

# 变异位点可视化

容器启动命令：

```
sudo docker run -it --name jbrowse2 -v /mnt/vol2_ws/test/wbzhao/wbzhao:/wbzhao -v /mnt/vol2_ws/test/wbzhao/wbzhao/html:/usr/share/nginx/html -p 8888:80 -d jbrowse2
```

！！根据实际需求修改挂载目录及端口

## 一、路径

10.0.1.1:/mnt/vol1/rendong/test/zhaowb\_test/html/

10.0.1.1:/mnt/vol1/rendong/test/zhaowb\_test/scripts/

## 二、镜像

镜像: jbrowse2:latest

## 三、文件

/mnt/vol1/rendong/test/zhaowb\_test/html/ 下全部文件

/mnt/vol1/rendong/test/zhaowb\_test/scripts 下 mutation\_sites\_vis.sh

## 四、命令及运行参数

tumor and normal

```
#generate somatic sites
docker exec -d jbrowse2 bash \
/mnt/vol1/rendong/test/zhaowb_test/scripts/mutation_sites_vis.sh \
-t 2000321 \
-n 2000322 \
-b /mnt/vol1/rendong/test/zhaowb_test/2000321/2.mapping/2000321.recal-H.bam \
-B /mnt/vol1/rendong/test/zhaowb_test/2000321/2.mapping/2000322.recal-H.bam \
-r /mnt/vol1/rendong/project_info/ref_file/hg19/hg19.fasta \
-s /mnt/vol1/rendong/test/zhaowb_test/2000321/3.somatic_VC/620.xls\
-o /mnt/vol1/rendong/test/zhaowb_test/2000321/url

#generate germline sites
docker exec -d jbrowse2 bash \
/mnt/vol1/rendong/test/zhaowb_test/scripts/mutation_sites_vis.sh \
-t 2000321 \
-n 2000322 \
-b /mnt/vol1/rendong/test/zhaowb_test/2000321/2.mapping/2000321.recal-H.bam \
-B /mnt/vol1/rendong/test/zhaowb_test/2000321/2.mapping/2000322.recal-H.bam \
-r /mnt/vol1/rendong/project_info/ref_file/hg19/hg19.fasta \
-s /mnt/vol1/rendong/test/zhaowb_test/2000321/3.germline_VC/genetic.xls \
-o /mnt/vol1/rendong/test/zhaowb_test/2000321/url
```

only tumor

```
#generate somatic sites
docker exec -d jbrowse2 bash \
/mnt/vol1/rendong/test/zhaowb_test/scripts/mutation_sites_vis.sh \
-t 2000321 \
-b /mnt/vol1/rendong/test/zhaowb_test/2000321/2.mapping/2000321.recal-H.bam \
-r /mnt/vol1/rendong/project_info/ref_file/hg19/hg19.fasta \
-s /mnt/vol1/rendong/test/zhaowb_test/2000321/3.somatic_VC/620.xls\
-o /mnt/vol1/rendong/test/zhaowb_test/2000321/url
```

only normal

```
#generate germline sites
docker exec -d jbrowse2 bash \
/mnt/vol1/rendong/test/zhaowb_test/scripts/mutation_sites_vis.sh \
-n 2000322 \
-B /mnt/vol1/rendong/test/zhaowb_test/2000321/2.mapping/2000322.recal-H.bam \
-r /mnt/vol1/rendong/project_info/ref_file/hg19/hg19.fasta \
-s /mnt/vol1/rendong/test/zhaowb_test/2000321/3.germline_VC/genetic.xls \
-o /mnt/vol1/rendong/test/zhaowb_test/2000321/url
```

参数	释义
-t	癌症样本编号，示例如上
-n	胚系样本编号，示例如上
-b	癌症样本bam文件，示例如上
-B	胚系样本bam文件，示例如上
-r	参考基因组
-s	变异位点列表，必须是常规的 620.xls/genetic.xls 的格式
-o	任务的结果输出目录 ,如 url/

五、结果说明

结果最终输出**1个文件夹**，包含**4/2个xls文件**，以及在  
10.0.1.1:/mnt/vol1/rendong/test/zhaowb\_test/html/ 中保存的项目ID对应变异位点的html存放目录：

文件	内容
somatic_url.xls	体系变异位点对应的url
germline_url.xls	胚系变异位点对应的url
620.xls	最后一列追加了url的620.xls
genetic.xls	最后一列追加了url的genetic.xls

