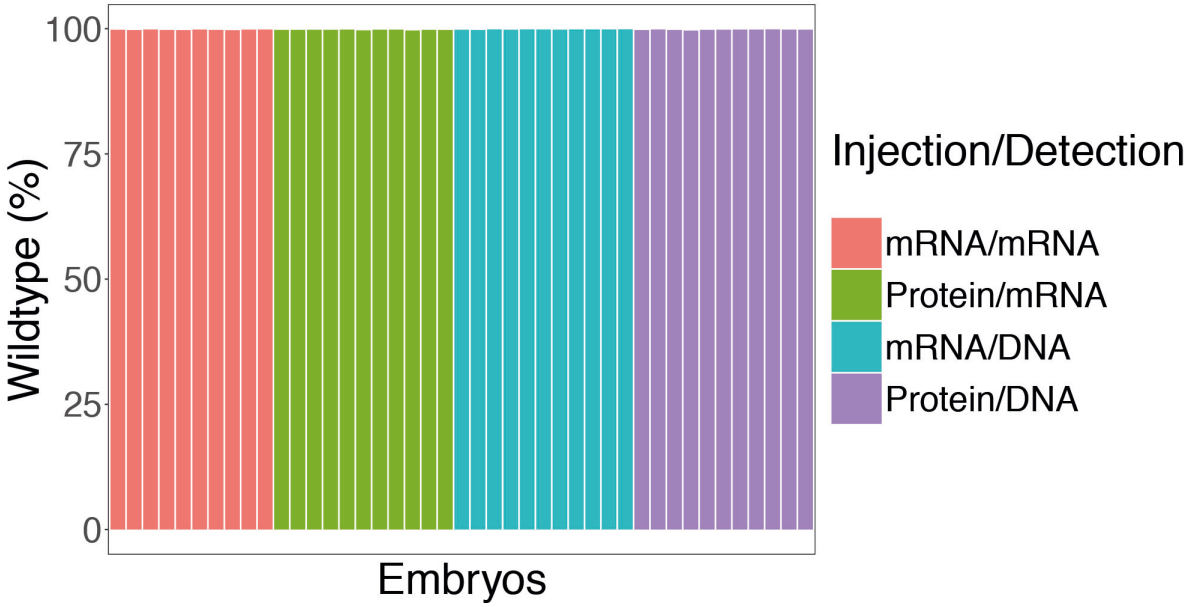
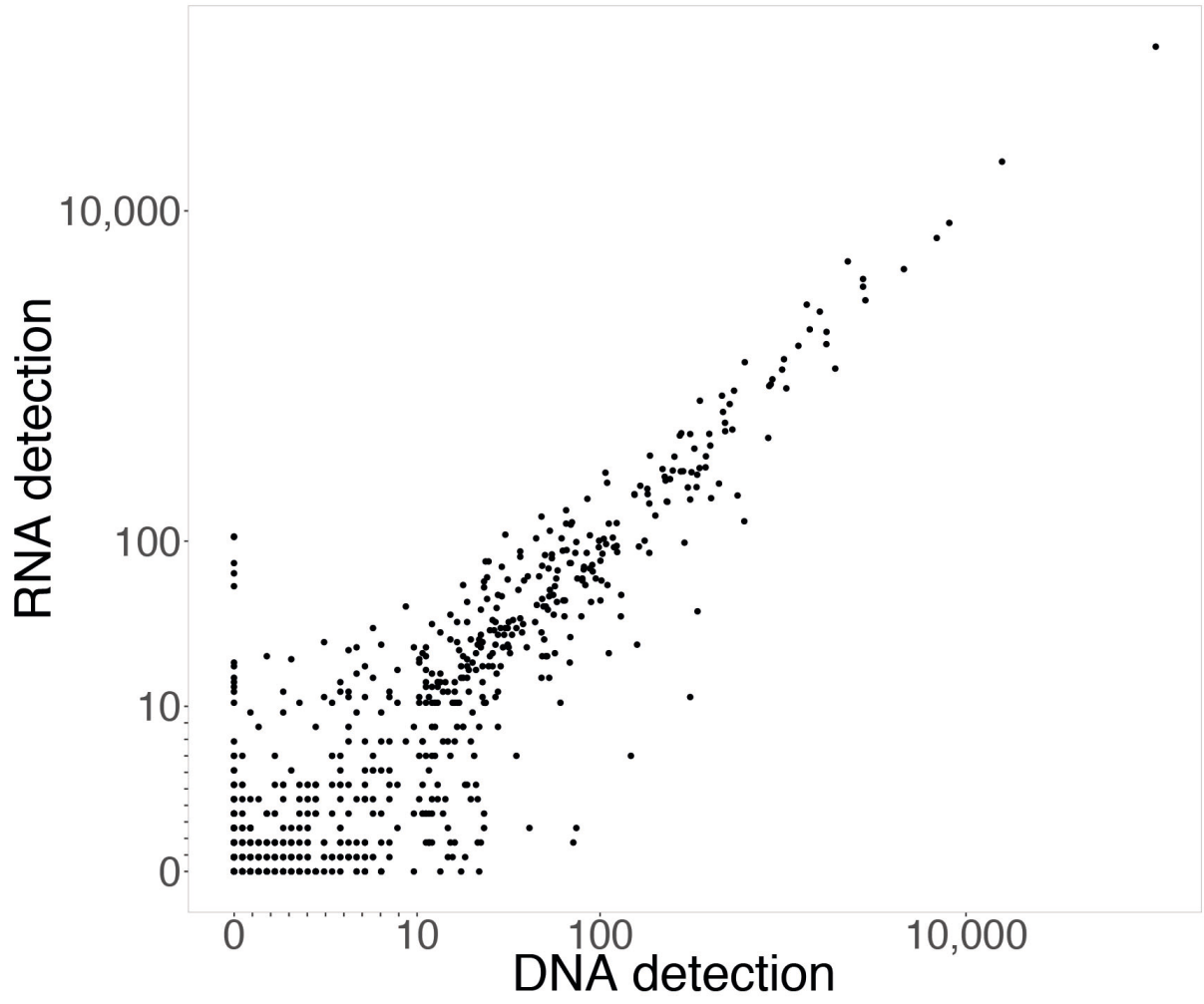
Supplementary Figure 1



