

## Legend Figure e-1

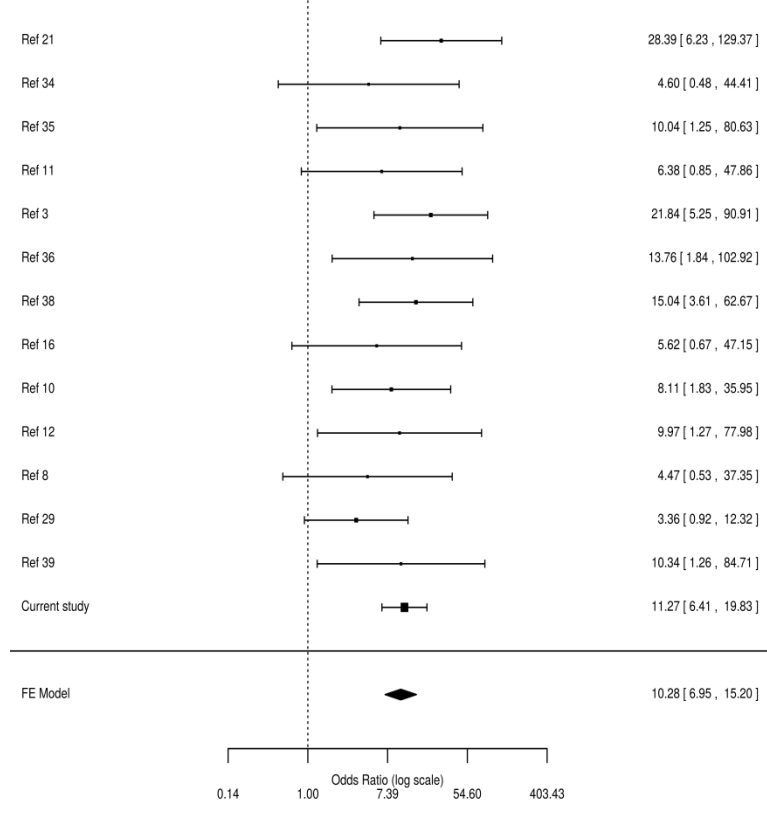
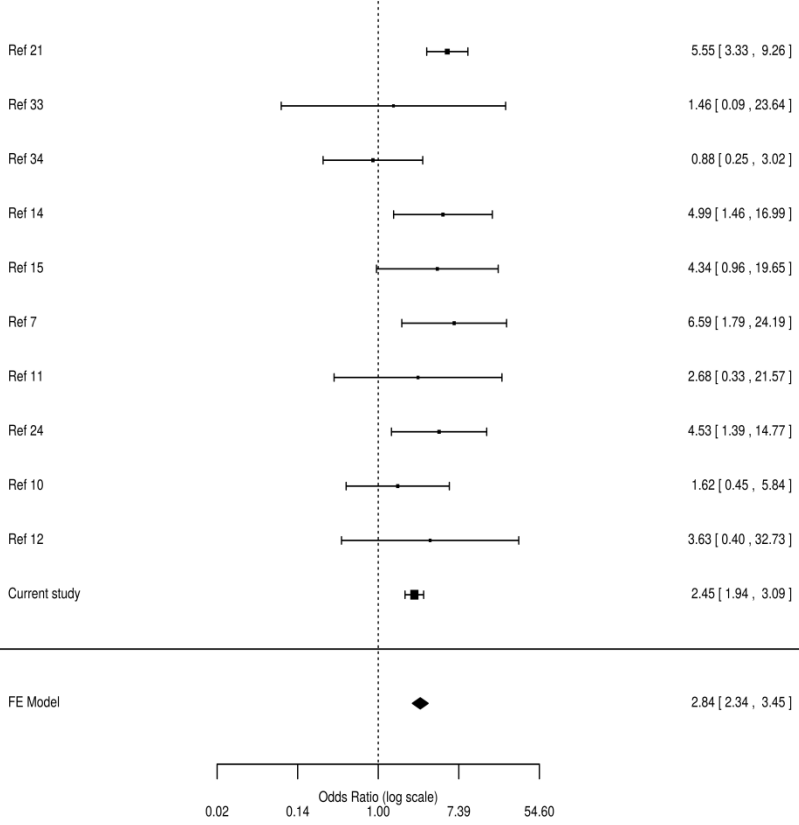
### Meta-analysis of mild and severe *GBA* mutations including the current study

