

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:31:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013282.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_SRR6013282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013282.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:31:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,939,836
Mapped reads	1,730,216 / 89.19%
Unmapped reads	209,620 / 10.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,623 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	67,752 / 3.49%
Duplication rate	3.15%
Clipped reads	733,205 / 37.8%

2.2. ACGT Content

Number/percentage of A's	31,985,717 / 27.59%
Number/percentage of C's	21,145,109 / 18.24%
Number/percentage of T's	36,967,780 / 31.89%
Number/percentage of G's	25,821,916 / 22.28%
Number/percentage of N's	1,594 / 0%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.3089
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2.4. Mapping Quality

Mean Mapping Quality	46.13
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2.5. Mismatches and indels

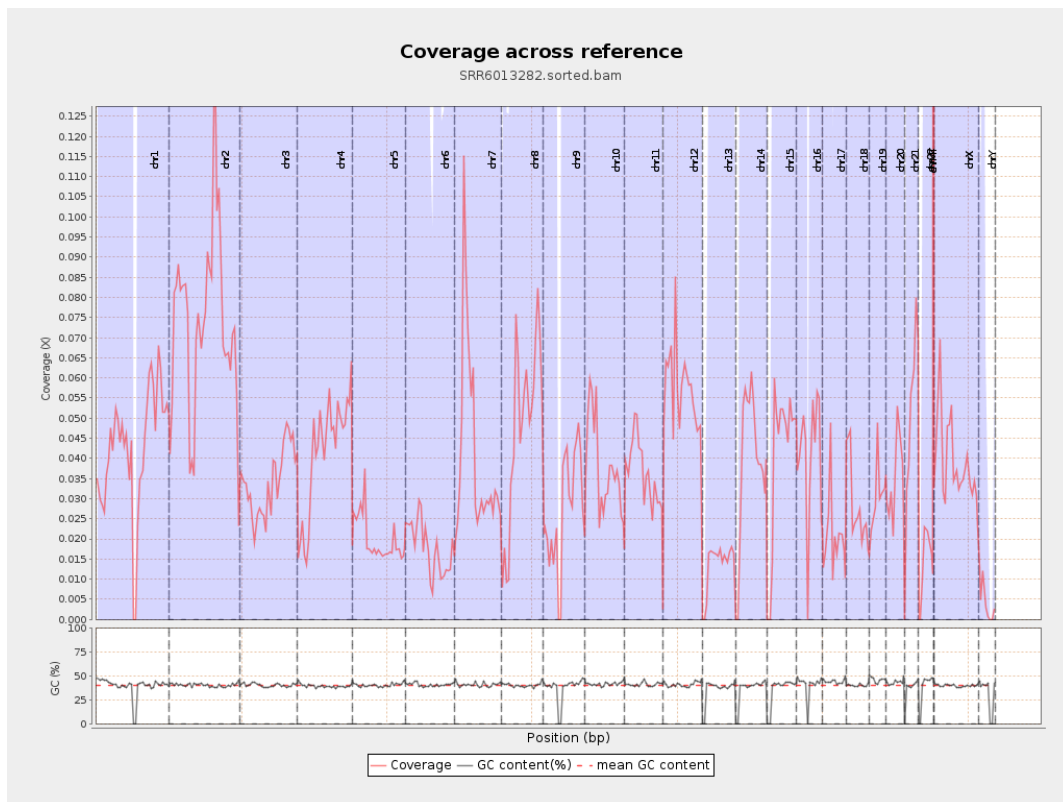
General error rate	0.7%
Mismatches	800,058
Insertions	7,969
Mapped reads with at least one insertion	0.46%
Deletions	27,444
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.34%

