

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:45:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004117.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_SRR6004117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:45:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,411,770
Mapped reads	2,384,638 / 69.89%
Unmapped reads	1,027,132 / 30.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,927 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	410,978 / 12.05%
Duplication rate	13.03%
Clipped reads	1,370,243 / 40.16%

2.2. ACGT Content

Number/percentage of A's	41,789,469 / 27.33%
Number/percentage of C's	27,064,594 / 17.7%
Number/percentage of T's	51,020,801 / 33.36%
Number/percentage of G's	33,023,362 / 21.6%
Number/percentage of N's	19,206 / 0.01%
GC Percentage	39.29%

2.3. Coverage

Mean	0.0494

Standard Deviation	0.5415
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2.4. Mapping Quality

Mean Mapping Quality	45.89
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2.5. Mismatches and indels

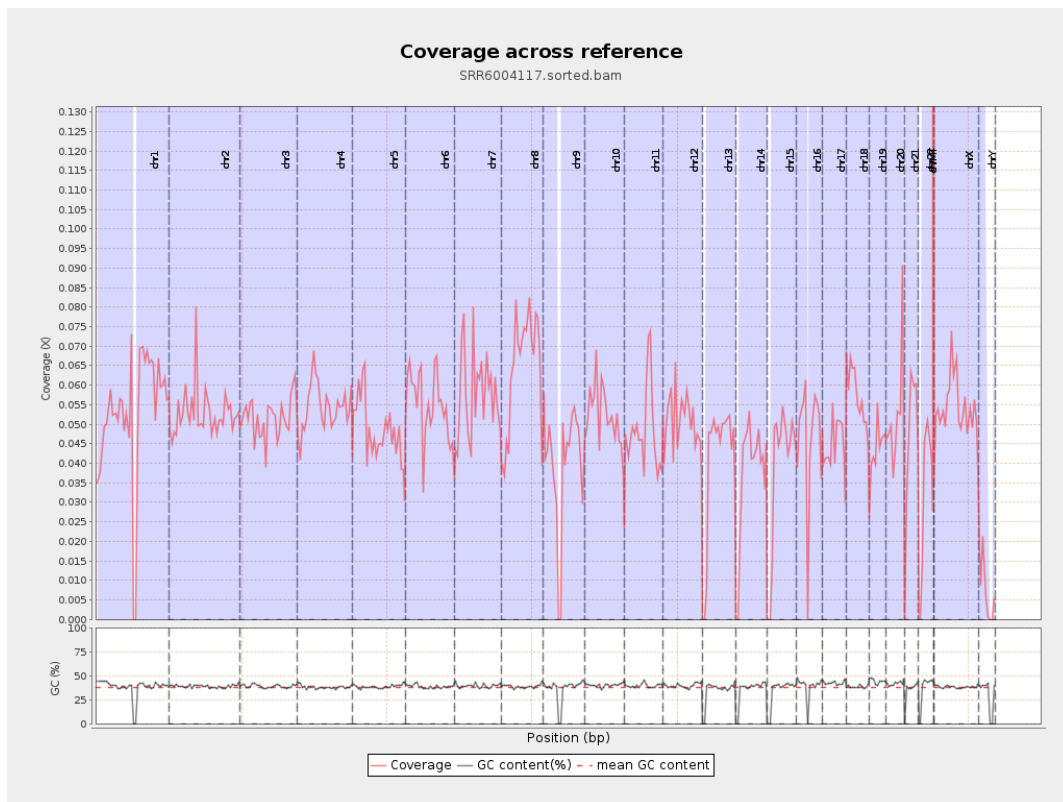
General error rate	1.14%
Mismatches	1,713,731
Insertions	13,773
Mapped reads with at least one insertion	0.57%
Deletions	53,045
Mapped reads with at least one deletion	2.19%
Homopolymer indels	48.15%

2.6. Chromosome stats

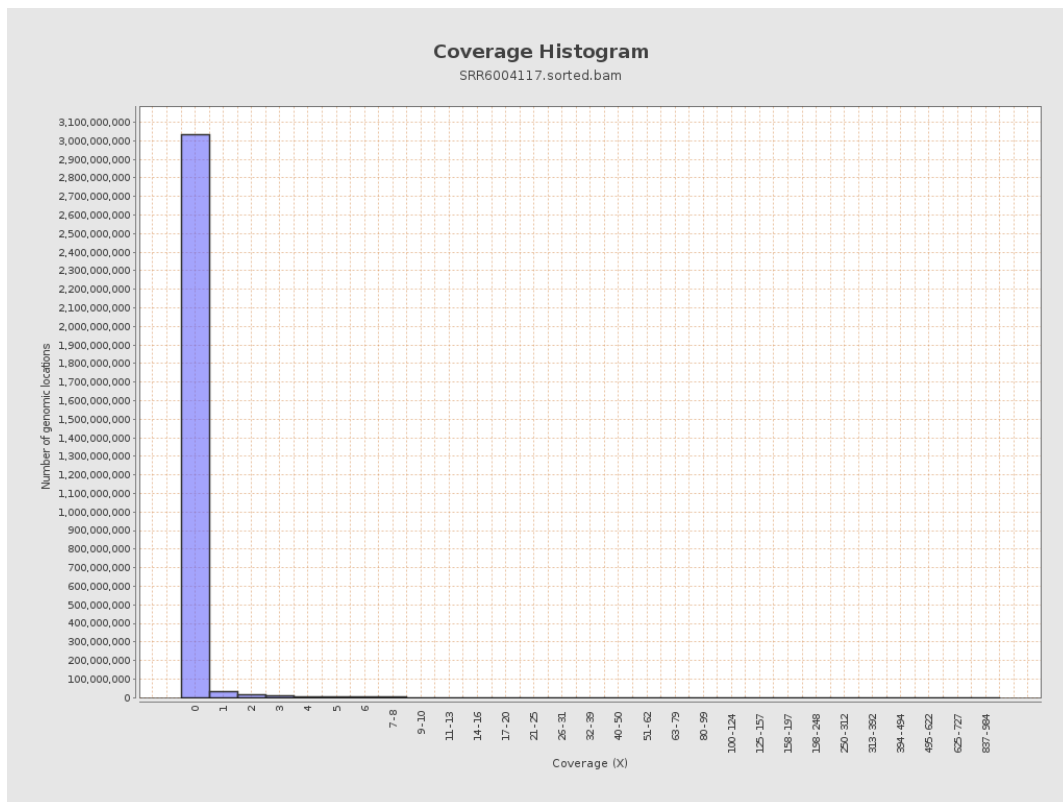
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13197372	0.0529	0.6976
chr2	243199373	12840313	0.0528	0.6549
chr3	198022430	10233236	0.0517	0.4562
chr4	191154276	10368609	0.0542	0.4788
chr5	180915260	8794705	0.0486	0.442
chr6	171115067	9352075	0.0547	0.5101
chr7	159138663	9272872	0.0583	0.6788

chr8	146364022	9395599	0.0642	0.75
chr9	141213431	5532678	0.0392	0.4691
chr10	135534747	7125761	0.0526	0.5138
chr11	135006516	6509429	0.0482	0.5206
chr12	133851895	6783735	0.0507	0.4564
chr13	115169878	4671838	0.0406	0.4116
chr14	107349540	3949634	0.0368	0.3932
chr15	102531392	3950488	0.0385	0.393
chr16	90354753	4207711	0.0466	0.4317
chr17	81195210	3600313	0.0443	0.43
chr18	78077248	4479672	0.0574	0.8861
chr19	59128983	2608342	0.0441	0.5169
chr20	63025520	3307720	0.0525	0.4631
chr21	48129895	2230532	0.0463	0.4362
chr22	51304566	1596287	0.0311	0.3316
chrMT	16571	169839	10.2492	8.8493
chrX	155270560	8404410	0.0541	0.4829
chrY	59373566	420357	0.0071	0.1533

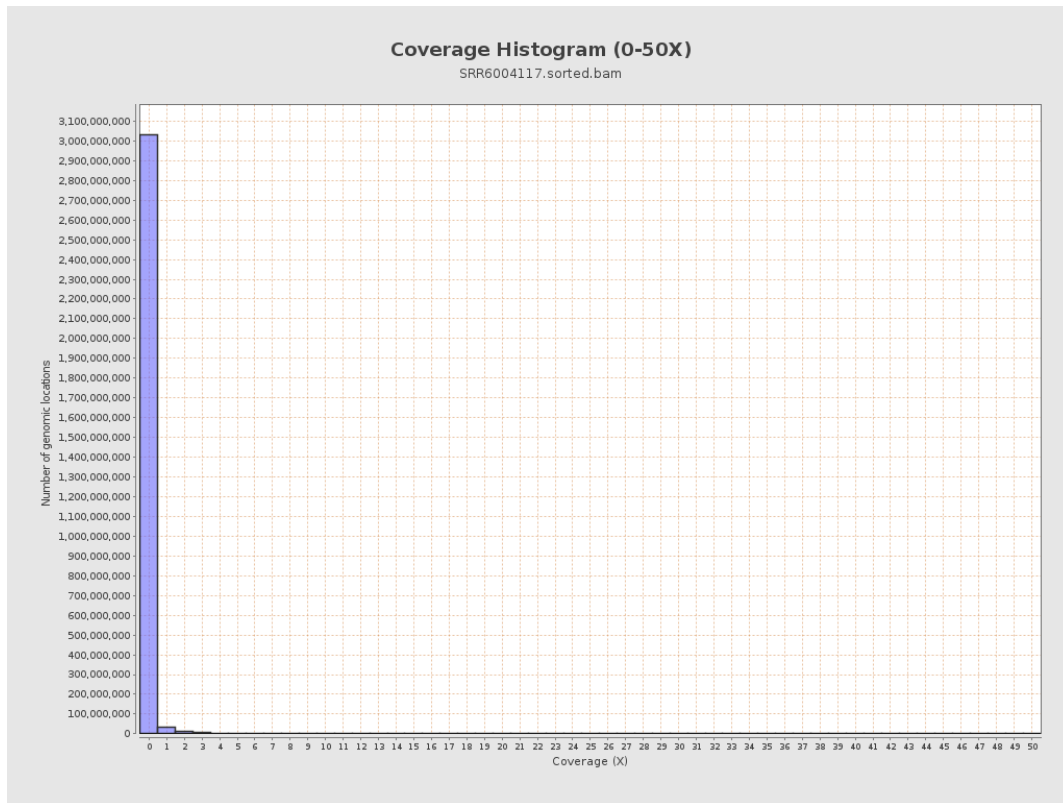
3. Results : Coverage across reference



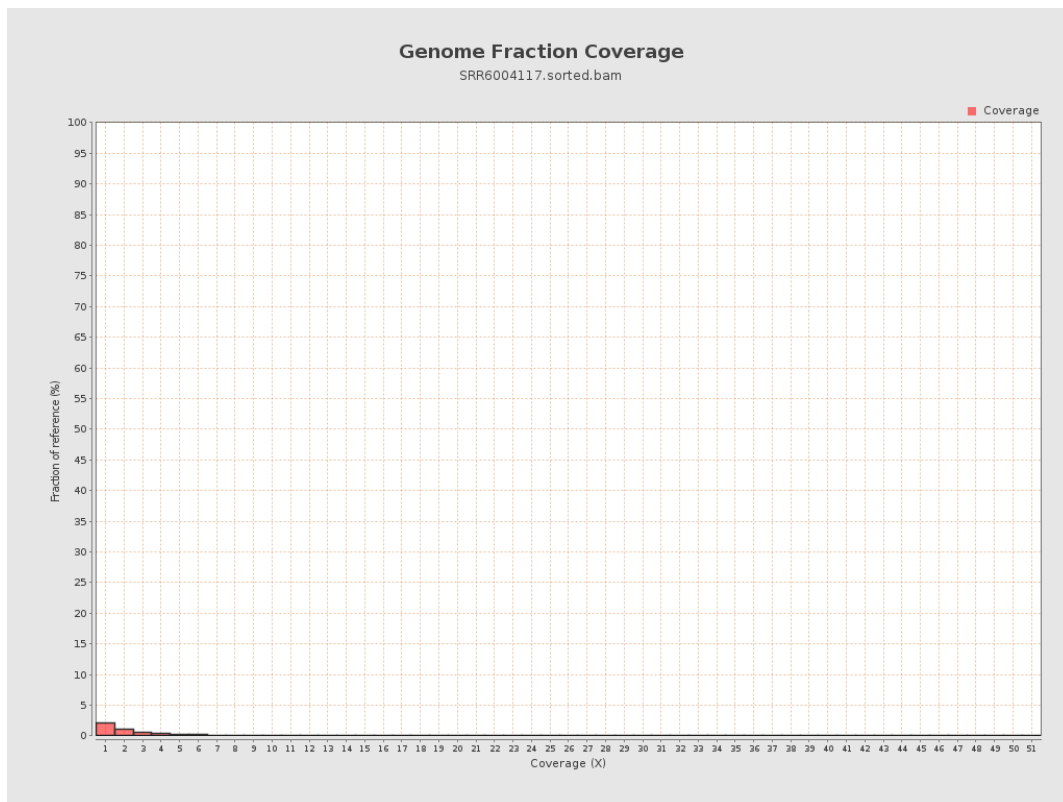
4. Results : Coverage Histogram



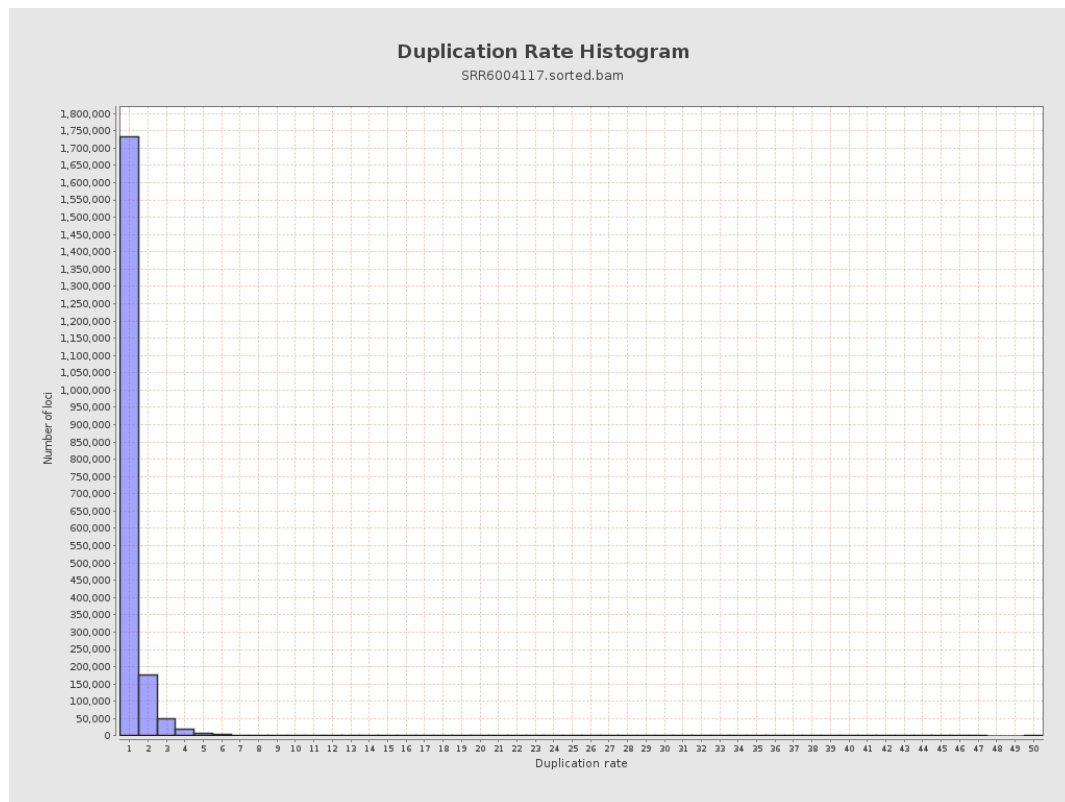
5. Results : Coverage Histogram (0-50X)



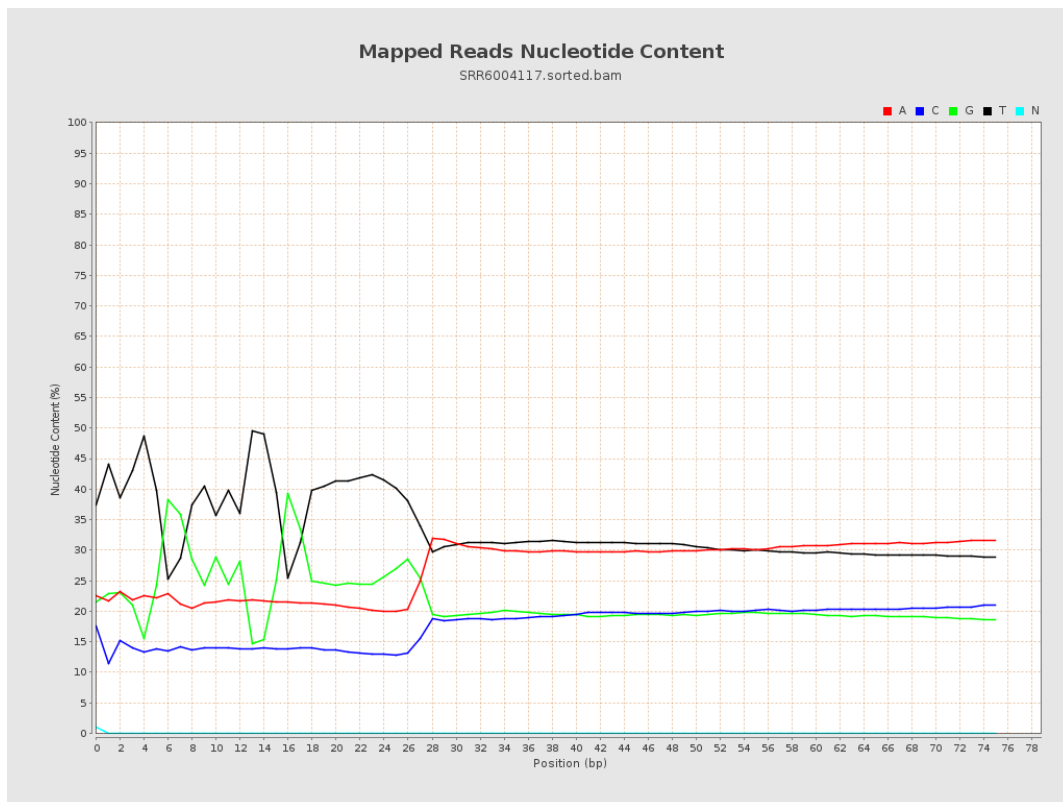
6. Results : Genome Fraction Coverage



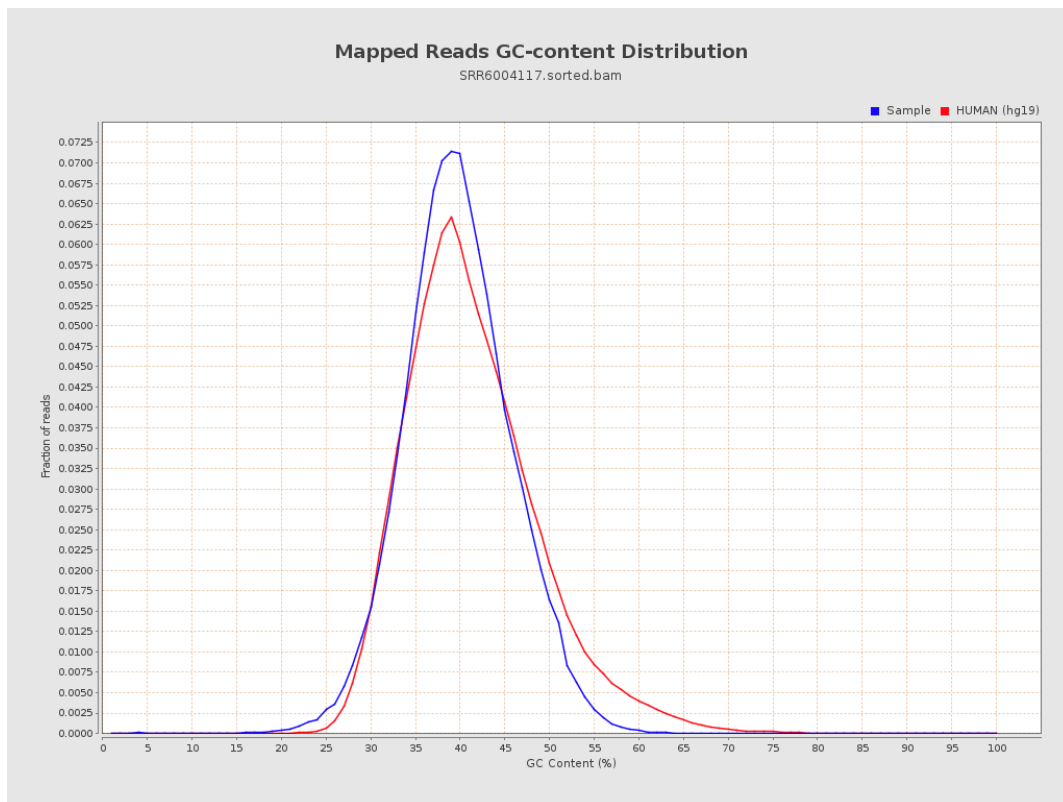
7. Results : Duplication Rate Histogram



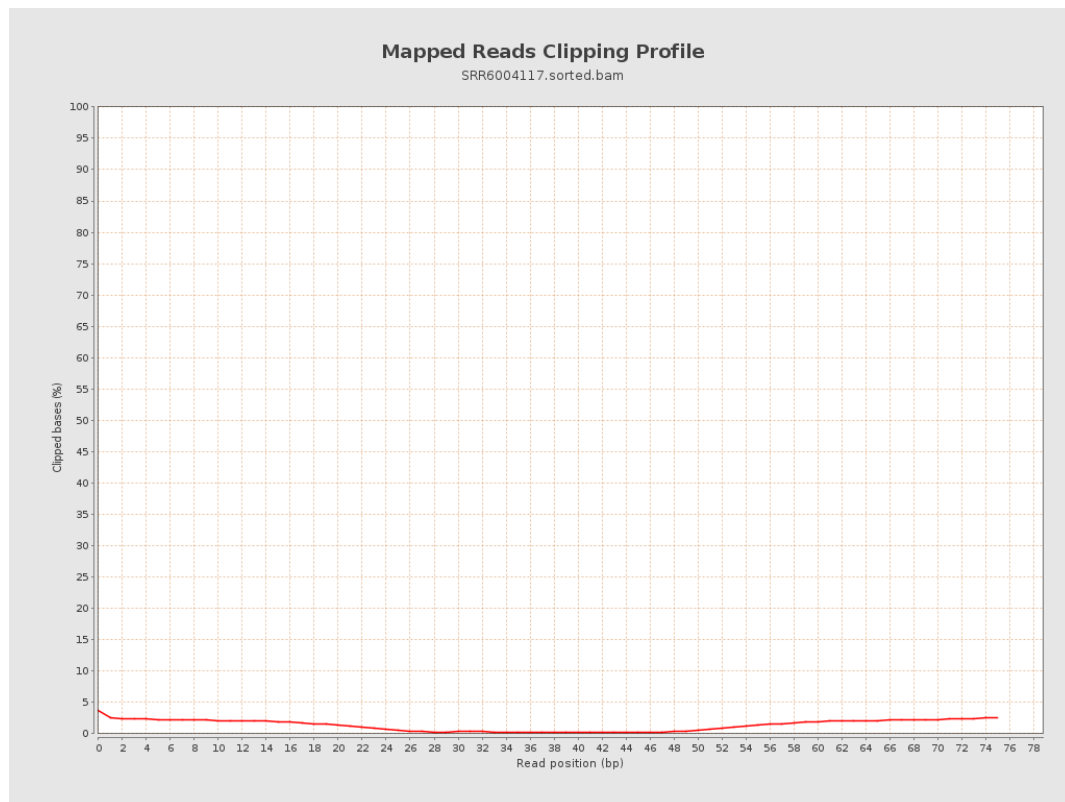
8. Results : Mapped Reads Nucleotide Content



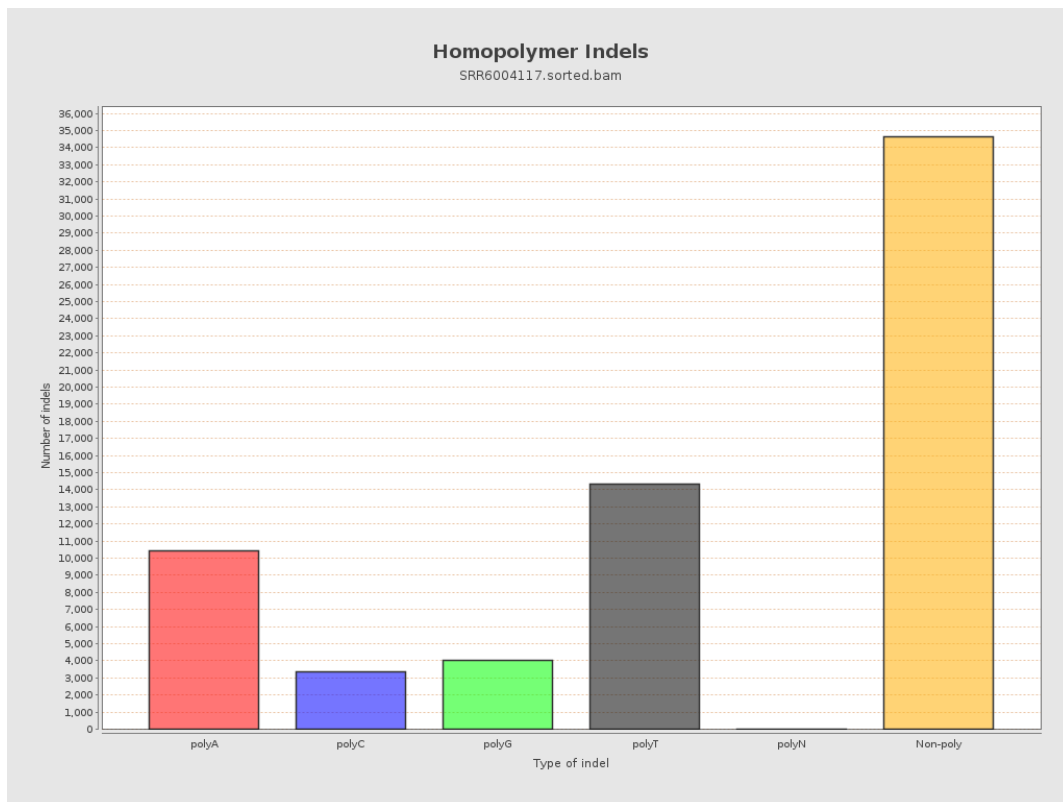
9. Results : Mapped Reads GC-content Distribution



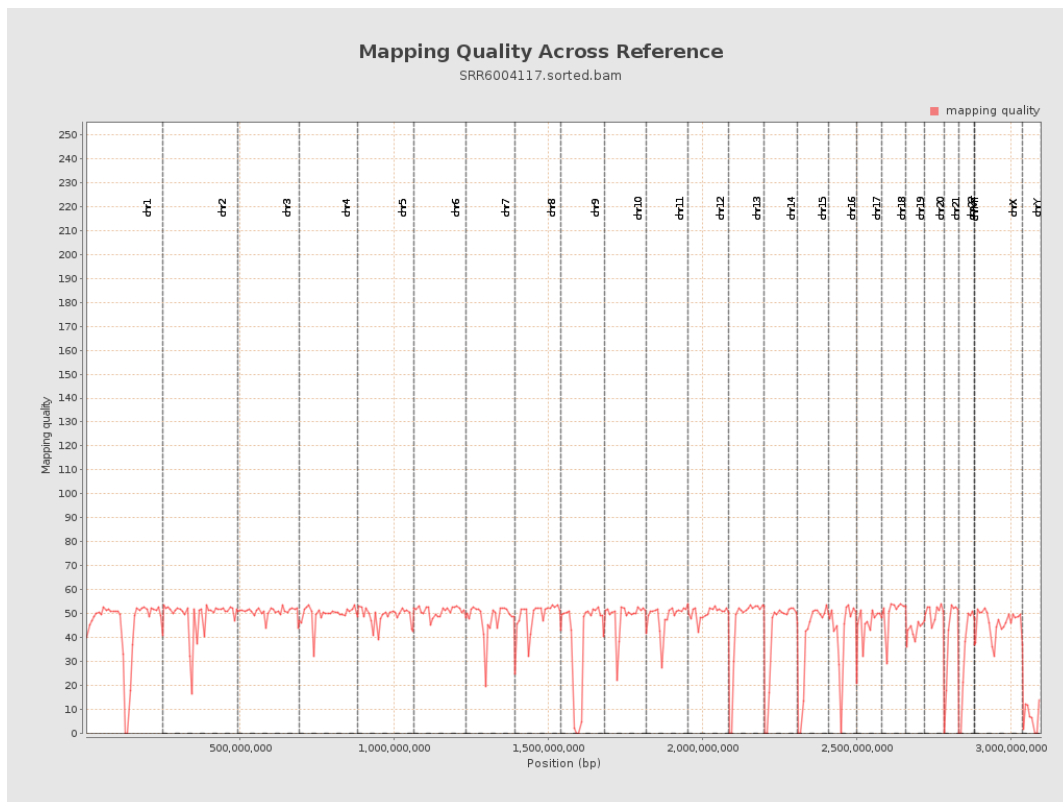
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

