Table S2. **Regression models for GABAAR mAb binding to unfixed murine brain.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  | #113-101 | #113-115 | #113-175 | #113-198 | #113-201 |
|  |  |  |  |  |  |  |
| Binding to murine GABAAR on brain sections | | | | |  |  |
| Curve fit | R² | 0.96 | 0.89 | 0.91 | 0.97 | 0.90 |
| MFImax | MFI | 121.4 | 118.3 | 75.8 | 121.4 | 114.7 |
| Std. Error | 3.3 | 3.6 | 2.2 | 2.6 | 7.7 |
| 95% CI | 115.0 - 128.0 | 111.3 - 125.3 | 71.5 - 80.3 | 115.9 - 127.1 | 101.4 – 134.5 |
| Half Max (= 50% MFImax) | Conc. | 2.5 | 0.16 | 0.27 | 0.72 | 6.6 |
| Std. Error | 0.25 | 0.035 | 0.039 | 0.073 | 1.33 |
| 95% CI | 2.0 - 3.0 | 0.11 - 0.21 | 0.20 - 0.36 | 0.57 – 0.90 | 4.5 - 10.4 |
| Binding to rat GABAAR overexpressed on HEK cells | | | | |  |  |
| Curve fit | R² | 0.98 | 0.98 | 0.91 | 0.97 | 0.96 |
| MFImax | MFI | 83 | 105.6 | 64.3 | 140.3 | 115.5 |
| Std. Error | 2.4 | 2.9 | 4.9 | 4.6 | 8.3 |
| 95% CI | 77.9 – 88.4 | 99.5- 111.9 | 54.5 – 75.3 | 130.4- 150.5 | 98.8 – 136.7 |
| Half Max (= 50% MFImax) | Conc. | 0.40 | 0.08 | 0.57 | 0.13 | 3.4 |
| Std. Error | 0.068 | 0.013 | 0.21 | 0.023 | 0.86 |
| 95% CI | 0.29 – 0.54 | 0.06 - 0.11 | 0.26 - 1.20 | 0.08 – 0.19 | 2.0 – 6.20 |
| Binding to human GABAAR overexpressed on HEK cells | | | | |  |  |
| Curve fit | R² | 0.94 | 0.98 | 0.98 | 0.97 | 0.98 |
| MFImax | MFI | 70.3 | 112.9 | 64.5 | 114.9 | 127 |
| Std. Error | 4.8 | 3.4 | 2.1 | 3.9 | 2.4 |
| 95% CI | 59.9 – 82 | 105.5 – 120.6 | 60.1 – 69.2 | 106.5 – 123.7 | 121.7 – 132.4 |
| Half Max (= 50% MFImax) | Conc. | 0.95 | 0.24 | 0.75 | 0.19 | 0.03 |
| Std. Error | 0.29 | 0.037 | 0.12 | 0.033 | 0.004 |
| 95% CI | 0.44 - 1.89 | 0.17 - 0.35 | 0.54 - 1.04 | 0.12 – 0.28 | 0.02 - 0.04 |

Parameter from best curve fit nonlinear regression models of one site-specific binding as calculated from MFI values of GABAAR mAb binding in serial dilutions to natively expressed receptors on unfixed murine brain sections or HEK cells overexpressing rat or human GABAAR as indicated. Regression models are based on the following equation: MFI = MFImax \* IgG concentration/(Half Max + IgG concentration). Calculated plateau MFI values are given as MFImax, from which concentration (Conc., in µg/ml) of 50% MFImax (Half Max) are derived.