

Supplement Figures S1-S3

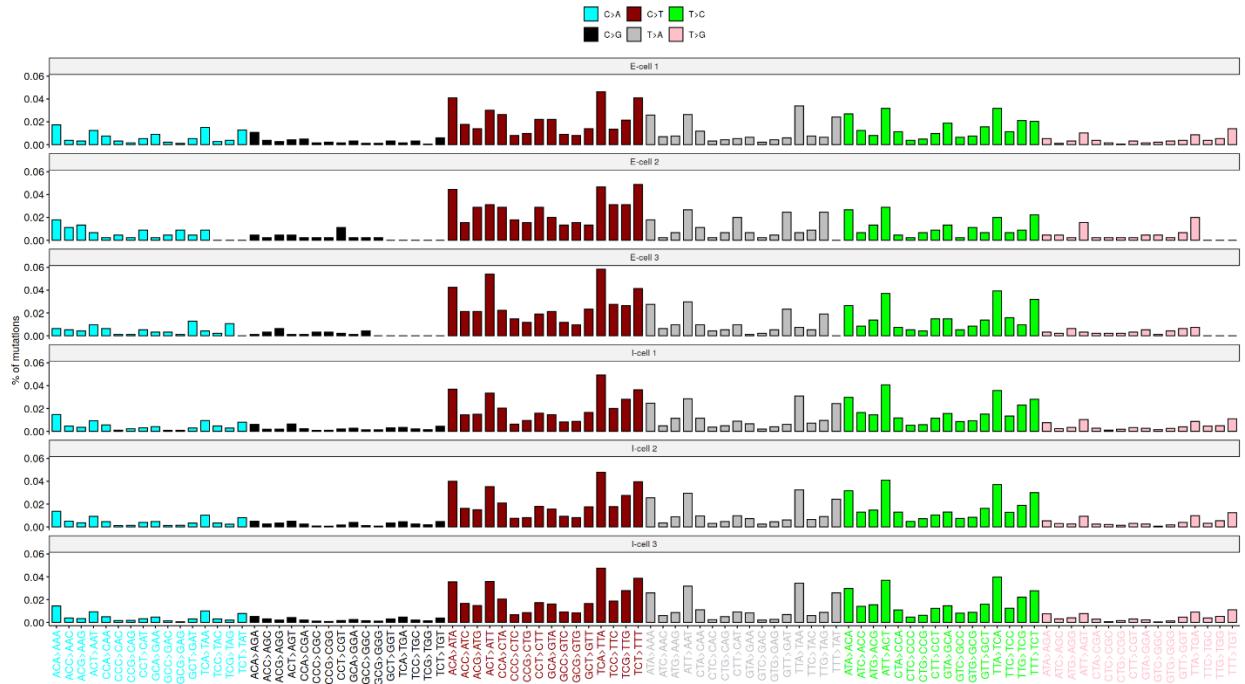


Fig. S1. Barplots of mutation types, including flanking bases, as a percentage of total mutations. Compare to [Fig 2b of Milholland et al, 2017, Nature communication.](#)

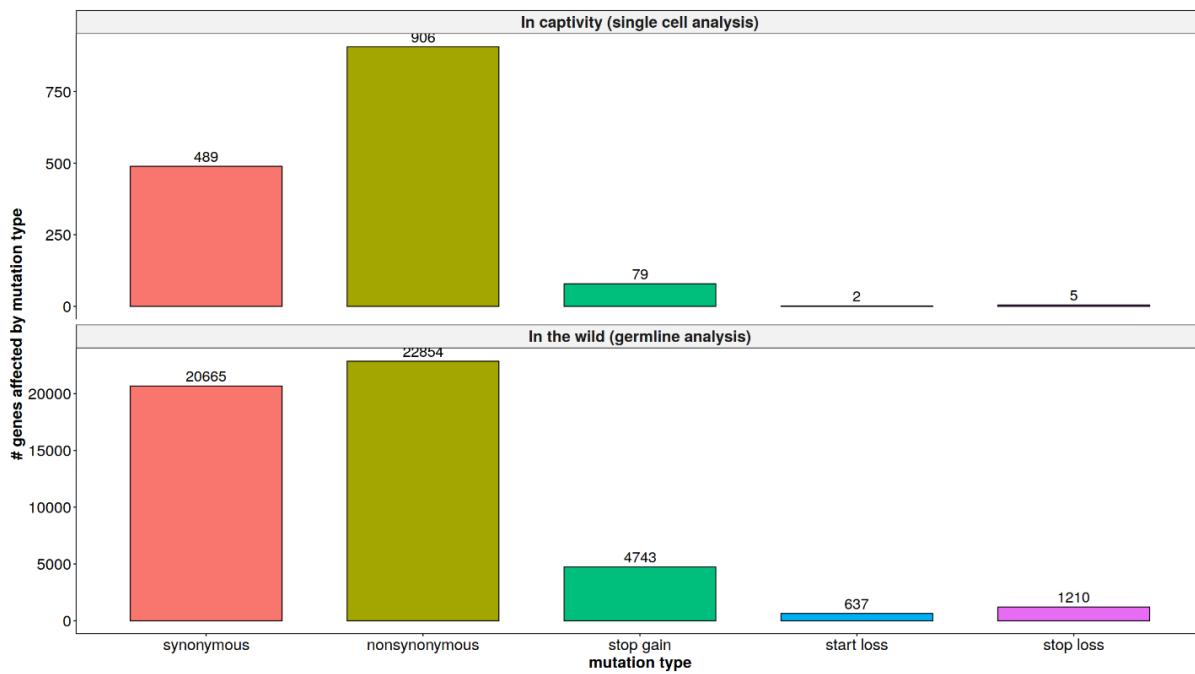


Fig. S2. Number of genes affected by different mutation types.

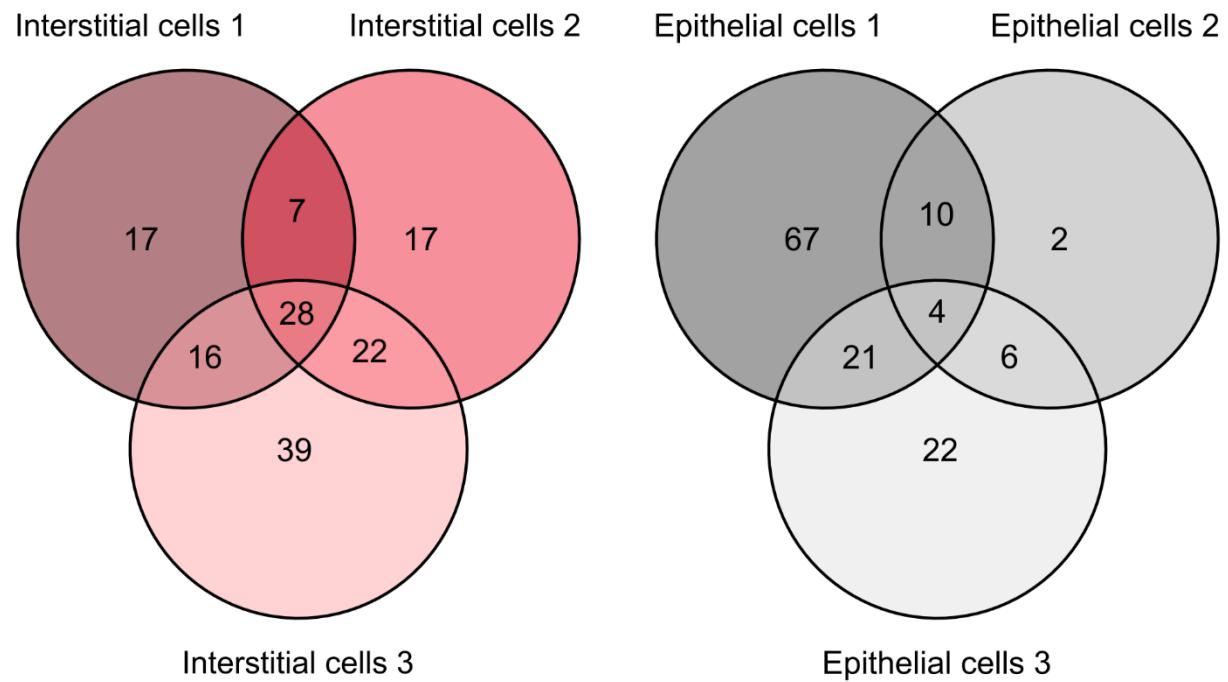


Fig. S3. Number of bases in million shared between the single-cell comparisons examined. Note that for each single-cell only genome positions were regarded with a read coverage ≥ 20 both in the respective single-cell and the merged mapping result of three single-cells of the opposite stem cell lineage. For this figure, the sets of genome positions fulfilling these criteria were intersected again between the comparisons of each stem cell lineage.