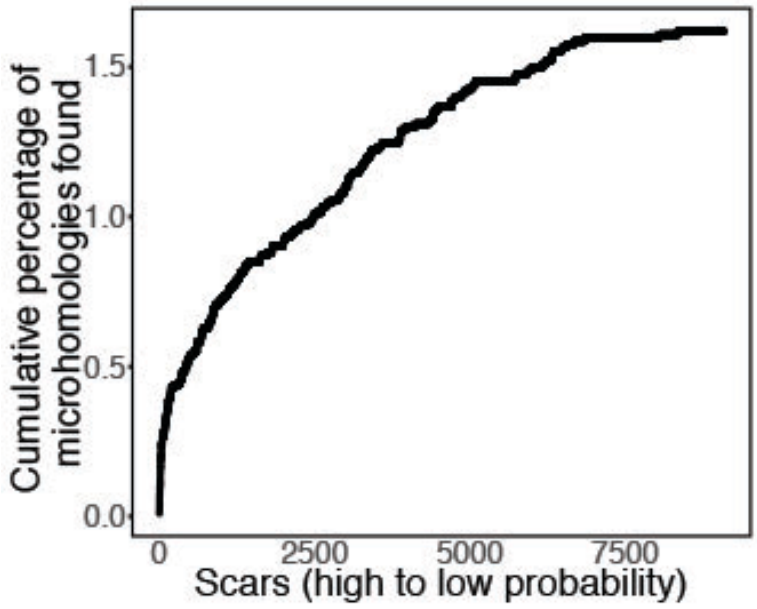
Supplementary Figure 1. Negative controls have over 99.6% wildtype GFP. Testing all combinations of Cas9 mRNA or protein injections and mRNA or DNA detection showed that no noticeable scars are created without the injection of sgRNA.

Supplementary Figure 2



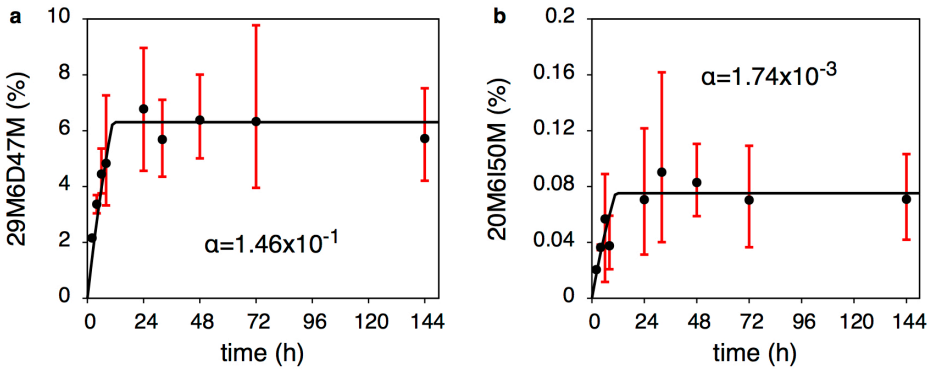
Supplementary Figure 2. Strong correlation between DNA and mRNA detection in the same embryo. Scar abundances in a 48 hpf embryo detected in DNA and mRNA have a Pearson correlation of 0.998.

