

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:33:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013180.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_SRR6013180 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013180.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:33:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013180.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,218,682
Mapped reads	1,074,513 / 88.17%
Unmapped reads	144,169 / 11.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,257 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	26,216 / 2.15%
Duplication rate	1.58%
Clipped reads	490,546 / 40.25%

2.2. ACGT Content

Number/percentage of A's	20,372,386 / 28.58%
Number/percentage of C's	13,073,120 / 18.34%
Number/percentage of T's	22,154,101 / 31.08%
Number/percentage of G's	15,677,323 / 21.99%
Number/percentage of N's	8,505 / 0.01%
GC Percentage	40.33%

2.3. Coverage

Mean	0.023

Standard Deviation	0.2469
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2.4. Mapping Quality

Mean Mapping Quality	43.75
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2.5. Mismatches and indels

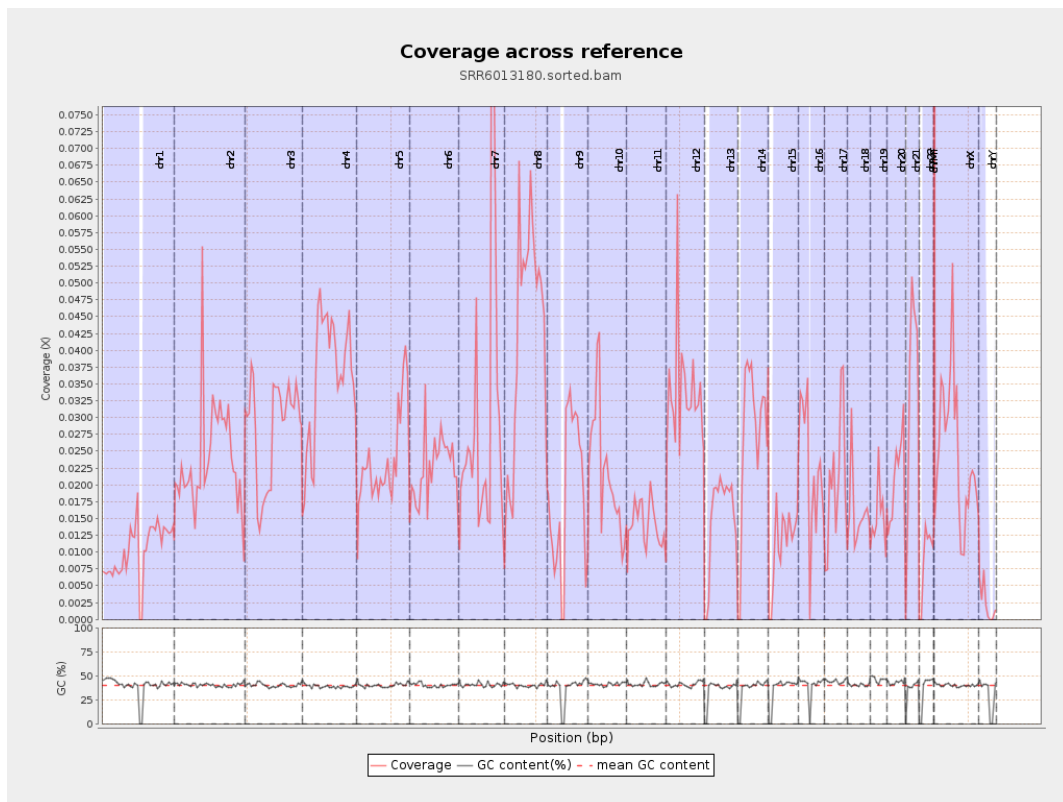
General error rate	0.84%
Mismatches	590,990
Insertions	5,634
Mapped reads with at least one insertion	0.52%
Deletions	21,678
Mapped reads with at least one deletion	1.99%
Homopolymer indels	45.85%

