*Table 3: Variants detected when comparing the same sample to different haplogroup genomes. 'Tool' refers to the variants detected when using the MitoCall tool, and 'Blast' refers to the variants detected when using the basic local alignment search tool. 'Multiple' refers to numbers found in the hundreds caused by the bisulfite treatment. 'C57BL/6Babr' refers to a deeper sequenced mouse oocyte discussed in Fig 2c.*

| Mutations | Ref (C57BL/6J) vs. C57BL/6Babr | C57BL/6NJ vs. C57BL/6Babr | | NZO/HiLtJ vs. C57BL/6Babr | |
|---|---|---|---|---|---|
| | | Tool | Blast | Tool | Blast |
| A > G | 1 | | | 4 | 17 |
| A > T | 1 | 1 | | 3 | 2 |
| C > A | 1 | 1 | | 3 | 3 |
| G > T,A | 1 | | | | |
| T > A | 1 | | | 2 | 1 |
| T > C | | 1 | | 22 | 22 |
| A > C | | | | 1 | 1 |
| G > T | | | | 1 | 1 |
| A deletion | | | 1 | | 2 |
| G deletion | | | | | 1 |
| C > T | multiple | multiple | 1 | multiple | 22 |
| G > A | multiple | multiple | | multiple | 15 |