**Additional Table 9:** TP (a), FP (b), FN (c), and TN (d) related to the studies reporting either directly the median ctDNA MAF value or enough data to allow a calculation.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **STUDY** | **MAF****(%)** | **a** | **b** | **c** | **d** |
| **Beaver** | Median =0,02 %Media =0,24 % | 13 | 0 | 1 | 15 |
| **Spoerke** | Median =2,43 %Media =6,51 %(all popul.) | 50 | 7 | 14 | 71 |
| **Chung** | Median =2,8 %Media =2,63 % | 3 | 0 | 0 | 11 |
| **Rothe** | Median =2,8 %Media =4,5 % | 3 | 1 | 1 | 12 |
| **Moreno****(a)+(b)** | Median =3 %Media =17,5 % | 19 | 0 | 3 | 54 |
| **Dawson** | Median =4 %(allmutations) | 12 | 0 | 0 | 18 |
| **Shatsky** | Median =9,6 %Media =17,6 % | 7 | 1 | 2 | 28 |