

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:15:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548960.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_SRR1548960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548960.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:15:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,551,623
Mapped reads	9,148,440 / 86.7%
Unmapped reads	1,403,183 / 13.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	518,398 / 4.91%
Duplication rate	3.5%
Clipped reads	819,410 / 7.77%

2.2. ACGT Content

Number/percentage of A's	100,121,578 / 27.71%
Number/percentage of C's	79,353,699 / 21.96%
Number/percentage of T's	102,192,326 / 28.28%
Number/percentage of G's	79,649,052 / 22.04%
Number/percentage of N's	519 / 0%
GC Percentage	44.01%

2.3. Coverage

Mean	0.1167
Standard Deviation	1.1737

2.4. Mapping Quality

Mean Mapping Quality	35
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2.5. Mismatches and indels

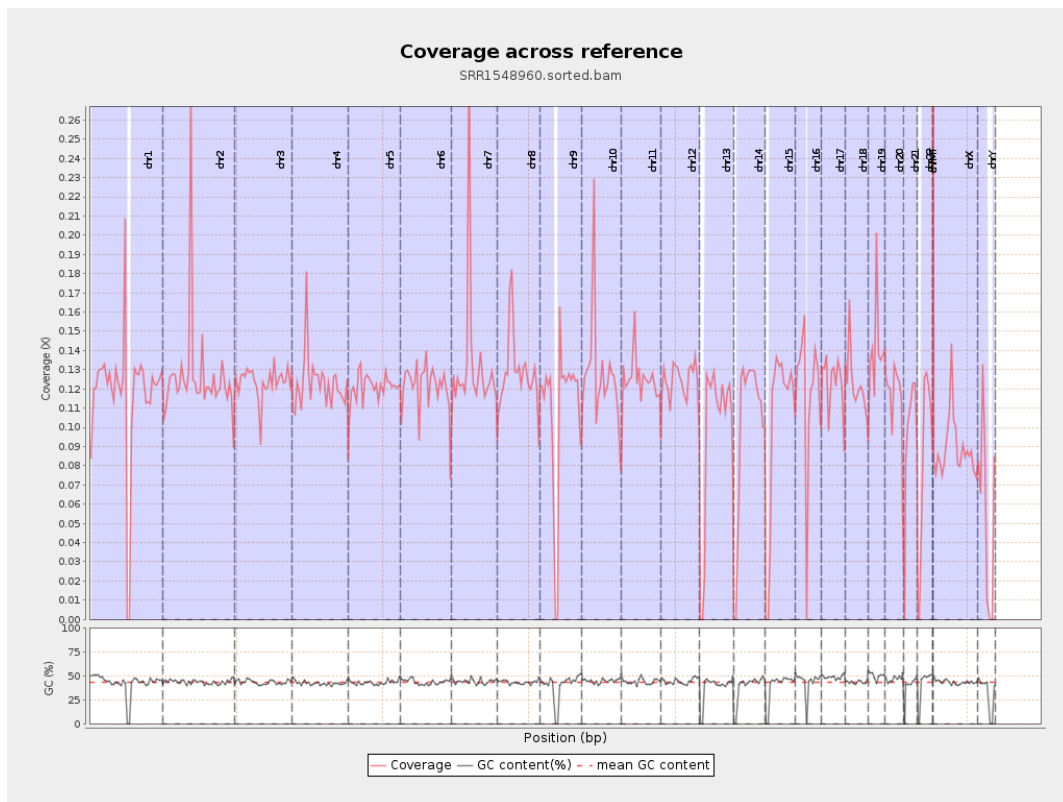
General error rate	0.33%
Mismatches	1,188,778
Insertions	12,746
Mapped reads with at least one insertion	0.14%
Deletions	25,991
Mapped reads with at least one deletion	0.28%
Homopolymer indels	37.5%

