

Table S1. Covariance parameter estimates and Wald Z-test of heavy peptide data using **Model 1**.

| Covariance Parameter | Estimate | Standard Error | Z Value | Probability > Z |
|---------------------------------------|-----------------|-----------------------|----------------|---------------------------|
| <i>tech_replicate(study)</i> | 0.0795 | 0.0795 | 1 | 0.1589 |
| <i>site</i> | 0.6446 | 0.4183 | 1.54 | 0.0617 |
| <i>peptide</i> | 1.1307 | 0.6591 | 1.72 | 0.0431 |
| <i>transition(peptide)</i> | 0.8387 | 0.2559 | 3.28 | 0.0005 |
| <i>study*site</i> | 0.1716 | 0.0771 | 2.23 | 0.013 |
| <i>study*peptide</i> | 0.0477 | 0.0248 | 1.92 | 0.0273 |
| <i>site*peptide</i> | 0.1445 | 0.0423 | 3.42 | 0.0003 |
| <i>study*transition(peptide)</i> | 0.0011 | 0.0007 | 1.73 | 0.0419 |
| <i>site*transition(peptide)</i> | 0.0618 | 0.0081 | 7.66 | <.0001 |
| <i>study*site*peptide</i> | 0.1790 | 0.0243 | 7.37 | <.0001 |
| <i>study*site*transition(peptide)</i> | 0 | . | . | . |
| <i>residual</i> | 0.7511 | 0.0046 | 162.28 | <.0001 |