

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:47:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524415.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_SRR10524415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524415.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:46:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,284,364
Mapped reads	1,179,842 / 91.86%
Unmapped reads	104,522 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,468 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	36,376 / 2.83%
Duplication rate	2.25%
Clipped reads	1,180,975 / 91.95%

2.2. ACGT Content

Number/percentage of A's	17,354,479 / 25.19%
Number/percentage of C's	12,722,761 / 18.46%
Number/percentage of T's	22,196,813 / 32.21%
Number/percentage of G's	16,620,706 / 24.12%
Number/percentage of N's	8,393 / 0.01%
GC Percentage	42.59%

2.3. Coverage

Mean	0.0223

Standard Deviation	0.2392
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2.4. Mapping Quality

Mean Mapping Quality	45.76
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2.5. Mismatches and indels

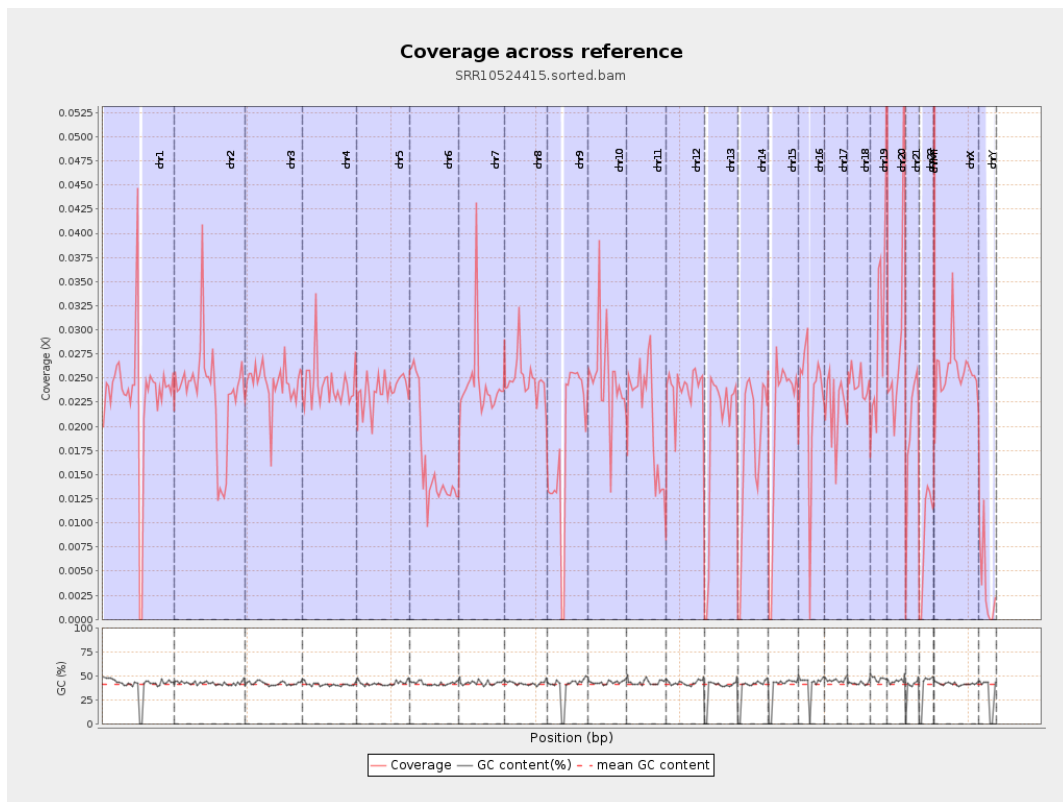
General error rate	0.5%
Mismatches	335,007
Insertions	4,552
Mapped reads with at least one insertion	0.38%
Deletions	12,620
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.19%

2.6. Chromosome stats

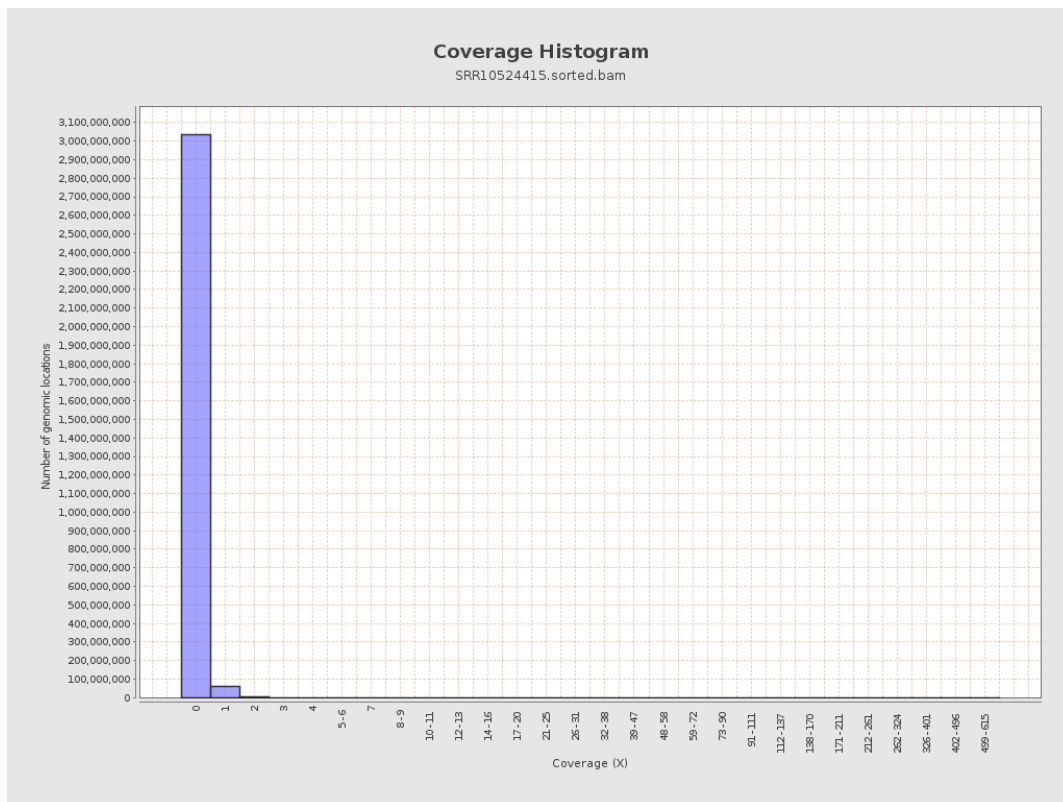
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5747164	0.0231	0.4951
chr2	243199373	5676702	0.0233	0.2525
chr3	198022430	4846658	0.0245	0.1666
chr4	191154276	4647675	0.0243	0.1779
chr5	180915260	4294205	0.0237	0.164
chr6	171115067	2787685	0.0163	0.145
chr7	159138663	3878535	0.0244	0.3258

chr8	146364022	3644916	0.0249	0.2329
chr9	141213431	2567125	0.0182	0.1783
chr10	135534747	3375201	0.0249	0.214
chr11	135006516	2867979	0.0212	0.1883
chr12	133851895	3204928	0.0239	0.1686
chr13	115169878	2218773	0.0193	0.148
chr14	107349540	1940169	0.0181	0.148
chr15	102531392	2102537	0.0205	0.1527
chr16	90354753	2049594	0.0227	0.1659
chr17	81195210	1792102	0.0221	0.1703
chr18	78077248	1908451	0.0244	0.2901
chr19	59128983	1837252	0.0311	0.3532
chr20	63025520	1852368	0.0294	0.1887
chr21	48129895	954121	0.0198	0.1644
chr22	51304566	464262	0.009	0.1003
chrMT	16571	48505	2.9271	2.6477
chrX	155270560	4010208	0.0258	0.187
chrY	59373566	205885	0.0035	0.101

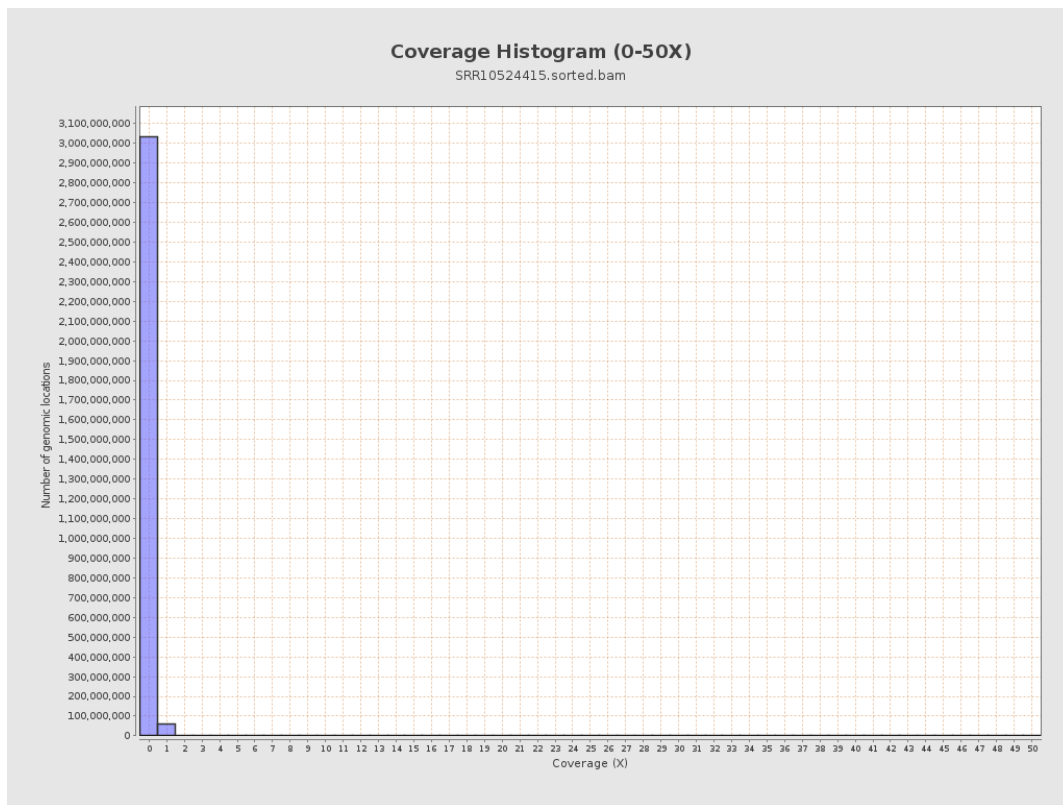
3. Results : Coverage across reference



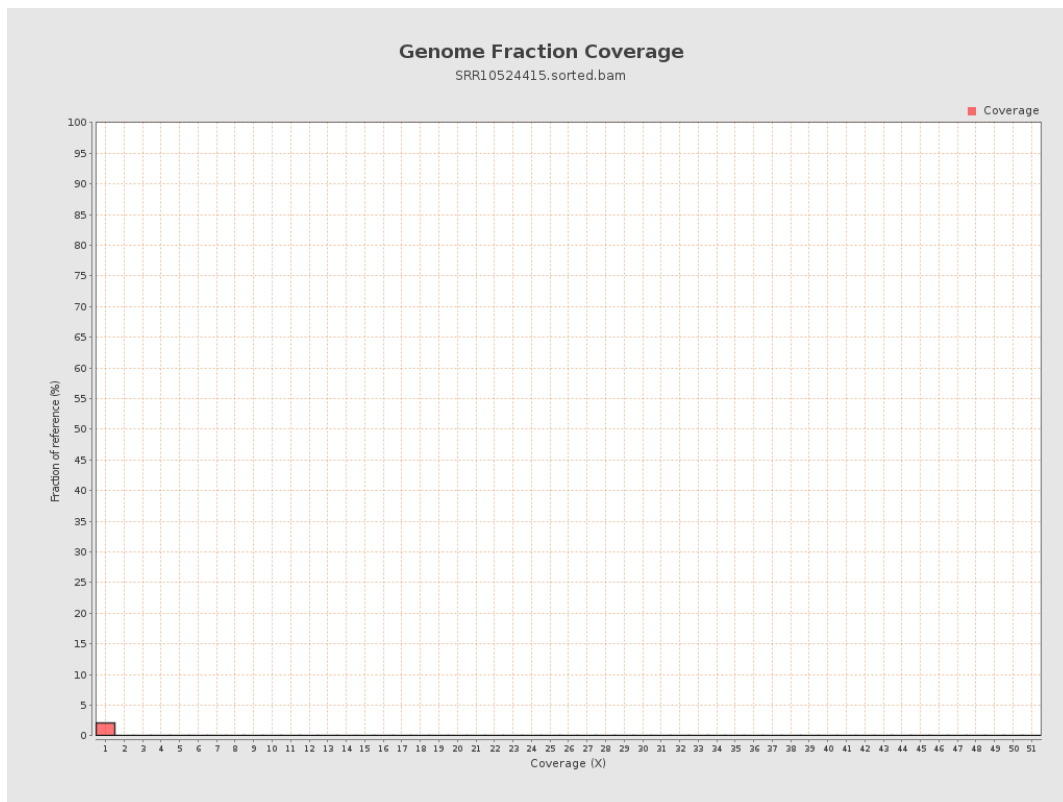
4. Results : Coverage Histogram



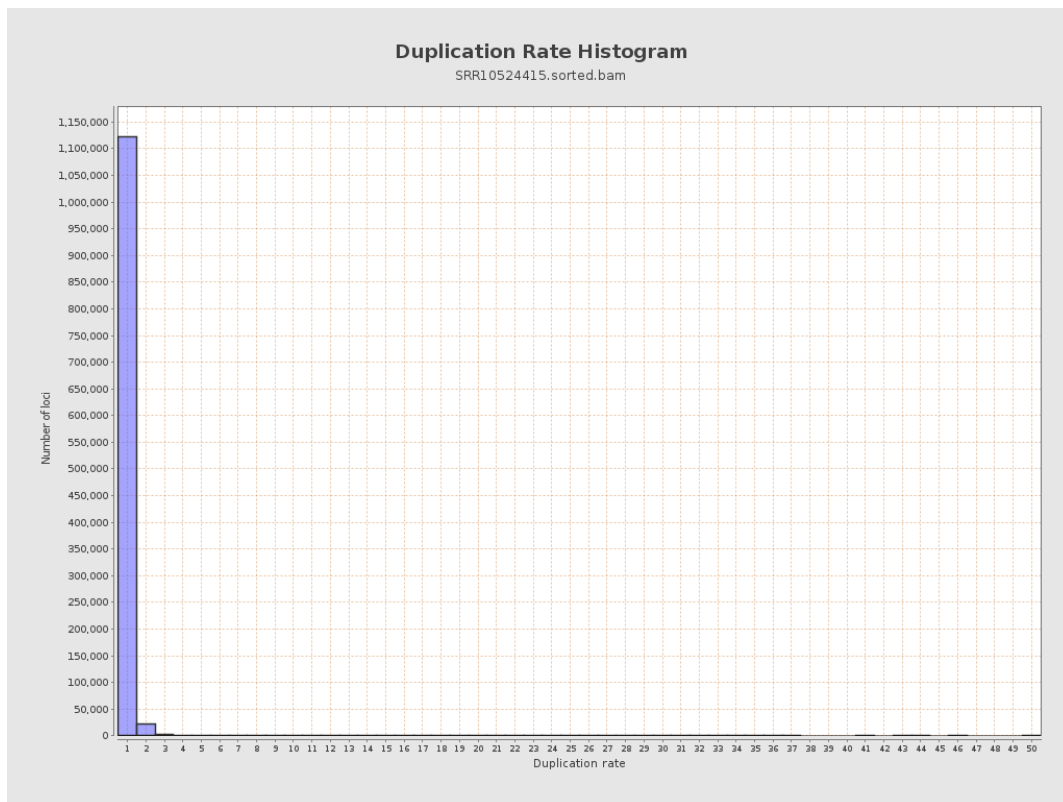
5. Results : Coverage Histogram (0-50X)



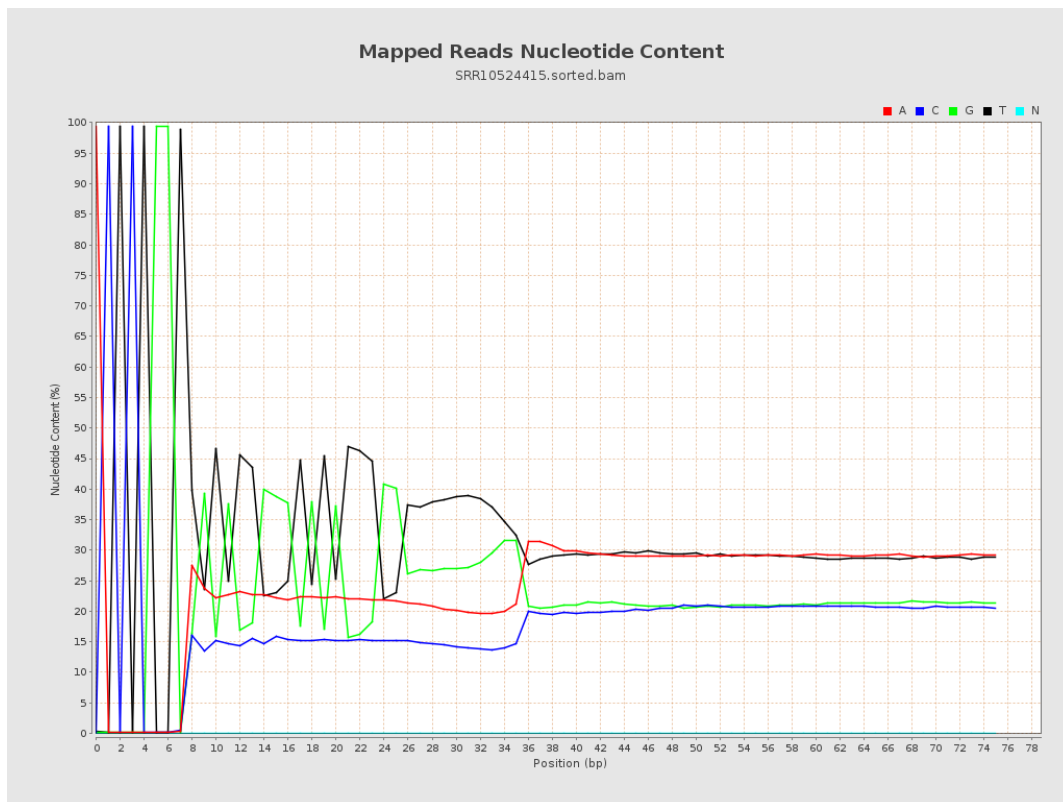
6. Results : Genome Fraction Coverage



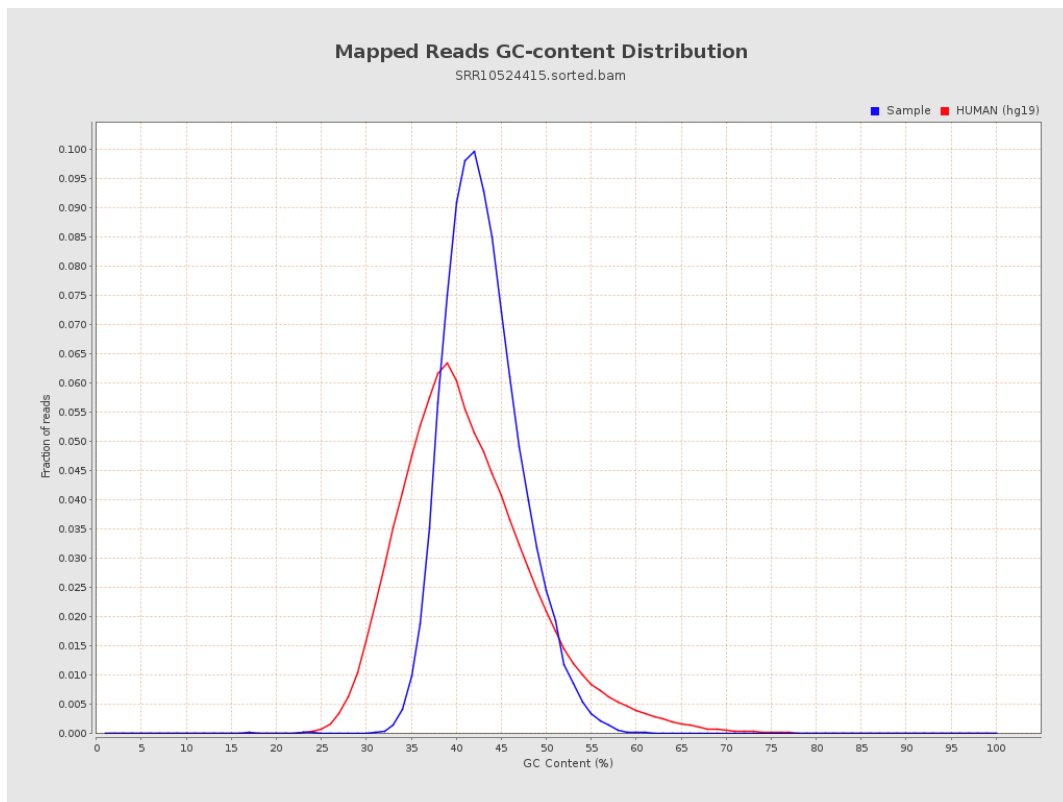
7. Results : Duplication Rate Histogram



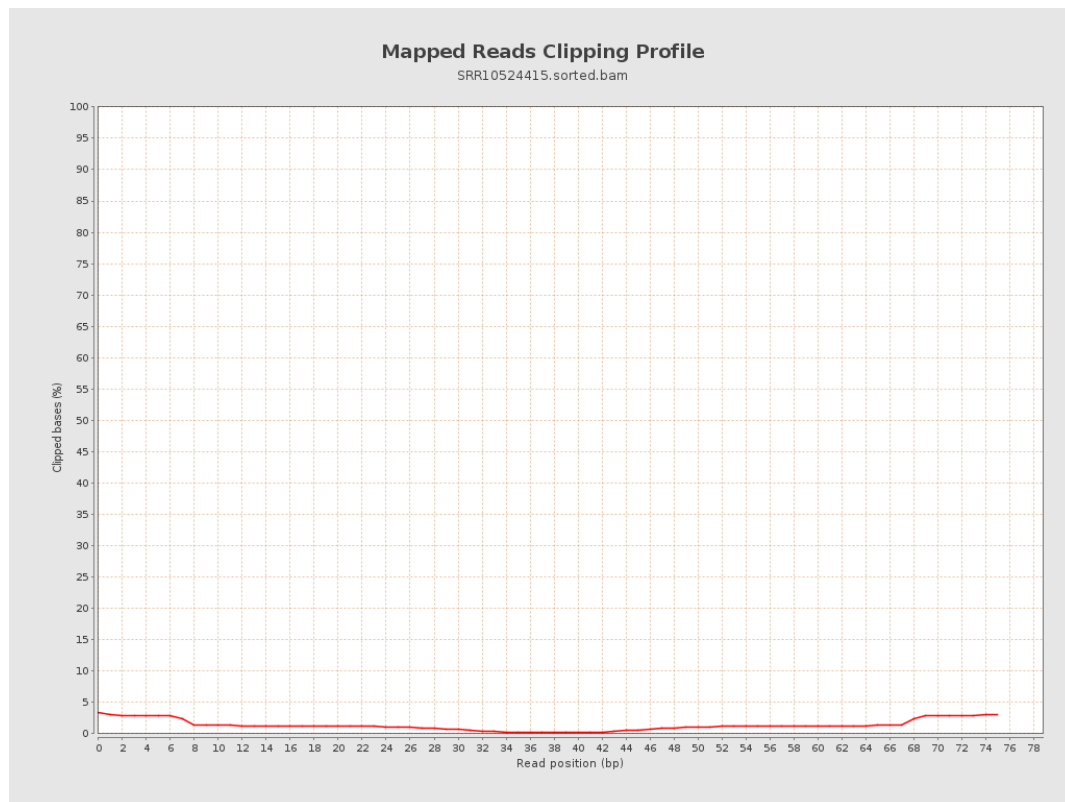
8. Results : Mapped Reads Nucleotide Content



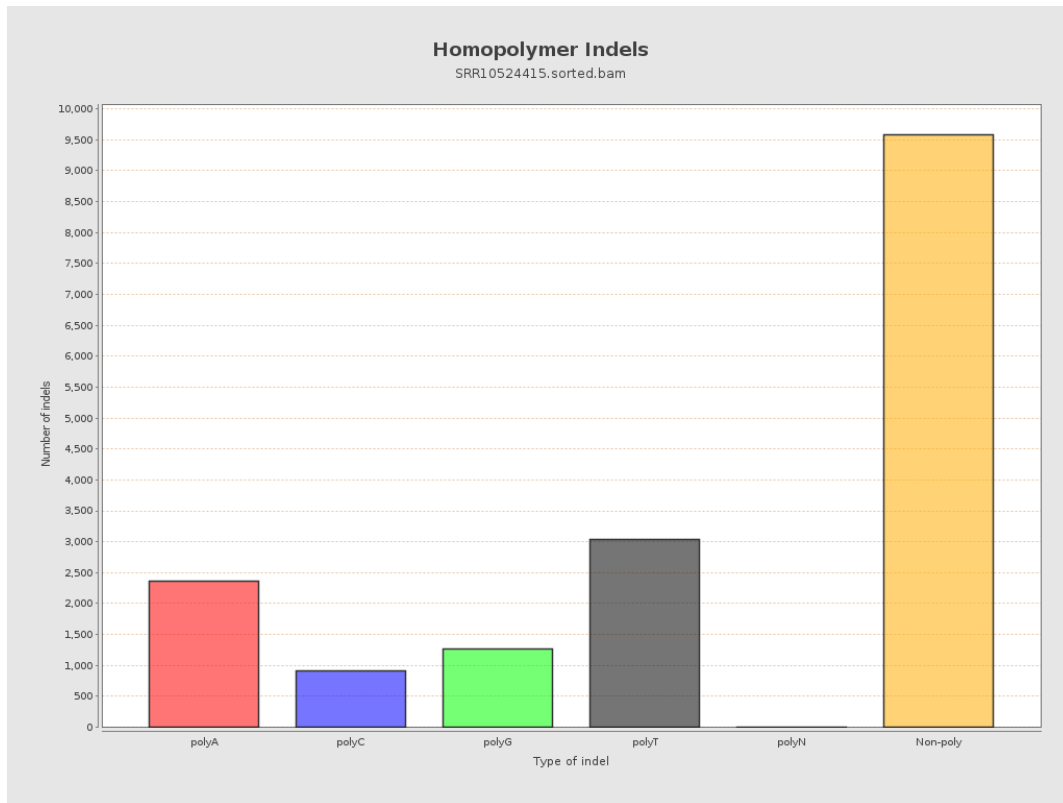
9. Results : Mapped Reads GC-content Distribution



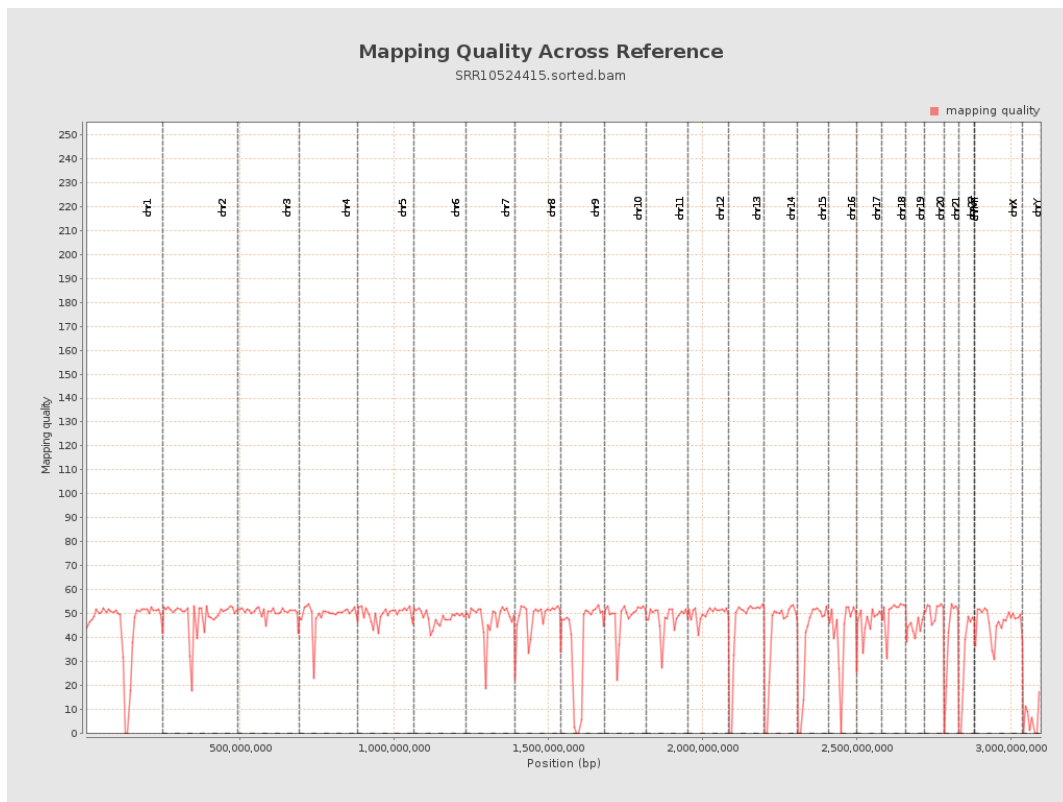
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

