

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:14:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013359.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_SRR6013359 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013359.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:14:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013359.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,922,310
Mapped reads	1,717,872 / 89.36%
Unmapped reads	204,438 / 10.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,485 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	69,993 / 3.64%
Duplication rate	2.94%
Clipped reads	671,655 / 34.94%

2.2. ACGT Content

Number/percentage of A's	33,336,347 / 28.5%
Number/percentage of C's	21,628,217 / 18.49%
Number/percentage of T's	37,012,683 / 31.64%
Number/percentage of G's	24,986,598 / 21.36%
Number/percentage of N's	25,697 / 0.02%
GC Percentage	39.85%

2.3. Coverage

Mean	0.0378

Standard Deviation	0.3927
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2.4. Mapping Quality

Mean Mapping Quality	46.5
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2.5. Mismatches and indels

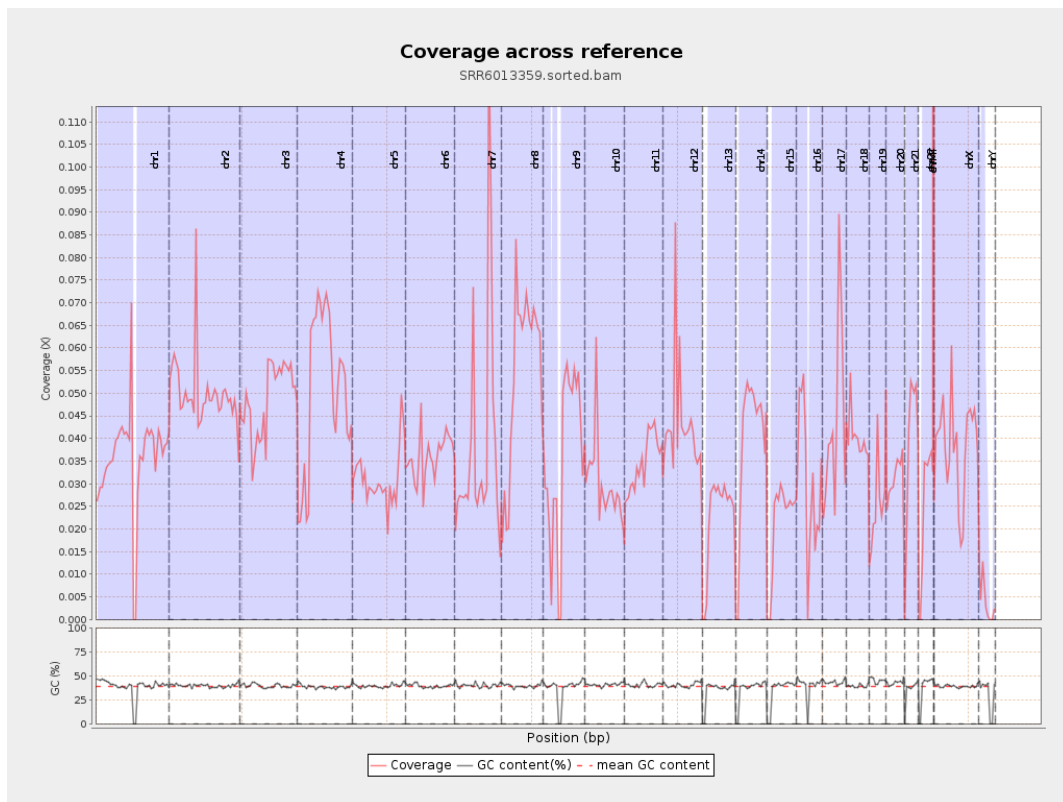
General error rate	0.79%
Mismatches	910,721
Insertions	8,716
Mapped reads with at least one insertion	0.5%
Deletions	26,154
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.91%

