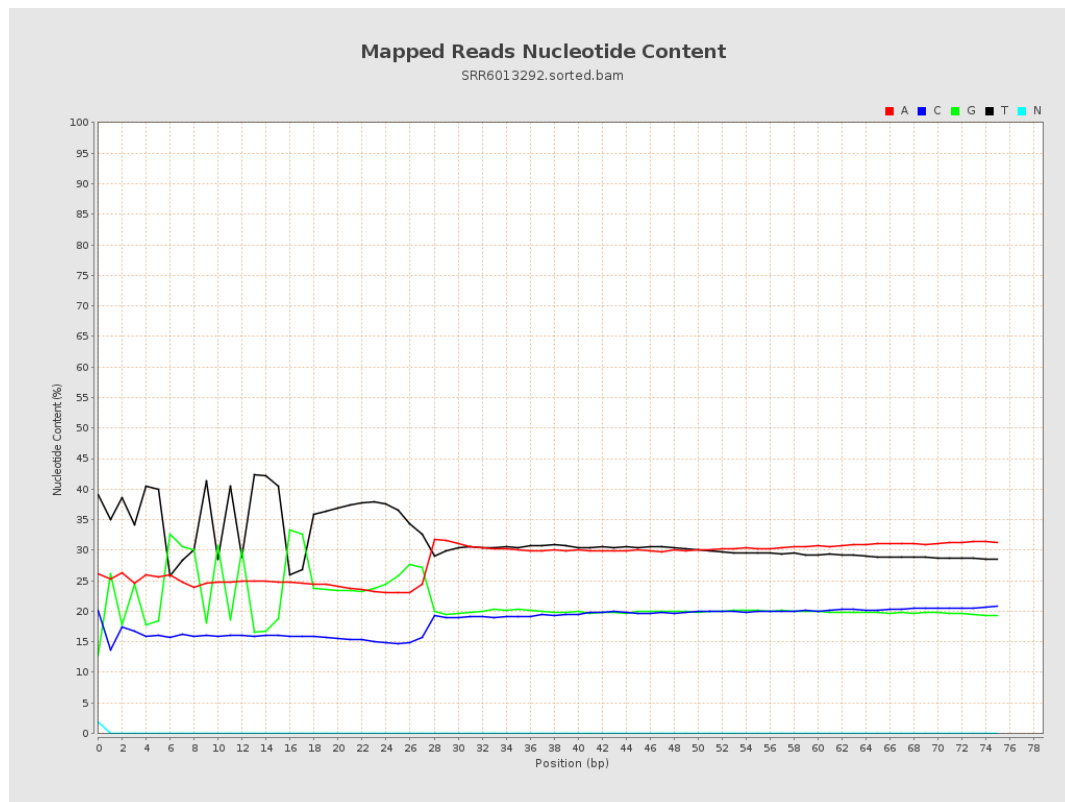
6. Results : Genome Fraction Coverage



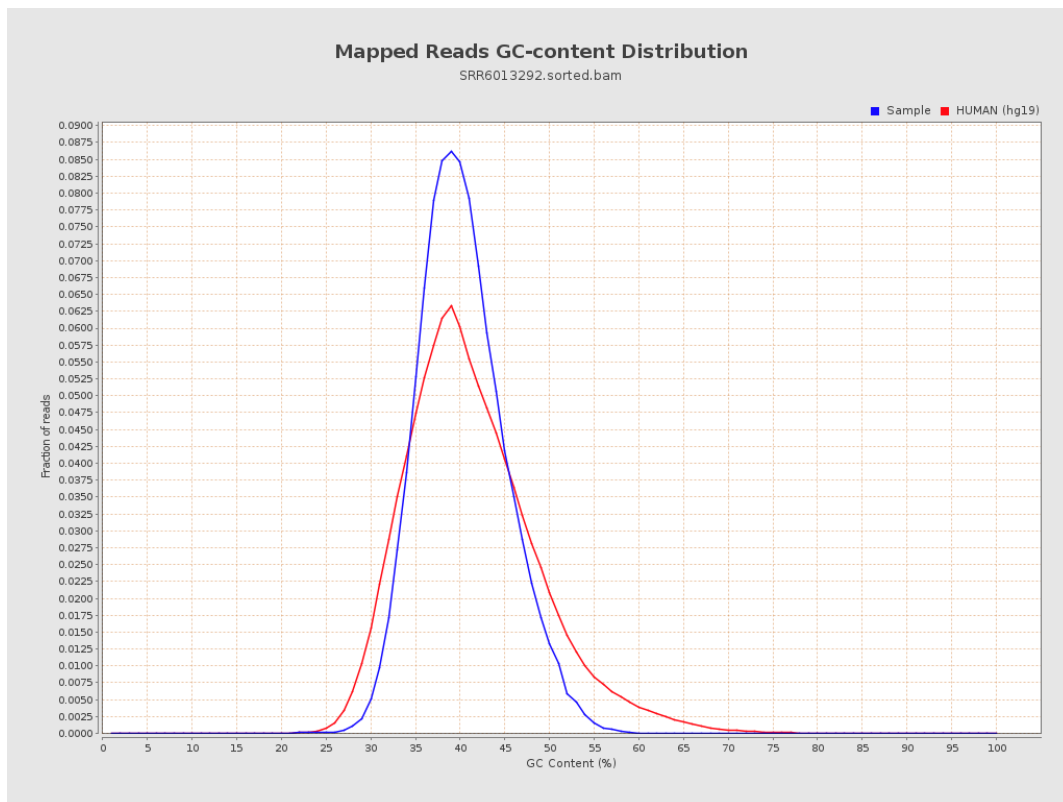
7. Results : Duplication Rate Histogram



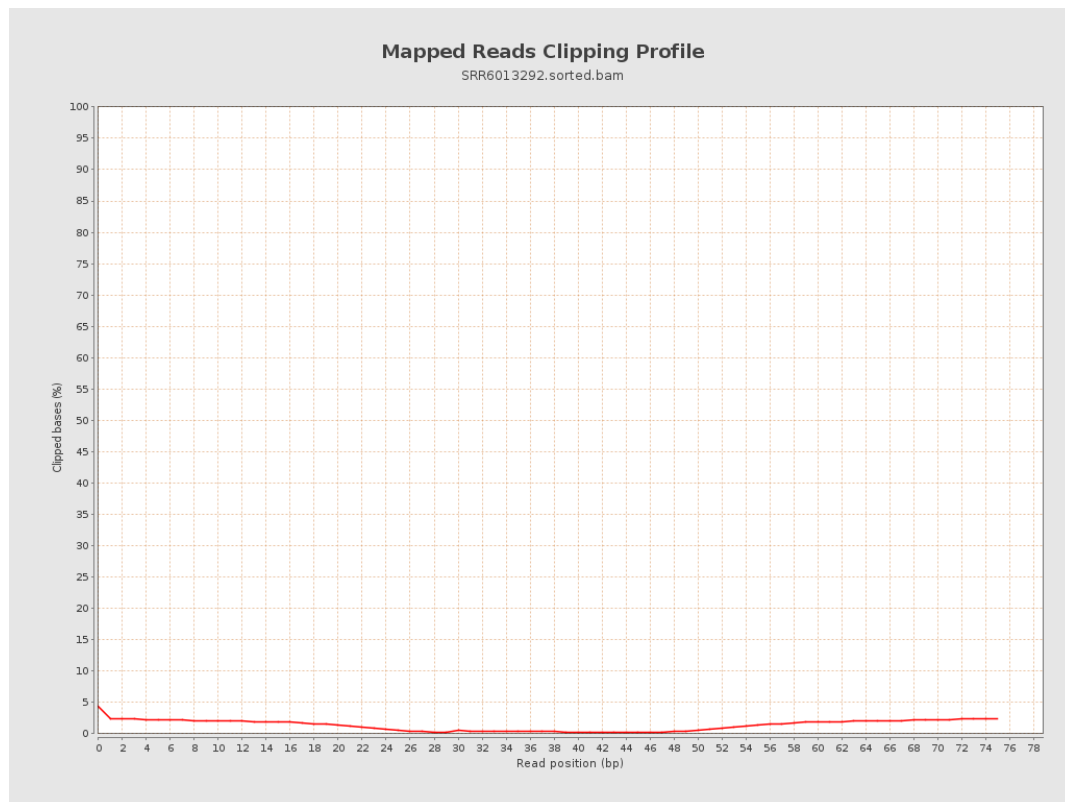
8. Results : Mapped Reads Nucleotide Content



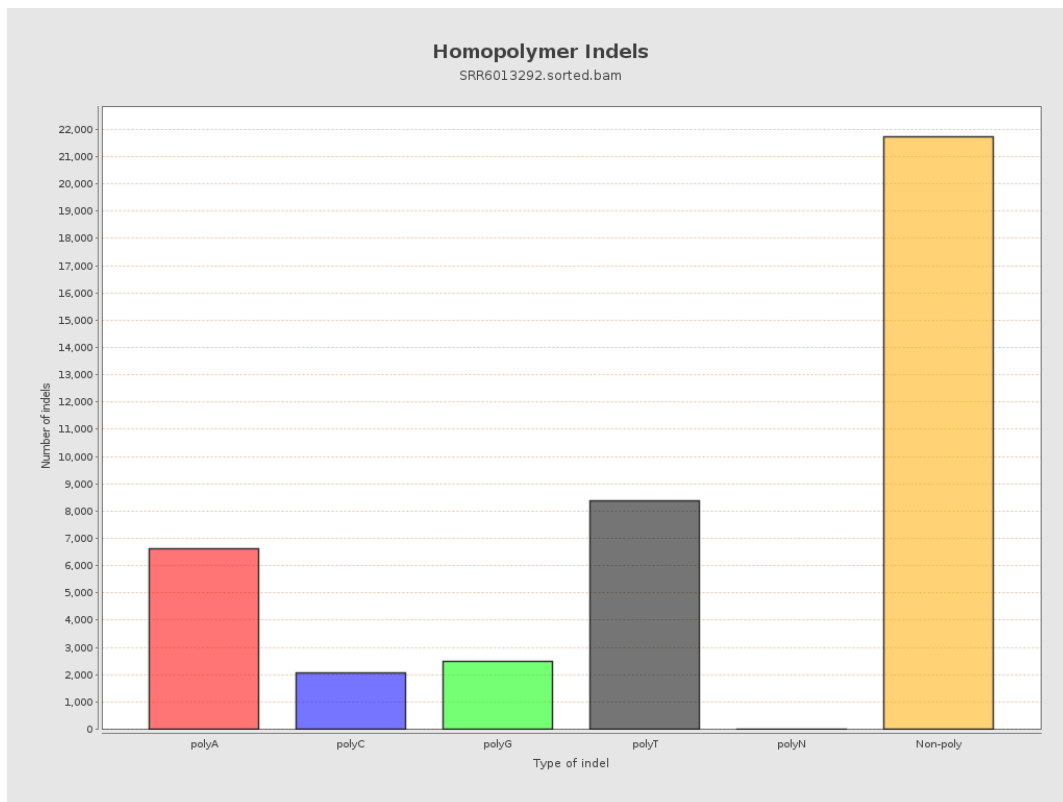
9. Results : Mapped Reads GC-content Distribution



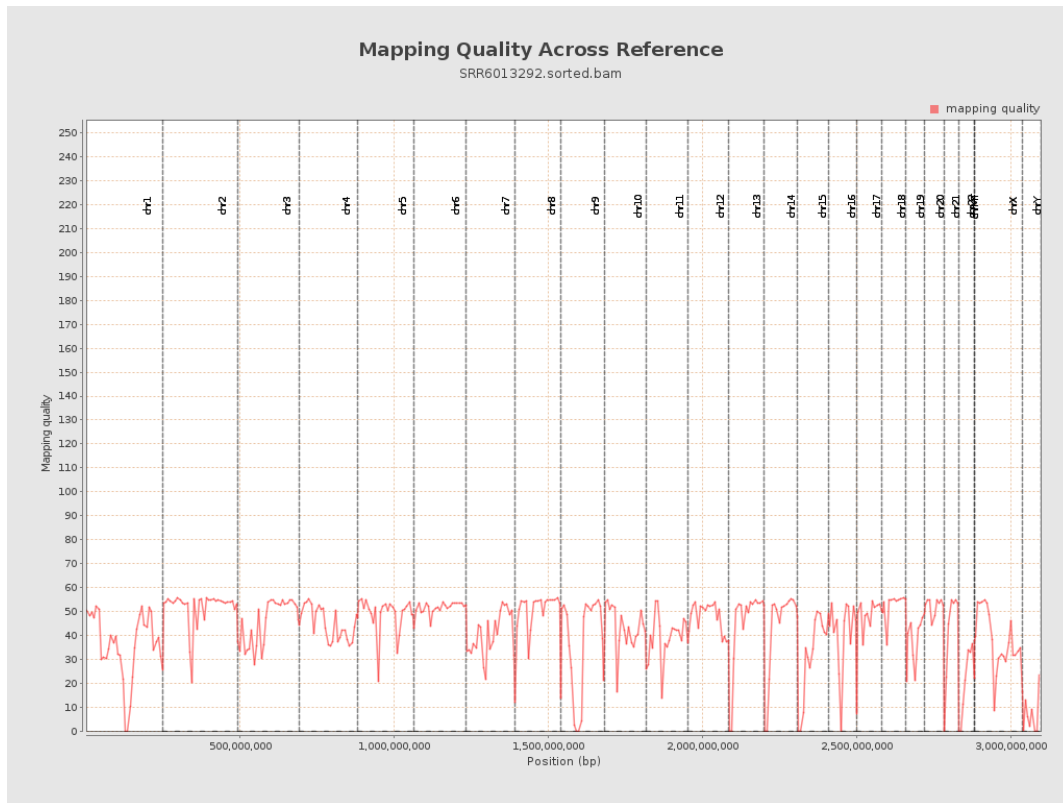
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

