Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/01/21 17:59:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR620533.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 SRR620533.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 21 17:59:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR620533.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,641,324
Mapped reads	7,440,598 / 50.82%
Unmapped reads	7,200,726 / 49.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	240 / 0%
Read min/max/mean length	30 / 49 / 49
Duplicated reads (estimated)	1,203,458 / 8.22%
Duplication rate	8.91%
Clipped reads	3,520,380 / 24.04%

2.2. ACGT Content

Number/percentage of A's	80,399,460 / 25.53%
Number/percentage of C's	53,363,349 / 16.94%
Number/percentage of T's	101,597,642 / 32.26%
Number/percentage of G's	79,415,412 / 25.22%
Number/percentage of N's	165,079 / 0.05%
GC Percentage	42.16%

2.3. Coverage

Mean	0.1018

Standard Deviation	1.393

2.4. Mapping Quality

Mean Mapping Quality	42.84

2.5. Mismatches and indels

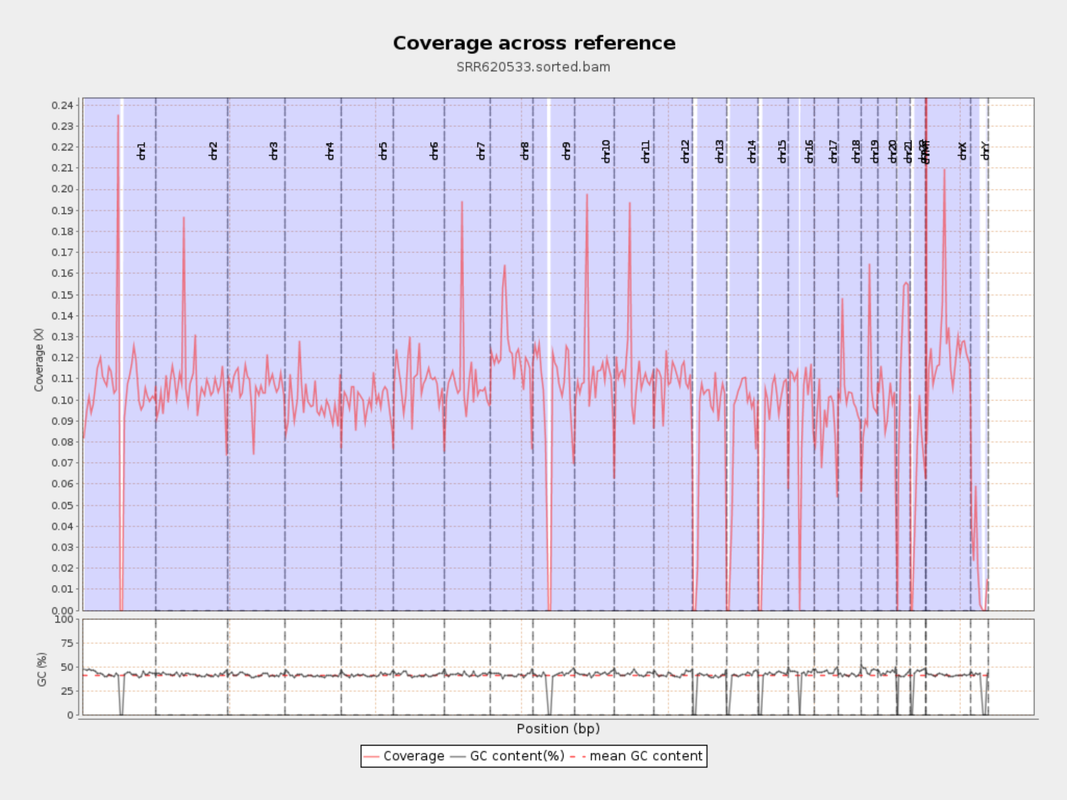
General error rate	0.68%
Mismatches	2,110,507
Insertions	21,207
Mapped reads with at least one insertion	0.28%
Deletions	52,838
Mapped reads with at least one deletion	0.7%
Homopolymer indels	41.82%