2.6. Chromosome stats

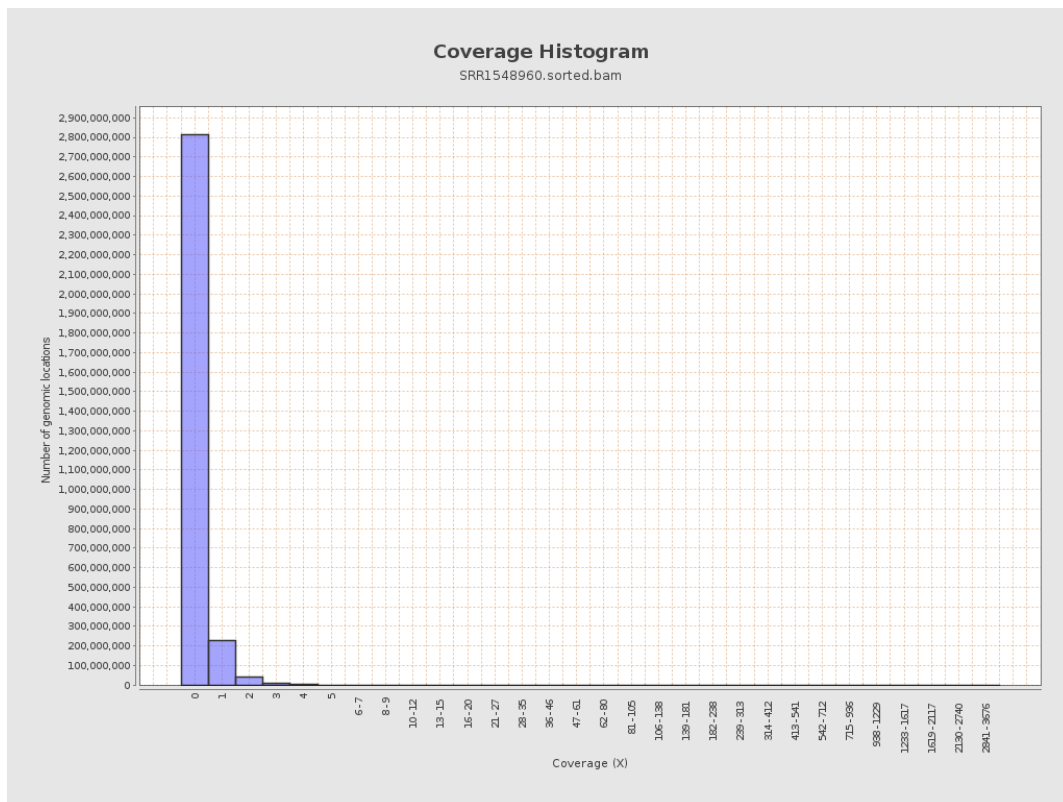
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29205545	0.1172	2.0317
chr2	243199373	30733788	0.1264	1.2666
chr3	198022430	24450772	0.1235	0.436
chr4	191154276	23544441	0.1232	0.5279
chr5	180915260	21894701	0.121	0.4652
chr6	171115067	20781377	0.1214	0.4866
chr7	159138663	21037211	0.1322	1.9755
chr8	146364022	18814403	0.1285	1.9512

chr9	141213431	15391468	0.109	1.3046
chr10	135534747	17286093	0.1275	0.9527
chr11	135006516	16813909	0.1245	0.7952
chr12	133851895	16707038	0.1248	0.506
chr13	115169878	11269943	0.0979	0.3726
chr14	107349540	10998973	0.1025	0.714
chr15	102531392	10380894	0.1012	0.4025
chr16	90354753	10483325	0.116	0.6067
chr17	81195210	10103564	0.1244	0.4933
chr18	78077248	9640384	0.1235	2.4382
chr19	59128983	8333917	0.1409	2.1219
chr20	63025520	7360359	0.1168	0.5042
chr21	48129895	4636004	0.0963	0.6382
chr22	51304566	4284949	0.0835	0.5641
chrMT	16571	10712	0.6464	1.0463
chrX	155270560	13798221	0.0889	0.6869
chrY	59373566	3388263	0.0571	0.5328

