Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/01/21 18:38:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR620537.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 SRR620537.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 21 18:38:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR620537.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,692,094
Mapped reads	8,242,821 / 49.38%
Unmapped reads	8,449,273 / 50.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	396 / 0%
Read min/max/mean length	30 / 49 / 49
Duplicated reads (estimated)	697,408 / 4.18%
Duplication rate	3.4%
Clipped reads	2,394,835 / 14.35%

2.2. ACGT Content

Number/percentage of A's	93,971,993 / 25.26%
Number/percentage of C's	78,702,036 / 21.15%
Number/percentage of T's	108,848,078 / 29.25%
Number/percentage of G's	90,513,766 / 24.33%
Number/percentage of N's	41,583 / 0.01%
GC Percentage	45.48%

2.3. Coverage

Mean	0.1202

Standard Deviation	1.3477

2.4. Mapping Quality

Mean Mapping Quality	36.13

2.5. Mismatches and indels

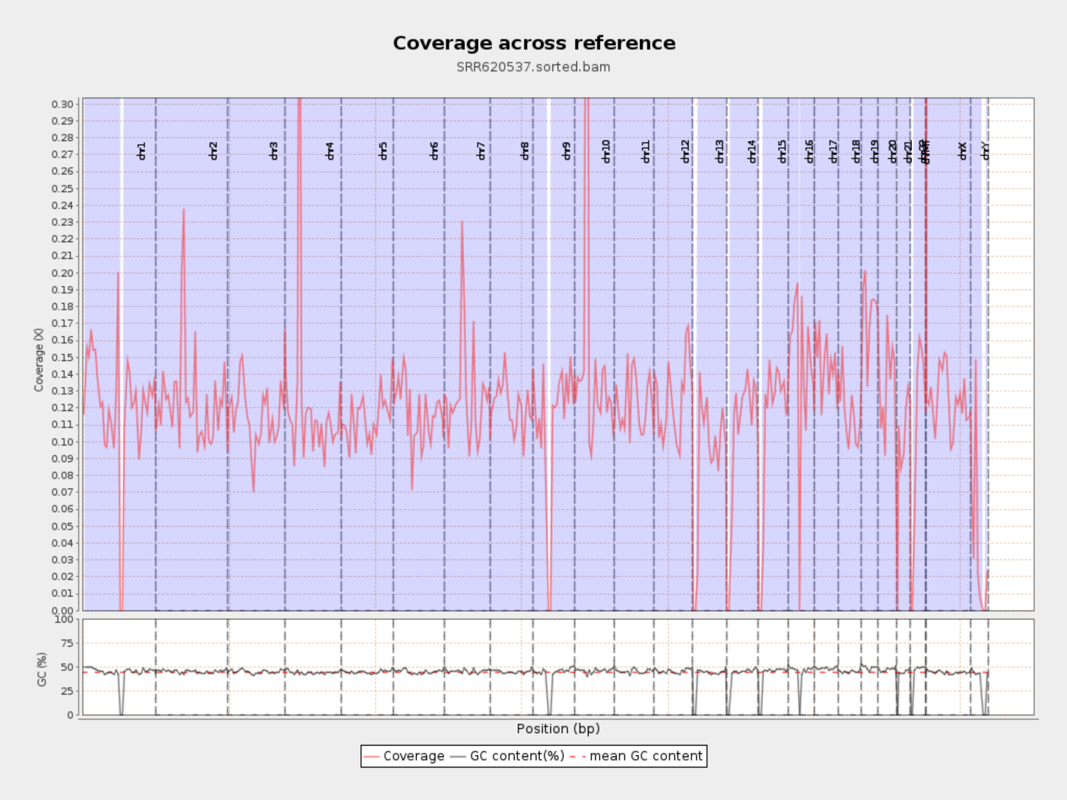
General error rate	0.72%
Mismatches	2,648,892
Insertions	25,787
Mapped reads with at least one insertion	0.31%
Deletions	58,282
Mapped reads with at least one deletion	0.68%
Homopolymer indels	35.56%

2.6. Chromosome stats

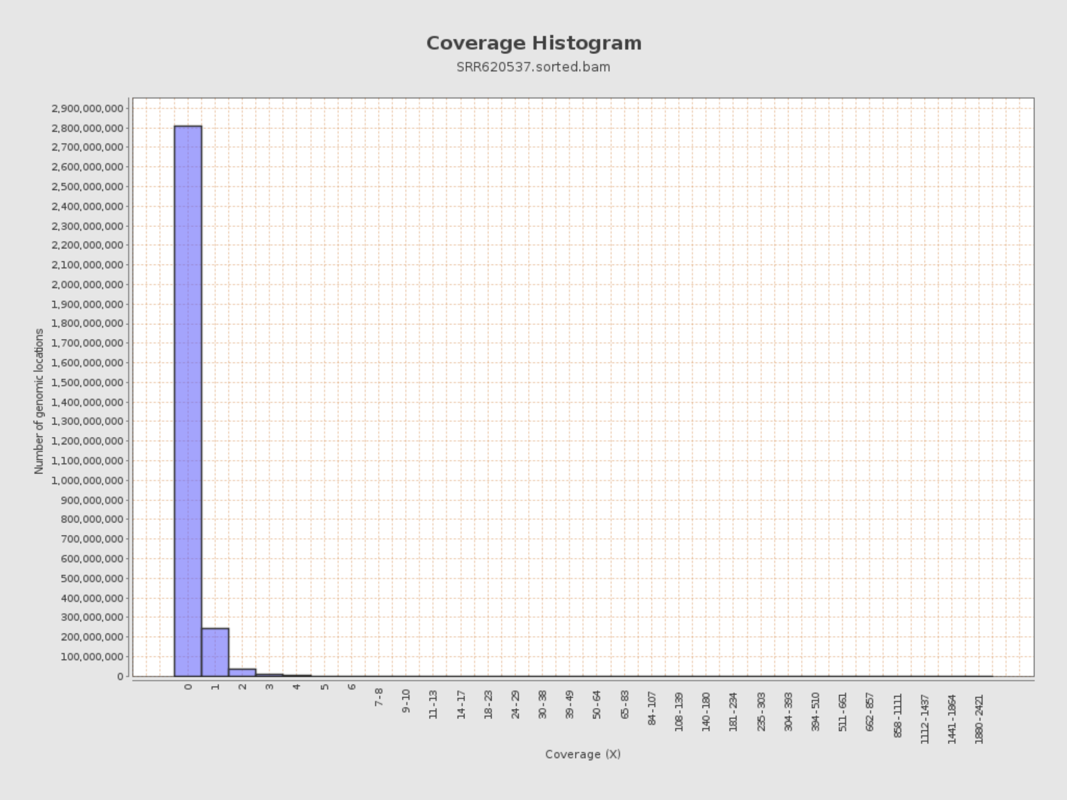
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30114425	0.1208	1.8741
chr2	243199373	30461396	0.1253	1.6662
chr3	198022430	22762278	0.1149	1.2666
chr4	191154276	23793087	0.1245	1.4636
chr5	180915260	20708299	0.1145	0.5705
chr6	171115067	19893913	0.1163	0.7326
chr7	159138663	20502234	0.1288	1.3889

chr8	146364022	17680133	0.1208	0.9659
chr9	141213431	15391037	0.109	0.9026
chr10	135534747	20699232	0.1527	3.2673
chr11	135006516	16552748	0.1226	1.14
chr12	133851895	16875396	0.1261	0.6291
chr13	115169878	10372794	0.0901	0.6155
chr14	107349540	11142248	0.1038	0.6883
chr15	102531392	10795269	0.1053	0.6475
chr16	90354753	12903248	0.1428	0.9615
chr17	81195210	11996129	0.1477	0.8711
chr18	78077248	9093944	0.1165	1.7328
chr19	59128983	10368981	0.1754	1.677
chr20	63025520	8408300	0.1334	0.7665
chr21	48129895	4784705	0.0994	0.875
chr22	51304566	5281077	0.1029	0.6026
chrMT	16571	56054	3.3827	3.0596
chrX	155270560	19345847	0.1246	0.8353
chrY	59373566	2181698	0.0367	1.1238

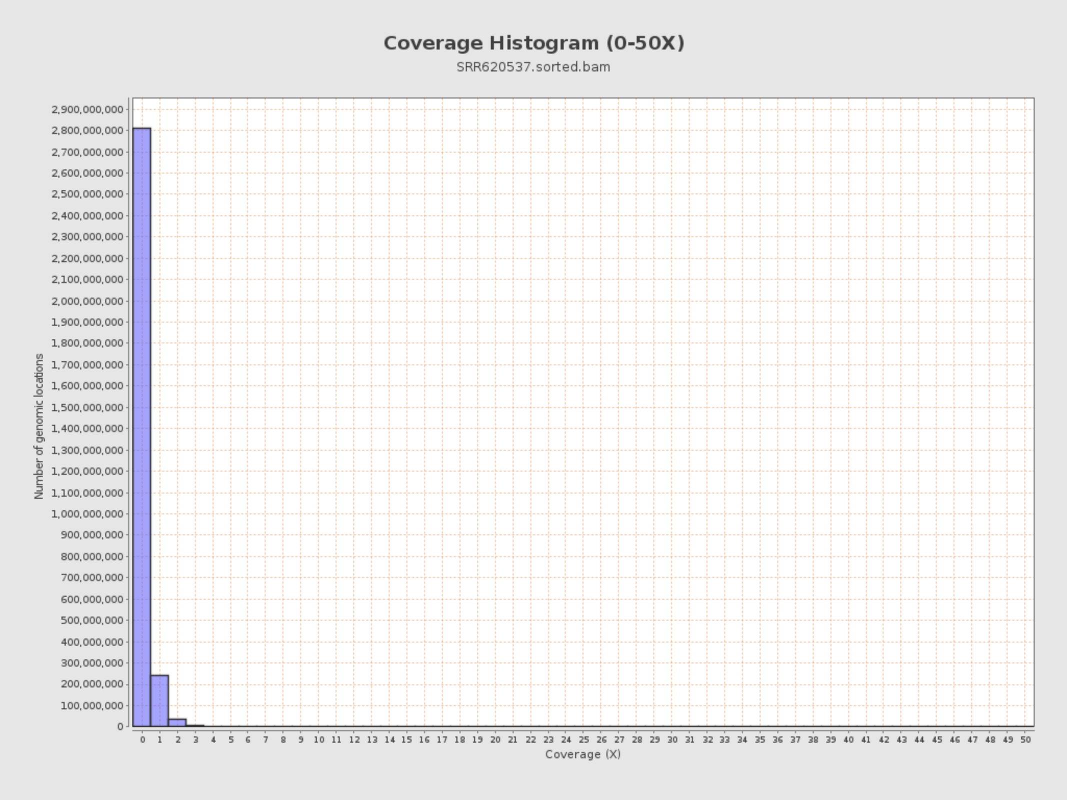
3. Results : Coverage across reference



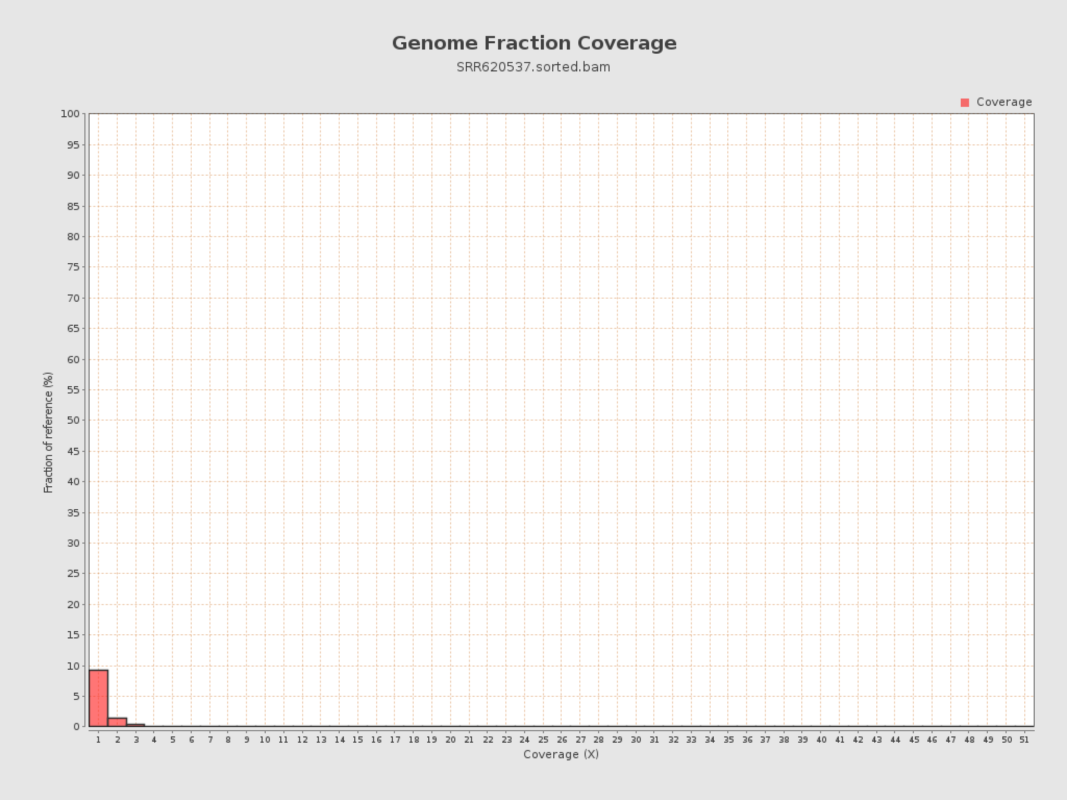
4. Results : Coverage Histogram



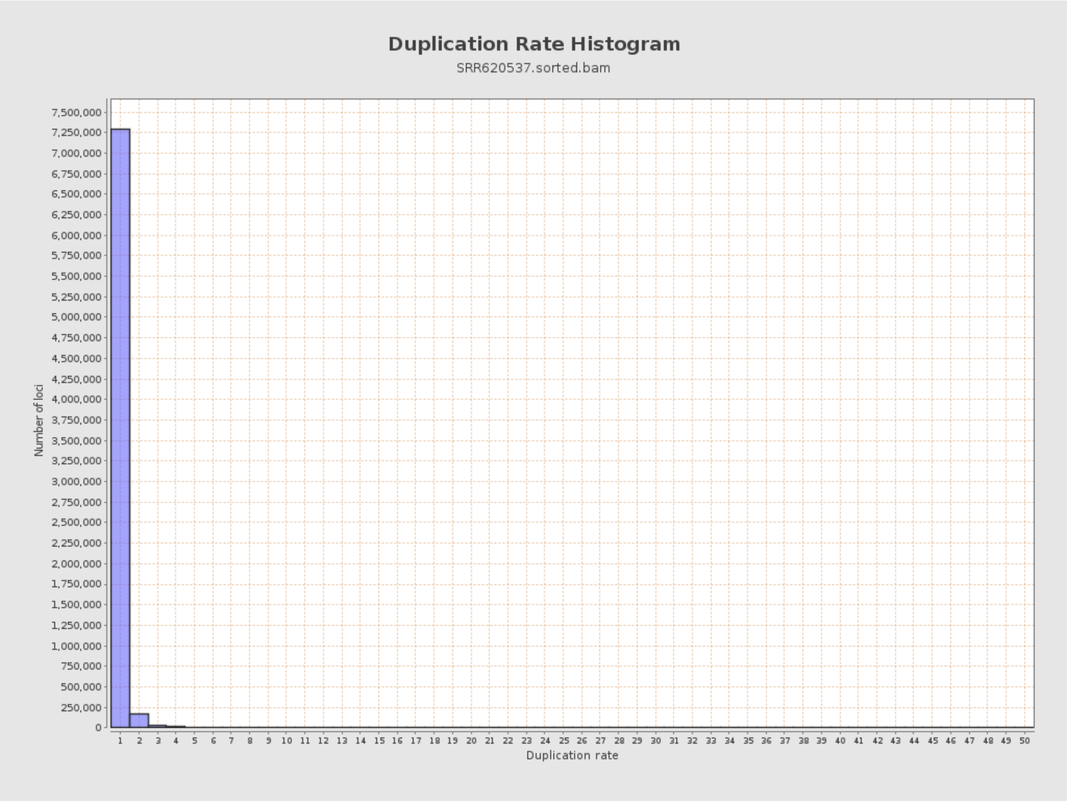
5. Results : Coverage Histogram (0-50X)



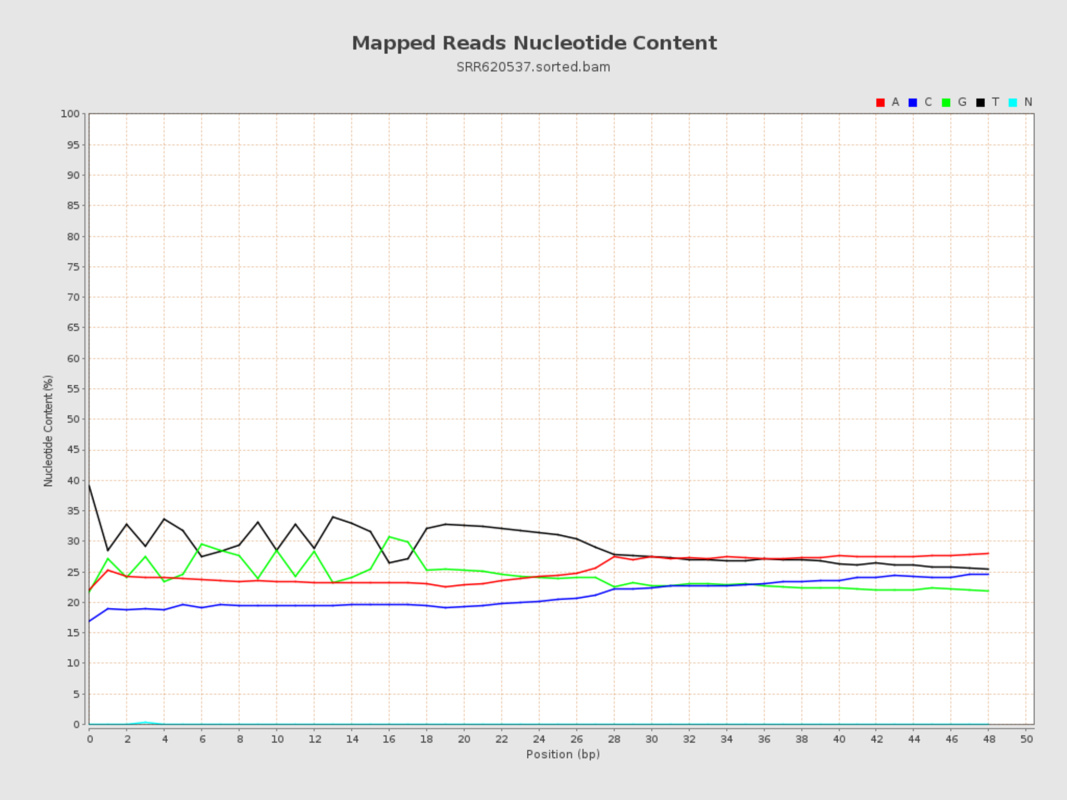
6. Results : Genome Fraction Coverage



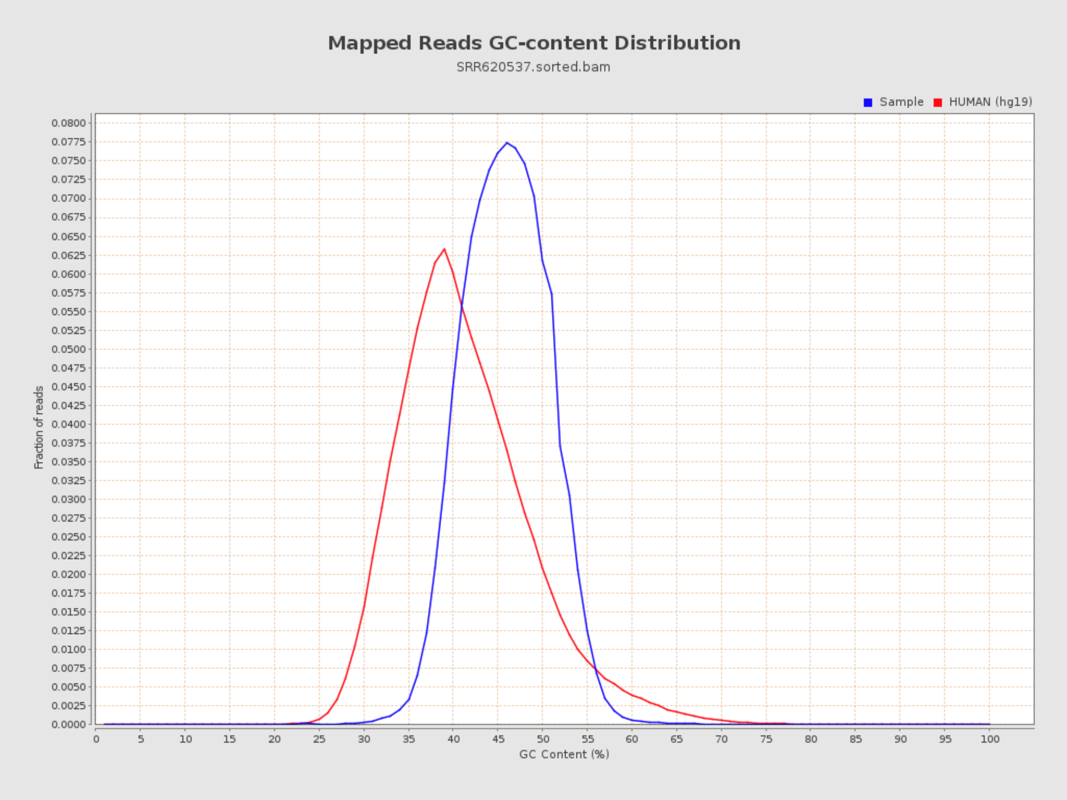
7. Results : Duplication Rate Histogram



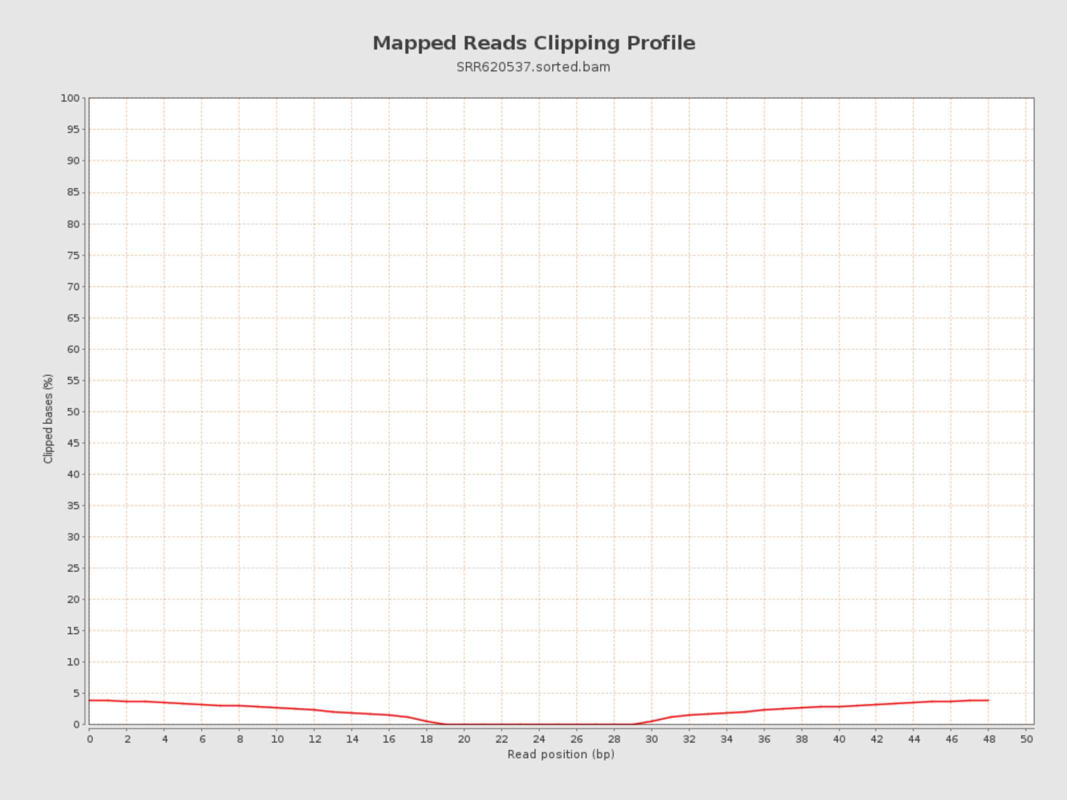
8. Results : Mapped Reads Nucleotide Content



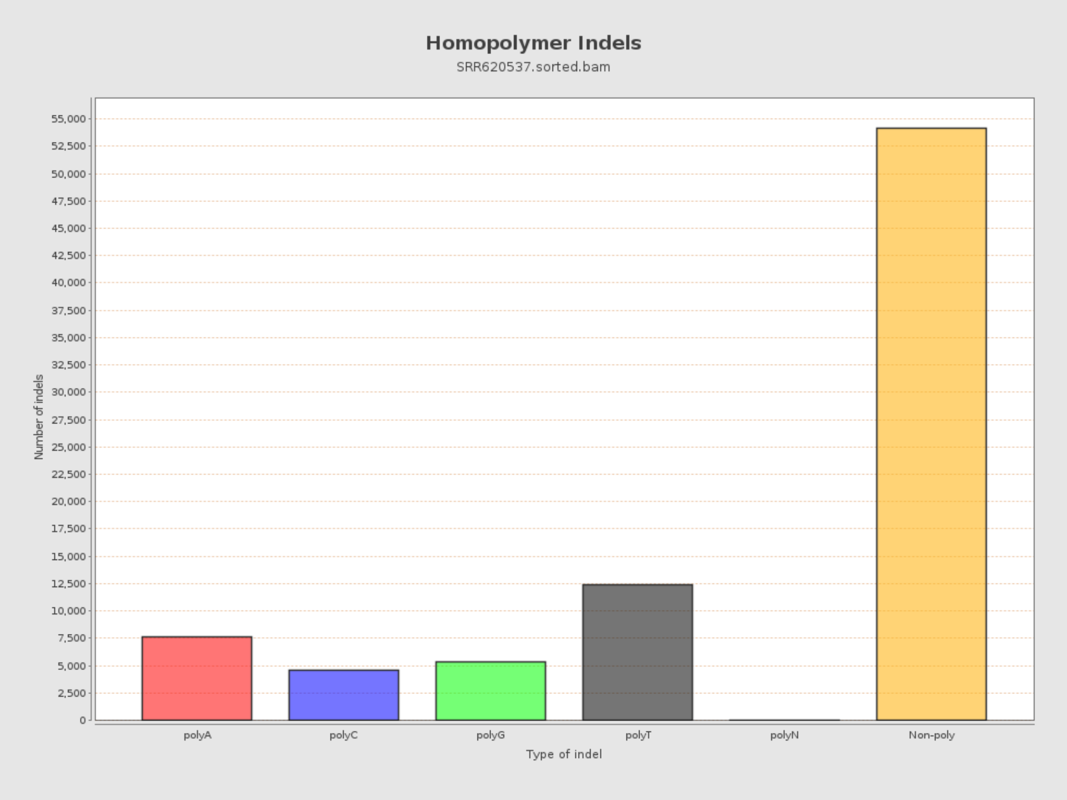
9. Results : Mapped Reads GC-content Distribution



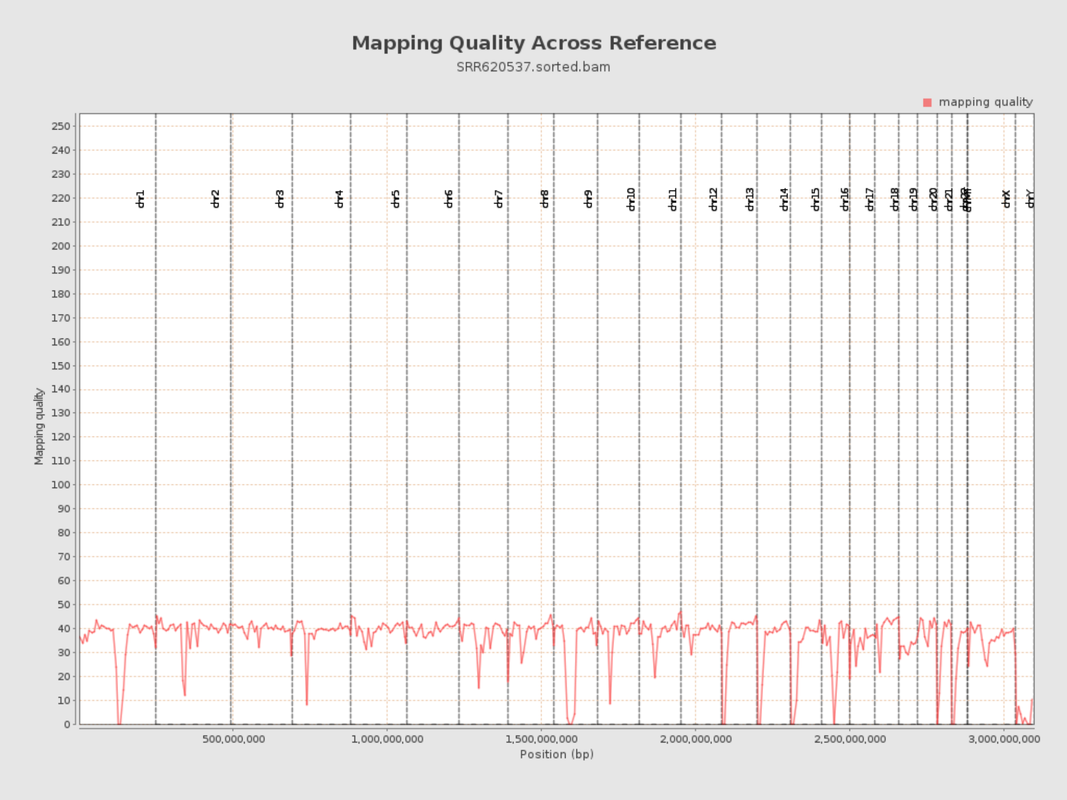
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram