

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:22:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013259.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_SRR6013259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013259.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:22:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,202,184
Mapped reads	1,588,994 / 72.16%
Unmapped reads	613,190 / 27.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,741 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	134,372 / 6.1%
Duplication rate	6.63%
Clipped reads	1,065,454 / 48.38%

2.2. ACGT Content

Number/percentage of A's	28,870,197 / 29.71%
Number/percentage of C's	18,768,688 / 19.32%
Number/percentage of T's	28,912,760 / 29.76%
Number/percentage of G's	20,612,308 / 21.21%
Number/percentage of N's	906 / 0%
GC Percentage	40.53%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.3788
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2.4. Mapping Quality

Mean Mapping Quality	45.33
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2.5. Mismatches and indels

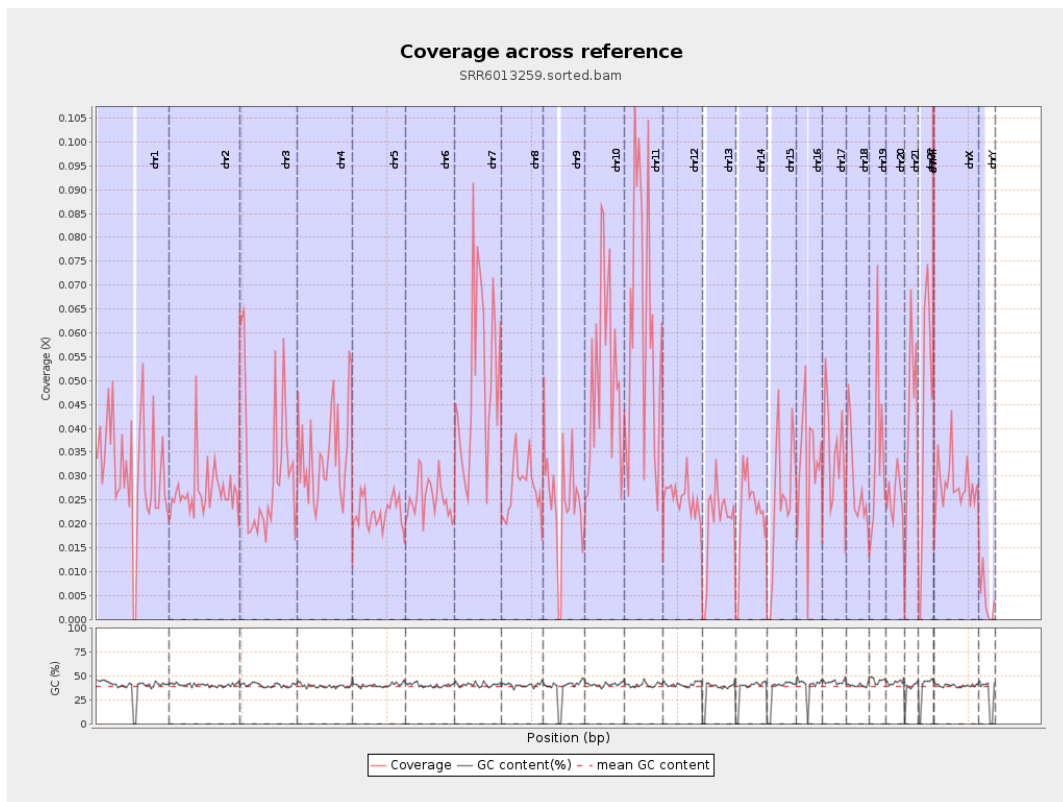
General error rate	0.78%
Mismatches	750,532
Insertions	6,415
Mapped reads with at least one insertion	0.4%
Deletions	21,867
Mapped reads with at least one deletion	1.36%
Homopolymer indels	45.04%

2.6. Chromosome stats

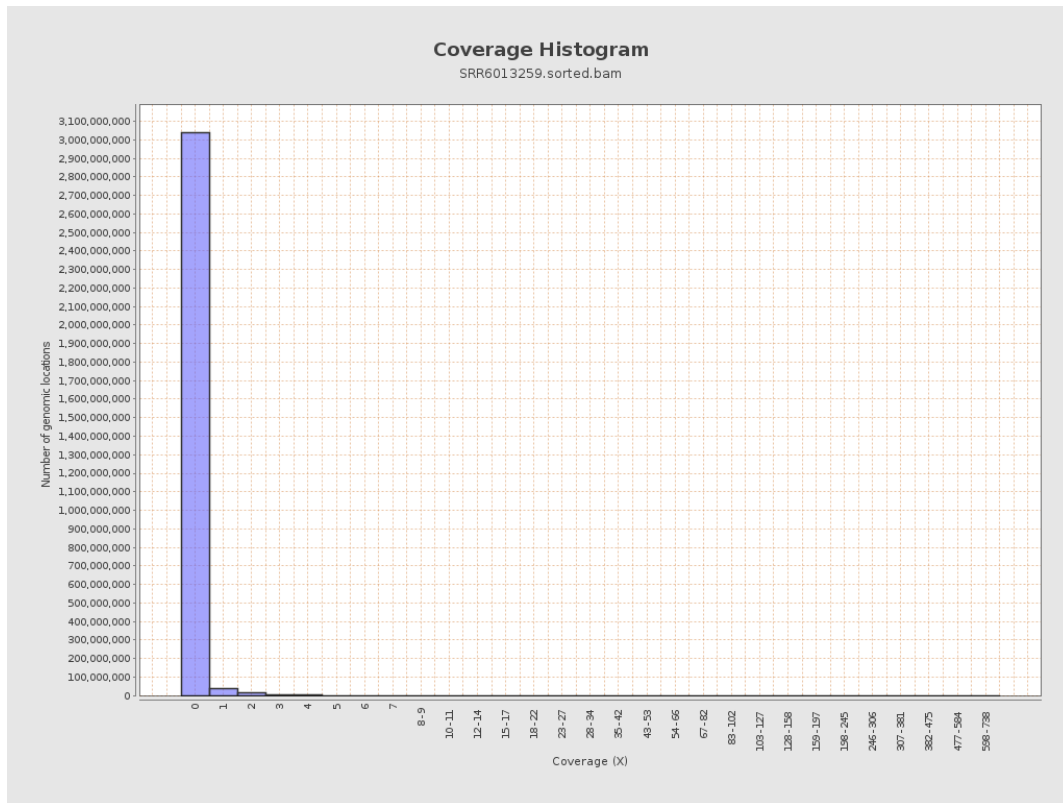
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7678509	0.0308	0.4822
chr2	243199373	6527065	0.0268	0.3347
chr3	198022430	6208285	0.0314	0.2935
chr4	191154276	6669864	0.0349	0.2855
chr5	180915260	4055289	0.0224	0.2264
chr6	171115067	4338900	0.0254	0.2504
chr7	159138663	8075333	0.0507	0.7526

chr8	146364022	4012402	0.0274	0.4581
chr9	141213431	3364765	0.0238	0.2954
chr10	135534747	6926019	0.0511	0.3822
chr11	135006516	8366763	0.062	0.6318
chr12	133851895	3385973	0.0253	0.2413
chr13	115169878	2295856	0.0199	0.212
chr14	107349540	2362506	0.022	0.2277
chr15	102531392	2532698	0.0247	0.2431
chr16	90354753	2999960	0.0332	0.2827
chr17	81195210	2753661	0.0339	0.3555
chr18	78077248	2250848	0.0288	0.506
chr19	59128983	2024121	0.0342	0.3752
chr20	63025520	1600661	0.0254	0.2409
chr21	48129895	1970680	0.0409	0.3136
chr22	51304566	2175890	0.0424	0.3738
chrMT	16571	21302	1.2855	2.0543
chrX	155270560	4360627	0.0281	0.2843
chrY	59373566	242817	0.0041	0.103

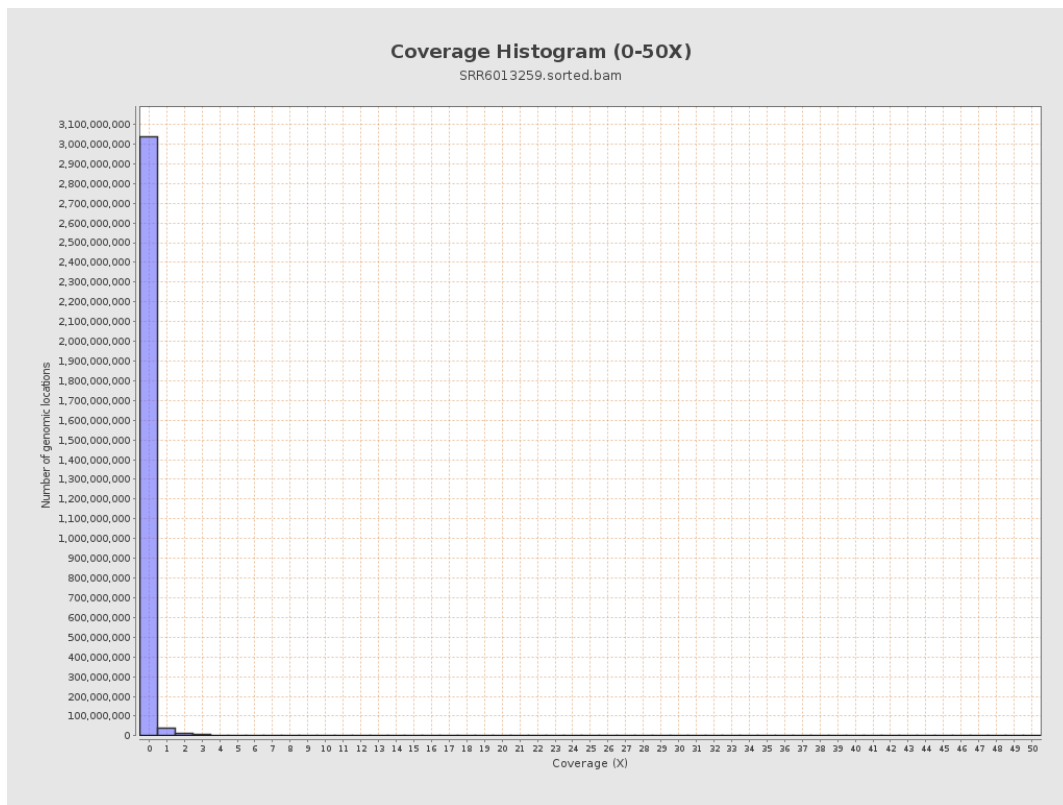
3. Results : Coverage across reference



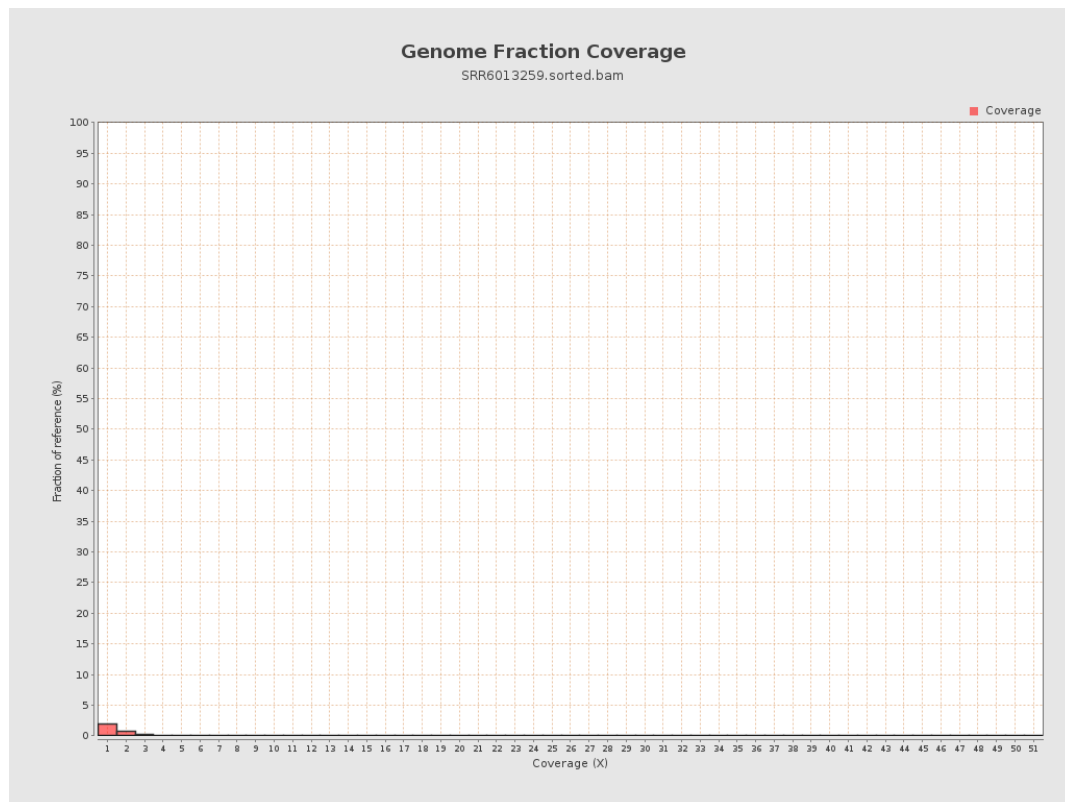
4. Results : Coverage Histogram



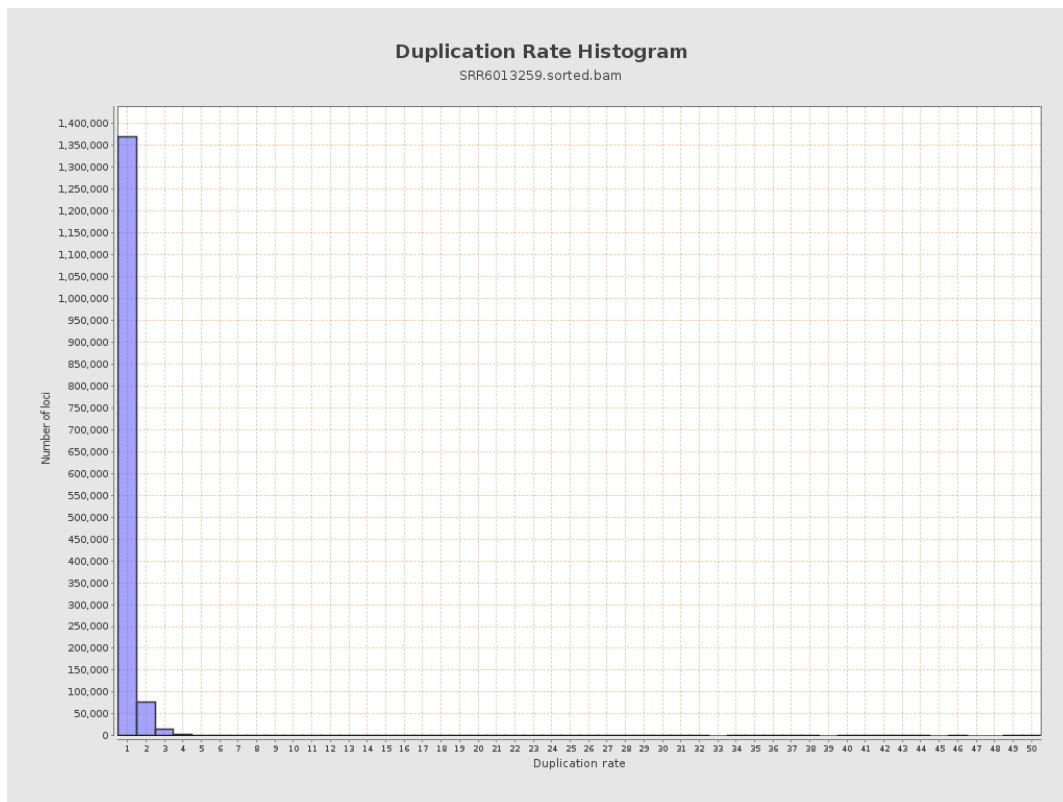
5. Results : Coverage Histogram (0-50X)



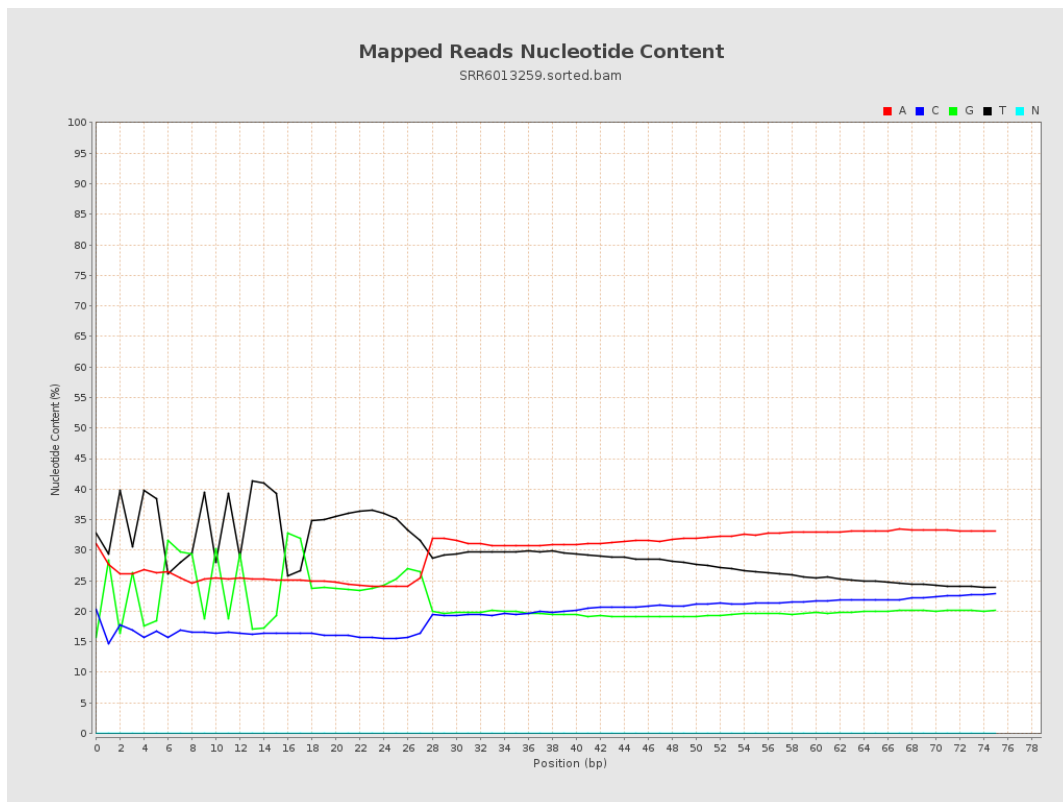
6. Results : Genome Fraction Coverage



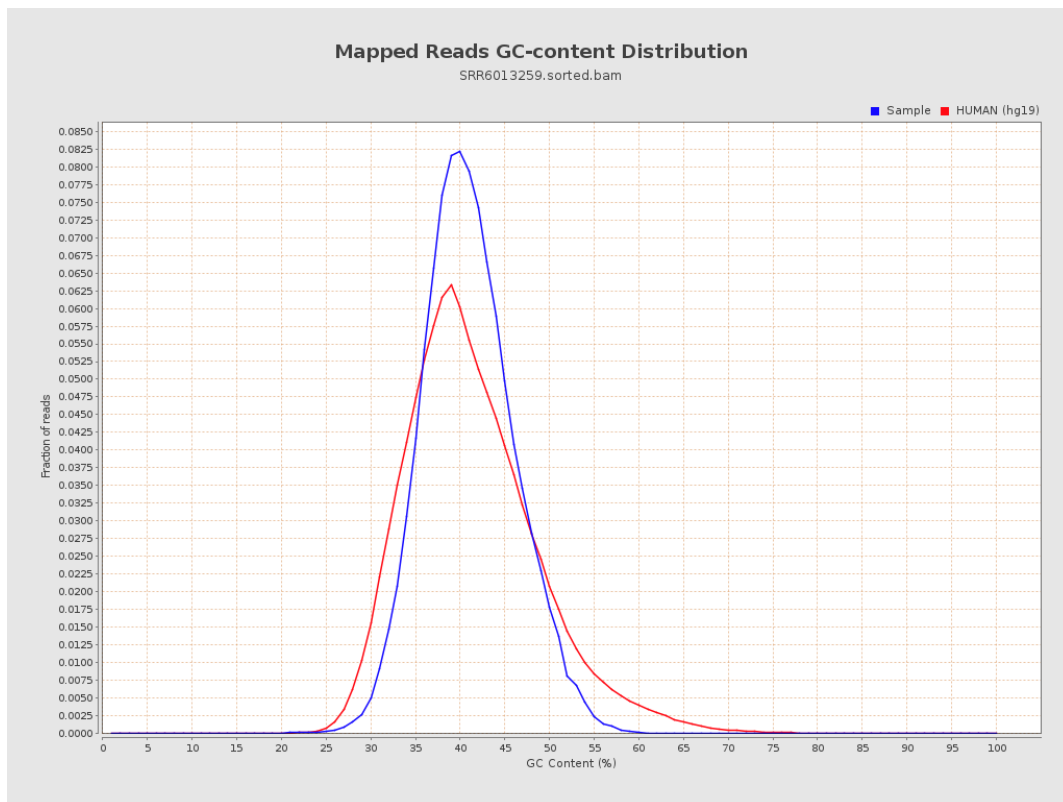