2.6. Chromosome stats

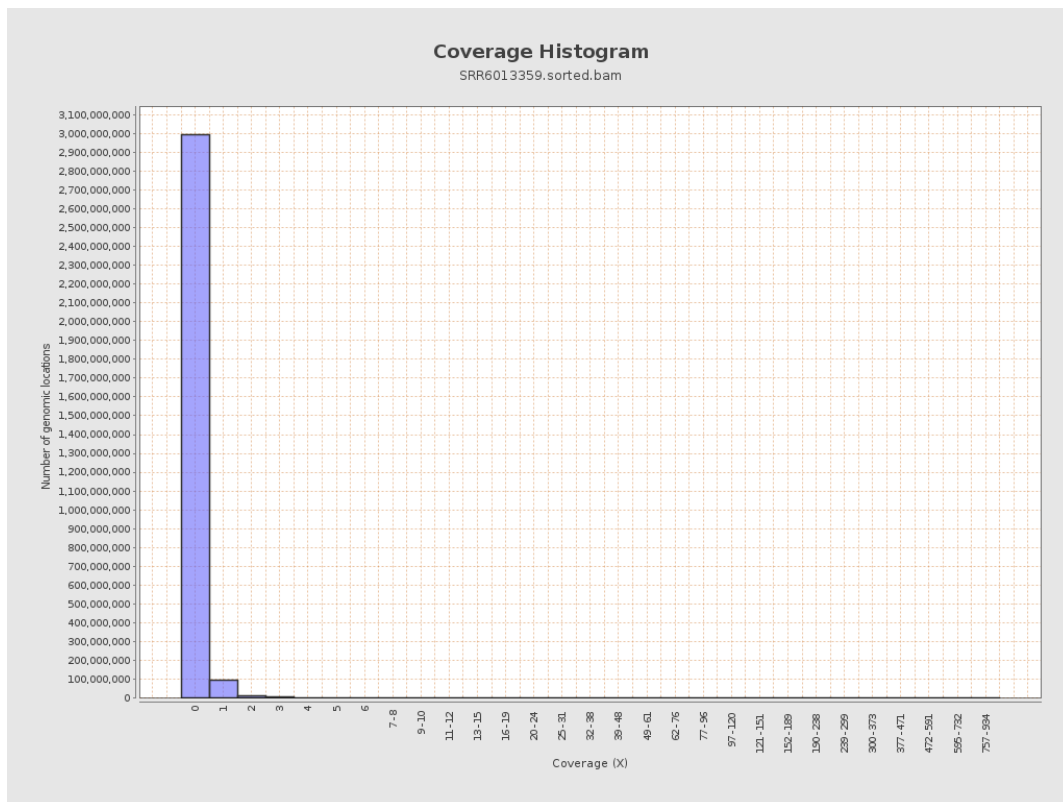
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8916818	0.0358	0.6534
chr2	243199373	12177220	0.0501	0.4496
chr3	198022430	9631217	0.0486	0.2437
chr4	191154276	9626256	0.0504	0.2727
chr5	180915260	5642408	0.0312	0.1964
chr6	171115067	6161161	0.036	0.2492
chr7	159138663	6222901	0.0391	0.6469

chr8	146364022	7997989	0.0546	0.6164
chr9	141213431	4989424	0.0353	0.3875
chr10	135534747	4081017	0.0301	0.3815
chr11	135006516	4661050	0.0345	0.2817
chr12	133851895	5782631	0.0432	0.2376
chr13	115169878	2573121	0.0223	0.1645
chr14	107349540	4243926	0.0395	0.2417
chr15	102531392	2194585	0.0214	0.1661
chr16	90354753	2760834	0.0306	0.224
chr17	81195210	3439996	0.0424	0.2457
chr18	78077248	3154267	0.0404	0.7491
chr19	59128983	1541028	0.0261	0.4854
chr20	63025520	1951597	0.031	0.2037
chr21	48129895	1863581	0.0387	0.2389
chr22	51304566	1262096	0.0246	0.1722
chrMT	16571	30417	1.8356	1.5947
chrX	155270560	5901064	0.038	0.244
chrY	59373566	228638	0.0039	0.1271

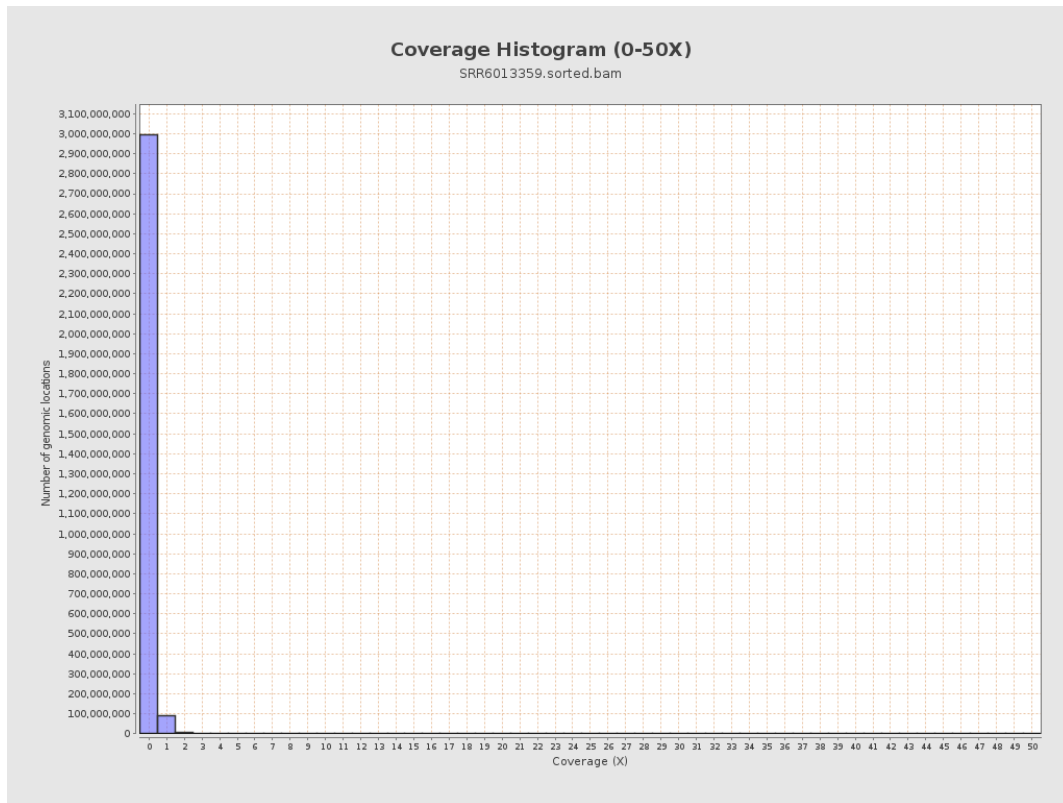
3. Results : Coverage across reference



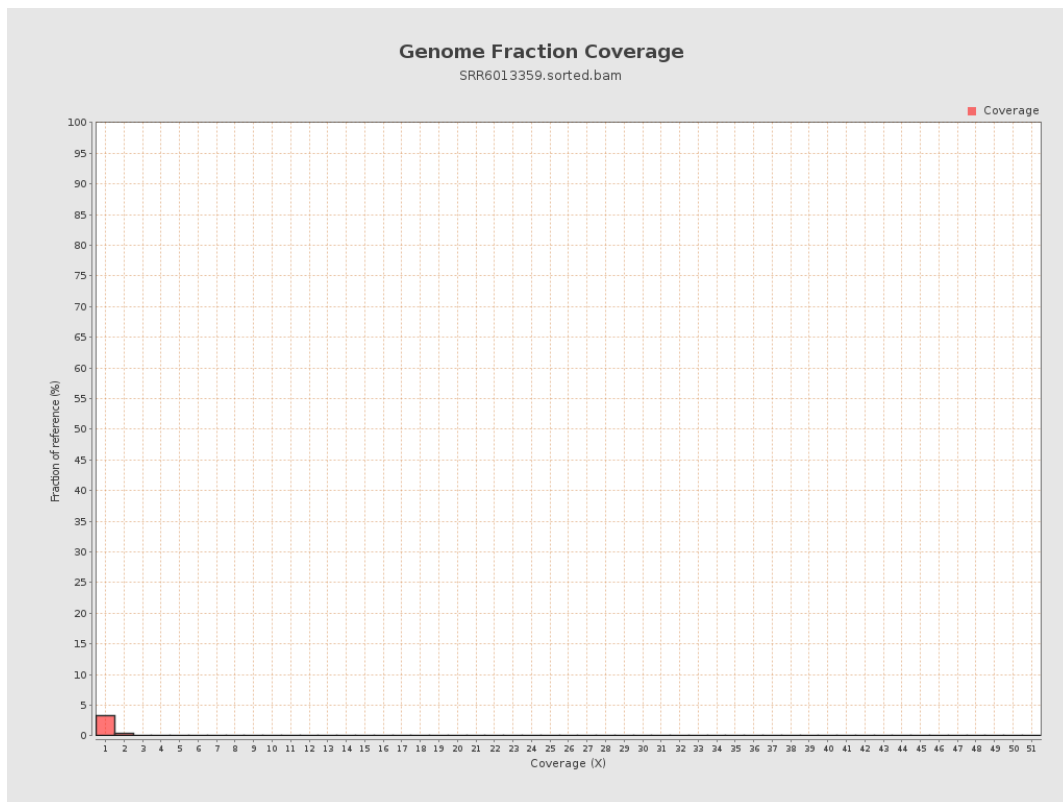
