

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:30:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240185.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_SRR6240185 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240185.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:30:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240185.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,415,650
Mapped reads	1,117,106 / 78.91%
Unmapped reads	298,544 / 21.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,432 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	110,027 / 7.77%
Duplication rate	7.8%
Clipped reads	497,715 / 35.16%

2.2. ACGT Content

Number/percentage of A's	21,363,698 / 28.53%
Number/percentage of C's	13,970,477 / 18.66%
Number/percentage of T's	23,716,022 / 31.67%
Number/percentage of G's	15,780,729 / 21.08%
Number/percentage of N's	42,609 / 0.06%
GC Percentage	39.74%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.3061
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	47.16
----------------------	-------

2.5. Mismatches and indels

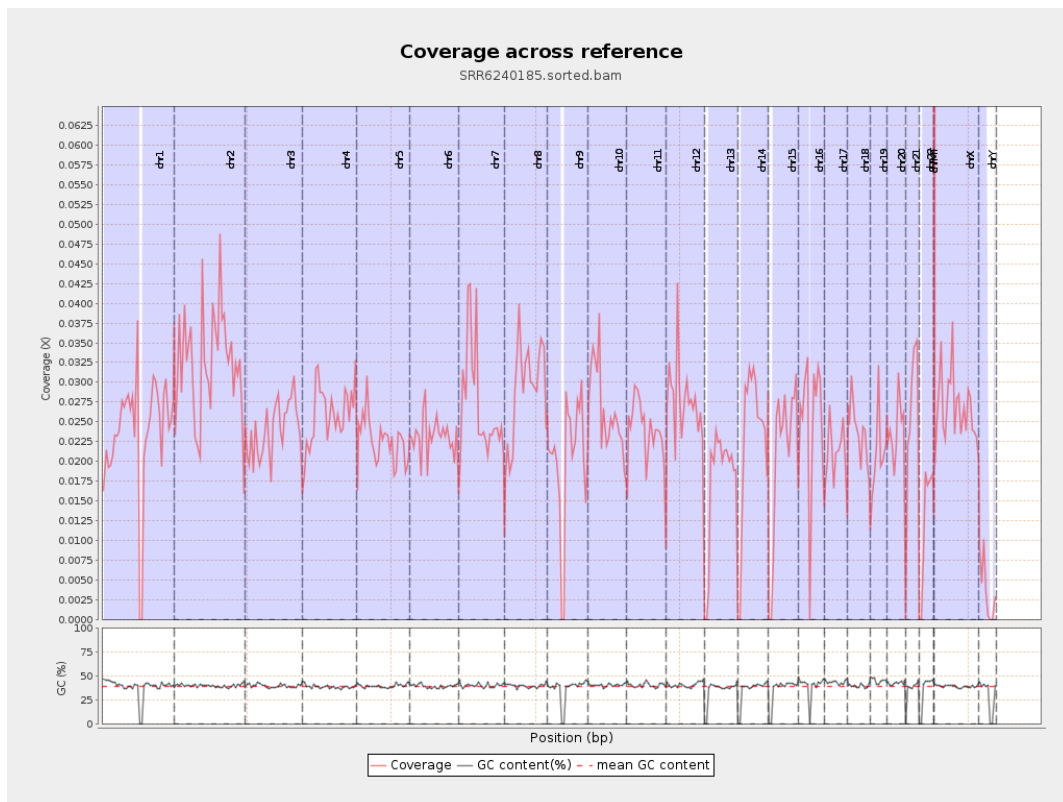
General error rate	0.91%
Mismatches	671,455
Insertions	5,521
Mapped reads with at least one insertion	0.49%
Deletions	19,247
Mapped reads with at least one deletion	1.71%
Homopolymer indels	47.98%