Ref – reference number

A) Forest plot of studies with data on mild *GBA* mutations, after excluding studies reporting zero cases with mild *GBA* mutations. The analysis included data from 11 studies with a total of 5,077 cases and 8,147 controls. *p* value for heterogeneity was 0.08. B) Forest plot of studies with data on severe *GBA* mutations, after excluding studies with zero cases with severe *GBA* mutations. The analysis included data from 14 studies with a total of 6,252 cases and 9,764 controls. *p* value for heterogeneity was 0.83. C) Forest plot of studies with data on mild *GBA* mutations, using a constant continuity correction of 0.5 for studies with zero cases with mild *GBA* mutations. The analysis included data from 31 studies with a total of 11,453 cases and 14,565 controls. *p* value for heterogeneity was 0.02. D) Forest plot of studies with data on severe *GBA* mutations, using a constant continuity correction of 0.5 for studies with zero cases with severe *GBA* mutations. The analysis included data from 31 studies with a total of 11,453 cases and 14,565 controls. *p* value for heterogeneity was 0.81.

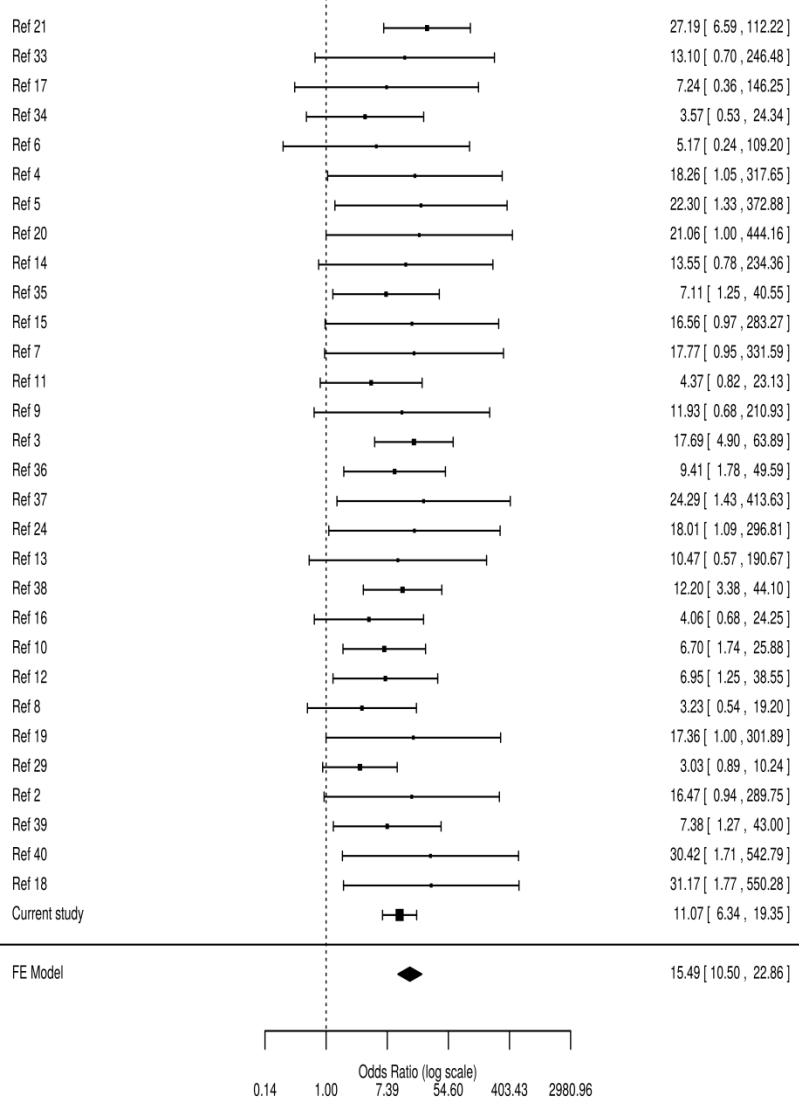
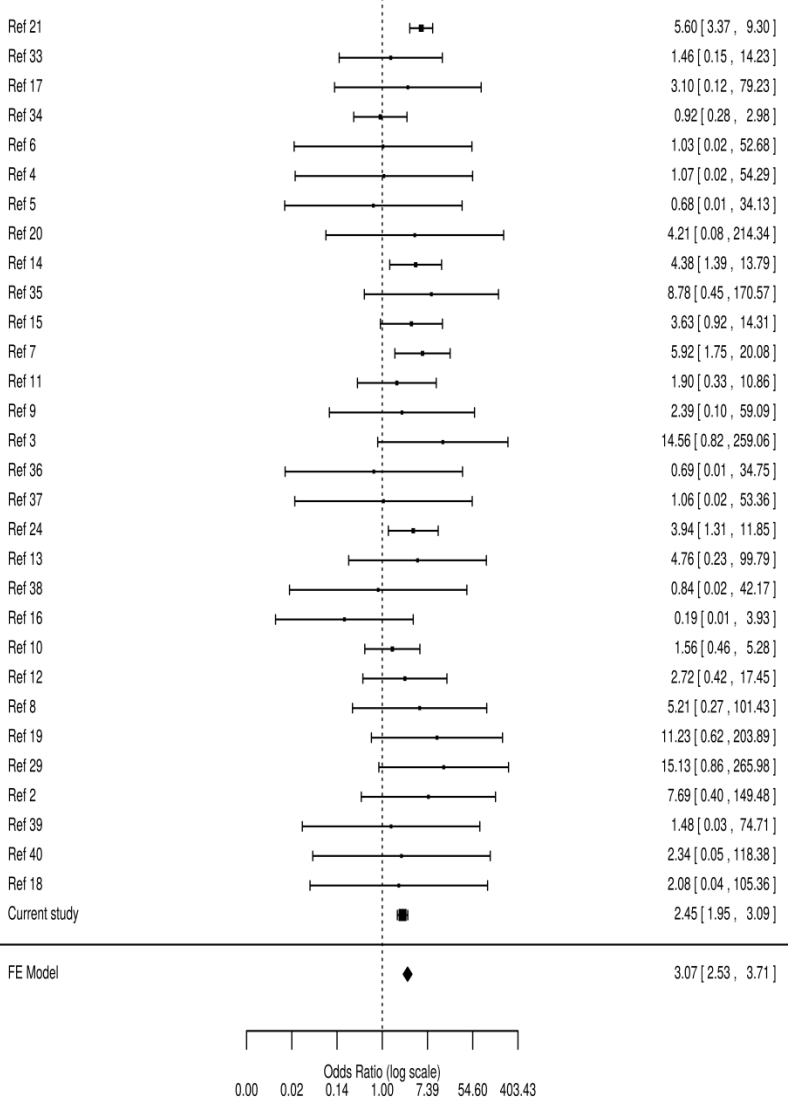
# Figure e-1 A

# B



# C

# D



## Legend Figure e-2

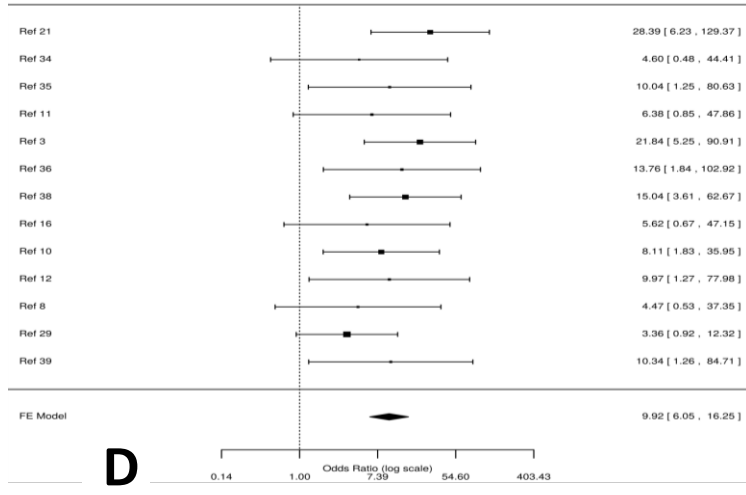
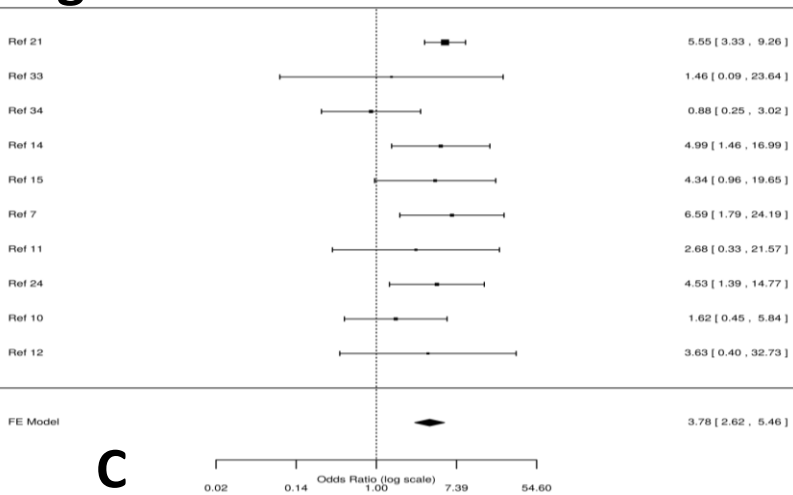
### Meta-analysis of mild and severe *GBA* mutations excluding the current study

Ref – reference number

A) Forest plot of studies with data on mild *GBA* mutations, after excluding studies with zero cases with mild *GBA* mutations. The analysis included data from 10 studies with a total of 3,356 cases and 4,248 controls.  $p$  value for heterogeneity was 0.22. B) Forest plot of studies with data on severe *GBA* mutations, after excluding studies with zero cases with severe *GBA* mutations. The analysis included data from 13 studies with a total of 5,252 cases and 5,959 controls.  $p$  value for heterogeneity was 0.78. C) Forest plot of studies with data on mild *GBA* mutations, using a constant continuity correction of 0.5 for studies with zero cases with mild *GBA* mutations. The analysis included data from 30 studies with a total of 10,453 cases and 10,760 controls.  $p$  value for heterogeneity was 0.06. D) Forest plot of studies with data on severe *GBA* mutations, using a constant continuity correction of 0.5 for studies with 0 cases with severe *GBA* mutations. The analysis included data from 30 studies with a total of 10,453 cases and 10,760 controls.  $p$  value for heterogeneity was 0.77. E) Forest plot of studies with data on mild *GBA* mutations, using an empirical continuity correction (see methods) for studies with zero cases with mild *GBA* mutations. The analysis included data from 30 studies with a total of 10,453 cases and 10,760 controls.  $p$  value for heterogeneity was 0.82. F) Forest plot of studies with data on severe *GBA* mutations, using an empirical continuity correction (see methods) for studies with zero cases with severe *GBA* mutations. The analysis included data from 30 studies with a total of 10,453 cases and 10,760 controls.  $p$  value for heterogeneity was 0.93.

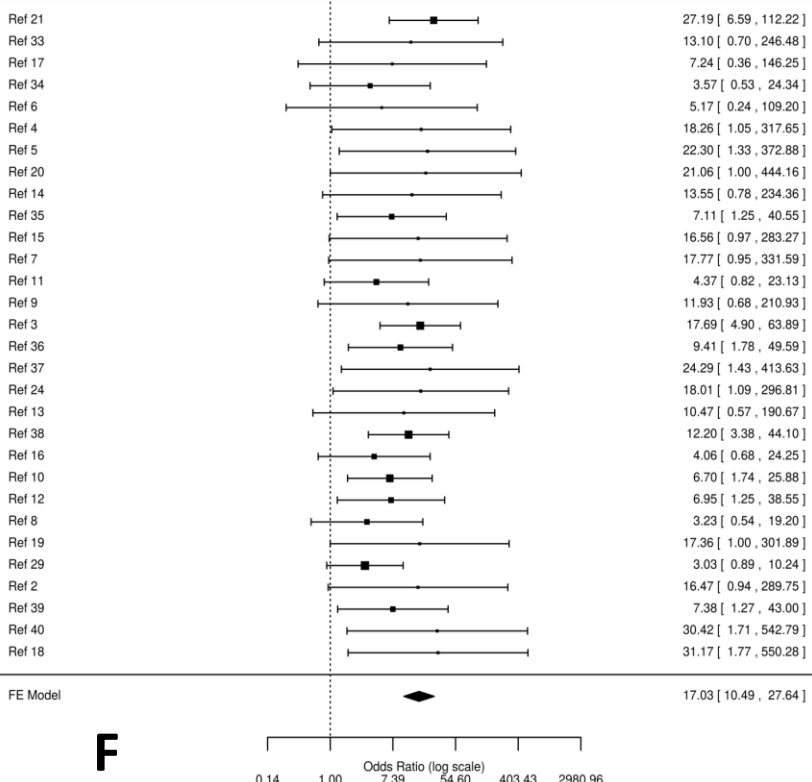
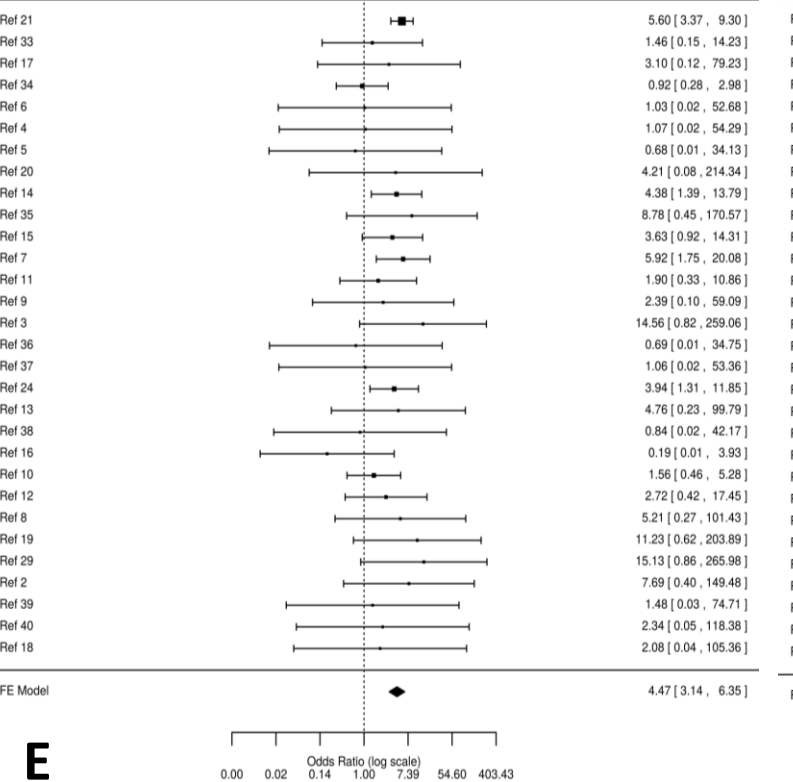
# Figure e-2 A

# B



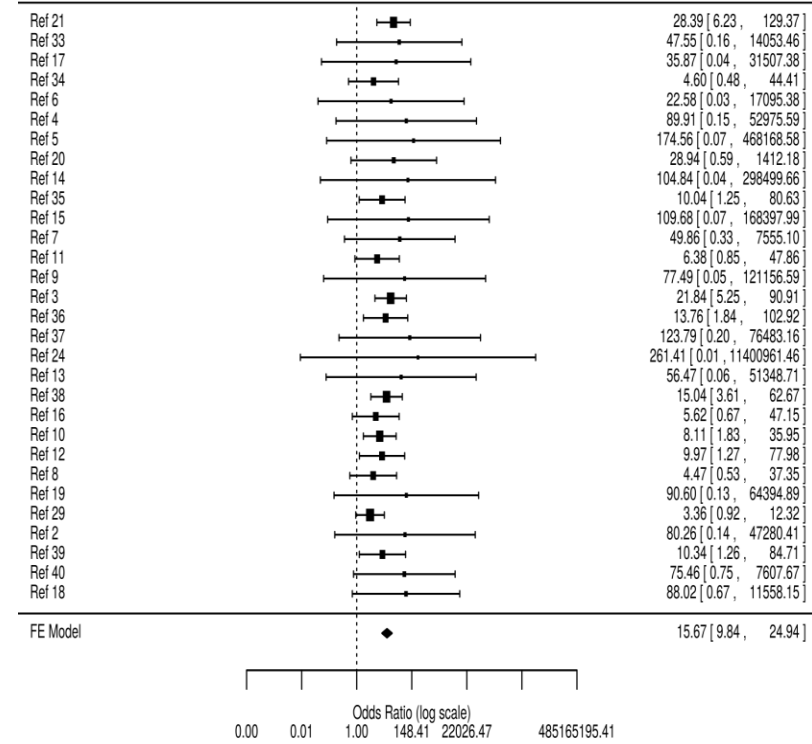
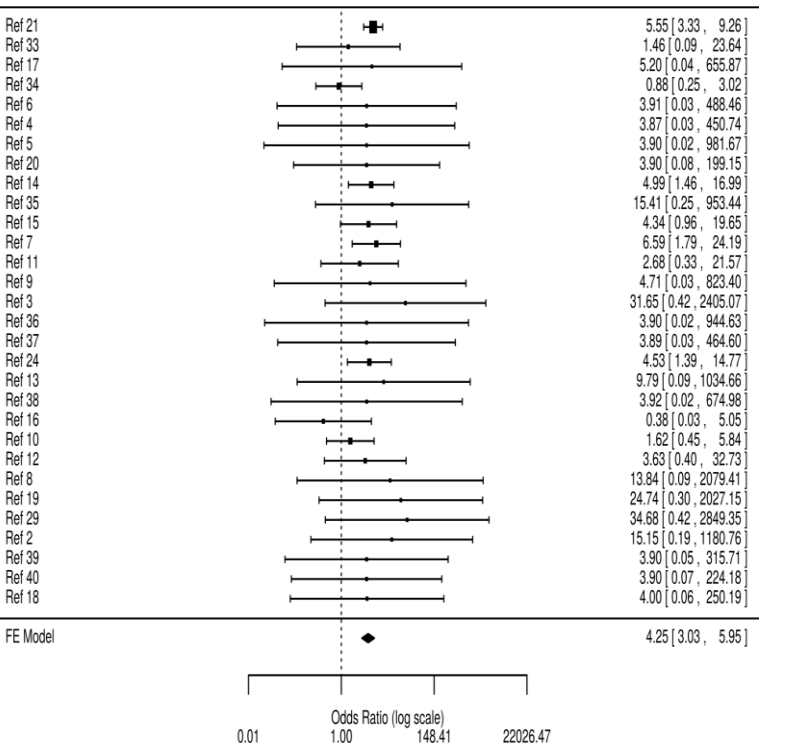
# C

# D



# E

# F



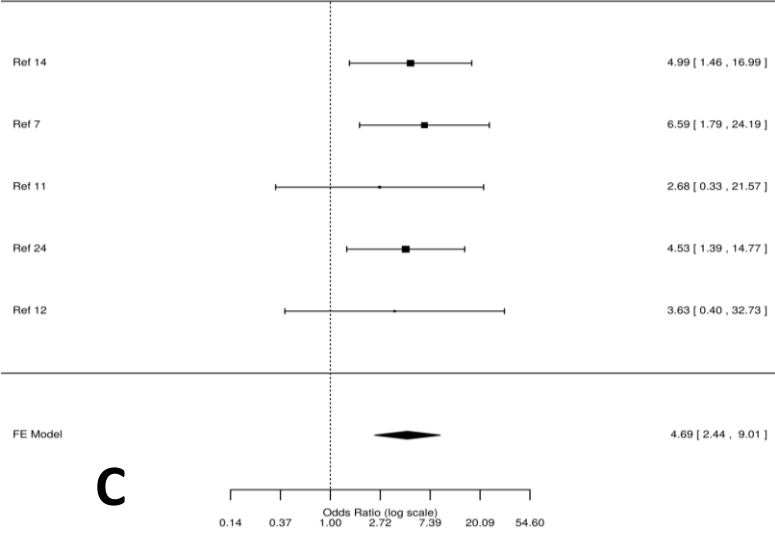
### Legend Figure e-3

#### Meta-analysis of studies with whole *GBA* gene sequencing data

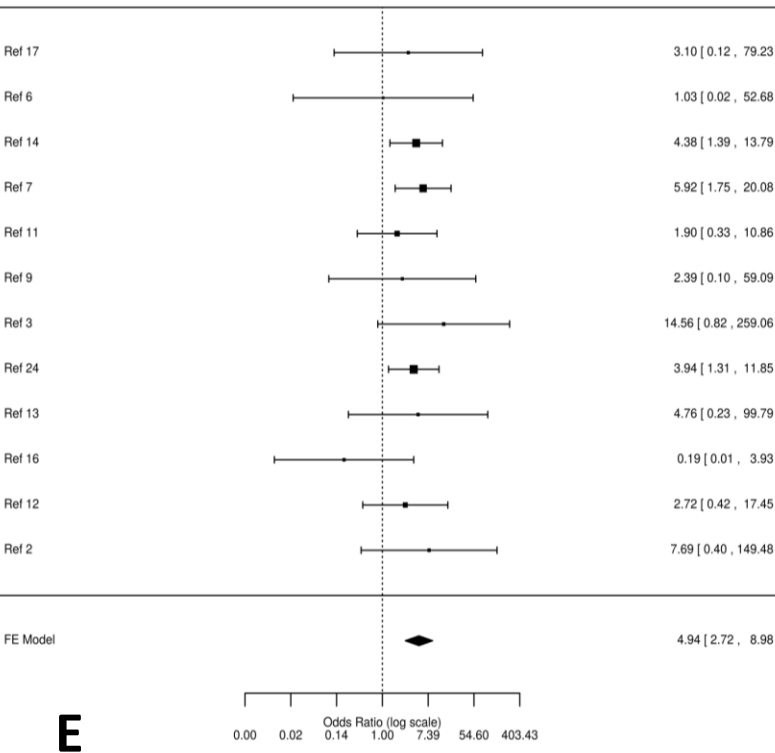
Ref – reference number

A) Forest plot of studies with data on mild *GBA* mutations, after excluding studies with zero cases with mild *GBA* mutations. The analysis included data from 5 studies with a total of 2,653 cases and 1,443 controls.  $p$  value for heterogeneity was 0.96. B) Forest plot of studies with data on severe *GBA* mutations, after excluding studies with zero cases with severe *GBA* mutations. The analysis included data from 4 studies with a total of 1,761 cases and 1,176 controls.  $p$  value for heterogeneity was 0.65. C) Forest plot of studies with data on mild *GBA* mutations, using a constant continuity correction of 0.5 for studies with zero cases with mild *GBA* mutations. The analysis included data from 12 studies with a total of 4,167 cases and 2,899 controls.  $p$  value for heterogeneity was 0.18. D) Forest plot of studies with data on severe *GBA* mutations, using a constant continuity correction of 0.5 for studies with zero cases with severe *GBA* mutations. The analysis included data from 12 studies with a total of 4,167 cases and 2,899 controls.  $p$  value for heterogeneity was 0.87. E) Forest plot of studies with data on mild *GBA* mutations, using an empirical continuity correction (see methods) for studies with 0 cases with mild *GBA* mutations. The analysis included data from 12 studies with a total of 4,167 cases and 2,899 controls.  $p$  value for heterogeneity was 0.71. F) Forest plot of studies with data on severe *GBA* mutations, using an empirical continuity correction (see methods) for studies with zero cases with severe *GBA* mutations. The analysis included data from 12 studies with a total of 4,167 cases and 2,899 controls.  $p$  value for heterogeneity was 0.95.

