

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:31:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082936.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_SRR3082936 /home/luna/Desktop/database/homo_hsa.fa SRR3082936.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:31:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,845,179
Mapped reads	1,699,817 / 92.12%
Unmapped reads	145,362 / 7.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,221 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	78,571 / 4.26%
Duplication rate	3.79%
Clipped reads	689,013 / 37.34%

2.2. ACGT Content

Number/percentage of A's	32,152,471 / 27.95%
Number/percentage of C's	21,138,680 / 18.37%
Number/percentage of T's	36,756,489 / 31.95%
Number/percentage of G's	24,990,656 / 21.72%
Number/percentage of N's	5,246 / 0%
GC Percentage	40.1%

2.3. Coverage

Mean	0.0372

Standard Deviation	0.3071
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2.4. Mapping Quality

Mean Mapping Quality	46.4
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2.5. Mismatches and indels

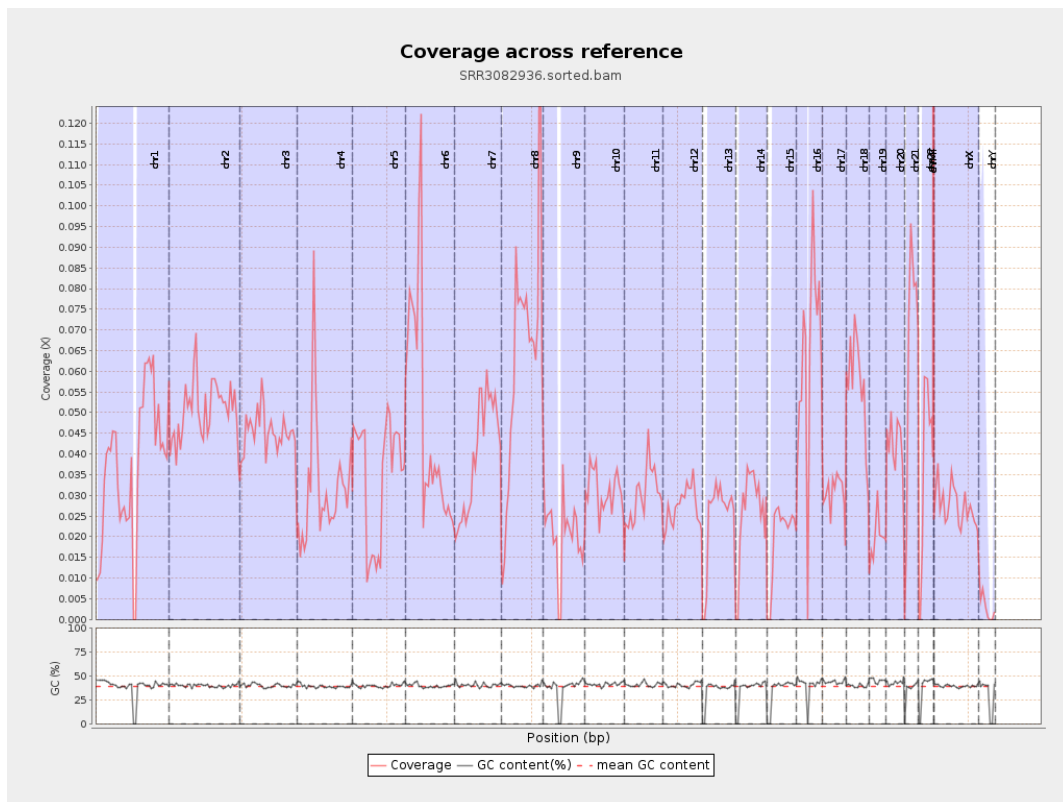
General error rate	0.73%
Mismatches	823,895
Insertions	9,669
Mapped reads with at least one insertion	0.56%
Deletions	27,620
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.39%