2.6. Chromosome stats

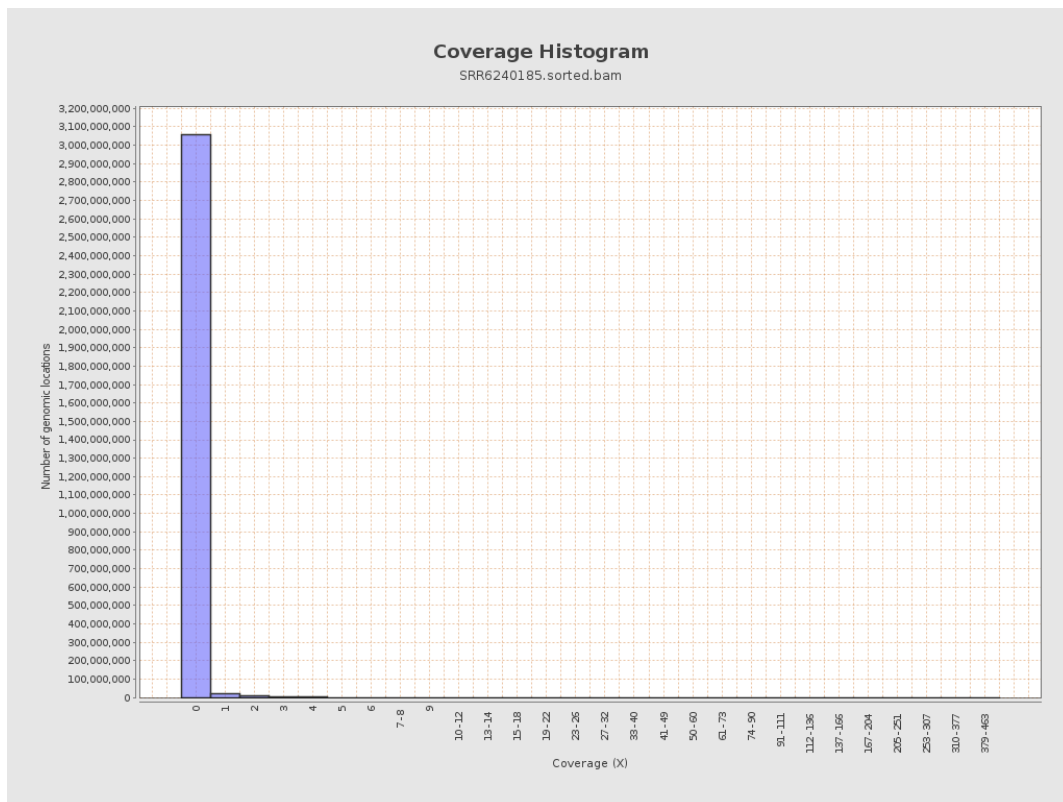
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5924495	0.0238	0.4456
chr2	243199373	7895948	0.0325	0.346
chr3	198022430	4745697	0.024	0.2549
chr4	191154276	4939489	0.0258	0.2673
chr5	180915260	4097719	0.0226	0.251
chr6	171115067	3953368	0.0231	0.2646
chr7	159138663	4308663	0.0271	0.3862

chr8	146364022	4275334	0.0292	0.393
chr9	141213431	2860183	0.0203	0.2686
chr10	135534747	3596714	0.0265	0.3092
chr11	135006516	3259718	0.0241	0.2951
chr12	133851895	3685054	0.0275	0.2738
chr13	115169878	1997807	0.0173	0.218
chr14	107349540	2457010	0.0229	0.2562
chr15	102531392	2144330	0.0209	0.2434
chr16	90354753	2207733	0.0244	0.2626
chr17	81195210	1709370	0.0211	0.2491
chr18	78077248	1845768	0.0236	0.3995
chr19	59128983	1245599	0.0211	0.3195
chr20	63025520	1476489	0.0234	0.2555
chr21	48129895	1243951	0.0258	0.2715
chr22	51304566	640694	0.0125	0.1792
chrMT	16571	18218	1.0994	1.9311
chrX	155270560	4162975	0.0268	0.2781
chrY	59373566	214605	0.0036	0.0936

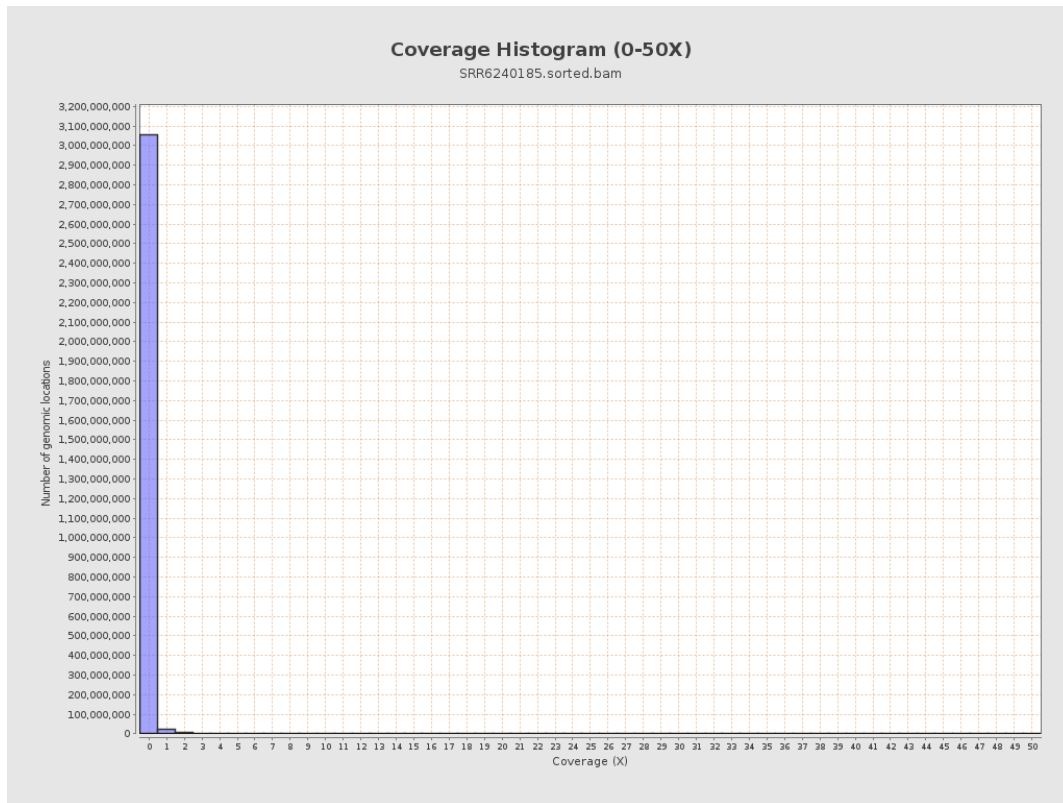
3. Results : Coverage across reference



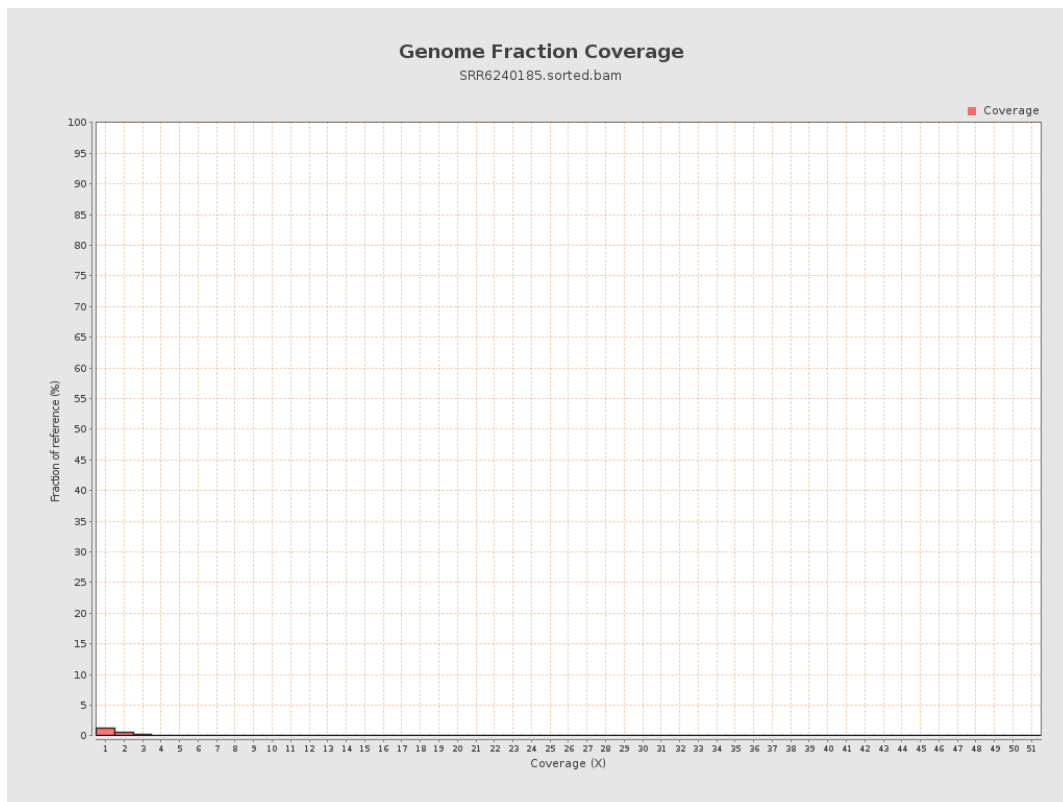
4. Results : Coverage Histogram



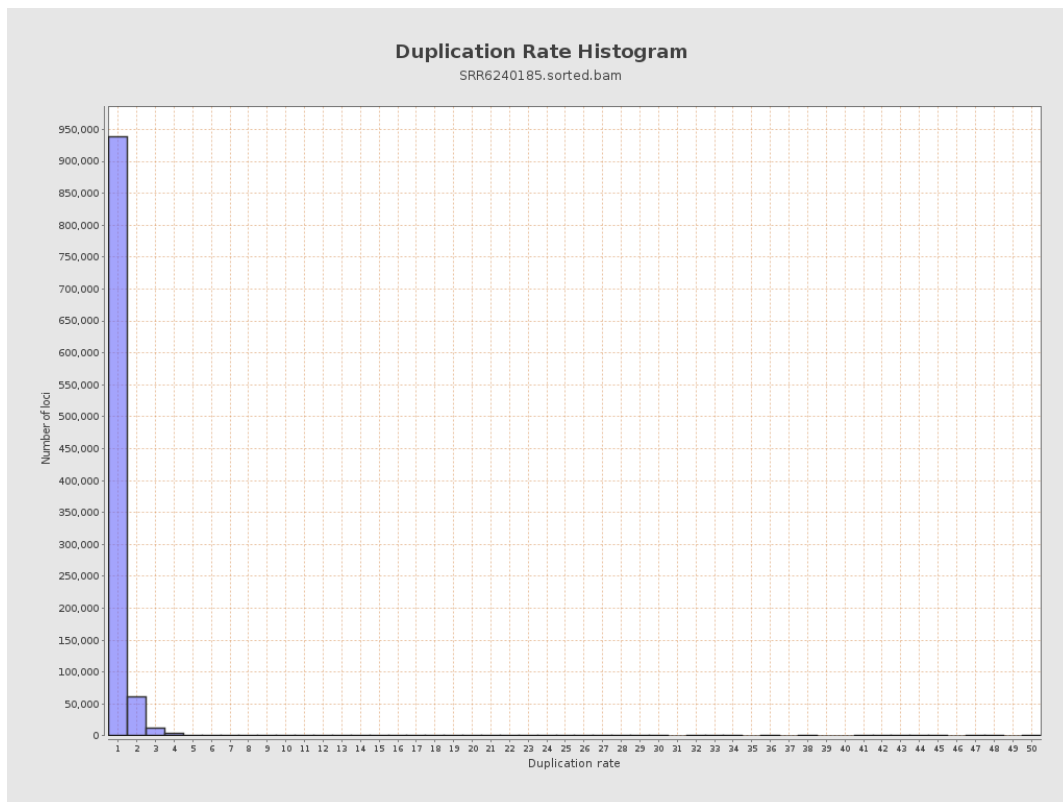
5. Results : Coverage Histogram (0-50X)



