

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:28:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819088.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_SRR1819088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:28:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,344,454
Mapped reads	1,195,444 / 88.92%
Unmapped reads	149,010 / 11.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,246 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	90,866 / 6.76%
Duplication rate	5.96%
Clipped reads	1,199,584 / 89.22%

2.2. ACGT Content

Number/percentage of A's	16,759,554 / 24.52%
Number/percentage of C's	12,137,648 / 17.76%
Number/percentage of T's	21,497,404 / 31.45%
Number/percentage of G's	17,959,752 / 26.27%
Number/percentage of N's	886 / 0%
GC Percentage	44.03%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2395
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2.4. Mapping Quality

Mean Mapping Quality	44.27
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2.5. Mismatches and indels

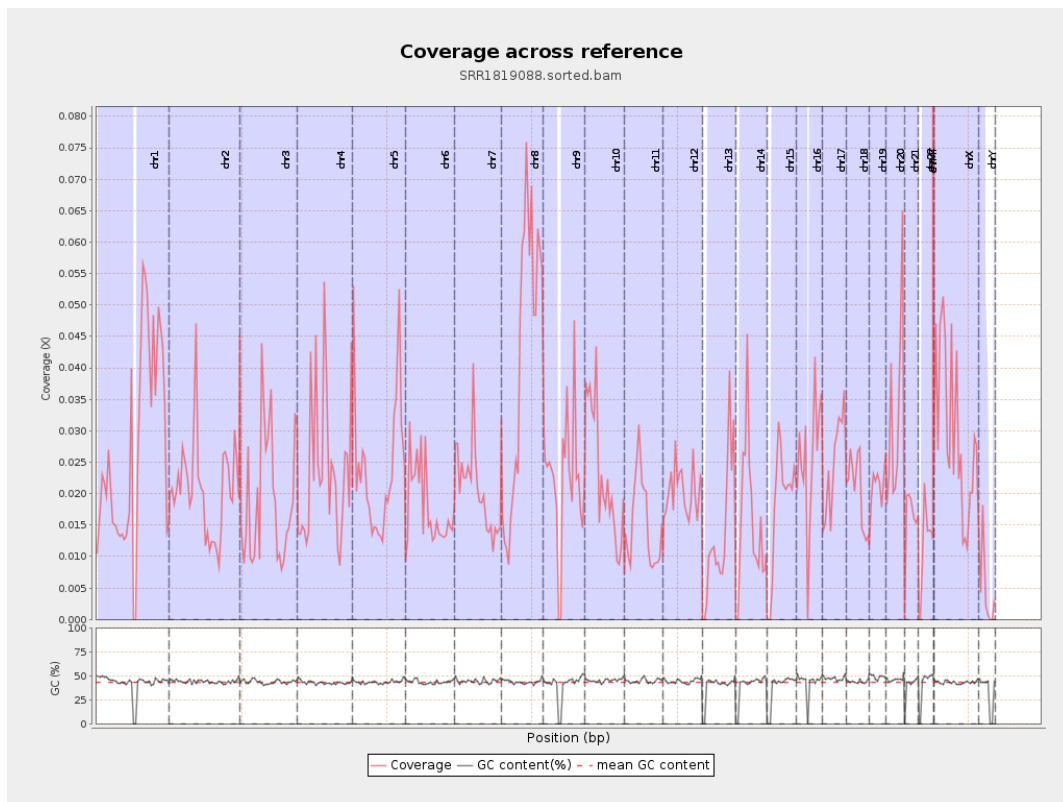
General error rate	0.67%
Mismatches	446,683
Insertions	4,308
Mapped reads with at least one insertion	0.36%
Deletions	25,512
Mapped reads with at least one deletion	2.11%
Homopolymer indels	41.5%

2.6. Chromosome stats

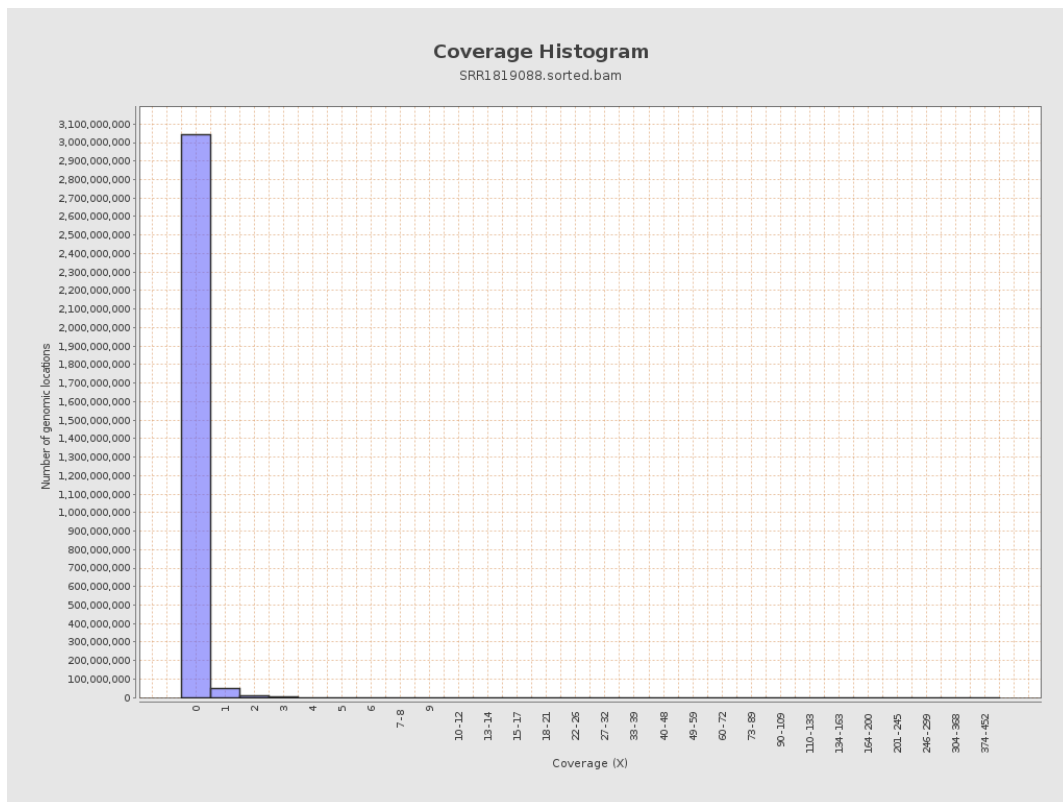
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6744386	0.0271	0.3701
chr2	243199373	5039086	0.0207	0.3158
chr3	198022430	3800352	0.0192	0.1666
chr4	191154276	4548576	0.0238	0.2208
chr5	180915260	4332432	0.0239	0.1864
chr6	171115067	3047871	0.0178	0.1808
chr7	159138663	3274206	0.0206	0.2789

chr8	146364022	5998479	0.041	0.2781
chr9	141213431	3129234	0.0222	0.2356
chr10	135534747	3126239	0.0231	0.2558
chr11	135006516	2049131	0.0152	0.2203
chr12	133851895	2726646	0.0204	0.1722
chr13	115169878	1564891	0.0136	0.1389
chr14	107349540	1661625	0.0155	0.1496
chr15	102531392	1891366	0.0184	0.1644
chr16	90354753	2326988	0.0258	0.2022
chr17	81195210	2021816	0.0249	0.2002
chr18	78077248	1598399	0.0205	0.3259
chr19	59128983	1265674	0.0214	0.2558
chr20	63025520	2057781	0.0326	0.2232
chr21	48129895	778329	0.0162	0.1782
chr22	51304566	587937	0.0115	0.1295
chrMT	16571	22356	1.3491	1.4419
chrX	155270560	4536883	0.0292	0.2213
chrY	59373566	268042	0.0045	0.1712

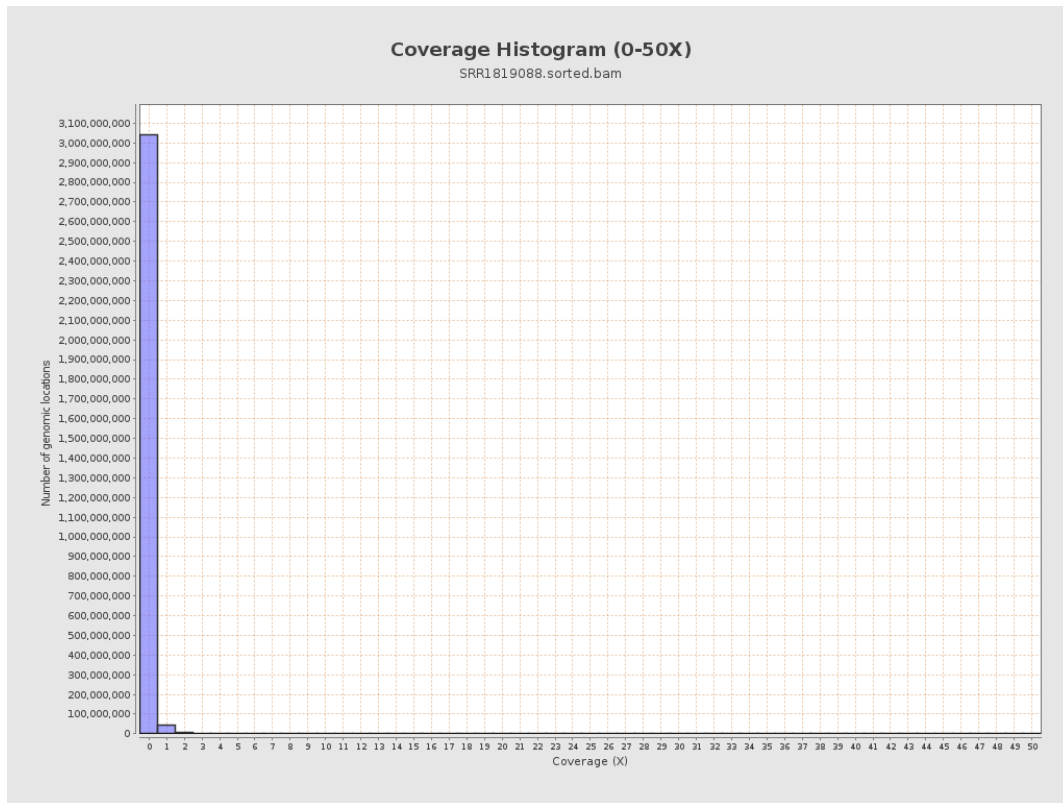
3. Results : Coverage across reference



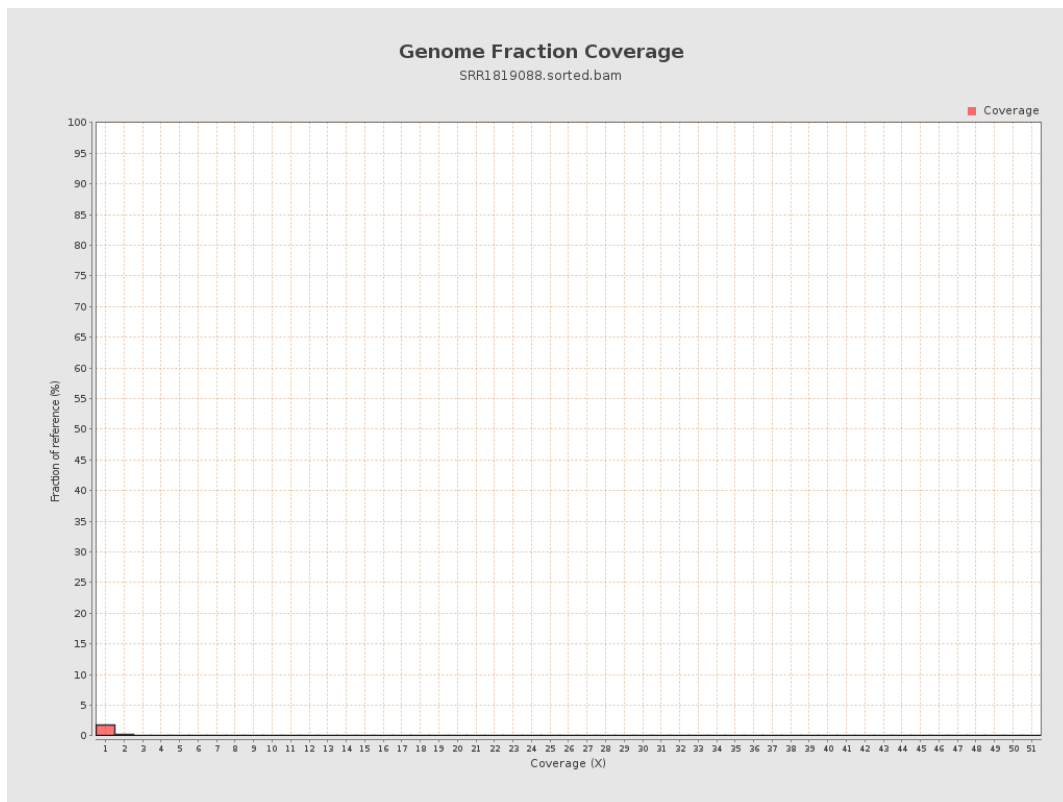
4. Results : Coverage Histogram



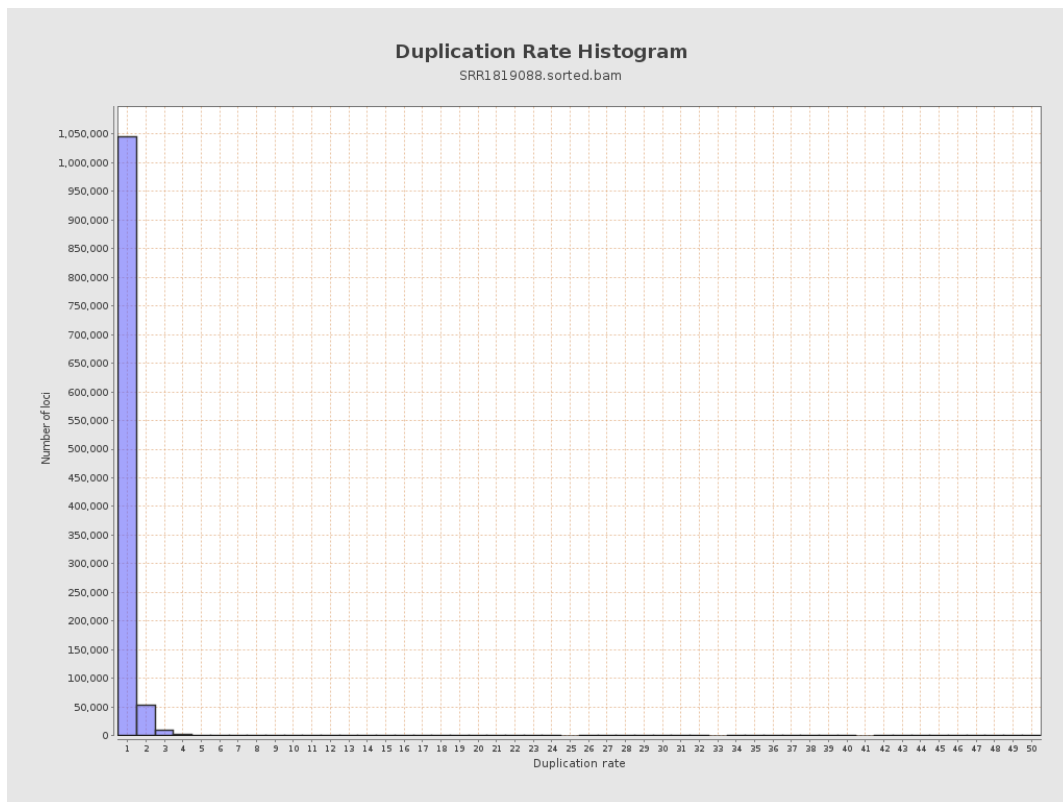
5. Results : Coverage Histogram (0-50X)



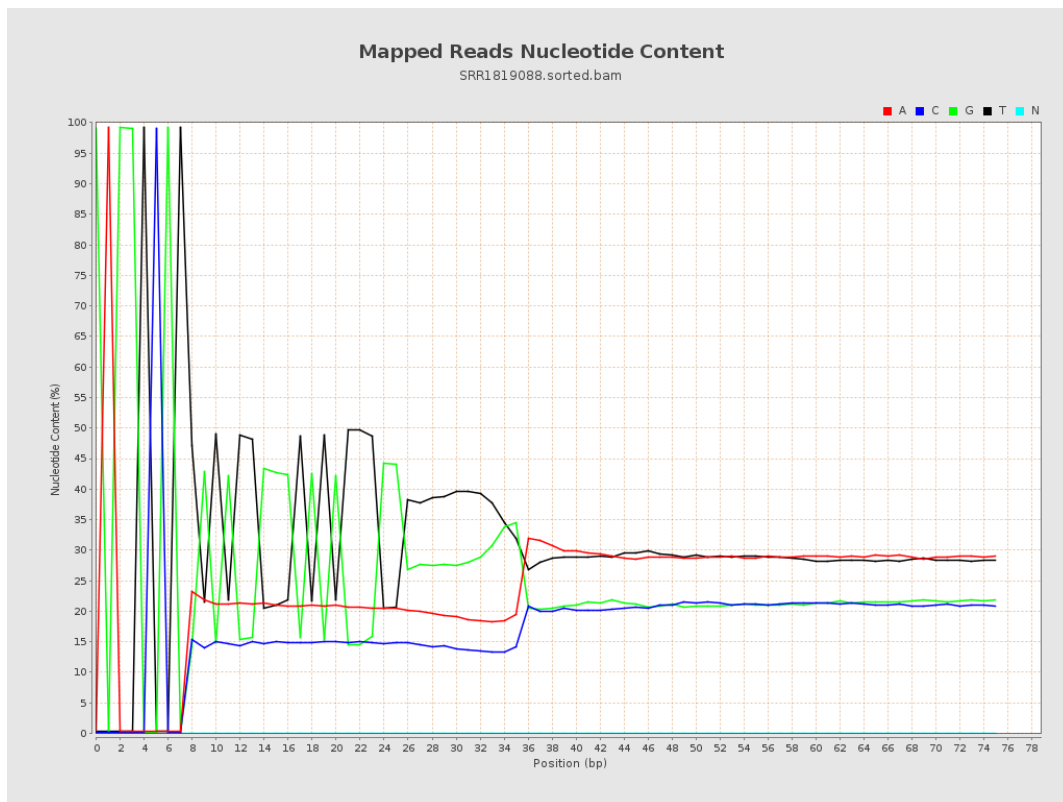
6. Results : Genome Fraction Coverage



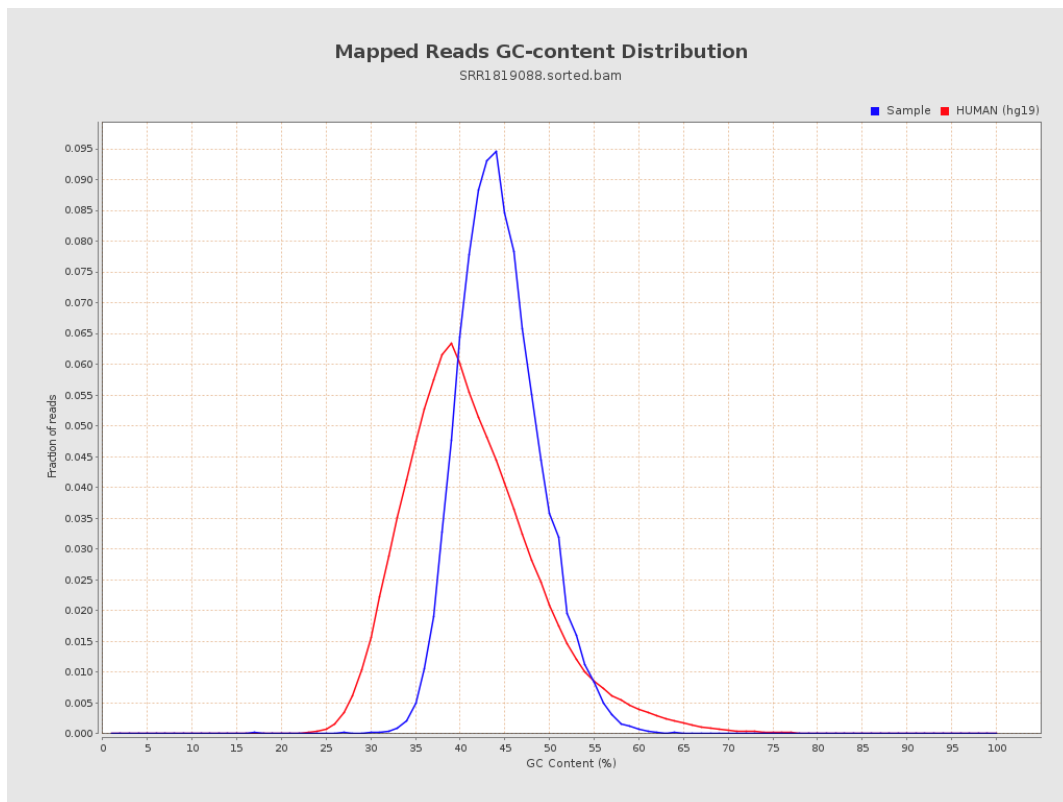
7. Results : Duplication Rate Histogram



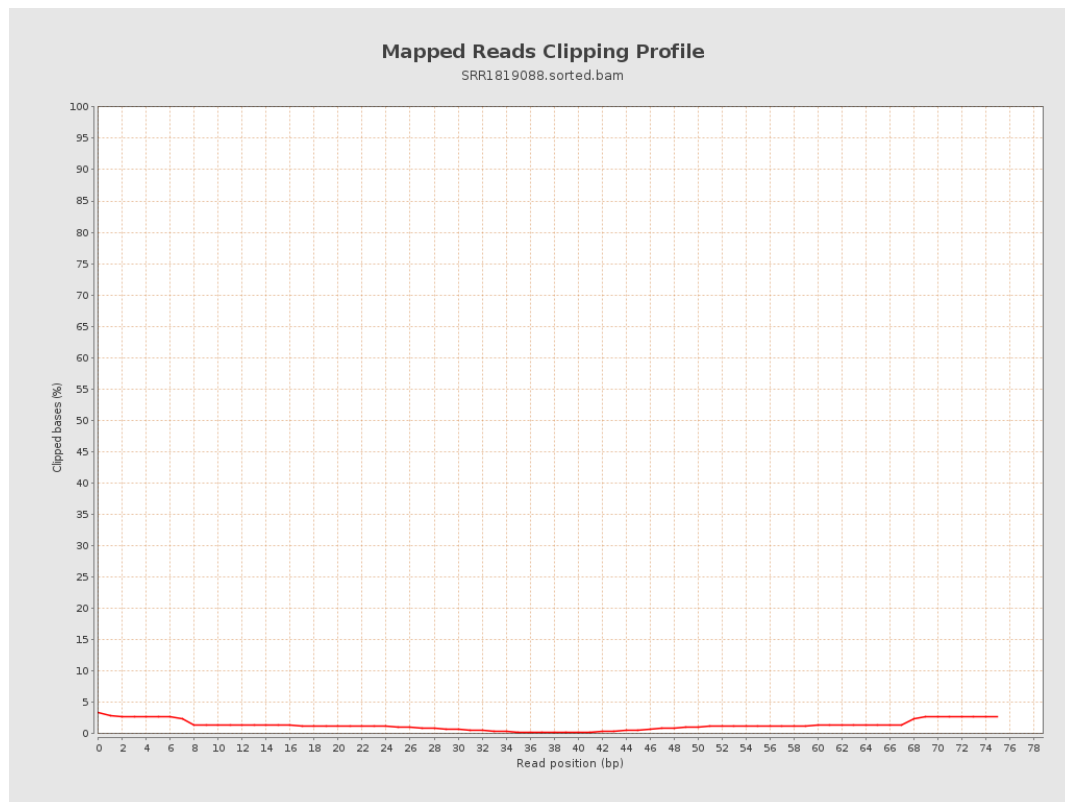
8. Results : Mapped Reads Nucleotide Content



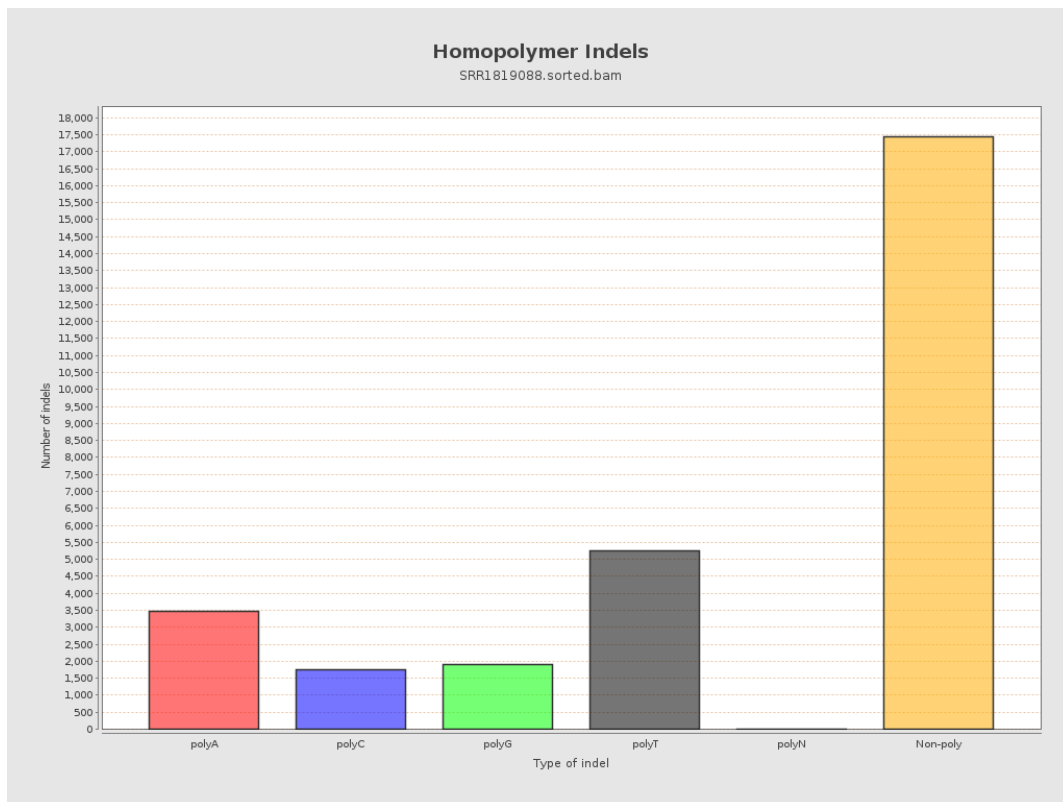
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

