Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/01/21 19:14:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR620540.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR620540.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 21 19:14:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR620540.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,319,331
Mapped reads	6,414,634 / 44.8%
Unmapped reads	7,904,697 / 55.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	123 / 0%
Read min/max/mean length	30 / 49 / 49
Duplicated reads (estimated)	1,158,315 / 8.09%
Duplication rate	8.38%
Clipped reads	2,281,520 / 15.93%

2.2. ACGT Content

Number/percentage of A's	74,223,698 / 26.24%
Number/percentage of C's	51,654,393 / 18.26%
Number/percentage of T's	87,904,079 / 31.07%
Number/percentage of G's	69,096,045 / 24.43%
Number/percentage of N's	4,032 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0914

Standard Deviation	1.043

2.4. Mapping Quality

Mean Mapping Quality	43.3

2.5. Mismatches and indels

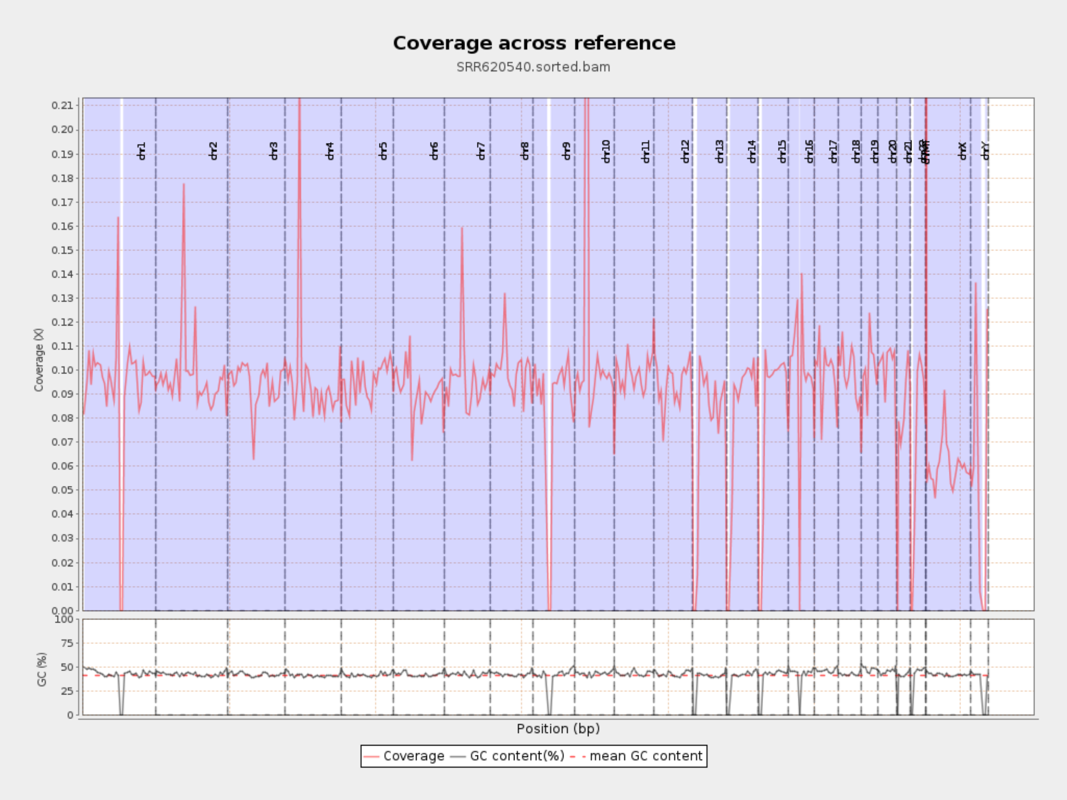
General error rate	0.71%
Mismatches	1,971,890
Insertions	20,364
Mapped reads with at least one insertion	0.32%
Deletions	47,244
Mapped reads with at least one deletion	0.73%
Homopolymer indels	42.06%

2.6. Chromosome stats

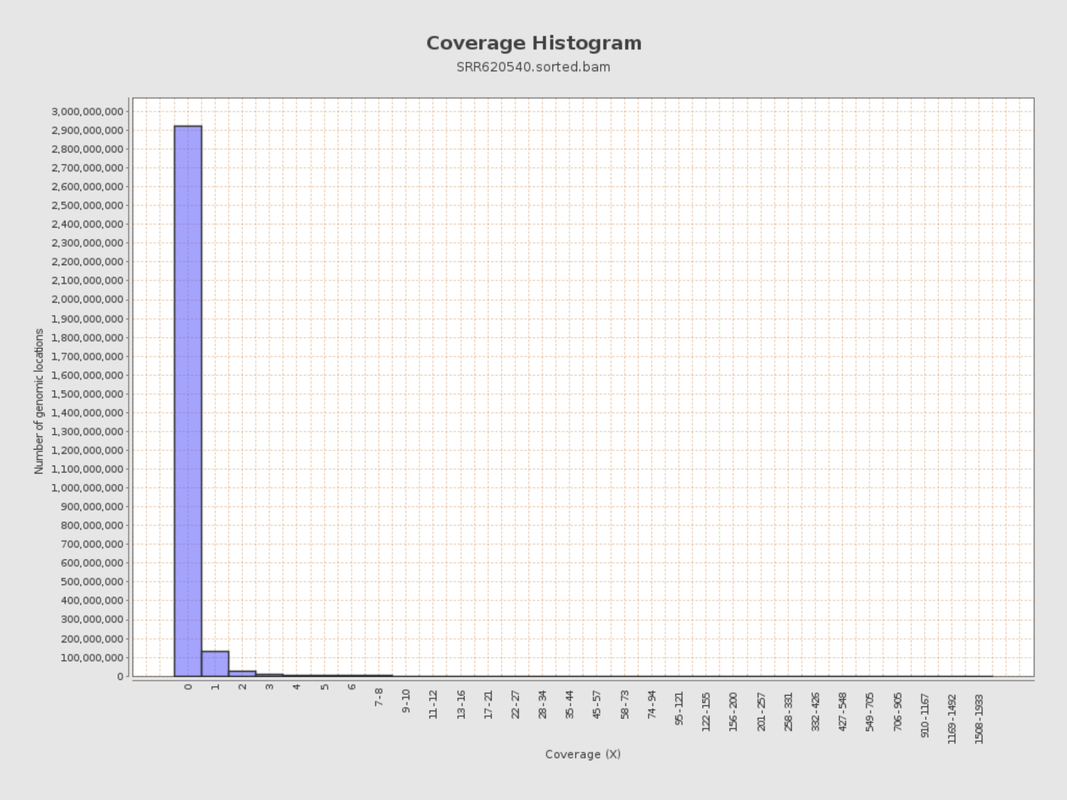
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23329993	0.0936	1.4177
chr2	243199373	23930280	0.0984	1.0362
chr3	198022430	18648948	0.0942	0.6731
chr4	191154276	18568969	0.0971	0.8688
chr5	180915260	17349486	0.0959	0.6507
chr6	171115067	15658158	0.0915	0.7721
chr7	159138663	15431758	0.097	1.1263

chr8	146364022	14564180	0.0995	0.9262
chr9	141213431	11692832	0.0828	0.7611
chr10	135534747	15233051	0.1124	2.4306
chr11	135006516	13205432	0.0978	1.0498
chr12	133851895	12683692	0.0948	0.6749
chr13	115169878	8673505	0.0753	0.6003
chr14	107349540	8560238	0.0797	0.6281
chr15	102531392	8332411	0.0813	0.6072
chr16	90354753	8740579	0.0967	0.8311
chr17	81195210	8086286	0.0996	0.7677
chr18	78077248	7736933	0.0991	1.8623
chr19	59128983	5902988	0.0998	1.033
chr20	63025520	6455078	0.1024	0.8585
chr21	48129895	3802707	0.079	0.7208
chr22	51304566	3528789	0.0688	0.573
chrMT	16571	84343	5.0898	6.4425
chrX	155270560	9412521	0.0606	0.7197
chrY	59373566	3338251	0.0562	0.7934

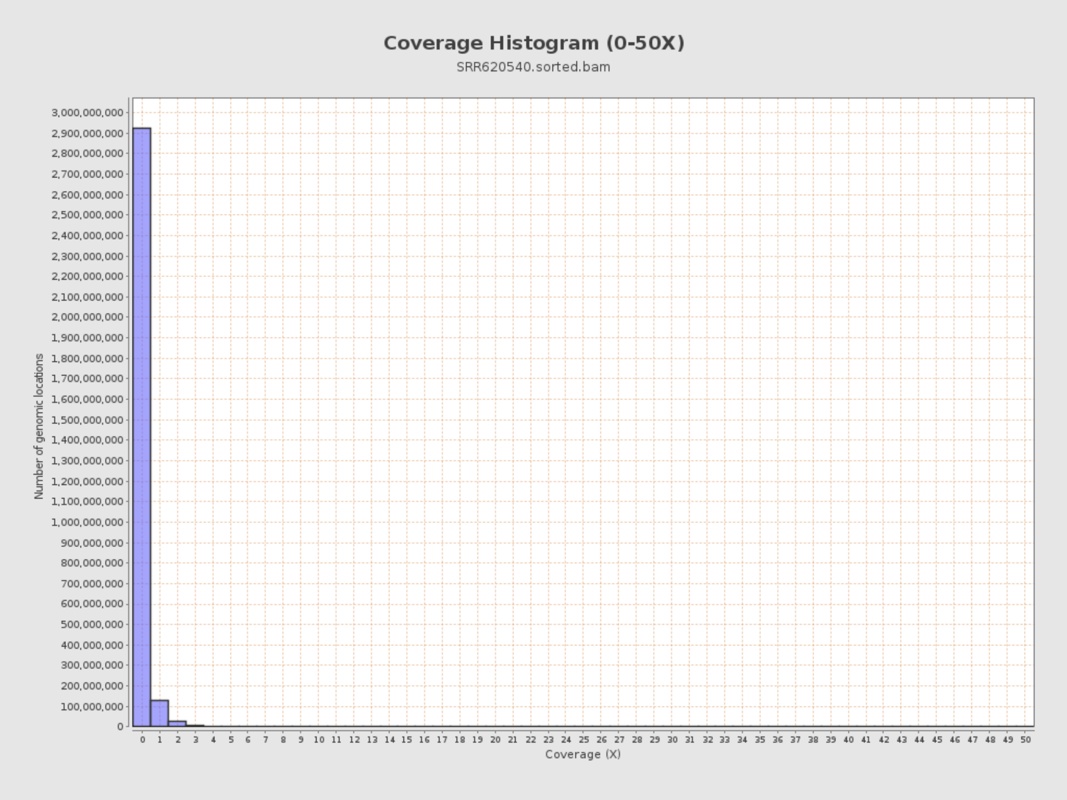
3. Results : Coverage across reference



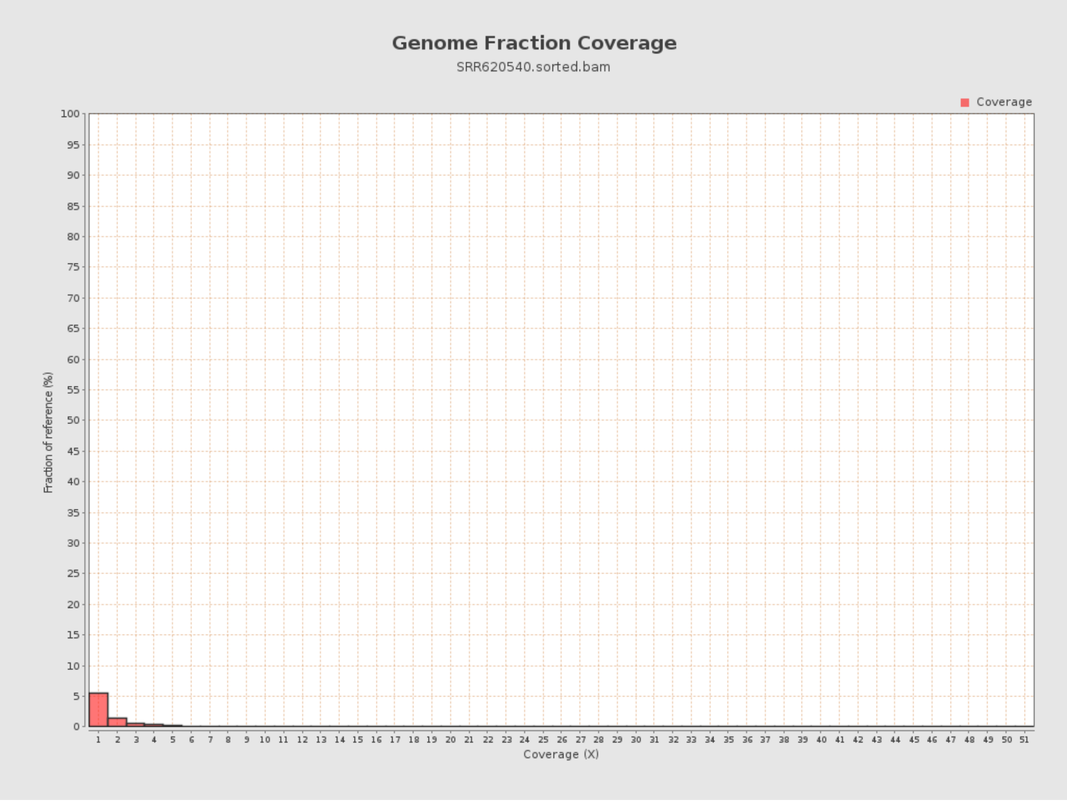
4. Results : Coverage Histogram



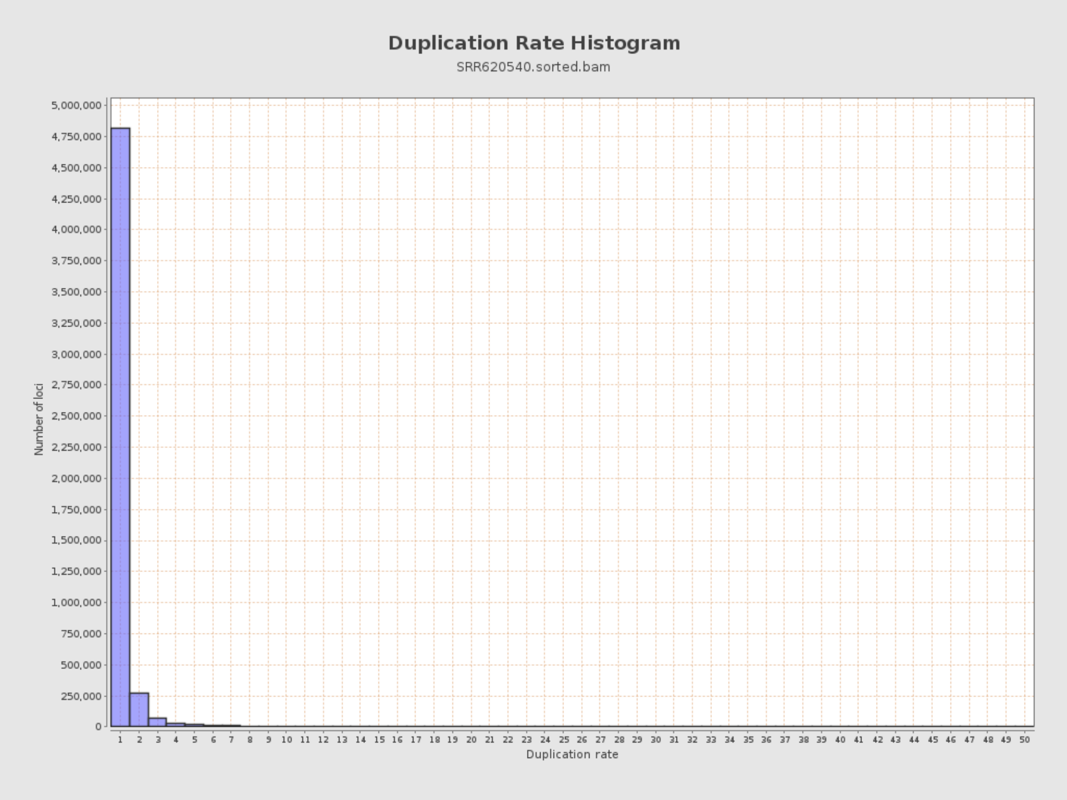
5. Results : Coverage Histogram (0-50X)



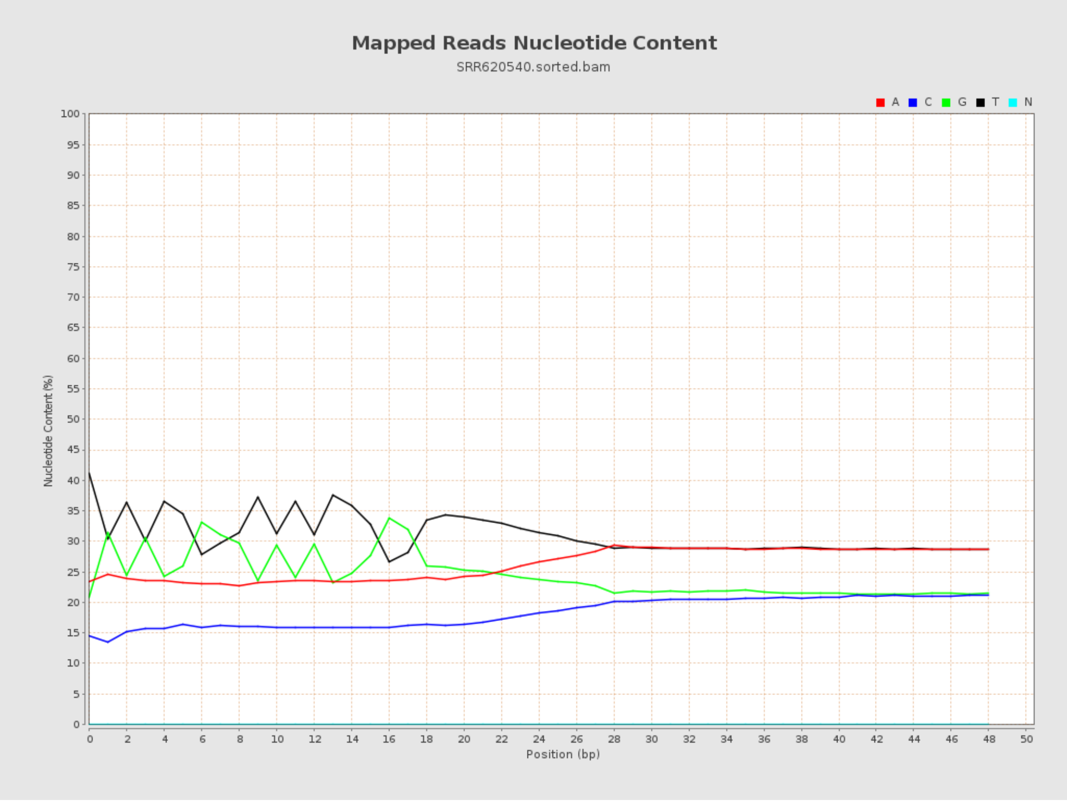
6. Results : Genome Fraction Coverage



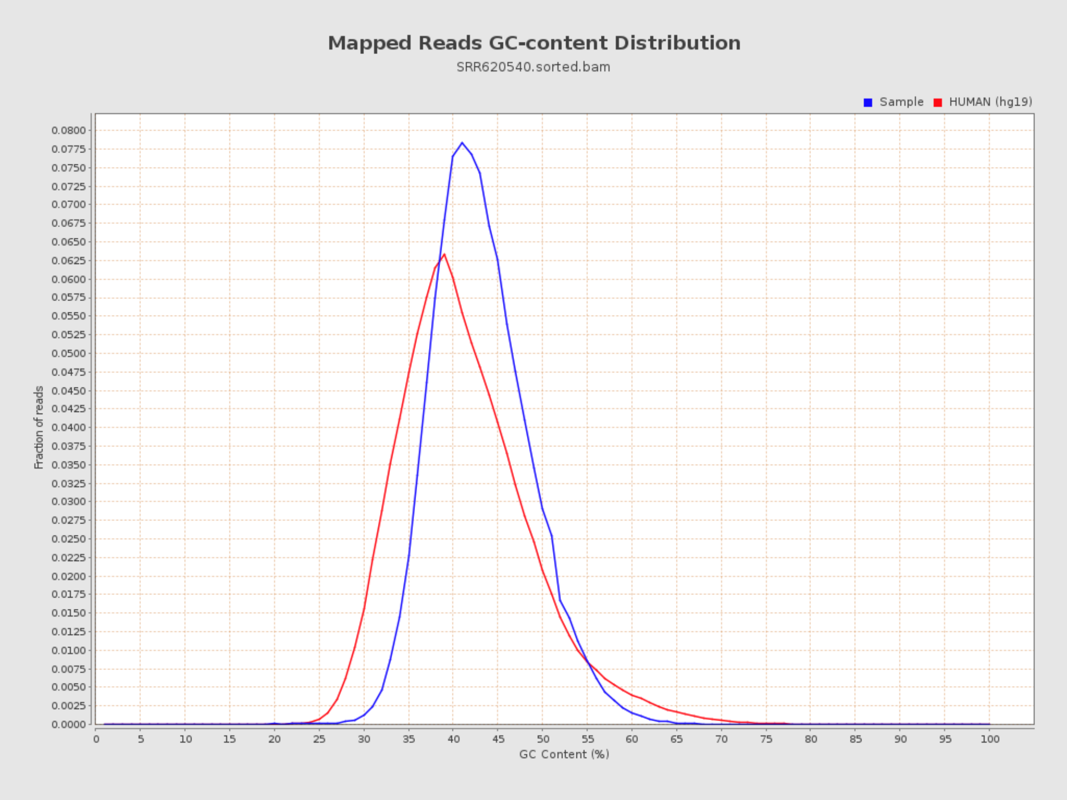
7. Results : Duplication Rate Histogram



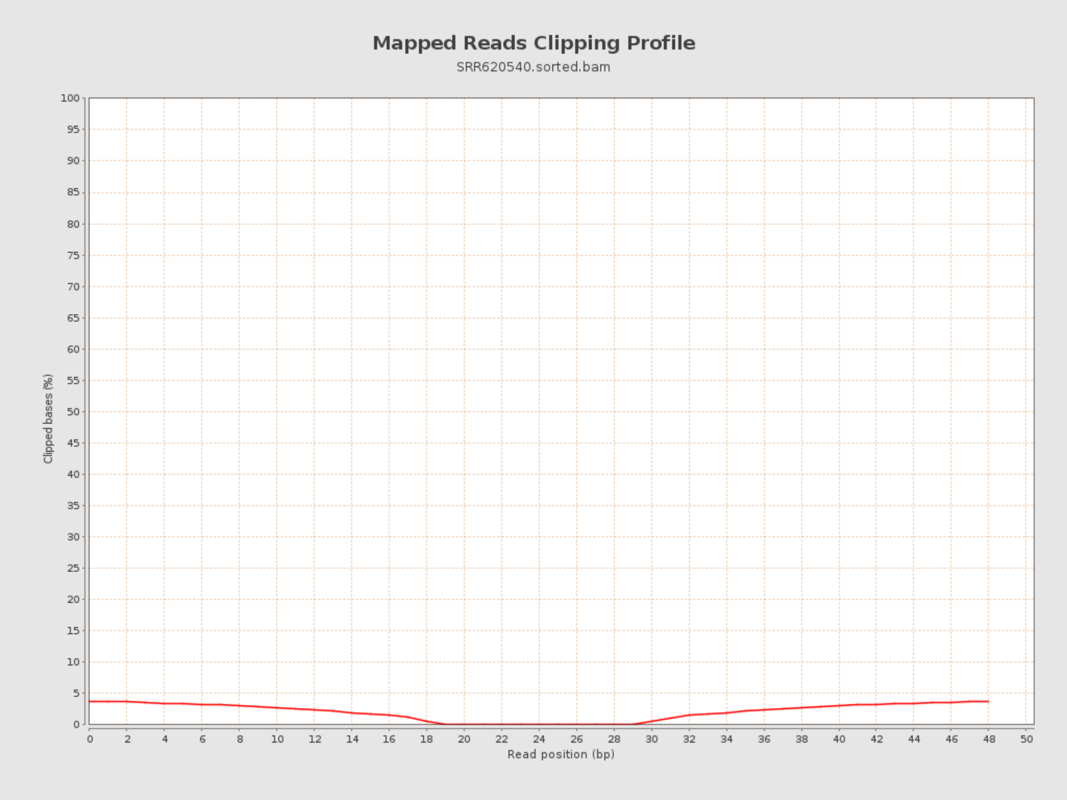
8. Results : Mapped Reads Nucleotide Content



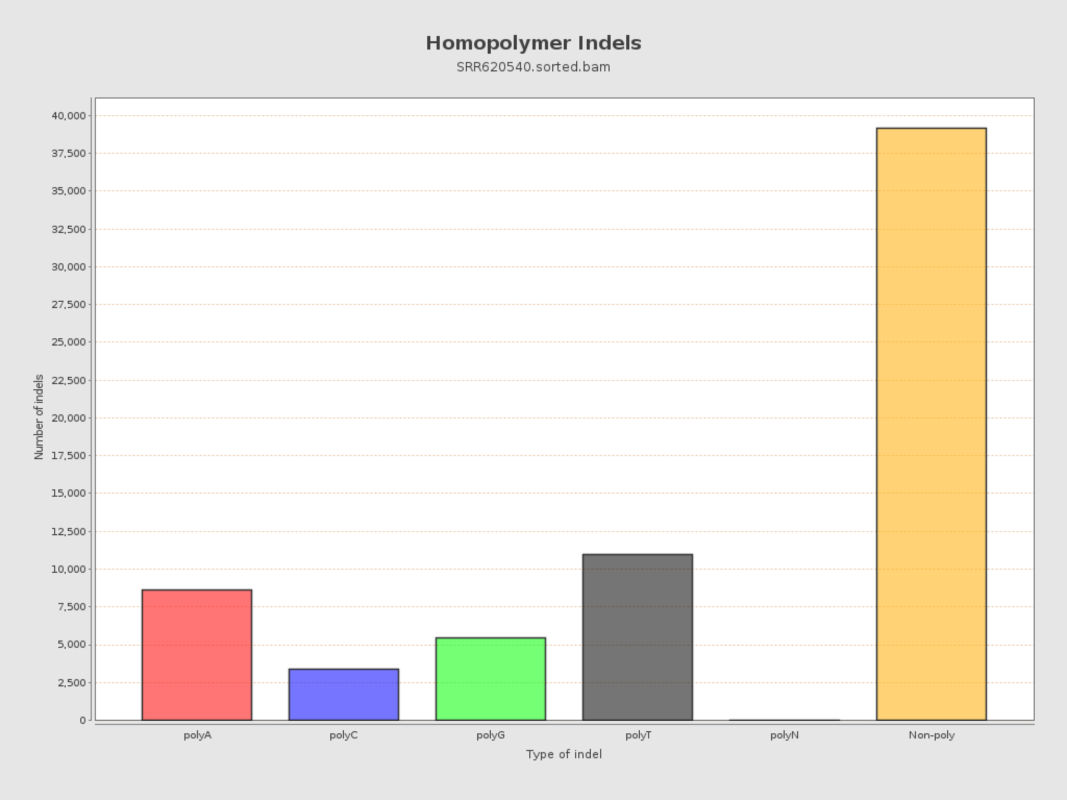
9. Results : Mapped Reads GC-content Distribution



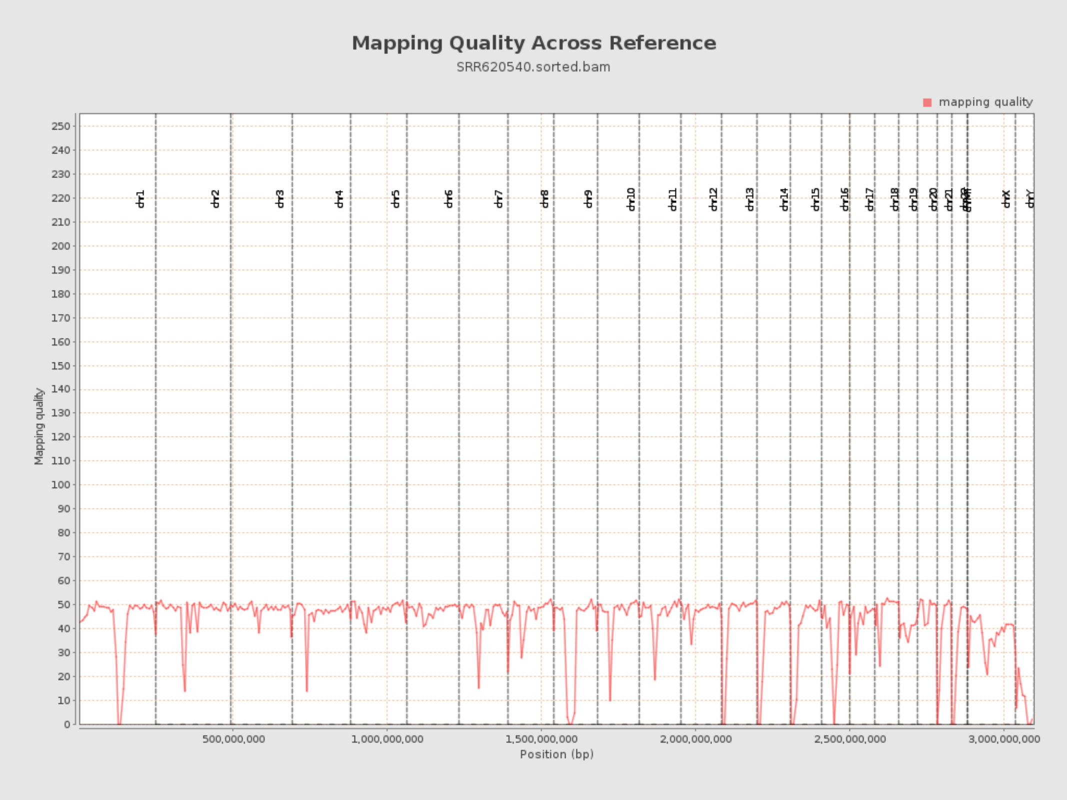
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram