

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:49:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236126.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_SRR6236126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:49:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	807,903
Mapped reads	692,857 / 85.76%
Unmapped reads	115,046 / 14.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,778 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	23,025 / 2.85%
Duplication rate	2.76%
Clipped reads	361,669 / 44.77%

2.2. ACGT Content

Number/percentage of A's	12,063,483 / 26.94%
Number/percentage of C's	7,971,395 / 17.8%
Number/percentage of T's	14,403,096 / 32.17%
Number/percentage of G's	10,316,335 / 23.04%
Number/percentage of N's	22,682 / 0.05%
GC Percentage	40.84%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1667
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2.4. Mapping Quality

Mean Mapping Quality	44.24
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2.5. Mismatches and indels

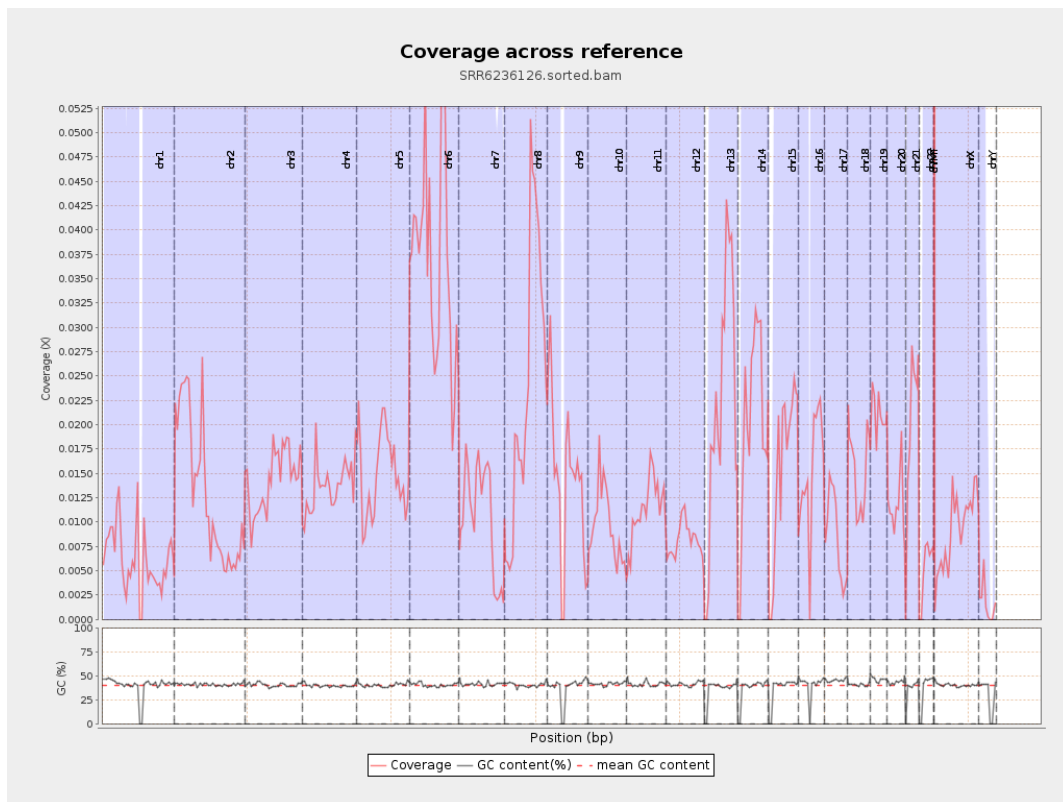
General error rate	0.86%
Mismatches	379,995
Insertions	3,180
Mapped reads with at least one insertion	0.46%
Deletions	14,012
Mapped reads with at least one deletion	2%
Homopolymer indels	45.45%