2.6. Chromosome stats

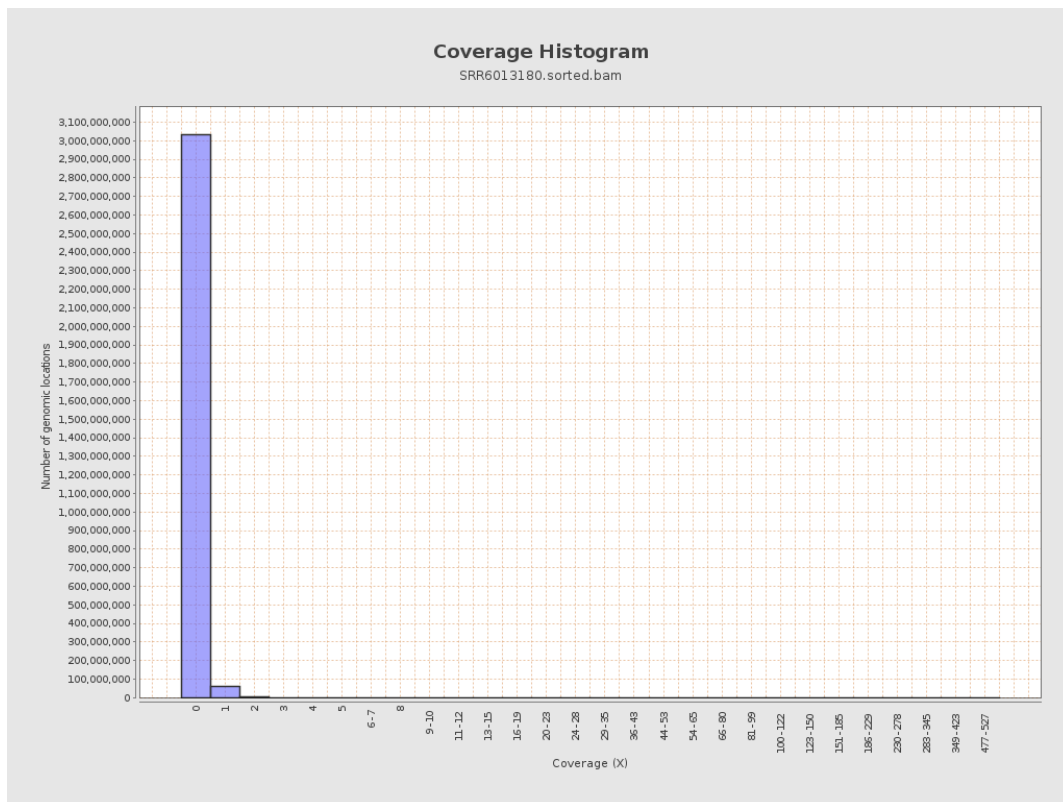
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2566086	0.0103	0.2349
chr2	243199373	5790507	0.0238	0.3088
chr3	198022430	5627882	0.0284	0.1772
chr4	191154276	6934618	0.0363	0.2049
chr5	180915260	4341786	0.024	0.1635
chr6	171115067	3850705	0.0225	0.2081
chr7	159138663	4725332	0.0297	0.3842

chr8	146364022	6300189	0.043	0.4003
chr9	141213431	2621244	0.0186	0.2554
chr10	135534747	2992030	0.0221	0.2788
chr11	135006516	1911252	0.0142	0.1849
chr12	133851895	4510359	0.0337	0.1946
chr13	115169878	1737376	0.0151	0.1279
chr14	107349540	2962421	0.0276	0.1938
chr15	102531392	1126754	0.011	0.1127
chr16	90354753	1997713	0.0221	0.1826
chr17	81195210	1660824	0.0205	0.173
chr18	78077248	1238613	0.0159	0.528
chr19	59128983	908138	0.0154	0.2462
chr20	63025520	1335470	0.0212	0.1653
chr21	48129895	1666368	0.0346	0.2049
chr22	51304566	473169	0.0092	0.1035
chrMT	16571	9522	0.5746	0.8097
chrX	155270560	3892222	0.0251	0.1966
chrY	59373566	142427	0.0024	0.0743

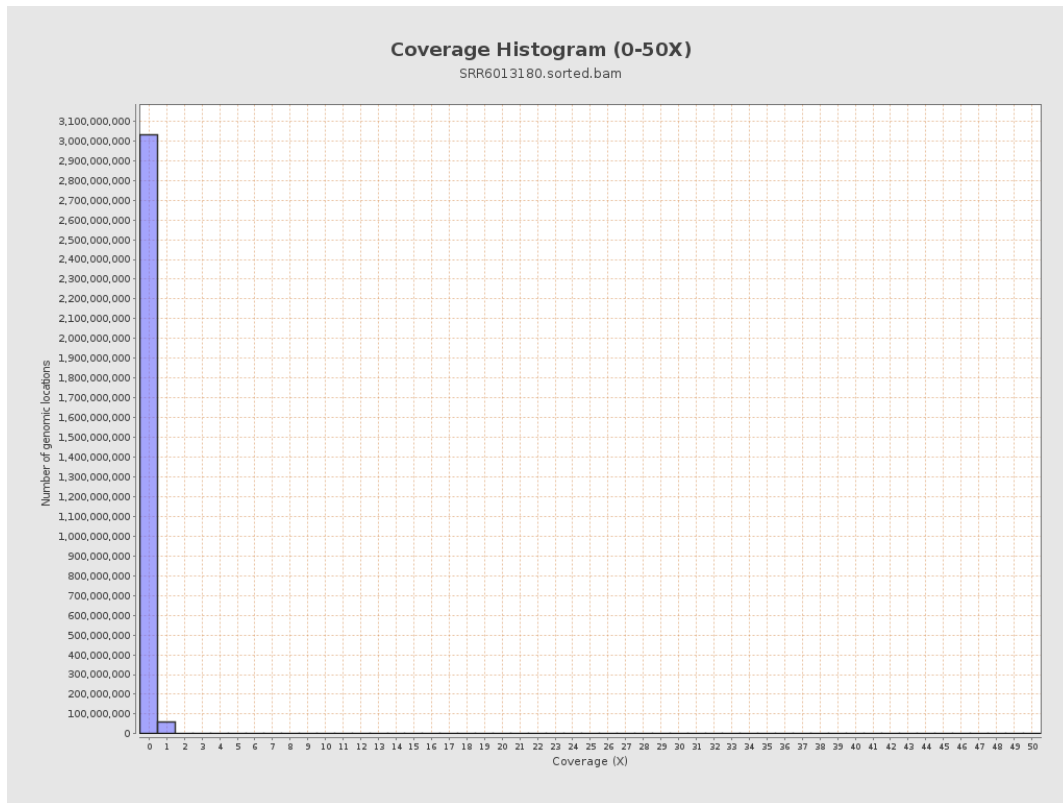
3. Results : Coverage across reference



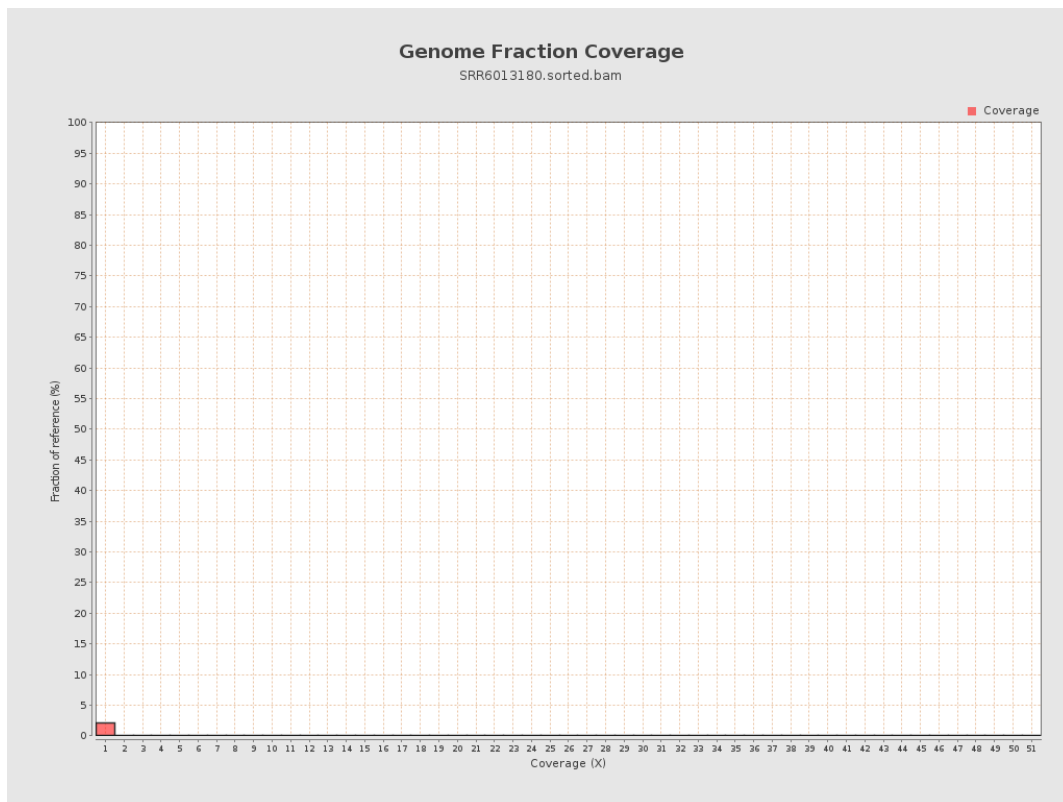
4. Results : Coverage Histogram



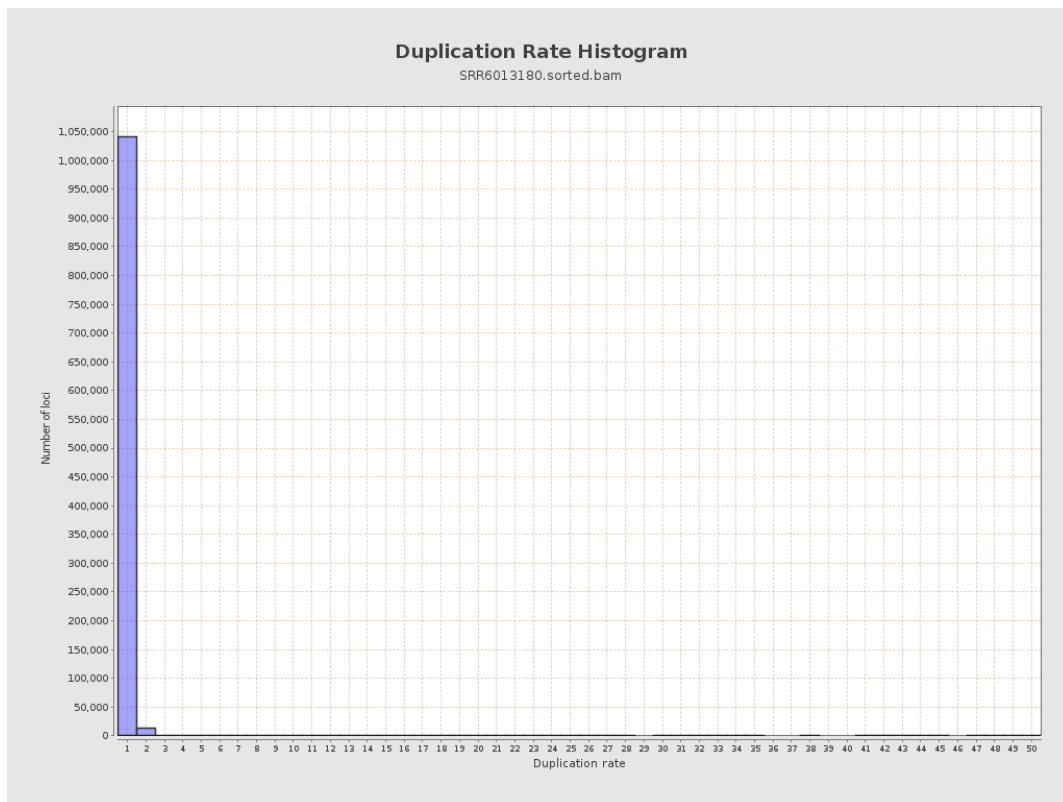
5. Results : Coverage Histogram (0-50X)



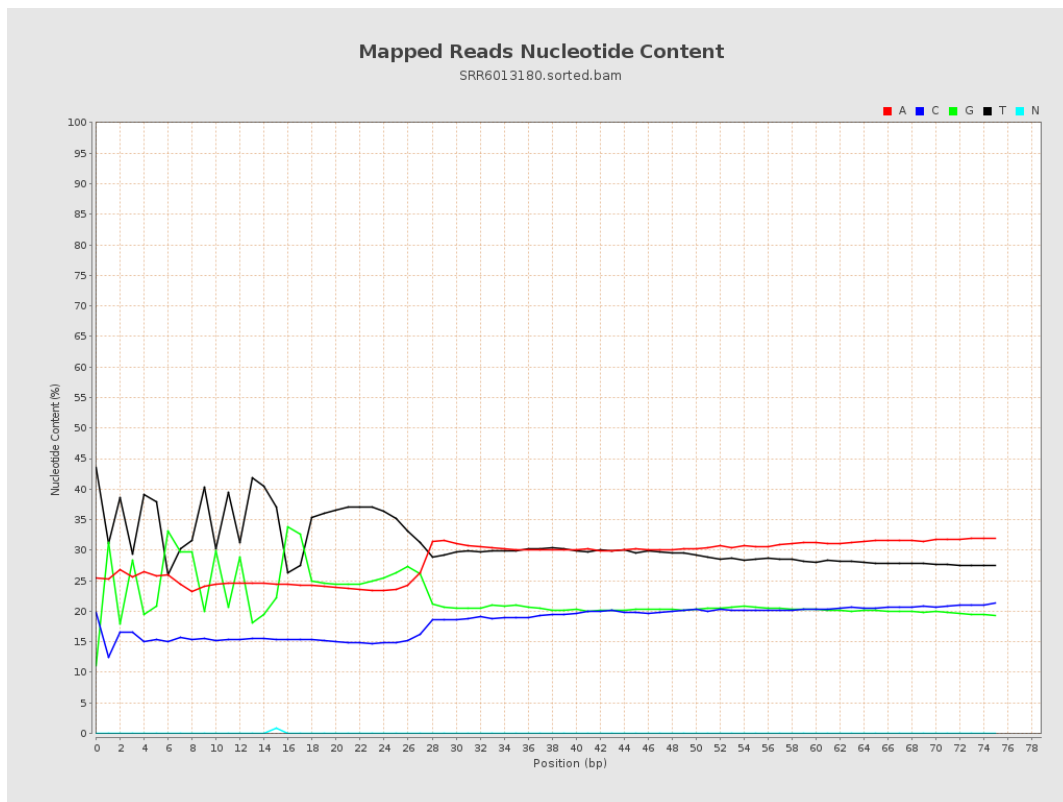
6. Results : Genome Fraction Coverage



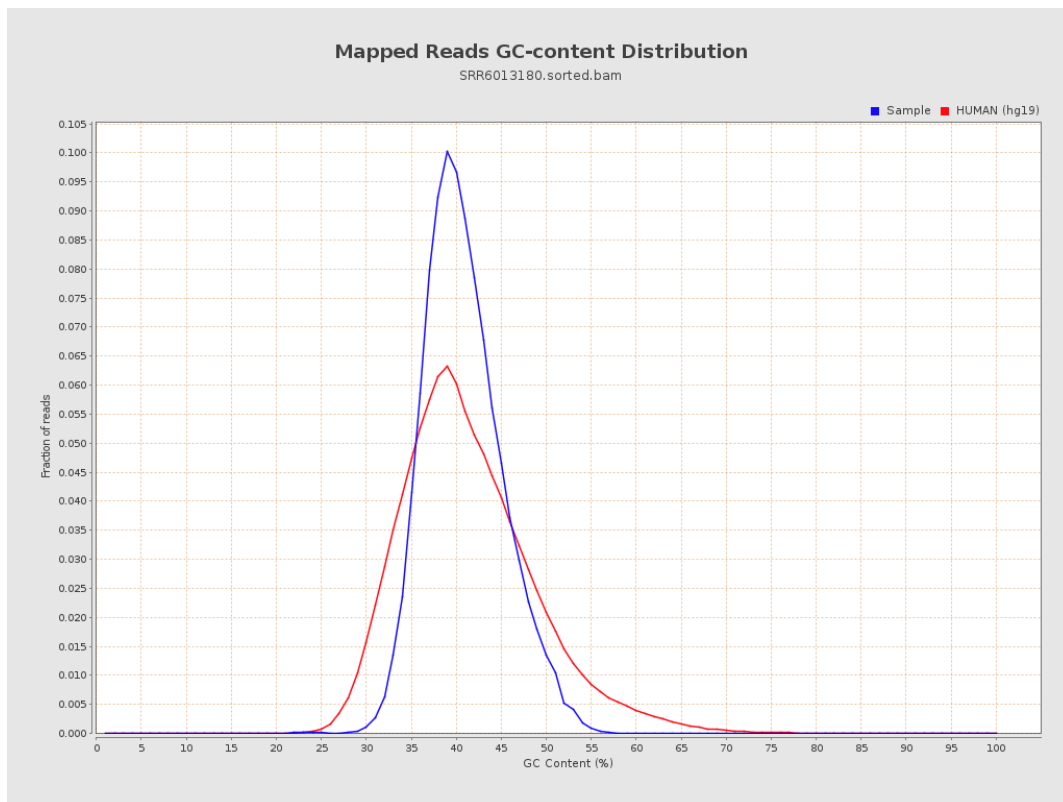
7. Results : Duplication Rate Histogram



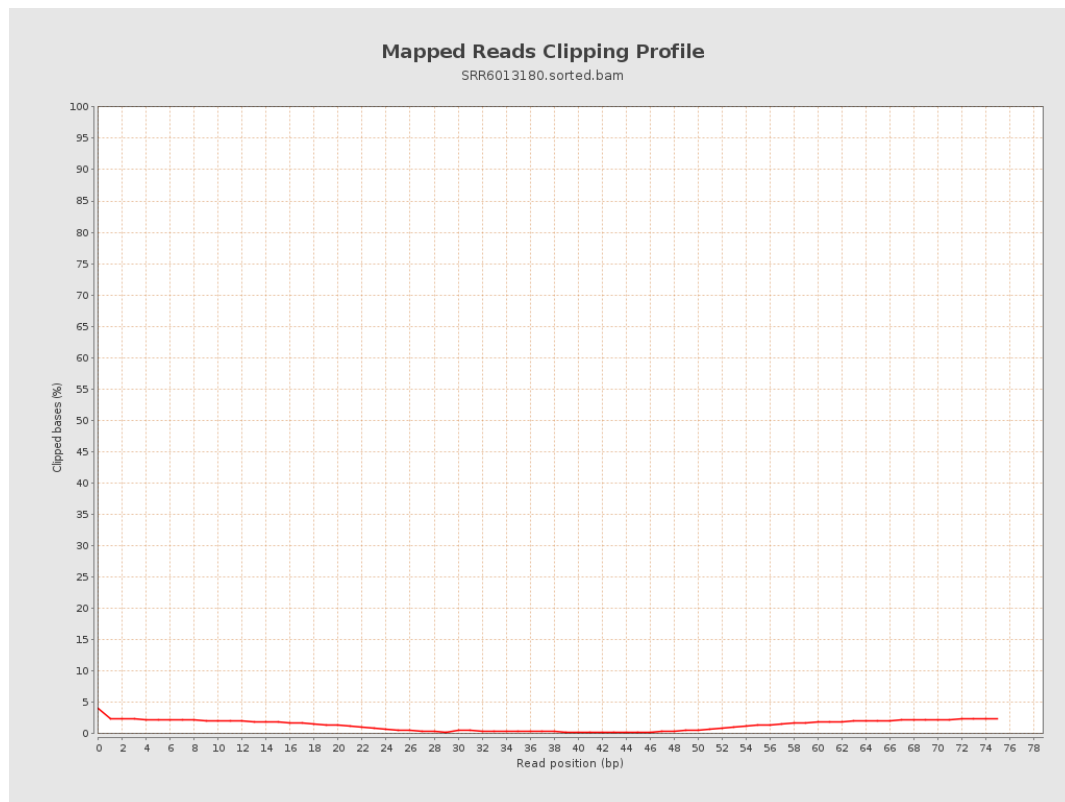
8. Results : Mapped Reads Nucleotide Content



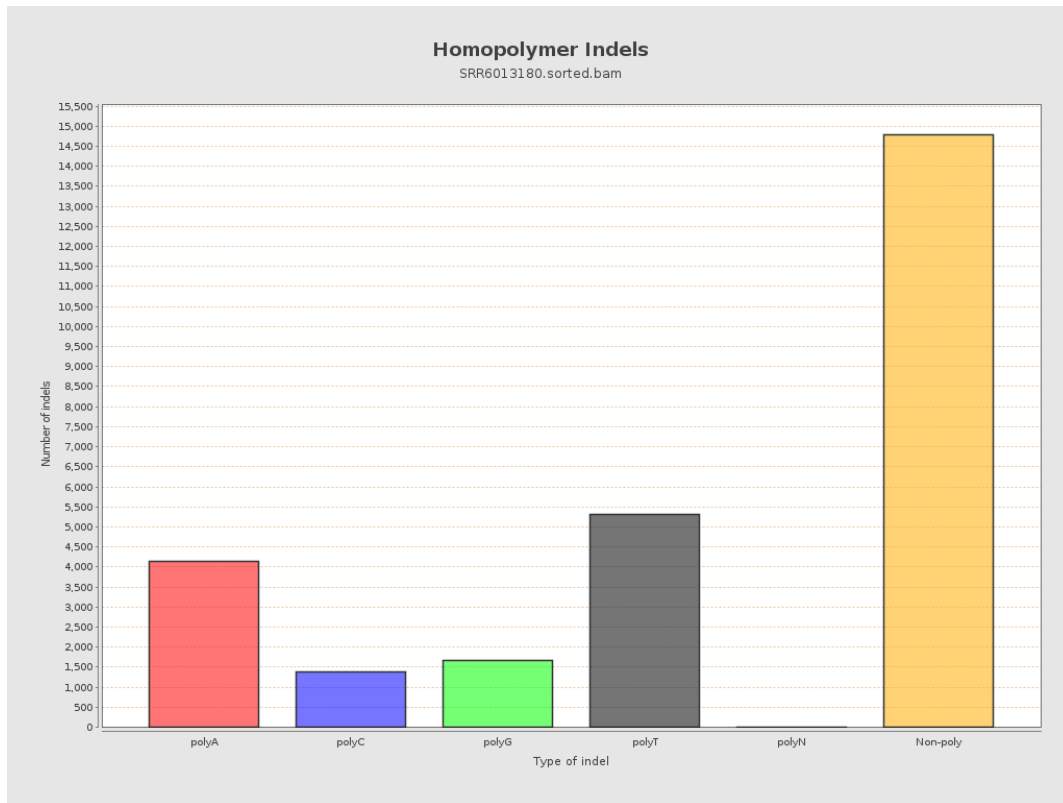
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

