Supplementary Table 3. Analysis of gene expression with microarray in NK150460 treated breast cancer cell lines.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Cell lines | CYP1A1 mRNA | | |  | CYP1B1 mRNA | | |
| 0 hr | 3 hr | 6 hr |  | 0 hr | 3 hr | 6 hr |
| T-47D | 1 | 81.9 | 112.7 |  | 1 | 6.8 | 4.1 |
| MCF-7 | 1 | 101.2 | 69.8 |  | 1 | 5.6 | 4.3 |
| SK-BR-3 | 1 | 100.4 | 119.7 |  | 1 | 10.9 | 7.4 |
| MM-231 | 1 | 2.1 | 1.9 |  | 1 | 2.2 | 2.2 |

For each cell line, the quantity of mRNA at each sampling point is indicated as fold-induction compared to the baseline.