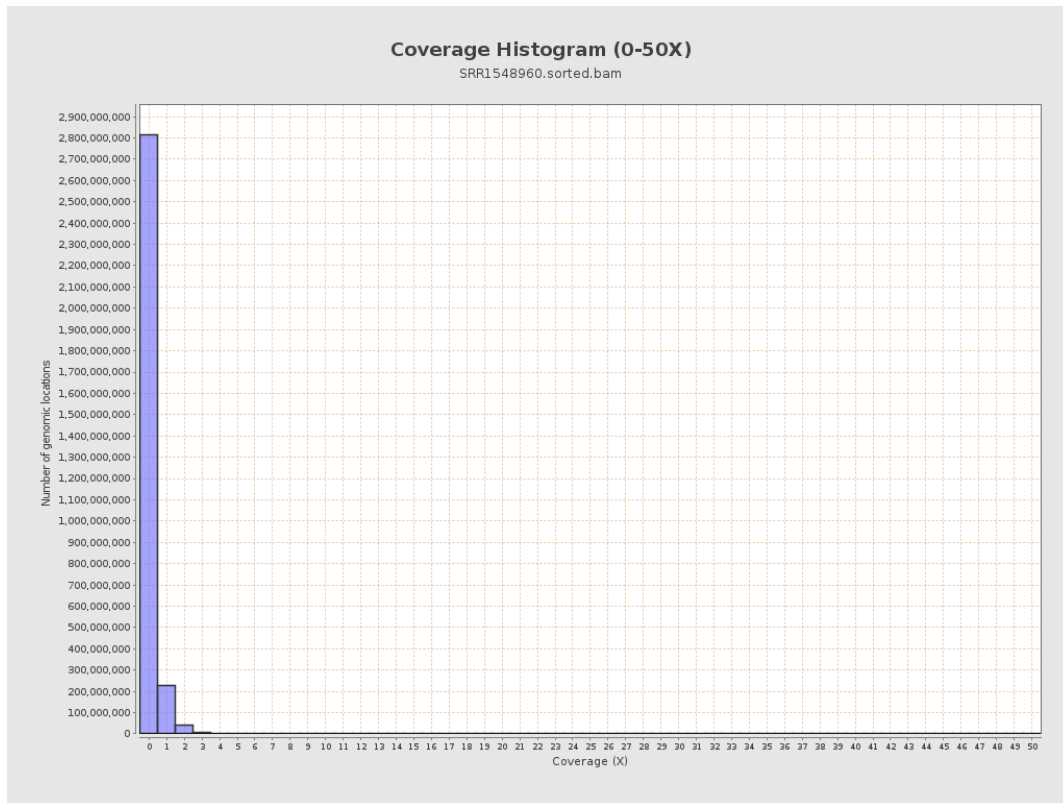
3. Results : Coverage across reference



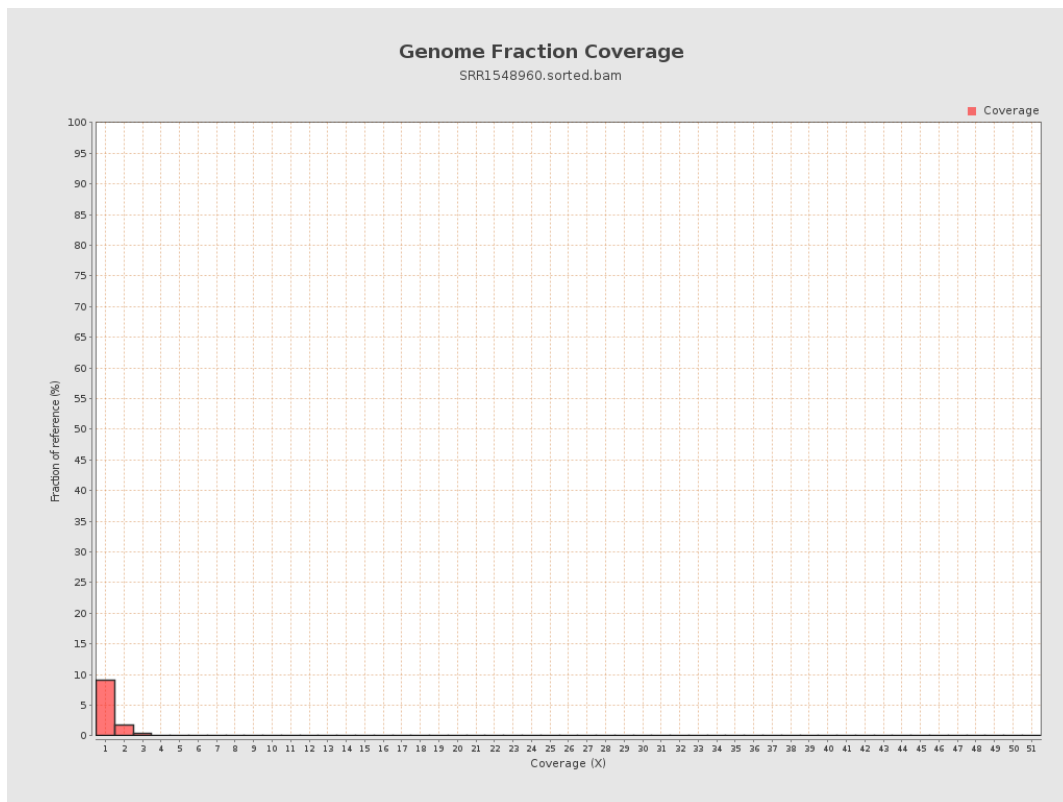