4. Results : Coverage Histogram



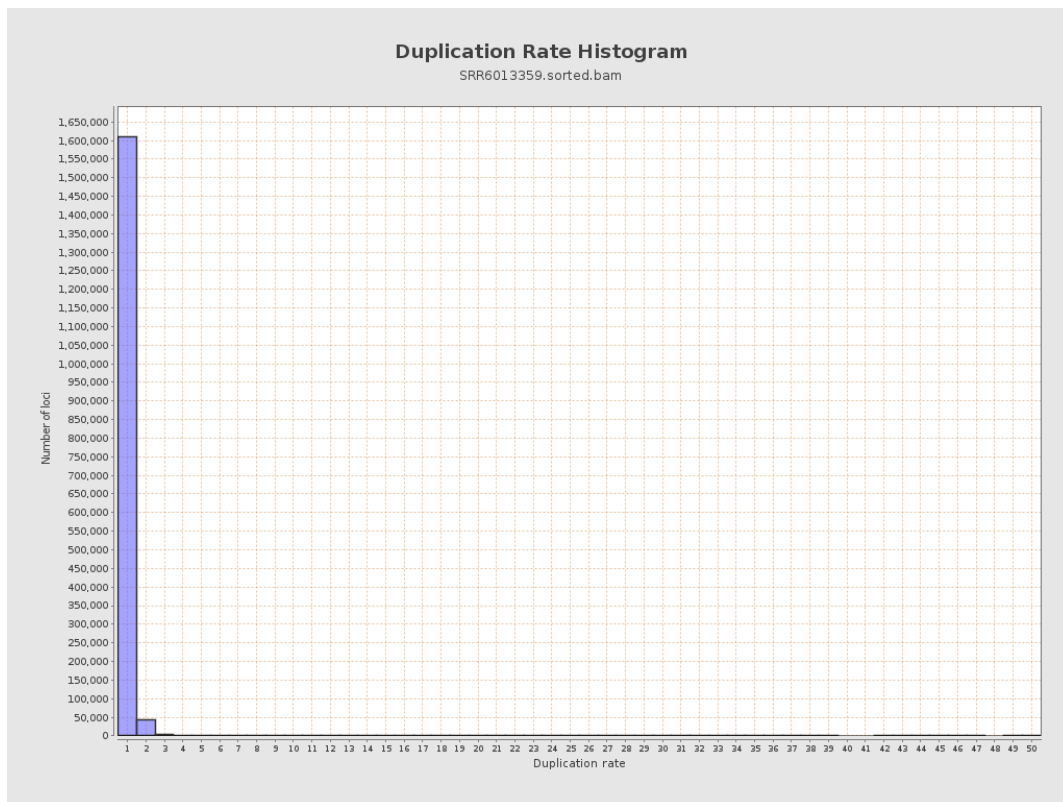
5. Results : Coverage Histogram (0-50X)



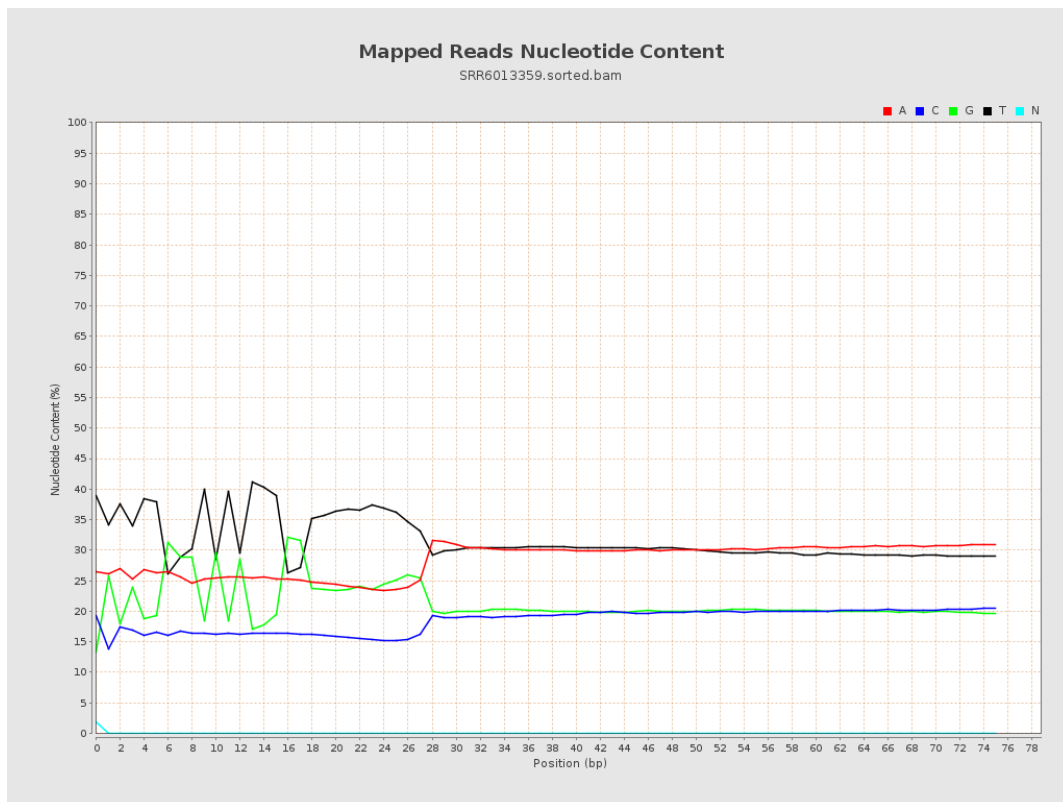
6. Results : Genome Fraction Coverage



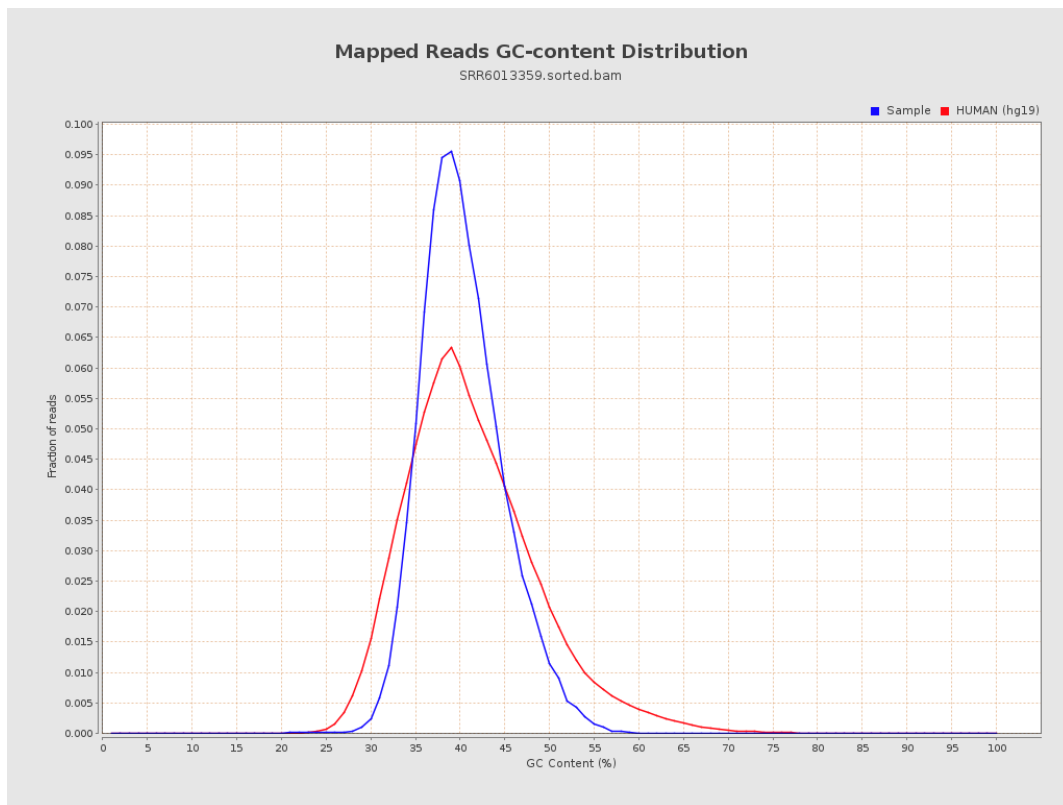
7. Results : Duplication Rate Histogram



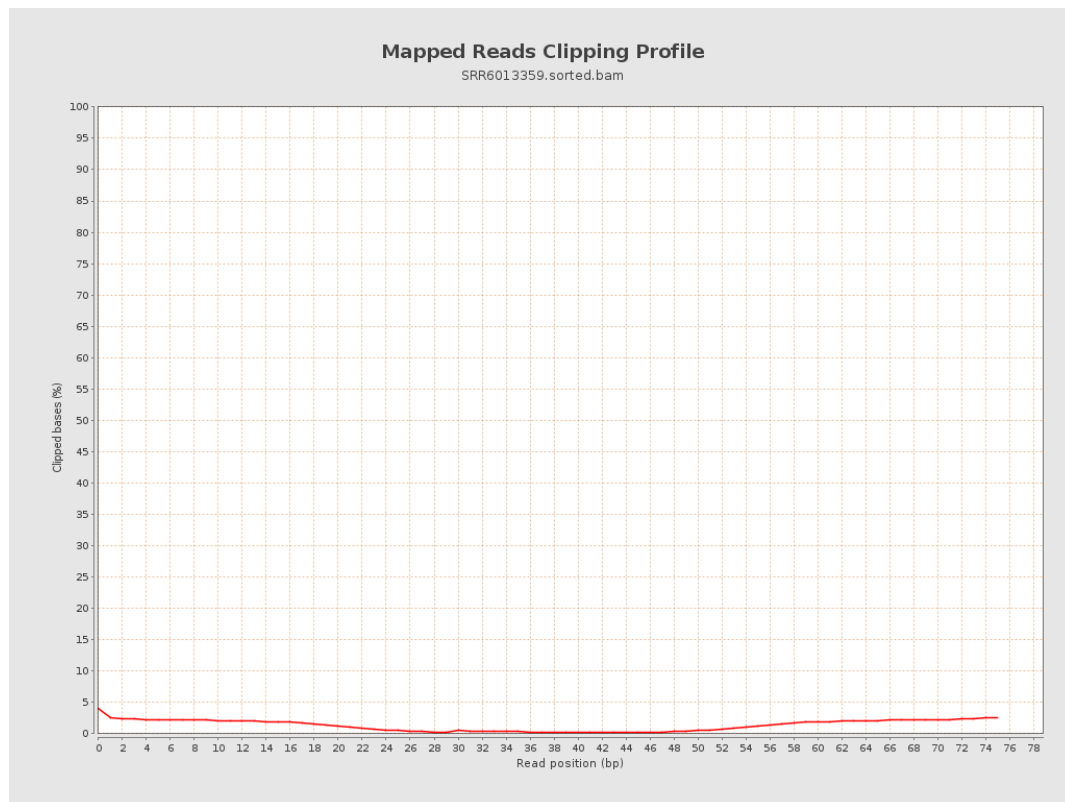
8. Results : Mapped Reads Nucleotide Content



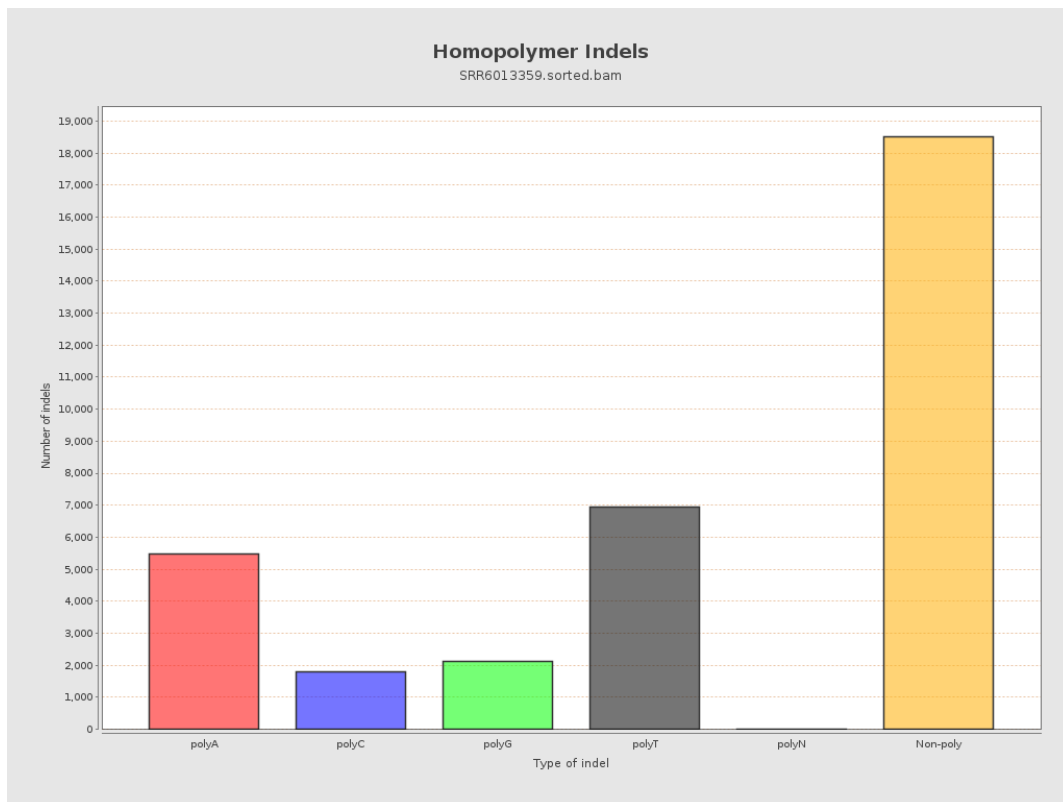
9. Results : Mapped Reads GC-content Distribution



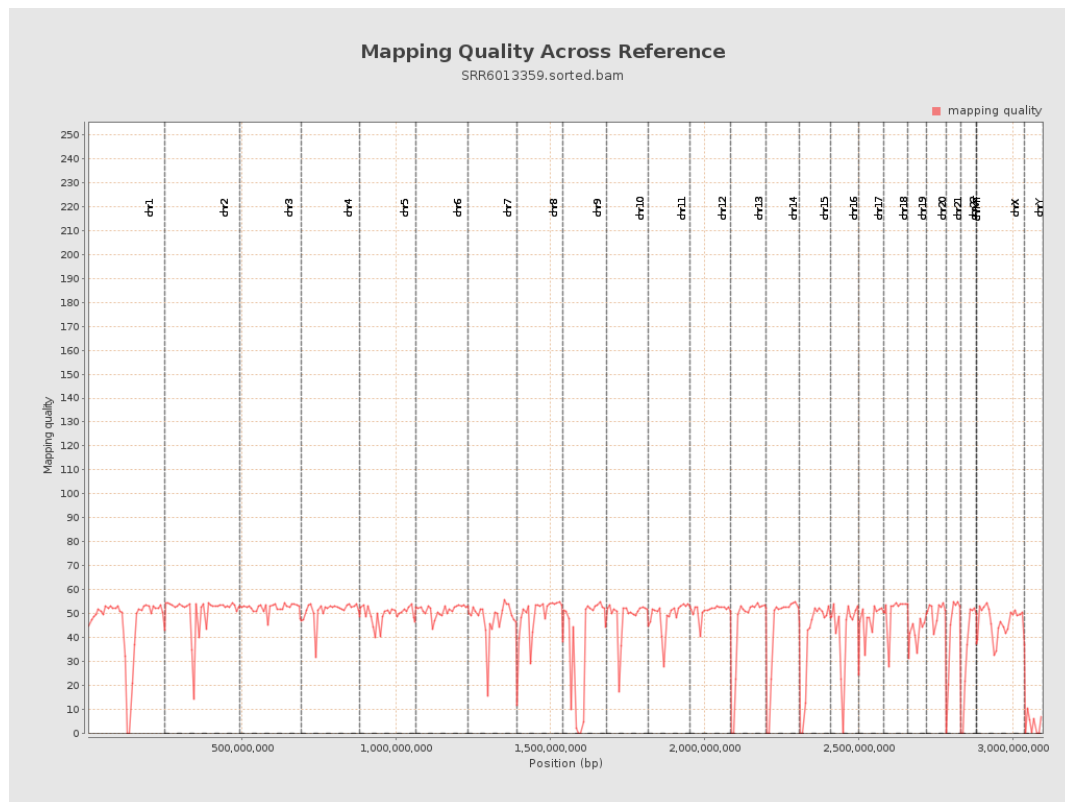
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

