

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:11:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549124.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_SRR1549124 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549124.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:11:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,446,038
Mapped reads	9,112,334 / 58.99%
Unmapped reads	6,333,704 / 41.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	793,659 / 5.14%
Duplication rate	7.03%
Clipped reads	919,413 / 5.95%

2.2. ACGT Content

Number/percentage of A's	98,355,870 / 27.39%
Number/percentage of C's	80,537,672 / 22.43%
Number/percentage of T's	99,424,307 / 27.69%
Number/percentage of G's	80,785,750 / 22.5%
Number/percentage of N's	14,461 / 0%
GC Percentage	44.92%

2.3. Coverage

Mean	0.116
Standard Deviation	0.8414

2.4. Mapping Quality

Mean Mapping Quality	39.55
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2.5. Mismatches and indels

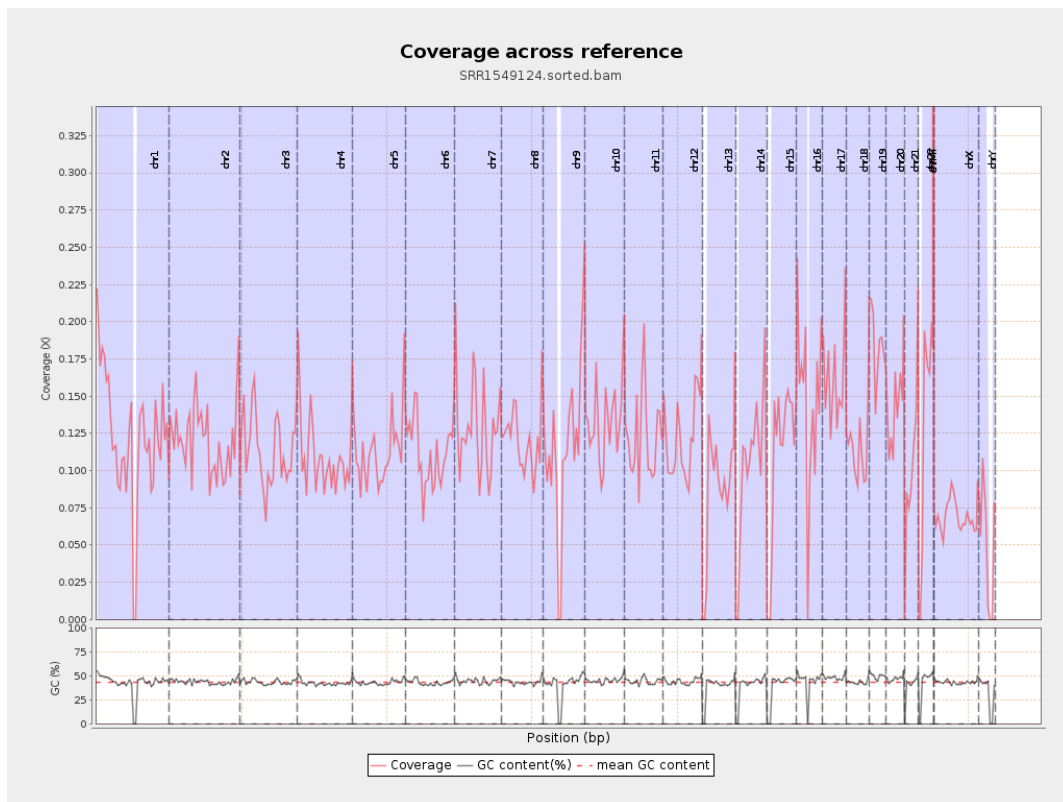
General error rate	0.38%
Mismatches	1,343,076
Insertions	13,238
Mapped reads with at least one insertion	0.15%
Deletions	34,319
Mapped reads with at least one deletion	0.38%
Homopolymer indels	43.06%

2.6. Chromosome stats

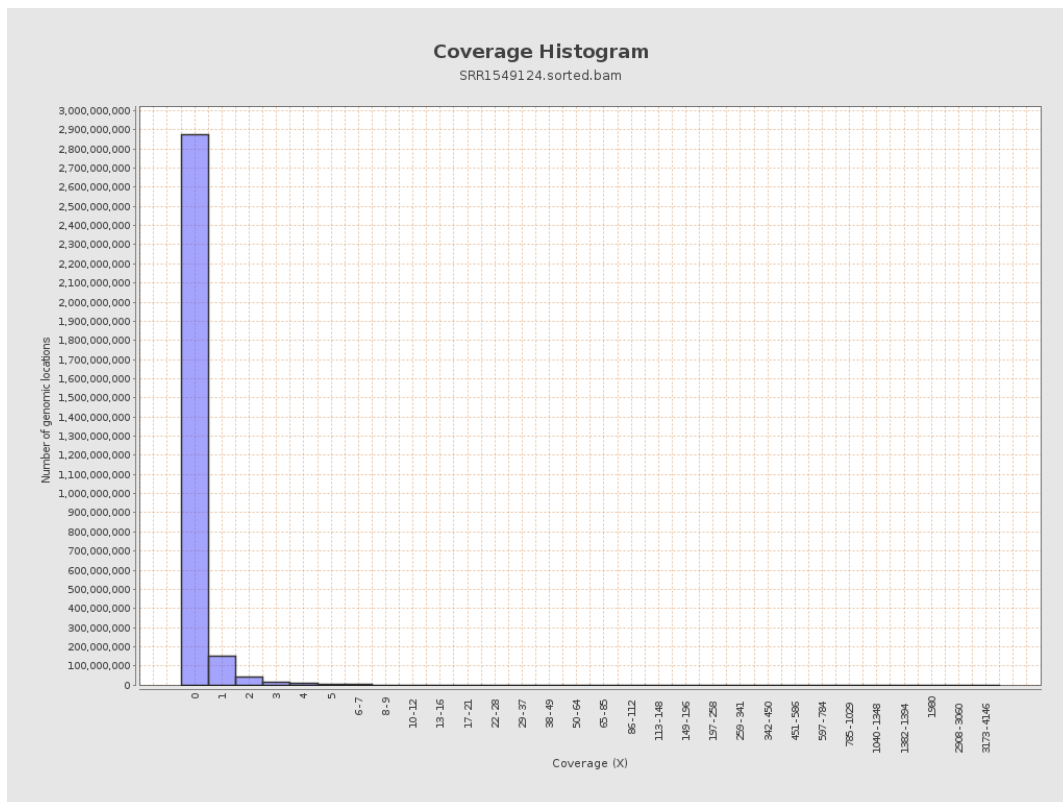
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	30197126	0.1212	1.1765
chr2	243199373	29356956	0.1207	0.7079
chr3	198022430	22419148	0.1132	0.5263
chr4	191154276	20674162	0.1082	0.5786
chr5	180915260	20389342	0.1127	0.5412
chr6	171115067	19240517	0.1124	0.5397
chr7	159138663	20217074	0.127	0.8244
chr8	146364022	17517116	0.1197	2.091

chr9	141213431	15787442	0.1118	0.6659
chr10	135534747	17723593	0.1308	0.7515
chr11	135006516	16811606	0.1245	0.6251
chr12	133851895	16323138	0.1219	0.5672
chr13	115169878	10029539	0.0871	0.4615
chr14	107349540	11138824	0.1038	0.8148
chr15	102531392	11390518	0.1111	0.519
chr16	90354753	13129144	0.1453	0.648
chr17	81195210	13156070	0.162	0.6505
chr18	78077248	8792129	0.1126	1.1839
chr19	59128983	10842610	0.1834	1.2878
chr20	63025520	8851862	0.1404	0.6333
chr21	48129895	4977480	0.1034	0.605
chr22	51304566	6379171	0.1243	0.5796
chrMT	16571	181415	10.9477	13.978
chrX	155270560	10739518	0.0692	0.4685
chrY	59373566	2895270	0.0488	0.5153

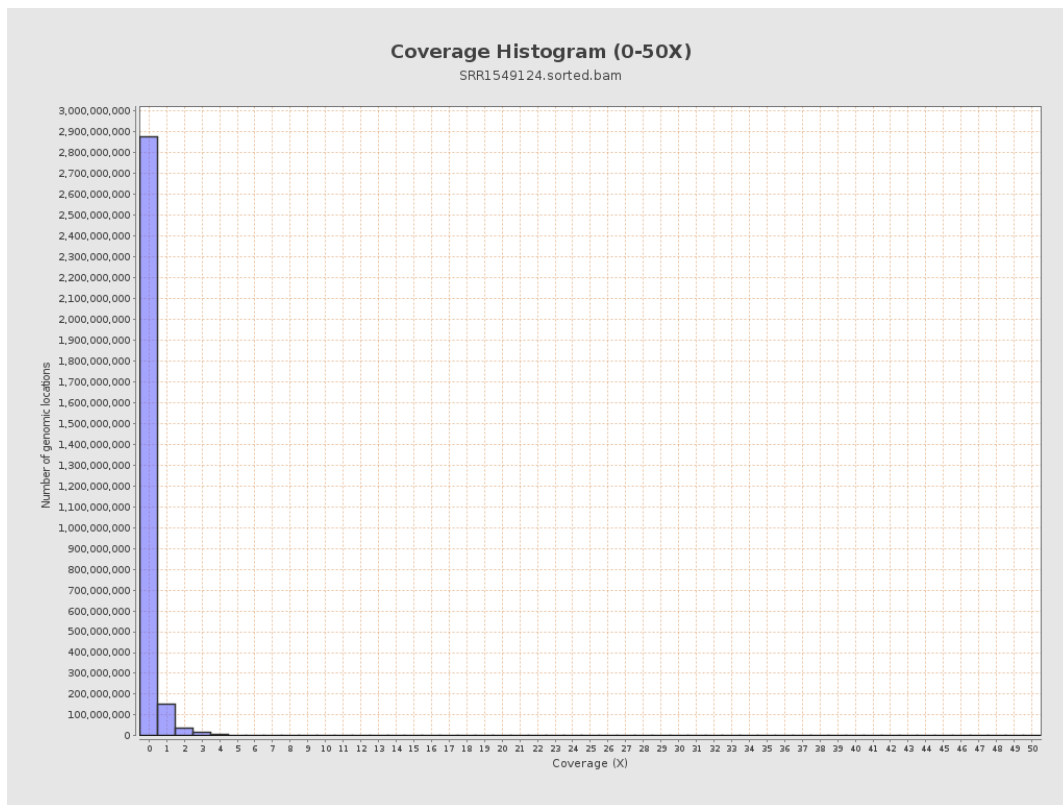
3. Results : Coverage across reference



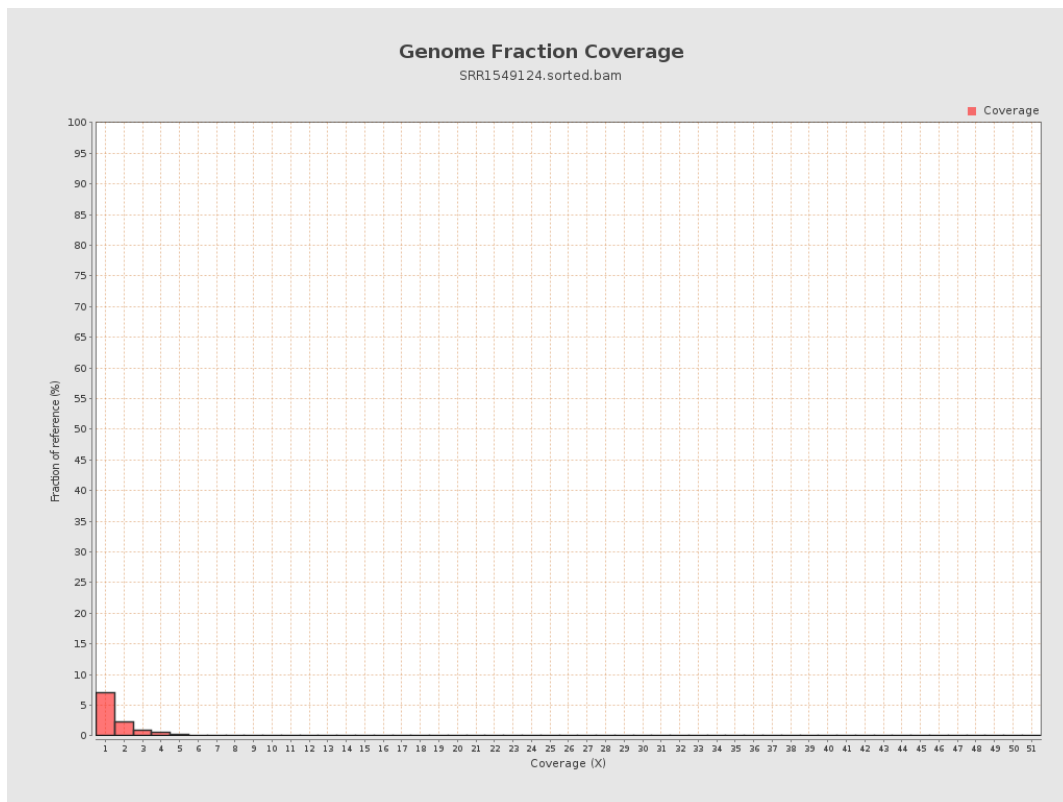
4. Results : Coverage Histogram



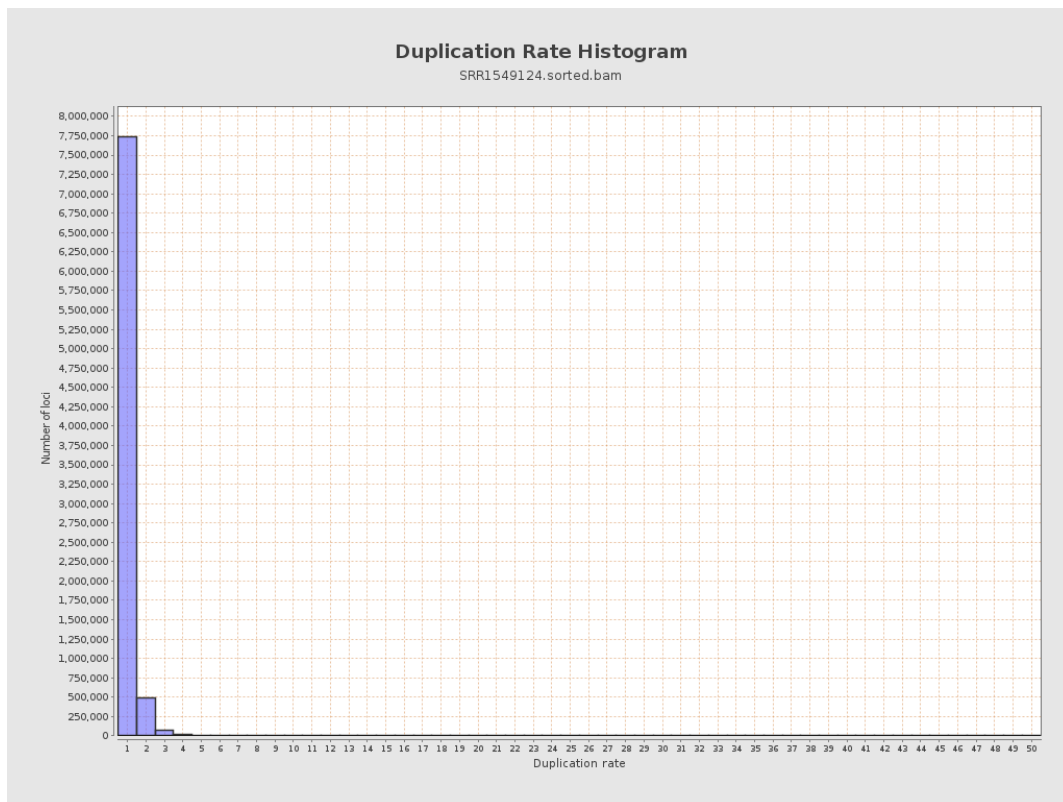
5. Results : Coverage Histogram (0-50X)



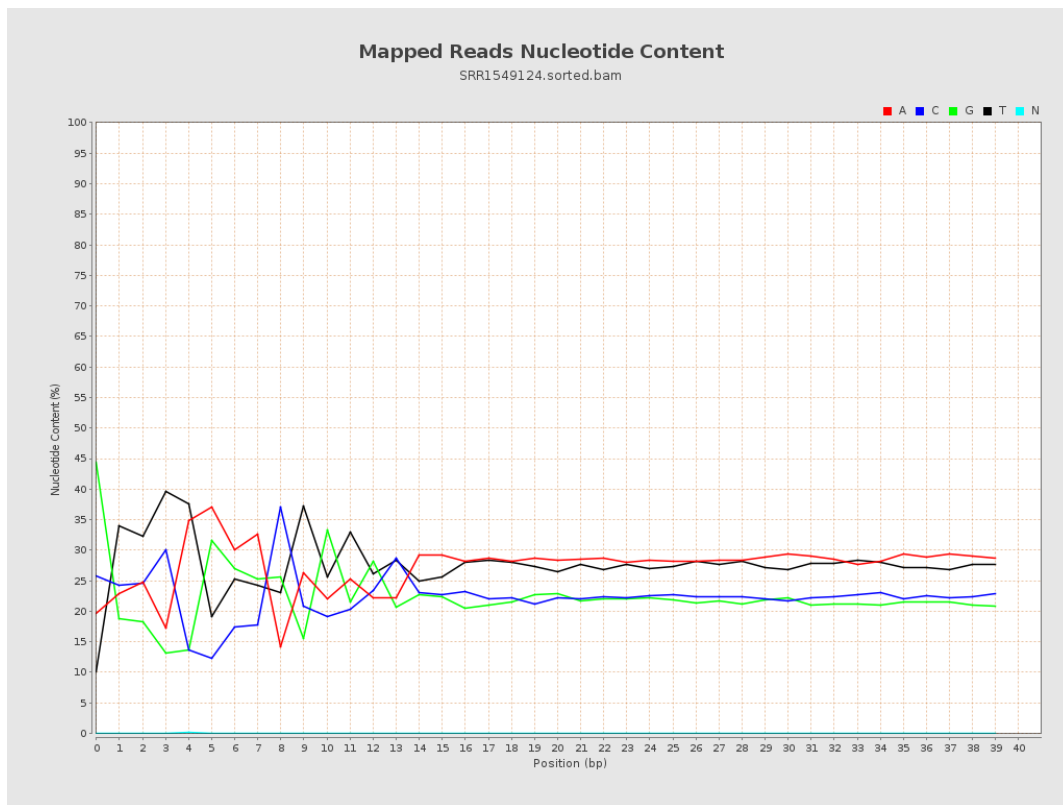
6. Results : Genome Fraction Coverage



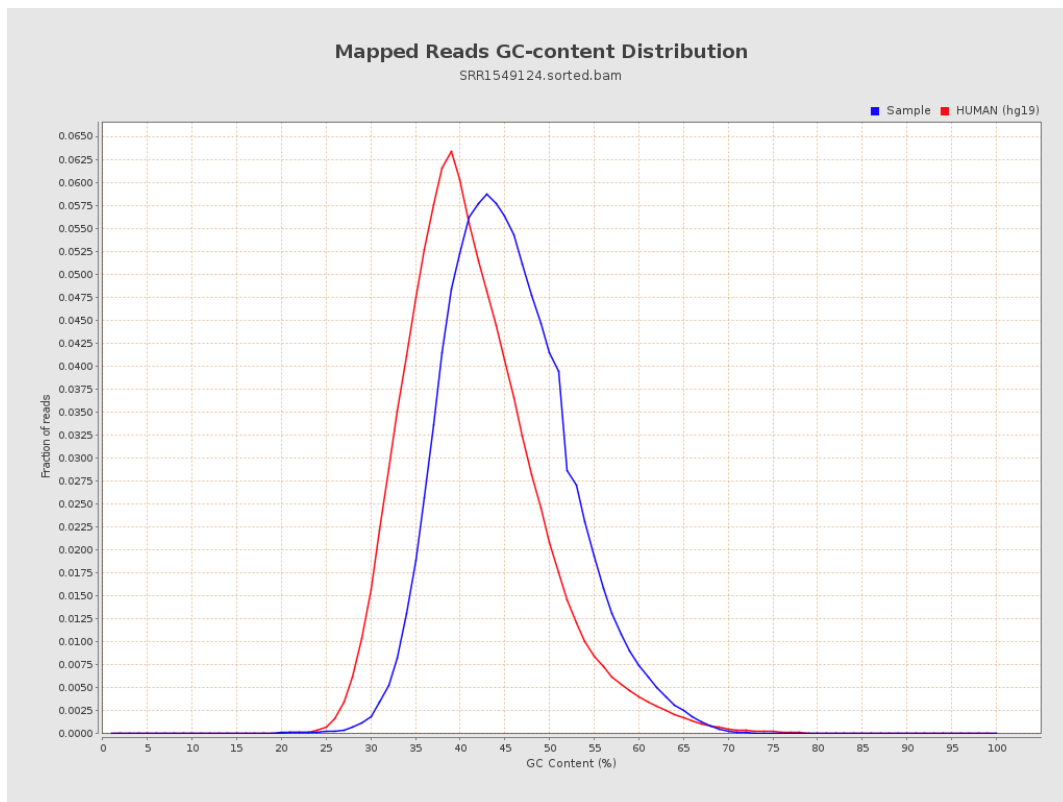
7. Results : Duplication Rate Histogram



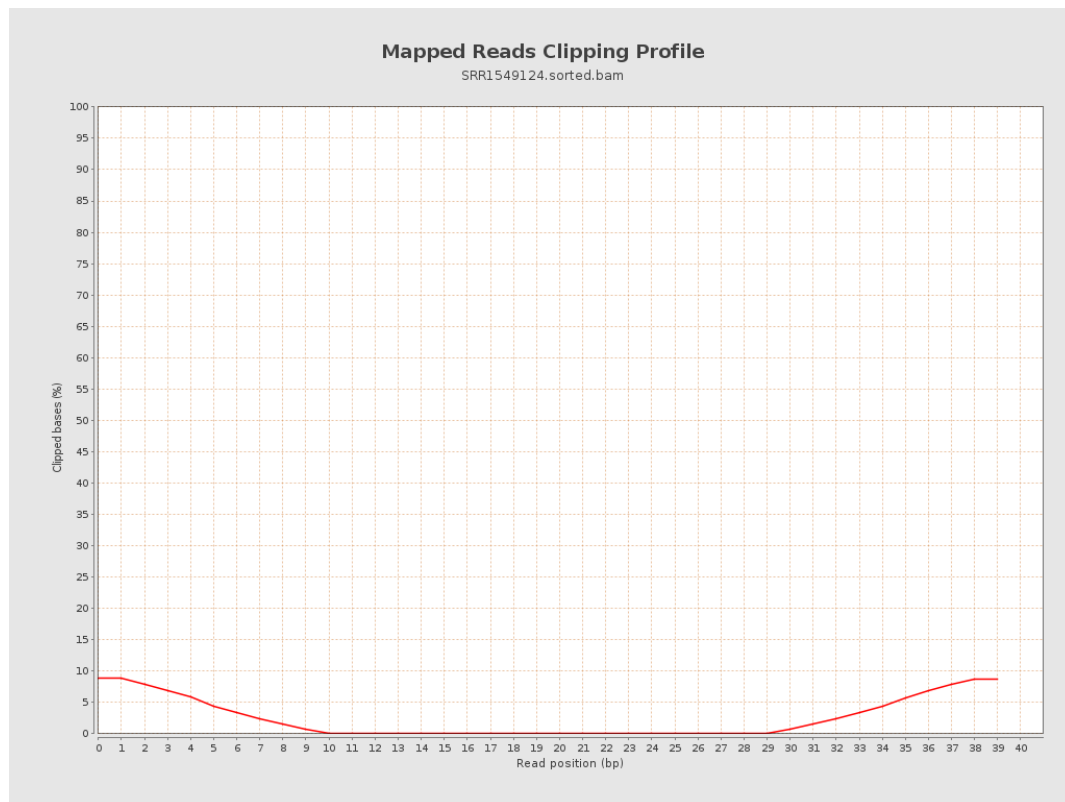
8. Results : Mapped Reads Nucleotide Content



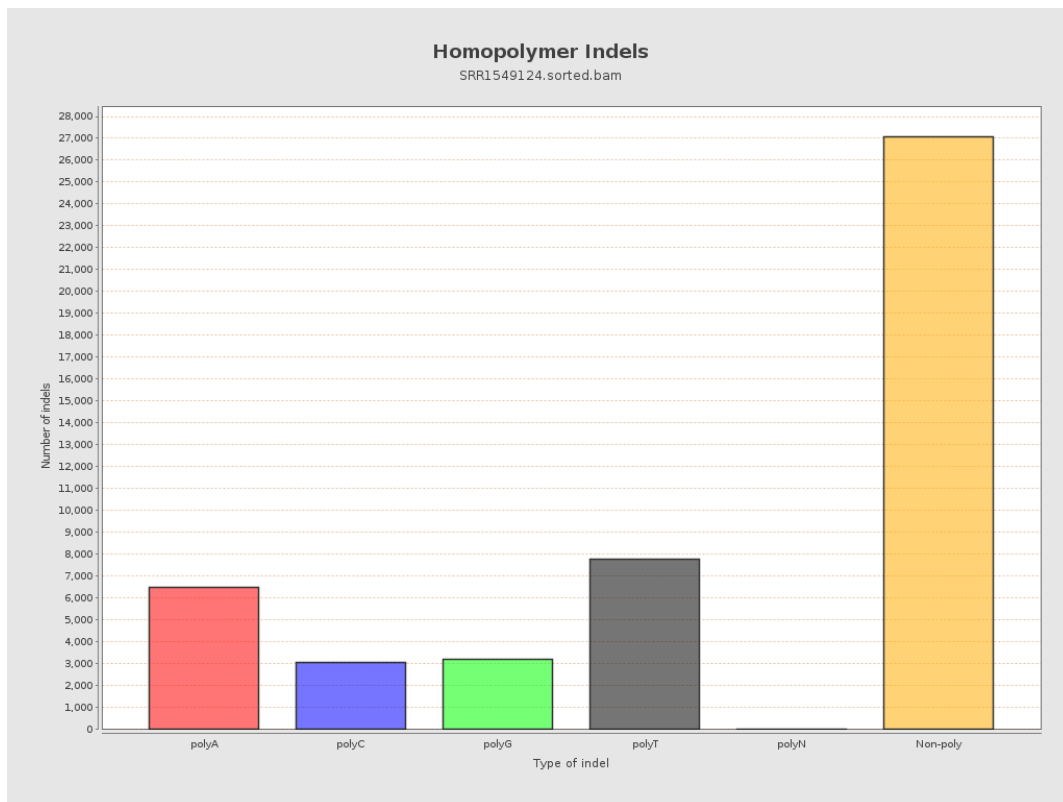
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

