TEST

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## 0.1 Functions

Table : CAPTION FOR TABLE

| Parameter | Estimate | Est.Error | l-95% CI | u-95% CI | Rhat | Bulk\_ESS | Tail\_ESS |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Group-Level Effects:** | | | | | | | |
| fkClientID (Number of levels: 1034) |  |  |  |  |  |  |  |
| sd(Intercept) | 0.10 | 0.01 | 0.08 | 0.12 | 1.00 | 599 | 1 106 |
| **Population-Level Effects:** | | | | | | | |
| Intercept | -0.03 | 0.04 | -0.11 | 0.04 | 1.00 | 4 700 | 5 335 |
| PHQ9\_baseline | -3.86 | 0.08 | -4.03 | -3.70 | 1.00 | 3 647 | 4 904 |
| PHQ9\_change | -2.45 | 0.13 | -2.70 | -2.20 | 1.00 | 1 342 | 3 300 |
| SOFAS\_baseline | 0.01 | 0.06 | -0.10 | 0.12 | 1.00 | 4 767 | 5 393 |
| SOFAS\_change | 0.41 | 0.07 | 0.27 | 0.55 | 1.00 | 6 621 | 6 049 |
| **Family Specific Parameters:** | | | | | | | |
| sigma | 0.10 | 0.00 | 0.09 | 0.10 | 1.01 | 661 | 1 473 |
| Formula: aqol6d\_total\_w ~ PHQ9\_baseline + PHQ9\_change + SOFAS\_baseline + SOFAS\_change + (1 | fkClientID) | | | | | | | |
| Family: gaussian Links: mu = log; sigma = identity Data: data\_tb (Number of observations: 1651) Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1; total post-warmup samples = 8000 | | | | | | | |
| Samples were drawn using sampling(NUTS). For each parameter, Bulk\_ESS and Tail\_ESS are effective sample size measures, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1). | | | | | | | |

Figure 1

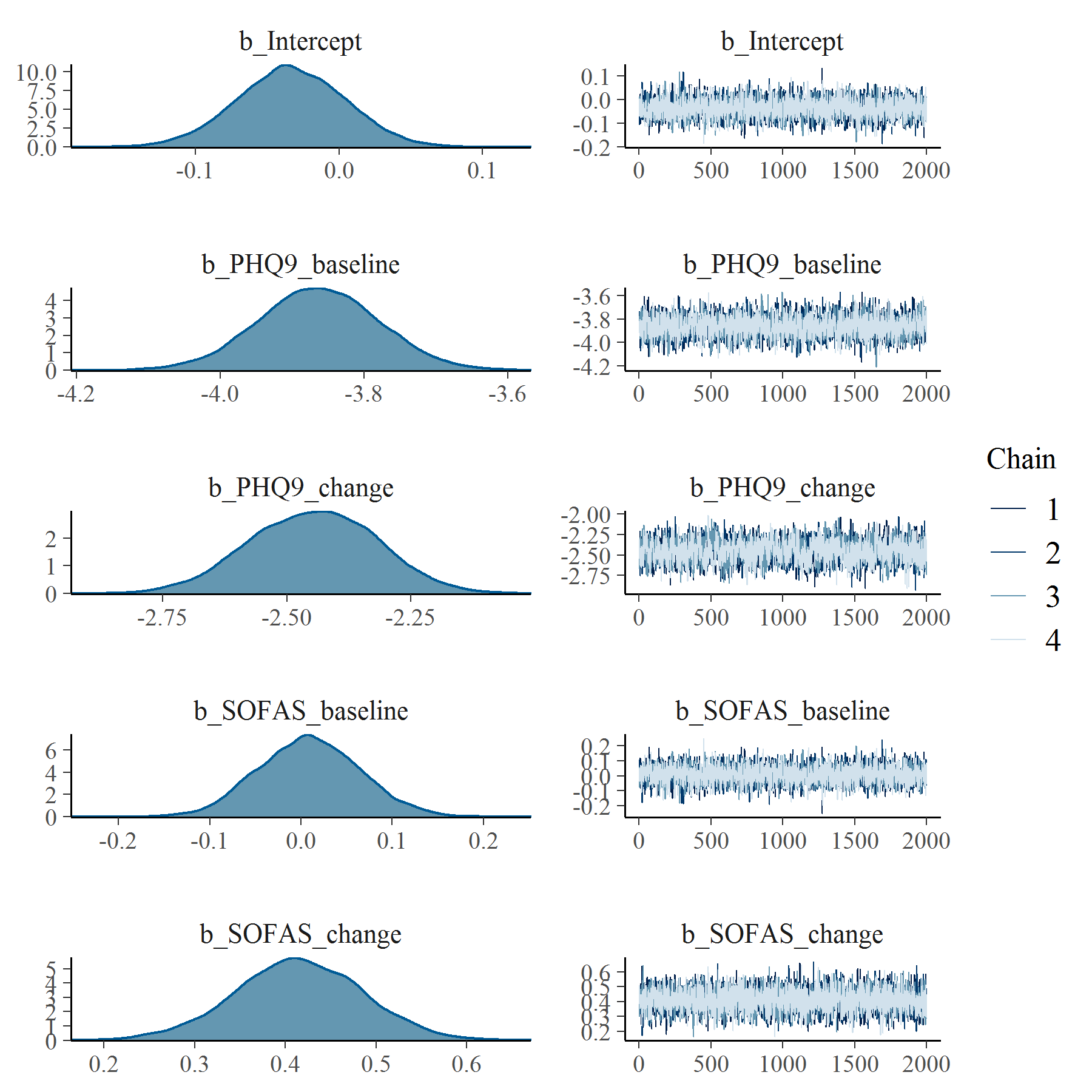


Figure : Caption 1

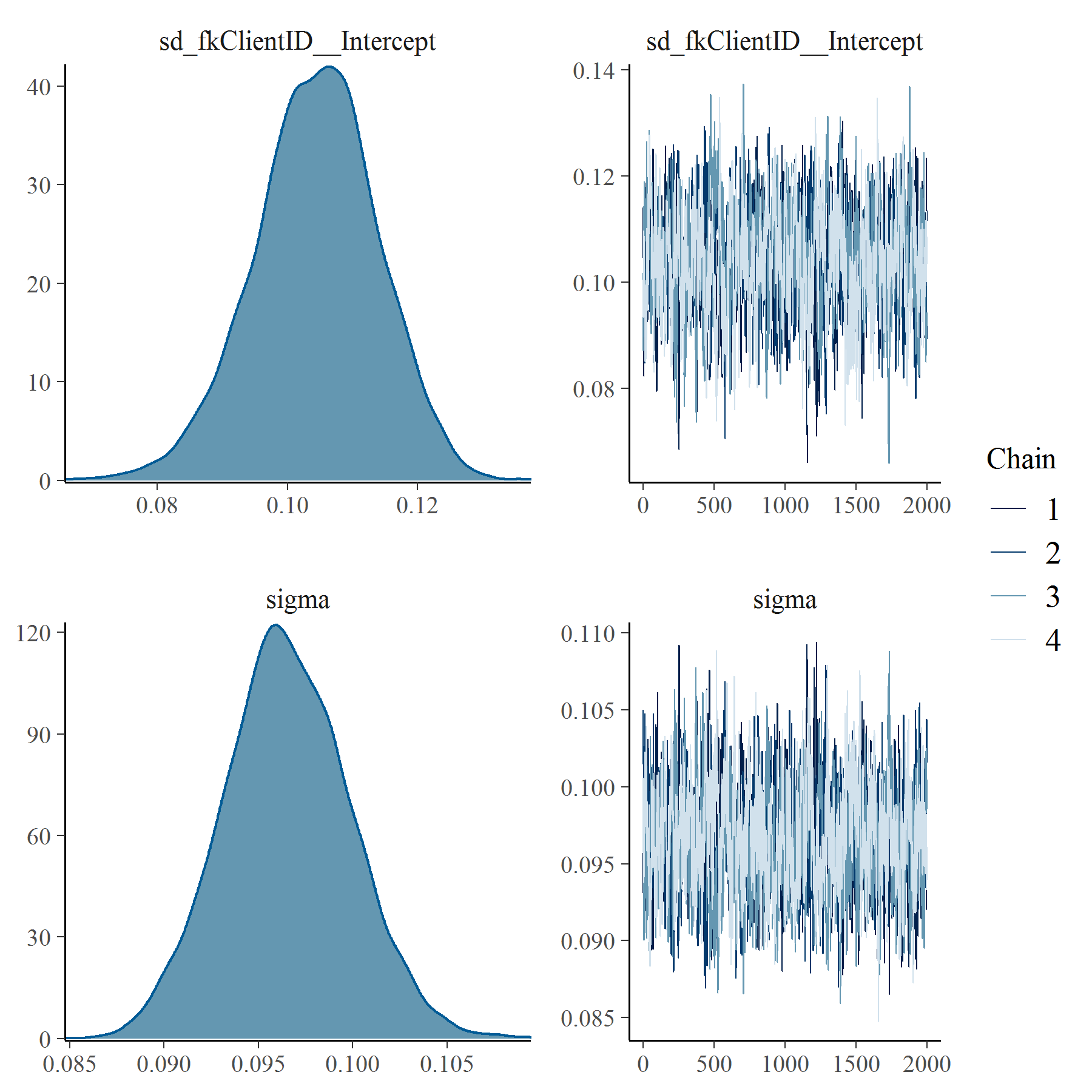


Figure : Caption 2

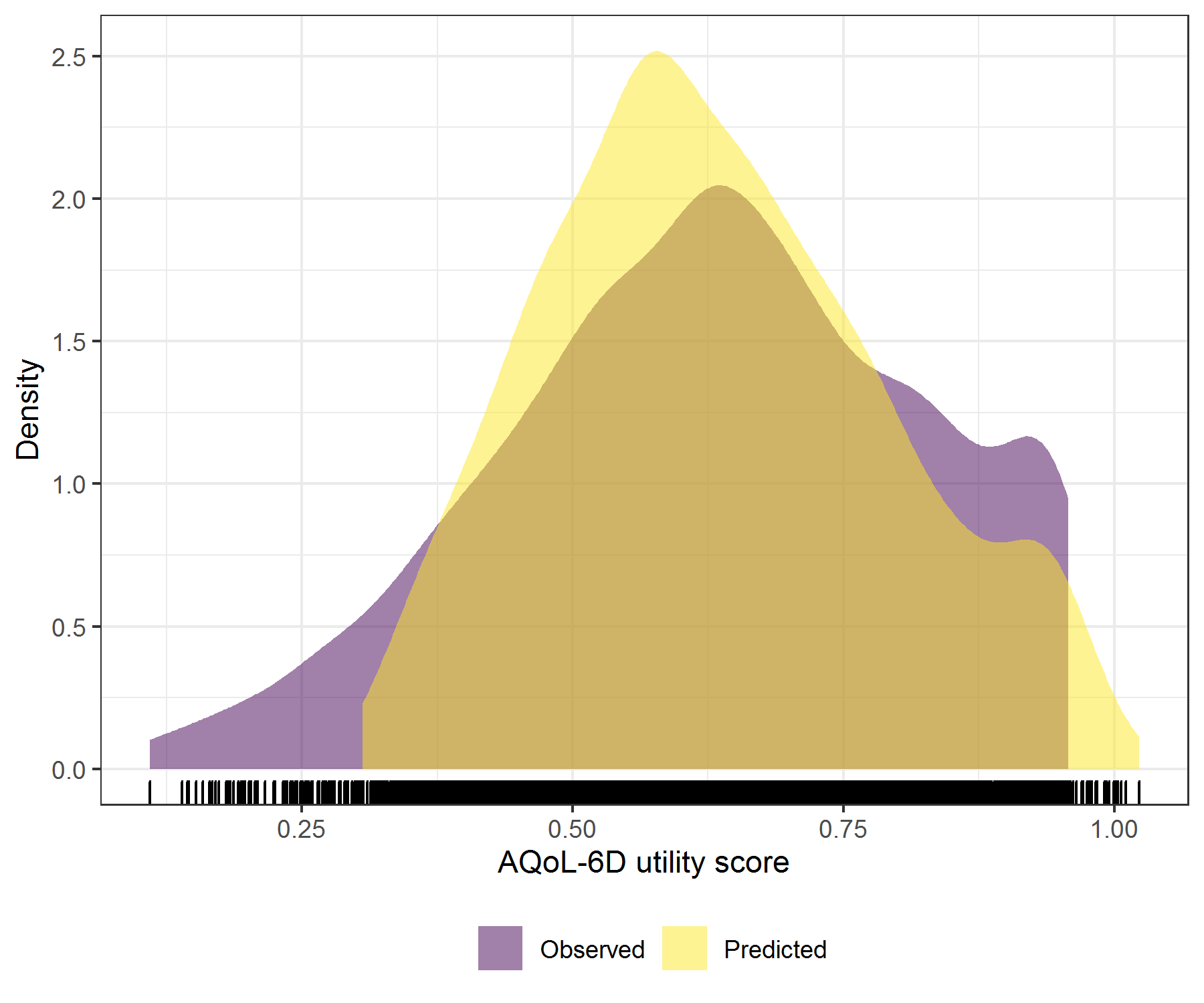


Figure : Caption 3

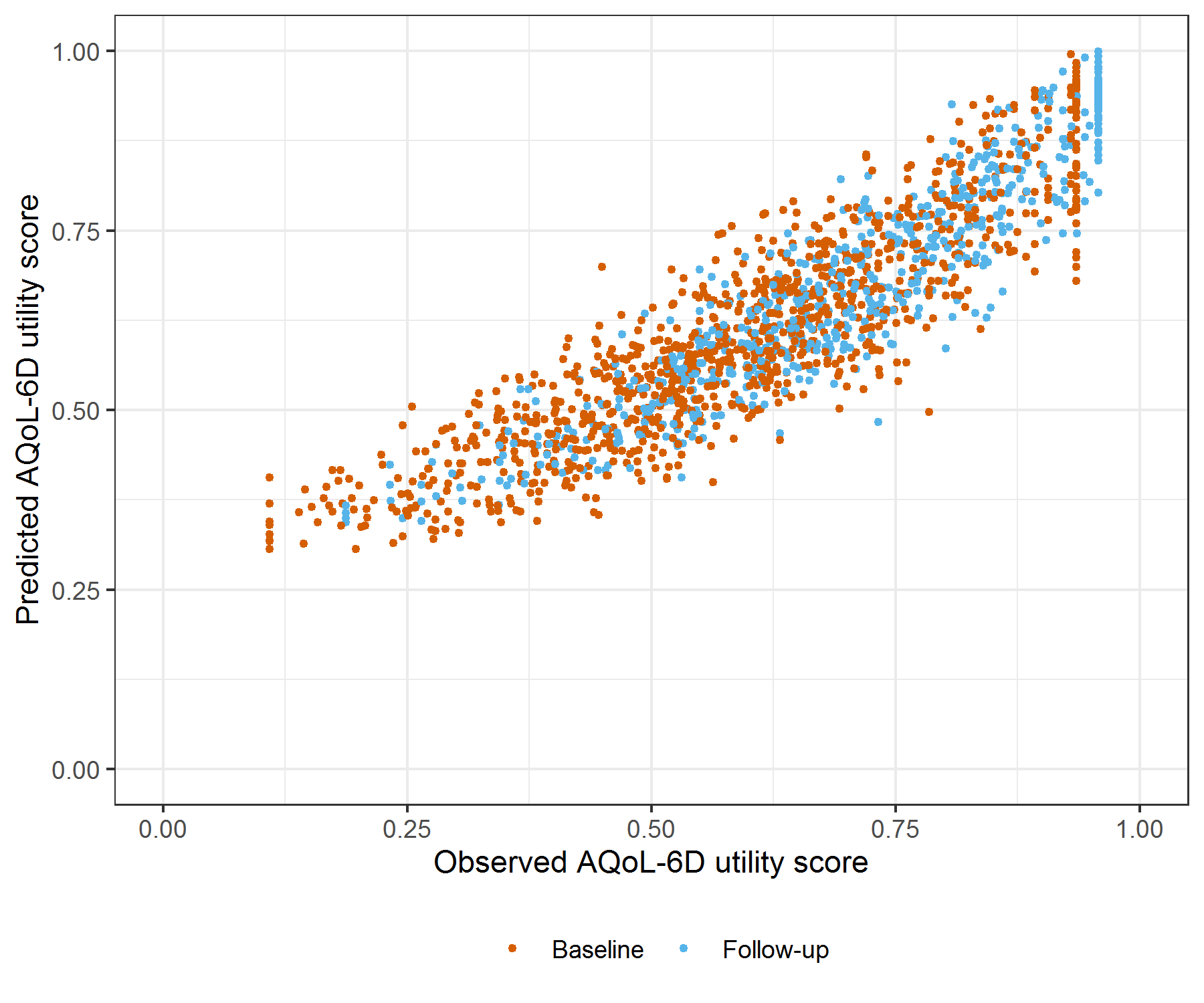


Figure : Caption 4

### TEST