2.6. Chromosome stats

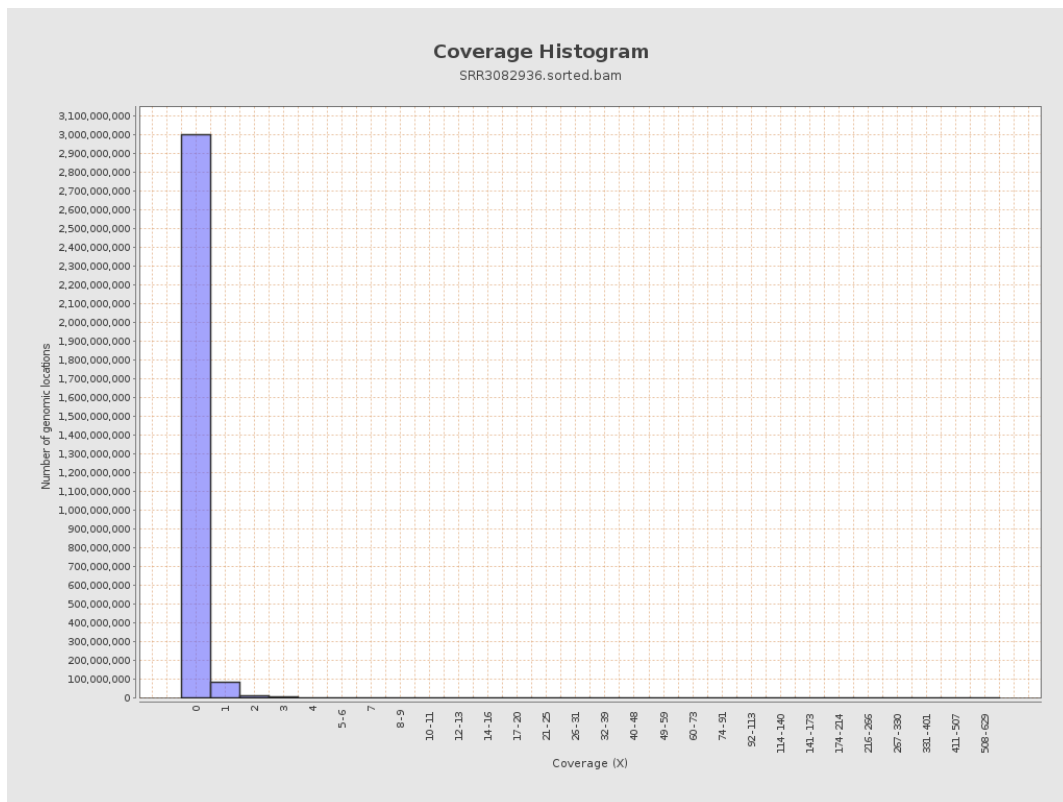
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9286657	0.0373	0.3776
chr2	243199373	12311658	0.0506	0.4358
chr3	198022430	8942157	0.0452	0.2422
chr4	191154276	6056846	0.0317	0.2105
chr5	180915260	6228470	0.0344	0.2127
chr6	171115067	8252097	0.0482	0.3311
chr7	159138663	6378018	0.0401	0.2926

chr8	146364022	9357259	0.0639	0.4254
chr9	141213431	2852638	0.0202	0.2859
chr10	135534747	4247244	0.0313	0.2383
chr11	135006516	4048525	0.03	0.2649
chr12	133851895	3662666	0.0274	0.1947
chr13	115169878	2776440	0.0241	0.1782
chr14	107349540	2782282	0.0259	0.2074
chr15	102531392	2043790	0.0199	0.1683
chr16	90354753	5750211	0.0636	0.3114
chr17	81195210	2464861	0.0304	0.2189
chr18	78077248	4442483	0.0569	0.7335
chr19	59128983	1183045	0.02	0.2905
chr20	63025520	2649383	0.042	0.2461
chr21	48129895	3064592	0.0637	0.2942
chr22	51304566	1861265	0.0363	0.2158
chrMT	16571	8949	0.54	0.8461
chrX	155270560	4259015	0.0274	0.2165
chrY	59373566	178054	0.003	0.0668

