

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:46:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818914.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_SRR1818914 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818914.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:46:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818914.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,255,833
Mapped reads	2,886,623 / 88.66%
Unmapped reads	369,210 / 11.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,407 / 1.15%
Read min/max/mean length	30 / 101 / 101.44
Duplicated reads (estimated)	826,467 / 25.38%
Duplication rate	23.75%
Clipped reads	2,910,237 / 89.39%

2.2. ACGT Content

Number/percentage of A's	78,662,350 / 29.4%
Number/percentage of C's	54,826,968 / 20.49%
Number/percentage of T's	74,937,888 / 28.01%
Number/percentage of G's	59,097,799 / 22.09%
Number/percentage of N's	3,801 / 0%
GC Percentage	42.58%

2.3. Coverage

Mean	0.0865

Standard Deviation	1.1377
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2.4. Mapping Quality

Mean Mapping Quality	49.26
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2.5. Mismatches and indels

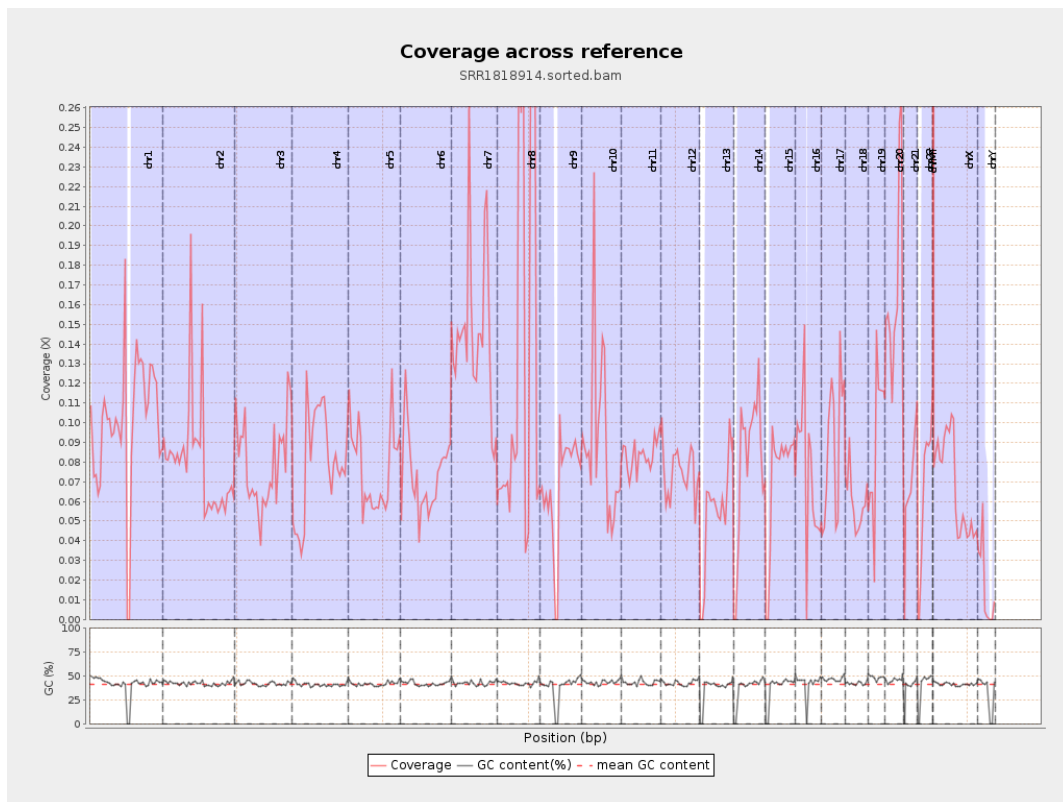
General error rate	0.63%
Mismatches	1,596,743
Insertions	39,493
Mapped reads with at least one insertion	1.32%
Deletions	85,580
Mapped reads with at least one deletion	2.89%
Homopolymer indels	41.2%

2.6. Chromosome stats

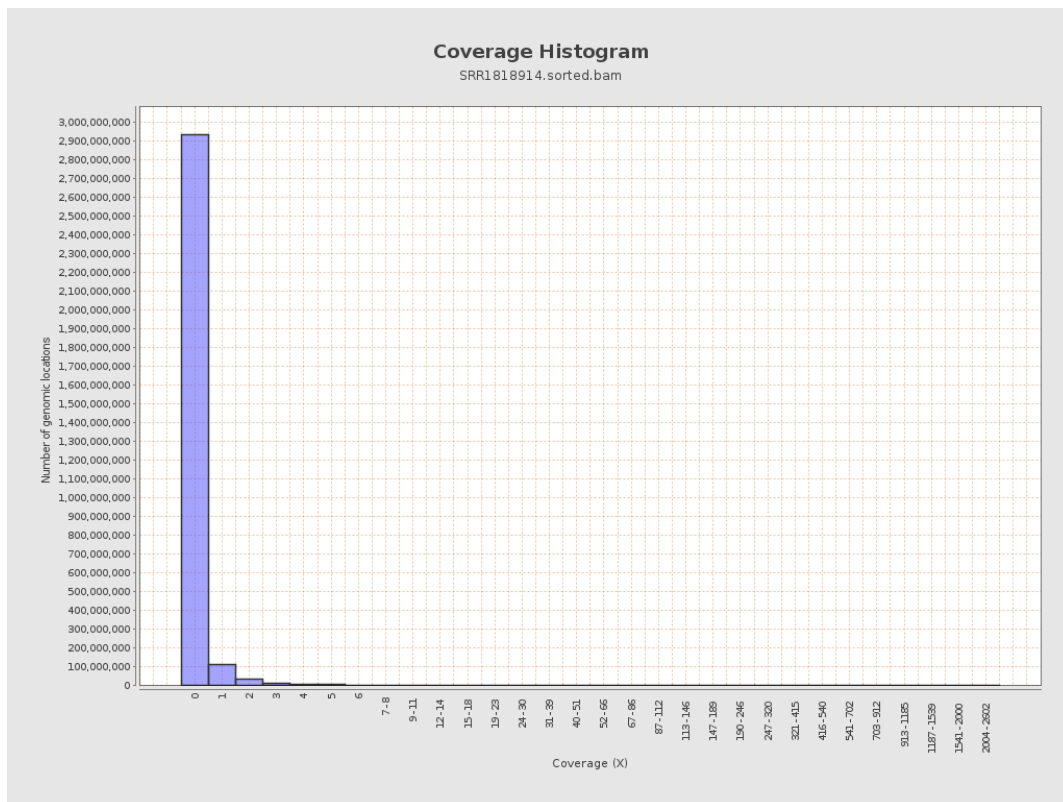
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24945402	0.1001	1.9225
chr2	243199373	19495530	0.0802	1.5471
chr3	198022430	15688319	0.0792	0.4199
chr4	191154276	15441319	0.0808	0.6077
chr5	180915260	13970932	0.0772	0.4463
chr6	171115067	12588525	0.0736	0.4704
chr7	159138663	23075360	0.145	2.5609

chr8	146364022	23982421	0.1639	0.8468
chr9	141213431	9603275	0.068	0.9068
chr10	135534747	12119634	0.0894	1.4588
chr11	135006516	11235806	0.0832	0.599
chr12	133851895	10021956	0.0749	0.4185
chr13	115169878	6324851	0.0549	0.3403
chr14	107349540	8727903	0.0813	0.4871
chr15	102531392	7255627	0.0708	0.3938
chr16	90354753	6688270	0.074	1.0966
chr17	81195210	7046950	0.0868	0.6501
chr18	78077248	4694459	0.0601	1.0784
chr19	59128983	5381973	0.091	1.8101
chr20	63025520	10807199	0.1715	0.6948
chr21	48129895	3326814	0.0691	0.4785
chr22	51304566	3197093	0.0623	0.4222
chrMT	16571	555926	33.5481	21.5318
chrX	155270560	10526408	0.0678	0.5044
chrY	59373566	997420	0.0168	1.2832

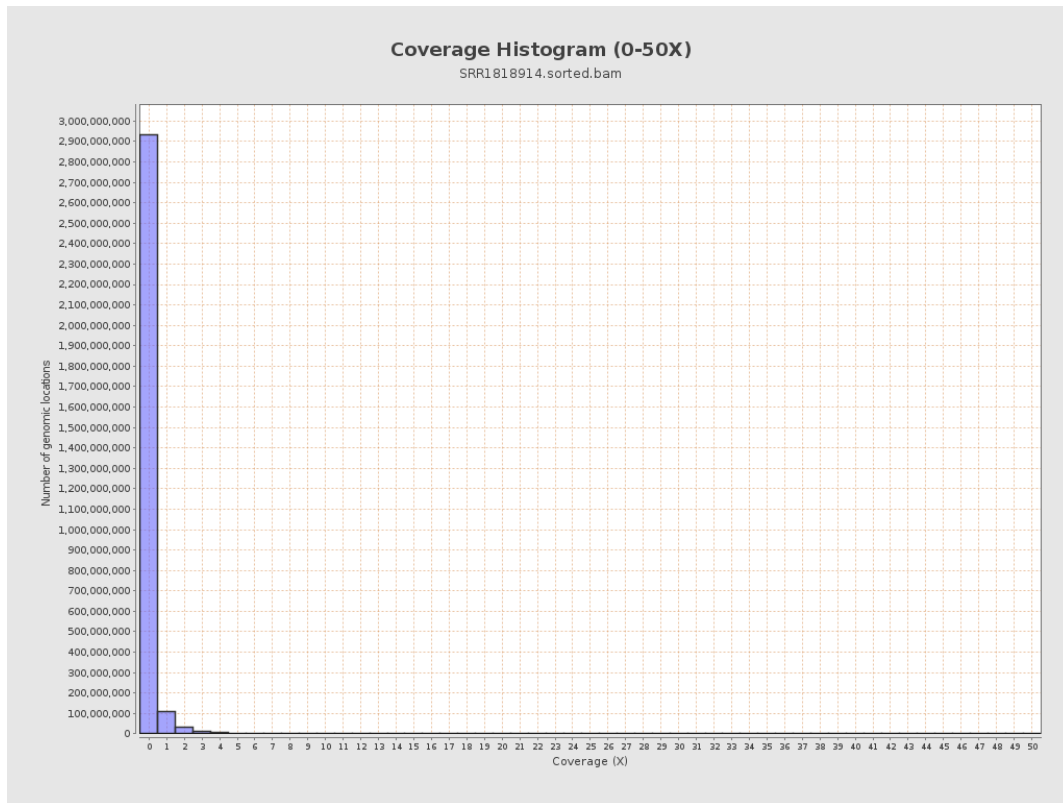
3. Results : Coverage across reference



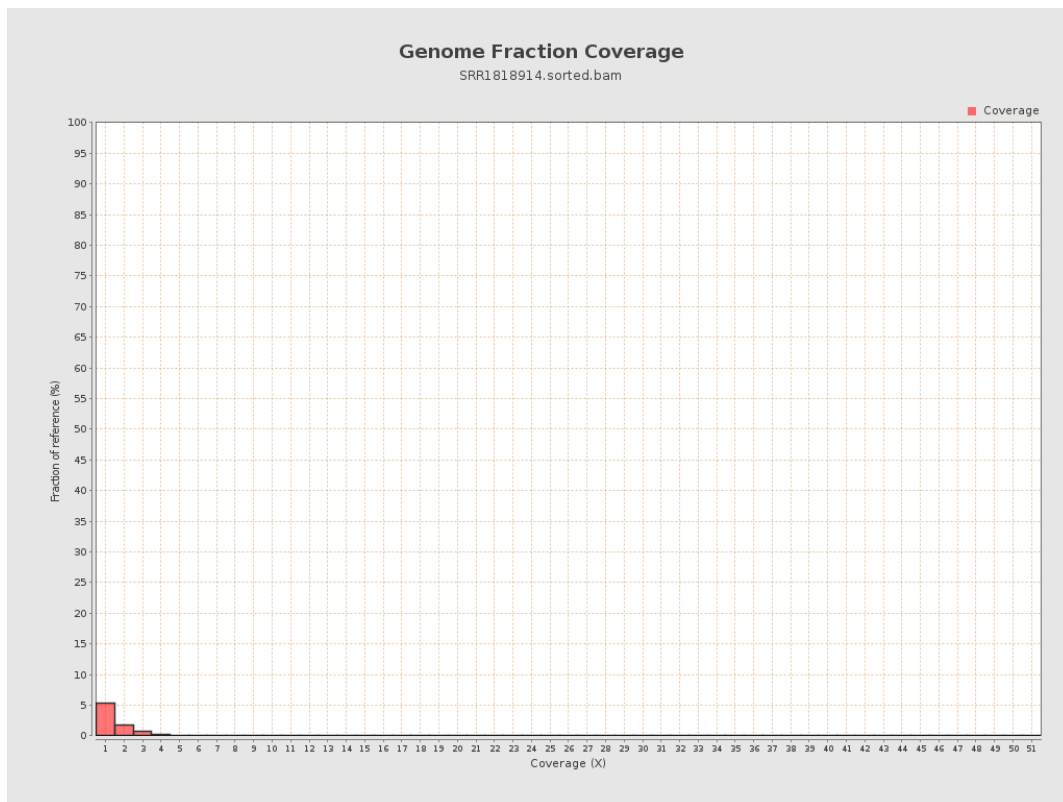
4. Results : Coverage Histogram



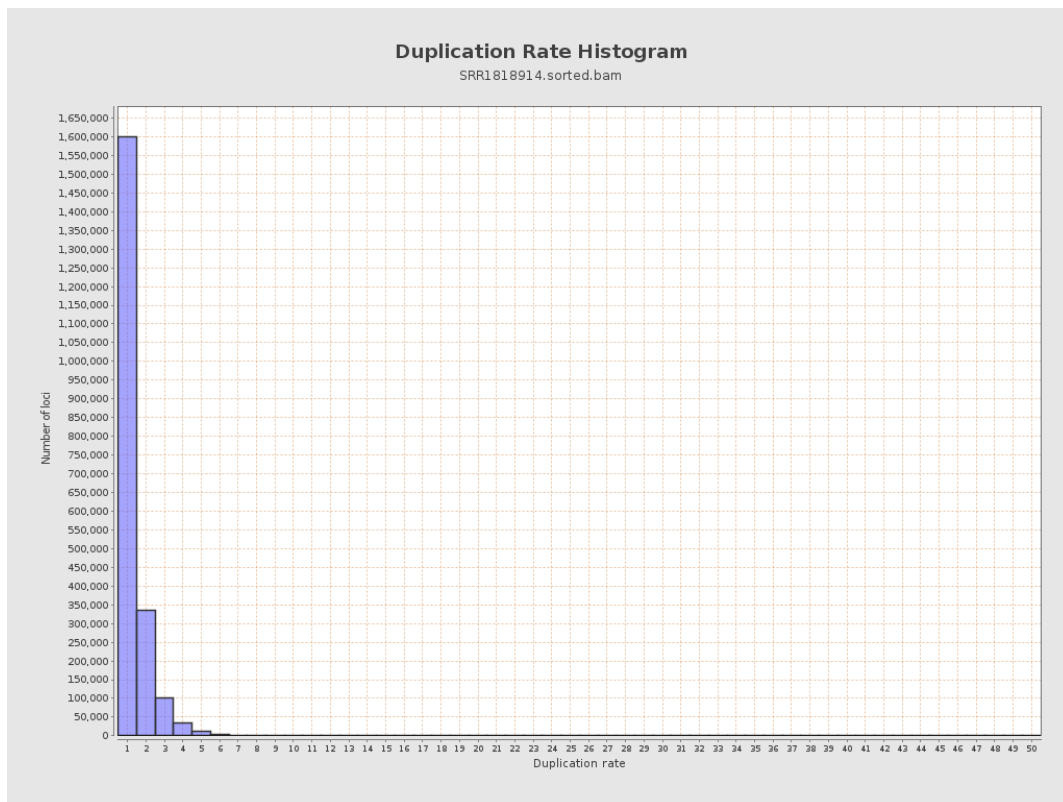
5. Results : Coverage Histogram (0-50X)



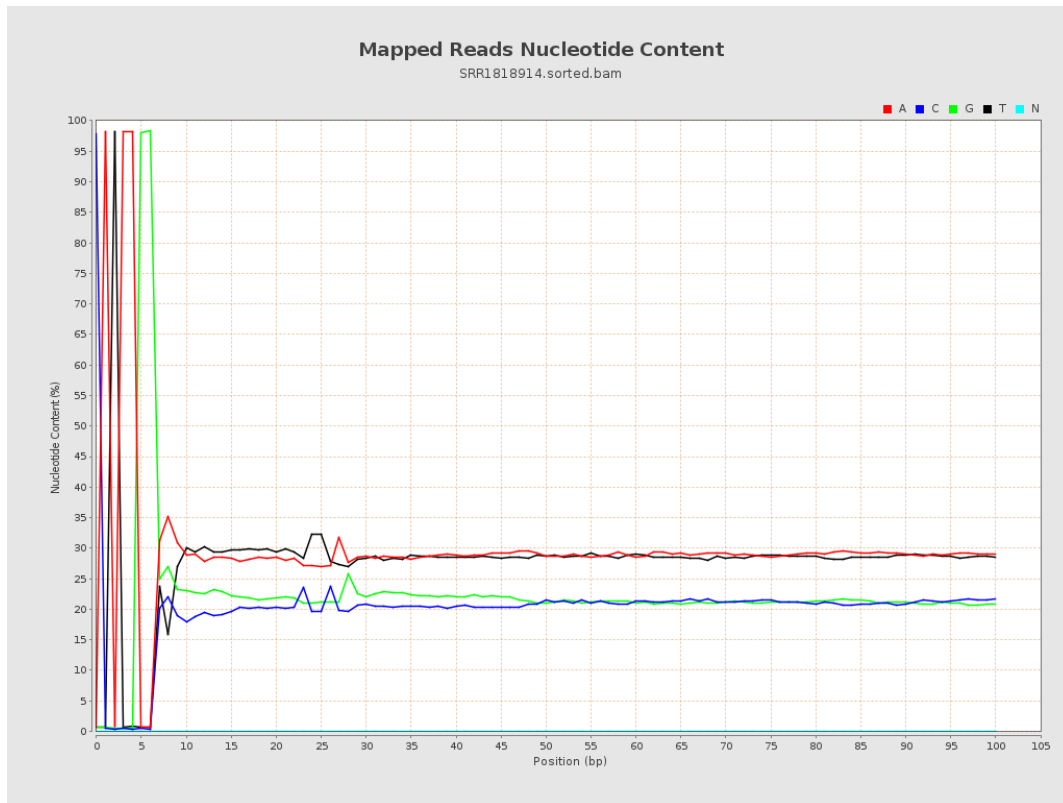
6. Results : Genome Fraction Coverage



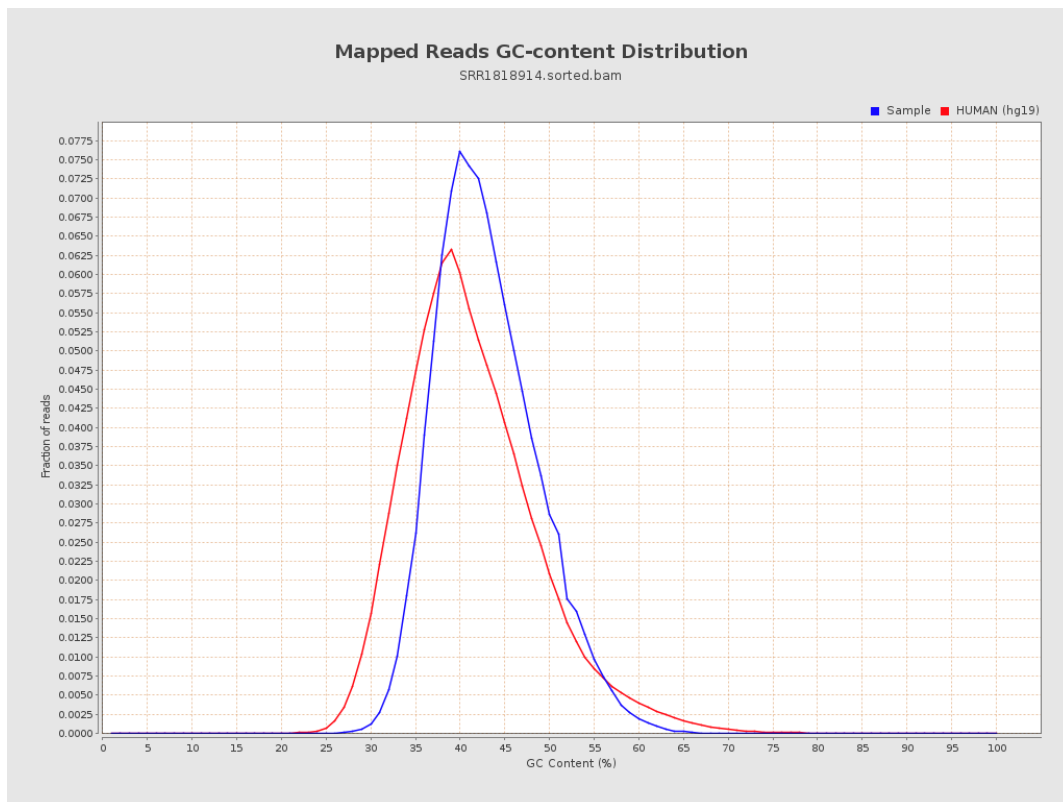
7. Results : Duplication Rate Histogram



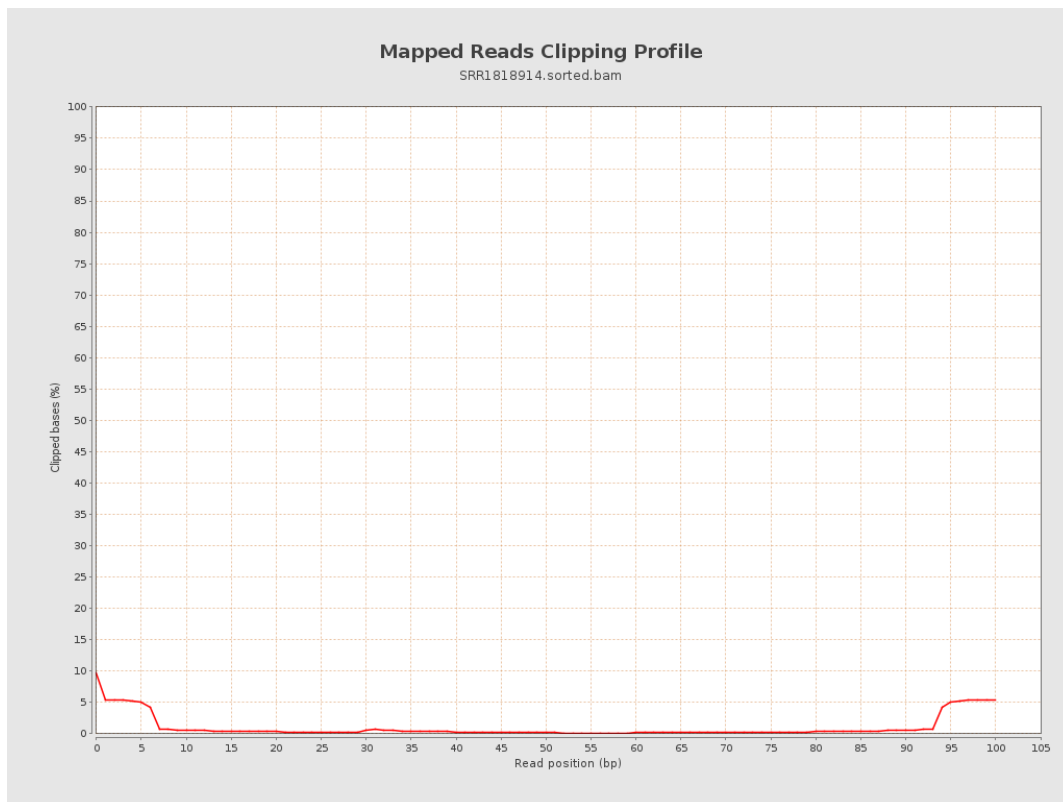
8. Results : Mapped Reads Nucleotide Content



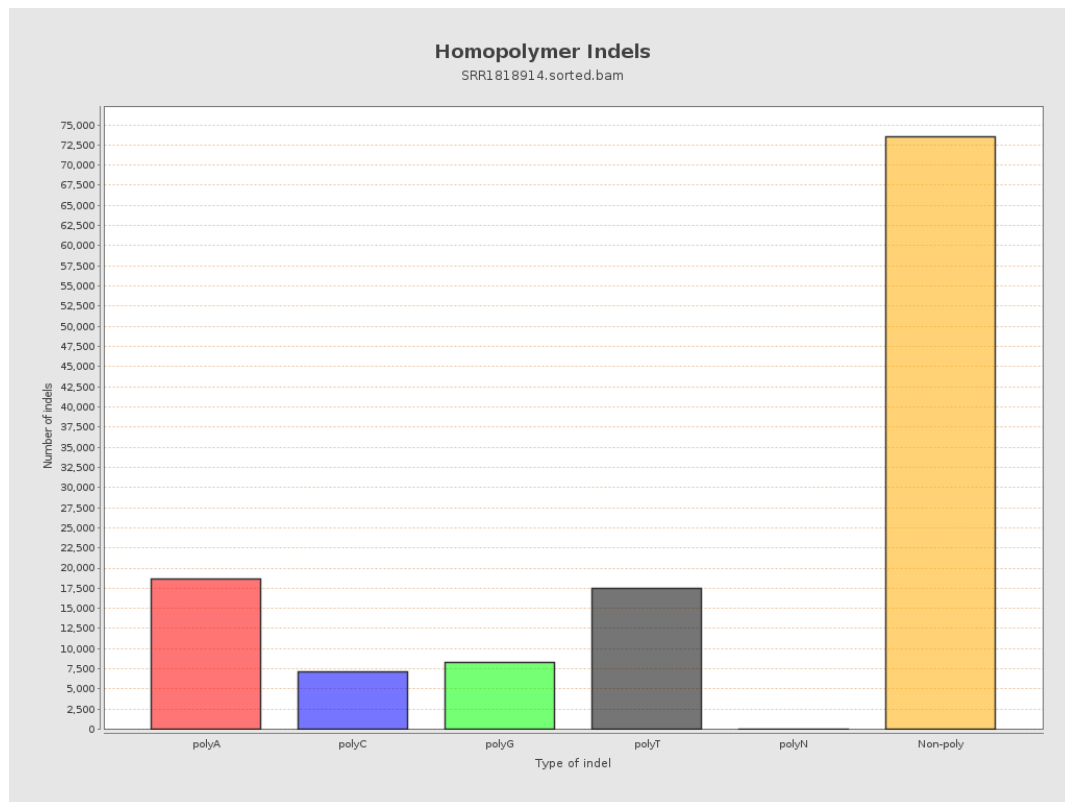
9. Results : Mapped Reads GC-content Distribution



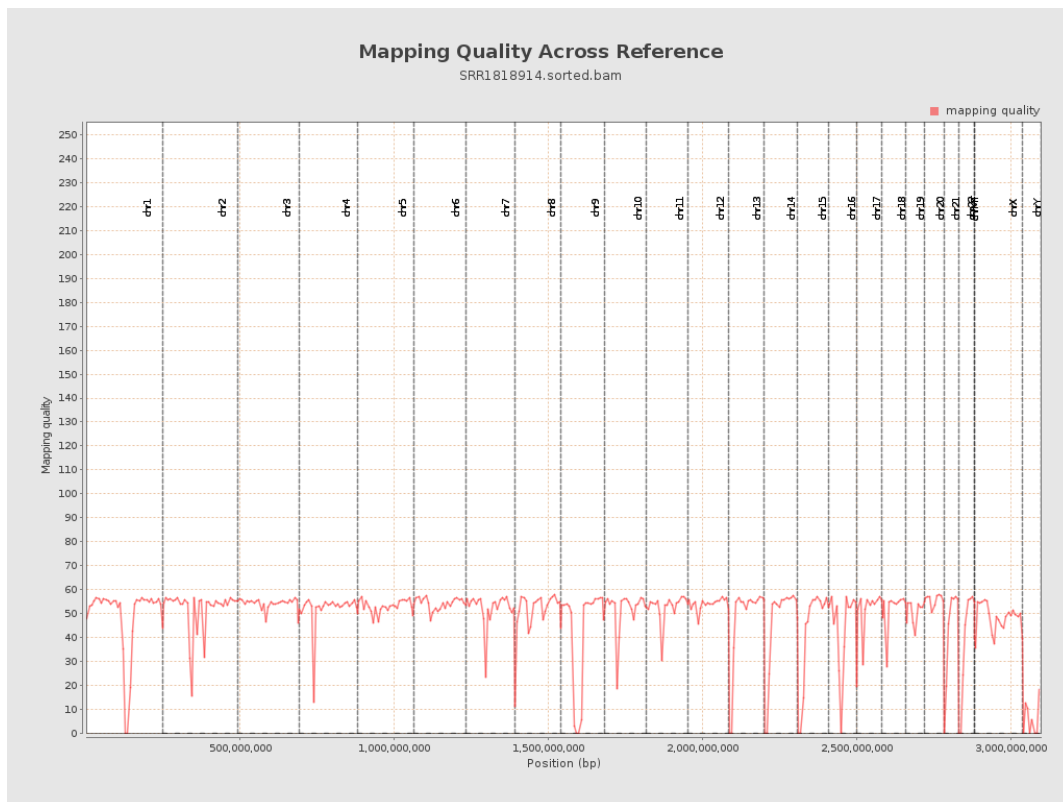
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