4. Results : Coverage Histogram



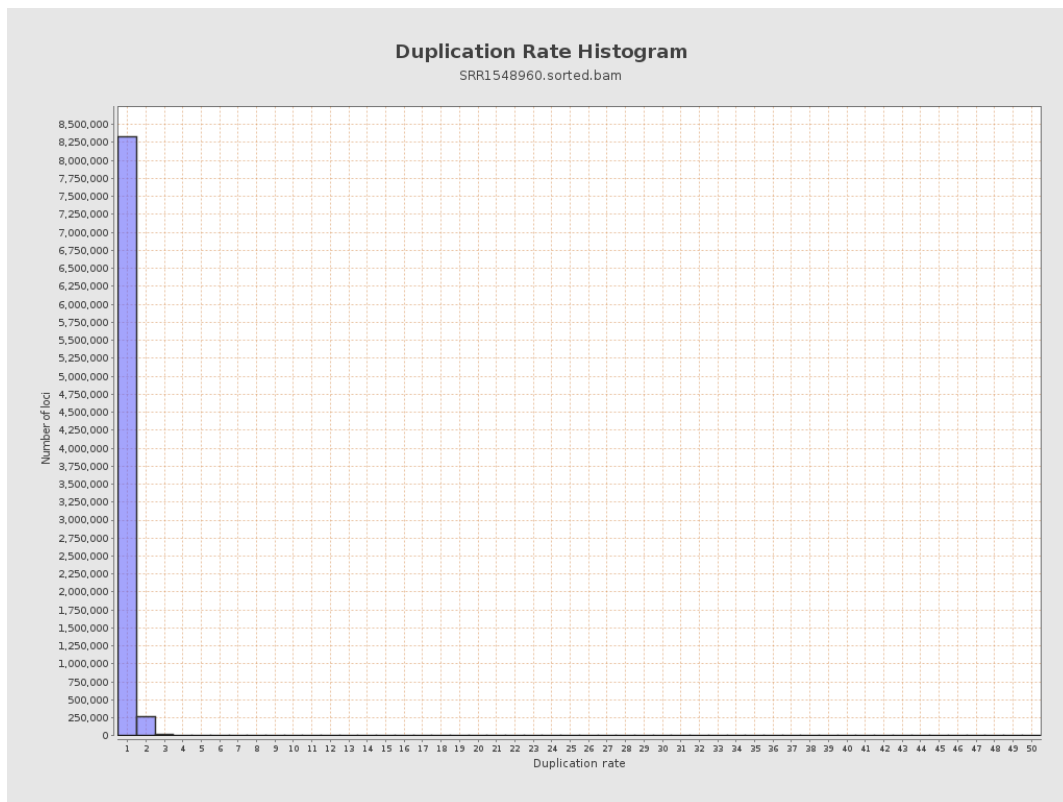
5. Results : Coverage Histogram (0-50X)



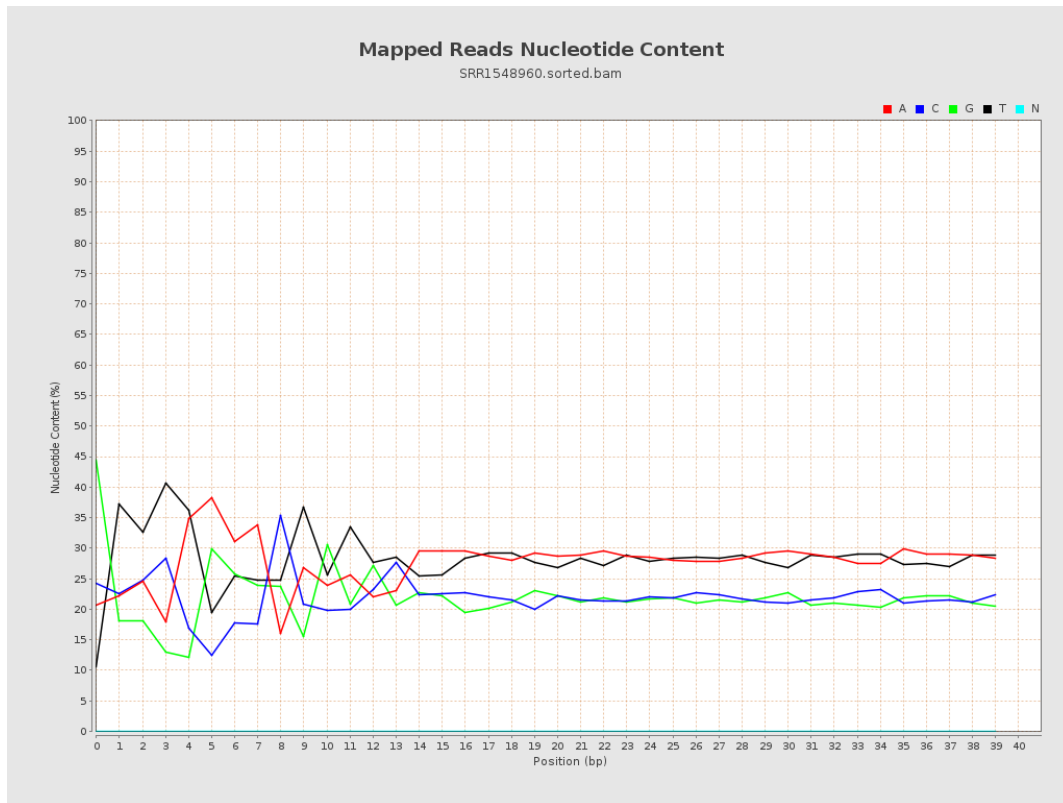
6. Results : Genome Fraction Coverage



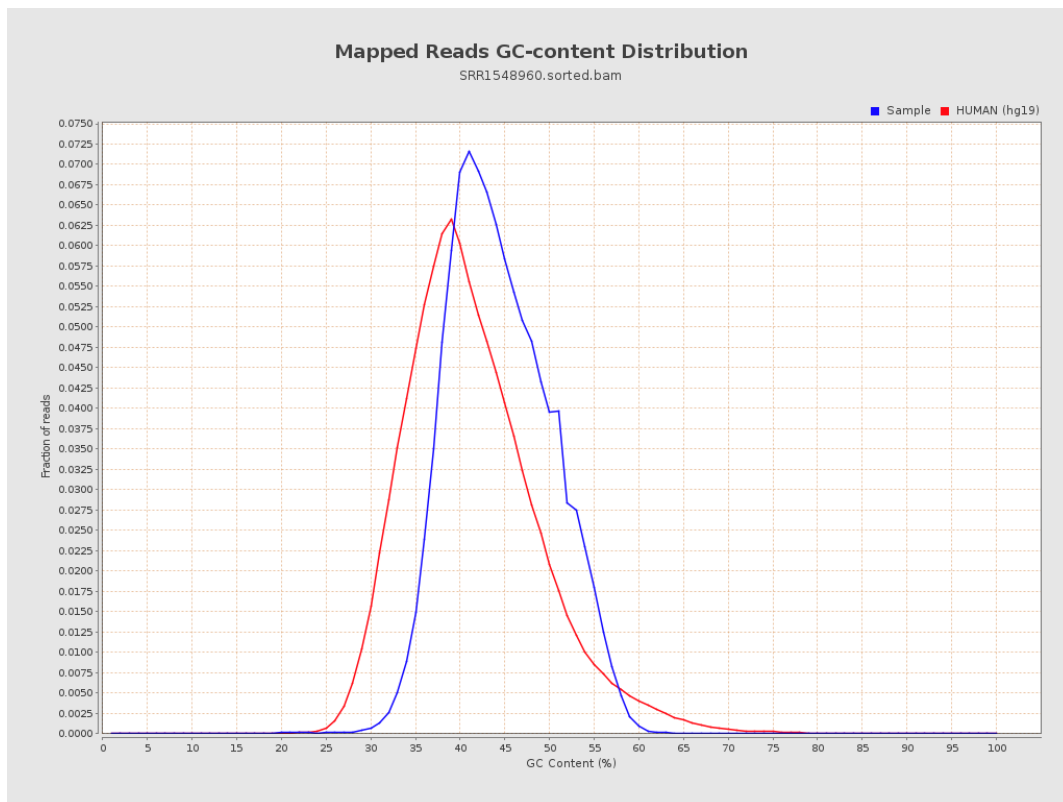
