

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:39:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818808.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_SRR1818808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818808.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:39:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818808.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	922,167
Mapped reads	893,955 / 96.94%
Unmapped reads	28,212 / 3.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,593 / 0.71%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	264,195 / 28.65%
Duplication rate	26.32%
Clipped reads	890,697 / 96.59%

2.2. ACGT Content

Number/percentage of A's	16,614,169 / 27.35%
Number/percentage of C's	12,852,944 / 21.16%
Number/percentage of T's	17,570,402 / 28.92%
Number/percentage of G's	13,705,800 / 22.56%
Number/percentage of N's	3,608 / 0.01%
GC Percentage	43.72%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.2652
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2.4. Mapping Quality

Mean Mapping Quality	47.76
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2.5. Mismatches and indels

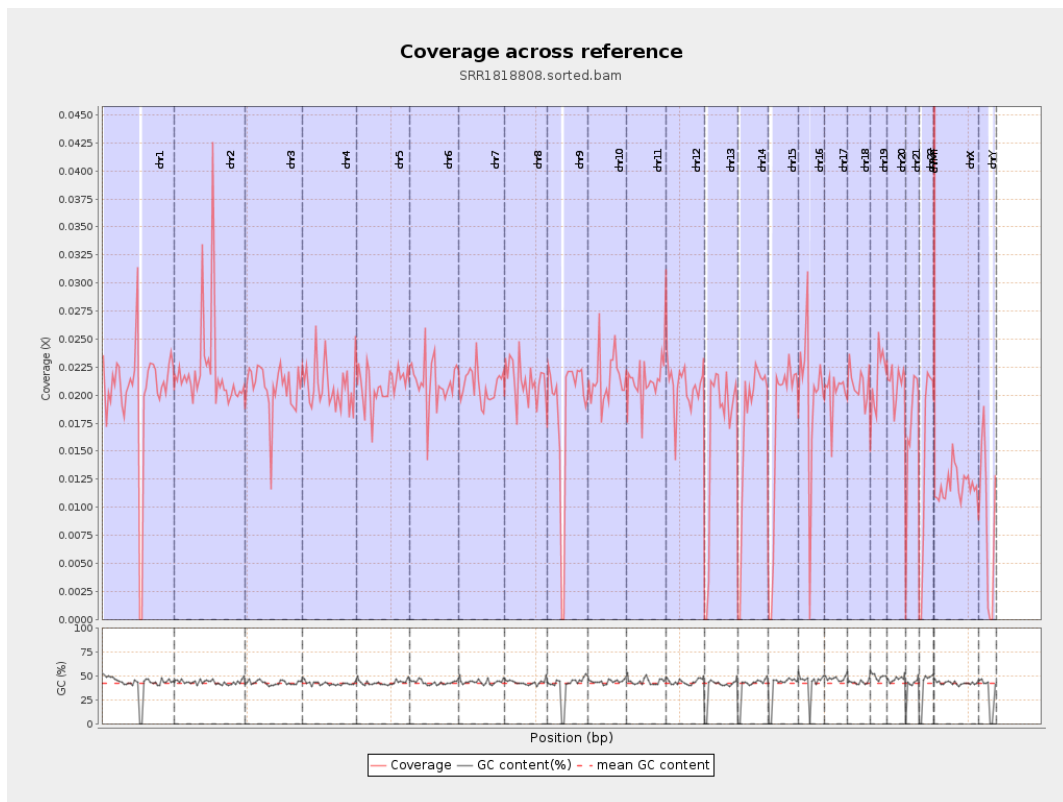
General error rate	0.53%
Mismatches	308,917
Insertions	6,999
Mapped reads with at least one insertion	0.77%
Deletions	15,740
Mapped reads with at least one deletion	1.74%
Homopolymer indels	43.69%