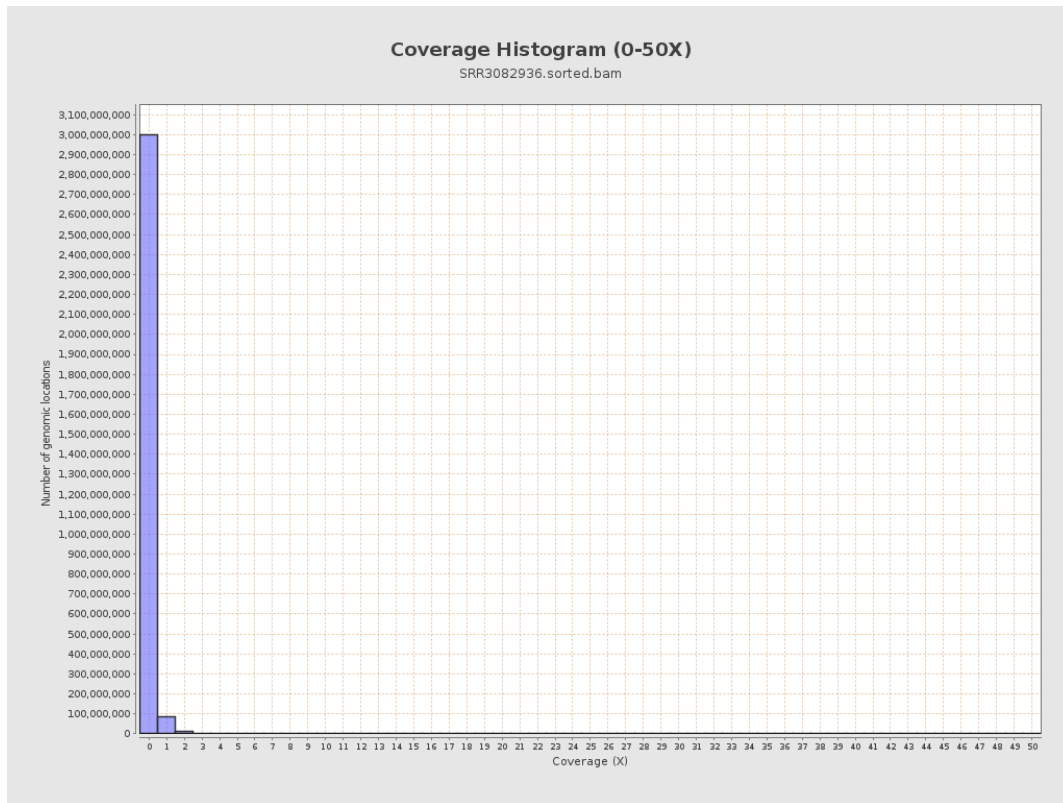
3. Results : Coverage across reference



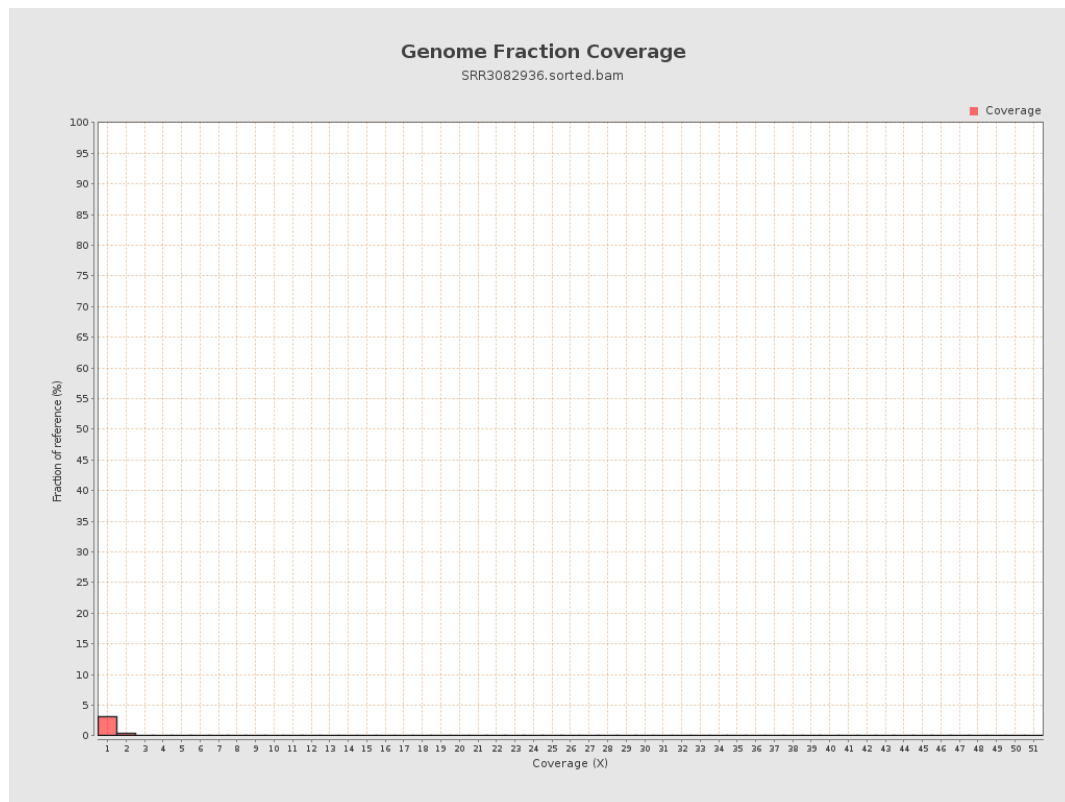
4. Results : Coverage Histogram



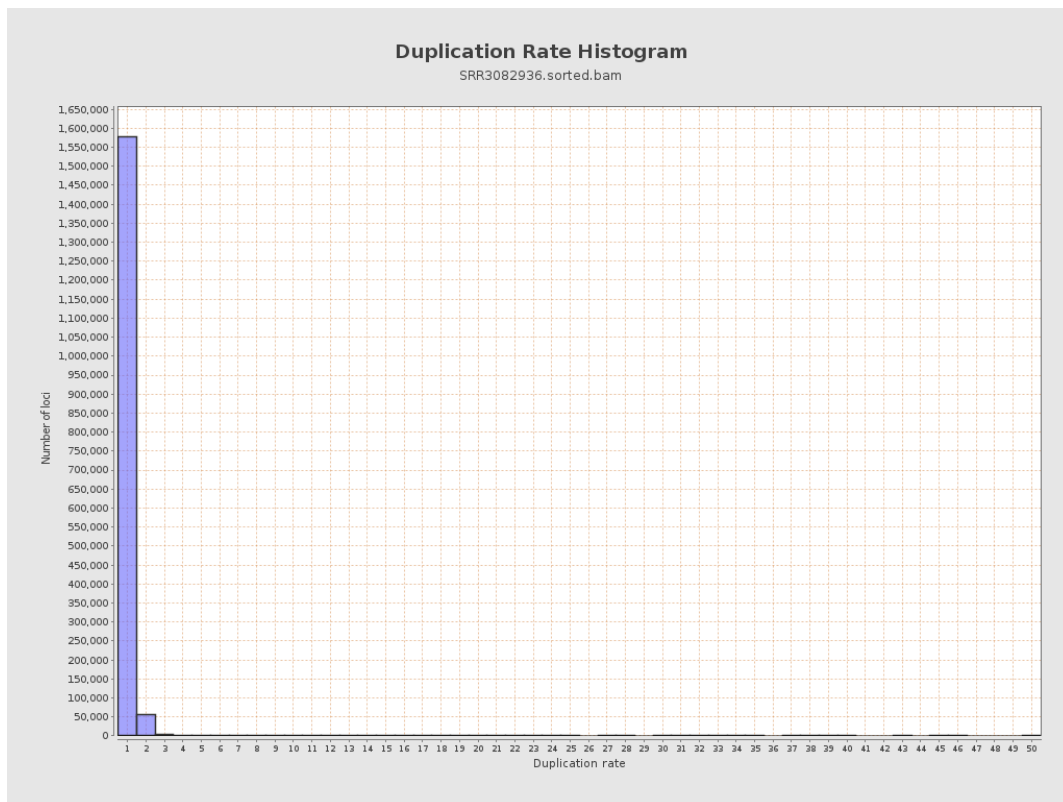
5. Results : Coverage Histogram (0-50X)



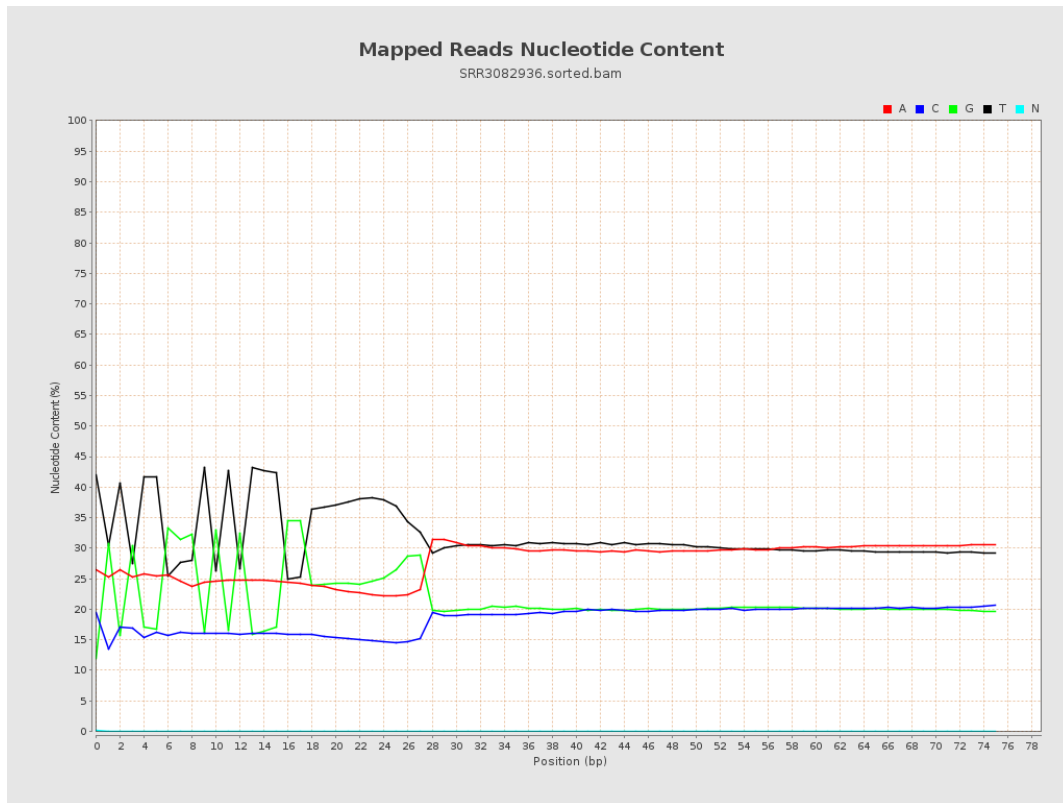
6. Results : Genome Fraction Coverage



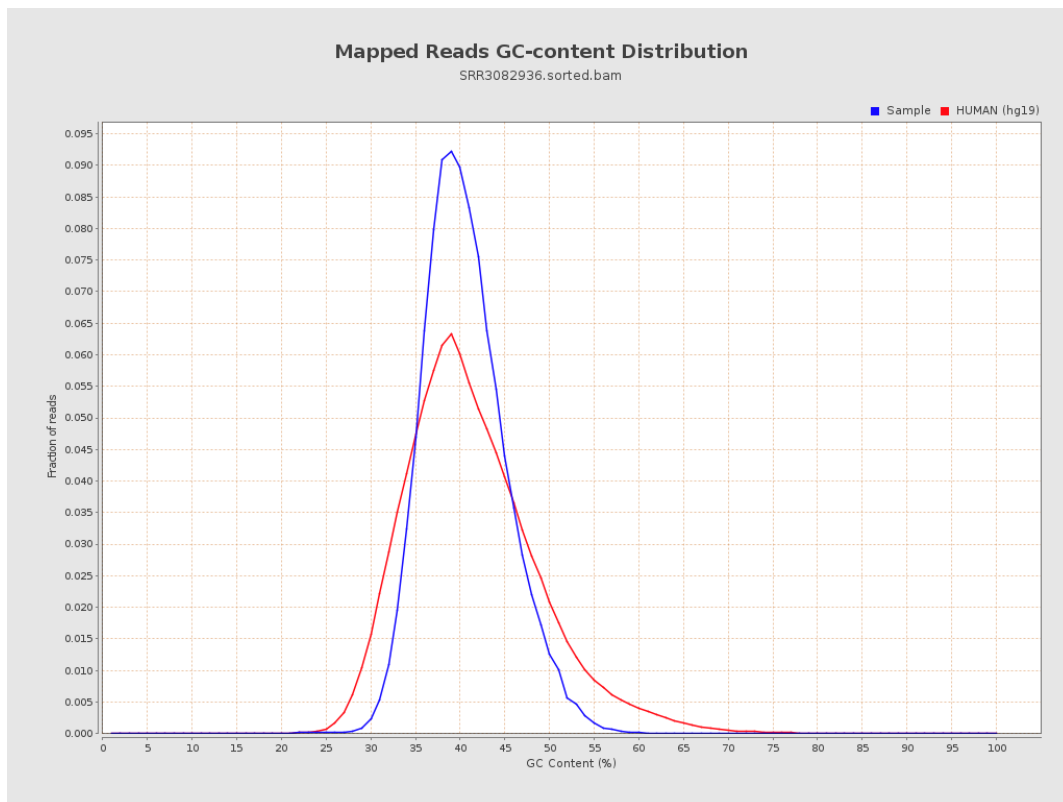
7. Results : Duplication Rate Histogram



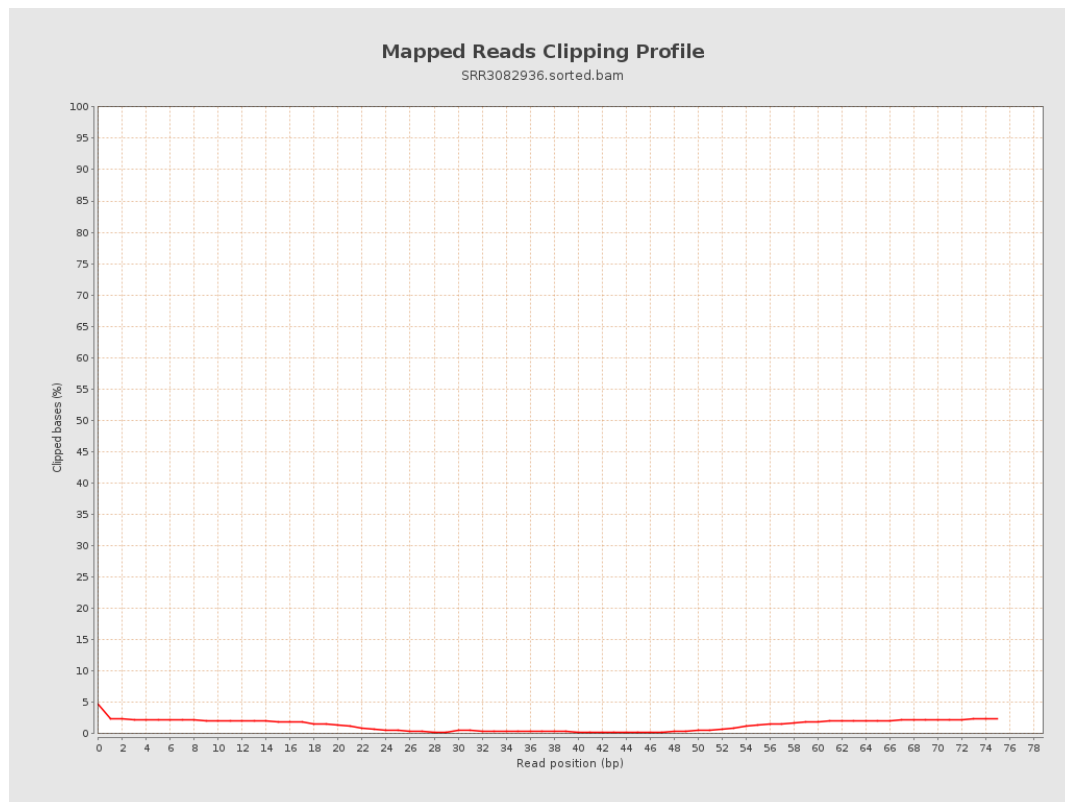
8. Results : Mapped Reads Nucleotide Content



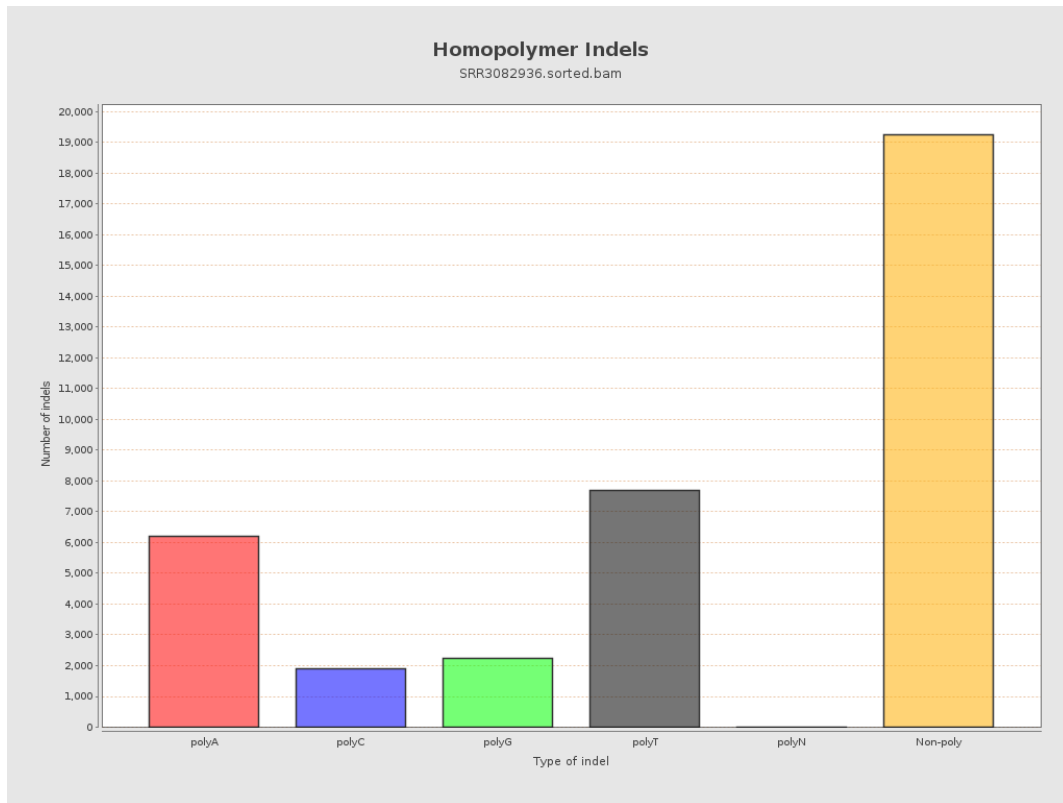
9. Results : Mapped Reads GC-content Distribution



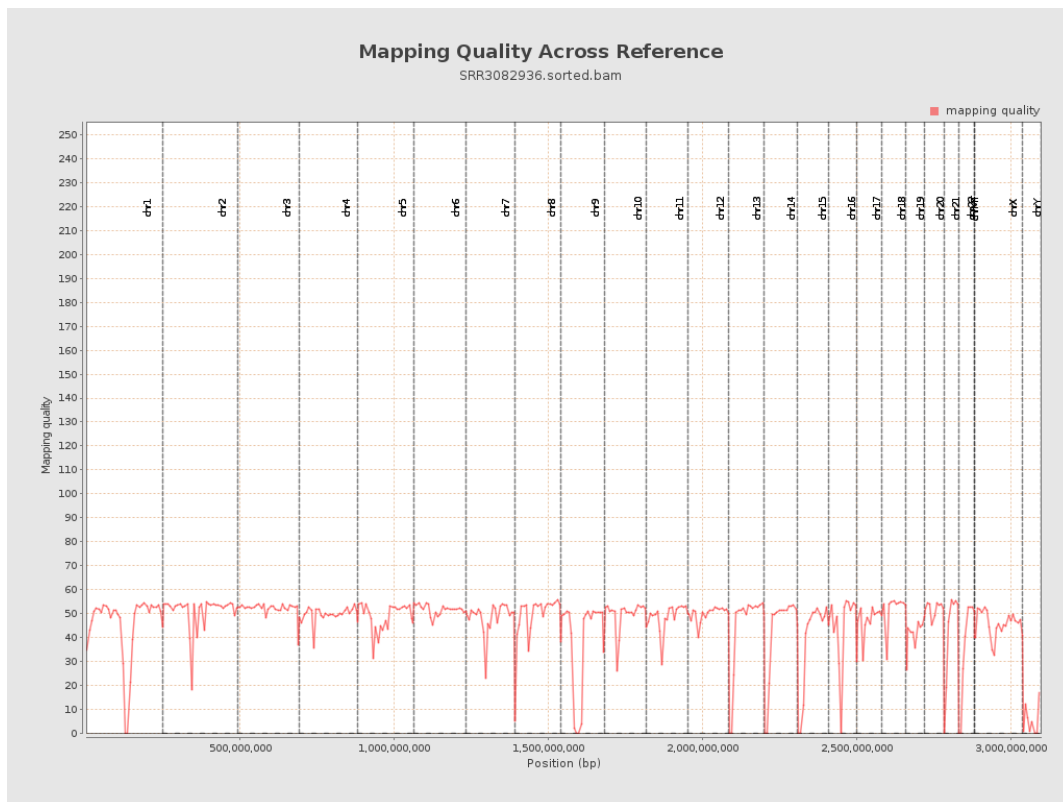
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

