Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 06:03:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089817.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_SRR089817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089817.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 06:03:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,400,750
Mapped reads	14,765,760 / 80.25%
Unmapped reads	3,634,990 / 19.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	736 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,548,620 / 13.85%
Duplication rate	12.36%
Clipped reads	1,730,991 / 9.41%

2.2. ACGT Content

Number/percentage of A's	204,623,682 / 29.56%
Number/percentage of C's	140,920,923 / 20.36%
Number/percentage of T's	198,828,689 / 28.73%
Number/percentage of G's	147,604,266 / 21.33%
Number/percentage of N's	180,816 / 0.03%
GC Percentage	41.68%

2.3. Coverage

Mean	0.2236

Standard Deviation	1.4211

2.4. Mapping Quality

Mean Mapping Quality	43.88

2.5. Mismatches and indels

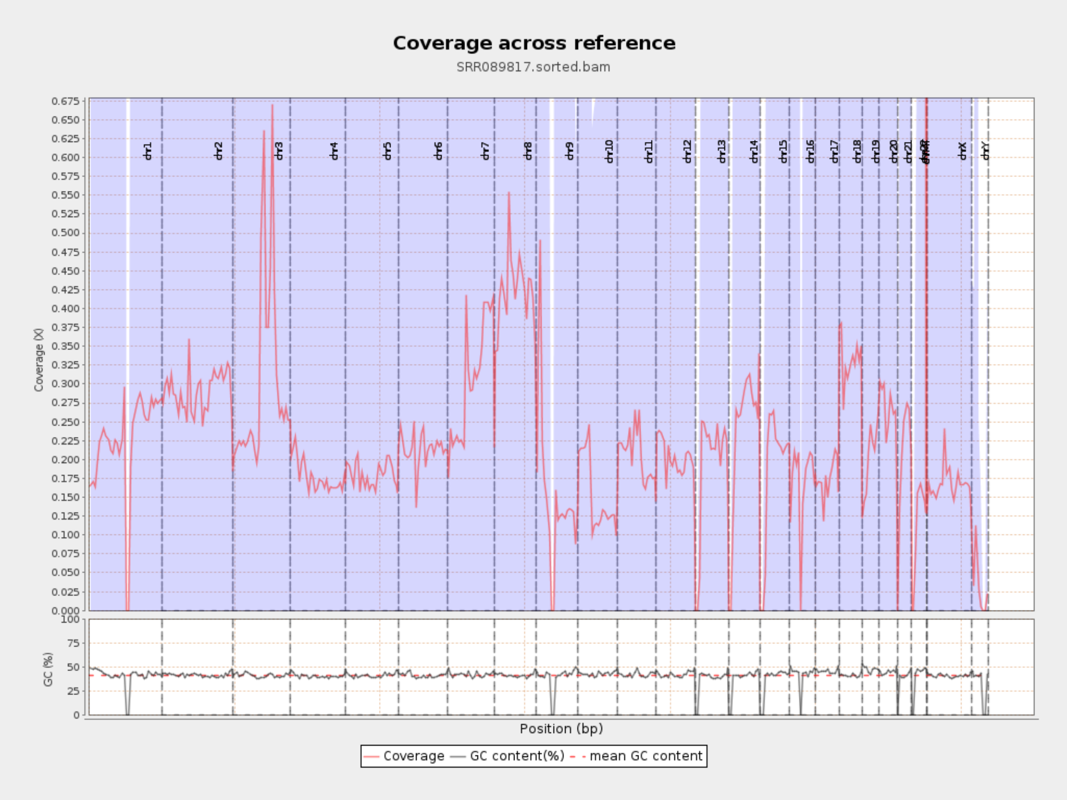
General error rate	0.53%
Mismatches	3,656,163
Insertions	28,192
Mapped reads with at least one insertion	0.19%
Deletions	86,694
Mapped reads with at least one deletion	0.59%
Homopolymer indels	46.04%

2.6. Chromosome stats

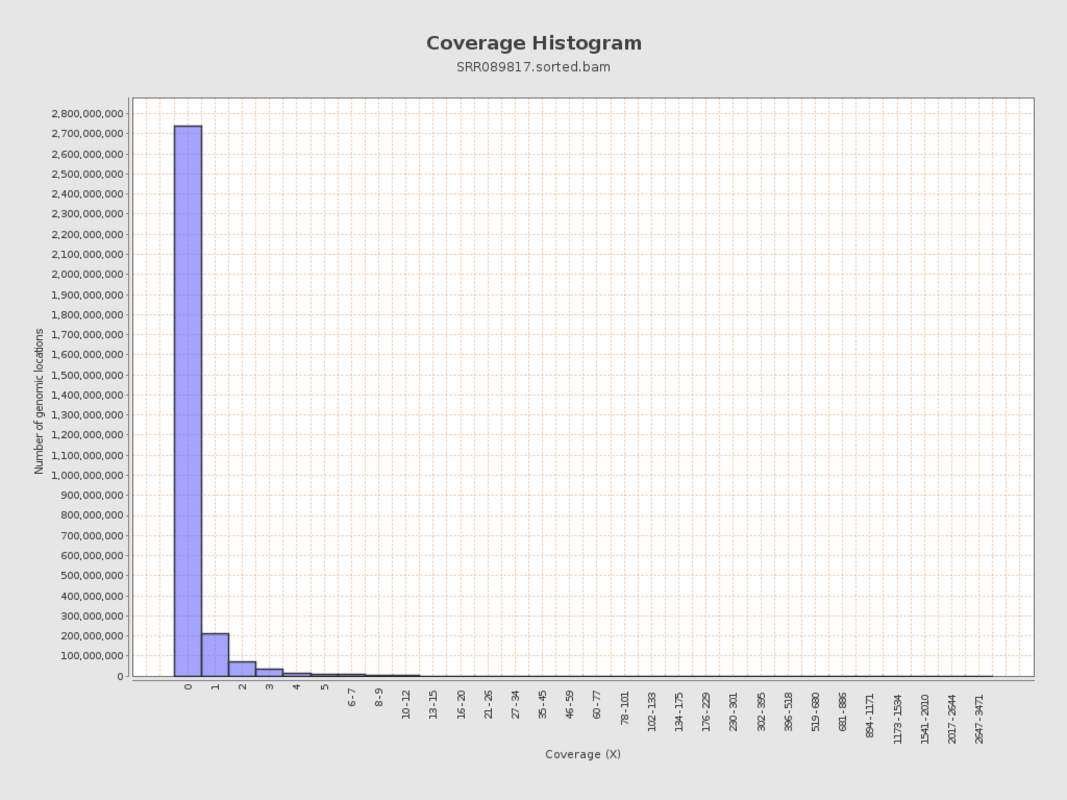
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	55784483	0.2238	2.1131
chr2	243199373	71024912	0.292	1.967
chr3	198022430	60235123	0.3042	1.0323
chr4	191154276	33839909	0.177	0.7824
chr5	180915260	32588898	0.1801	0.7745
chr6	171115067	36591927	0.2138	0.9635
chr7	159138663	48947250	0.3076	2.7739

chr8	146364022	61983367	0.4235	2.1374
chr9	141213431	21681758	0.1535	1.0962
chr10	135534747	20852314	0.1539	1.068
chr11	135006516	27781993	0.2058	1.1715
chr12	133851895	26974403	0.2015	0.8454
chr13	115169878	21854873	0.1898	0.776
chr14	107349540	24920871	0.2321	0.8976
chr15	102531392	18876305	0.1841	0.7667
chr16	90354753	15411221	0.1706	0.8062
chr17	81195210	14059480	0.1732	0.8419
chr18	78077248	25847807	0.3311	1.748
chr19	59128983	12114385	0.2049	1.4104
chr20	63025520	16811034	0.2667	0.9991
chr21	48129895	9817534	0.204	0.9415
chr22	51304566	5624550	0.1096	0.5956
chrMT	16571	690191	41.6505	28.1917
chrX	155270560	26058213	0.1678	0.9897
chrY	59373566	1915522	0.0323	1.1685

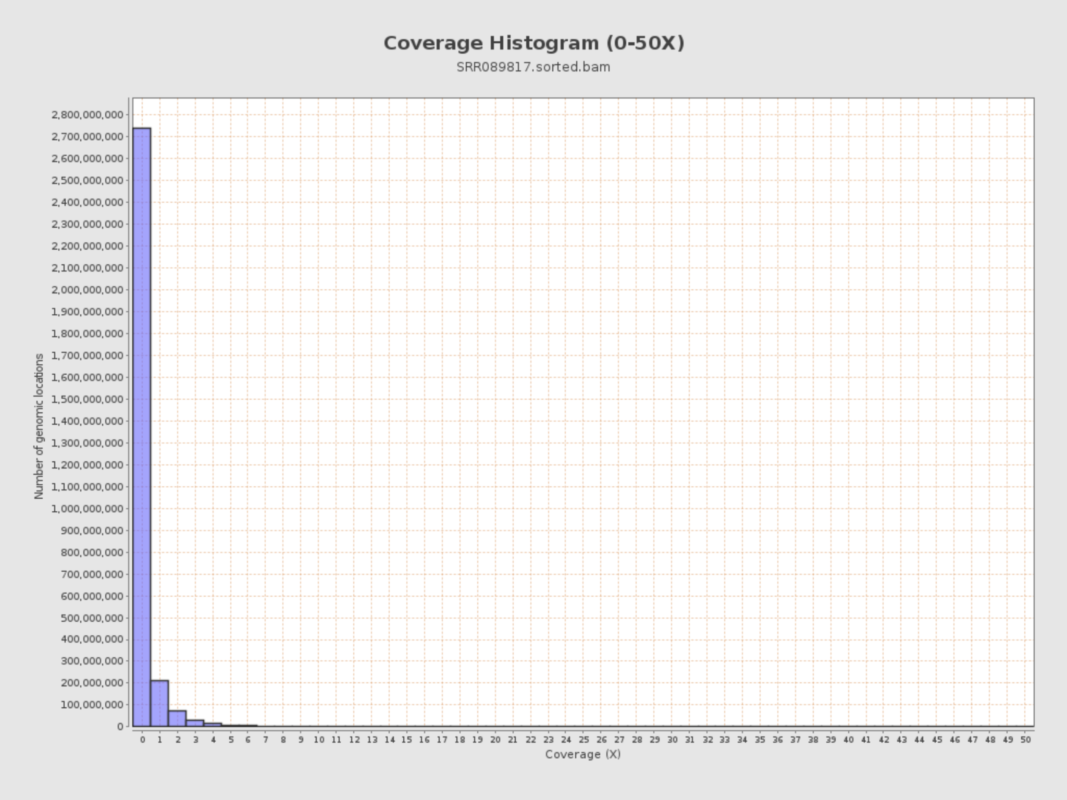
3. Results : Coverage across reference



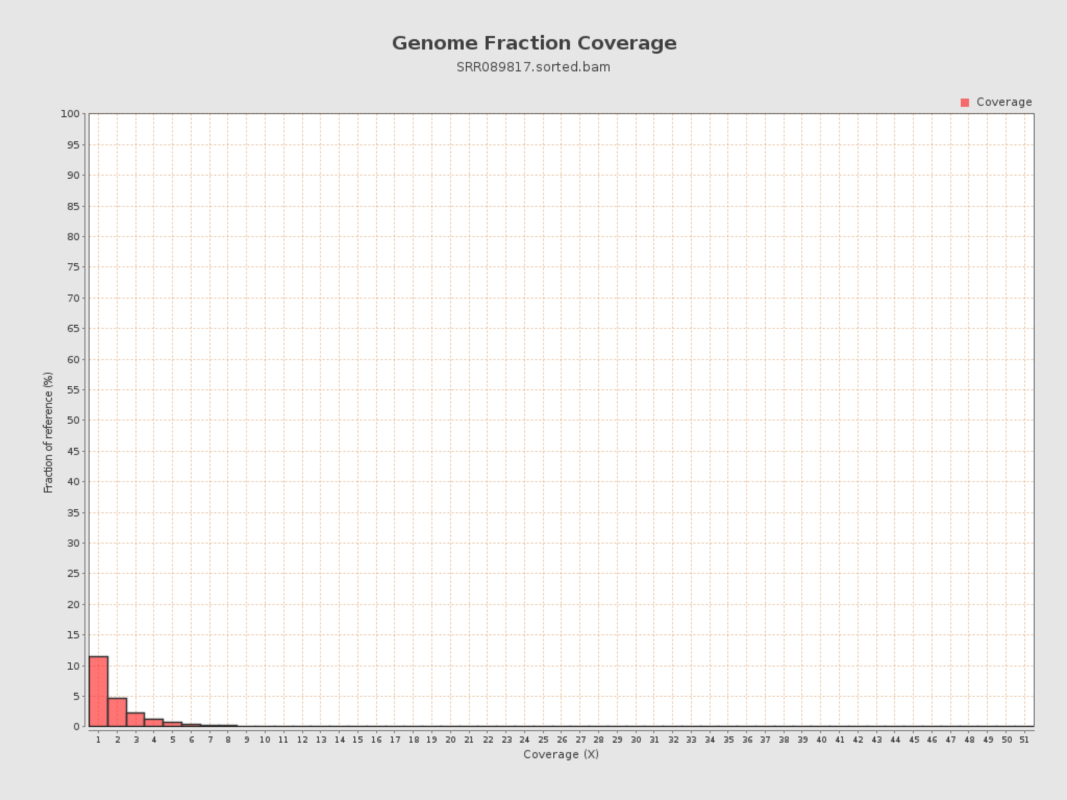
4. Results : Coverage Histogram



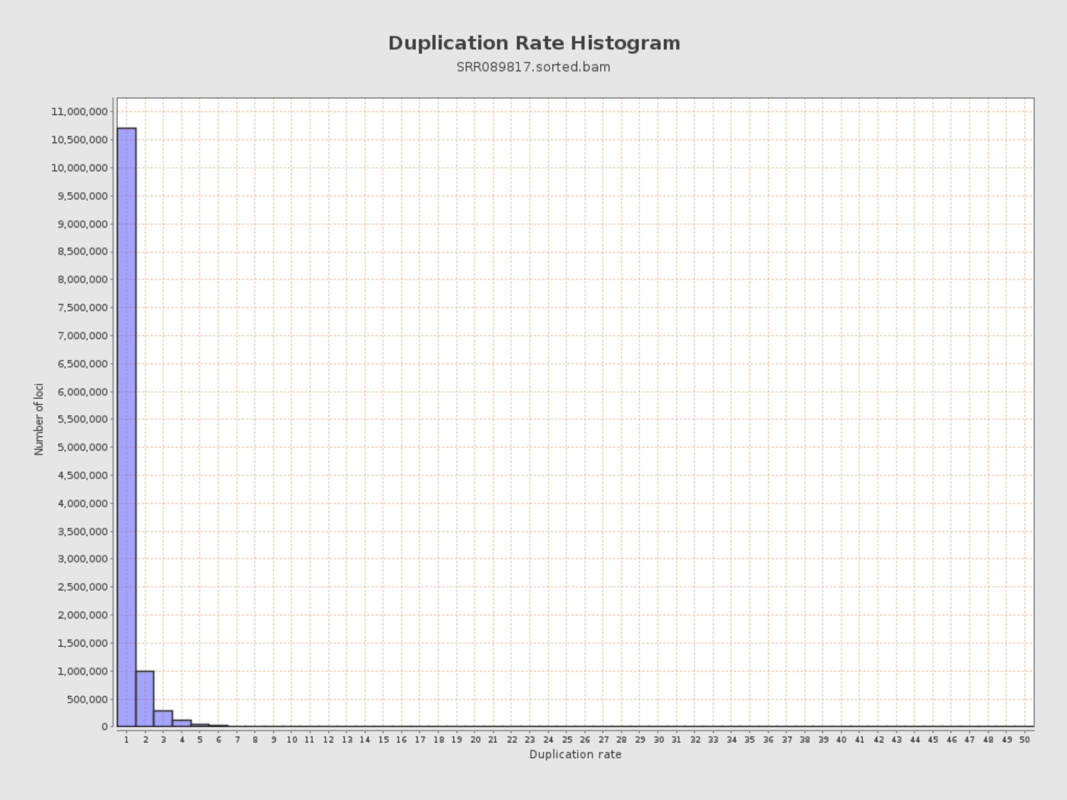
5. Results : Coverage Histogram (0-50X)



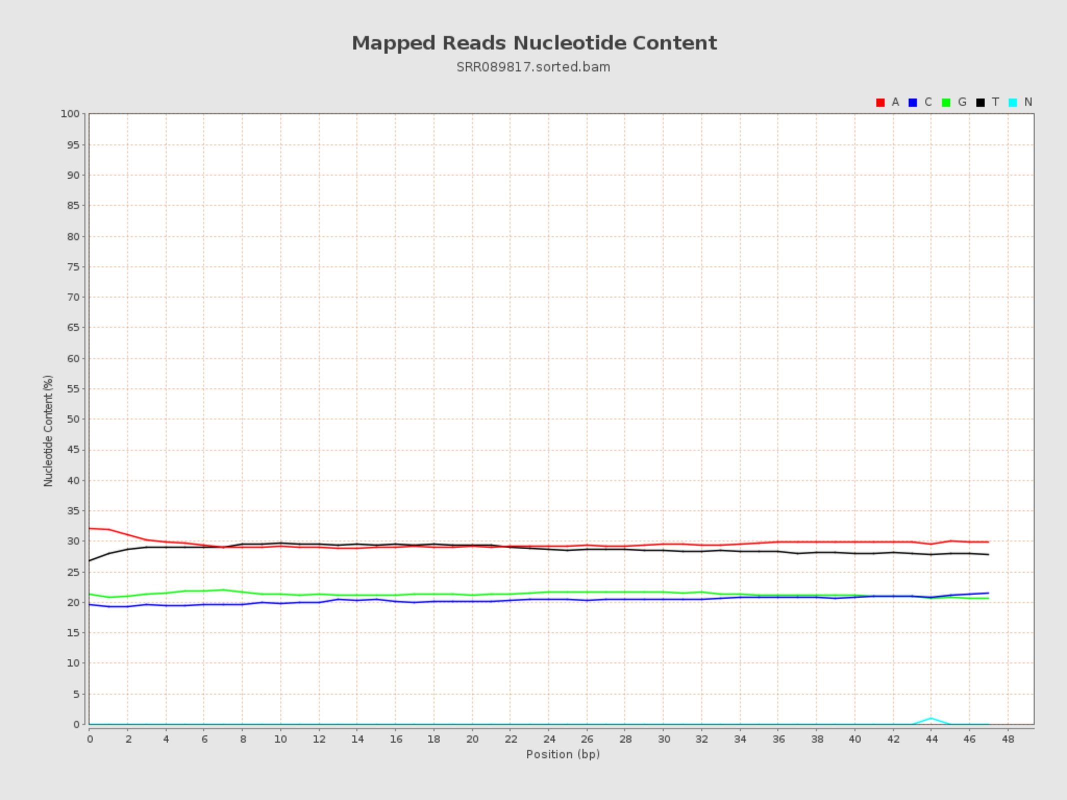
6. Results : Genome Fraction Coverage



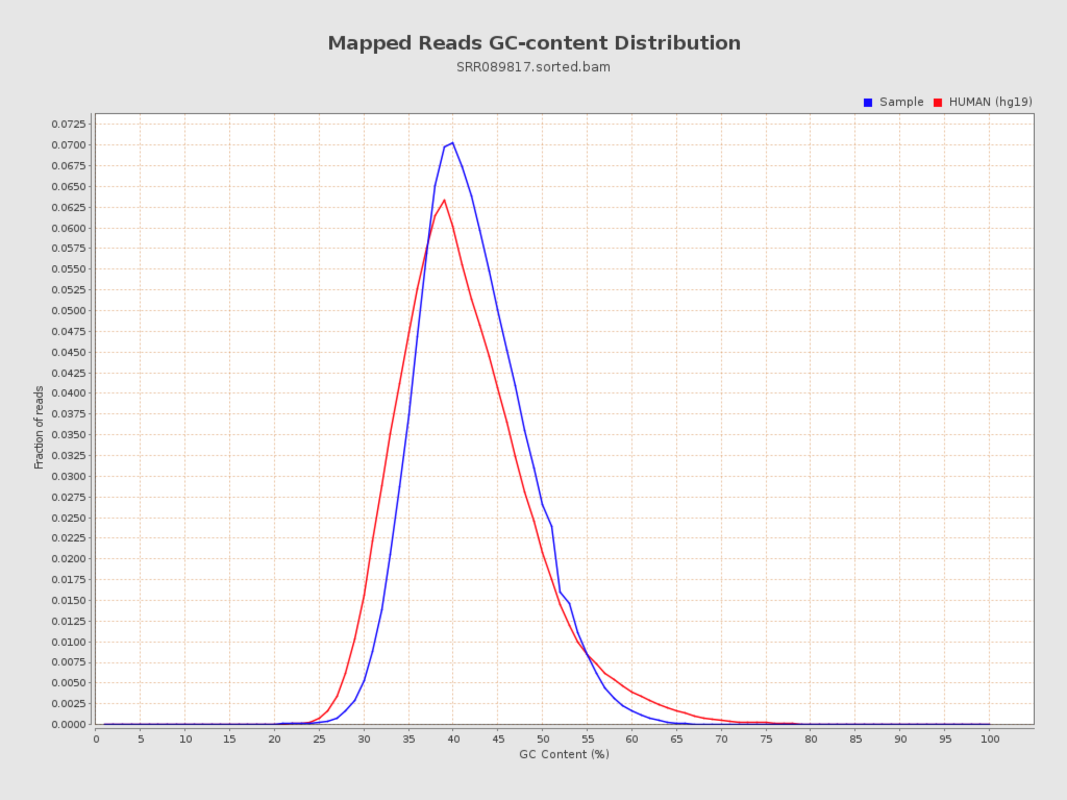
7. Results : Duplication Rate Histogram



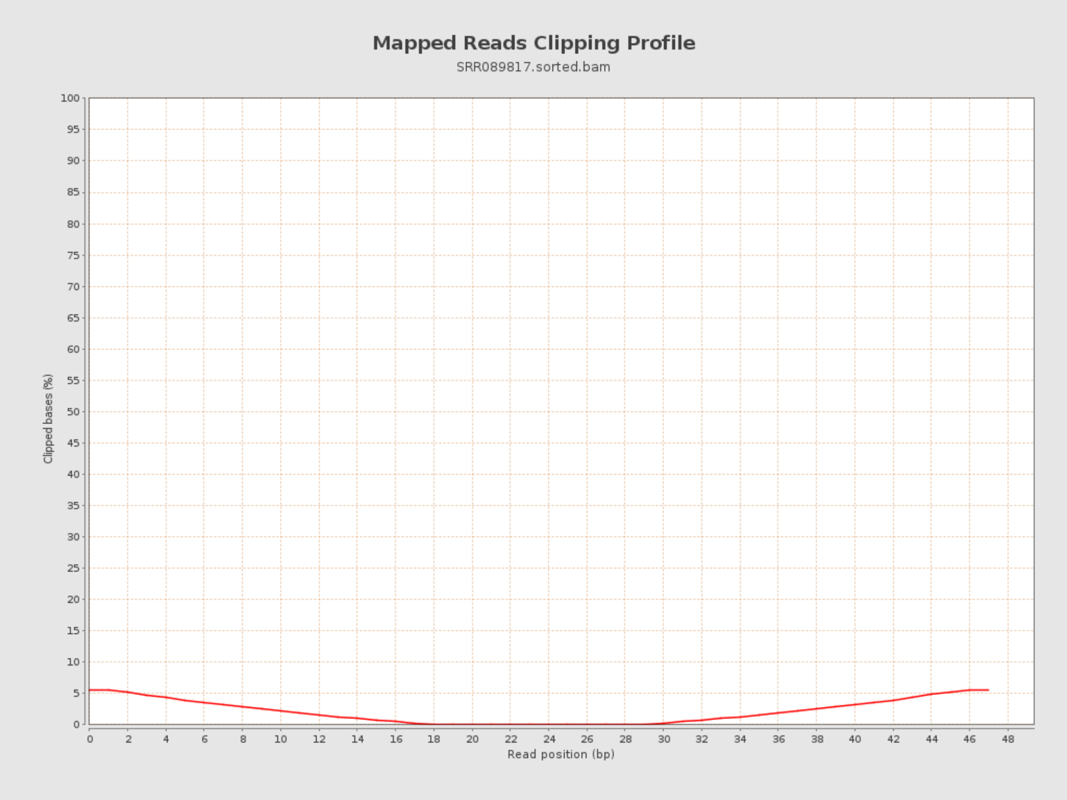
8. Results : Mapped Reads Nucleotide Content



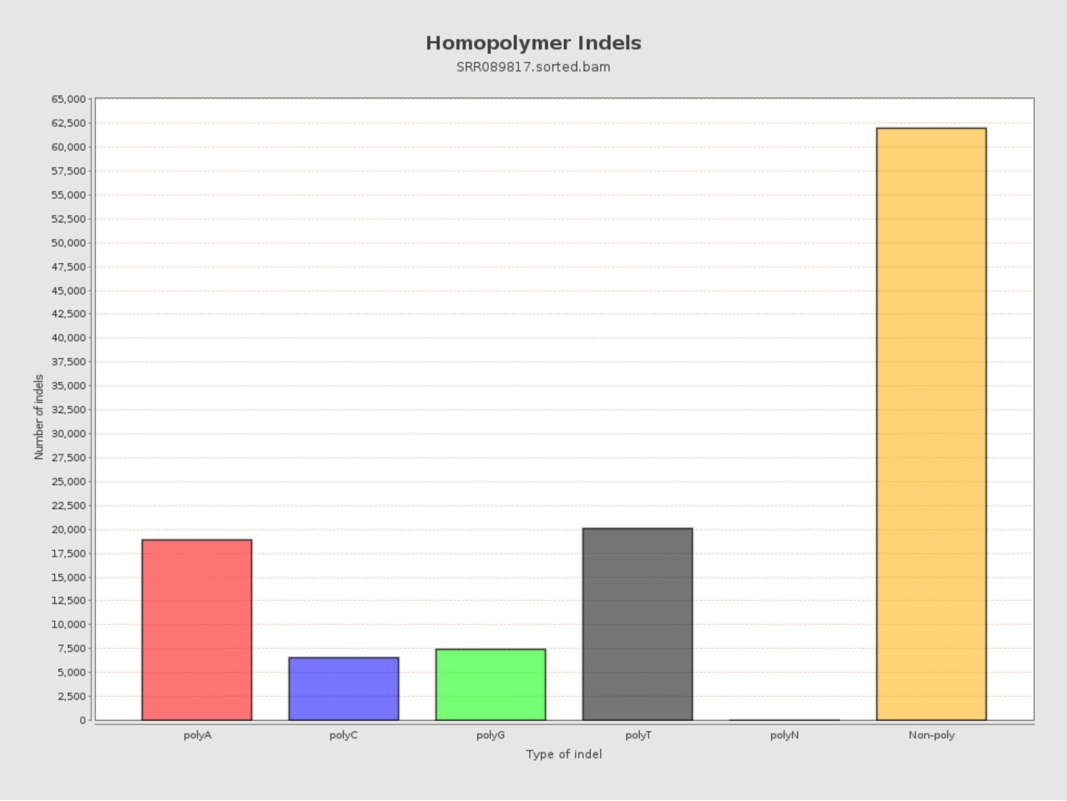
9. Results : Mapped Reads GC-content Distribution



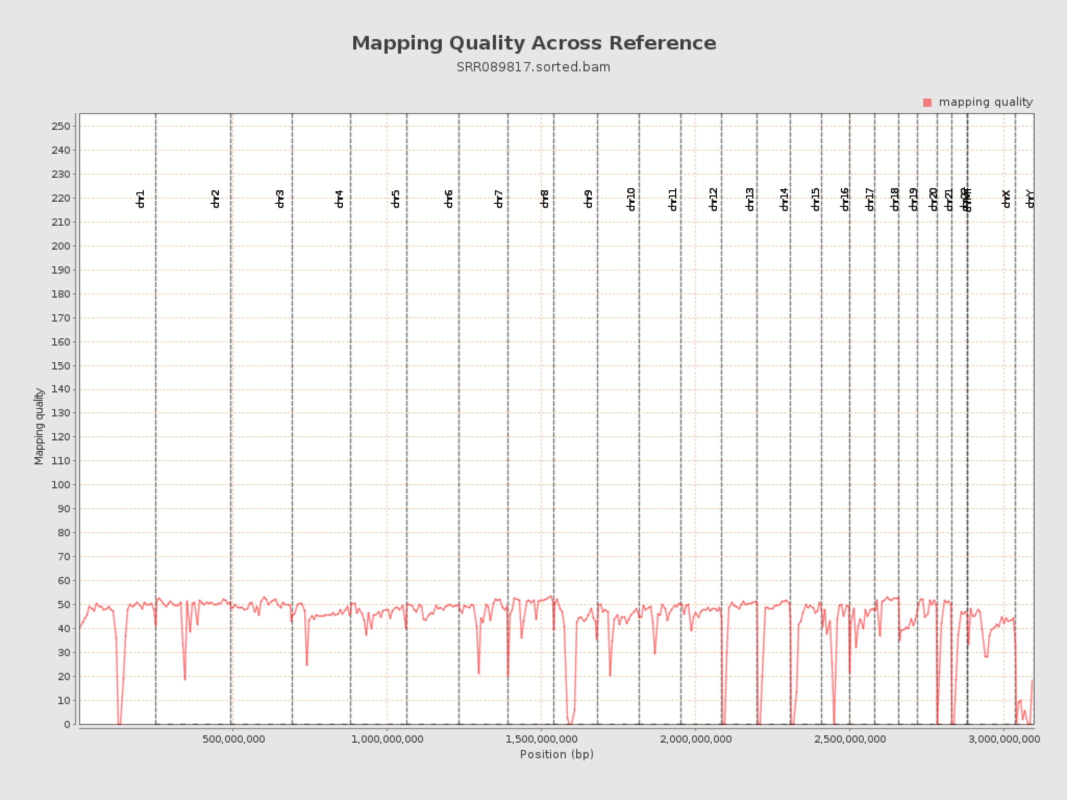
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram