

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:36:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818813.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_SRR1818813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818813.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:36:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	800,019
Mapped reads	778,266 / 97.28%
Unmapped reads	21,753 / 2.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,478 / 0.81%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	217,055 / 27.13%
Duplication rate	25.06%
Clipped reads	779,351 / 97.42%

2.2. ACGT Content

Number/percentage of A's	15,306,229 / 28.97%
Number/percentage of C's	11,734,803 / 22.21%
Number/percentage of T's	14,812,511 / 28.03%
Number/percentage of G's	10,986,471 / 20.79%
Number/percentage of N's	3,378 / 0.01%
GC Percentage	43%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.2285
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2.4. Mapping Quality

Mean Mapping Quality	47.75
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2.5. Mismatches and indels

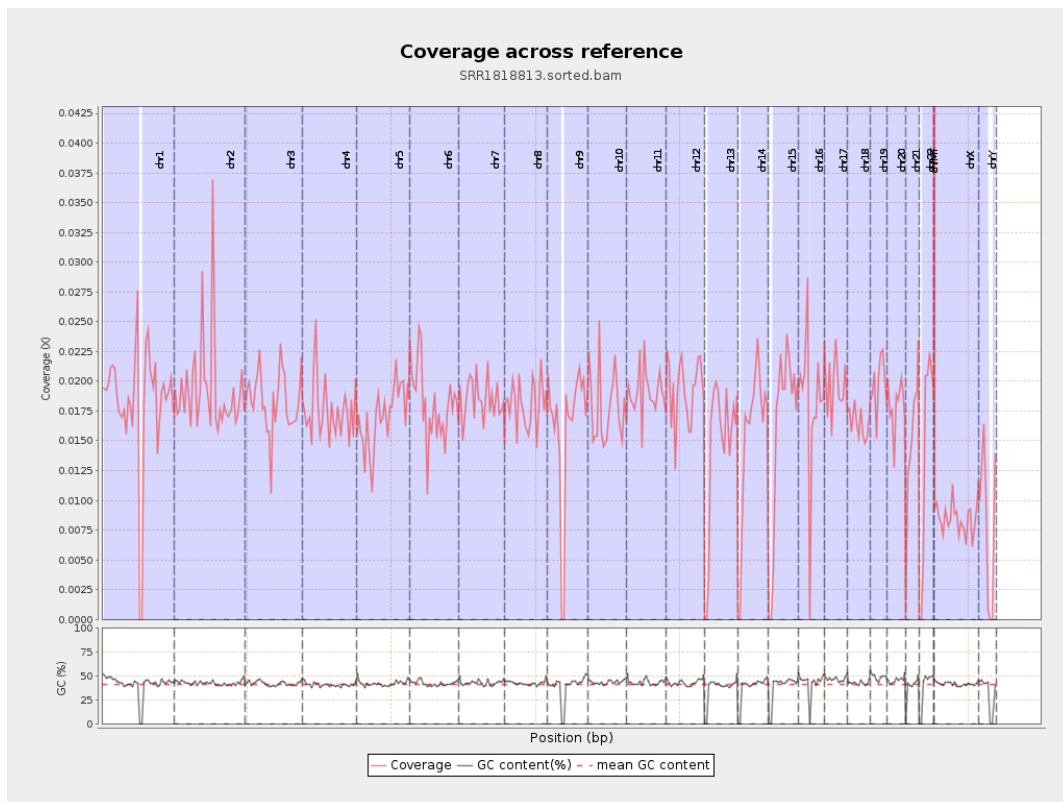
General error rate	0.54%
Mismatches	271,603
Insertions	6,348
Mapped reads with at least one insertion	0.81%
Deletions	13,489
Mapped reads with at least one deletion	1.71%
Homopolymer indels	42.04%

2.6. Chromosome stats

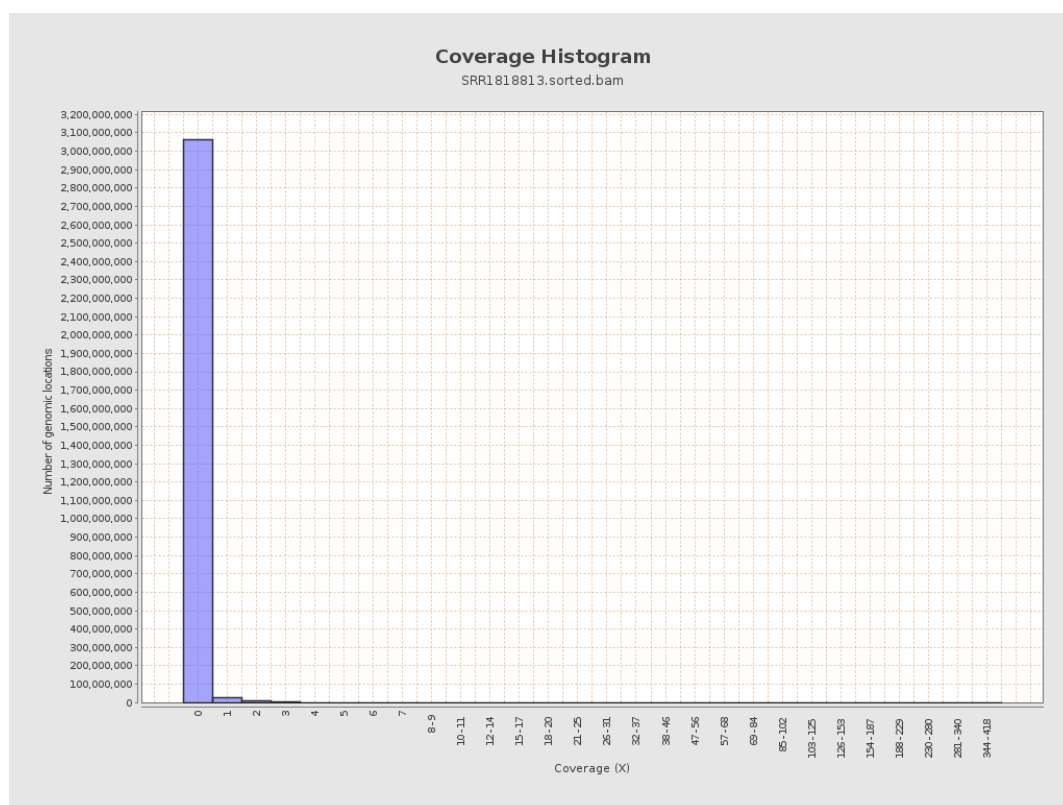
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4539897	0.0182	0.3082
chr2	243199373	4674859	0.0192	0.3338
chr3	198022430	3626134	0.0183	0.1909
chr4	191154276	3355723	0.0176	0.2034
chr5	180915260	3092612	0.0171	0.1895
chr6	171115067	3087206	0.018	0.1952
chr7	159138663	2953768	0.0186	0.216

chr8	146364022	2644325	0.0181	0.2037
chr9	141213431	2278625	0.0161	0.208
chr10	135534747	2427145	0.0179	0.2323
chr11	135006516	2589365	0.0192	0.21
chr12	133851895	2570846	0.0192	0.2012
chr13	115169878	1645653	0.0143	0.1694
chr14	107349540	1645349	0.0153	0.1828
chr15	102531392	1648013	0.0161	0.1799
chr16	90354753	1630694	0.018	0.271
chr17	81195210	1580937	0.0195	0.2072
chr18	78077248	1284009	0.0164	0.229
chr19	59128983	1168435	0.0198	0.2648
chr20	63025520	1125567	0.0179	0.1989
chr21	48129895	718942	0.0149	0.1777
chr22	51304566	721956	0.0141	0.1799
chrMT	16571	68130	4.1114	4.0309
chrX	155270560	1311046	0.0084	0.1407
chrY	59373566	475927	0.008	0.3313

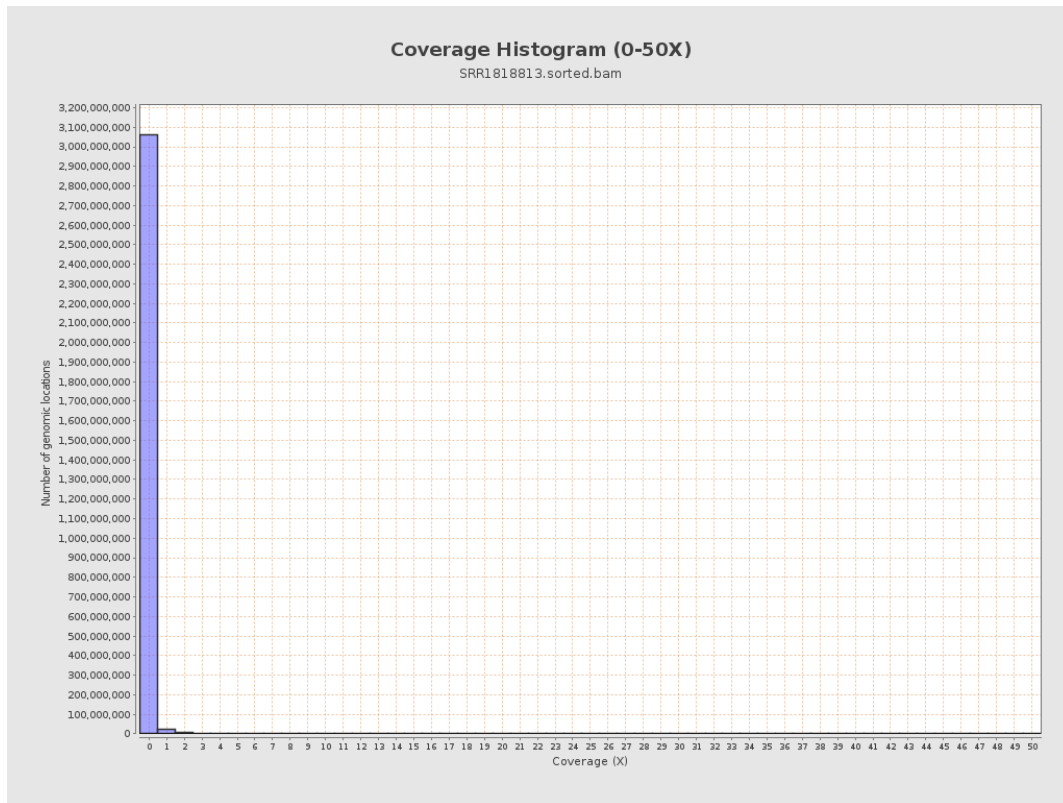
3. Results : Coverage across reference



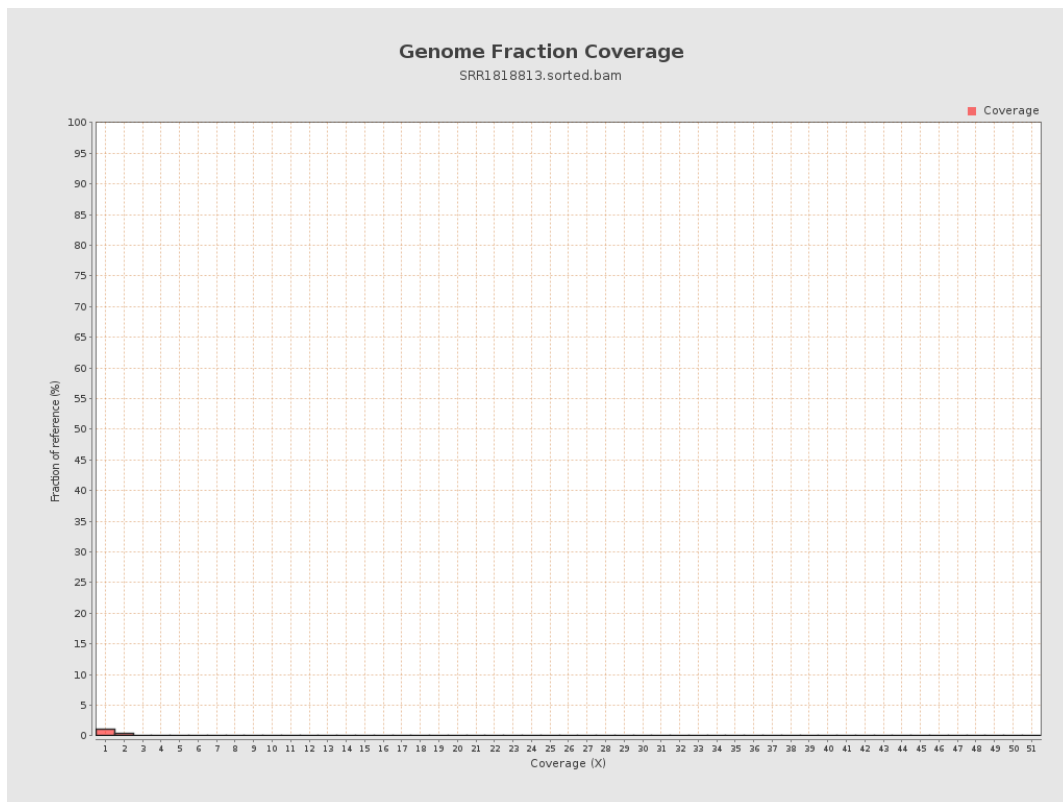
4. Results : Coverage Histogram



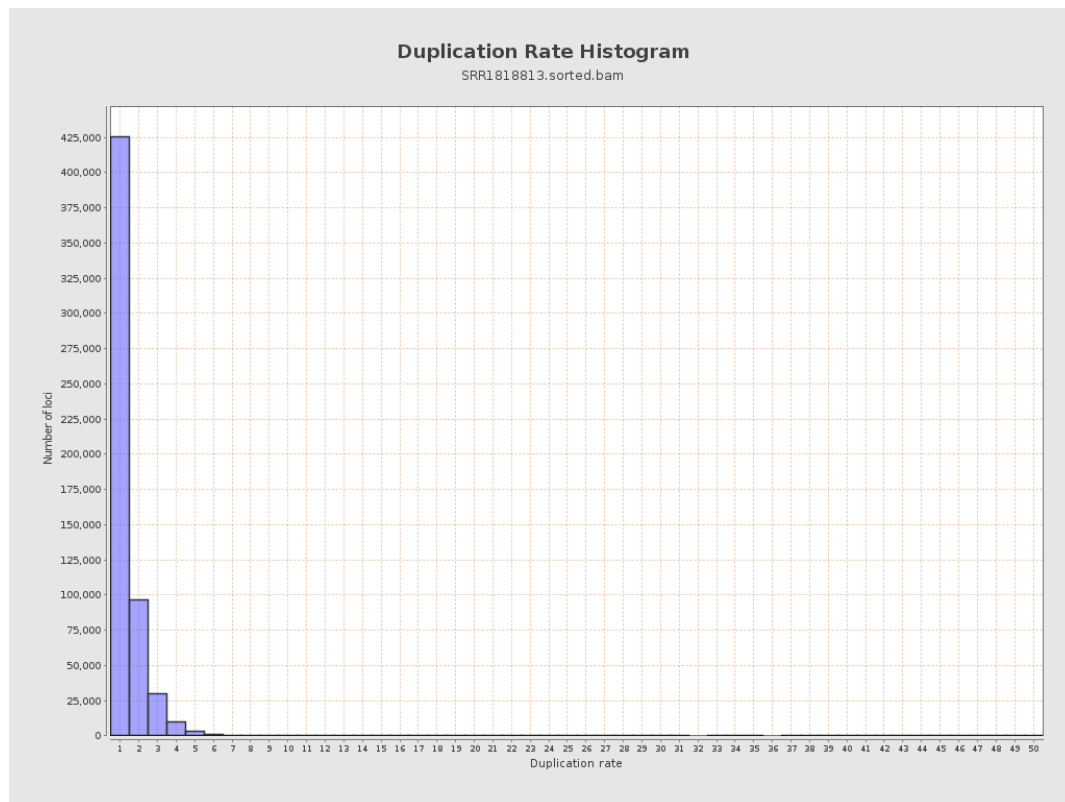
5. Results : Coverage Histogram (0-50X)



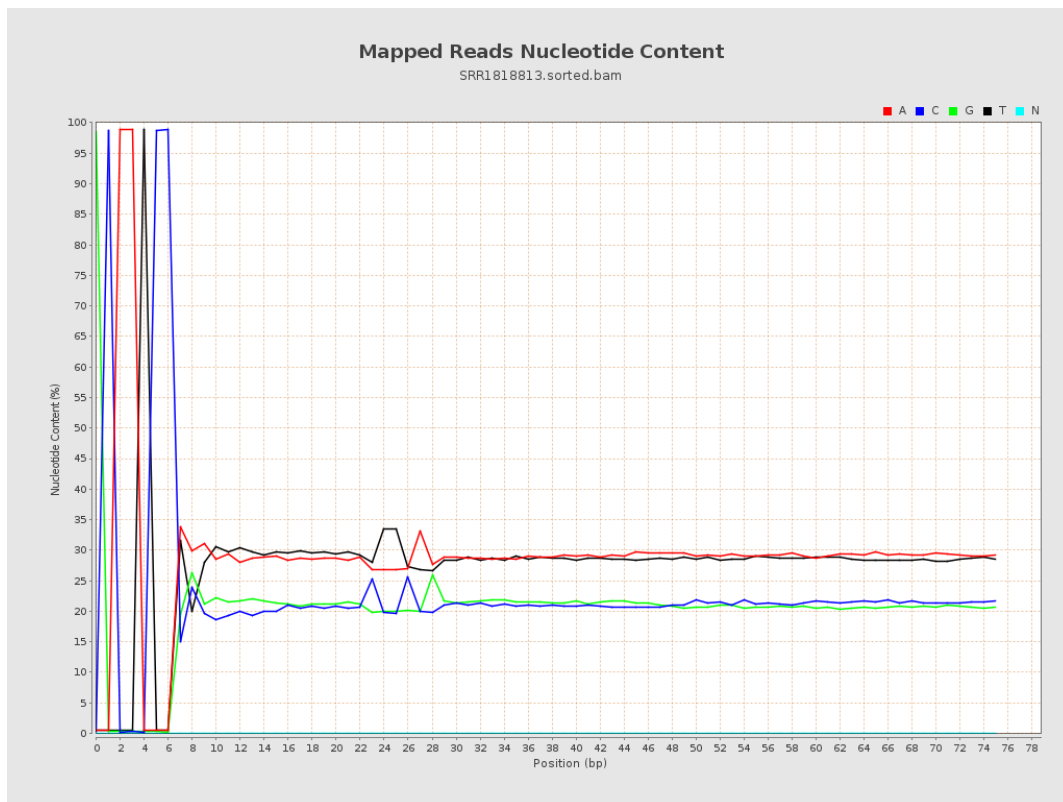
6. Results : Genome Fraction Coverage



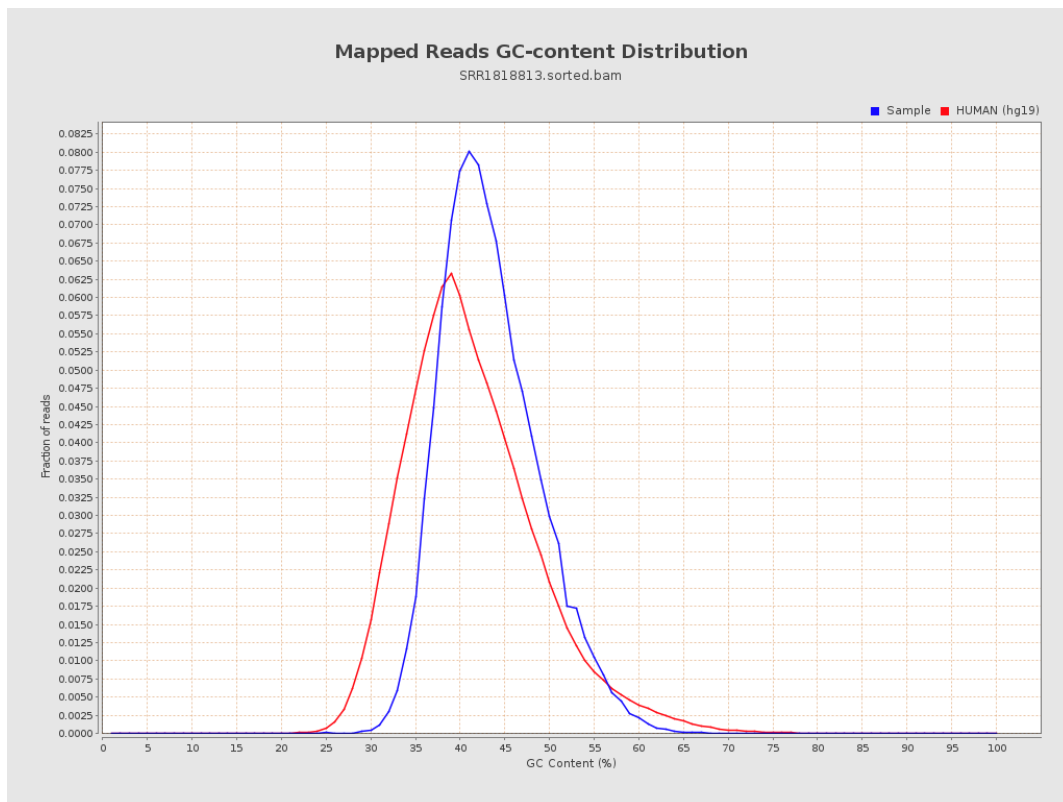
7. Results : Duplication Rate Histogram



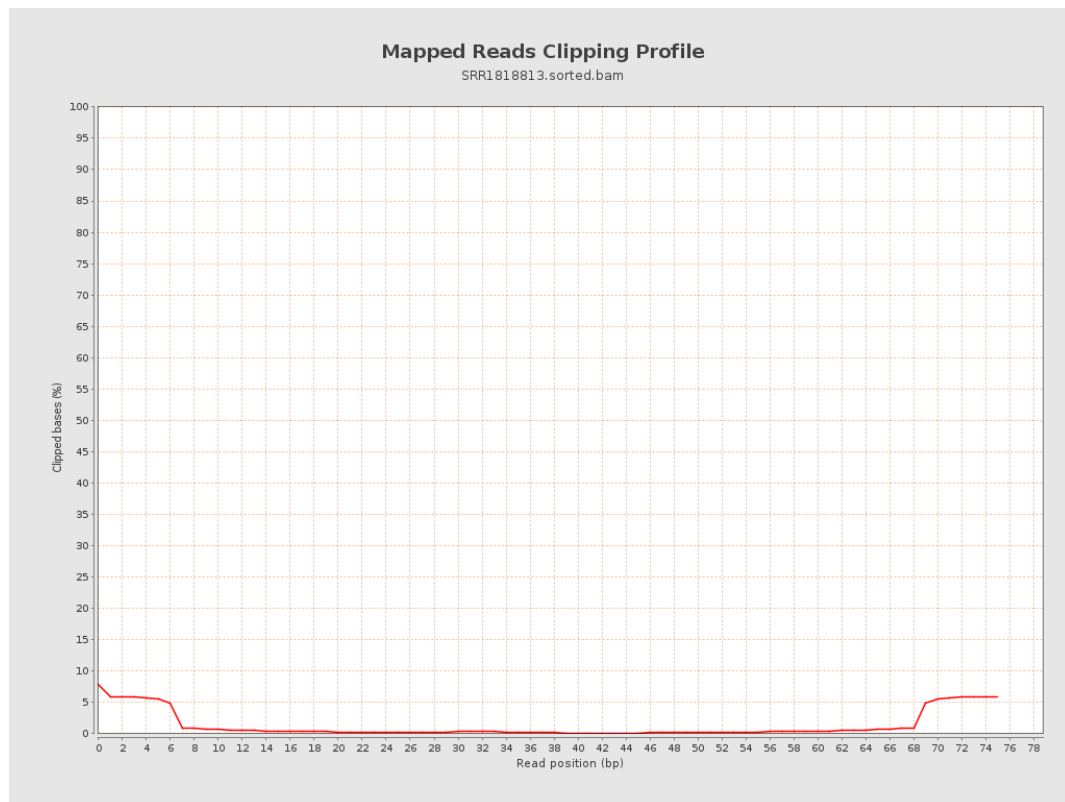
8. Results : Mapped Reads Nucleotide Content



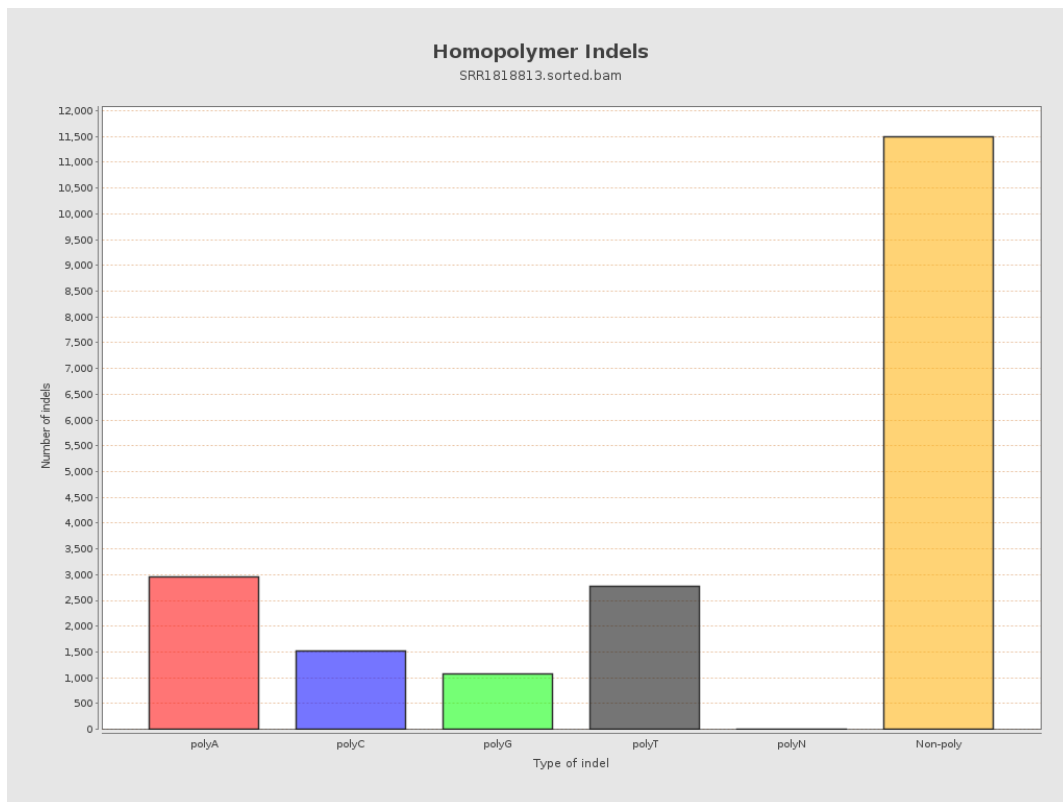
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

