Table 1: **Drug mixture - 200 ppb**

For **new** and **old** MS settings analytes with corresponding *Internal Standard*

| Analyte Information | | Differences as *Analyte* - *IS* | | | Normalisation as *analyte\_height/IS\_height* | |
| --- | --- | --- | --- | --- | --- | --- |
| Analyte Name | Molecular formula | Retention Time ,<br>min | Drift Time ,<br>ms | Mass Error,<br>ppm | OLD | NEW |
| *Methamphetamine-d9* | | | | | | |
| Phentermine*1* | C10H15N | 0.017 | 0.000 | 1.115 | 0.642 | 0.365 |
| Methamphetamine*1* | C10H15N | 0.017 | 0.000 | 1.115 | 0.642 | 0.365 |
|  | | | | | | |
| MDMA | C11H15NO2 | 0.015 | -0.024 | -1.235 | 1.716 | 1.290 |
| MDEA | C12H17NO2 | 0.012 | -0.024 | -0.635 | 1.663 | 2.001 |
| Benzoylecgonine | C16H19NO4 | 0.000 | 0.000 | -0.404 | 2.419 | 2.320 |
| THC-COOH | C21H28O4 | -0.002 | -0.095 | *2*-11.002 | 3.269 | 2.502 |
| *1*Isomeric compounds. They have been matched to the same feature, hence, the reason for the identical values. | | | | | | |
| *2*The large mass error difference between \*analyte\* and \*IS\* is due to a larger mass error for the corresponding IS (10.9 compared to analyte -0.101) | | | | | | |