Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/01/21 18:16:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR620535.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 SRR620535.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 21 18:16:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR620535.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,649,196
Mapped reads	5,920,024 / 61.35%
Unmapped reads	3,729,172 / 38.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	736 / 0.01%
Read min/max/mean length	30 / 49 / 49
Duplicated reads (estimated)	367,597 / 3.81%
Duplication rate	3.74%
Clipped reads	1,534,162 / 15.9%

2.2. ACGT Content

Number/percentage of A's	72,568,613 / 26.96%
Number/percentage of C's	52,050,465 / 19.34%
Number/percentage of T's	82,795,076 / 30.76%
Number/percentage of G's	60,883,284 / 22.62%
Number/percentage of N's	871,744 / 0.32%
GC Percentage	41.96%

2.3. Coverage

Mean	0.087

Standard Deviation	0.8672

2.4. Mapping Quality

Mean Mapping Quality	42.46

2.5. Mismatches and indels

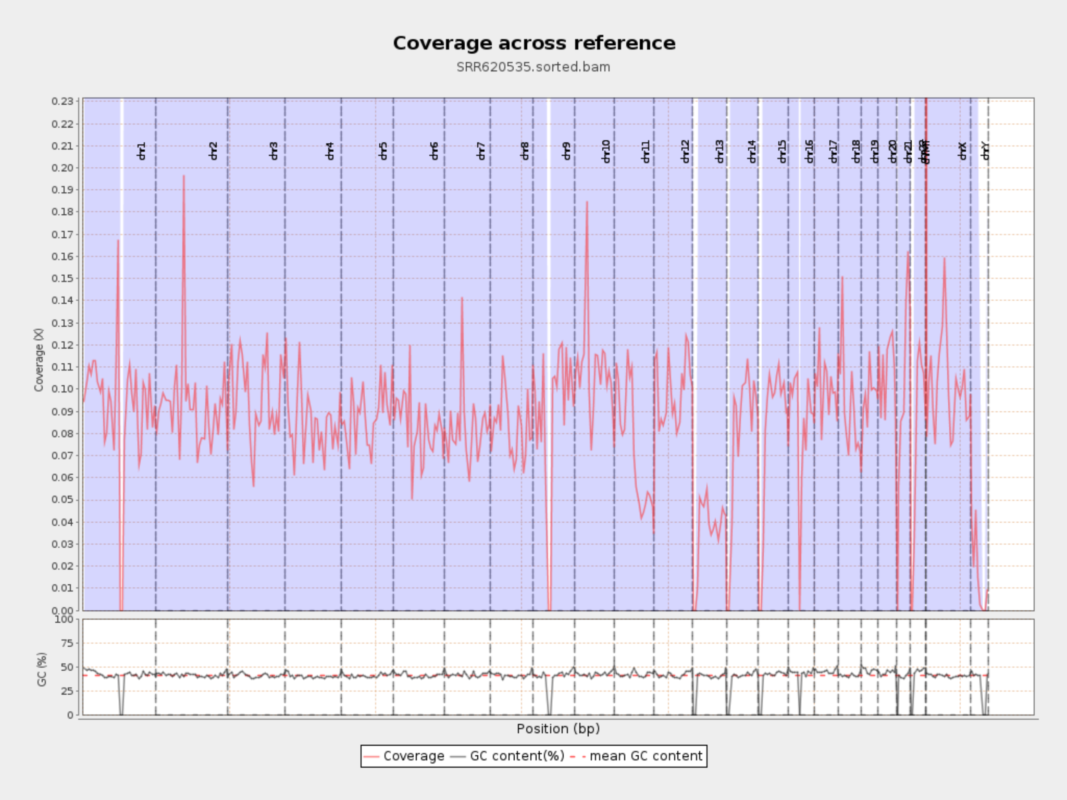
General error rate	1.19%
Mismatches	3,167,209
Insertions	16,557
Mapped reads with at least one insertion	0.28%
Deletions	42,452
Mapped reads with at least one deletion	0.71%
Homopolymer indels	46.48%

2.6. Chromosome stats

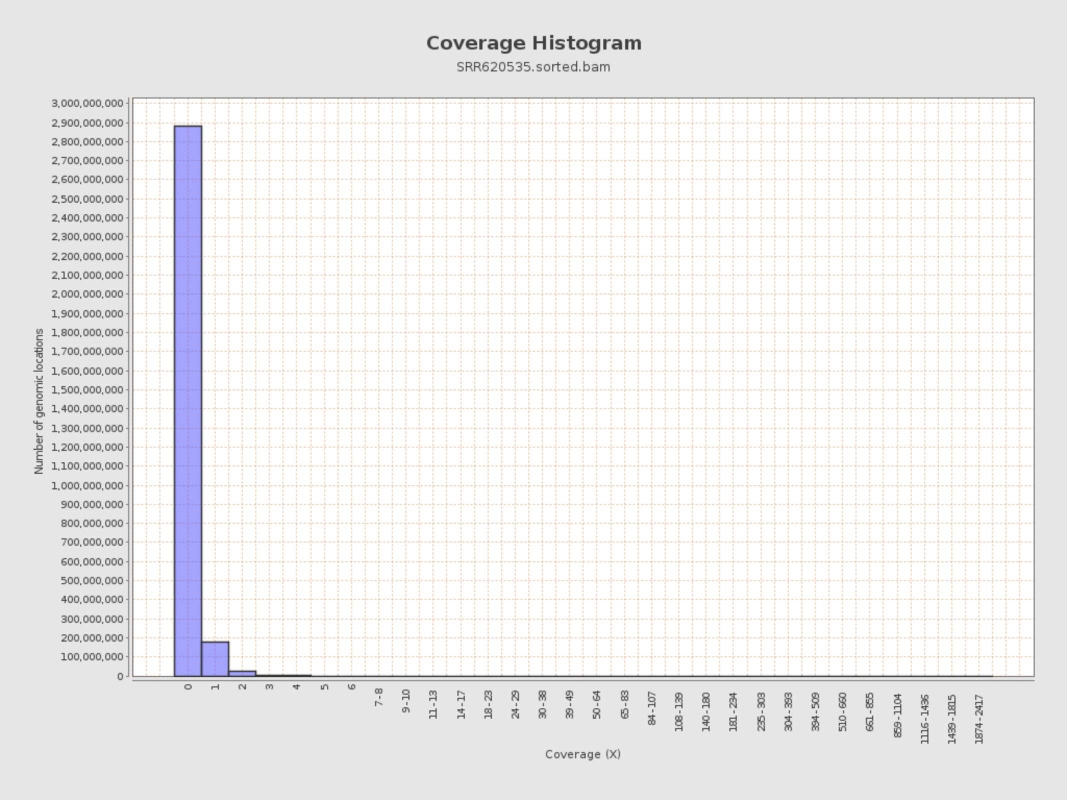
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22920921	0.092	1.4804
chr2	243199373	22693786	0.0933	0.9119
chr3	198022430	19083810	0.0964	0.445
chr4	191154276	16285179	0.0852	0.4501
chr5	180915260	15969664	0.0883	0.3959
chr6	171115067	14177856	0.0829	0.7499
chr7	159138663	13149379	0.0826	0.8942

chr8	146364022	12083967	0.0826	1.0032
chr9	141213431	12395054	0.0878	0.7937
chr10	135534747	14835957	0.1095	0.812
chr11	135006516	9945694	0.0737	0.9201
chr12	133851895	13380822	0.1	0.4472
chr13	115169878	4132381	0.0359	0.2706
chr14	107349540	8491136	0.0791	0.4007
chr15	102531392	8122103	0.0792	0.3667
chr16	90354753	7477687	0.0828	0.4278
chr17	81195210	8250332	0.1016	0.592
chr18	78077248	7302943	0.0935	2.5626
chr19	59128983	5709184	0.0966	0.9694
chr20	63025520	6875039	0.1091	0.5323
chr21	48129895	4798277	0.0997	0.4837
chr22	51304566	3920139	0.0764	0.3486
chrMT	16571	496354	29.9532	24.5504
chrX	155270560	15814764	0.1019	0.6505
chrY	59373566	922128	0.0155	0.2549

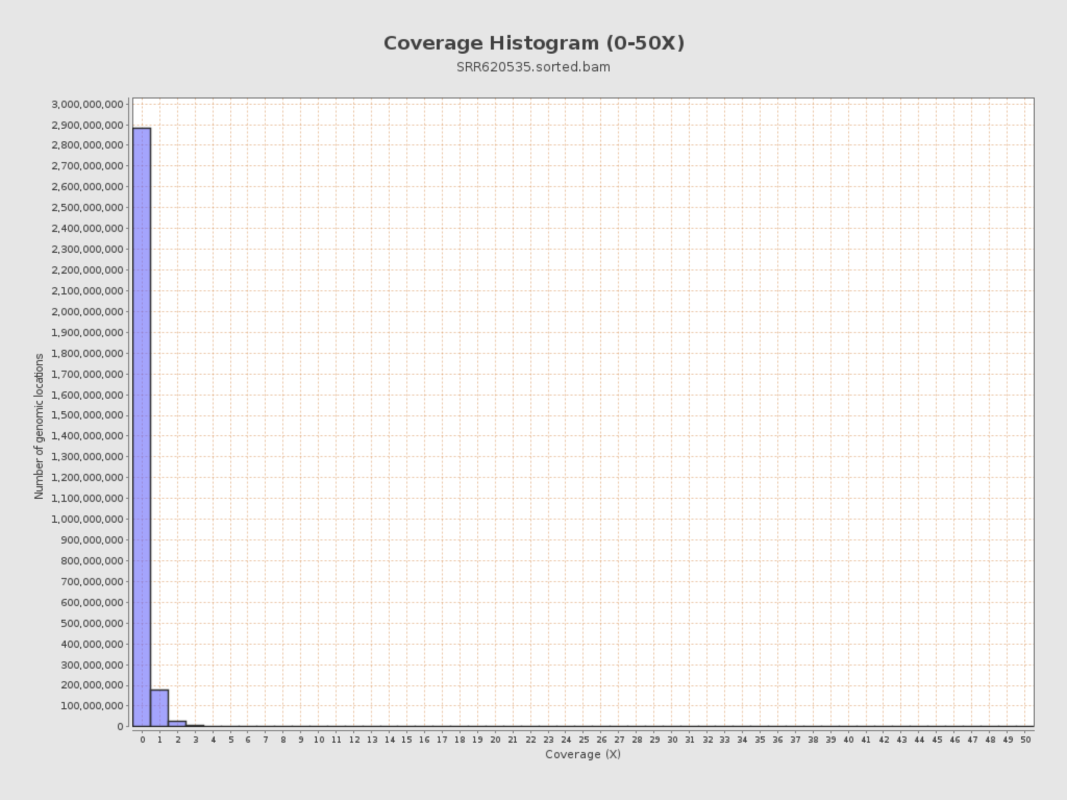
3. Results : Coverage across reference



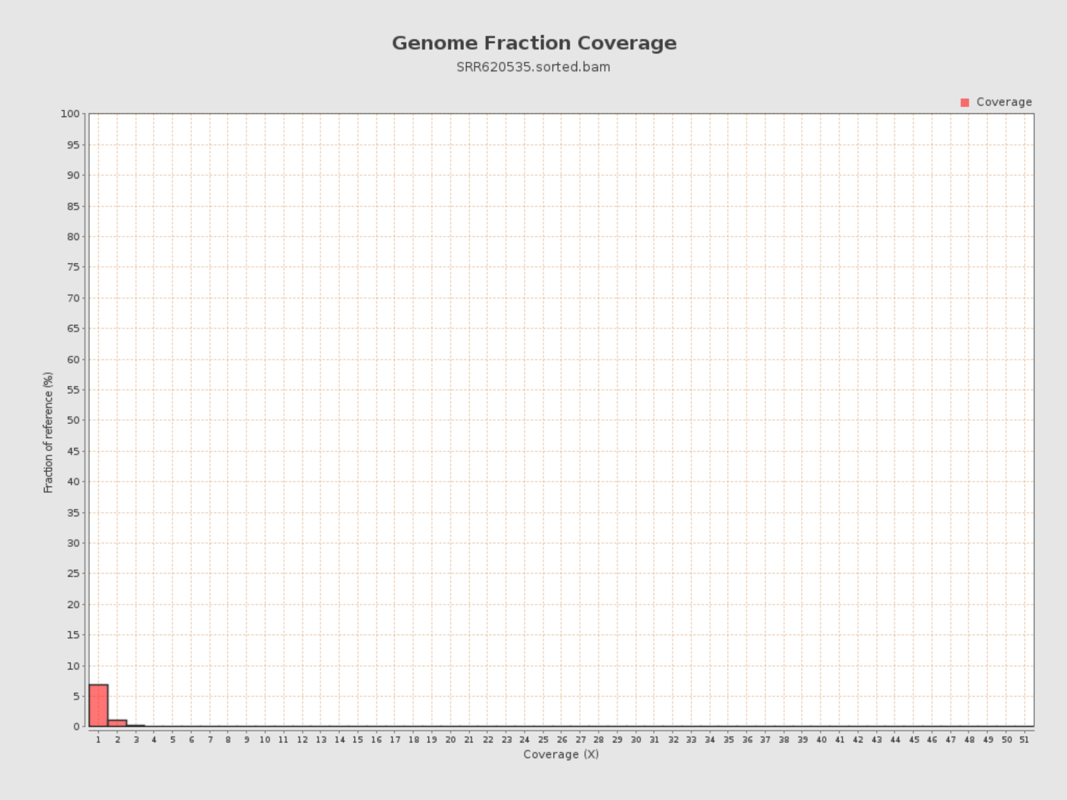
4. Results : Coverage Histogram



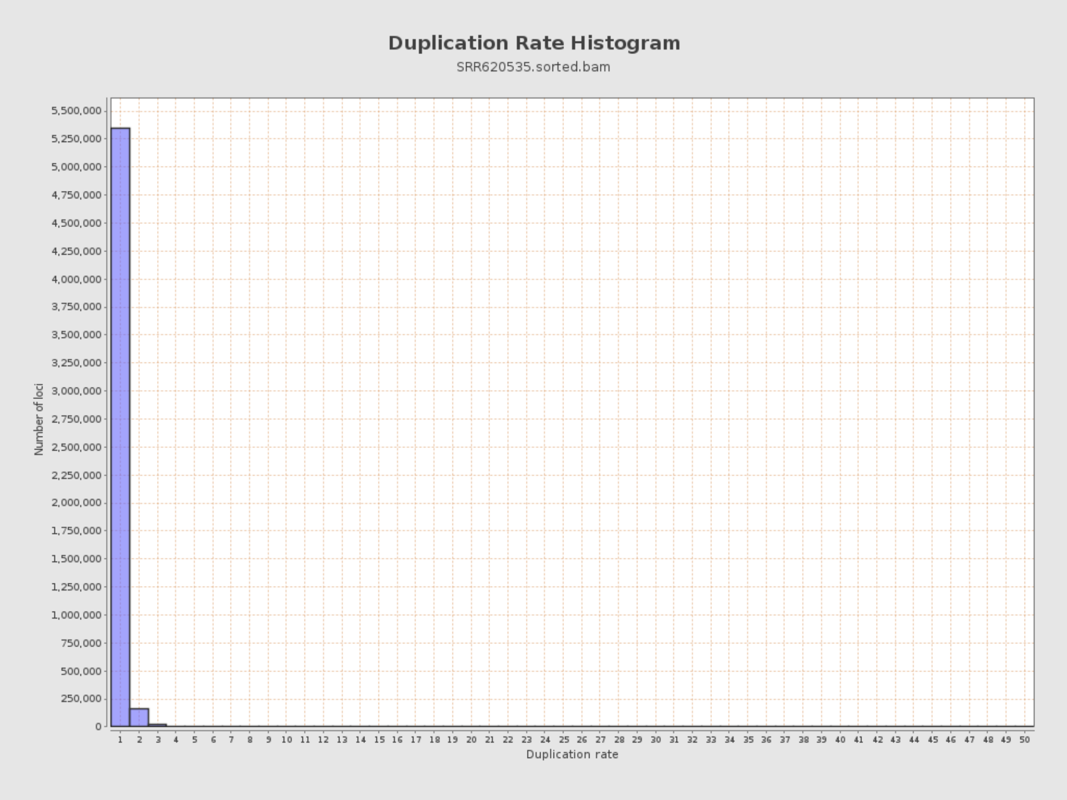
5. Results : Coverage Histogram (0-50X)



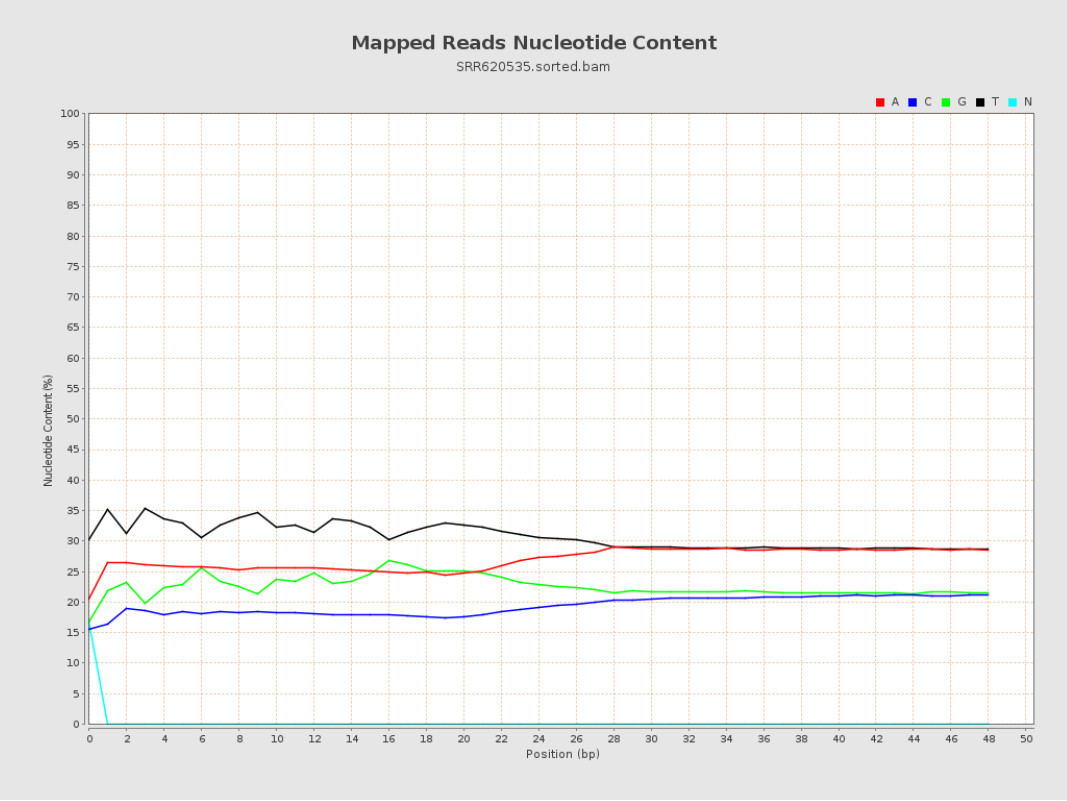
6. Results : Genome Fraction Coverage



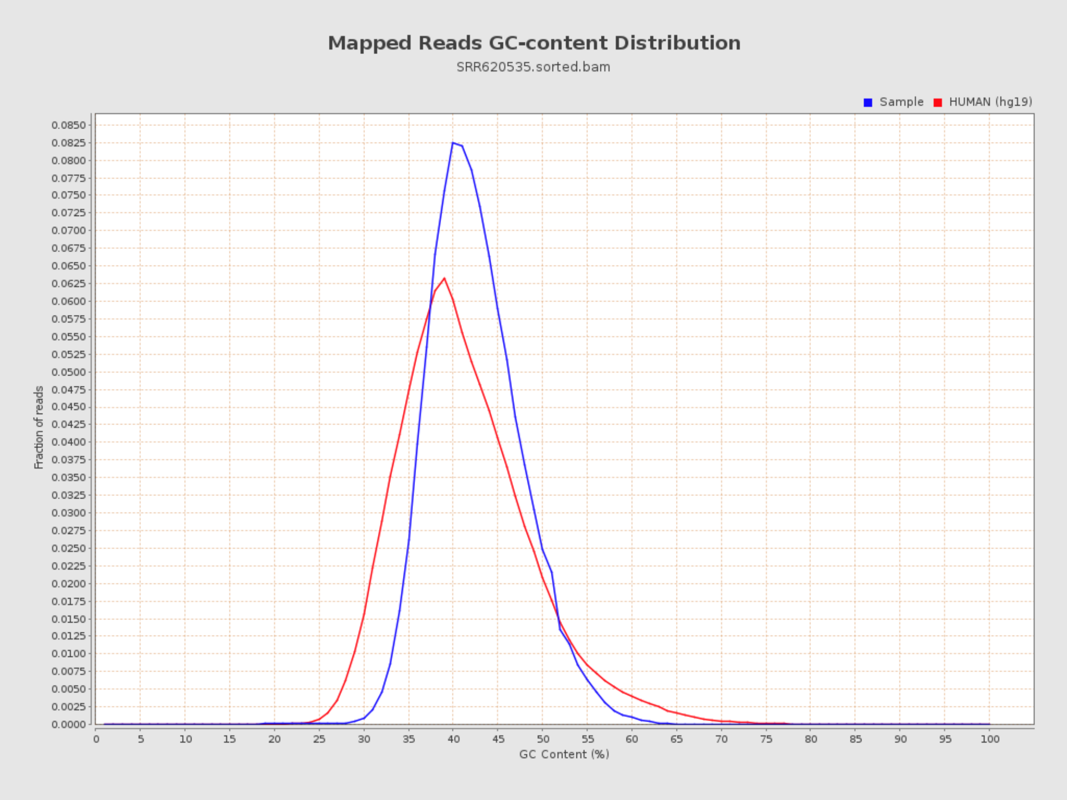