2.6. Chromosome stats

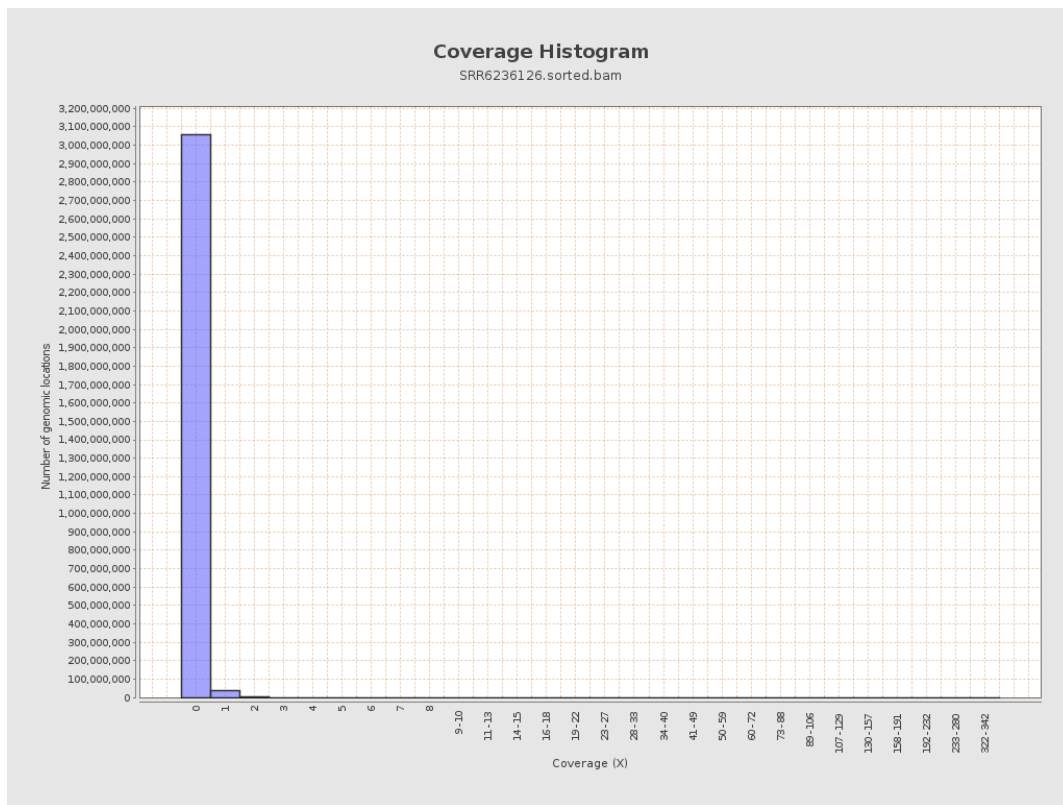
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1515688	0.0061	0.228
chr2	243199373	3136832	0.0129	0.1714
chr3	198022430	2841565	0.0143	0.1271
chr4	191154276	2617353	0.0137	0.131
chr5	180915260	2687785	0.0149	0.1305
chr6	171115067	6484230	0.0379	0.2884
chr7	159138663	1671267	0.0105	0.1182

chr8	146364022	3578480	0.0244	0.2676
chr9	141213431	2062481	0.0146	0.1535
chr10	135534747	1294498	0.0096	0.1259
chr11	135006516	1538099	0.0114	0.1282
chr12	133851895	1080826	0.0081	0.0983
chr13	115169878	2552301	0.0222	0.1589
chr14	107349540	2140328	0.0199	0.1532
chr15	102531392	1594355	0.0155	0.1362
chr16	90354753	1352205	0.015	0.1358
chr17	81195210	696890	0.0086	0.108
chr18	78077248	1163343	0.0149	0.2087
chr19	59128983	1248416	0.0211	0.2068
chr20	63025520	727597	0.0115	0.1158
chr21	48129895	980013	0.0204	0.1575
chr22	51304566	275084	0.0054	0.0771
chrMT	16571	19592	1.1823	1.3044
chrX	155270560	1441407	0.0093	0.1076
chrY	59373566	100937	0.0017	0.0605

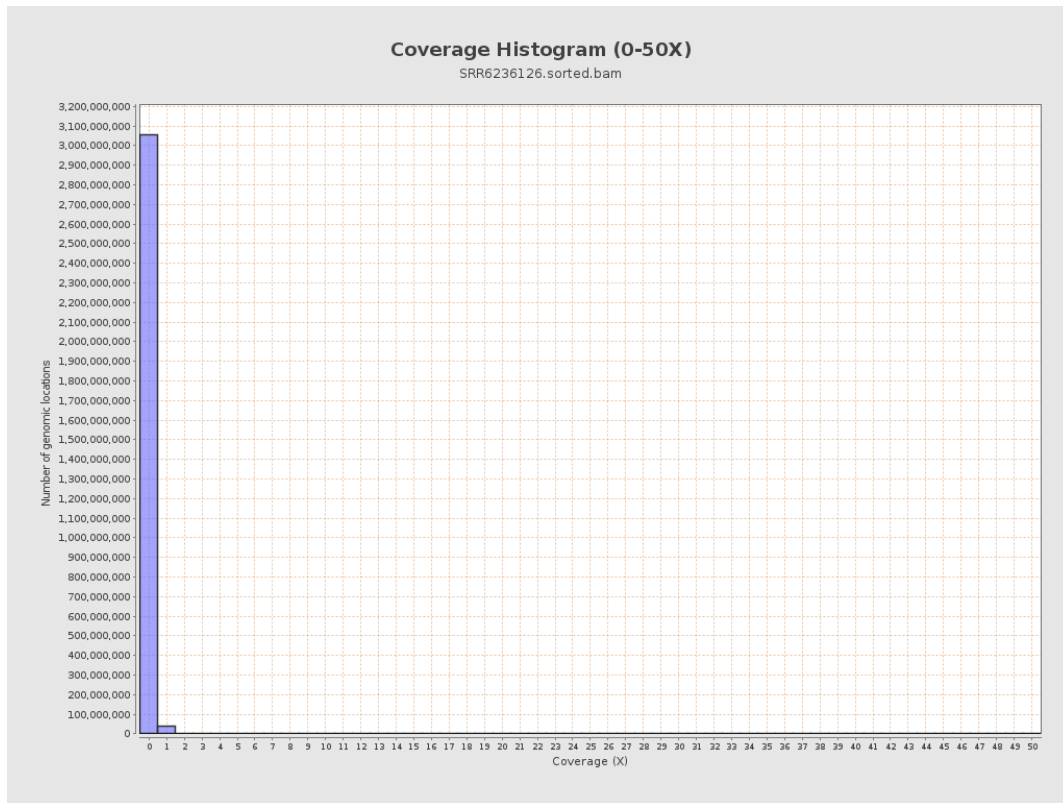
3. Results : Coverage across reference



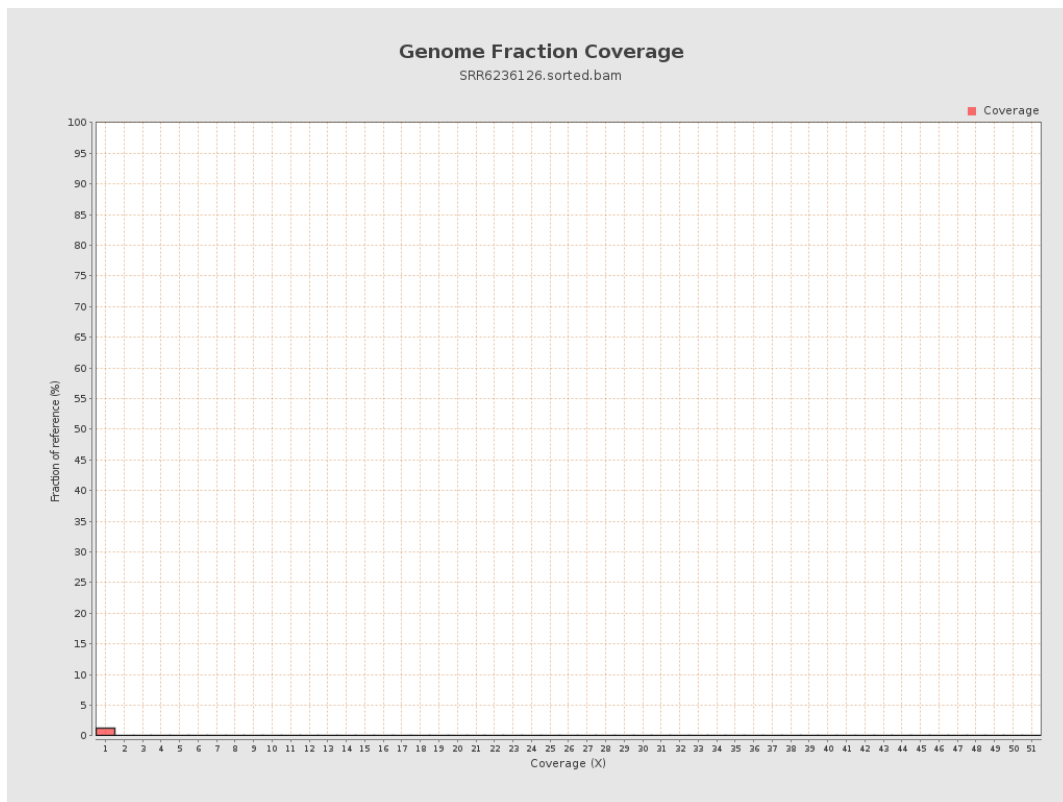