Supplementary Figure 3



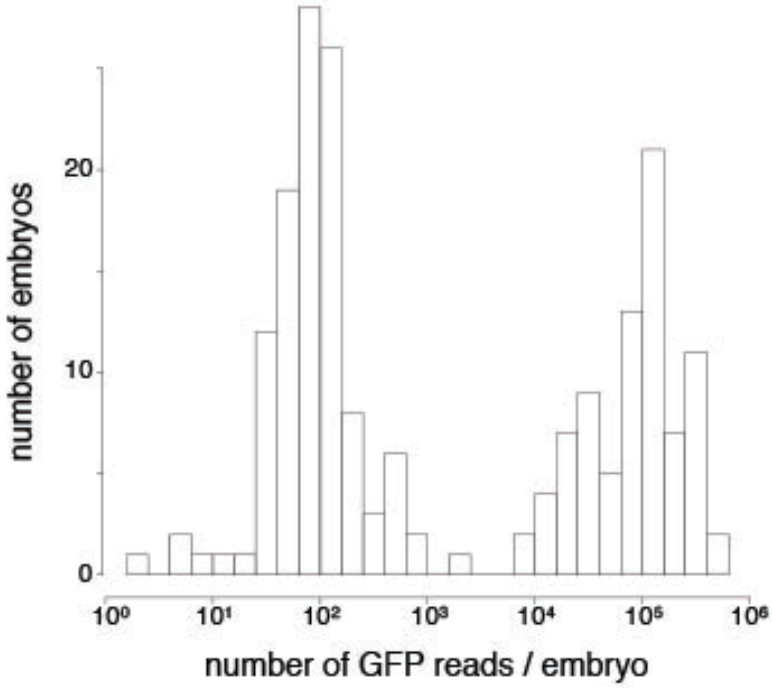
Supplementary Figure 3. The most probable scars are enriched in microhomologies. We sorted over 9000 scars by frequency of occurrence (x-axis), and we determined which percentage of scars exhibit a microhomology (y-axis, cumulative plot). For details on the calculation see Materials and Methods.

Supplementary Figure 4



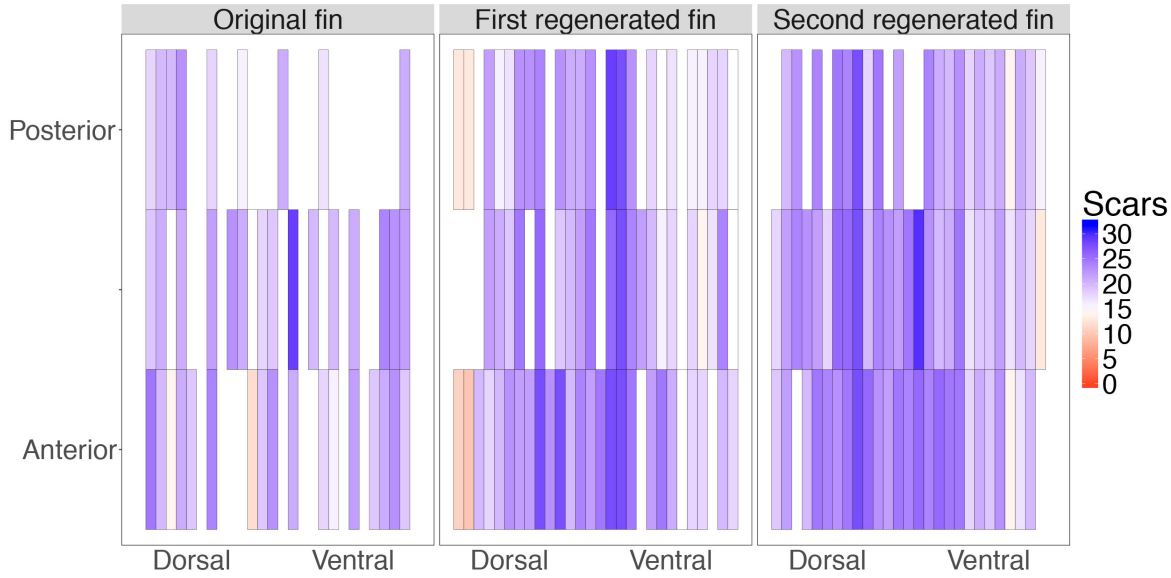
Supplementary Figure 4. Average fraction of two different scars as a function of time. Experimental determination (black dots and red error bars) and fit to equation S2 (solid black line). Error bars are 95% confidence intervals.

Supplementary Figure 5



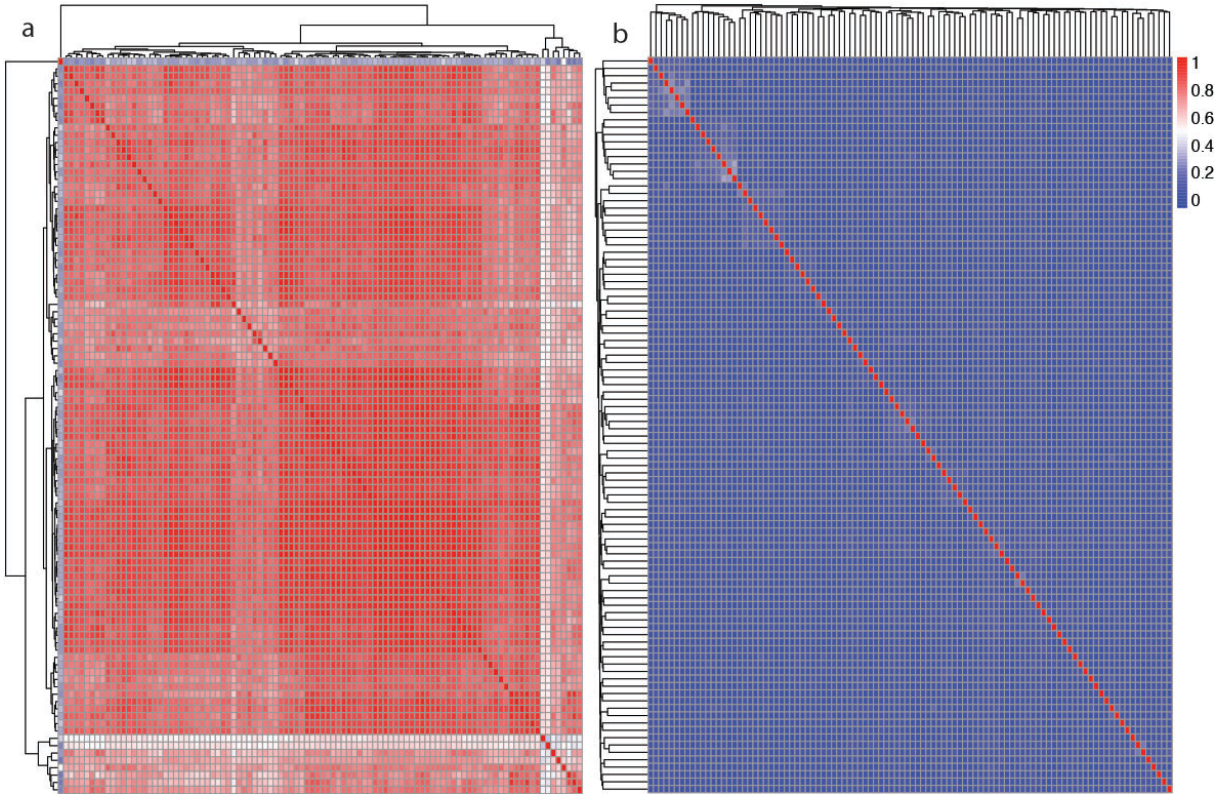
Supplementary Figure 5. Histogram of GFP reads in a collection of F1 embryos. Scarred heterozygote parent crossed with a wildtype parent. We detected a bimodal distribution, with approximately half of the embryos expressing GFP, as expected for a transgene that is integrated on one chromosome.

Supplementary Figure 6



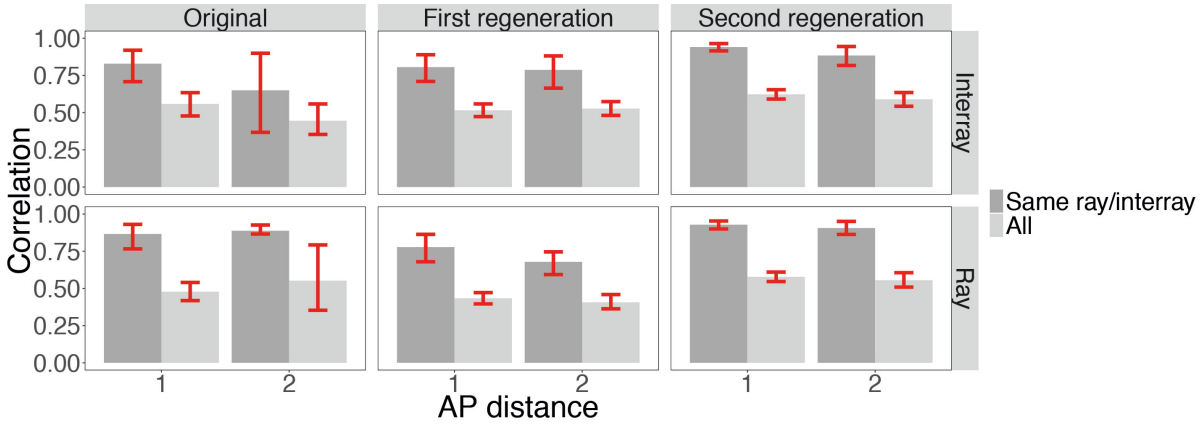
Supplementary Figure 6. Each fin piece has between 10 and 30 distinct scars. We count scars that generate at least 0.1% of all reads in a sample. Pieces that did not pass our data quality filter are shown as blank.

Supplementary Fig. 7



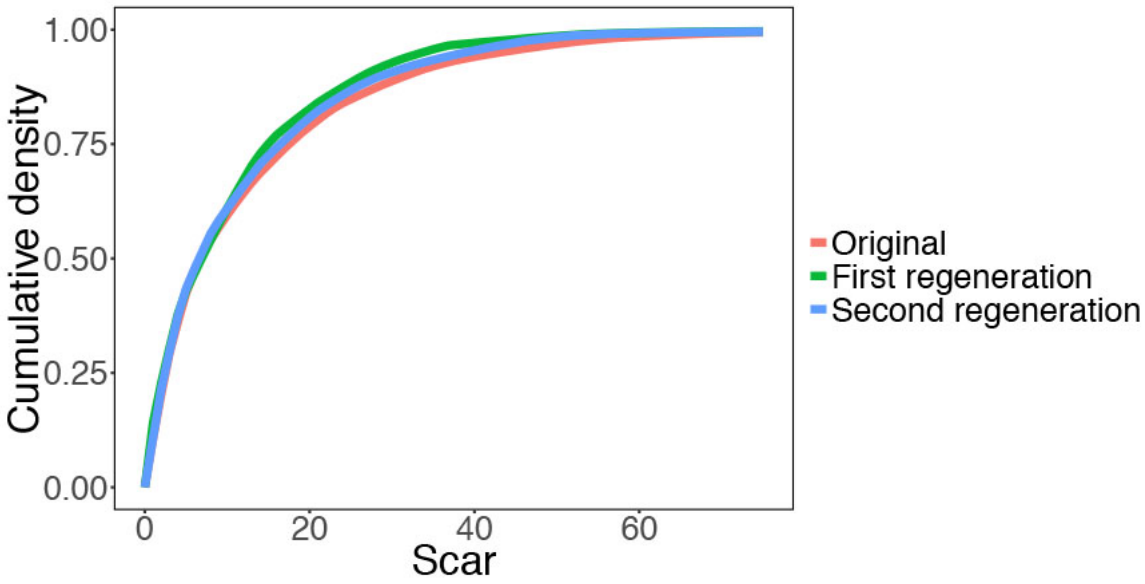
Supplementary Fig. 7. Pairwise Pearson correlations of scar abundance between different embryos from the dynamics data. (a) Without normalization, and (b) after normalization by scar probability**.** This strategy was successful in removing correlations between different embryos caused by repeated creation of the same scars (see also Materials and Methods).

Supplementary Figure 8



Supplementary Figure 8. In the original as well as the regenerated fins, we find a strong correlation within rays or interrays. Correlations of scar abundances between pieces taken at different AP distances within the same rays and interrays. Correlations across all rays/interrays are shown for comparison.

Supplementary Figure 9



Supplementary Figure 9. Cumulative distribution of the number of different scars in the original and two regenerated fins. The number of scars is reduced only mildly in the regenerated fins.

Supplementary Table 1. Scar zoology. Ten most prevalent single deletions, single insertions and complex scars. Probabilities are obtained from the fit to Equation S2.

	CIGAR	Sequence	Probability
Single deletions	29M6D47M	CATCGAGGACGGCAGCGTGCAGCTCGCCGACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$1.44 * 10^{-1}$
	26M3D50M	CGAGGACGGCAGCGTGCAGCTCGCCGACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$7.54 * 10^{-2}$
	27M11D49M	CACAACATCGAGGACGGCAGCGTGCAGCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$7.00 * 10^{-2}$
	31M18D45M	GATCCGCCACAACATCGAGGACGGCAGCGTGCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$6.50 * 10^{-2}$
	27M2D49M	GAGGACGGCAGCGTGCAGCTCGCCGACCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$3.65 * 10^{-2}$
	33M21D43M	CAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$2.78 * 10^{-2}$
	27M9D49M	CAACATCGAGGACGGCAGCGTGCAGCTCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$2.68 * 10^{-2}$
	30M10D46M	ACAACATCGAGGACGGCAGCGTGCAGCTCGCCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$2.66 * 10^{-2}$
	27M6D49M	CATCGAGGACGGCAGCGTGCAGCTCGCCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$2.65 * 10^{-2}$
	27M7D49M	ACATCGAGGACGGCAGCGTGCAGCTCGCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$9.67 * 10^{-3}$
Single insertions	25M1I50M	GACGGCAGCGTGCAGCTCGCCGACCAACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$2.45 * 10^{-2}$
	22M3I51M	CGGCAGCGTGCAGCTCGCCGACCAGCAGAACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$2.57 * 10^{-3}$
	25M1I50M	GACGGCAGCGTGCAGCTCGCCGACCTTGTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$2.20 * 10^{-3}$
	20M6I50M	CAGCGTGCAGCTCGCCGACCAGCAGAACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$1.82 * 10^{-3}$
	21M5I50M	GCAGCGTGCAGCTCGCCGACCAGCAGACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$1.67 * 10^{-3}$
	23M1I52M	GACGGCAGCGTGCAGCTCGCCGACCCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$9.75 * 10^{-4}$
	17M8I51M	GCGTGCAGCTCGCCGACCAGCAGAACACCACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$9.48 * 10^{-4}$
	26M1I49M	GACGGCAGCGTGCAGCTCGCCGACCAGCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$9.37 * 10^{-4}$
	16M4I56M	GGCAGCGTGCAGCTCGAACACCGCCCTCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$7.28 * 10^{-4}$
	20M4I52M	GGCAGCGTGCAGCTCGCCGAACACCCCCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$7.20 * 10^{-4}$
Complex scars	21M6I2M1D47M	GCAGCGTGCAGCTCGCCGACCAGCAGAACACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$2.17 * 10^{-3}$
	24M6D5M1D47M	ACATCGAGGACGGCAGCGTGCAGCAGAACACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$1.88 * 10^{-3}$
	24M4D2M2D50M	CATCGAGGACGGCAGCGTGCAGCTGAACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$1.44 * 10^{-3}$
	20M4I2M2D50M	ACGGCAGCGTGCAGCTCGCCAGCAGAACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$8.21 * 10^{-4}$
	23M3D7M2D46M	ATCGAGGACGGCAGCGTGCAGCTCGAACACCCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$7.91 * 10^{-4}$
	20M3D5M1I50M	GAGGACGGCAGCGTGCAGCTCTACCAACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$7.25 * 10^{-4}$
	28M1I1M12D46M	CACAACATCGAGGACGGCAGCGTGCAGCGTCCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$6.24 * 10^{-4}$
	25M4D4M3D47M	ACATCGAGGACGGCAGCGTGCAGCTGAACACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$5.79 * 10^{-4}$
	19M3I5M2D49M	GACGGCAGCGTGCAGCTCGTCCTCGTCCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$5.52 * 10^{-4}$
	27M4D5M5D44M	CAACATCGAGGACGGCAGCGTGCAGCTGACCATGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC	$5.49 * 10^{-4}$