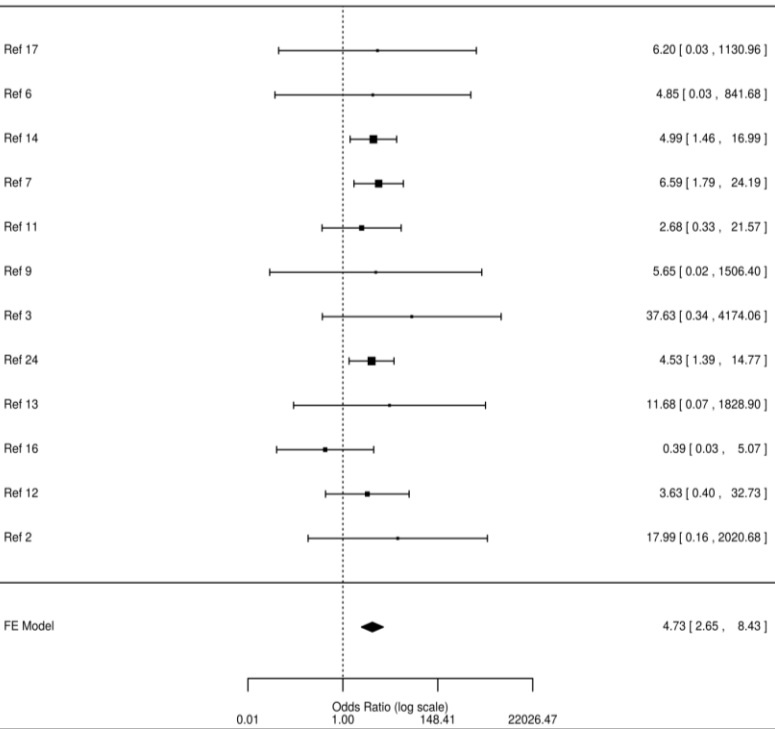
# Figure e-3 A



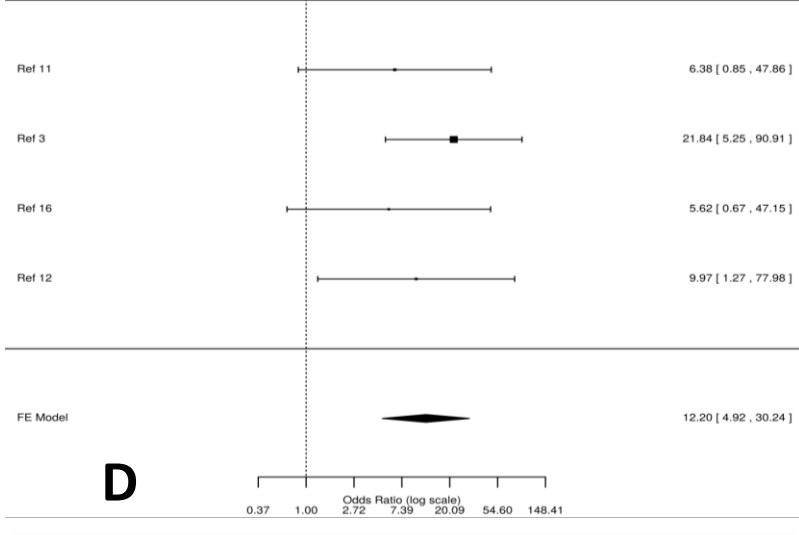
**C**



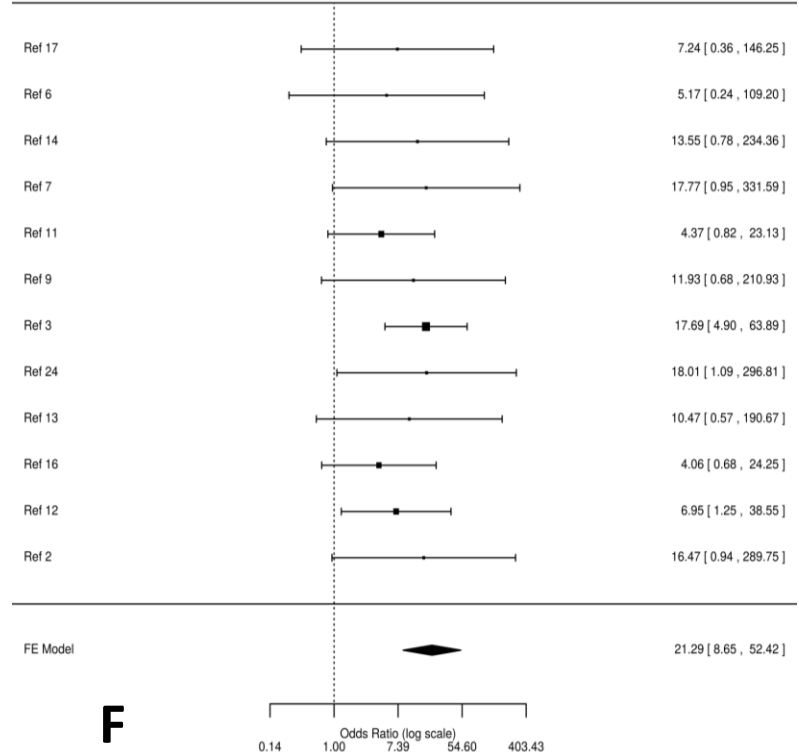
**E**



**B**



**D**



**F**