2.6. Chromosome stats

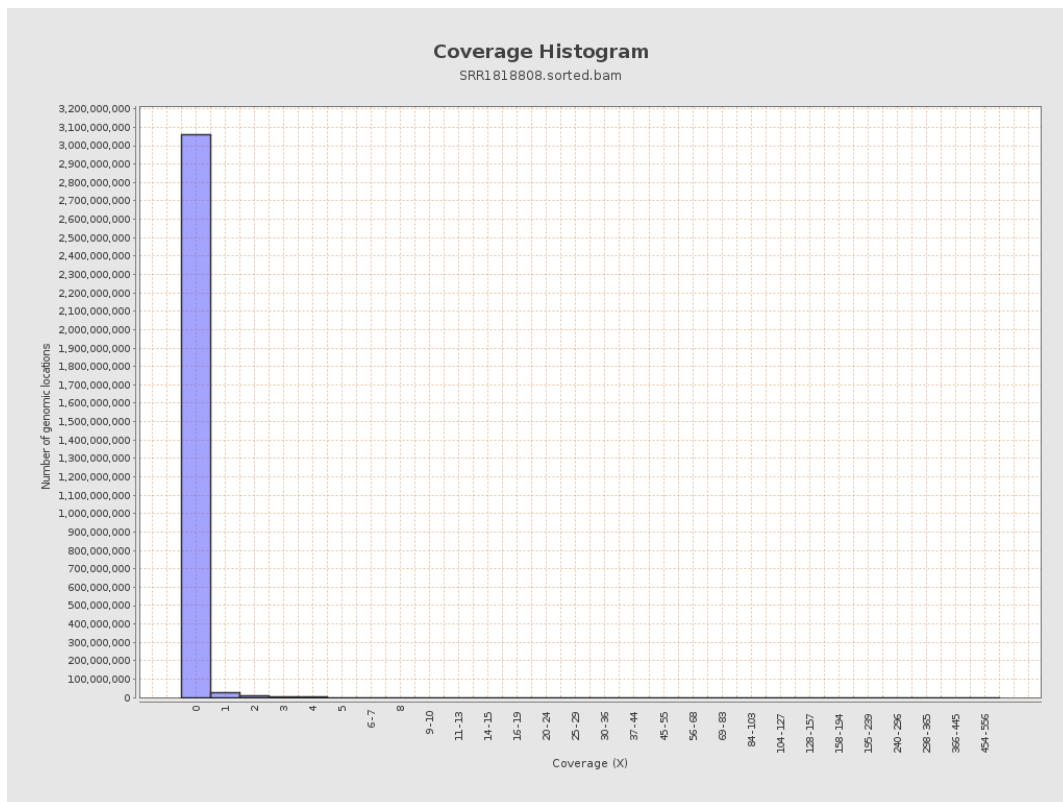
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5018539	0.0201	0.3329
chr2	243199373	5387762	0.0222	0.4295
chr3	198022430	4092595	0.0207	0.2119
chr4	191154276	3987487	0.0209	0.2313
chr5	180915260	3768887	0.0208	0.2186
chr6	171115067	3614548	0.0211	0.2333
chr7	159138663	3315172	0.0208	0.2395

chr8	146364022	3108016	0.0212	0.2321
chr9	141213431	2628338	0.0186	0.2318
chr10	135534747	2912321	0.0215	0.2697
chr11	135006516	2869412	0.0213	0.2339
chr12	133851895	2774498	0.0207	0.2187
chr13	115169878	1928892	0.0167	0.1886
chr14	107349540	1873101	0.0174	0.215
chr15	102531392	1764472	0.0172	0.1941
chr16	90354753	1796313	0.0199	0.2903
chr17	81195210	1646366	0.0203	0.2183
chr18	78077248	1640675	0.021	0.2824
chr19	59128983	1271409	0.0215	0.311
chr20	63025520	1328506	0.0211	0.2273
chr21	48129895	824221	0.0171	0.2051
chr22	51304566	753131	0.0147	0.1968
chrMT	16571	74328	4.4854	4.7584
chrX	155270560	1861419	0.012	0.1739
chrY	59373566	531904	0.009	0.4278