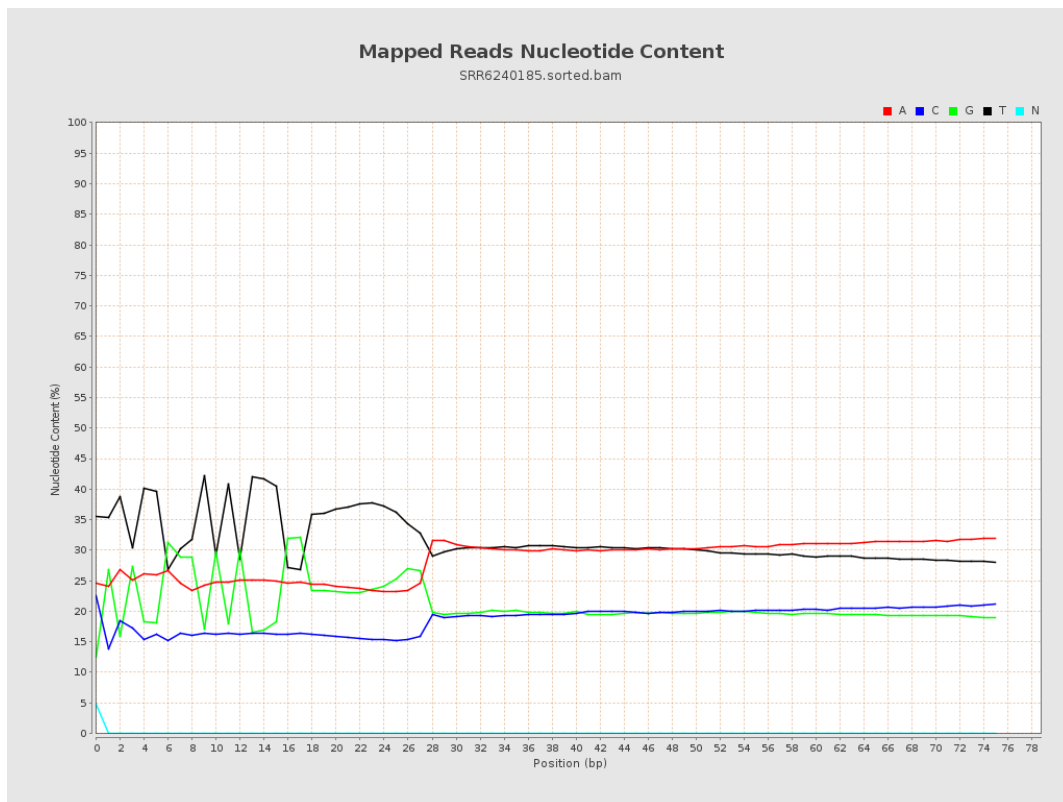
6. Results : Genome Fraction Coverage



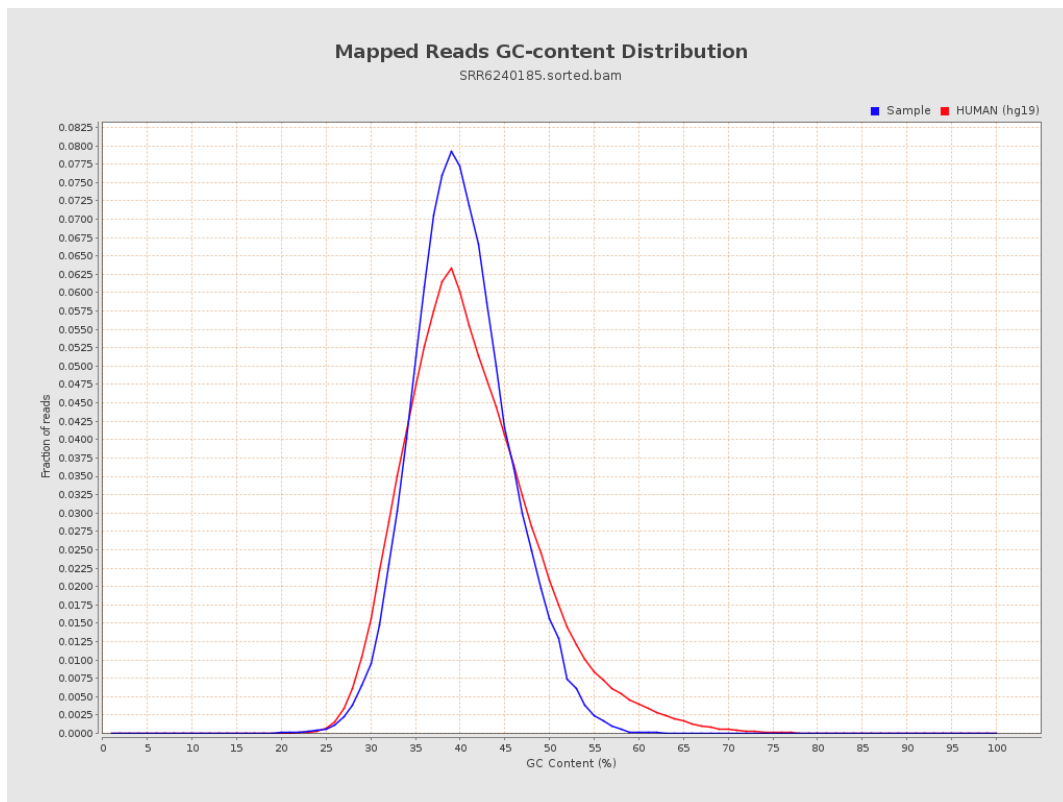