4. Results : Coverage Histogram



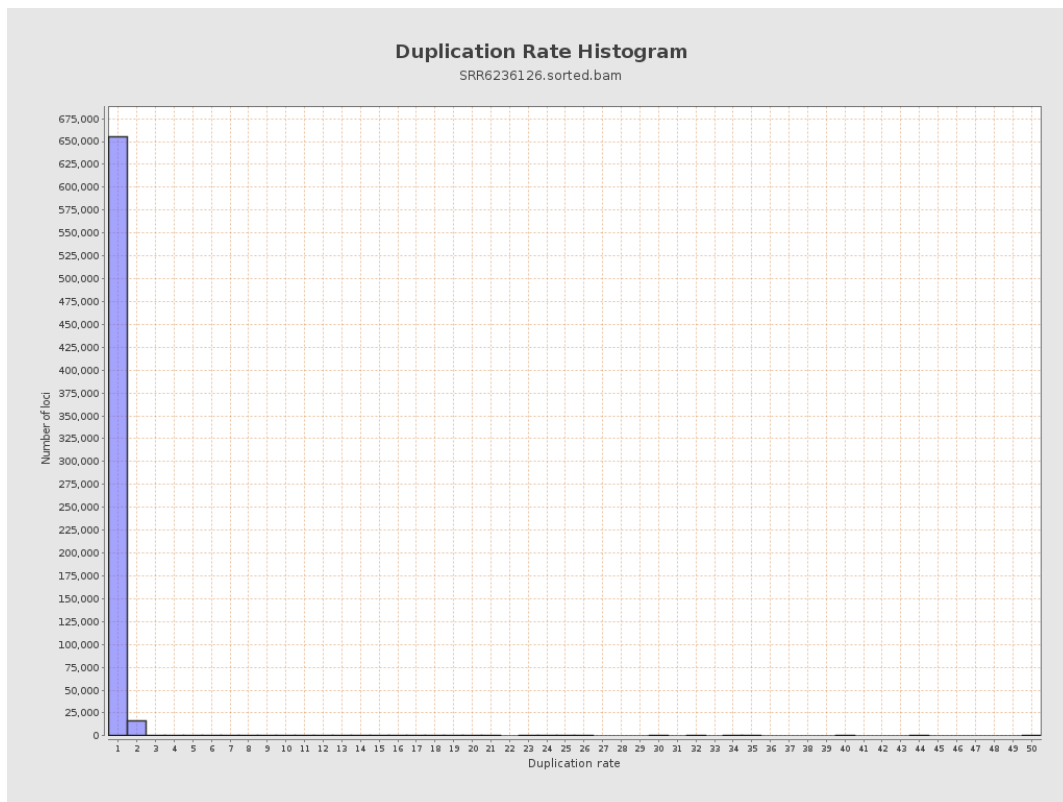
5. Results : Coverage Histogram (0-50X)



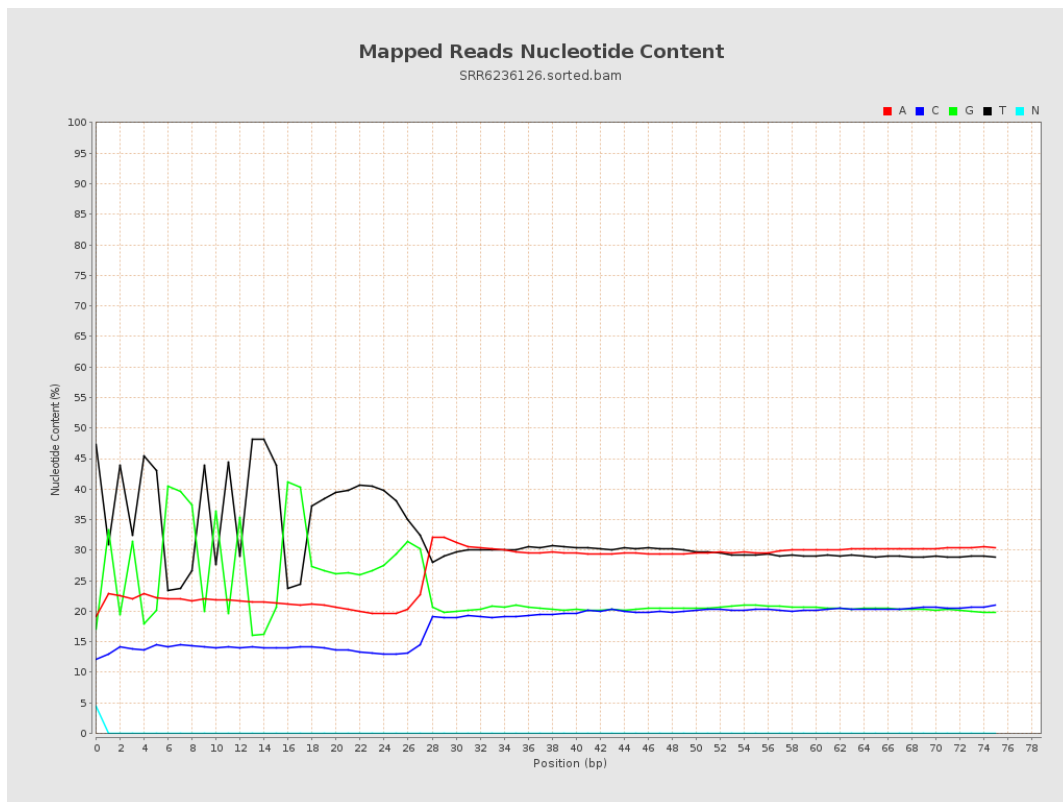
6. Results : Genome Fraction Coverage



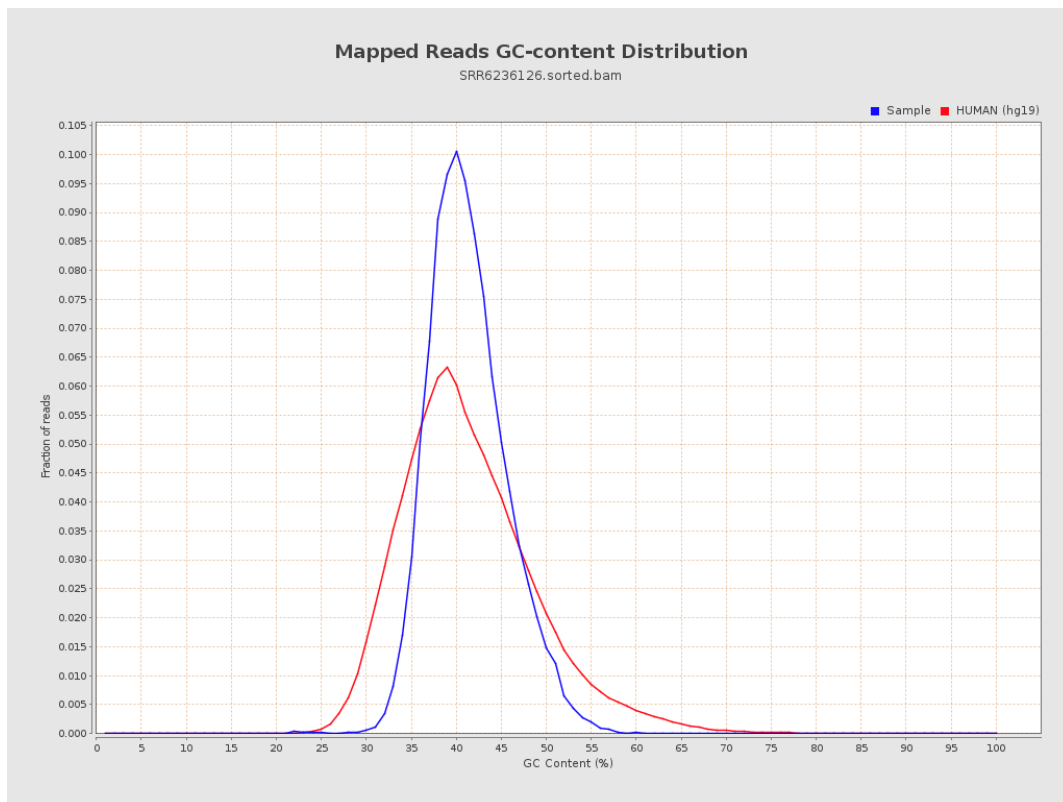
7. Results : Duplication Rate Histogram



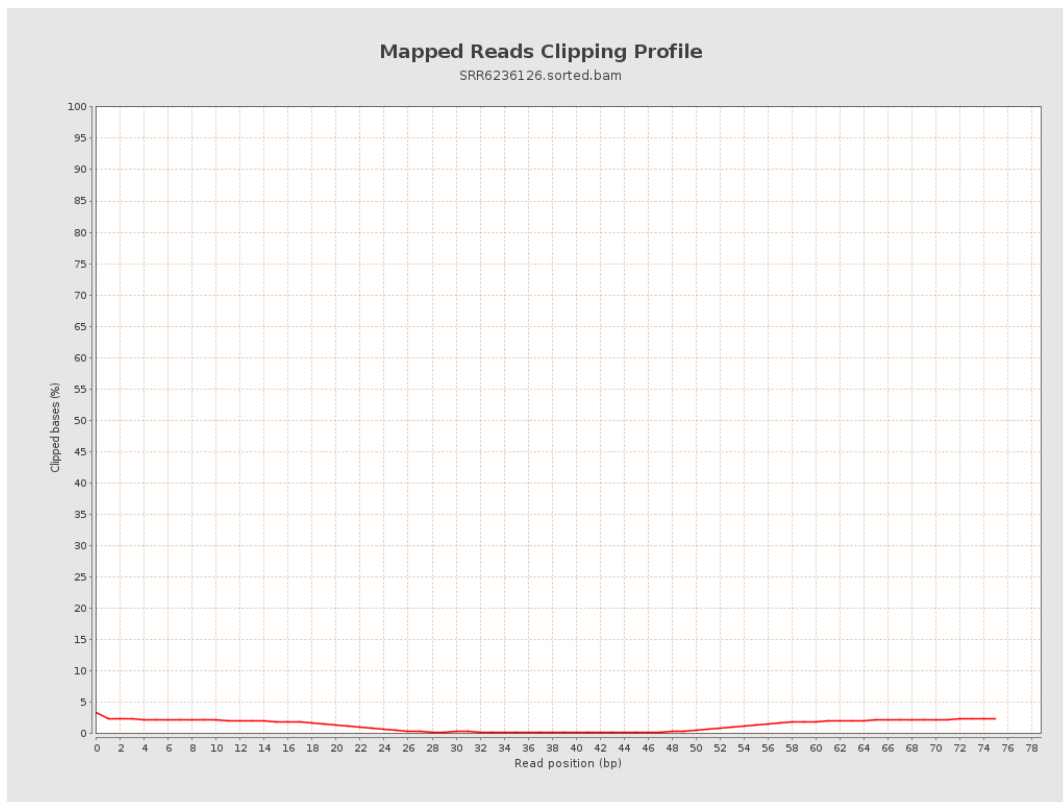
8. Results : Mapped Reads Nucleotide Content



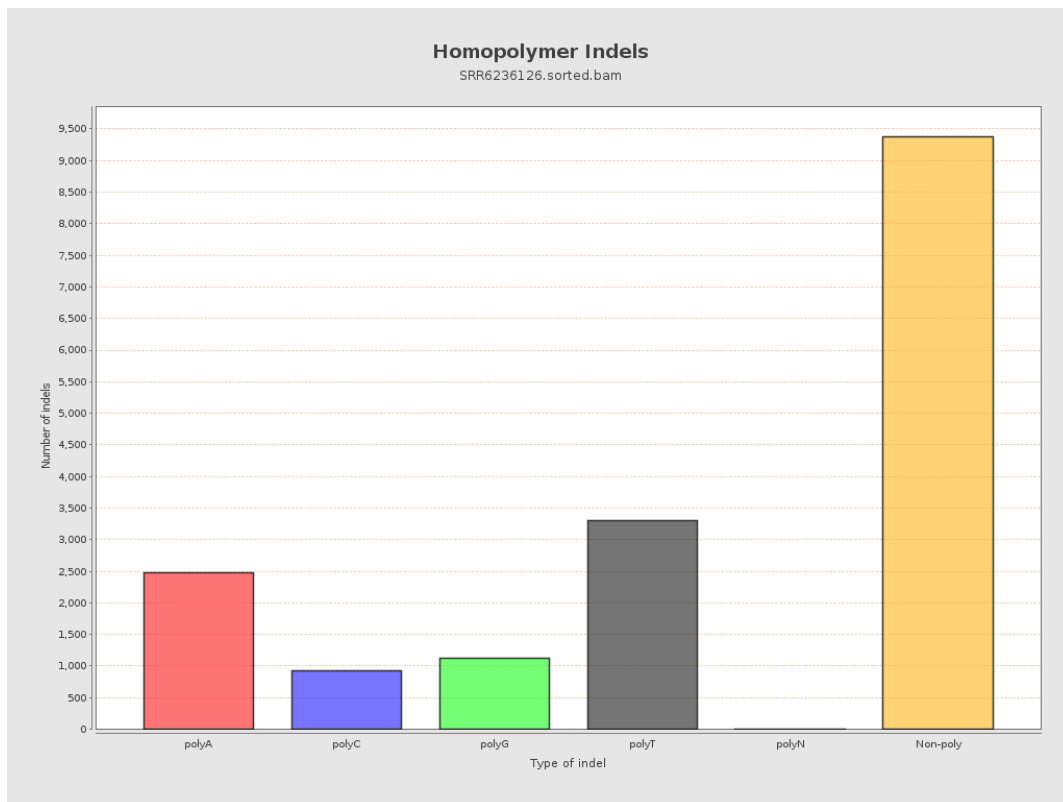
9. Results : Mapped Reads GC-content Distribution



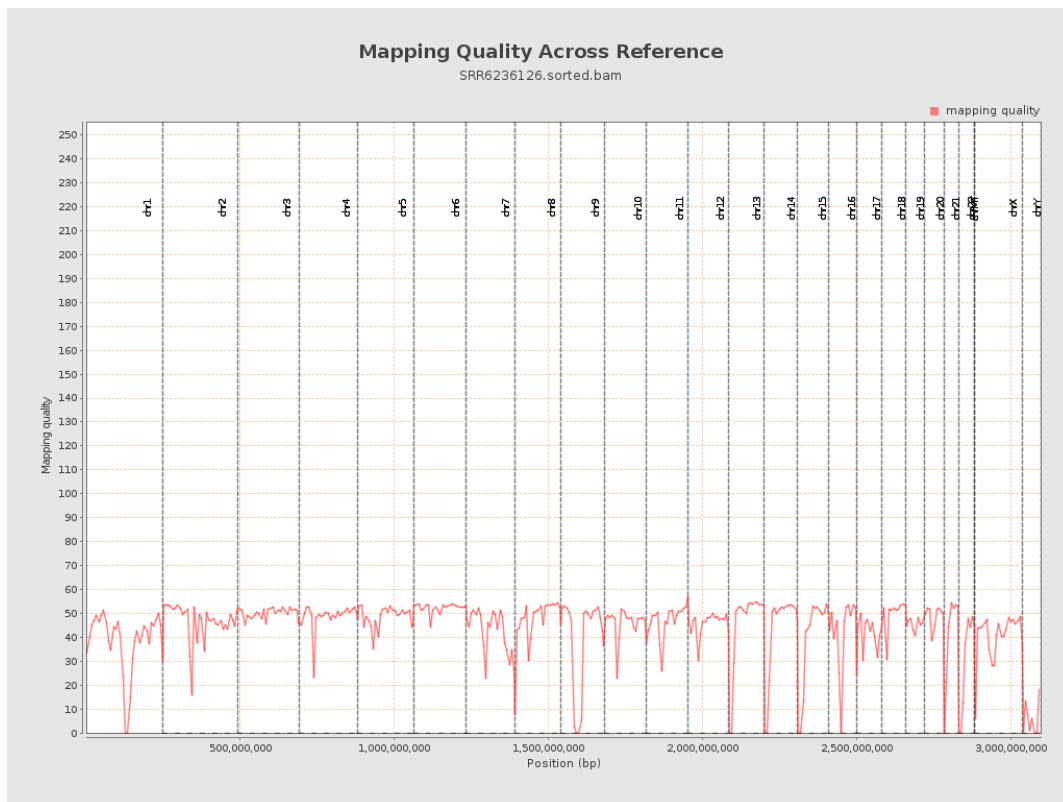
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