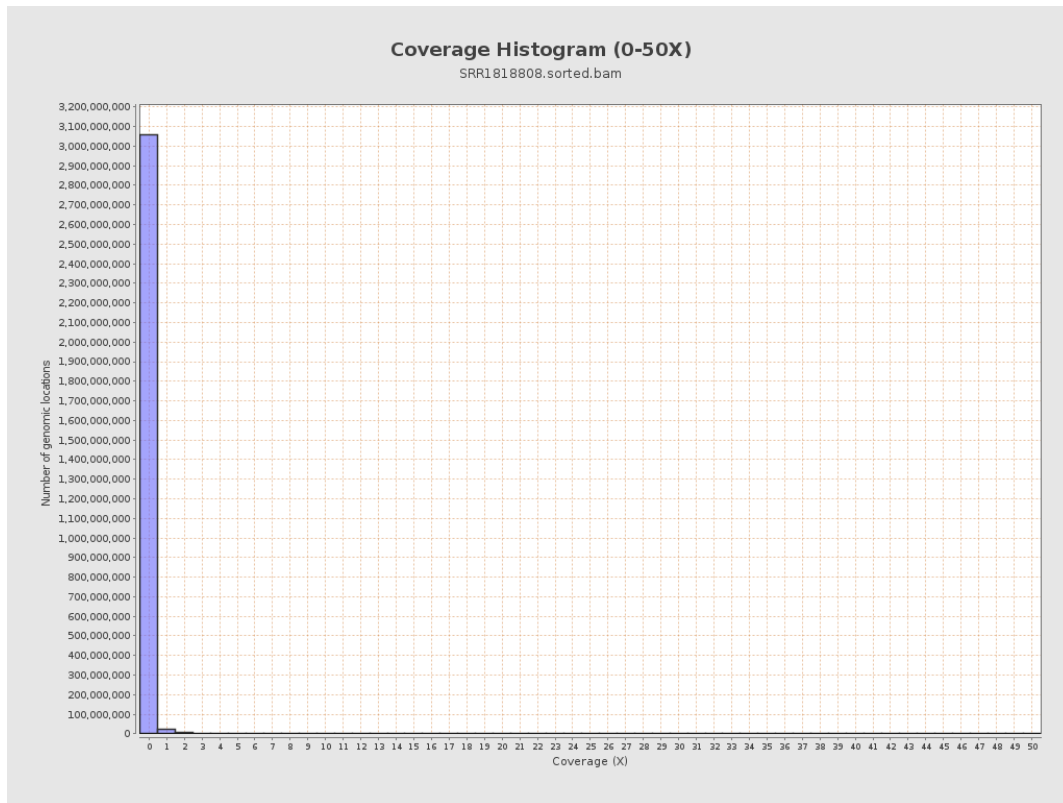
3. Results : Coverage across reference



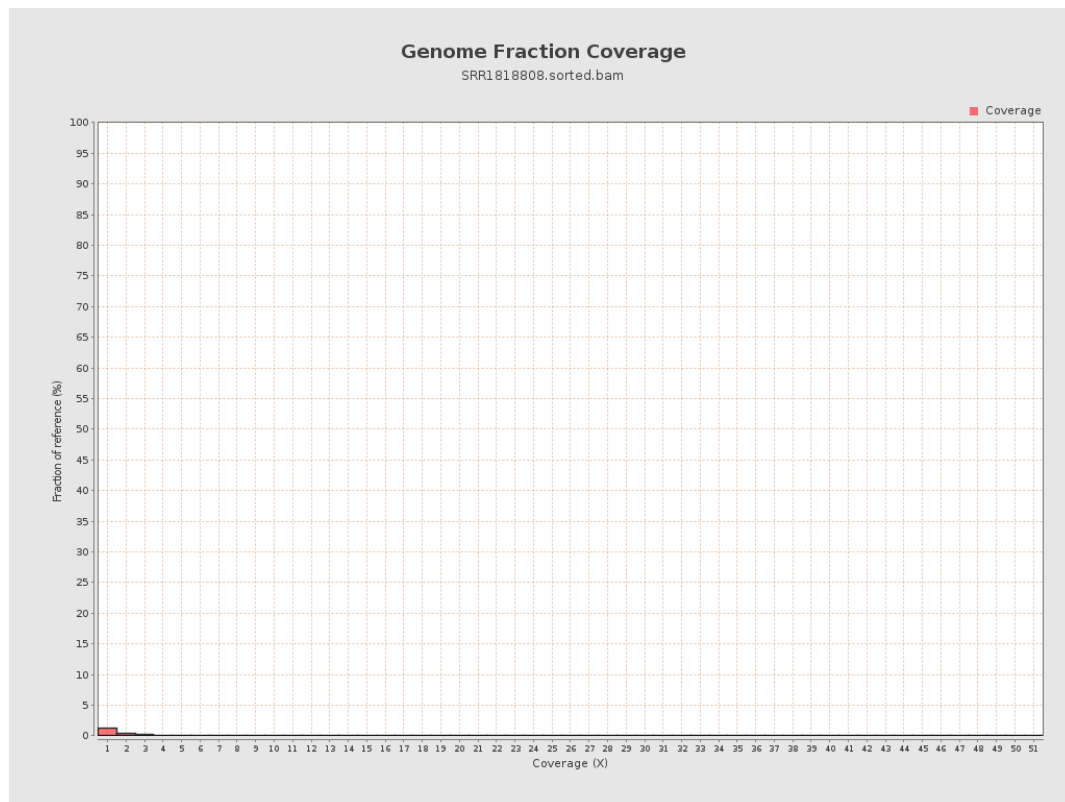
4. Results : Coverage Histogram



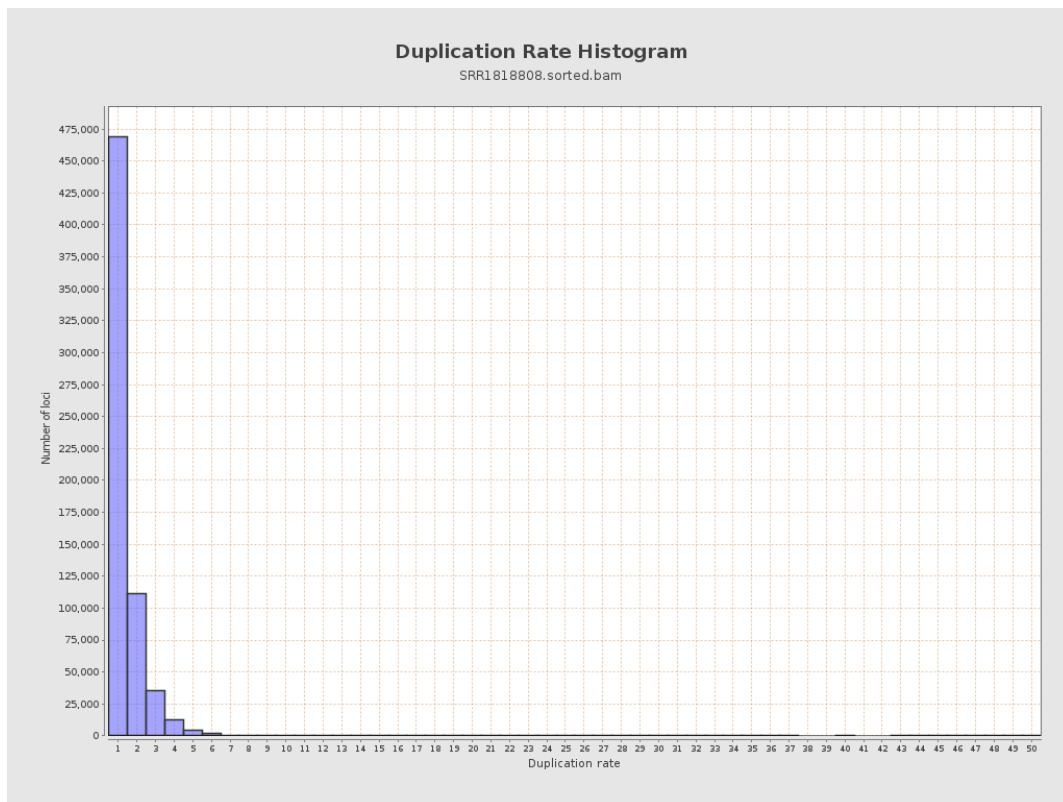
5. Results : Coverage Histogram (0-50X)



