**Table 3**. **Methylation-induced mutation spectra at the $\lambda$ cII locus in wild-type or ß-pol null MEFs**

| Mutation type | Spontaneous | | | MMS | | | Fold MMS-induced change |
|---|---|---|---|---|---|---|---|
| | No. | % | Mutation frequency, $\times 10^{-5}$ | No. | % | Mutation frequency, $\times 10^{-5}$ | |
| **Wild type** | | | | | | | |
| G:C to A:T | 39 | 30 | **4.2** | 46 | 29.1 | **3.2** | – |
| A:T to G:C | 24 | 18.4 | **2.6** | 12 | 7.6 | **0.8** | – |
| G:C to T:A | 23 | 17.7 | **2.5** | 45 | 28.5 | **3.1** | 1.2 |
| G:C to C:G | 17 | 13 | **1.8** | 18 | 11.4 | **1.2** | – |
| A:T to T:A | 9 | 6.9 | **1.0** | 22 | 13.9 | **1.5** | 1.6 |
| A:T to C:G | 18 | 13.8 | **1.9** | 15 | 9.5 | **1.1** | – |
| Total | 130 | | | 158 | | | |
| **ß-pol null** | | | | | | | |
| G:C to A:T | 24 | 24.5 | **5.6** | 29 | 19.6 | **10.4** | 1.9 |
| A:T to G:C | 8 | 7.8 | **1.8** | 20 | 13.5 | **7.2** | 4 |
| G:C to T:A | 21 | 20.6 | **4.7** | 39 | 26.4 | **14** | 3 |
| G:C to C:G | 24 | 23.5 | **5.4** | 24 | 16.2 | **8.6** | 1.6 |
| A:T to T:A | 10 | 9.8 | **2.3** | 21 | 14.2 | **7.5** | 3.3 |
| A:T to C:G | 15 | 14.7 | **3.4** | 15 | 10.1 | **5.4** | 3.3 |
| Total | 102 | | | 148 | | | |

The mutant frequencies used in the calculation of MMS-induced mutation frequencies were $1.1 \times 10^{-4}$ and $5.3 \times 10^{-4}$ for wild-type and ß-pol null cells, respectively. These values are graphically represented in Fig. 2. Mutation frequencies were calculated by multiplying the fraction of each class of mutations observed by the average spontaneous mutant frequency. For example, the frequency of spontaneous G:C to C:G mutations in wild-type cells was calculated as follows: $(0.13)(1.4 \times 10^{-4}) = 1.8 \times 10^{-5}$. Fold change is calculated by dividing the mutation frequency of a given type mutation on MMS-treated cells by the frequency of the same type of mutation in control cells