

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:41:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716182.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_SRR9716182 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716182.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:41:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716182.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,154,314
Mapped reads	1,903,686 / 88.37%
Unmapped reads	250,628 / 11.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,236 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	52,448 / 2.43%
Duplication rate	1.94%
Clipped reads	1,906,128 / 88.48%

2.2. ACGT Content

Number/percentage of A's	26,572,748 / 24.5%
Number/percentage of C's	20,533,847 / 18.93%
Number/percentage of T's	34,592,723 / 31.89%
Number/percentage of G's	26,779,141 / 24.69%
Number/percentage of N's	897 / 0%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.275
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2.4. Mapping Quality

Mean Mapping Quality	42.08
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2.5. Mismatches and indels

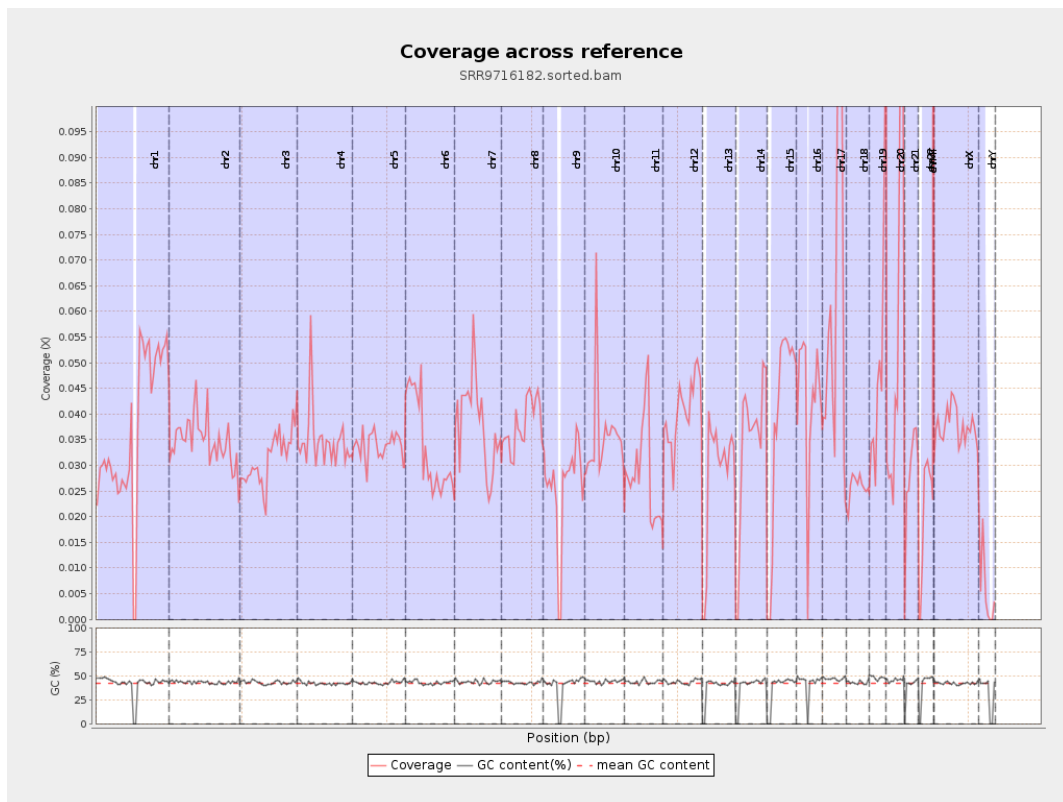
General error rate	0.54%
Mismatches	567,734
Insertions	8,823
Mapped reads with at least one insertion	0.46%
Deletions	19,927
Mapped reads with at least one deletion	1.04%
Homopolymer indels	39.67%

2.6. Chromosome stats

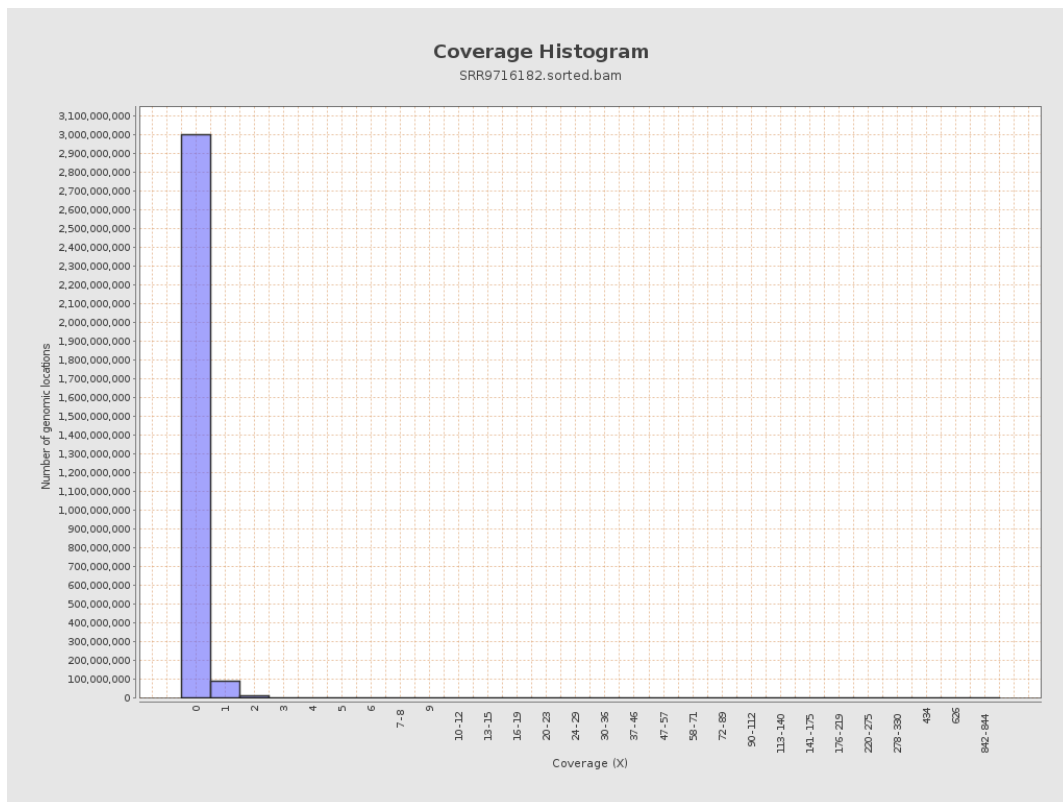
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9141580	0.0367	0.3267
chr2	243199373	8464251	0.0348	0.4117
chr3	198022430	6176267	0.0312	0.1972
chr4	191154276	6600638	0.0345	0.2321
chr5	180915260	6118101	0.0338	0.2019
chr6	171115067	5742181	0.0336	0.2411
chr7	159138663	6099381	0.0383	0.3856

chr8	146364022	5568439	0.038	0.2542
chr9	141213431	3613433	0.0256	0.2079
chr10	135534747	4831535	0.0356	0.3622
chr11	135006516	3859663	0.0286	0.2346
chr12	133851895	5433663	0.0406	0.2217
chr13	115169878	3248275	0.0282	0.185
chr14	107349540	3640398	0.0339	0.2128
chr15	102531392	4013246	0.0391	0.2231
chr16	90354753	3869199	0.0428	0.2493
chr17	81195210	4965679	0.0612	0.2907
chr18	78077248	2010072	0.0257	0.3314
chr19	59128983	2976813	0.0503	0.3365
chr20	63025520	3571580	0.0567	0.2823
chr21	48129895	1355761	0.0282	0.203
chr22	51304566	1031509	0.0201	0.1565
chrMT	16571	10325	0.6231	1.1014
chrX	155270560	5835517	0.0376	0.2304
chrY	59373566	333965	0.0056	0.1607

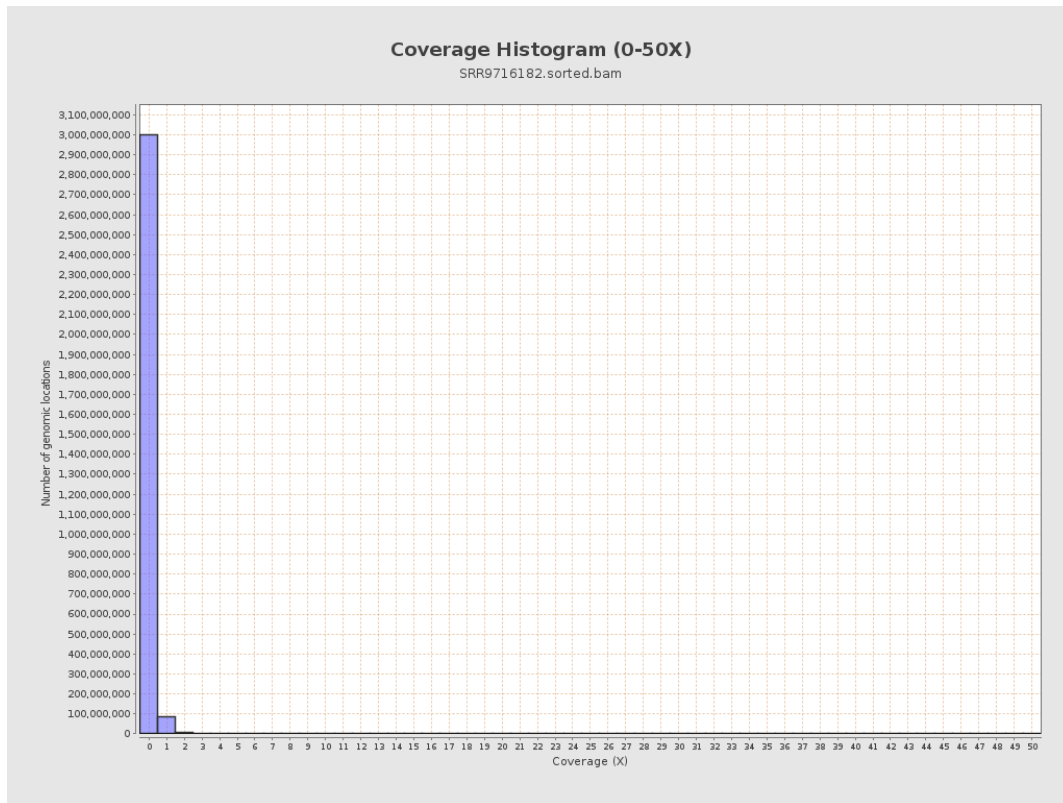
3. Results : Coverage across reference



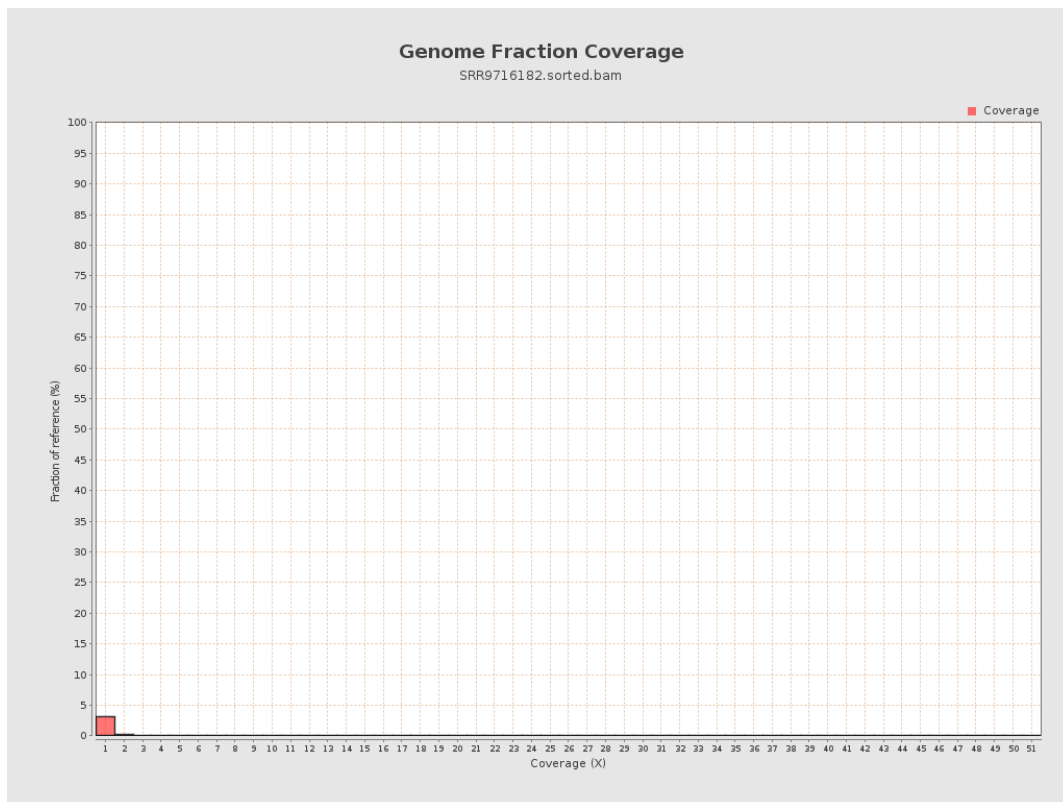
4. Results : Coverage Histogram



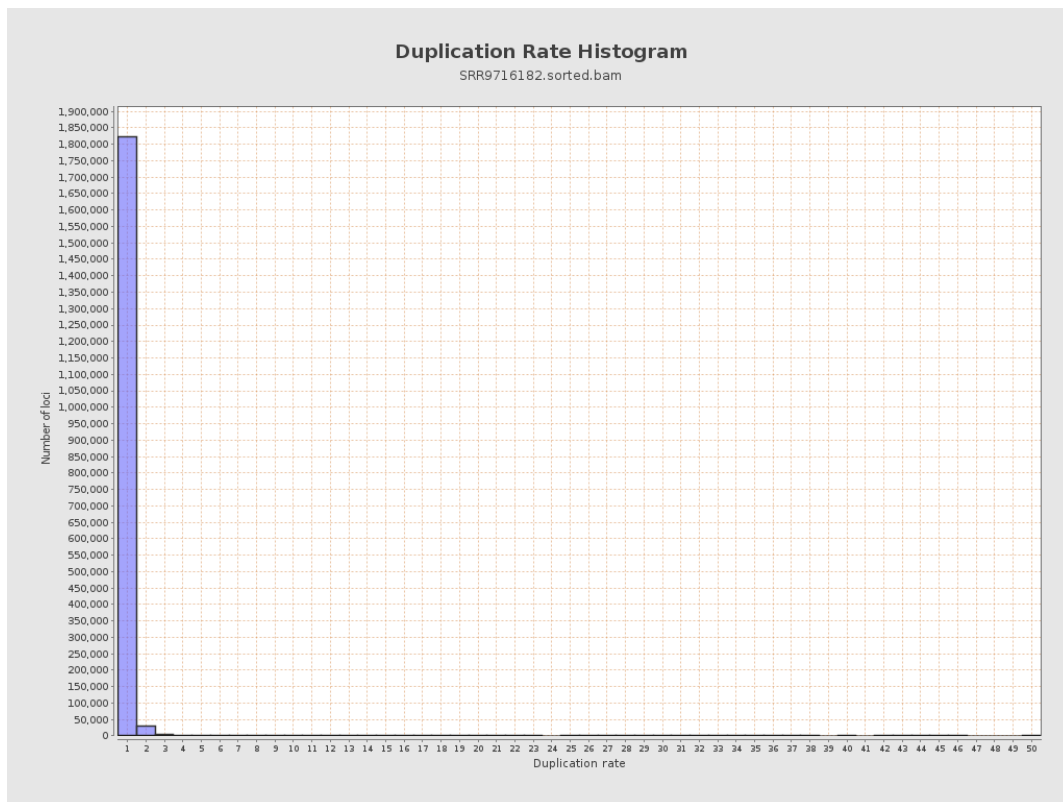
5. Results : Coverage Histogram (0-50X)



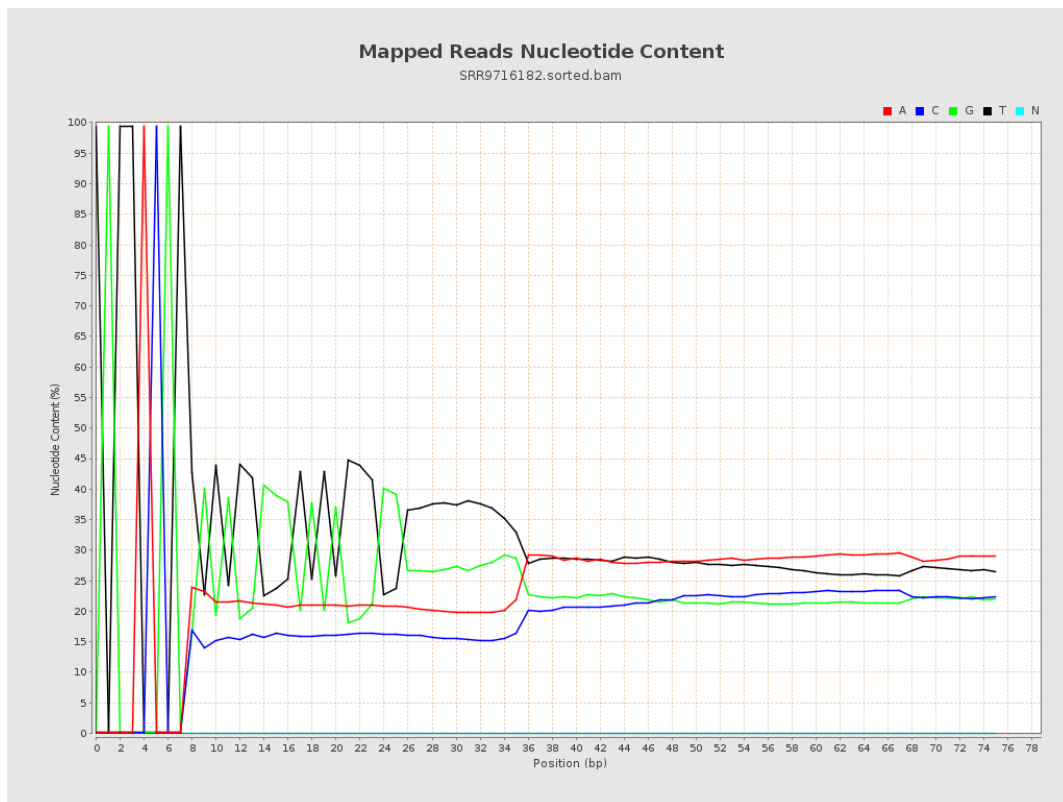
6. Results : Genome Fraction Coverage



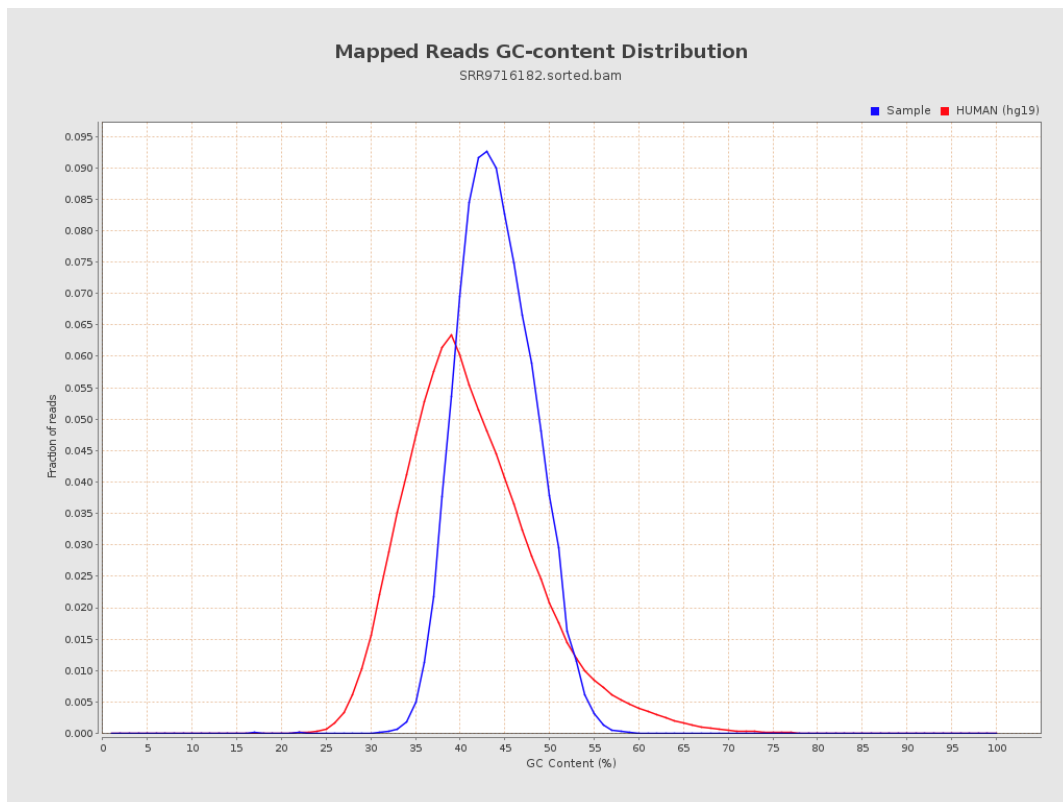
7. Results : Duplication Rate Histogram



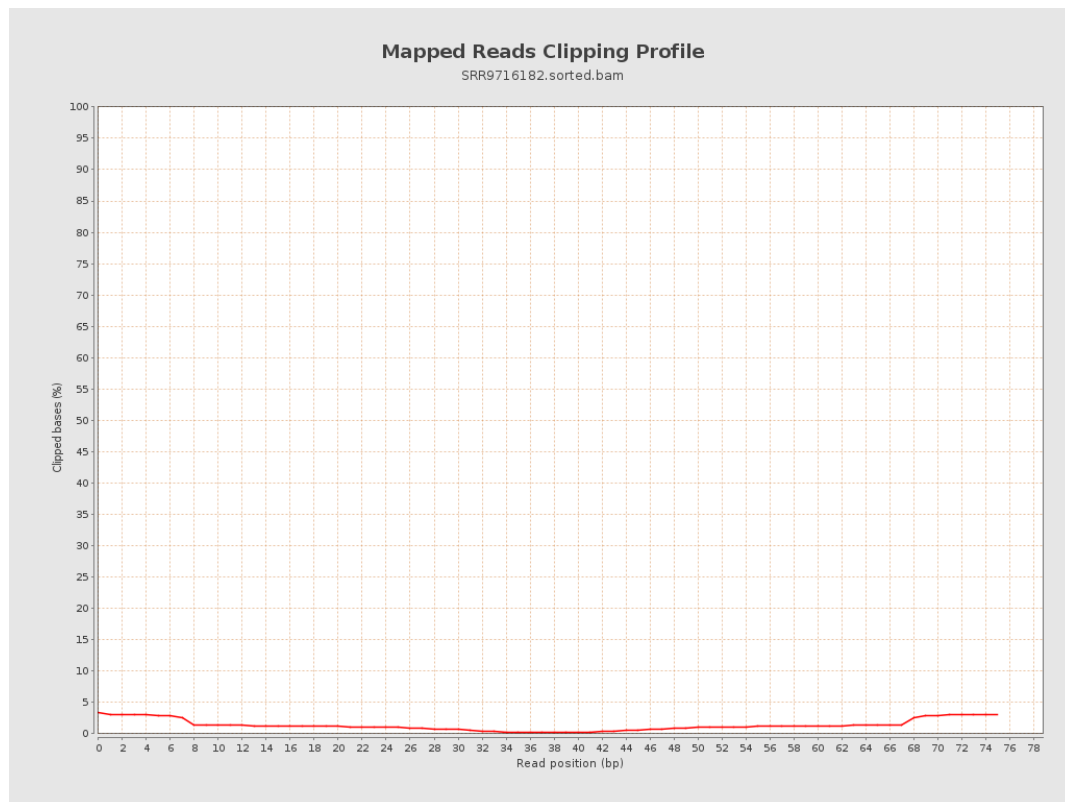
8. Results : Mapped Reads Nucleotide Content



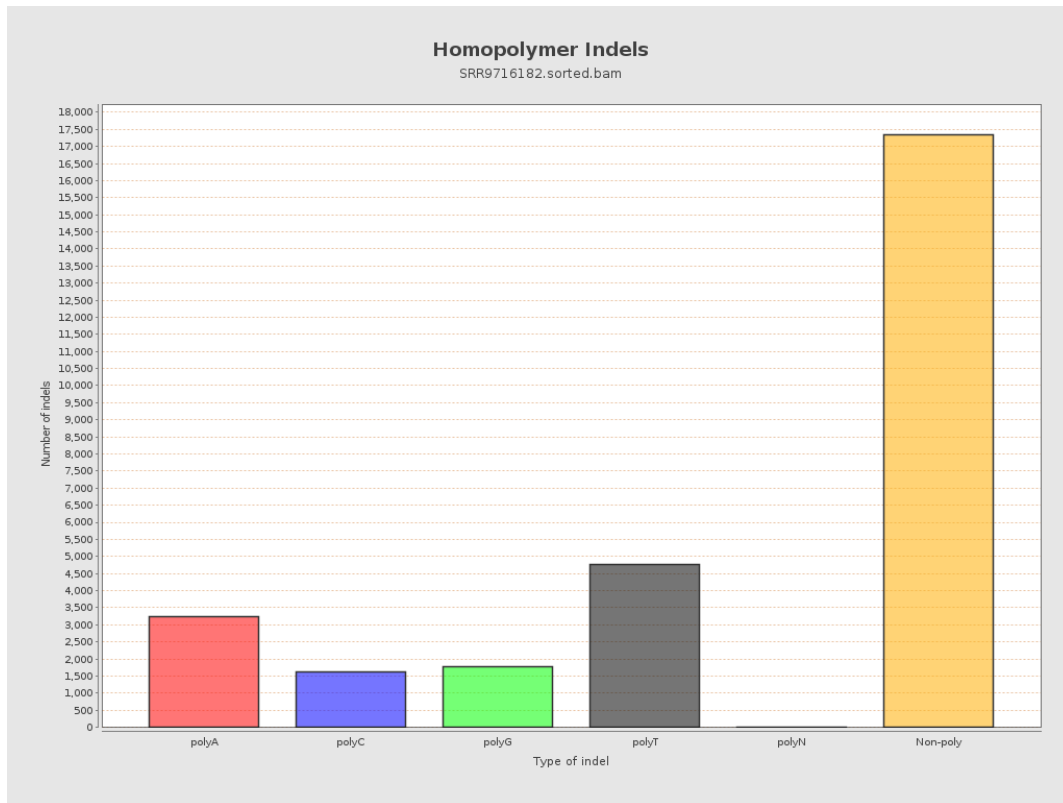
9. Results : Mapped Reads GC-content Distribution



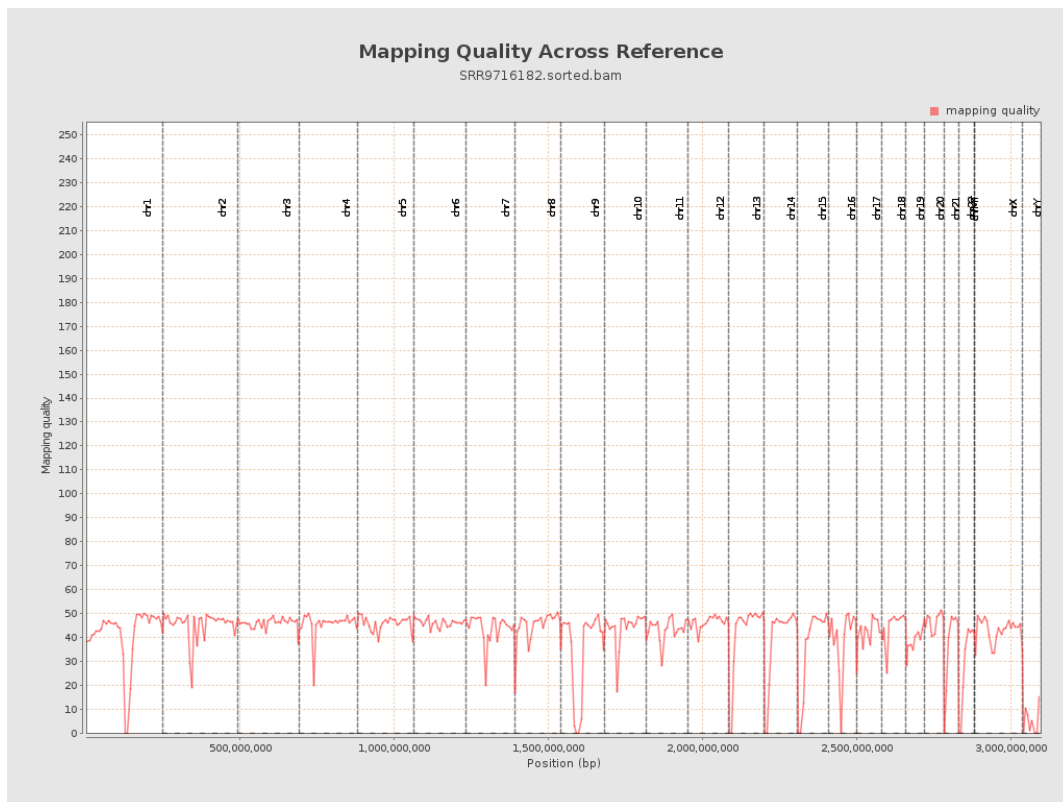
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

