

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:59:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085033.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_SRR3085033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085033.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:59:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,195,751
Mapped reads	2,880,204 / 90.13%
Unmapped reads	315,547 / 9.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,875 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	103,685 / 3.24%
Duplication rate	2.82%
Clipped reads	1,415,986 / 44.31%

2.2. ACGT Content

Number/percentage of A's	53,209,627 / 27.94%
Number/percentage of C's	37,019,980 / 19.44%
Number/percentage of T's	57,738,795 / 30.32%
Number/percentage of G's	42,429,618 / 22.28%
Number/percentage of N's	20,299 / 0.01%
GC Percentage	41.72%

2.3. Coverage

Mean	0.0615

Standard Deviation	0.4281
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2.4. Mapping Quality

Mean Mapping Quality	43.97
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2.5. Mismatches and indels

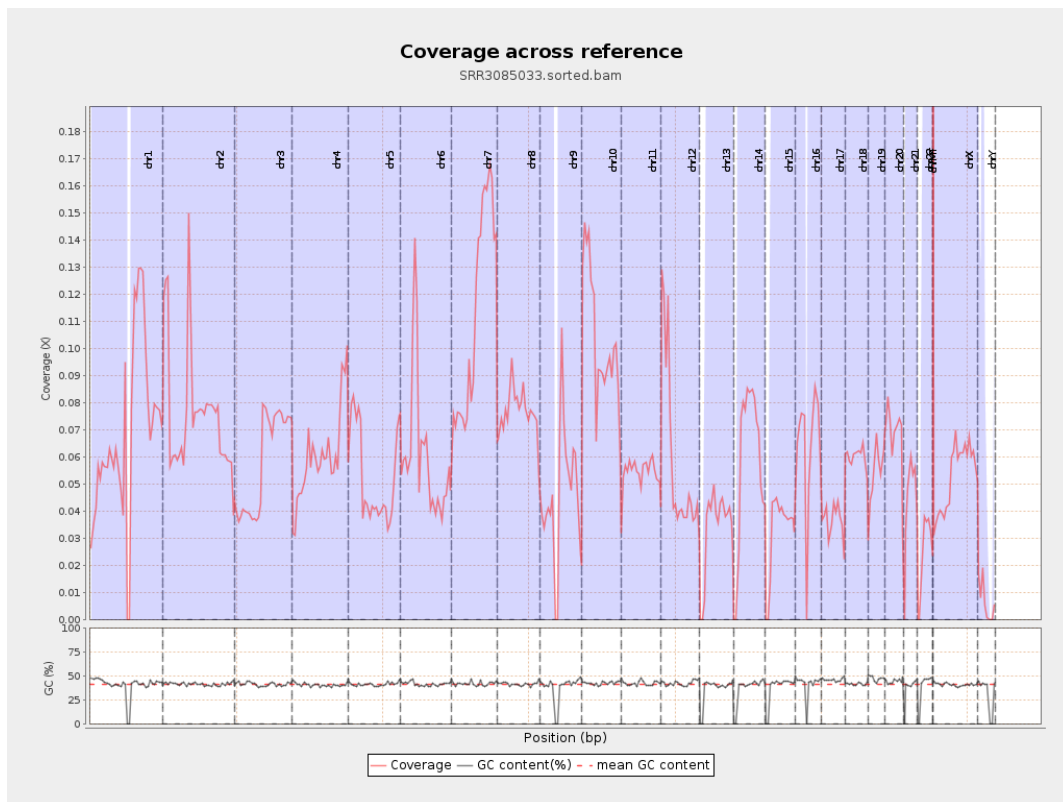
General error rate	0.92%
Mismatches	1,719,650
Insertions	13,782
Mapped reads with at least one insertion	0.47%
Deletions	39,031
Mapped reads with at least one deletion	1.34%
Homopolymer indels	45.84%

2.6. Chromosome stats

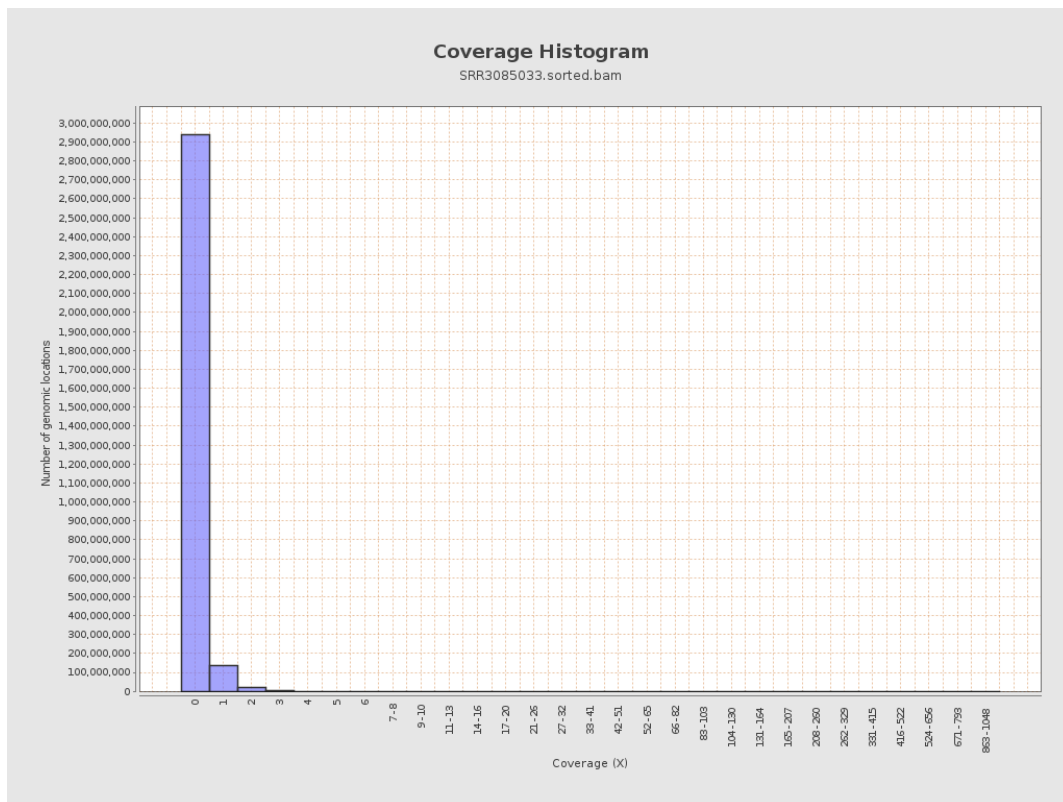
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17066905	0.0685	0.6318
chr2	243199373	18657664	0.0767	0.5584
chr3	198022430	11367725	0.0574	0.2827
chr4	191154276	11547436	0.0604	0.2909
chr5	180915260	9562911	0.0529	0.2671
chr6	171115067	10451913	0.0611	0.3875
chr7	159138663	17859353	0.1122	0.5154

chr8	146364022	11252837	0.0769	0.7073
chr9	141213431	6572443	0.0465	0.3888
chr10	135534747	14123001	0.1042	0.5938
chr11	135006516	7395584	0.0548	0.3991
chr12	133851895	7886865	0.0589	0.2891
chr13	115169878	3895258	0.0338	0.2112
chr14	107349540	6465092	0.0602	0.2968
chr15	102531392	3308644	0.0323	0.2218
chr16	90354753	5669729	0.0627	0.3107
chr17	81195210	3018318	0.0372	0.2455
chr18	78077248	4706938	0.0603	0.6019
chr19	59128983	3277313	0.0554	0.5074
chr20	63025520	4408329	0.0699	0.309
chr21	48129895	2131248	0.0443	0.2569
chr22	51304566	1276688	0.0249	0.1806
chrMT	16571	10750	0.6487	1.1004
chrX	155270560	8189738	0.0527	0.3026
chrY	59373566	382706	0.0064	0.1273

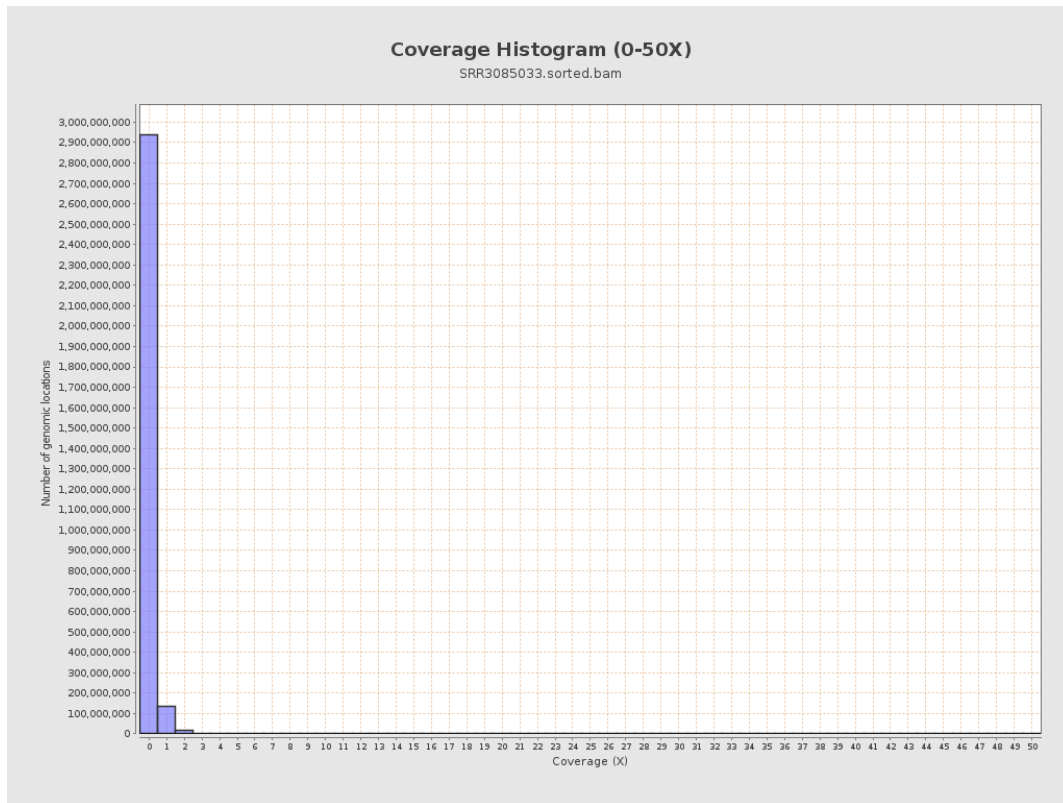
3. Results : Coverage across reference



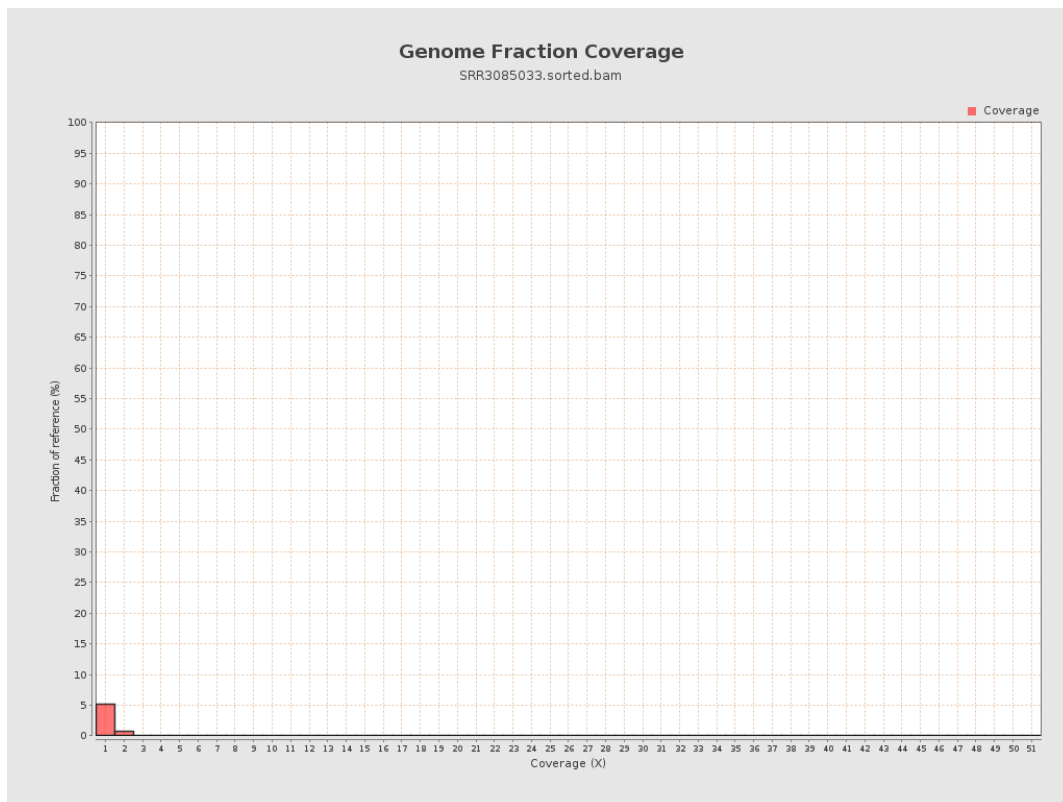
4. Results : Coverage Histogram



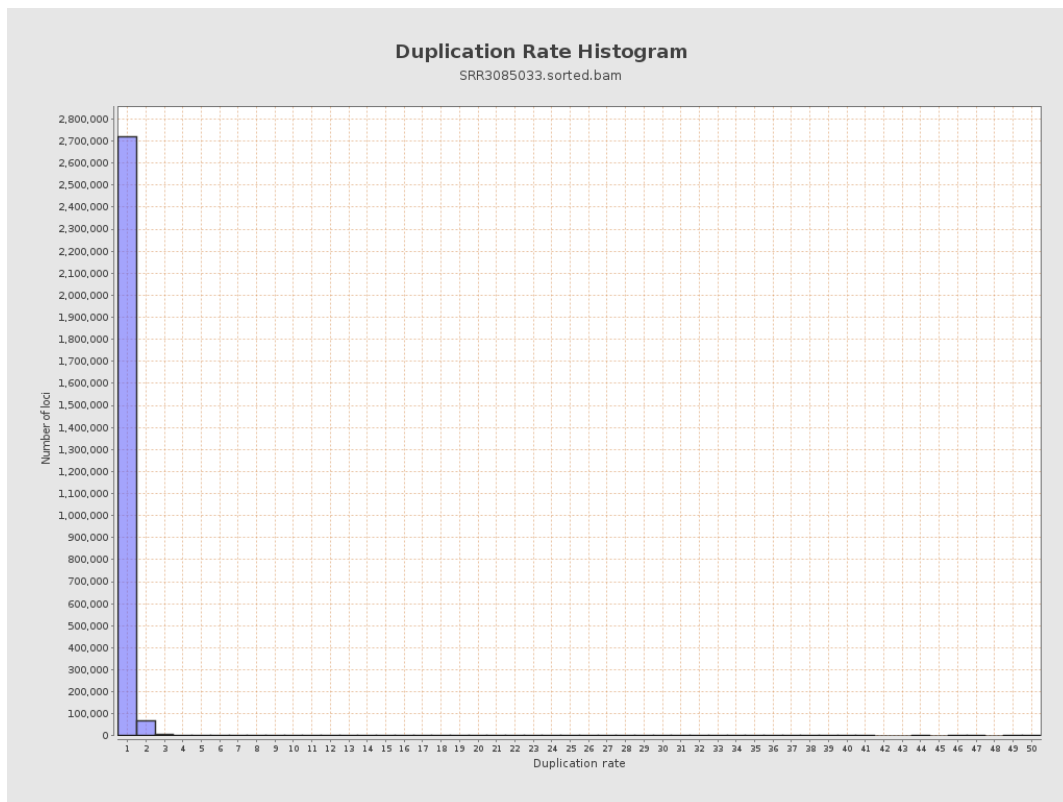
5. Results : Coverage Histogram (0-50X)



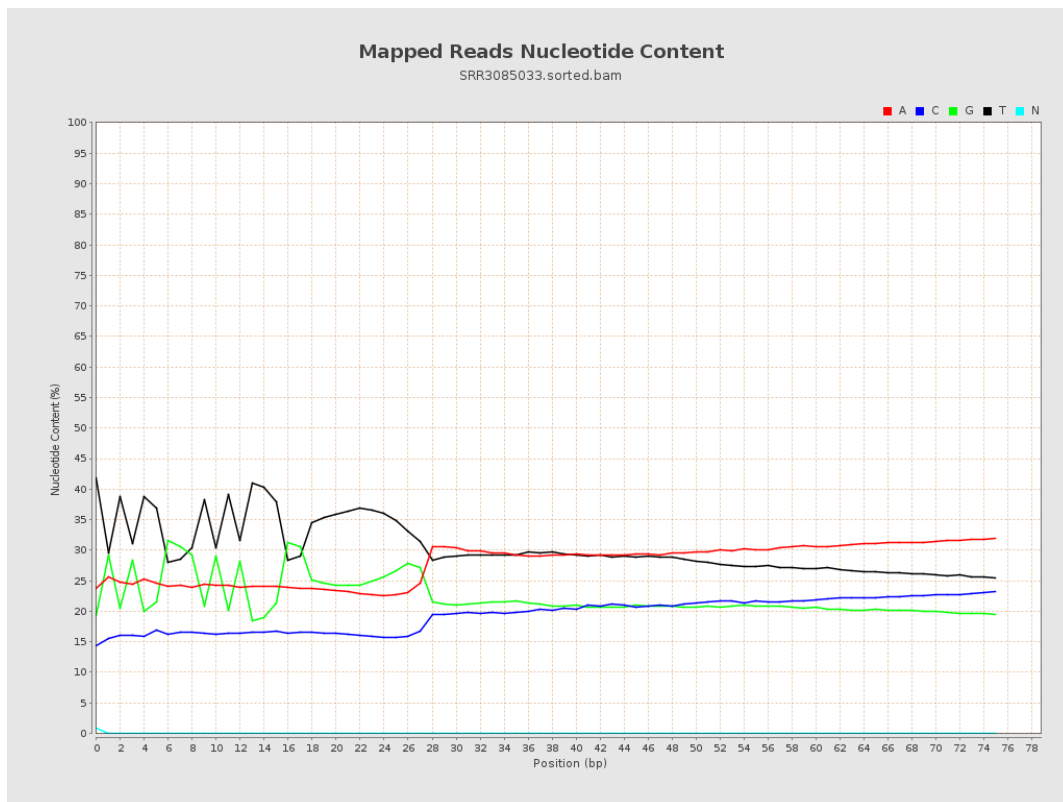
6. Results : Genome Fraction Coverage



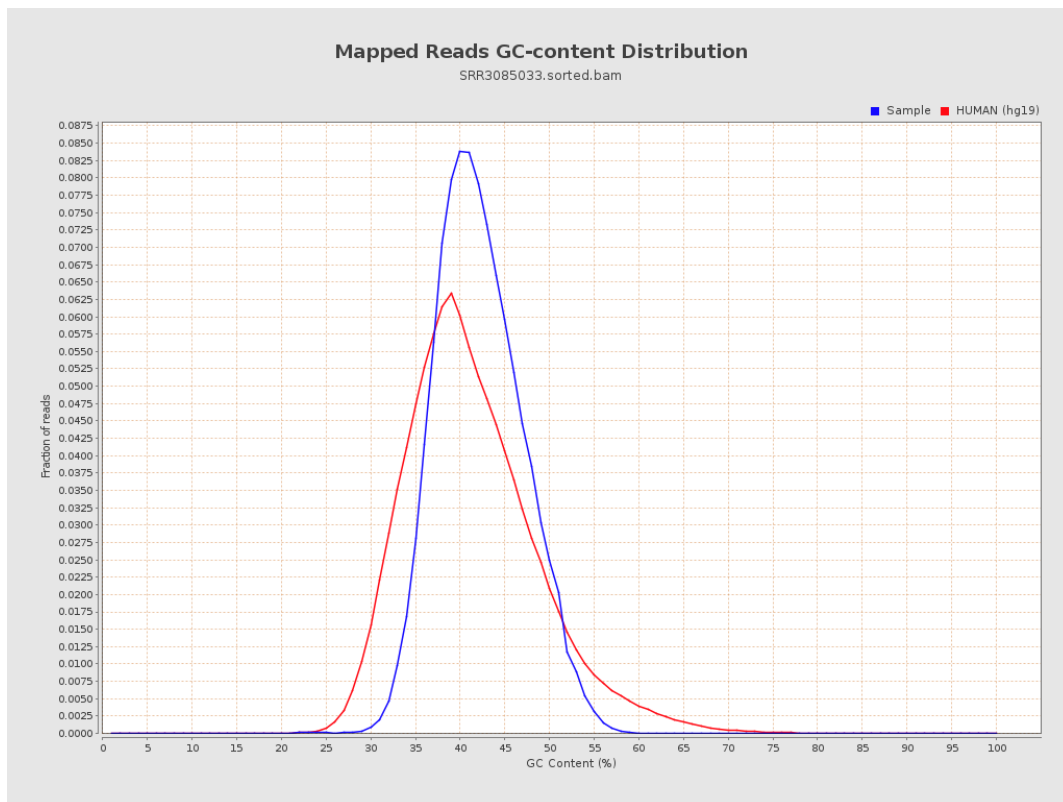
7. Results : Duplication Rate Histogram



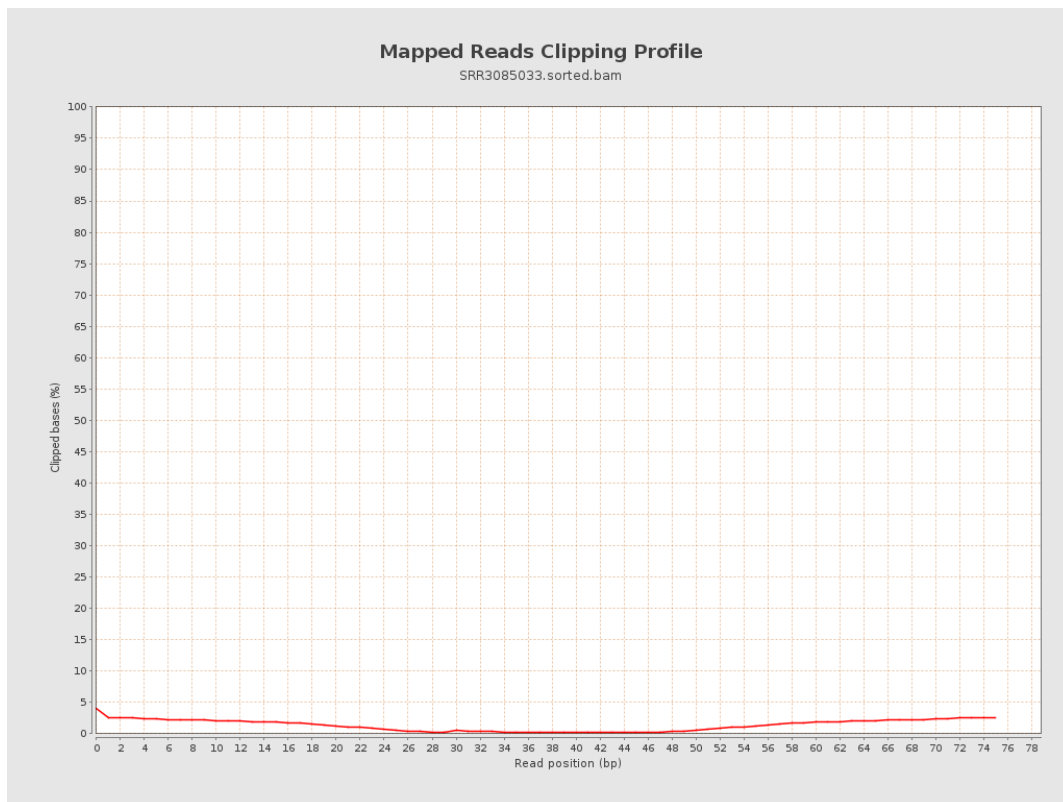
8. Results : Mapped Reads Nucleotide Content



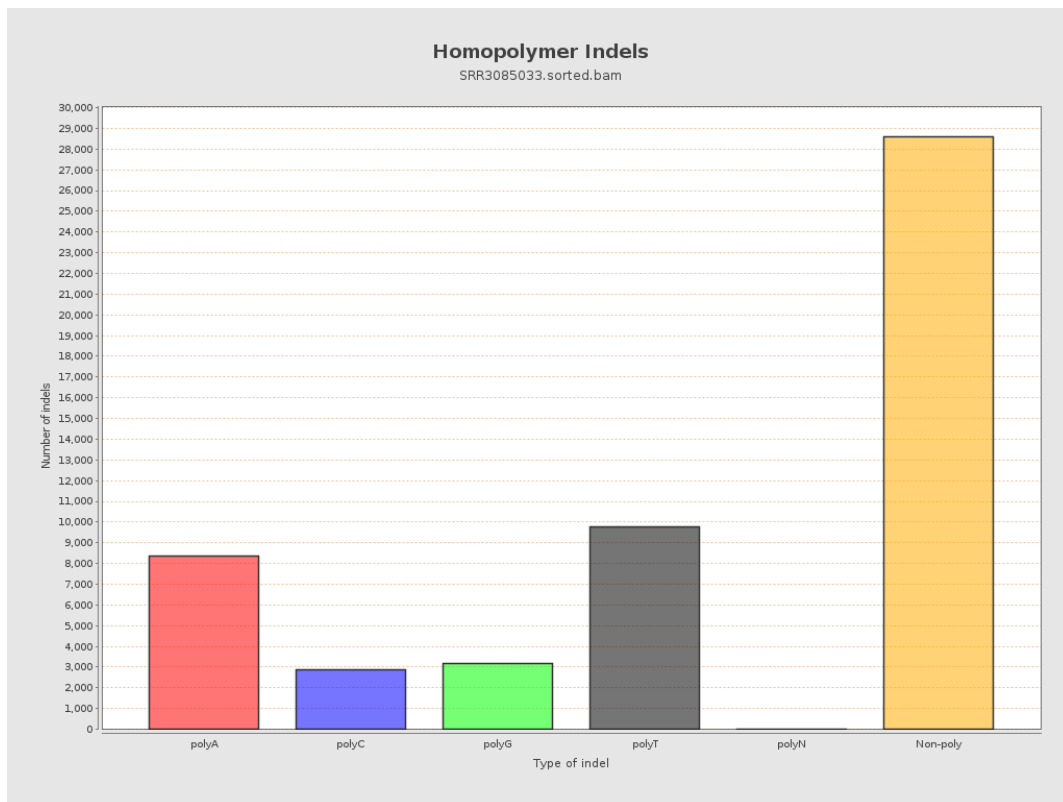
9. Results : Mapped Reads GC-content Distribution



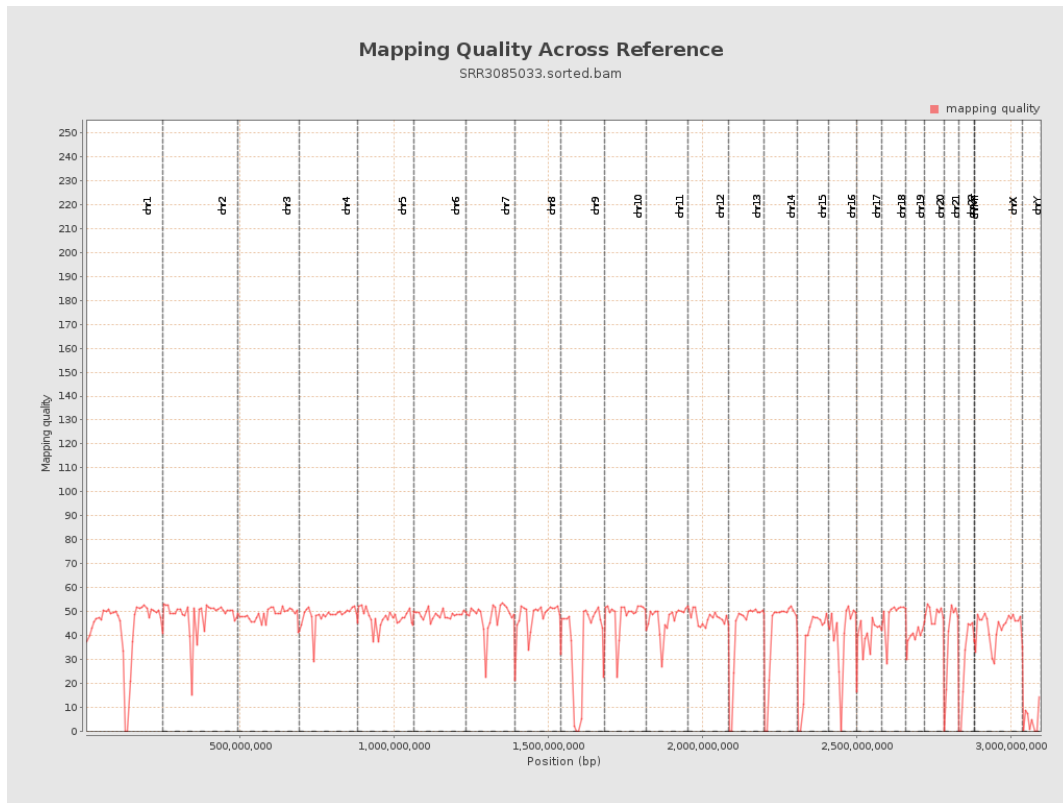
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