7. Results : Duplication Rate Histogram



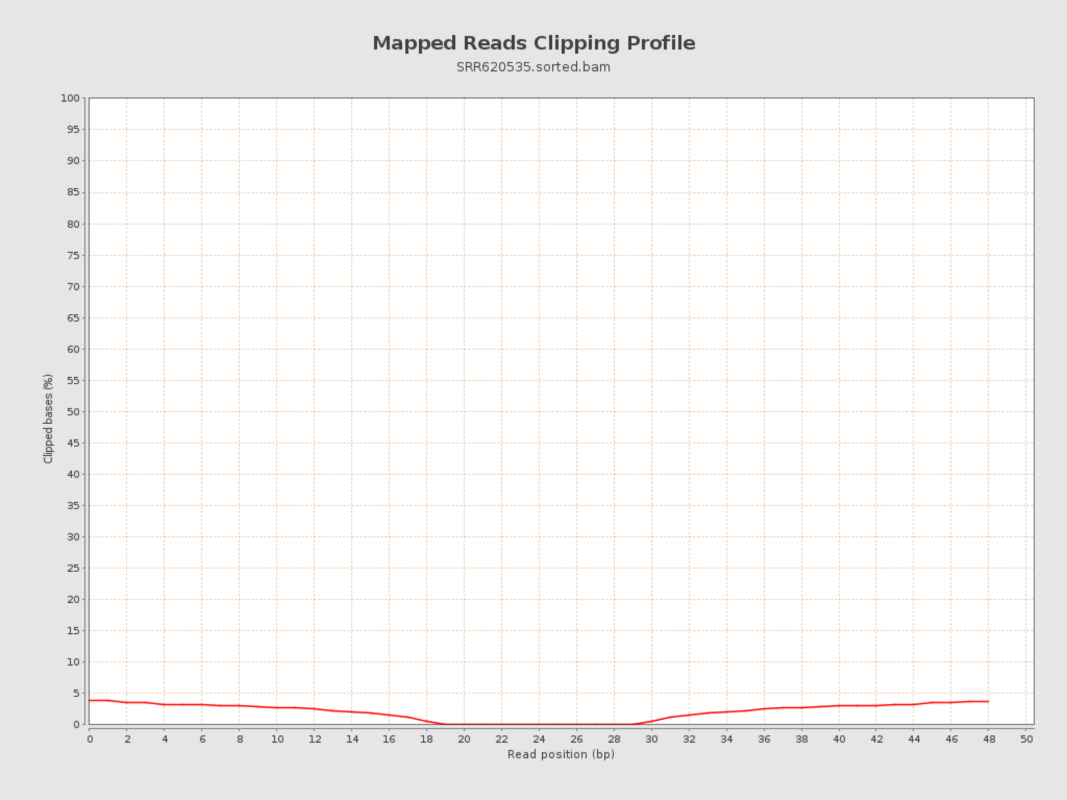
8. Results : Mapped Reads Nucleotide Content



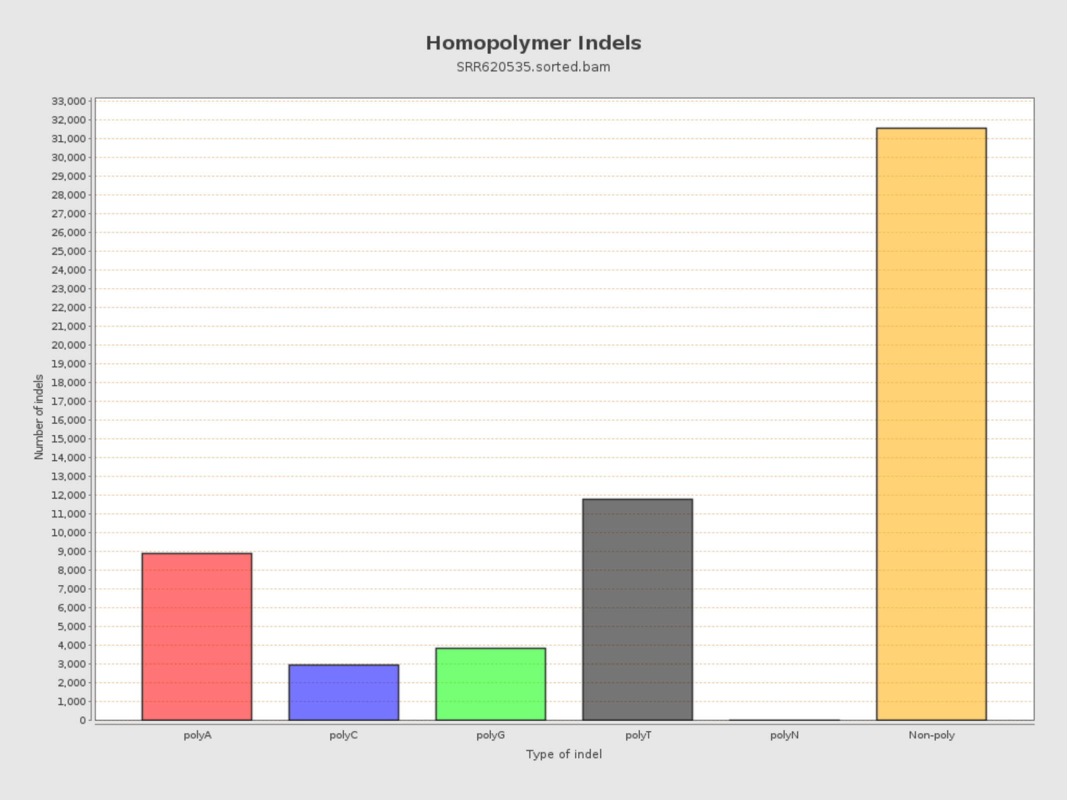
9. Results : Mapped Reads GC-content Distribution



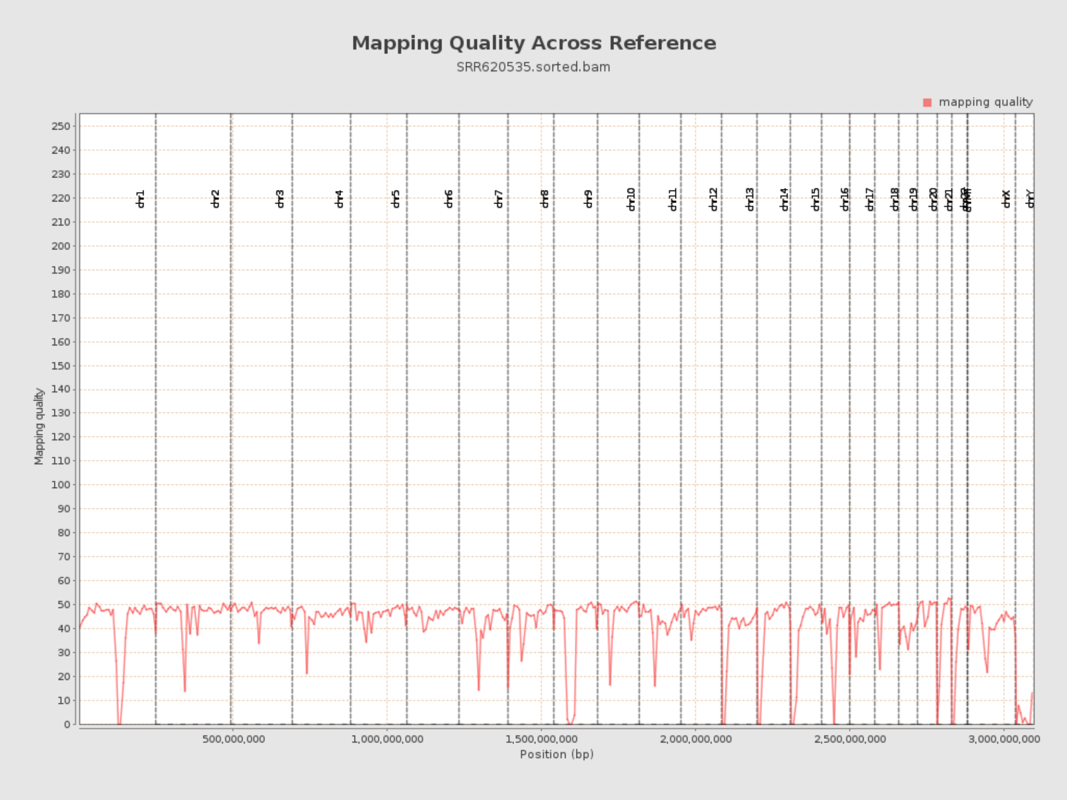
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram