

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:17:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240180.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_SRR6240180 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240180.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:17:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240180.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,615,911
Mapped reads	1,255,321 / 77.69%
Unmapped reads	360,590 / 22.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,507 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	128,997 / 7.98%
Duplication rate	8.1%
Clipped reads	605,774 / 37.49%

2.2. ACGT Content

Number/percentage of A's	24,074,895 / 28.93%
Number/percentage of C's	15,669,311 / 18.83%
Number/percentage of T's	26,008,359 / 31.25%
Number/percentage of G's	17,398,635 / 20.91%
Number/percentage of N's	63,006 / 0.08%
GC Percentage	39.74%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.3478
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2.4. Mapping Quality

Mean Mapping Quality	47.06
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2.5. Mismatches and indels

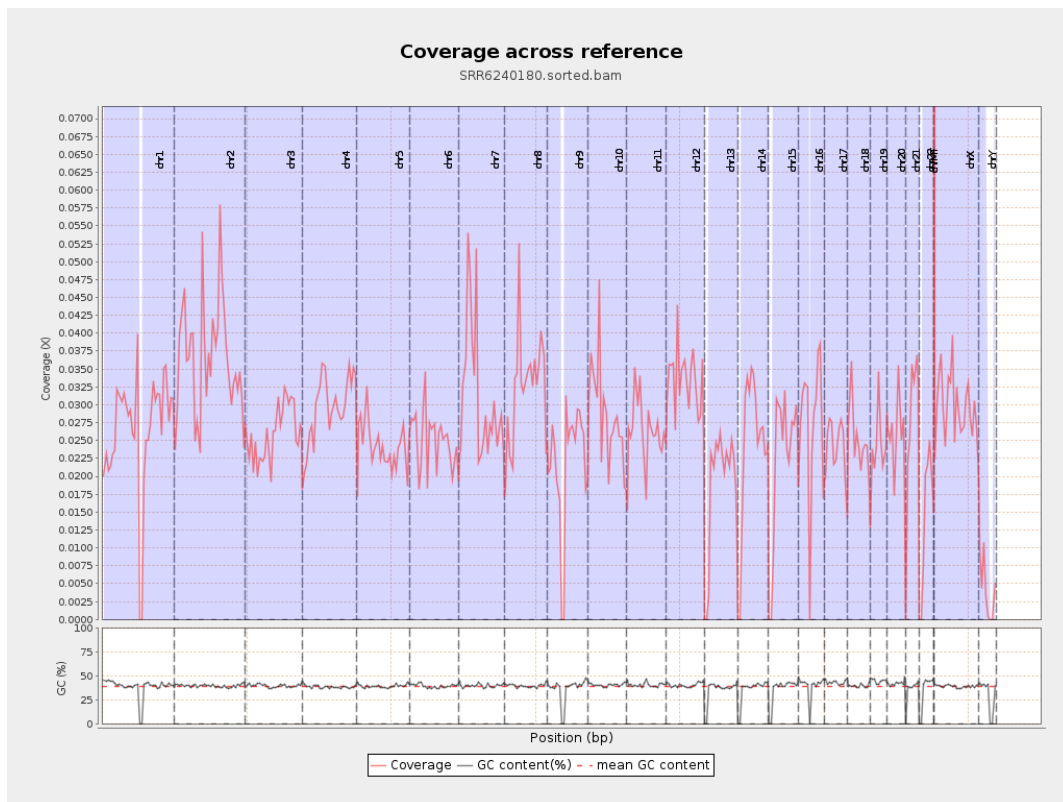
General error rate	0.91%
Mismatches	748,647
Insertions	5,786
Mapped reads with at least one insertion	0.46%
Deletions	22,196
Mapped reads with at least one deletion	1.75%
Homopolymer indels	48.33%

2.6. Chromosome stats

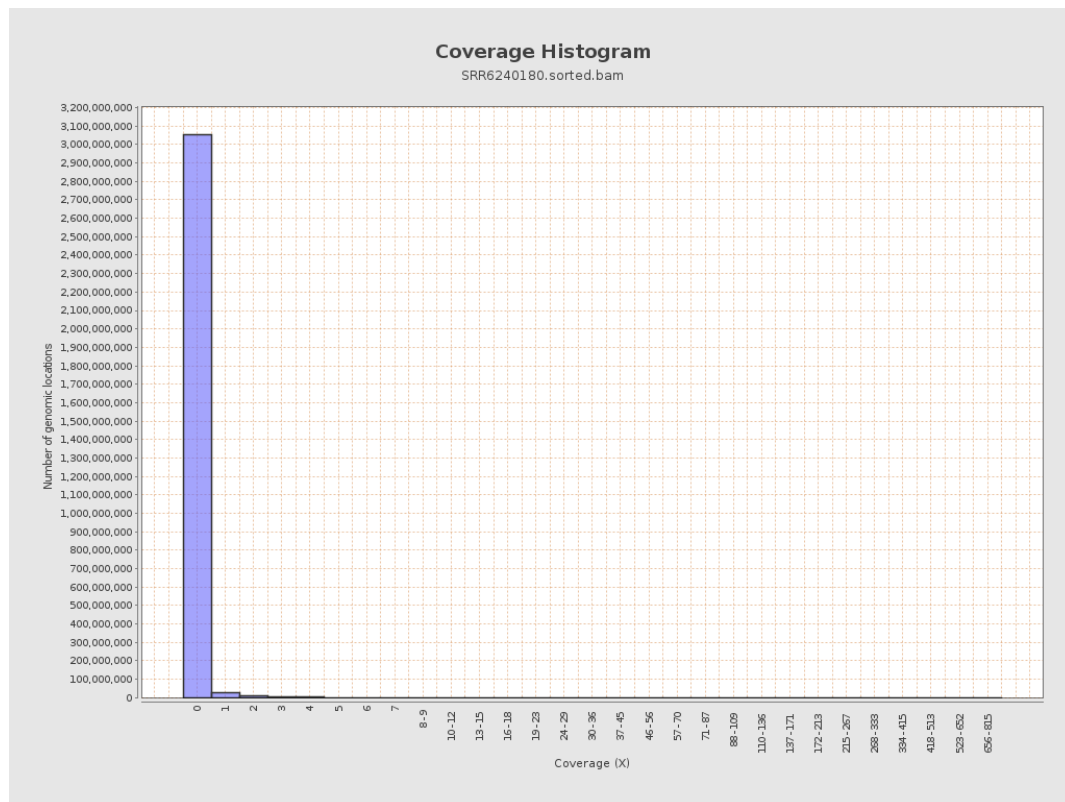
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6596536	0.0265	0.4694
chr2	243199373	8929160	0.0367	0.3721
chr3	198022430	5136307	0.0259	0.2711
chr4	191154276	5646302	0.0295	0.5076
chr5	180915260	4398600	0.0243	0.2638
chr6	171115067	4287072	0.0251	0.2784
chr7	159138663	4970224	0.0312	0.4744

chr8	146364022	4760578	0.0325	0.41
chr9	141213431	3092957	0.0219	0.3028
chr10	135534747	3868996	0.0285	0.3263
chr11	135006516	3566085	0.0264	0.3168
chr12	133851895	4489566	0.0335	0.3115
chr13	115169878	2168175	0.0188	0.2302
chr14	107349540	2621836	0.0244	0.2707
chr15	102531392	2299404	0.0224	0.2583
chr16	90354753	2419988	0.0268	0.278
chr17	81195210	1955899	0.0241	0.277
chr18	78077248	1986644	0.0254	0.451
chr19	59128983	1450040	0.0245	0.3422
chr20	63025520	1629336	0.0259	0.266
chr21	48129895	1344577	0.0279	0.2898
chr22	51304566	744209	0.0145	0.1967
chrMT	16571	12716	0.7674	1.6624
chrX	155270560	4640236	0.0299	0.2991
chrY	59373566	237183	0.004	0.0974

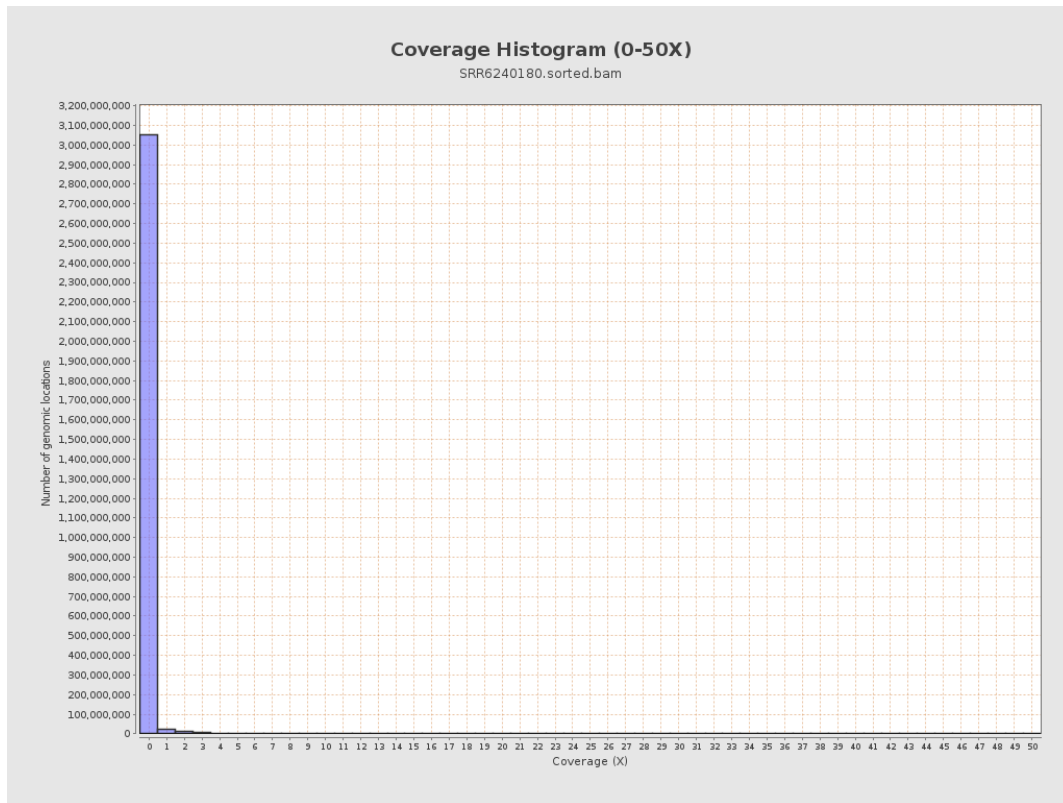
3. Results : Coverage across reference



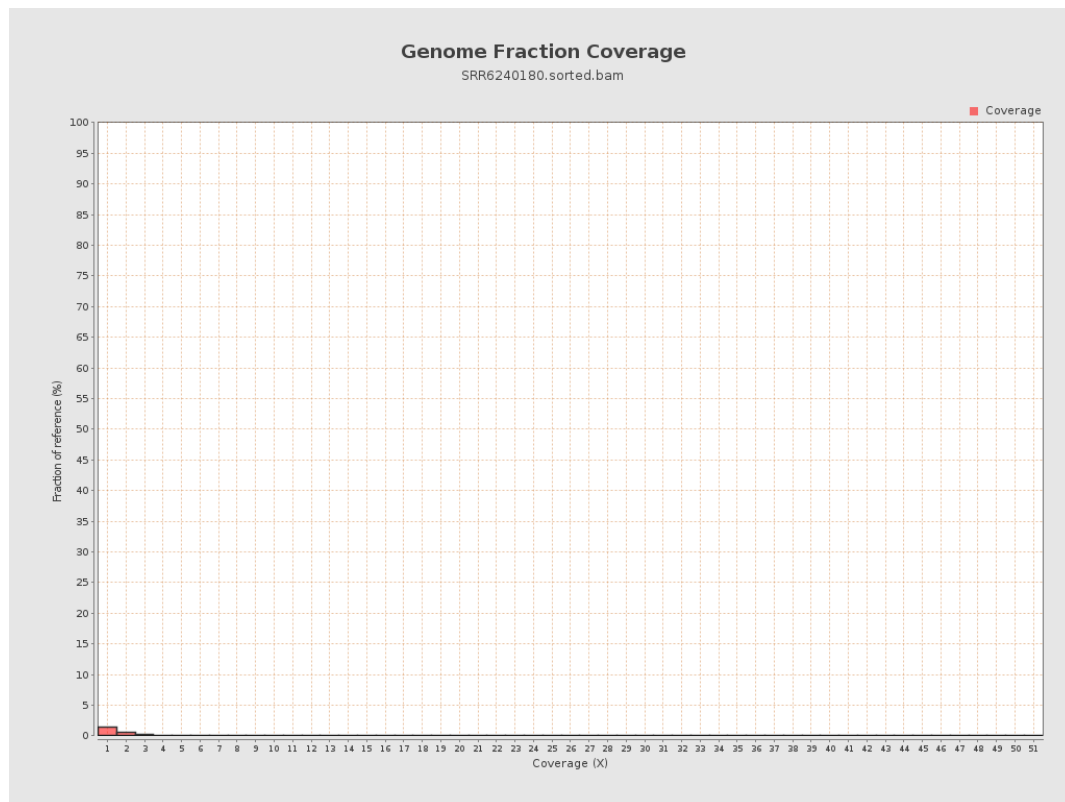
4. Results : Coverage Histogram



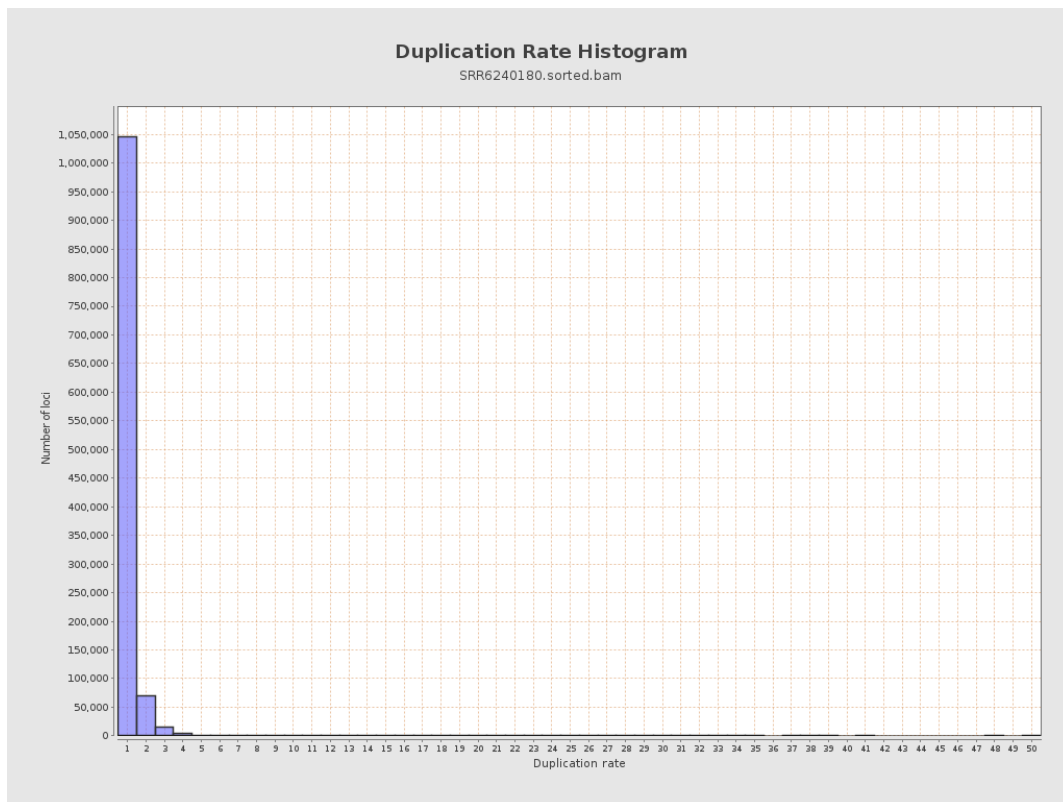
5. Results : Coverage Histogram (0-50X)



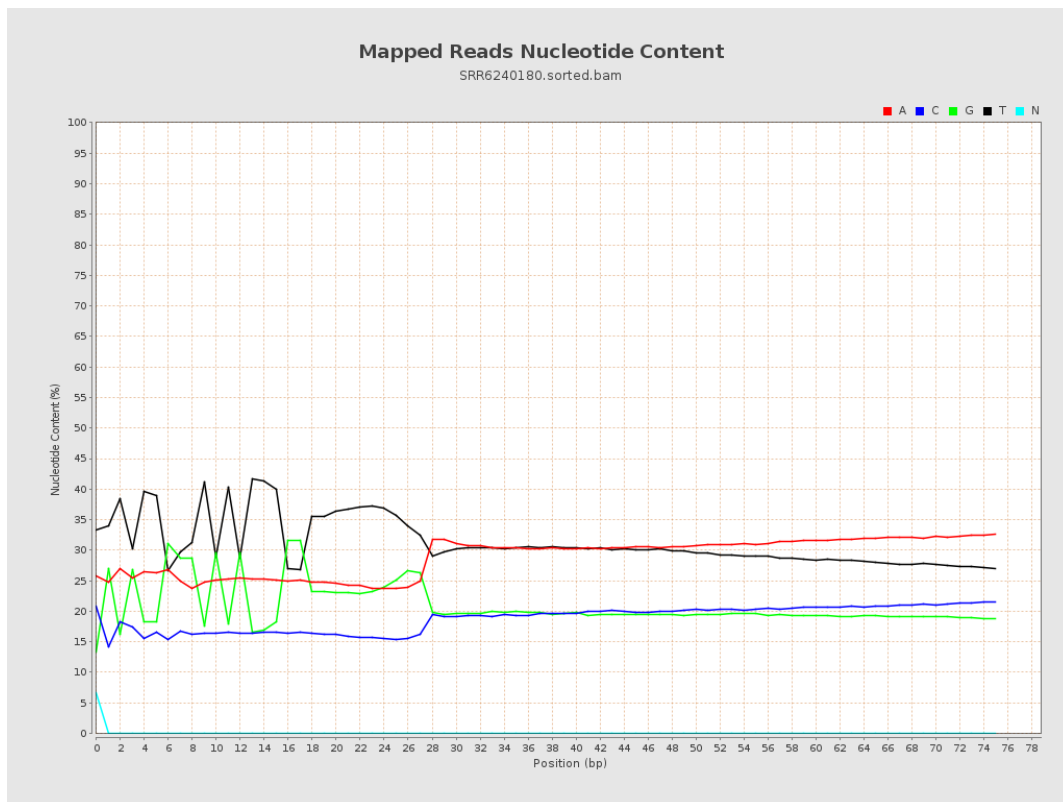
6. Results : Genome Fraction Coverage



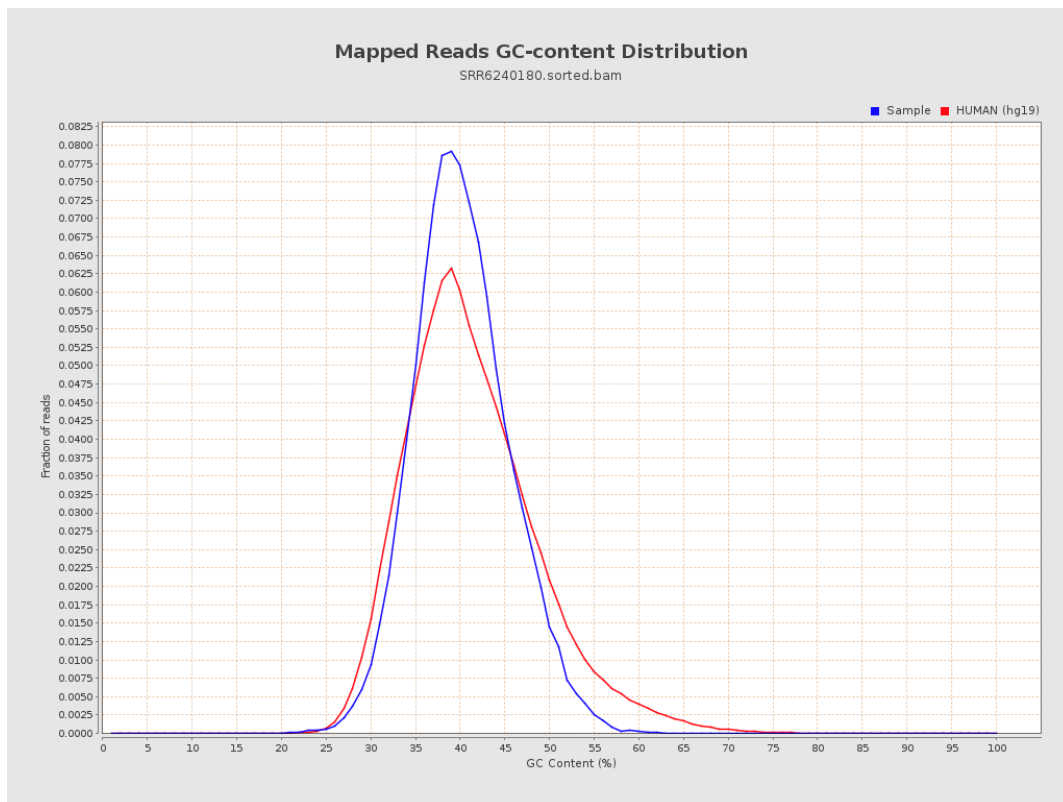
7. Results : Duplication Rate Histogram



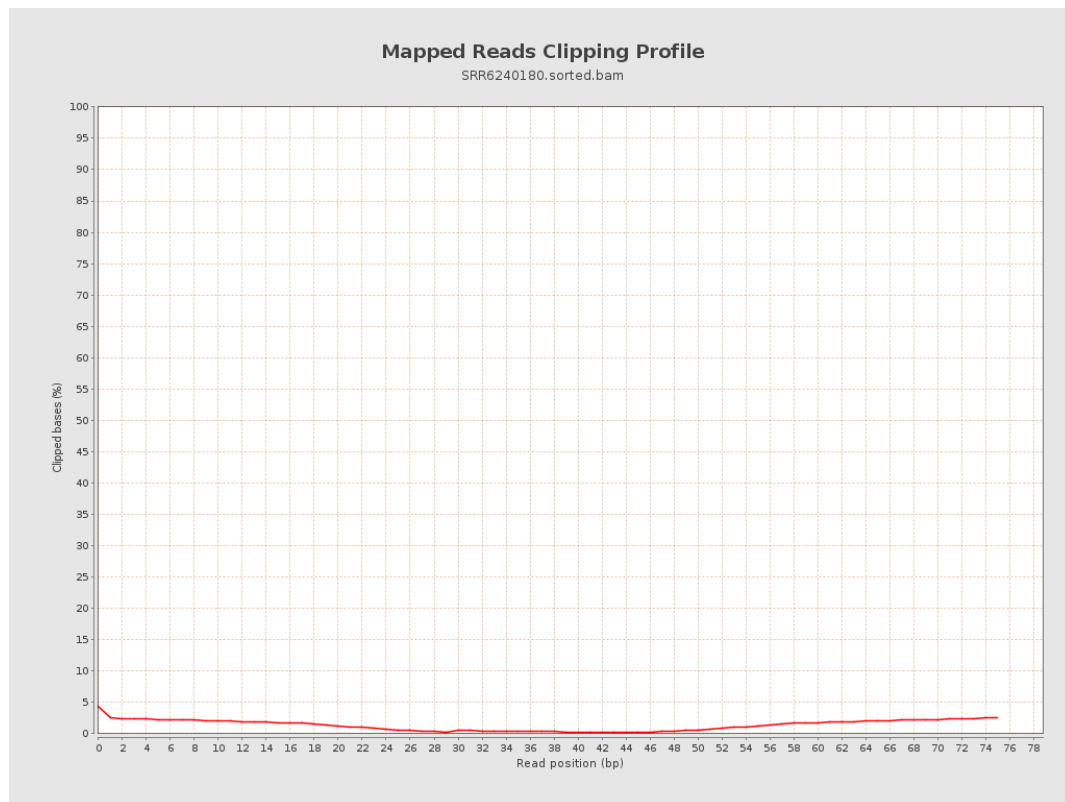
8. Results : Mapped Reads Nucleotide Content



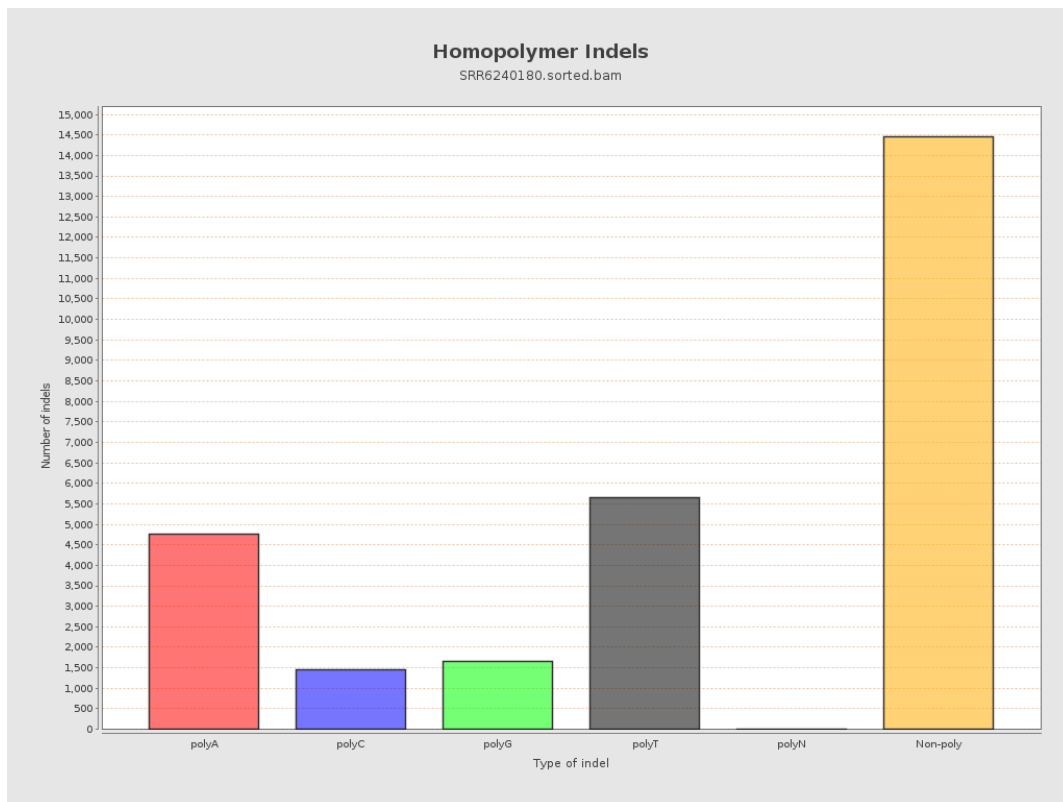
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