2.6. Chromosome stats

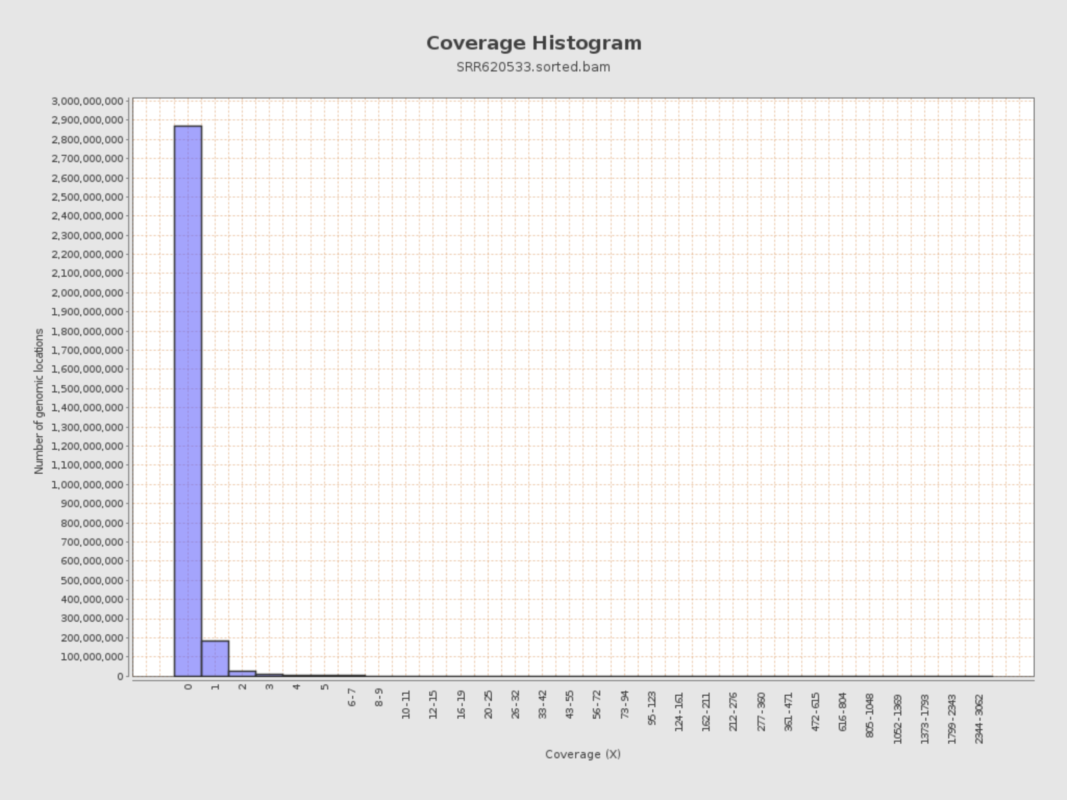
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25608065	0.1027	2.5583
chr2	243199373	26166488	0.1076	0.8778
chr3	198022430	21049276	0.1063	0.6203
chr4	191154276	18884279	0.0988	0.821
chr5	180915260	17883566	0.0989	0.5624
chr6	171115067	18705316	0.1093	0.6594
chr7	159138663	17284044	0.1086	1.5382

chr8	146364022	17710023	0.121	1.4997
chr9	141213431	13820288	0.0979	0.9079
chr10	135534747	15410625	0.1137	1.075
chr11	135006516	15333258	0.1136	3.6453
chr12	133851895	14679234	0.1097	0.6547
chr13	115169878	9772516	0.0849	0.5173
chr14	107349540	8994987	0.0838	0.5406
chr15	102531392	8575517	0.0836	0.4871
chr16	90354753	8464122	0.0937	0.572
chr17	81195210	7313759	0.0901	0.6888
chr18	78077248	8140572	0.1043	2.2217
chr19	59128983	5955839	0.1007	1.6495
chr20	63025520	6232624	0.0989	0.6796
chr21	48129895	5546770	0.1152	0.6555
chr22	51304566	2989187	0.0583	0.3788
chrMT	16571	123490	7.4522	12.0646
chrX	155270560	19238528	0.1239	1.2692
chrY	59373566	1134239	0.0191	0.3886

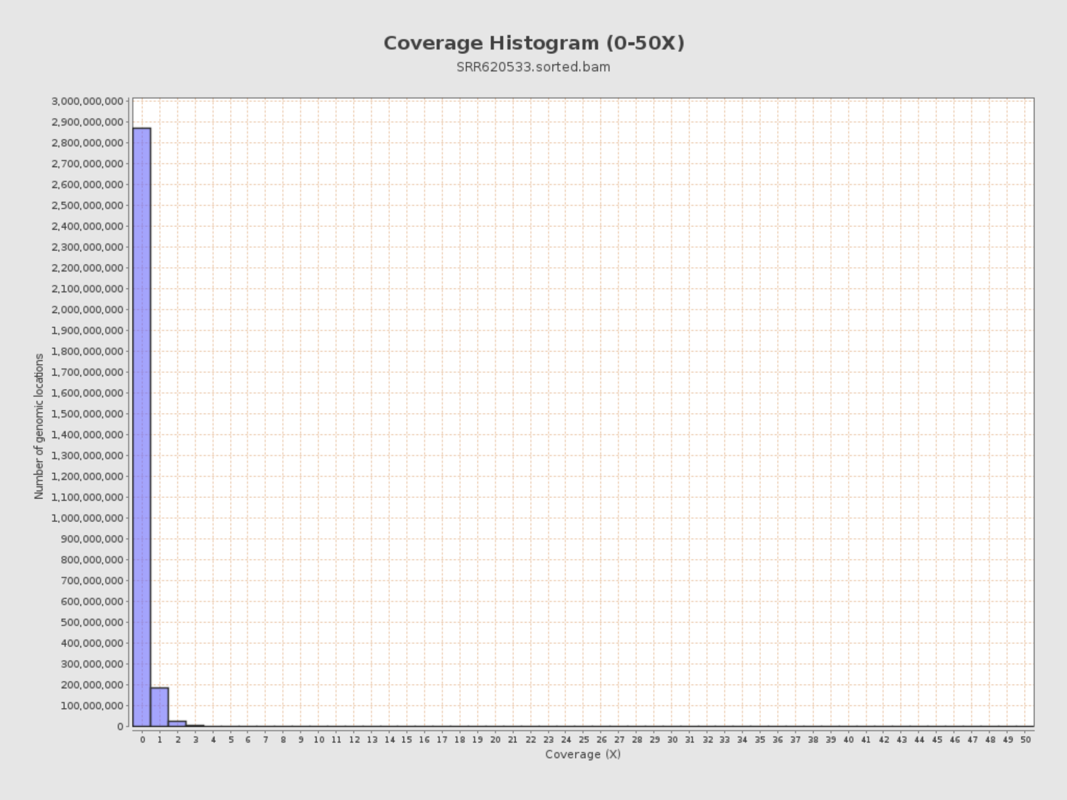
3. Results : Coverage across reference



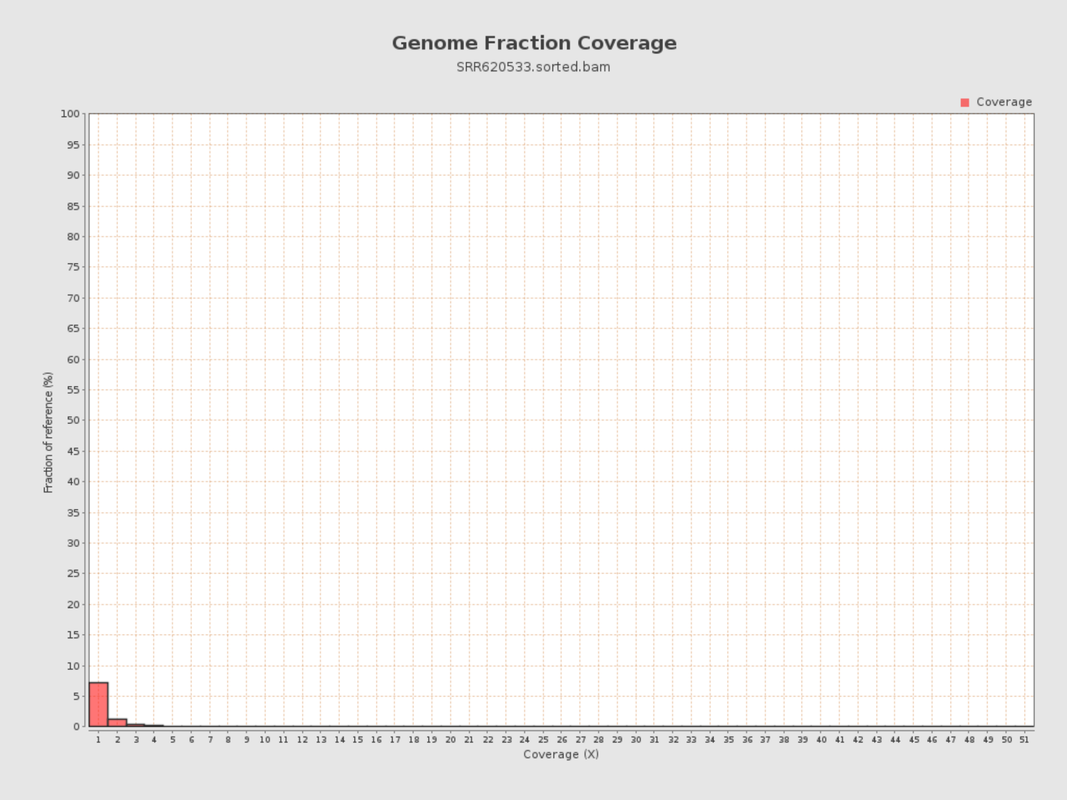
4. Results : Coverage Histogram



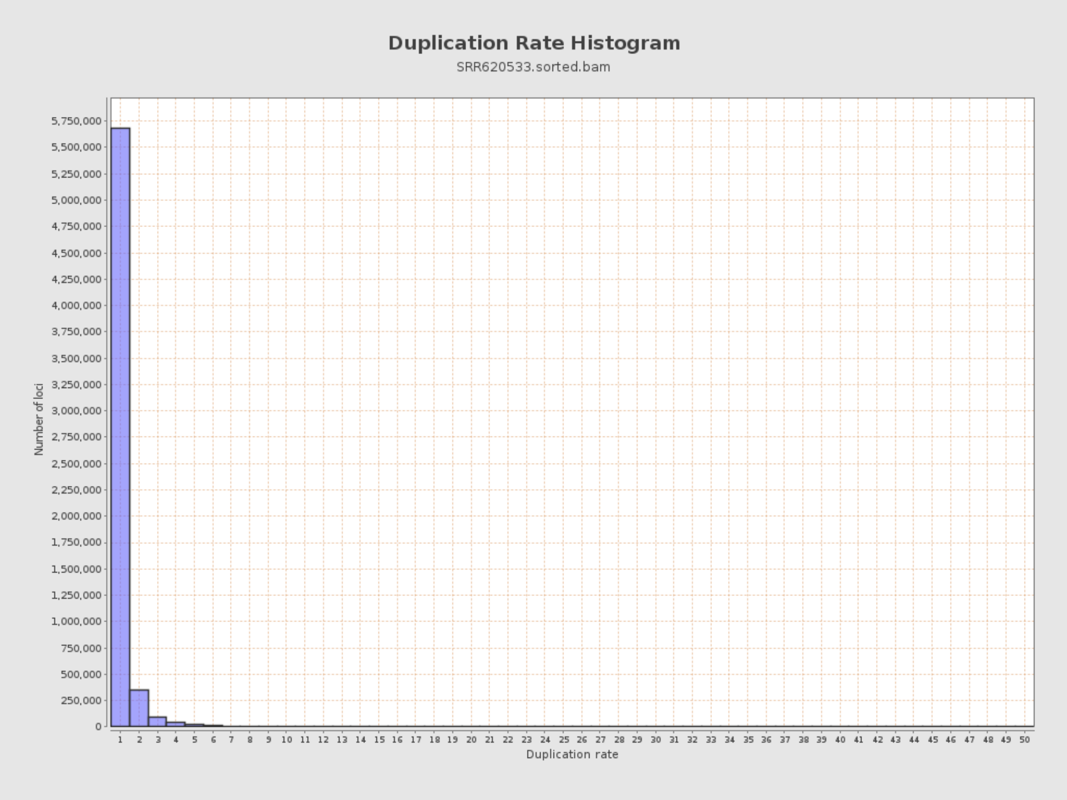
5. Results : Coverage Histogram (0-50X)



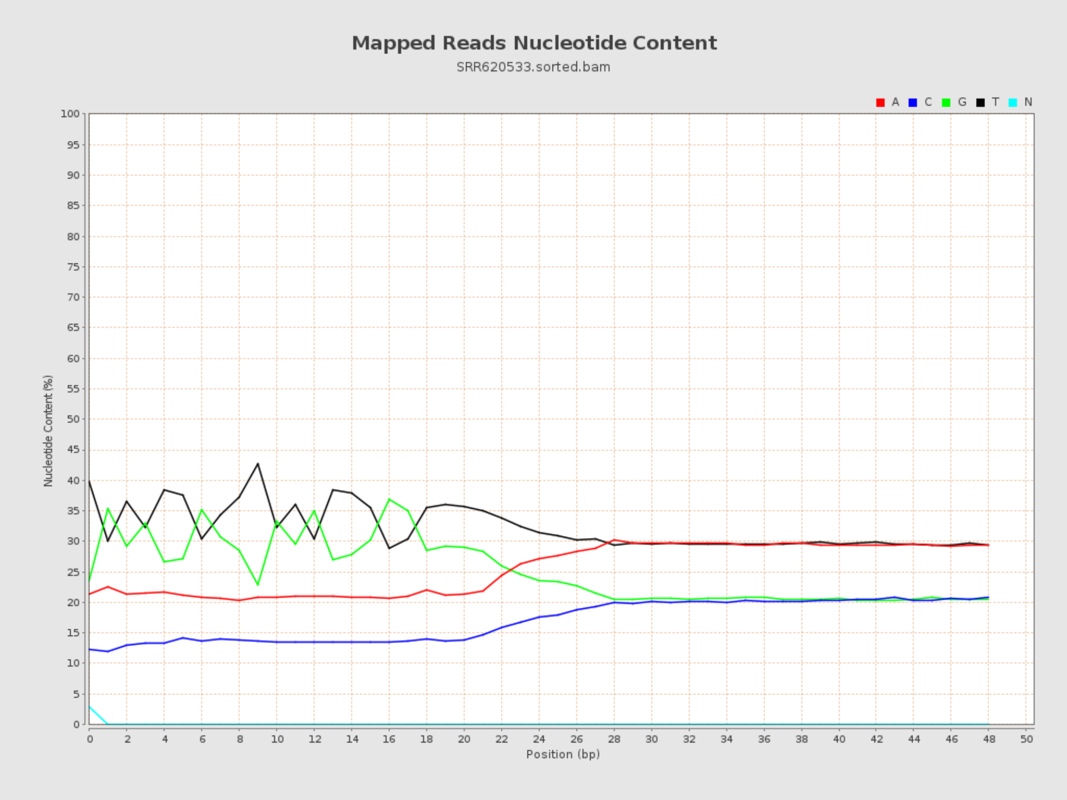
6. Results : Genome Fraction Coverage



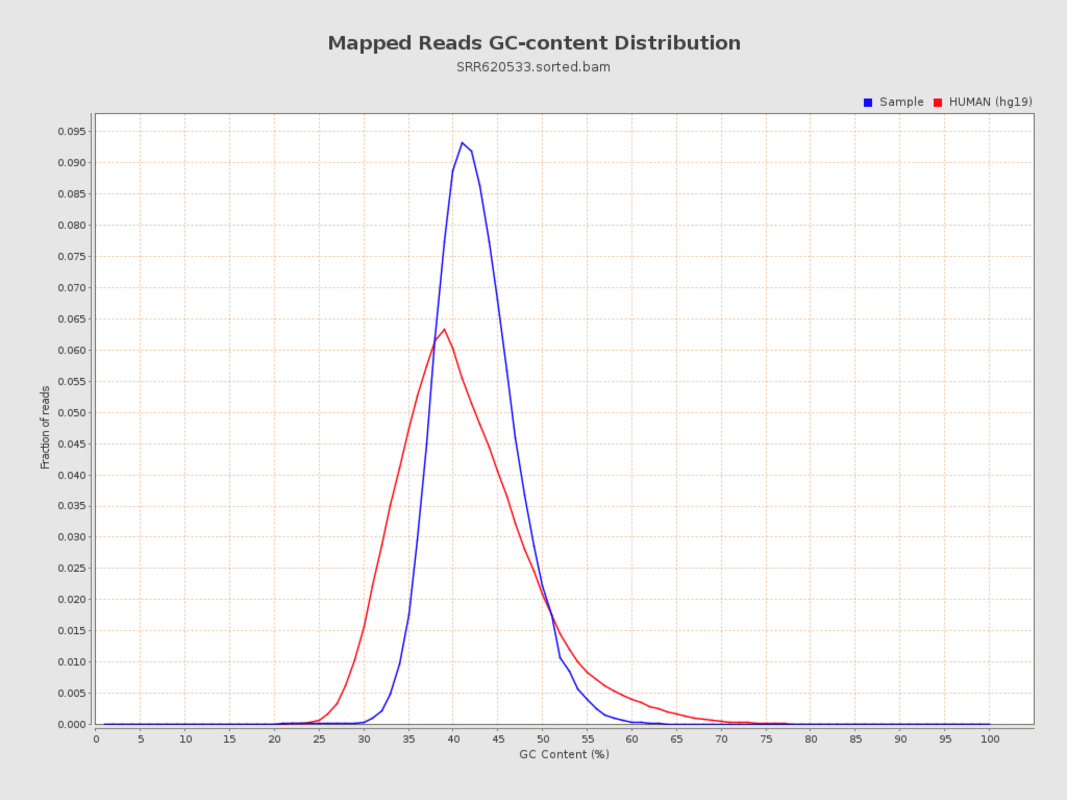
