

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:53:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717036.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_SRR9717036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717036.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:53:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,837,125
Mapped reads	1,665,470 / 90.66%
Unmapped reads	171,655 / 9.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,880 / 2.44%
Read min/max/mean length	30 / 101 / 101.88
Duplicated reads (estimated)	47,761 / 2.6%
Duplication rate	1.81%
Clipped reads	1,707,107 / 92.92%

2.2. ACGT Content

Number/percentage of A's	33,849,793 / 26.66%
Number/percentage of C's	25,367,205 / 19.98%
Number/percentage of T's	37,774,020 / 29.75%
Number/percentage of G's	29,946,790 / 23.59%
Number/percentage of N's	15,491 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.041

Standard Deviation	0.3609
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2.4. Mapping Quality

Mean Mapping Quality	45.54
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2.5. Mismatches and indels

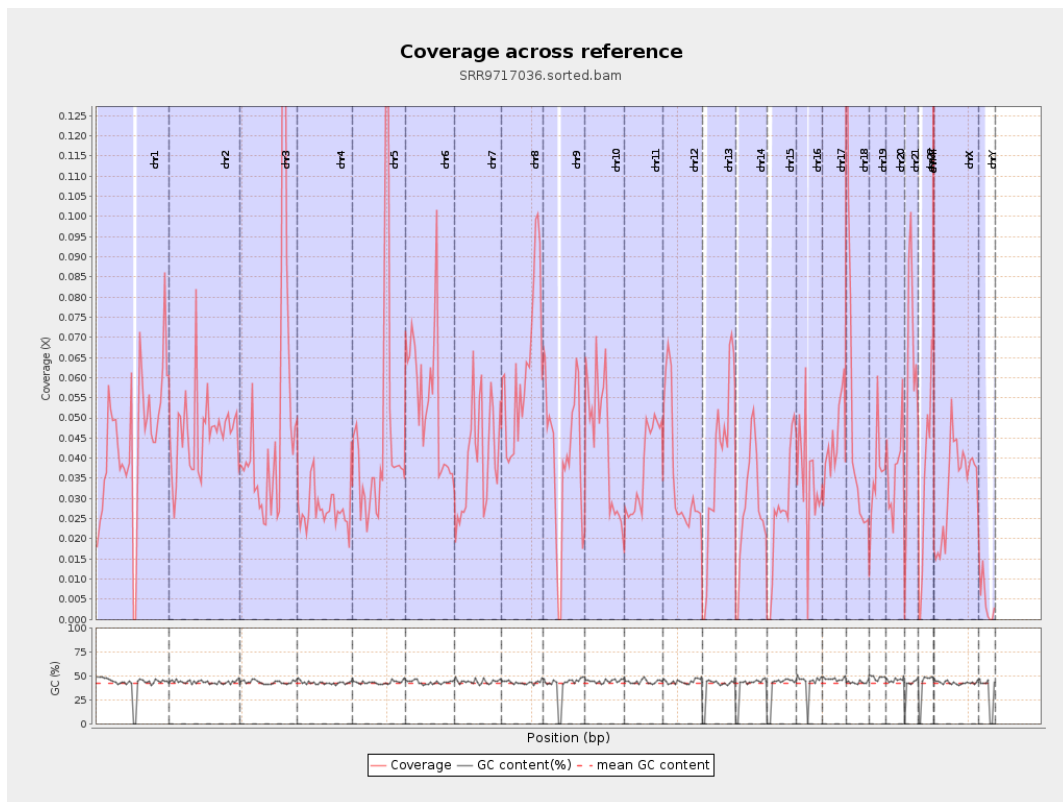
General error rate	0.79%
Mismatches	975,544
Insertions	11,345
Mapped reads with at least one insertion	0.67%
Deletions	28,077
Mapped reads with at least one deletion	1.66%
Homopolymer indels	39.86%

2.6. Chromosome stats

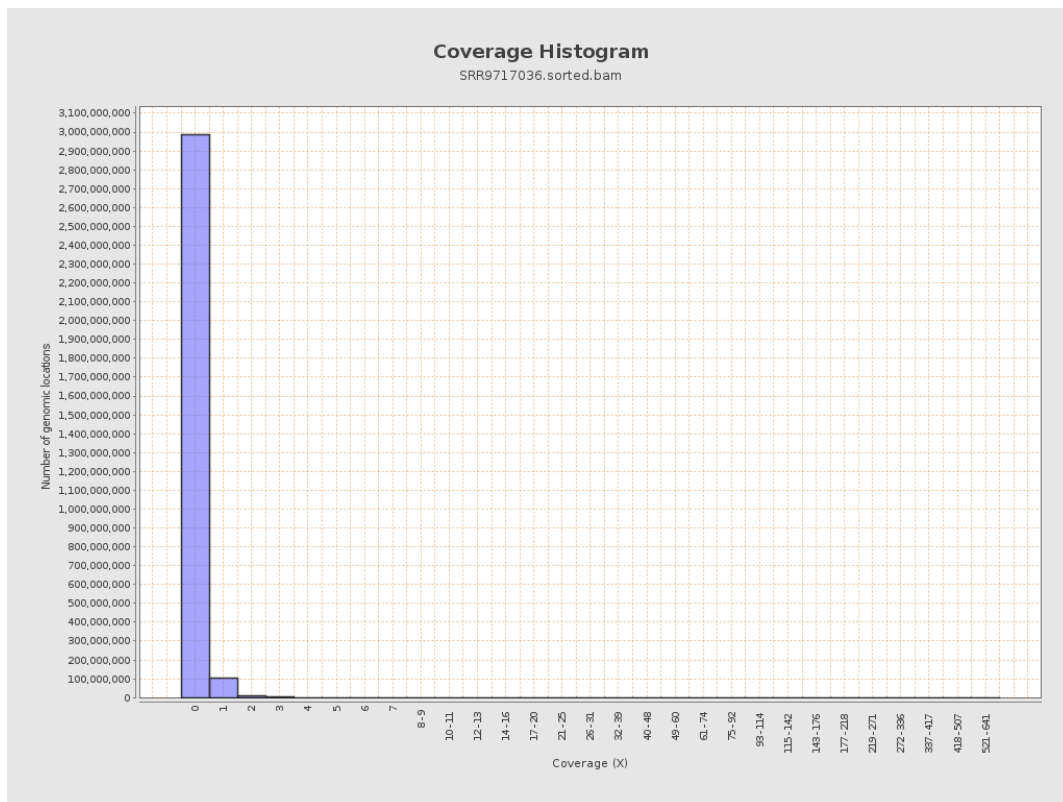
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10969997	0.044	0.5366
chr2	243199373	11185679	0.046	0.5358
chr3	198022430	9703295	0.049	0.2511
chr4	191154276	5258785	0.0275	0.1958
chr5	180915260	8175060	0.0452	0.2381
chr6	171115067	9336101	0.0546	0.2978
chr7	159138663	6432775	0.0404	0.5192

chr8	146364022	9157156	0.0626	0.4785
chr9	141213431	5599519	0.0397	0.3375
chr10	135534747	6023624	0.0444	0.3464
chr11	135006516	5083336	0.0377	0.2998
chr12	133851895	4666950	0.0349	0.2071
chr13	115169878	4511367	0.0392	0.2177
chr14	107349540	2995045	0.0279	0.2079
chr15	102531392	2742139	0.0267	0.179
chr16	90354753	3101332	0.0343	0.2385
chr17	81195210	3593810	0.0443	0.2617
chr18	78077248	3875640	0.0496	0.6558
chr19	59128983	2158754	0.0365	0.425
chr20	63025520	2351105	0.0373	0.2492
chr21	48129895	2869507	0.0596	0.2826
chr22	51304566	1777848	0.0347	0.2088
chrMT	16571	3980	0.2402	1.2742
chrX	155270560	5157026	0.0332	0.2515
chrY	59373566	272254	0.0046	0.1403

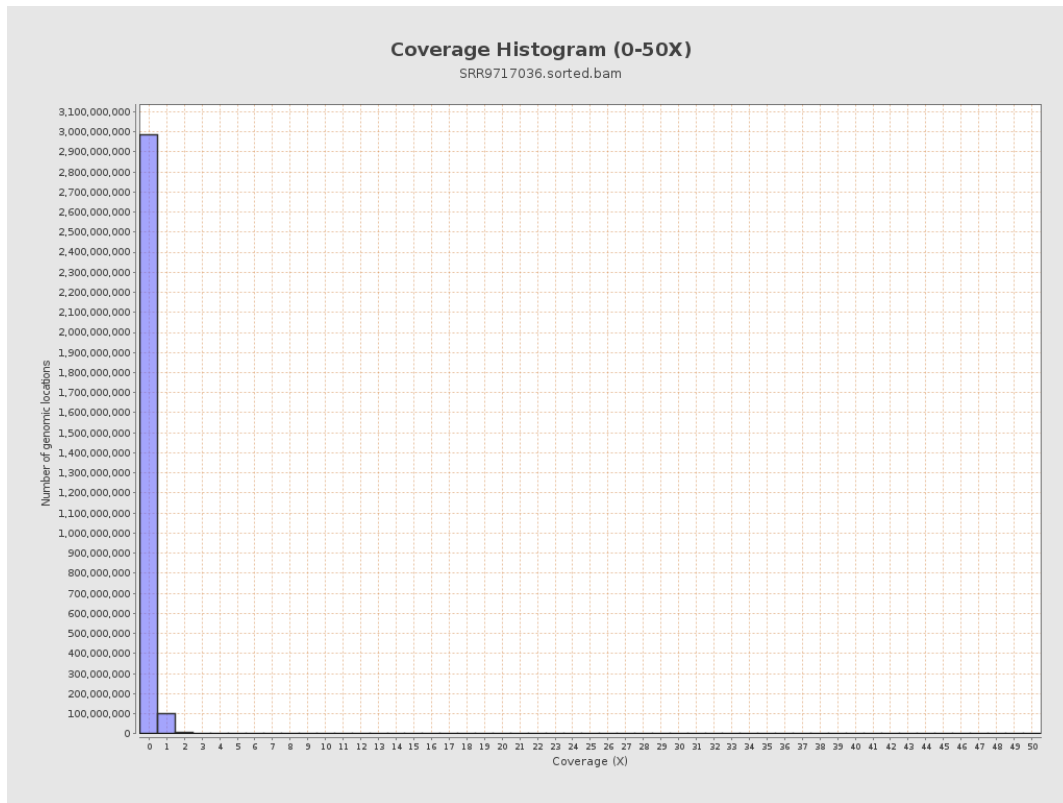
3. Results : Coverage across reference



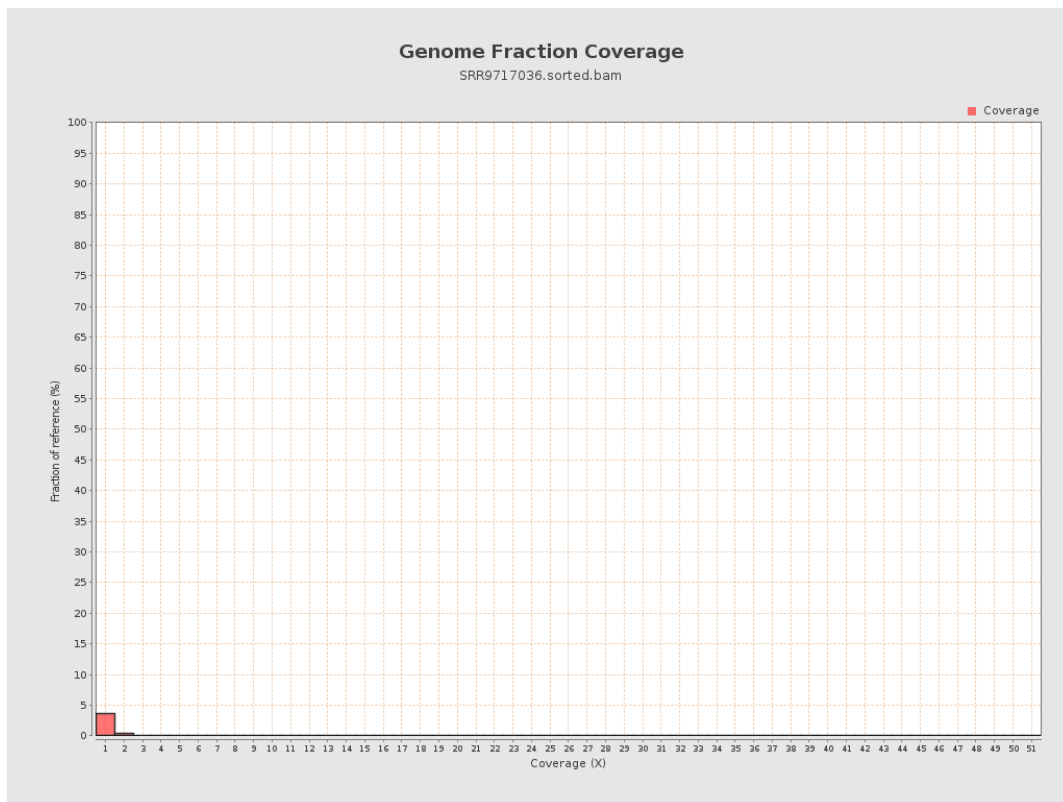
4. Results : Coverage Histogram



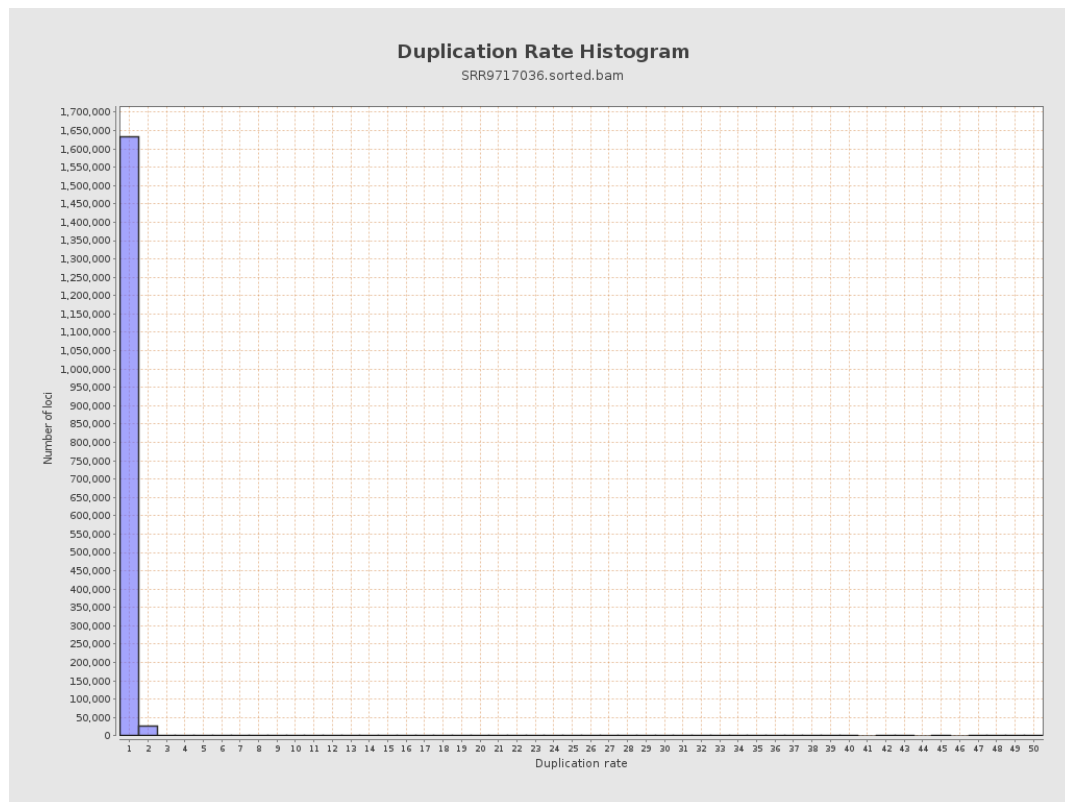
5. Results : Coverage Histogram (0-50X)



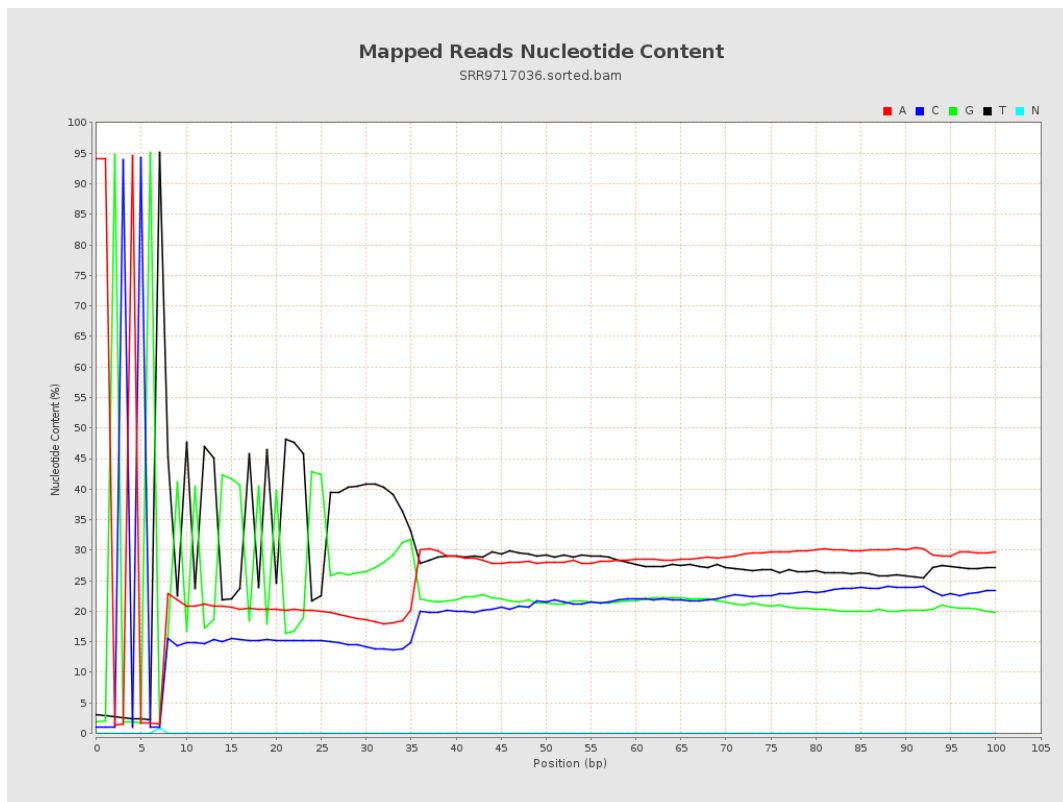
6. Results : Genome Fraction Coverage



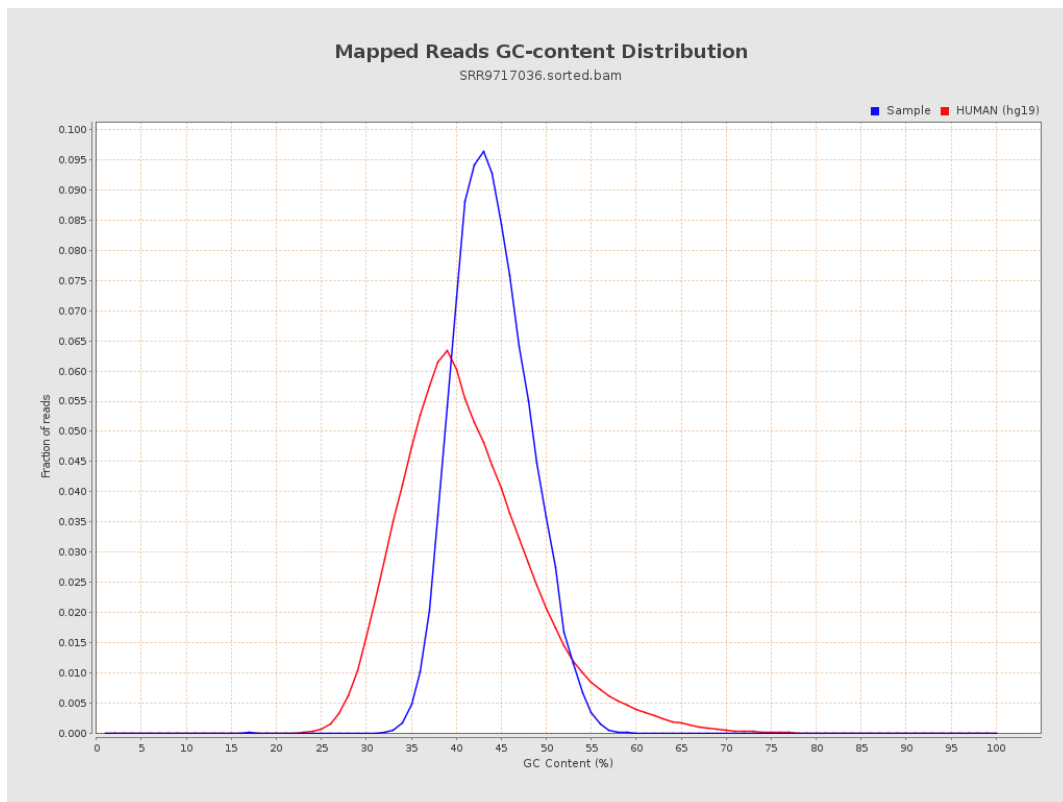
7. Results : Duplication Rate Histogram



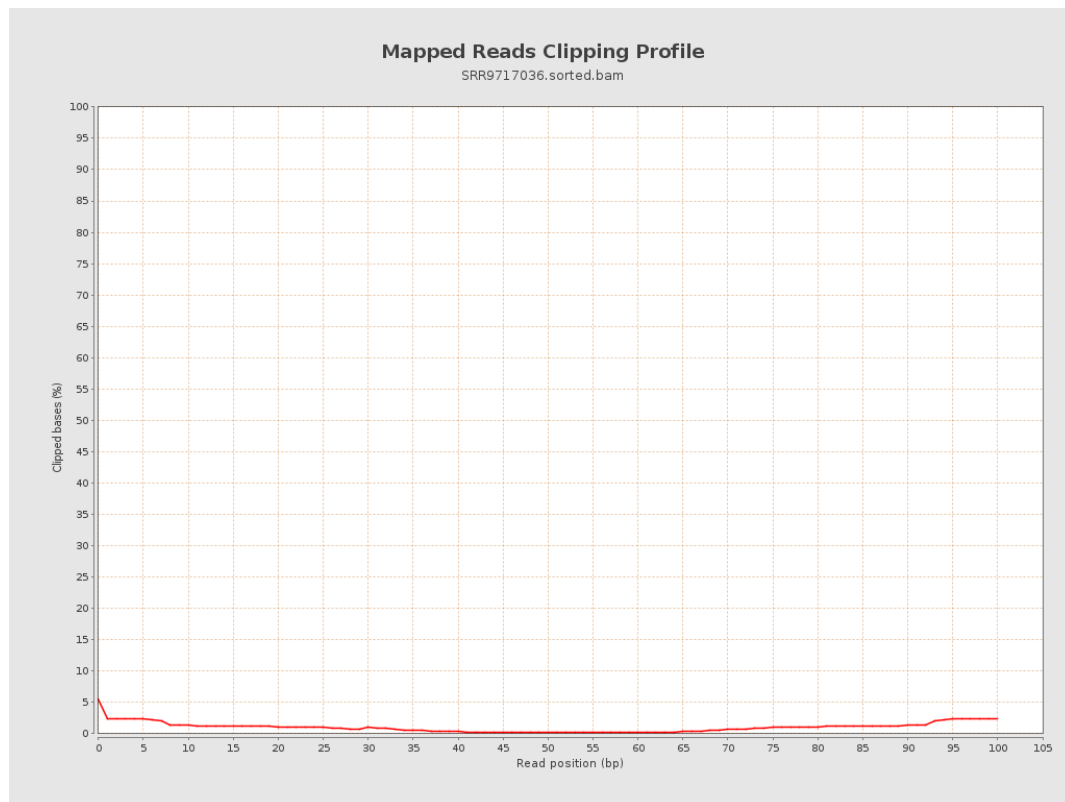
8. Results : Mapped Reads Nucleotide Content



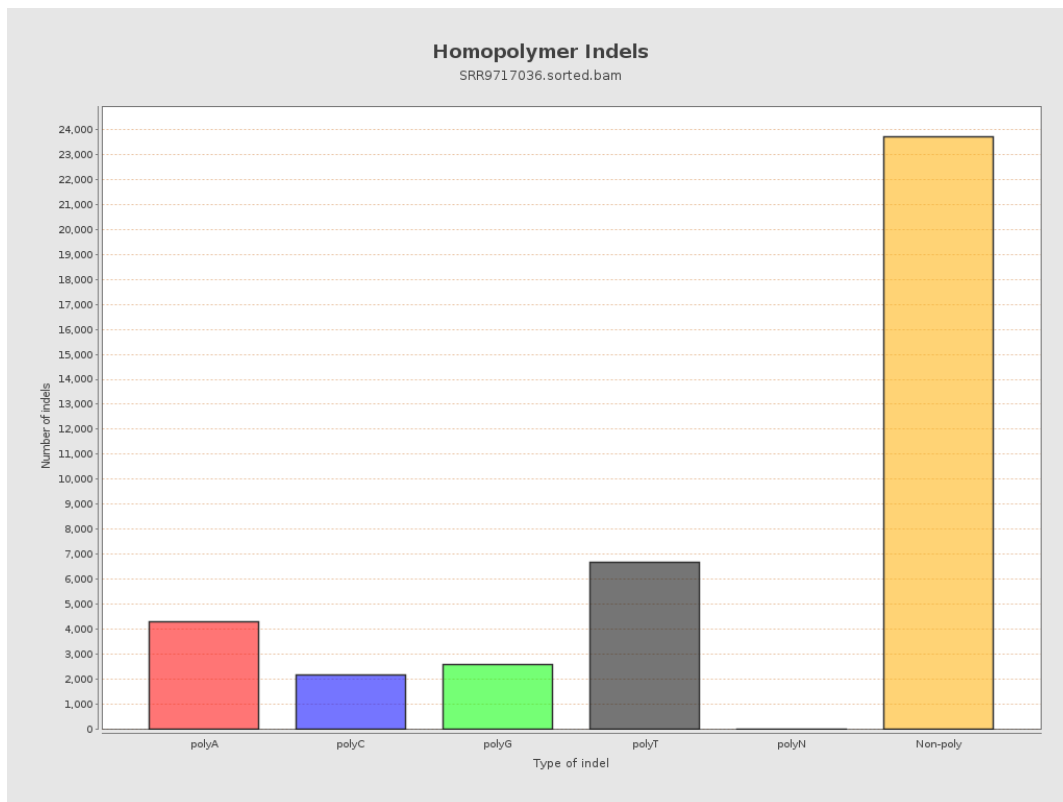
9. Results : Mapped Reads GC-content Distribution



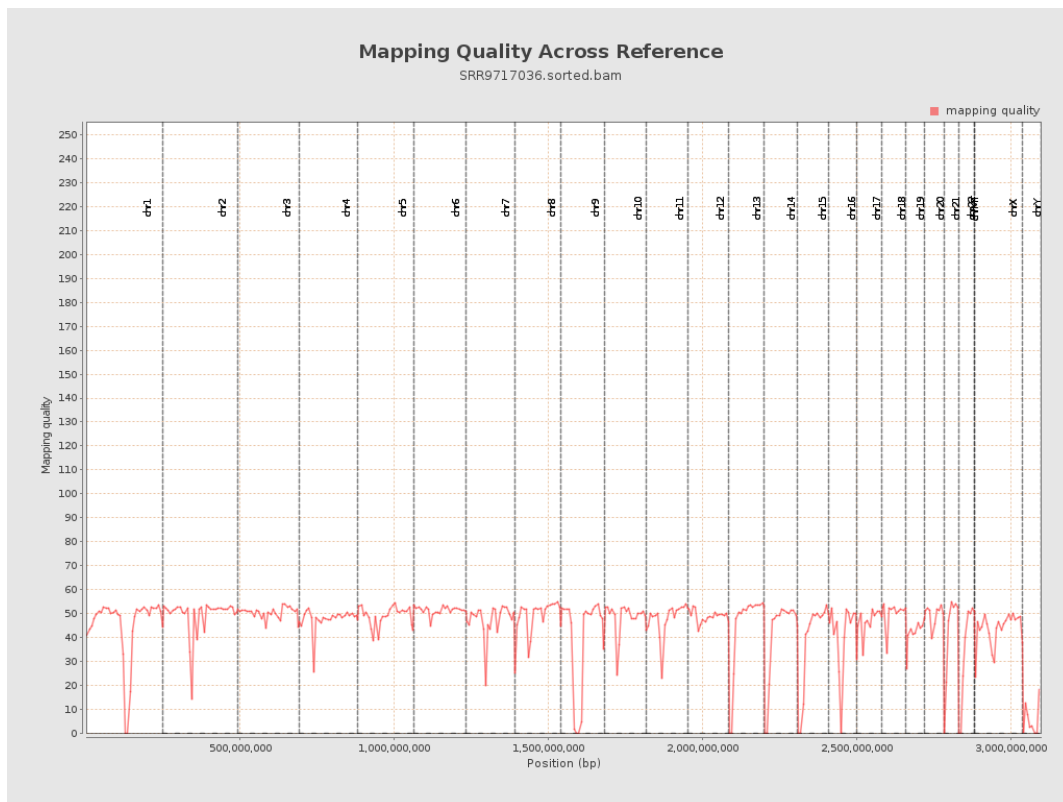
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