2.6. Chromosome stats

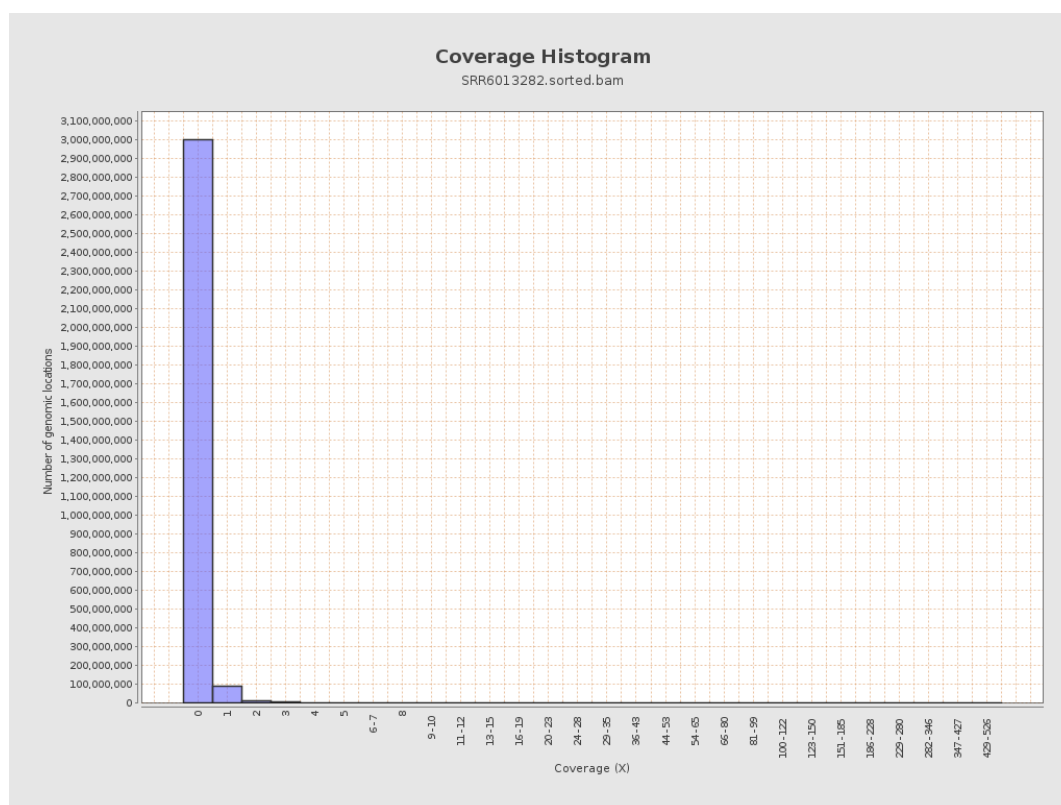
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10608975	0.0426	0.4736
chr2	243199373	17931905	0.0737	0.4251
chr3	198022430	6741140	0.034	0.21
chr4	191154276	7875922	0.0412	0.2492
chr5	180915260	3621304	0.02	0.1633
chr6	171115067	3049801	0.0178	0.174
chr7	159138663	6559675	0.0412	0.4688

chr8	146364022	6993492	0.0478	0.3446
chr9	141213431	3895096	0.0276	0.2758
chr10	135534747	5170738	0.0382	0.3226
chr11	135006516	4876854	0.0361	0.3205
chr12	133851895	7607911	0.0568	0.2746
chr13	115169878	1554692	0.0135	0.1328
chr14	107349540	4215564	0.0393	0.2332
chr15	102531392	4192452	0.0409	0.2373
chr16	90354753	3663037	0.0405	0.236
chr17	81195210	1671818	0.0206	0.1947
chr18	78077248	2223860	0.0285	0.4649
chr19	59128983	1807521	0.0306	0.3344
chr20	63025520	2202271	0.0349	0.217
chr21	48129895	2422613	0.0503	0.2696
chr22	51304566	720985	0.0141	0.1317
chrMT	16571	12303	0.7424	0.9877
chrX	155270560	6101262	0.0393	0.252
chrY	59373566	248094	0.0042	0.1022

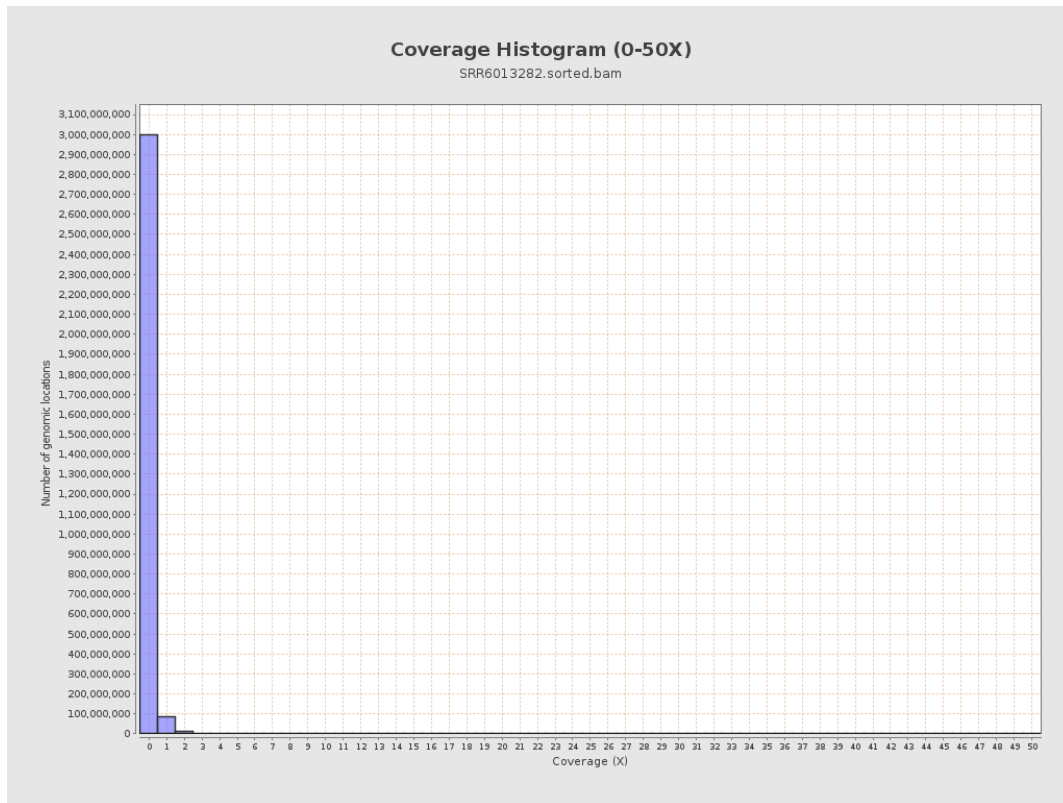
3. Results : Coverage across reference



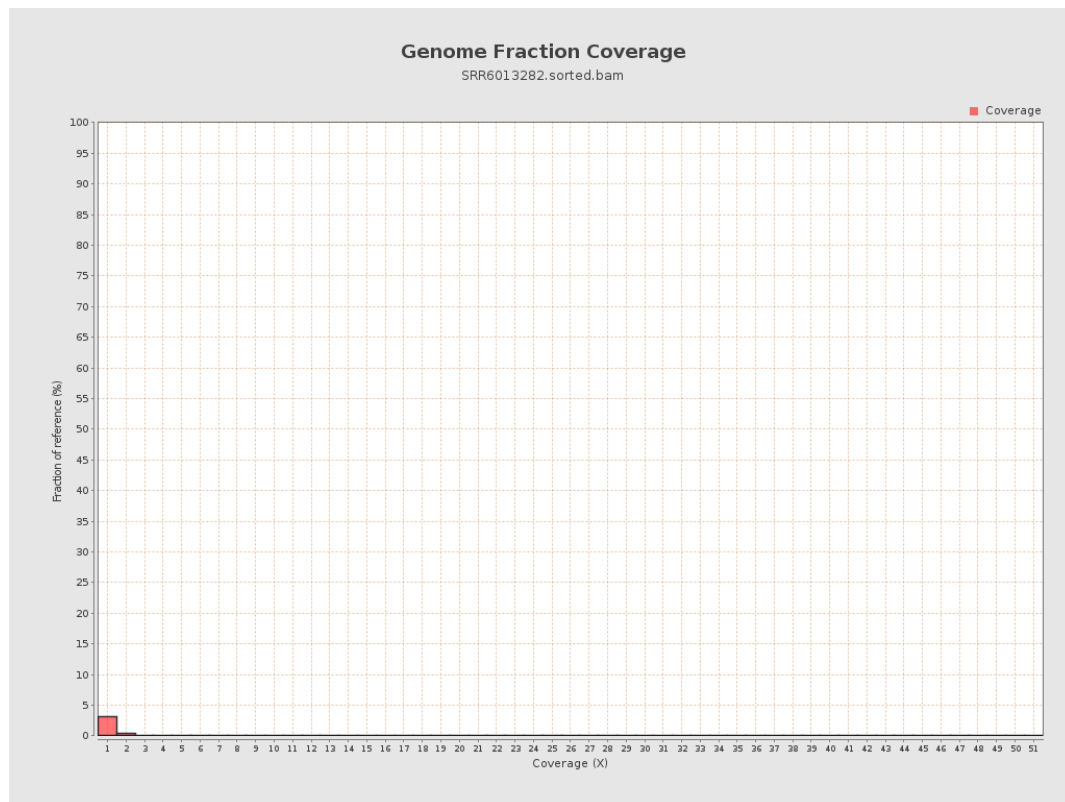
4. Results : Coverage Histogram



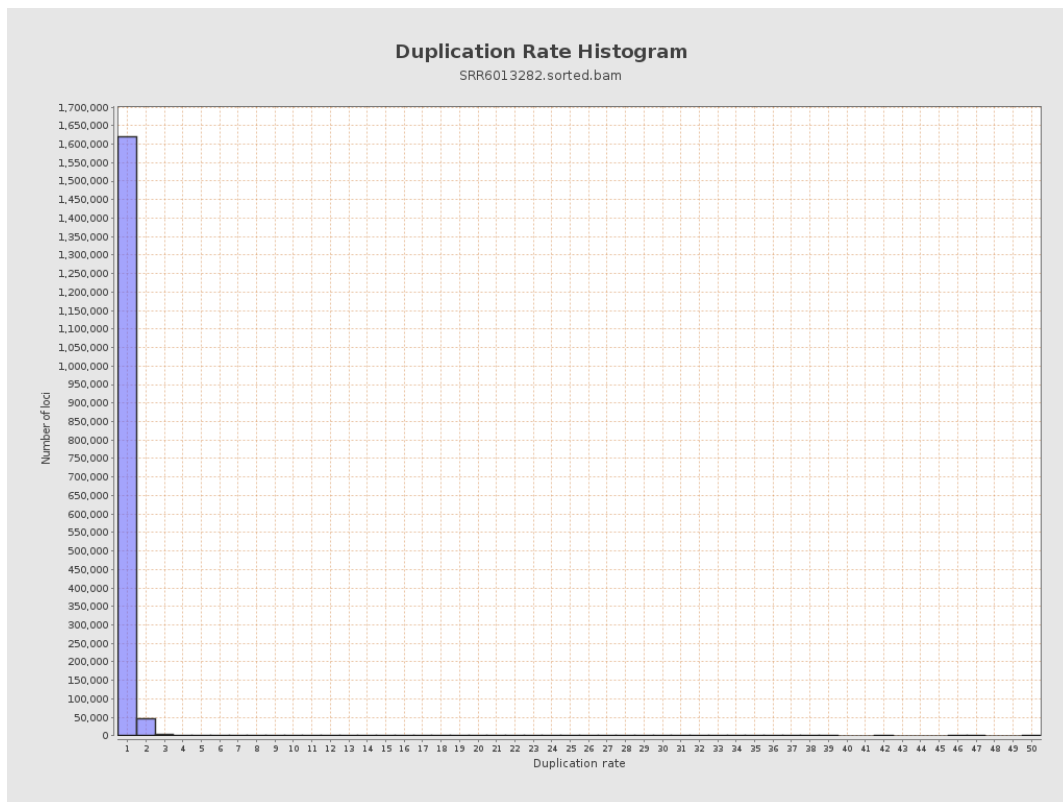
5. Results : Coverage Histogram (0-50X)



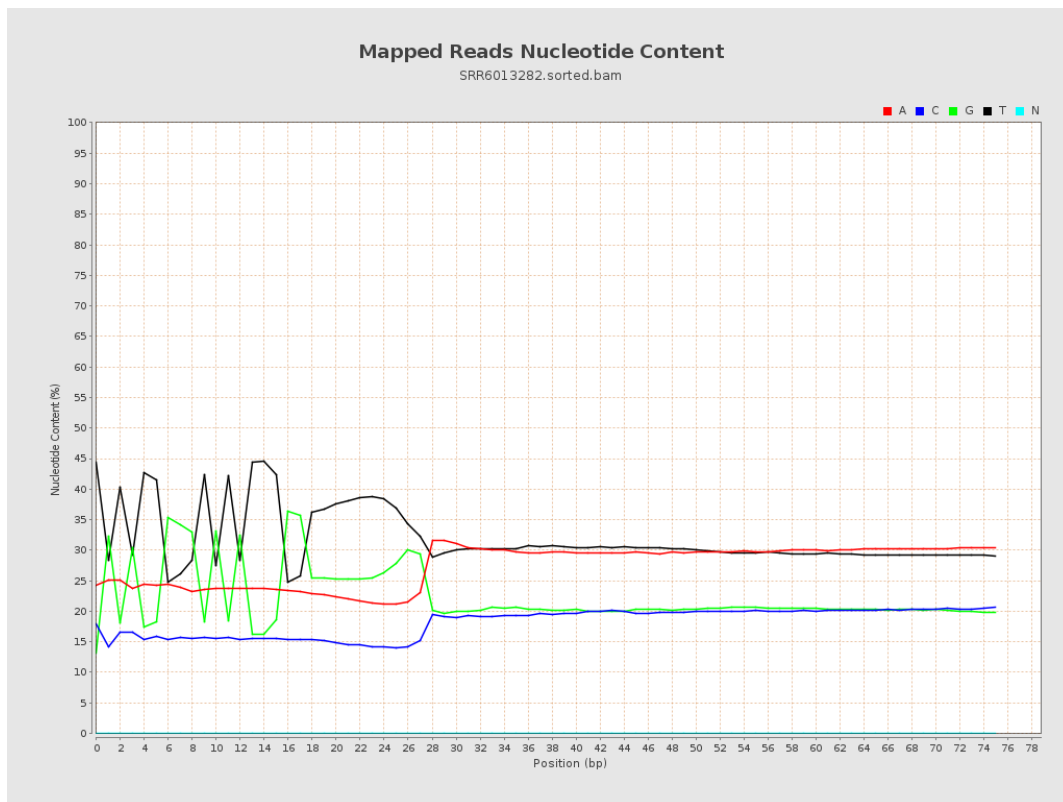
6. Results : Genome Fraction Coverage



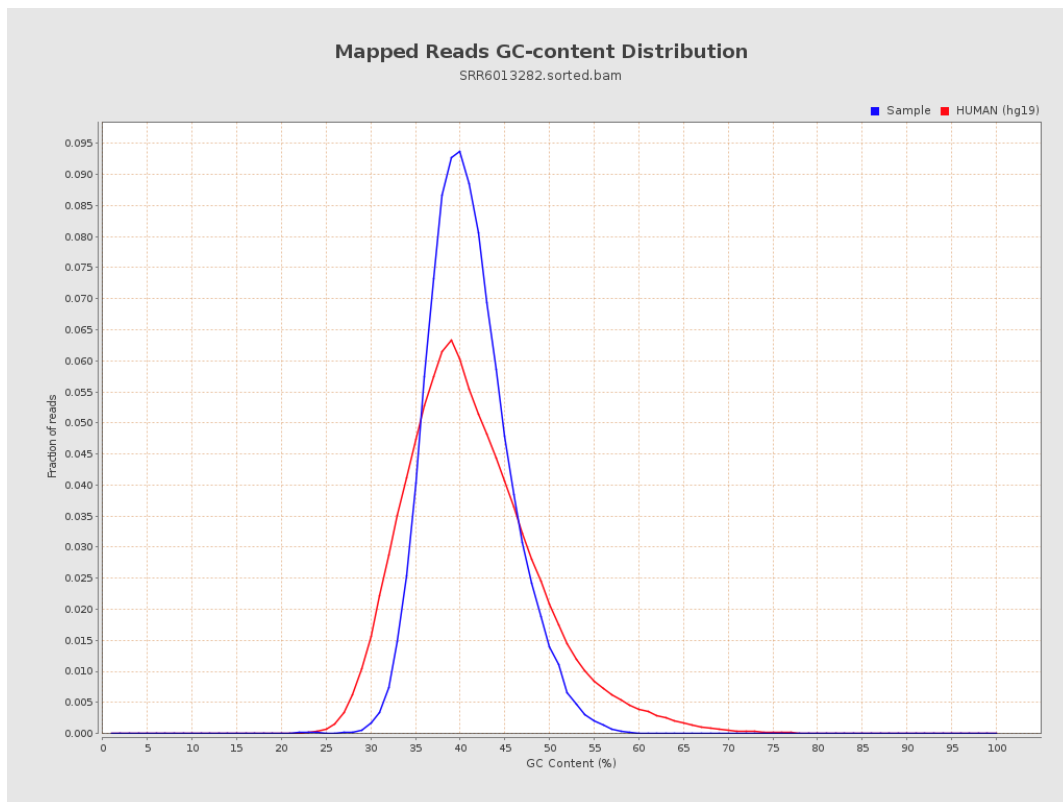
7. Results : Duplication Rate Histogram



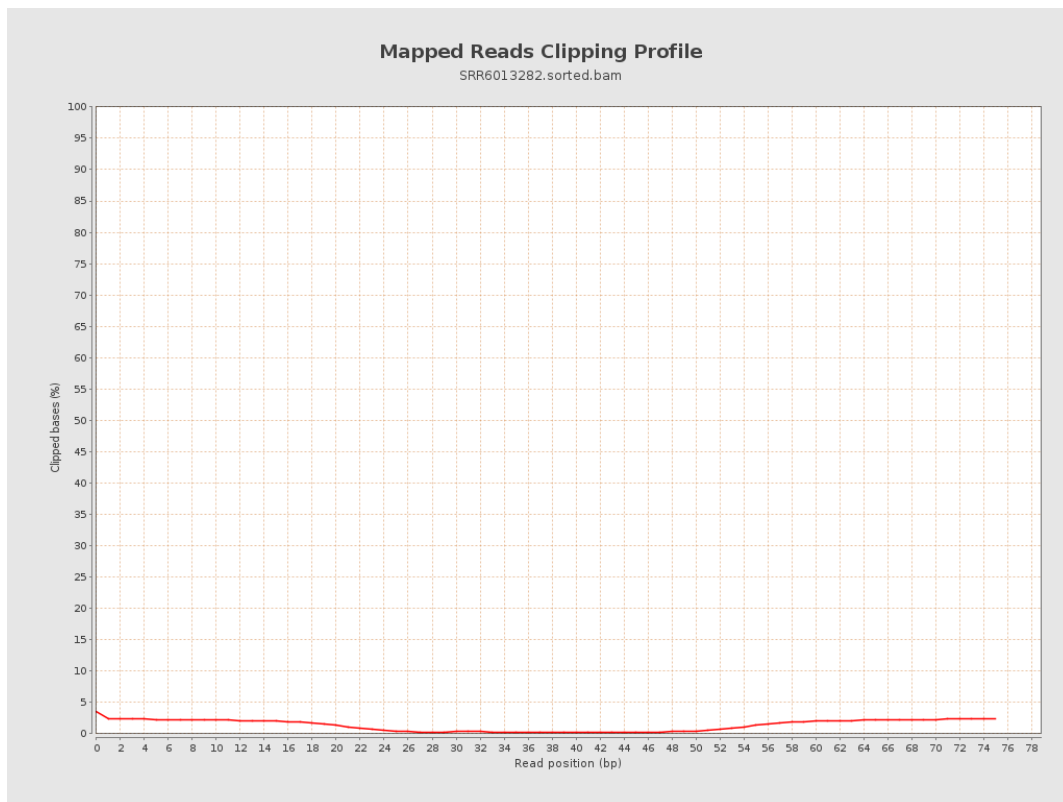
8. Results : Mapped Reads Nucleotide Content



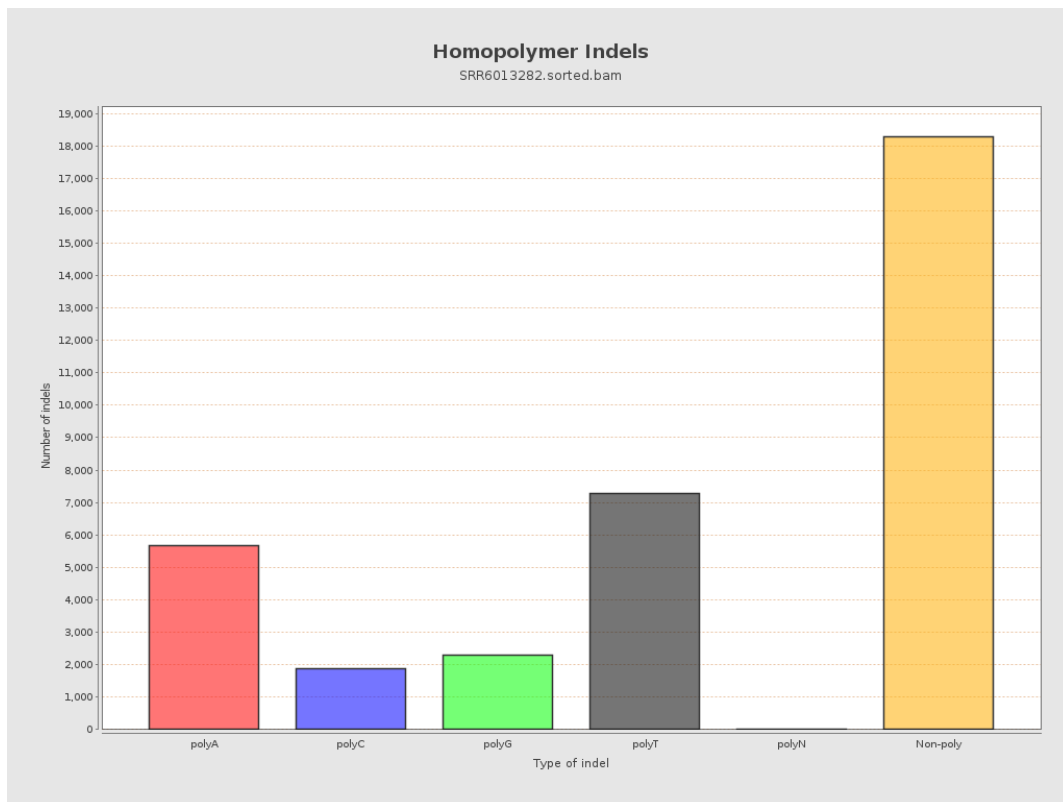
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

