

# Modified *Graphtyper* for variant discovery and genotyping in cattle

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The most convenient way to run a *Graphtyper* version compiled for the bovine chromosome complement is to use Docker (which deals with all required dependencies). The command below starts to download modified *Graphtyper* software hosted at the Dockerhub:

```
docker run --rm cdanang/graphtyper_cattle graphtyper
```

We built the docker images using *Ubuntu* 18.04 as a base image. If you are working on a Linux 64-bit machine you could also get a static executable with command below. We placed the *Graphtyper* binary in `/usr/local/bin` and executing command below will copy the *Graphtyper* binary from docker images to the current working directory:

```
docker run --rm -v ${PWD}:/io cdanang/graphtyper_cattle \  
cp /usr/local/bin/graphtyper /io  
  
### And then run the software as a standard binary  
./graphtyper
```

If you prefer to modify and build a modified version of *Graphtyper* for the bovine chromosome complement directly from the source, please follow the instructions below:

1. Clone the *Graphtyper Github* at this [link](#)

```
git clone --recursive https://github.com/DecodeGenetics/graphtyper.git
```

2. Create a new `branch` at this specific commit tag. We built *graphtyper* at this specific commit hash (04ab5ee460fa36129fb0d8ea5d4b72adc3836f52), to compile at the same software version that we use in the paper, please use this commit tag. We named the `branch` as *cattle modification*

```
git checkout -b cattle_modification \  
04ab5ee460fa36129fb0d8ea5d4b72adc3836f52
```

3. Change directory into *graphtyper/* and modify the chromosomal specifications in the files *include/graphtyper/graph/absolute\_position.hpp* & *src/typer/vcf.cpp* using UMD 3.1 cattle chromosomal names and lengths. The first modification enables all cattle chromosomes (esp. for chromosome number > 23) as the current software release set the maximum allowed length for each chromosomes according to the human *GRCh37* and *GRCh38*. The second modifications are required that the respective chromosomal information is written to the *vcf header*.
  
4. Make sure that these dependencies are installed:
  - C++ compiler with C++11 supported (we tested gcc 4.8.5 or gcc 6.3.0 to build the software)
  - Boost>=1.57.0
  - zlib>=1.2.8
  - libbz2
  - liblzma
  - Autotools, Automake, libtool, Make, and CMake>=2.8.8
  
5. Follow installation procedures as below. This will put the software in *release-build/bin/graphtyper*

```
mkdir -p release-build && cd release-build
cmake ..
make -j4 graphtyper
bin/graphtyper # Run Graphtyper with modified cattle chromosome
specifications
```