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Subject: Re: 2017 Ghana Maternal Health Survey  
Posted by [lmallick](#) on Mon, 19 Aug 2019 19:50:43 GMT

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Then I would try to collapse the BQ file to what would be the caseid in an IR file: qhclust qhnumber qline using a count of each of the dummy pregnancy variables that you could create using the line above.

Does this help:

```
use GHBQ7IFL.DTA, clear
```

```
gen wt = qweight/1000000
```

```
ta pregout, gen(pregout_dummy)  
sort qhclust qhnumber qline  
collapse (count) live = pregout_dummy1 ///  
  still = pregout_dummy2 ///  
  miscar = pregout_dummy3 ///  
  abor = pregout_dummy4 ///  
  , by(qhclust qhnumber qline)
```

```
save GHpregout.dta, replace
```

```
use GHIQ7IFL.dta, clear
```

```
merge 1:1 qhclust qhnumber qline using GHpregout
```

Once merged, you could create a binary variable for ever had an abortion (Y/N) if abor is greater than or equal to 1. Then you could cross tab with q578\_1.