**Figure 3 – source data 1. Statistical evaluation of flow cytometry data using various cell lines incubated with rhDAO-WT and rhDAO-R568S/R571T heparin-binding motif mutant.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Cell line | Normality by Shapiro-Wilk test | Equality of Variances | NC vs. R568S/R571T | NC vs.WT | R568S/R571T vs. WT |
| **CHO-K1\*** | **Yes** | **No** | **p < 0.05** |
| **HDF\*\*** | **Yes** | **Yes** |
| **HDMVEC\*** | **Yes** | **No** |
| **HeLa\*** | **Yes** | **No** |
| **HepG2\*** | **Yes** | **No** |
| **HUVEC\*** | **Yes** | **No** |
| **LHCN-M2\*** | **Yes** | **No** |
| **PODO\*** | **Yes** | **No** |
| **SK-Hep1\*** | **Yes** | **No** |

The cells were incubated with Alexa488-labeled rhDAO-WT and rhDAO-R568S/R571T (no DAO added = negative control) and 500 cells per sample were analyzed flow cytometrically (n = 4 biological replicates, 2 individual experiments in duplicate). The significance of differences in fluorescence intensities (median) of the negative control (NC), rhDAO-WT and rhDAO-R568S/R571T was tested. All comparisons were statistically significant with p-values < 0.05.

\* = Welch’s-ANOVA and Games-Howell test; \*\* = ANOVA and Tukey’s HSD test