7. Results : Duplication Rate Histogram



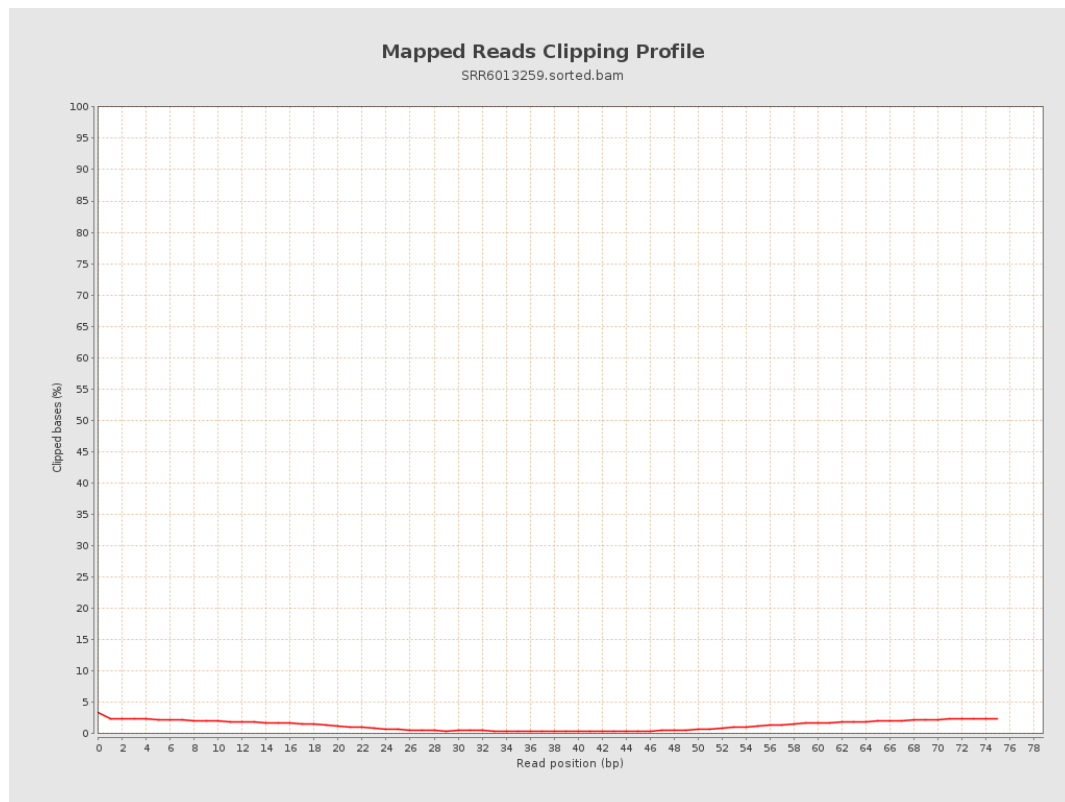
8. Results : Mapped Reads Nucleotide Content



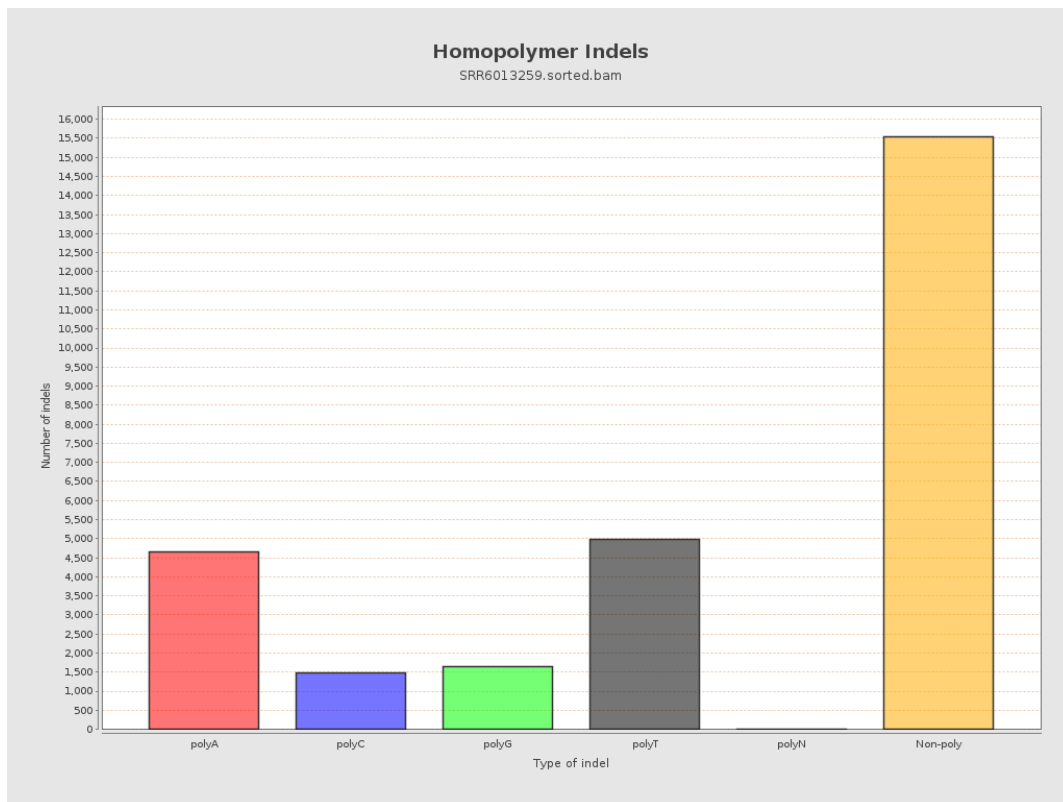
9. Results : Mapped Reads GC-content Distribution



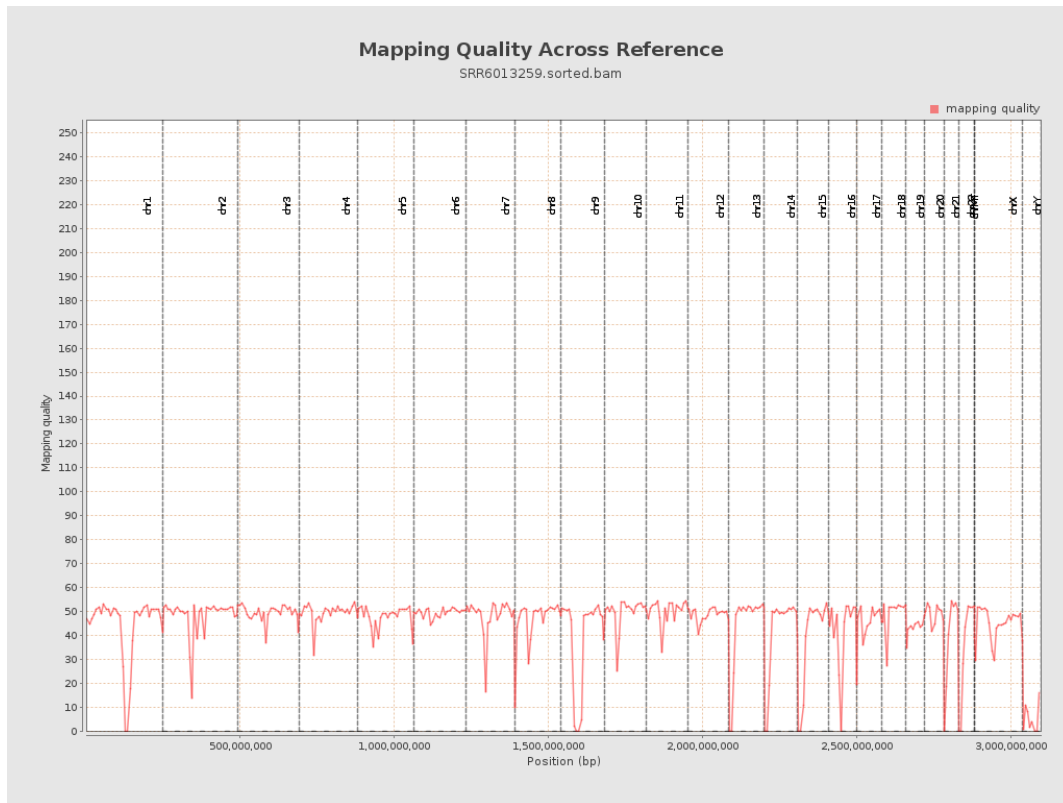
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