7. Results : Duplication Rate Histogram



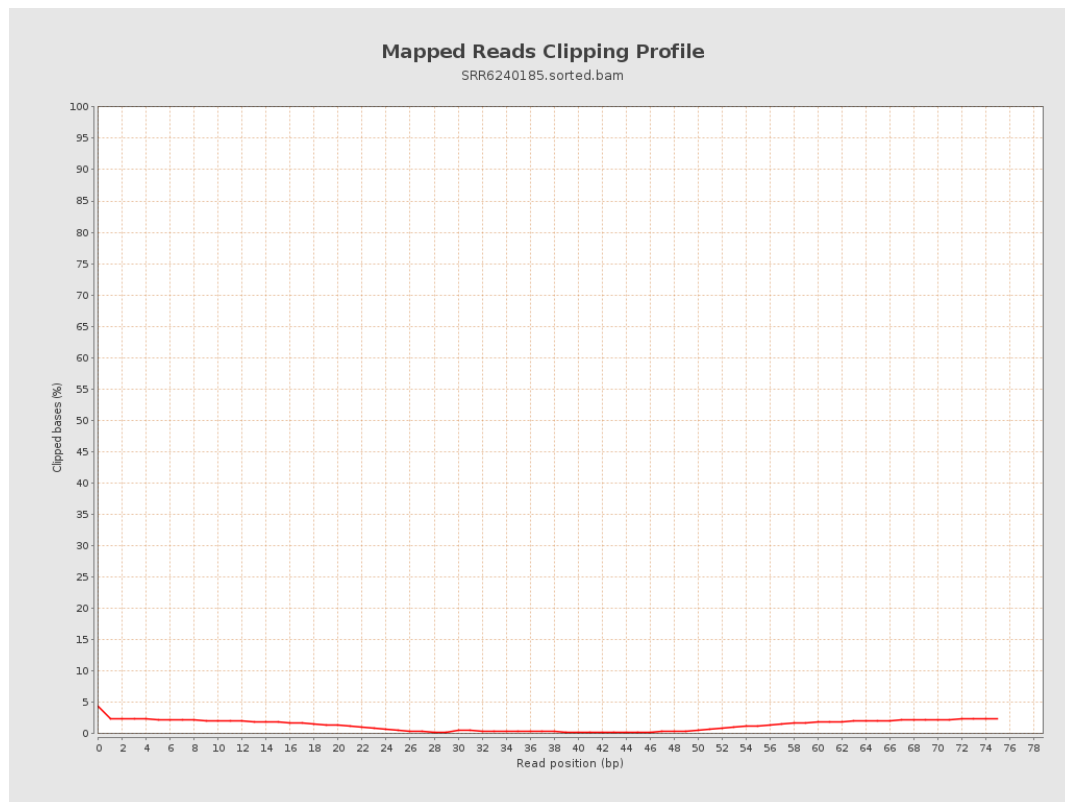
8. Results : Mapped Reads Nucleotide Content



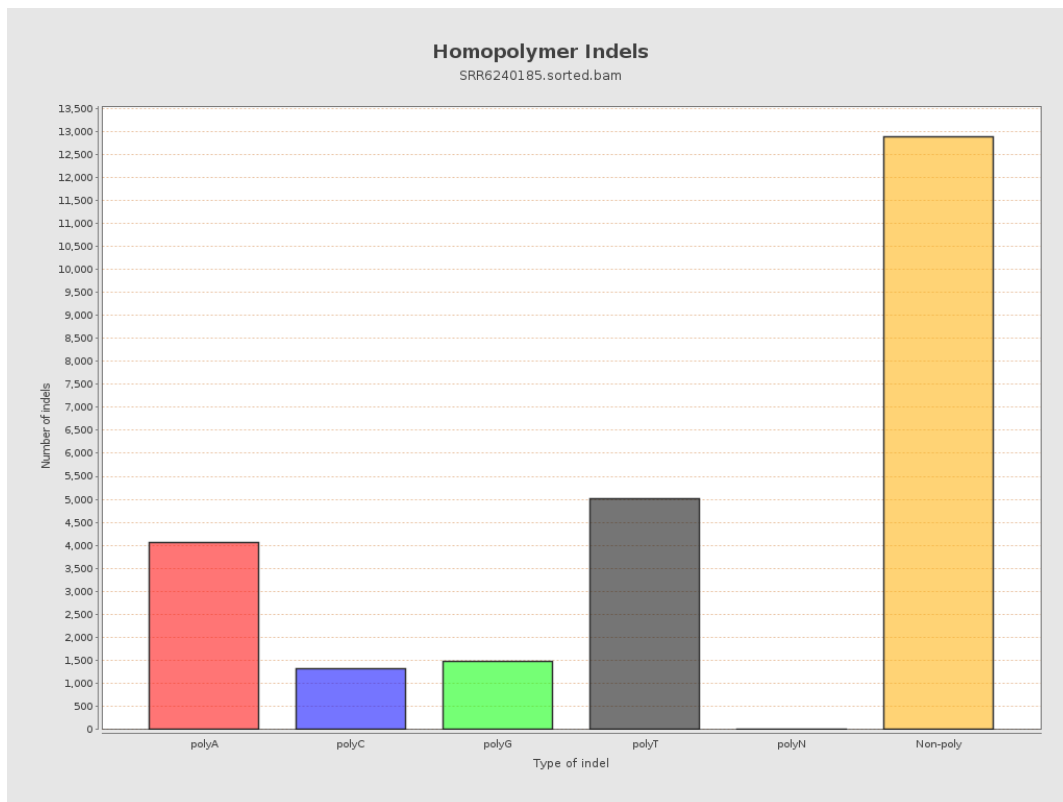
9. Results : Mapped Reads GC-content Distribution



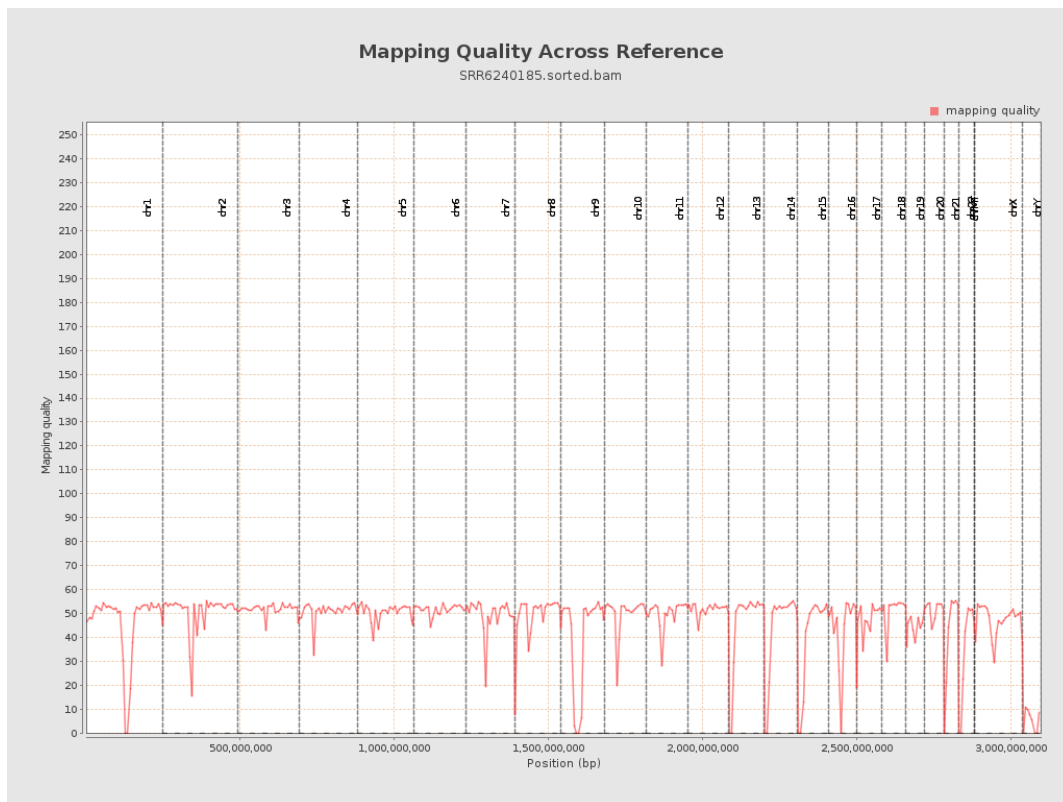
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

