. use "C:\Users\ASUS\Desktop\Small-molecule TKI\Stata\OS\NMA-OS-ID changed-Component1.dta", clear

. network import, studyvar(id_name)treat(intervention2 intervention1)effect(logoshr)stderr(selogoshr)

Importing from pairs format

Reference treatment: 1

All treatments: 1 10 12 17 18 2 21 3 4 8 9

. network convert augmented

Converting pairs to augmented ...

. network meta c,fixed

Warning: can't check for disconnected network

Warning: can't check df for inconsistency

Warning: can't check df for heterogeneity

Command is: mvmeta logoshr_S , fixed longparm suppress(uv mm) vars(logoshr_10 logoshr_12 logoshr_17 logoshr_18 logoshr_21 logo

> shr_3 logoshr_4 logoshr_8 logoshr_9)

Note: using method fixed

Note: using variables logoshr_10 logoshr_12 logoshr_17 logoshr_18 logoshr_2 logoshr_21 logoshr_3 logoshr_4 logoshr_8 logoshr_9

Note: 11 observations on 10 variables

Multivariate meta-analysis

Variance-covariance matrix = (none)

Method = fixed Number of dimensions = 10

Number of observations = 11

```
Coef. Std. Err. z P>|z| [95% Conf. Interval]
------
logoshr_10 |
 logoshr_12 |
 .-----+-----+
logoshr_17 |
 logoshr_18 |
 _cons | .5103245 .2225387 2.29 0.022 .0741567 .9464923
-----+-----+
logoshr_2
 -----+----+
logoshr_21 |
 _cons | .2933531 .4057721 0.72 0.470 -.5019457 1.088652
-----+-----+
logoshr_3
 _cons | .2443648 .2204231 1.11 0.268 -.1876566 .6763862
logoshr_4
```