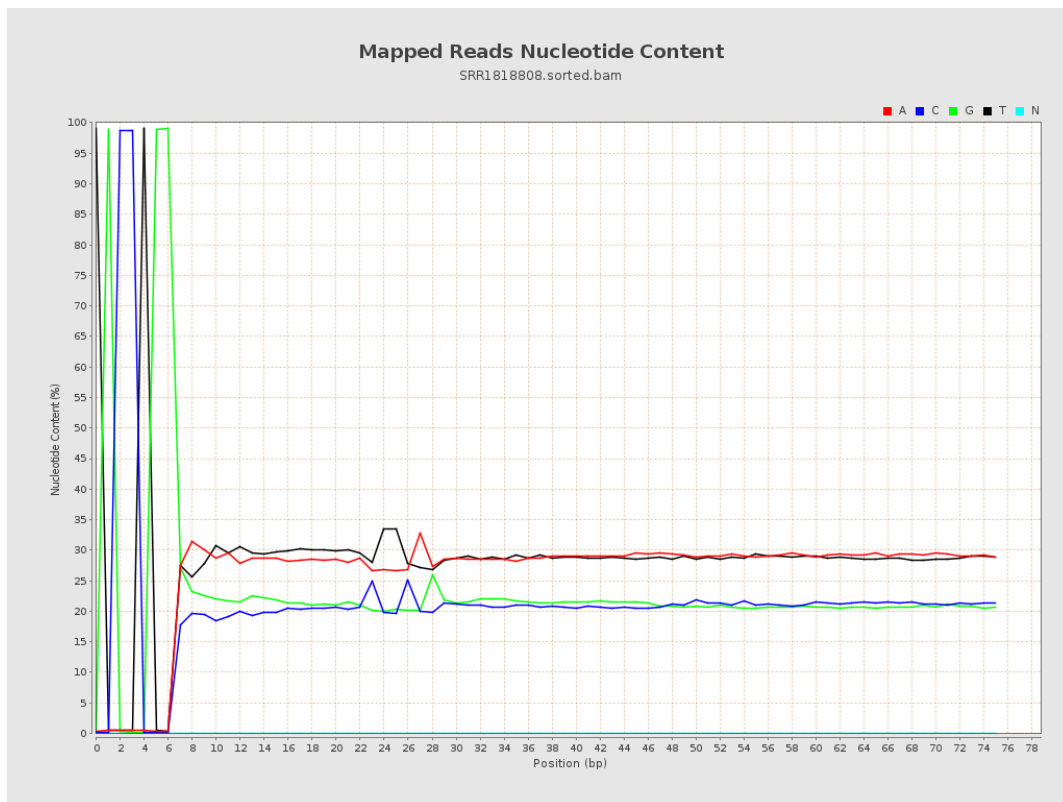
6. Results : Genome Fraction Coverage



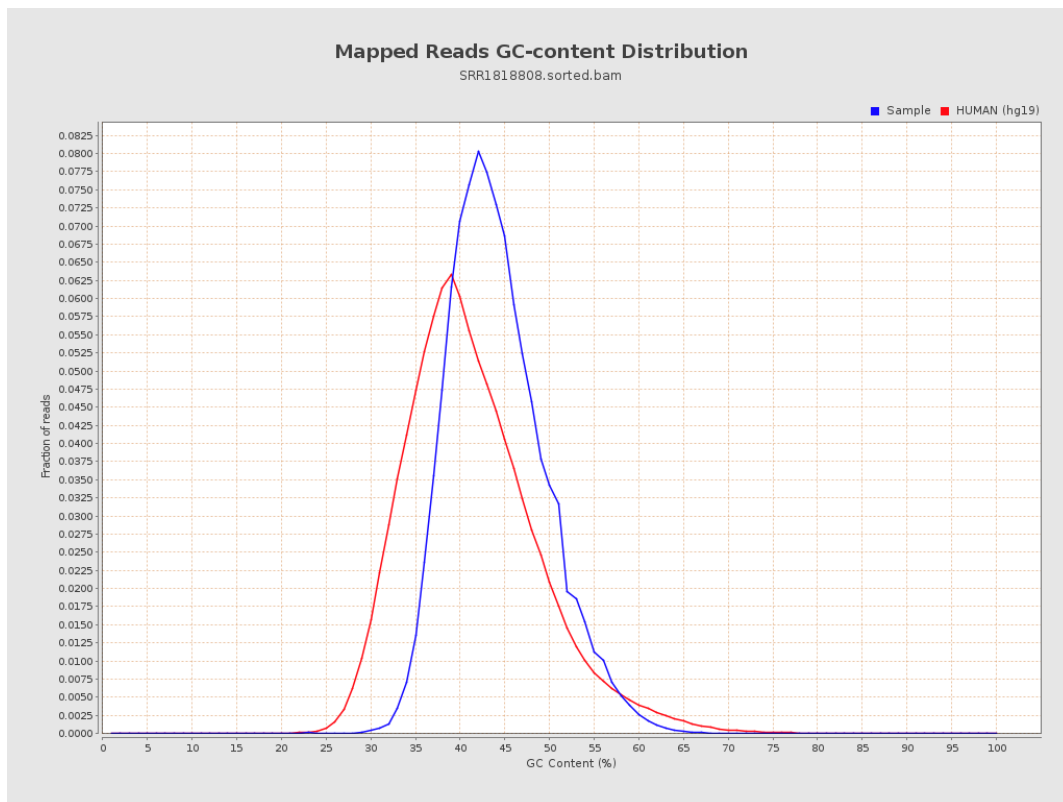
7. Results : Duplication Rate Histogram



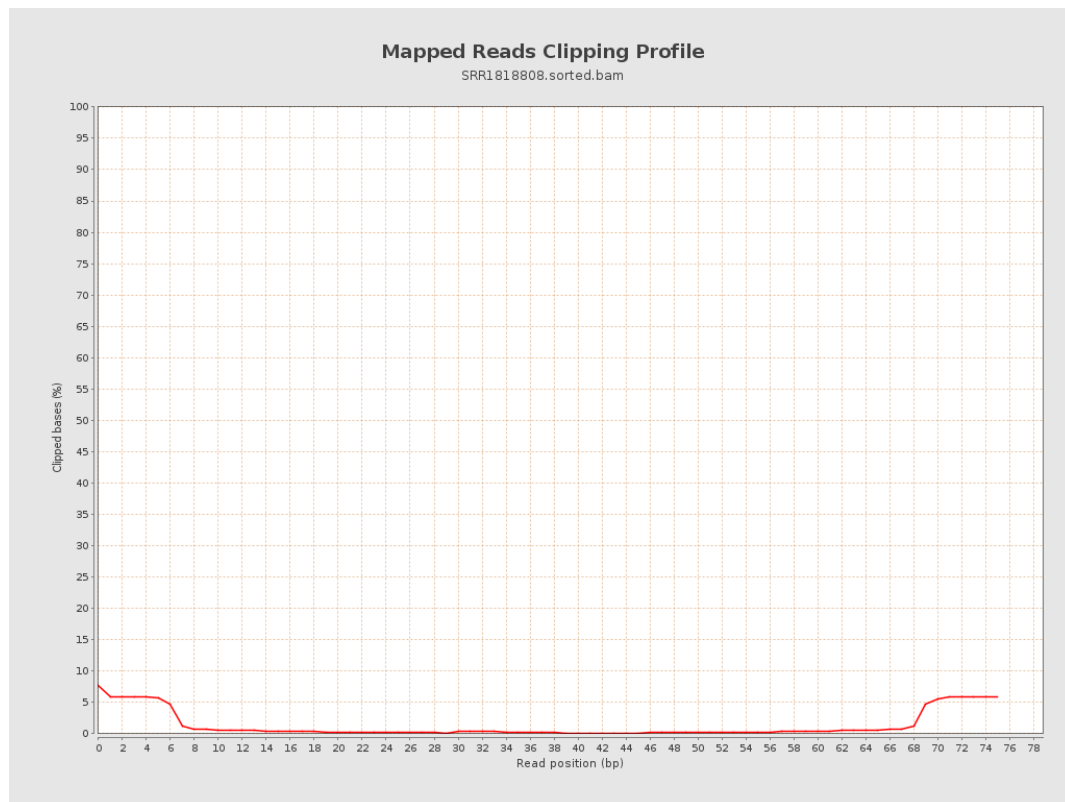
8. Results : Mapped Reads Nucleotide Content



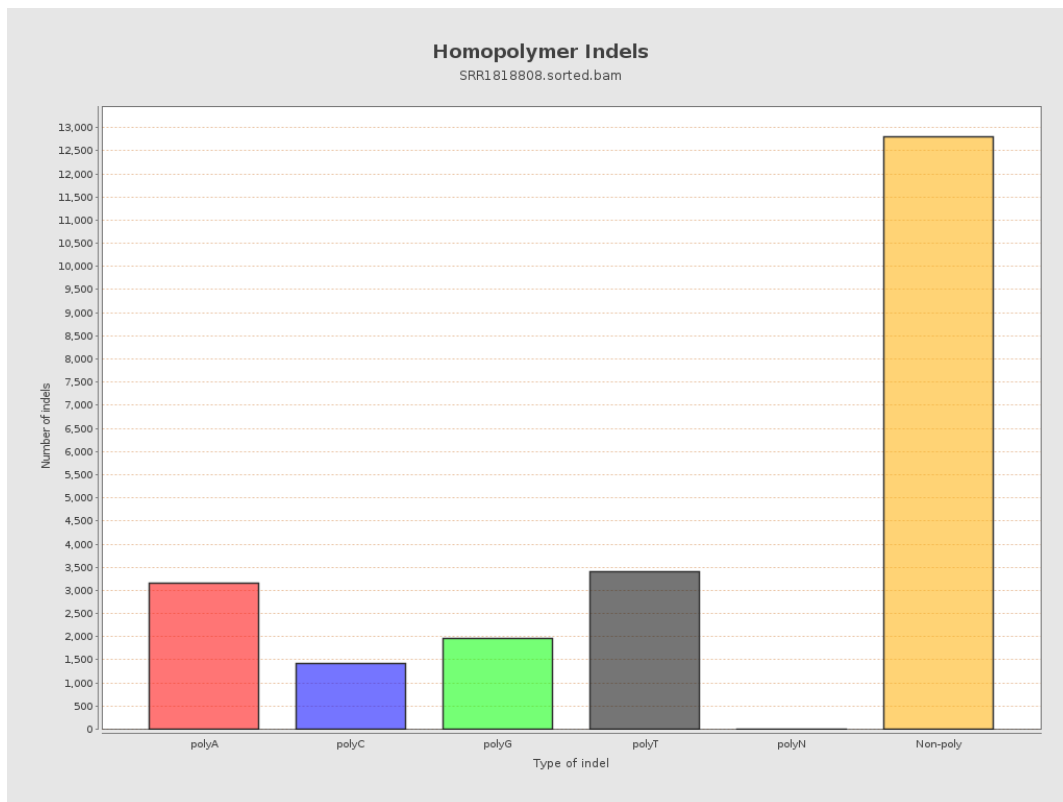
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

