Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/01/21 18:08:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR620534.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 SRR620534.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 21 18:08:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR620534.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,128,791
Mapped reads	2,952,510 / 41.42%
Unmapped reads	4,176,281 / 58.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	60 / 0%
Read min/max/mean length	30 / 49 / 49
Duplicated reads (estimated)	394,493 / 5.53%
Duplication rate	9.05%
Clipped reads	1,033,432 / 14.5%

2.2. ACGT Content

Number/percentage of A's	30,559,993 / 23.85%
Number/percentage of C's	21,957,324 / 17.13%
Number/percentage of T's	46,362,024 / 36.18%
Number/percentage of G's	29,260,012 / 22.83%
Number/percentage of N's	7,774 / 0.01%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0414

Standard Deviation	0.6711

2.4. Mapping Quality

Mean Mapping Quality	42

2.5. Mismatches and indels

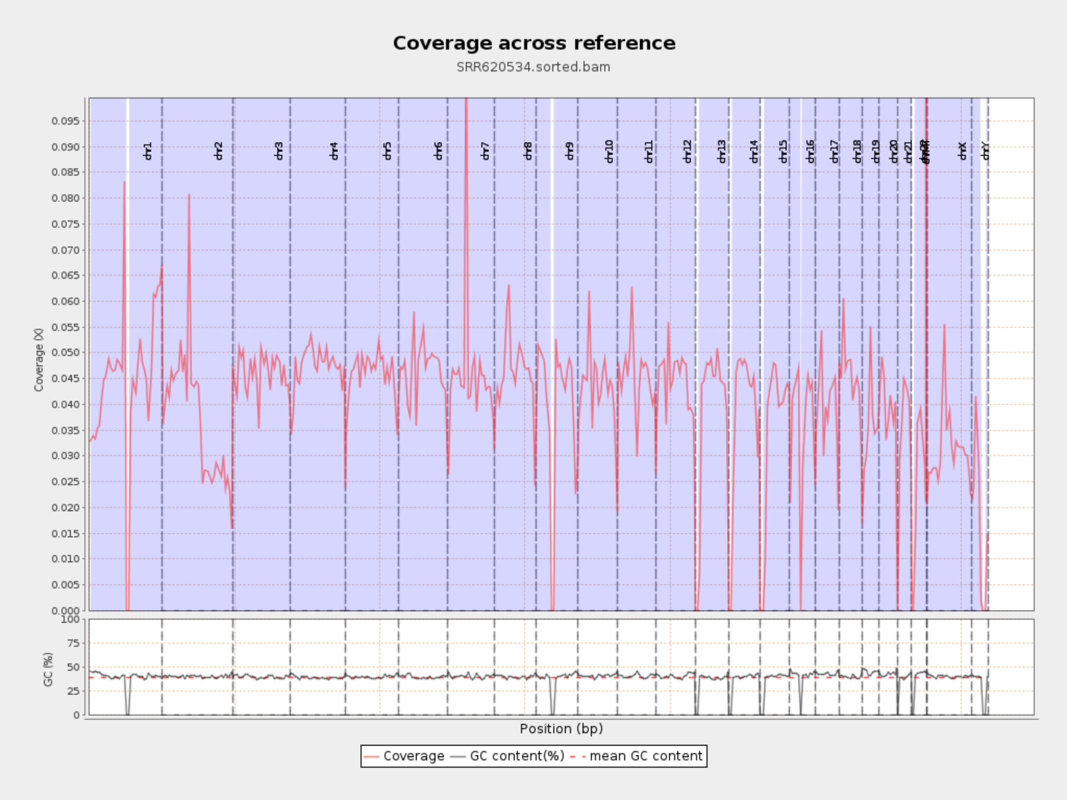
General error rate	0.92%
Mismatches	1,163,312
Insertions	7,810
Mapped reads with at least one insertion	0.26%
Deletions	20,727
Mapped reads with at least one deletion	0.7%
Homopolymer indels	47.3%

2.6. Chromosome stats

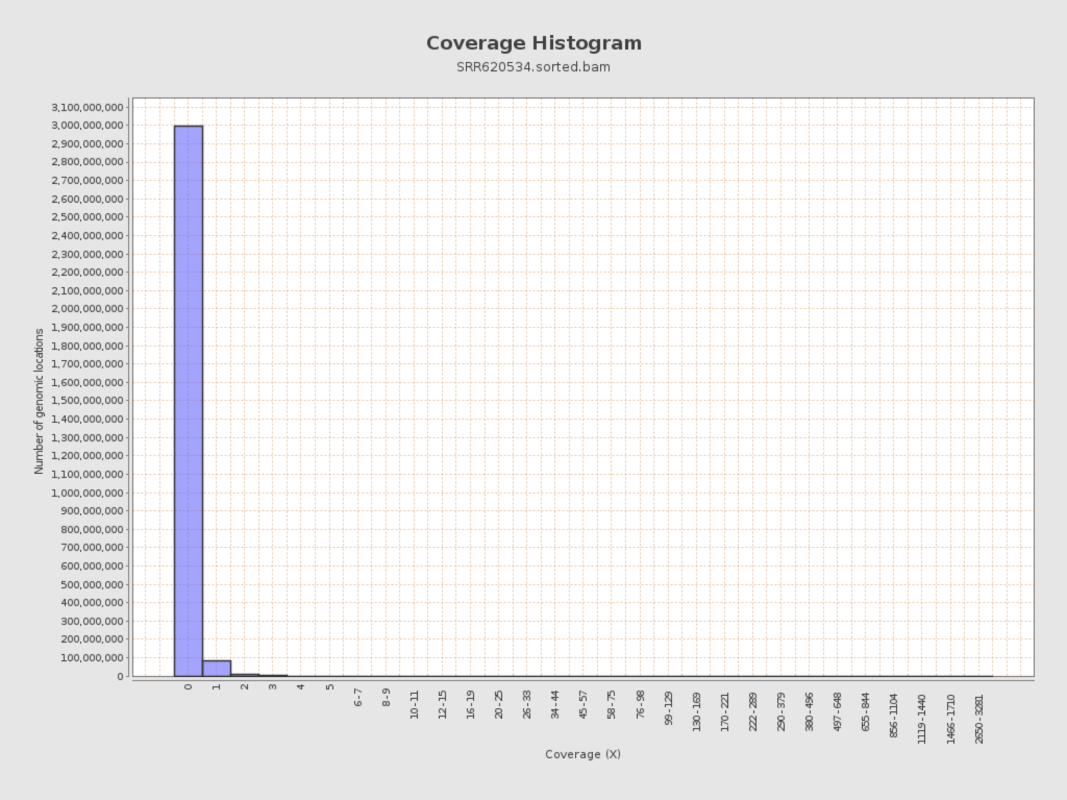
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11072289	0.0444	0.9826
chr2	243199373	9059932	0.0373	0.4562
chr3	198022430	9147141	0.0462	0.3671
chr4	191154276	9070378	0.0475	0.574
chr5	180915260	8328220	0.046	0.3184
chr6	171115067	7990655	0.0467	0.3839
chr7	159138663	7511509	0.0472	1.7324

chr8	146364022	6749331	0.0461	0.6287
chr9	141213431	5596029	0.0396	0.6108
chr10	135534747	5920944	0.0437	0.4329
chr11	135006516	6071544	0.045	0.7536
chr12	133851895	5977658	0.0447	0.3684
chr13	115169878	4332226	0.0376	0.3445
chr14	107349540	3981179	0.0371	0.3025
chr15	102531392	3528204	0.0344	0.3723
chr16	90354753	3261304	0.0361	0.2823
chr17	81195210	3181397	0.0392	0.3757
chr18	78077248	3593860	0.046	1.0755
chr19	59128983	2115731	0.0358	0.5485
chr20	63025520	2493267	0.0396	0.3723
chr21	48129895	1632016	0.0339	0.3689
chr22	51304566	1212118	0.0236	0.2525
chrMT	16571	500844	30.2241	34.2118
chrX	155270560	4887439	0.0315	0.517
chrY	59373566	962489	0.0162	0.1928

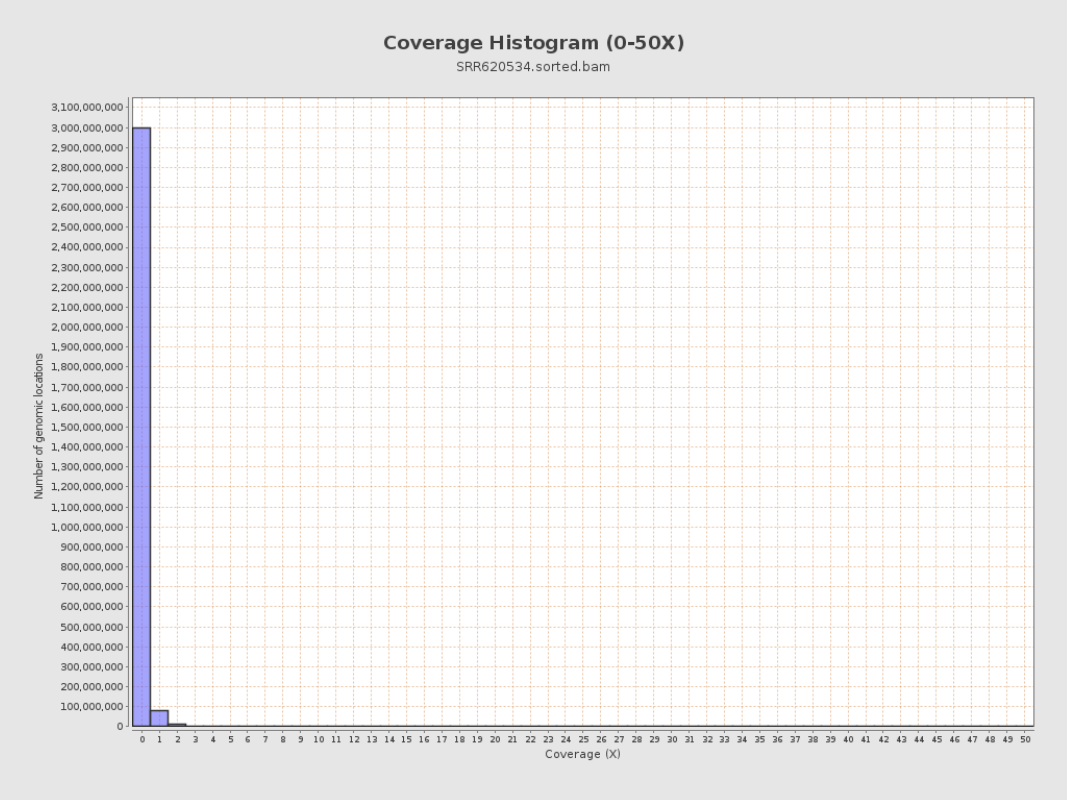
3. Results : Coverage across reference



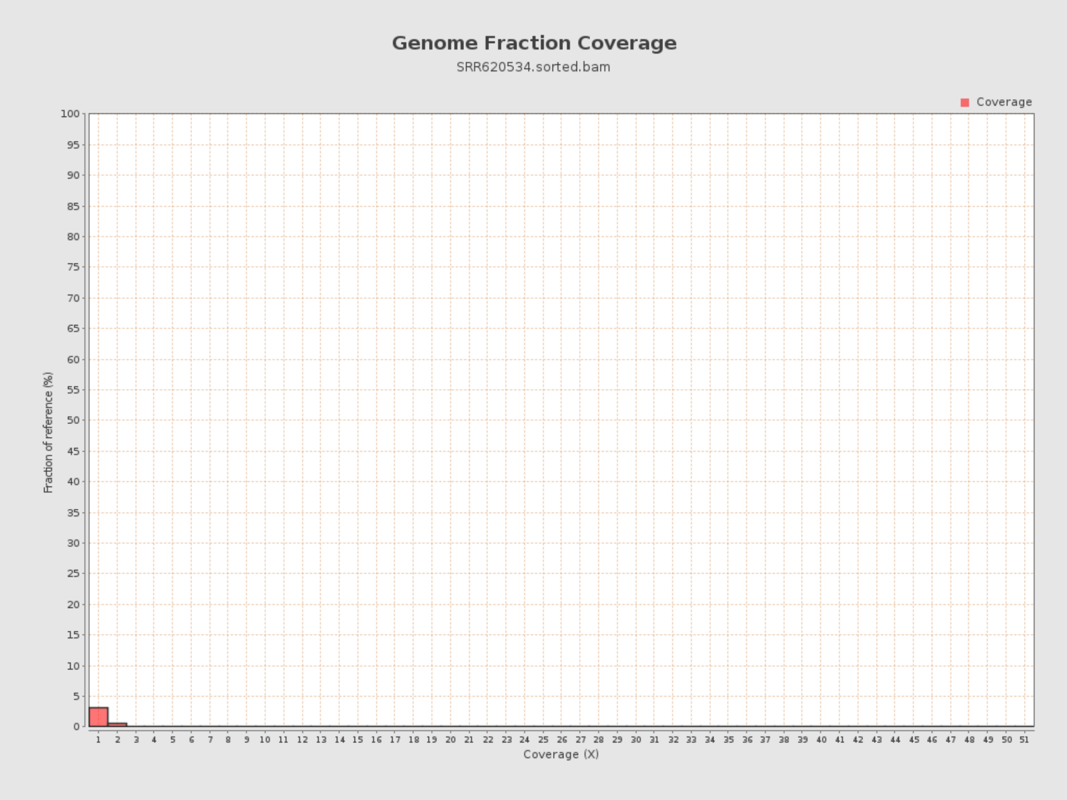
4. Results : Coverage Histogram



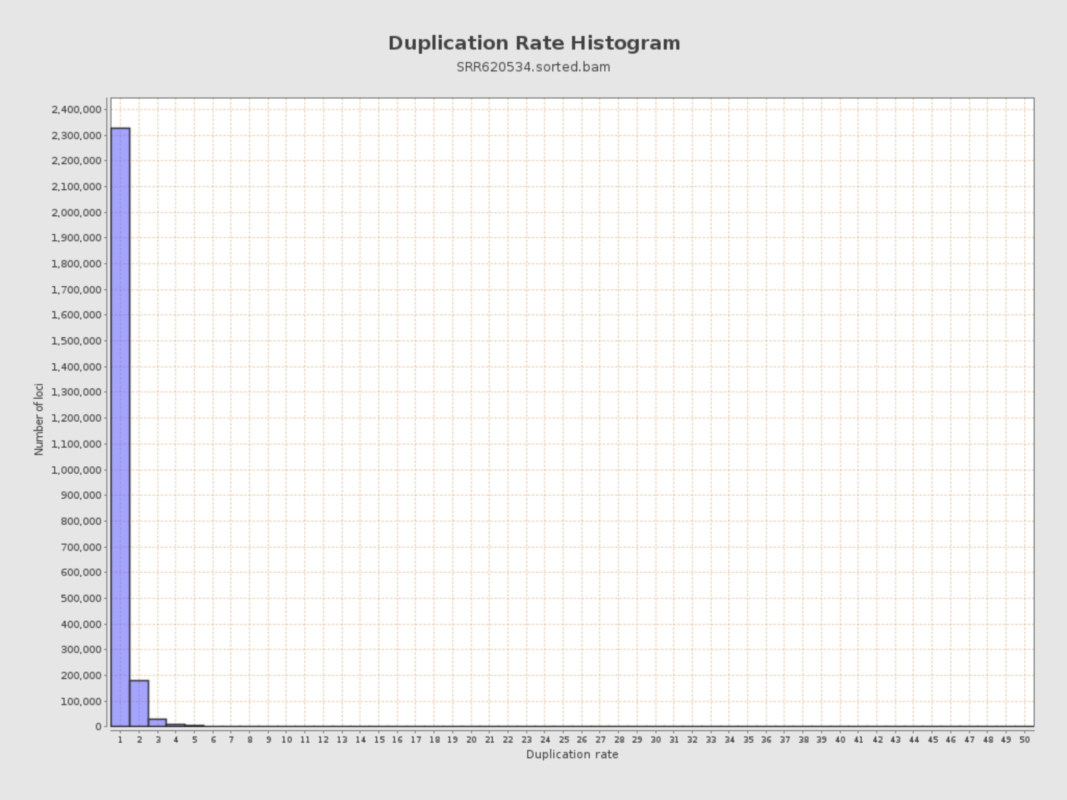
5. Results : Coverage Histogram (0-50X)



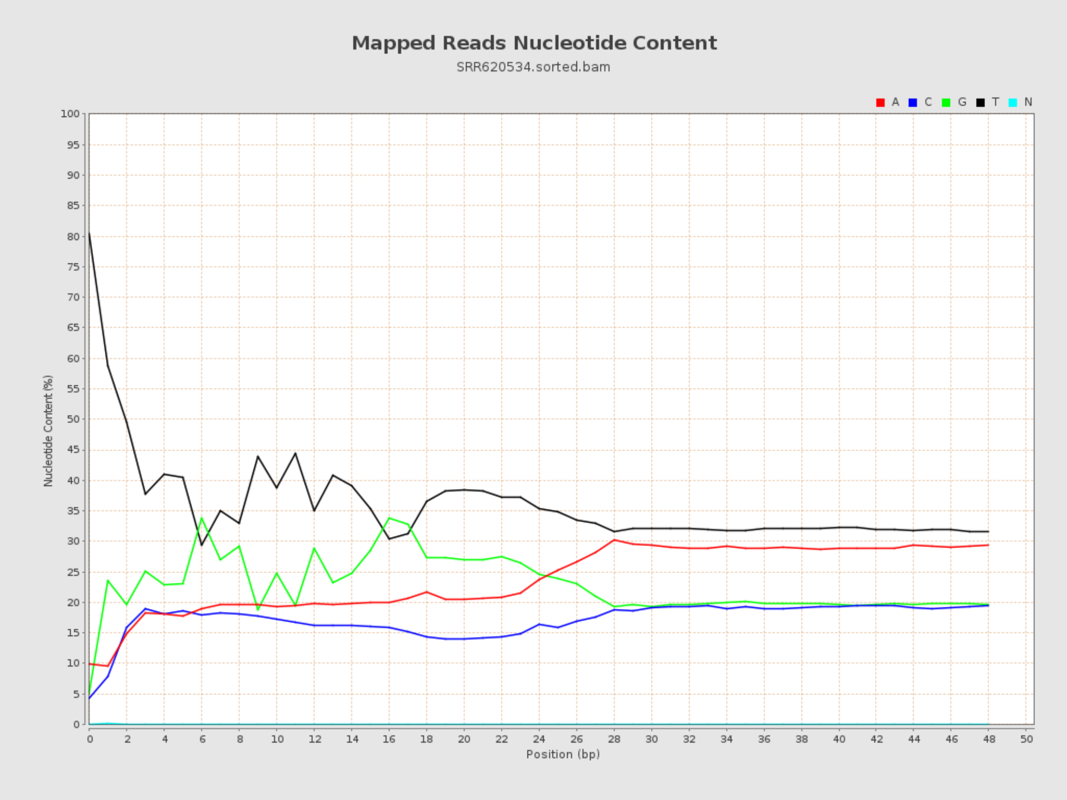
6. Results : Genome Fraction Coverage



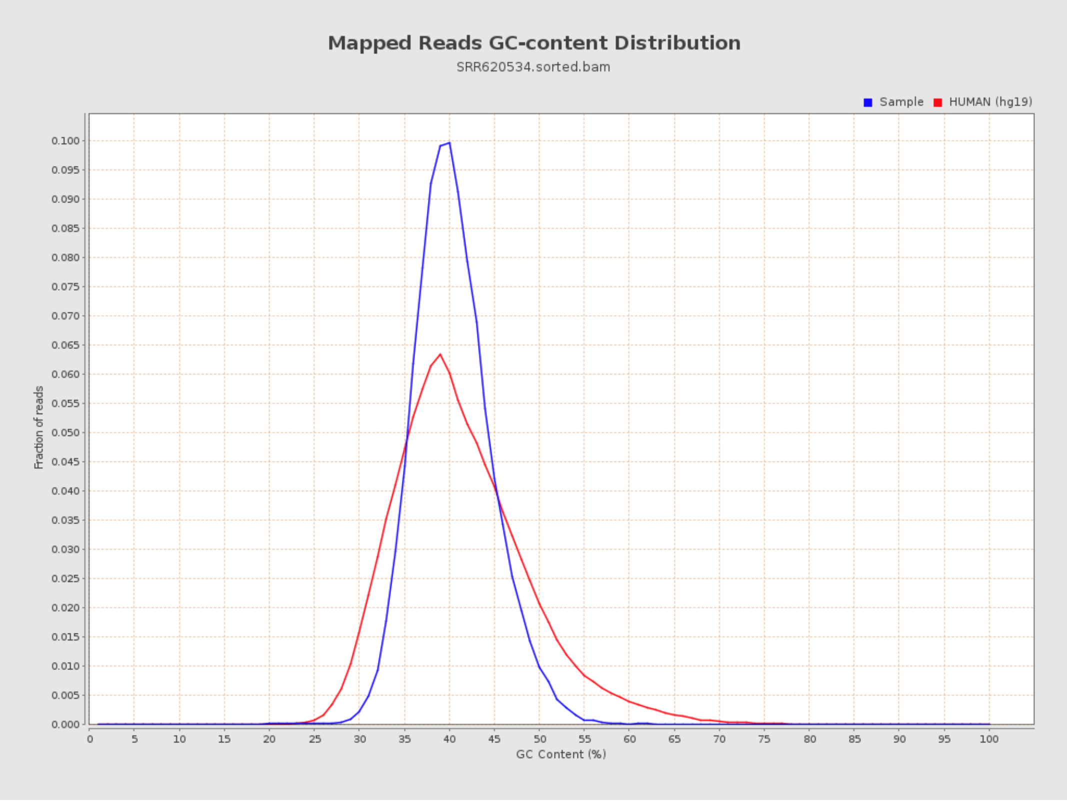
7. Results : Duplication Rate Histogram



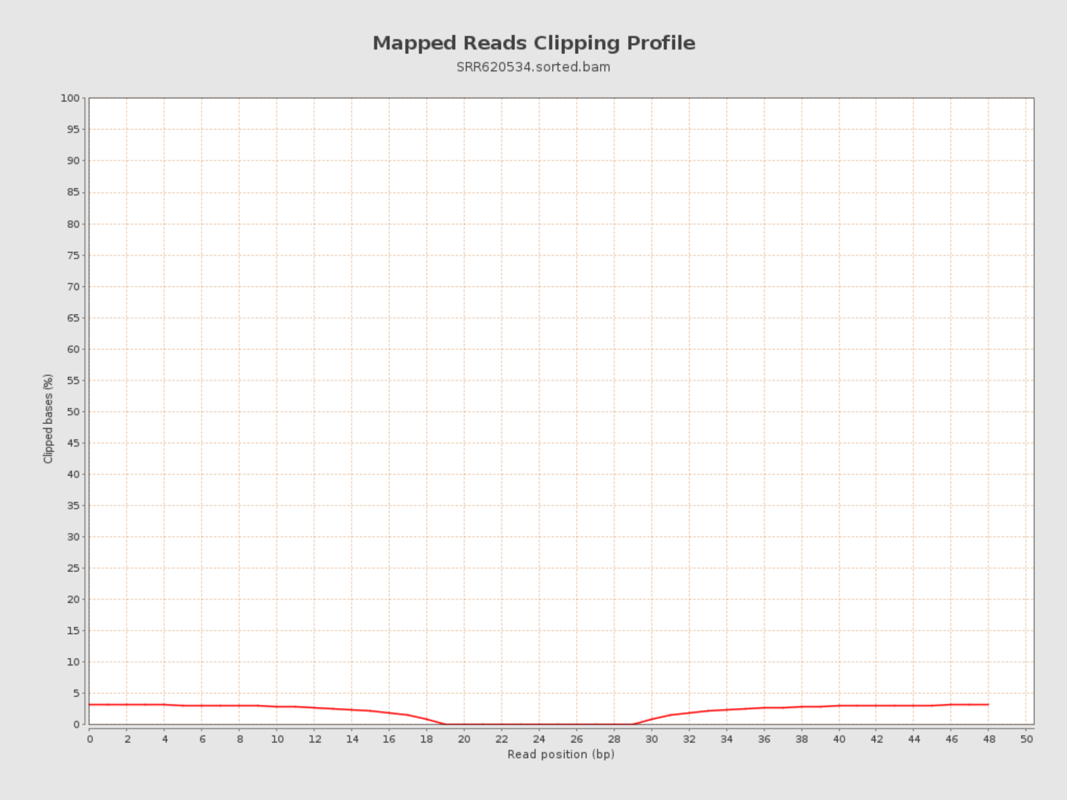
8. Results : Mapped Reads Nucleotide Content



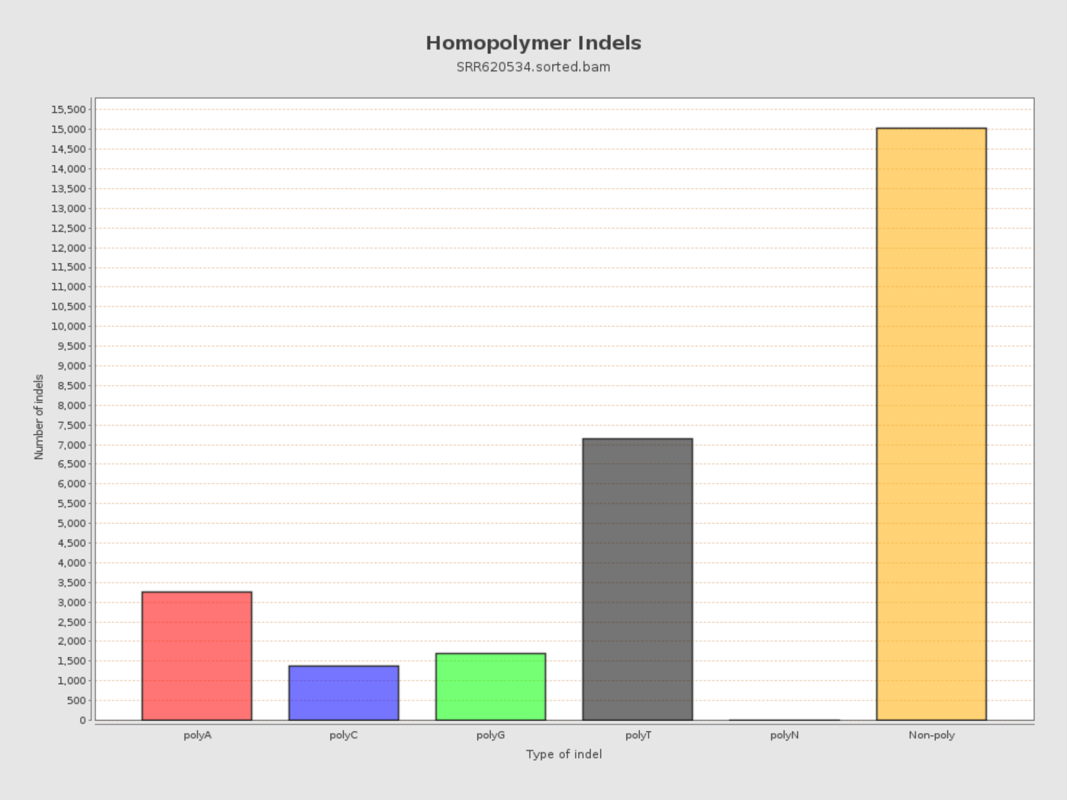
9. Results : Mapped Reads GC-content Distribution



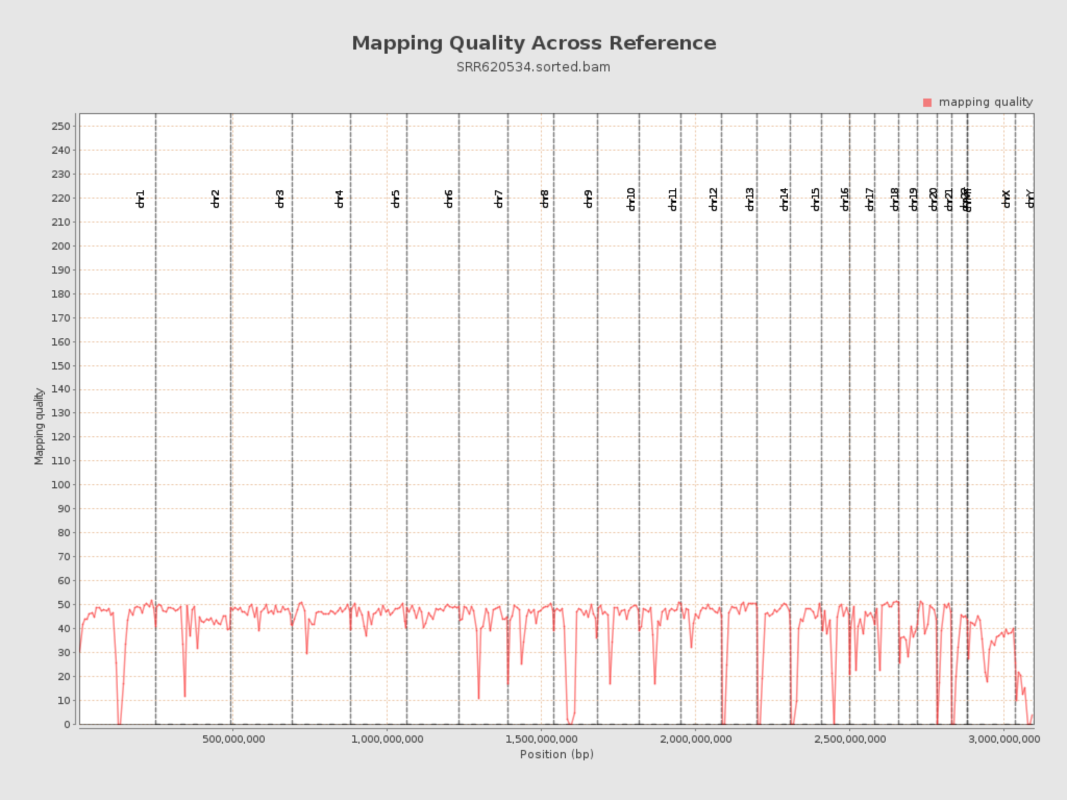
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram