

Fig S1. Real data introduces noise/missing data that masks mutation type pattern. At the center is an example distribution of mosaic and germline scores for generated calls. Arrows show *NxN* pairwise binary matrices for select calls. **A)** An ideal matrix for a germline variant. Calls for the variant are made in all but one cell. **B)** A matrix for a germline variant that is similar to example in A, however there are multiple cells for which call was not made. **C)** This call exhibits pattern that is a "combination" of patterns for germline variant and mosaic mutations. This call is thus a mosaic mutation that is present in high fraction cells and is missed when comparing cells to bulk. **D)** An ideal matrix for a mosaic mutation showing that the mutation is present in only one cell. **E)** An example of a matrix for a mosaic mutation present in 3 cells. One cell exhibits an ideal pattern (i.e., a call is made when comparing to each other cell), but other two cells have missing calls. **F)** A noisy call with pattern not matching to either germline variant or mosaic mutation.