7. Results : Duplication Rate Histogram



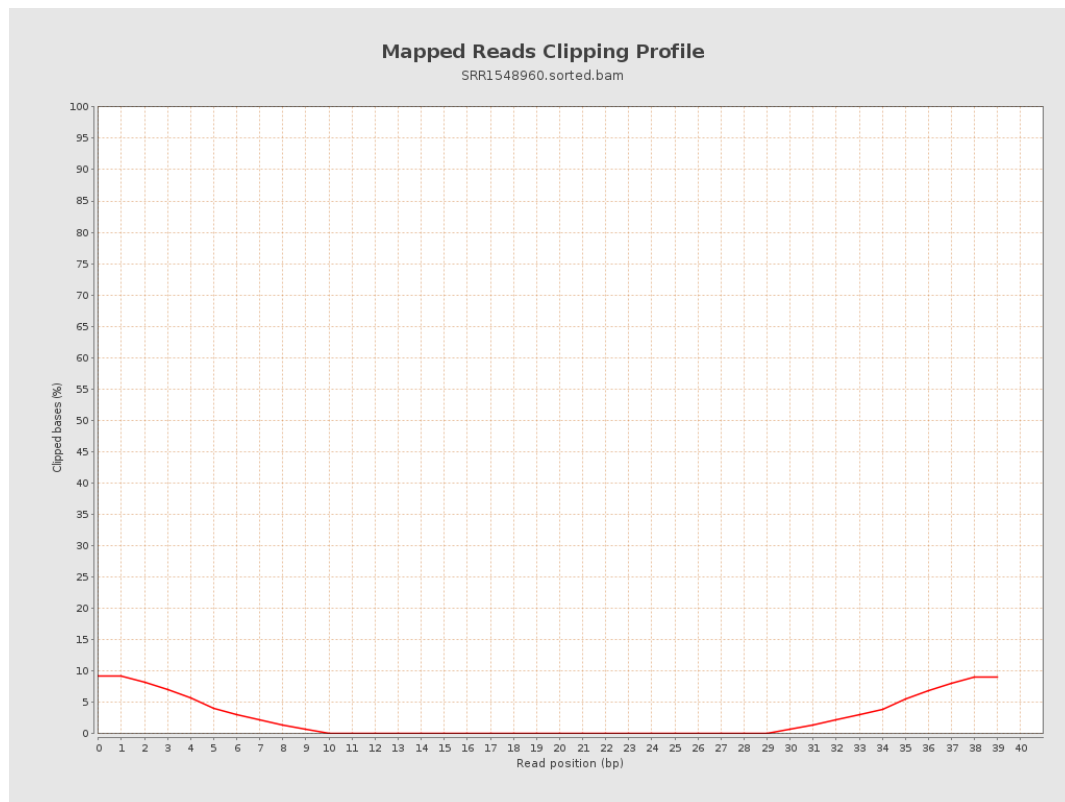
8. Results : Mapped Reads Nucleotide Content



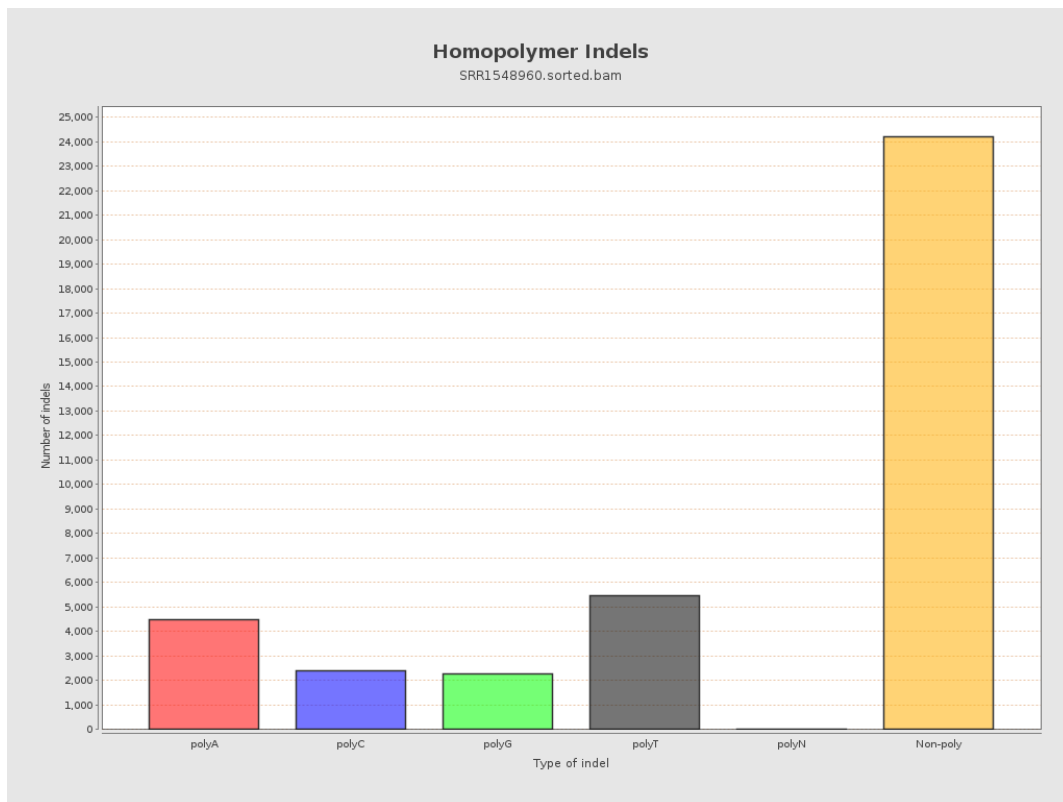
9. Results : Mapped Reads GC-content Distribution



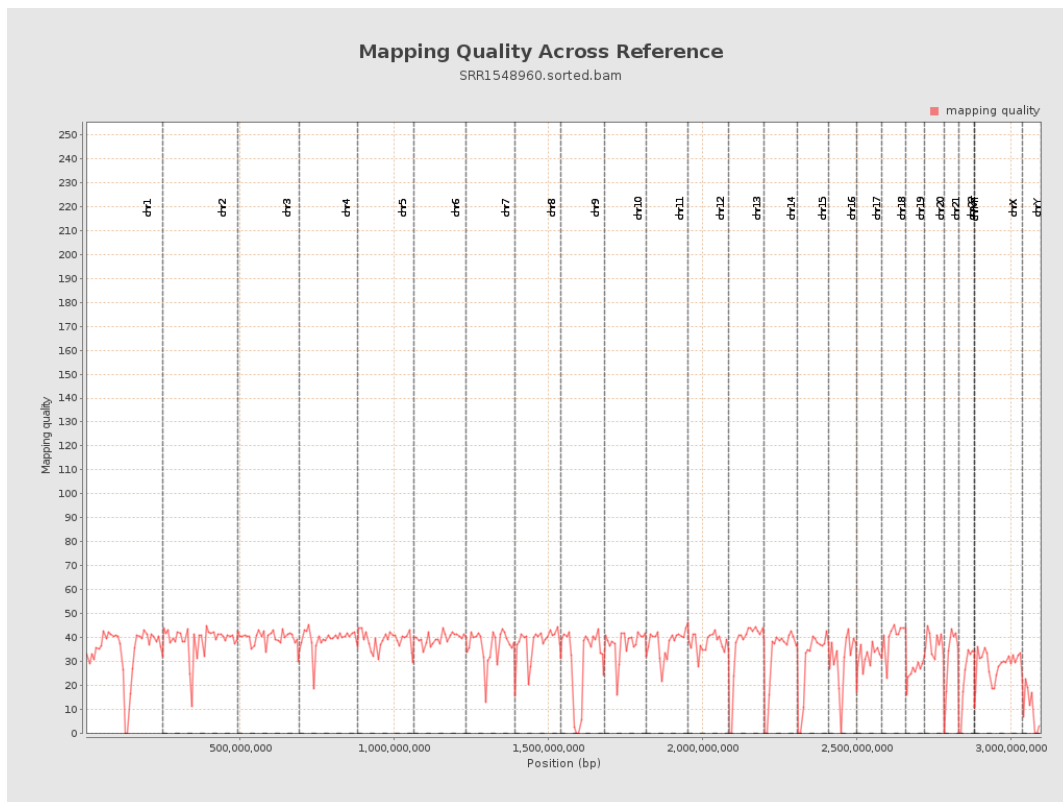
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