7. Results : Duplication Rate Histogram



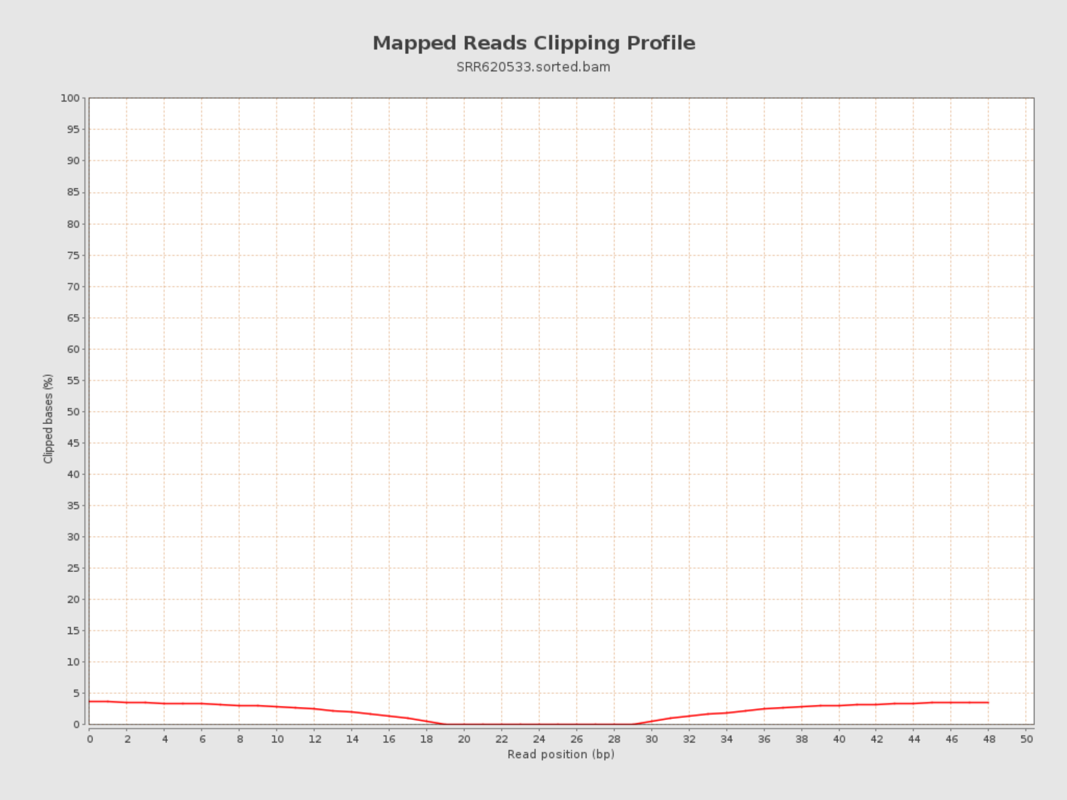
8. Results : Mapped Reads Nucleotide Content



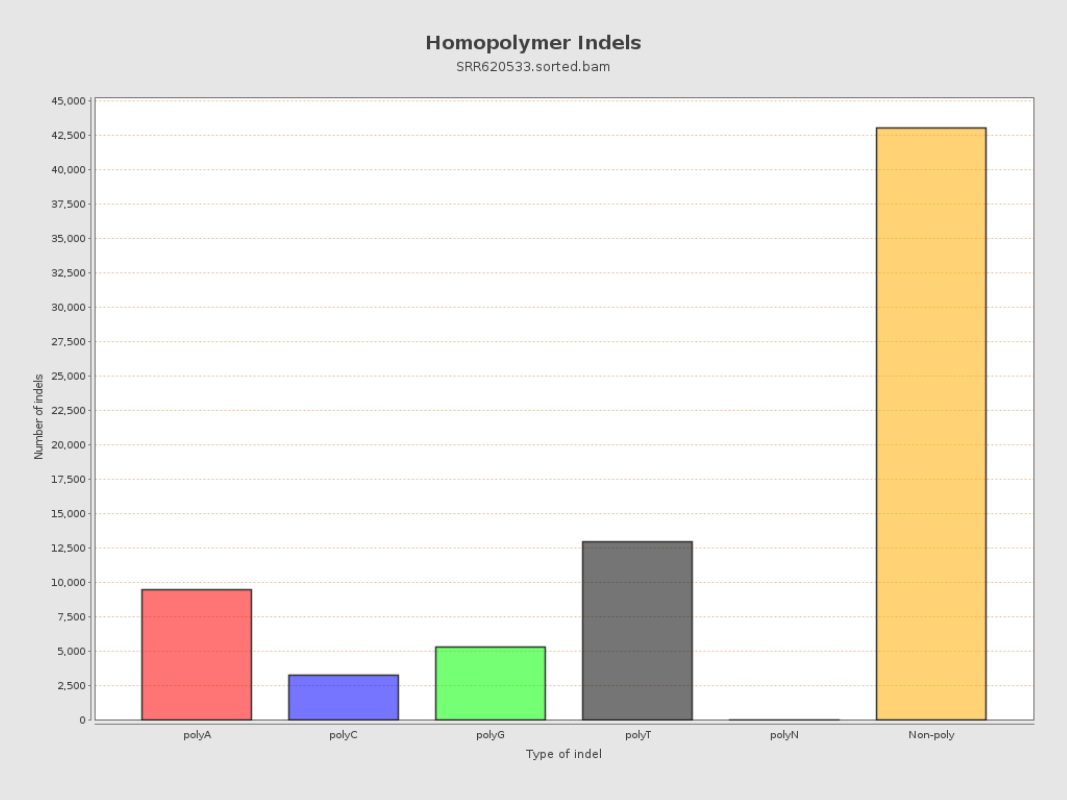
9. Results : Mapped Reads GC-content Distribution



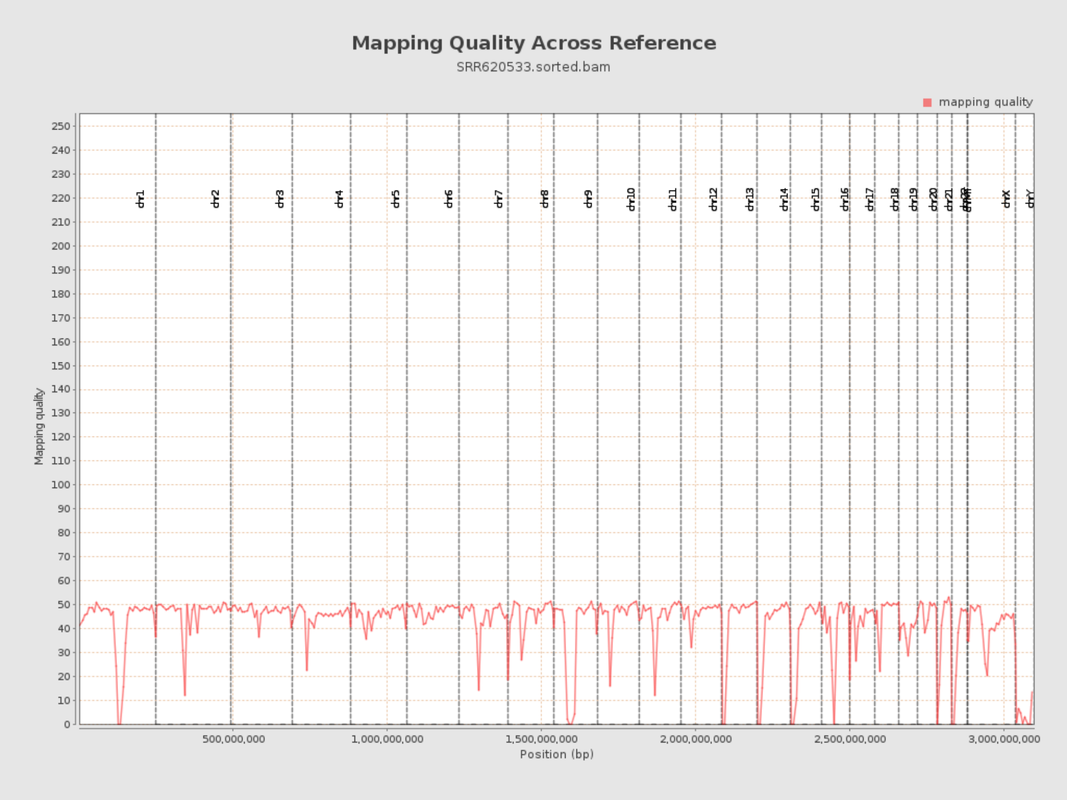
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram