

Figure S5

### HO-induced DSB

**CAAATTTGGAATCG**CTTTAGTTTCAGCTTCCGC**AACA**      GTATAATTAAACCTG**ATTGGAATCGCATA**  
**GTTTAAACCTTAGC**GAAAATCAAAGTCGAAAGGCG      **TTGT**CATATTAAAATATTGGGAC**TAAACCTTAGCGTAT**  
*ILV1prm*    overhang

coded name	joint type	joint sequence
D+0_M4_L0_R0	precise	<pre>         TTTTAGTTTCAGCTTCCGC<b>AACA</b>GTATAATTAAACCTG         AAAATCAAAGTCGAAAGGCG<b>TGT</b>CATATTAAAATATTGGGAC         ...         microhomology       </pre>
D-4_M0_L4_R4	resected blunt	<pre>         TTTTAGTTTCAGCTTCCGC<b>AACA</b>GTATAATTAAACCTG         AAAATCAAAGTCGAAAGGCG<b>TGT</b>CATATTAAAATATTGGGAC         → ←       </pre>
D+2_M1_L0_R1	+CA	<pre>         TTTTAGTTTCAGCTTCCGC<b>AACA</b><b>CA</b>GTATAATTAAACCTG         AAAATCAAAGTCGAAAGGCG<b>TG</b><b>TGT</b>CATATTAAAATATTGGGAC         ...       </pre>
D-3_M2_L3_R2	-ACA	<pre>         TTTTAGTTTCAGCTTCCGC<b>AG</b>TATAATTAAACCTG         AAAATCAAAGTCGAAAGGCG<b>GT</b>CATATTAAAATATTGGGAC         ...       </pre>
D+4_M0_L0_R0	fill-in blunt	<pre>         TTTTAGTTTCAGCTTCCGC<b>AACA</b><b>AAC</b>GTATAATTAAACCTG         AAAATCAAAGTCGAAAGGCG<b>TTGT</b><b>TTGT</b>CATATTAAAATATTGGGAC       </pre>
D+6_M0_L0_R0_I(AC)	fill-in plus	<pre>         TTTTAGTTTCAGCTTCCGC<b>AACA</b><b>ACA</b><b>AAC</b>GTATAATTAAACCTG         AAAATCAAAGTCGAAAGGCG<b>TG</b><b>TG</b><b>TG</b>CATATTAAAATATTGGGAC       </pre>

**D**= delta, the number of bases lost/gained

**M**= the number of bases of microhomology

**L**= the number of bases deleted on the left overhang

**R**= the number of bases deleted on the right overhang

**I**= insertional nucleotides