|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Target** | **Description** | **Figure** | **Sequence of repair template (5’ to 3’)** | **Relatedguide** | **Repair ID** |
| *Cbr ben-1* | *Cbr* co-injection marker |  | GGGAAGTGATTTCCGACGAGCACGGAATTCAACCTGATGGAACCTACATATGGTGGAGAGAGTGACTTGCAGCTCGAGCGCATCAATGTCTACTACAACG | crispr\_bf39 | BF-2036 |
| *Cbr rex-4* | *Cbr rex-4* MEX (-13.8) scrambled | Figure 9, Figure 9—Figure supplement 1 | GGCCAATTGGCATGGGCTGCCTGCTAACCTTTCCCTGCCTACGCATATTTGATAAGTGATGACTGCGCGGACAAAAGAGGGAAACTAGTGGCCTGCTACCCGAGAAAGAGAGA | crispr\_bf77 | BF-2470 |
| *Cbr rex-4* | *Cbr rex-4* MEX II (-19.09) scrambled | Figure 9, Figure 9—Figure supplement 1 | GCATTCCTCAACCCGCAAAGAGAAGTCAATCGCGCAGATATTGTAATTGTTGCTGCTGCAGTCACTGTGCTCGCTCTGACTGCCTGCTAACCTTTCCCTGCCTACGCATATTTTATATGAACAGGGTGCG | crispr\_bf80 | QY070t |
| *Cbr rex-4* | *Cbr rex-4* MEX II (-19.09) scrambled and MEX (-13.8) scrambled  | Figure 9, Figure 9—Figure supplement 1 | GCATTCCTCAACCCGCAAAGAGAAGTCAATCGCGCAGATATTGTAATTGTTGCTGCTGCAGTCACTGTGCTCGCTCTGACTGCCTGCTAACCTTTCCCTGCCTACGCATATTTGATAAGTGATGACTGCG | crispr\_bf80 | QY071t |
| *Cbr rex-7* | *Cbr rex-7* MEX (-18.72) scrambled | Figure 11, Figure 11—Figure supplement 1 | CGTCCTGTTCATTGCAATAAACTGGTGGGAGTTTTTCCAATCTGAGATTTGTGAGCAGTAGTGACAACAGTGATTTAATTTTATGTTCATGAAGTTTTCAGGTTTTTTGCAT | crispr\_bf79 | BF-2472 |
| *Cbr rex-7* | *Cbr rex-7* MEX (-12.26) scrambled, andMEX (-12.58) scrambled | Figure 11, Figure 11—Figure supplement 1 | TCAGGTTTTTTGCATAAAATGCACAATATTCTGAGAAATGTTGTCTTAATCTCGCGTCGTCGTGTTCTCTTCGCACGCAATTTAAGAGTCAGTGTCAGAGGAGAAGACAAATTTGAGGGACCTCTTCTCTTATTTTTTTTTCGCAAAGT | crQY011,crQY015 | QY087t |
| *Cbr rex-3* | *Cbr rex-3* MEX II (-20.04) scrambled | Figure 10, Figure 10—Figure supplement 1 | GCAAAGTCAACATGTGTATTTTCCGTGAAAGGACATATGCAAAGGGGTGTCTGTCGAGCTCGCTGTGCTGACGAGAGCAGCTCATAGAGCGTAAATGGGCATTGCCCTCCGCGCAGATACGCGCGTTAAGCCATACCACACATATAACC | crQY013 | QY154t |
| *Cbr rex-3* | *Cbr rex-3* MEX II (-12.36) scrambled | Figure 10, Figure 10—Figure supplement 1 | TTGATCACACAGTCTTCTTGATGTGCAAGCTAGCTATTTCGAGTAGTTGGAAAATCAAAATTCTATAGTAATACTGTGATAATCATACATCTGTATAGCTACGATGATTTTGAGGAAATGTTTAATAGAAACGTGAAAAAAAGAAATAT | crQY014 | QY155t |

| **Target** | **Description** | **Figure** | **Sequence of repair template (5’ to 3’)** | **Relatedguide** | **Repair ID** |
| --- | --- | --- | --- | --- | --- |
| *Cel dpy-10* | *Cel* co-injection marker |  | CACTTGAACTTCAATACGGCAAGATGAGAATGACTGGAAACCGTACCGCATGCGGTGCCTATGGTAGCGGAGCTTCACATGGCTTCAGACCAACAGCCTAT | crispr\_bf32 | BF-1813 |
| *Cel rex-33* | 3 *Cel* MEX motifs replaced by *Cbr* MEX motifs in *Cel rex-33* | Figure 12, Figure 13 | CGTTCAAACAGTCTTTCCTGCAAGCACAGACACTCAAACGTGAGTAATTATTATATGGGCAGGGACACCCAATCGATTGCCCATTTACGAATGCGGCAGGGGGTCACCATAGATAGTAATTGGGAAGGGAAGATTTACCGCCTTTCGCTTATTTAGTAGGGCACGCAAATTAGTATGCTT | crQY016 | QY199t |
| *Cel rex-33* | 3 *Cel* MEX motifs scrambled | Figure 12, Figure 13 | CGTTCAAACAGTCTTTCCTGCAAGCACAGACACTCAAACGTGAGTAATTATTTTAGTCGACGTGACACCCAATCGATTGCCCATTTACATTGCGCTCGAGCGCTCACCATAGATAGGTATGACGCGACGCTGATTTACCGCCTTTCGCTTATTTAGTAGGGCACGCAAATTAGTATGCTT | crQY016 | QY214t |
| *Cel rex-33* | 3 *Cel* MEX motifs with C4G substitution | Figure 13 | CGTTCAAACAGTCTTTCCTGCAAGCACAGACACTCAAACGTGAGTAATTATTTTAAGGGAAGGGACACCCAATCGATTGCCCATTTACATTTGGGGCAGGGGGTCACCATAGATAGGTATCGGGCAGGGAAGATTTACCGCCTTTCGCTTATTTAGTAGGGCACGCAAATTAGTATGCTT | crQY016 | QY245t |
| *Cel rex-33* | 3 *Cel* MEX motifs replaced by *Cbr* MEX motifs with G7C substitution | Figure 13 | CGTTCAAACAGTCTTTCCTGCAAGCACAGACACTCAAACGTGAGTAATTATTATATGCGCAGGGACACCCAATCGATTGCCCATTTACGAATGCCGCAGGGGGTCACCATAGATAGTAATTGCGAAGGGAAGATTTACCGCCTTTCGCTTATTTAGTAGGGCACGCAAATTAGTATGCTT | crQY016 | QY244t |
| *Cel rex-39* | 2 *Cel* MEX II motifs replaced by *Cbr* MEX II motifs in *Cel rex-39* | Figure 12 | TTTCATAACACAACAAGACCGAATAAATATAACACTTATTCCTCCTGCCTACTTCCACAACGCGCGAAGTAACAAGTAACTACTTCGCGCGTTGTGGAAGTAGGCAGGAGGATTTTCAAGAAACATGTGCATGAGTGCATTTCAAAATTC | crQY017 | QY208t |
| *Cel* Xsite 2 | *Cel* X site 2 insertion of *Cbr rex-2* | Figure 5 | GAACATGTCGAACACGTACATGACGACTGCTTAAAAGTTGAAAATTTCCCATATCCGTTTCTCATTTTATGTAGTCTCTTTCAGTAATCGTATTCAGCACGTTCGAAAGTACCTTTGTACAAATTTTGAGCTAATTCTCAACGCCCCTCTGAAAACACTTCCCTTGTGAGTTTGAACGGTTTCAGTACAACCATATGGTCAGGGGAACTAAAAAACTAGAAATTCATTACTCGAACATACTGTAGTTATCCCACCATCGCAAATTTGATCGAGTCAACCTCTGCGAAAACGCAAAATAGAAAGGACCACCACACACAAAACGCCCACGTAAACACTGCCCCCTTCCGAGATAAAACATTGAGTGATAACTCTCCTTTTCCGTTTTTCTGAGCGTTTCGCATTTTGGCACGGATCAGTTTCTAATCCACAACTTTAAAAAAATCAAAAATTTTCTTCGAAATTCGAAAGAAAATAAGGAGATTTTTTGACAAGTGAAAAATGAACTCATTCAGTAAGAACGCATATTGTTTCTCAATATTTCTTTTCTATCGTGAAAACGCT TCAACAATCGTTACAAAACTTCATTGGCTACTAACGATTTTGCAATTTTACATTATACTTTGTTTGTGAGTTTCAGGAAACTTGTGAATTCGTTCAAACCCTTCAGAATCAG | CS568 | ER567 |
| *Cel* Xsite 2 | *Cel* X site 2 insertion of *Cel rex-32* | Figure 5 | GTCGAACACGTACATGACGACTGCTTAAAAGTTGAAAATTTCCCATATCCGTTTCTCATTTTATGTAGTCTCTTTCAGGAGACAAAAAGGAAAAAATGAAATTGGACAACCCCATAAATTTCATGAATTTTTAAAACTTCTTGCAGGAATATAAATTACTCTAATTAAAGTTTTTTTGTTTGAAAATTTTTTGATAGGCCCAAATACATACTTATCTCTAAAAAAATTACTTTTGAATTCGTTCATTCAATGTGTAAAATCTAAACAAAAGTGACCCCCCTTGTCCAAATATTTTATCCACGAGACTAGGTACACCTCCCTTCGCGATAAATAATTGGTACATCATTTTATCCACAGGGCTACTTCCTCCCTGCGCGATAAATTTAAAATTTTATAACTCTTTGGGTAACTAATTTTGGCAATATTTTCTTATTTTTTCACATCAACAAAAATATTTCAAGTCTAAAAGTTGCAATAAATGCAGTTCAGAGGAAAATTGAGTCGTGTGCGAATAACGAGGAAAAAGACAGACCCATACTTCCTCCCTGCGCGATACGATCTCTATCGACTTTTCTGGTTTTATTGTTTGGCAATGTTTATTAAATTACTCCAAAGATCAAGAAAACAATTATGAAAATTCGAGGAGGTGTAAAATAGAAAATGTTGCAGTTGTGGCTACTAACGATTTTGCAATTTTACATTATACTTTGTTTGTGAGTTTCAGGAAACTTGTGAATTCGTTCAAACCC | CS568 | ER577 |
| *Cel* X site 2 | *Cel* X site 2 insertion of *Cbr rex-9* | Figure 5 | GTCGAACACGTACATGACGACTGCTTAAAAGTTGAAAATTTCCCATATCCGTTTCTCATTTTATGTAGTCTCTTTCAGGCAAATTTGAGCTTTCACCTTGATCTCAATTGTACATAATATTTCATGACATTTTTTGTATAAATGTGTTTTCTCATCACTCGATTTTCTTCTGCCAAAAAATAGAGCACTCCATTCCAAAAATAGTATGTCTACGACATTCTCCGCTAATTGTAGTCTTCTGAACACCTCCTTTCGCATGTAAGACGCTGATGGATATAAGATACGAACAGGGTGCAAGGACCCGCGCACGTGCCTTGAATAGACGCTGTTAAAAAGGGCAGACGGCCAGATGGAAGACGTTTCGGAGACAGCGAGGCGGACGAAACGAGTATGTGAGGCCCATTACAACGTCTAATCCATTGGAGGAGAGAGGTTTGCAAAGGGGTGACTGGGGCGACCAGCATTTTTATGTTTGATGGATGTGACCGGGAAAATGACGGGTTGTCATCAGTGCAAGGTGACACAAAAAAACCGACAGTAGAATGGTAGTTTTTTTTTGCAATTTAAACGTTATCCATCATATTACGGTAGTGGAGGAGTAGTGACACCGCTAAATGCATCTGATAAGTTTTATCAGGGTAGTCAAGATGATTTTTGCAACAAATTTTGAACTGTACTTTGTGGCTACTAACGATTTTGCAATTTTACATTATACTTTGTTTGTGAGTTTCAGGAAACTTGTGAATTCG | CS568 | ER581 |
| *Cel X site 2* | *Cel* X site 2 insertion of *Cbr rex-7* | Figure 5 | GTCGAACACGTACATGACGACTGCTTAAAAGTTGAAAATTTCCCATATCCGTTTCTCATTTTATGTAGTCTCTTTCAGGTCAGTTGATCACTTTCTGATAATTCTTACATGAACCAAAACAAATTTGCTTGAAATTGAAAGTTGAACTGCTCATTTCATTAGAGTGTTTACGCTATTTTTCGAAAATTTGTTTAAAAGTATACT | CS568 | ER586 |
|  |  |  | TGAAACGTAGCAAAAAGCTTACTGAAAGAAAACGGAAATGTTTCATTTTAATTGATTTTGTCCGGTGTTTTTGTTAAATCAGCTTTATCGTTTCCTGAAATTTTCGAGATTTGCCCGACCGTCCTGTTCATTGCAATAAACTGGTGGGAGTTTTTCCAATCTGAGATTTTATATGGGCAGGGACAACAGTGATTTAATTTTATGTTCATGAAGTTTTCAGGTTTTTTGCATAAAATGCACAATATTCTGAGAAATGTTGTCTTAATCCCCTGCCGCATTCTTCTCTTCGCACGCAATTTAAGTAATTGGGAAGGGGGAGAAGACAAATTTGAGGGACCTCTTCTCTTATTTTTTTTTCGCAAAGTAGCAGCAATGAATTTTGCGATAAAAAGGATTCTACAAGTCGTTTTCTATTTTCCTTCCTTTTCCAGTGGAAACTCTTCAAACAGACCAAATATTTTGCACTCTGTTGTCATGTGGCTACTAACGATTTTGCAATTTTACATTATACTTTGTTTGTGAGTTTCAGGAAACTTGTGAATTCGTTCAAACCC |  |  |
| *Cel X site 2* | *Cel* X site 2 insertion of *Cbr rex-4* | Figure 5 | GTCGAACACGTACATGACGACTGCTTAAAAGTTGAAAATTTCCCATATCCGTTTCTCATTTTATGTAGTCTCTTTCAGGTATGAAATTTGAAGTGTTTGAATATATACTCTCTGCACTCCGACTATTTTACAGTGCGACTGGCAAATCTCACTGAATGAGTAAGGTCAACTGACAATCAACAAAGATATAATTCCAAAGTTTTCTCATTTCTTGAATATAAGTATTTGATGTTTGAAAAAATCGGCATTTCTTGCAAATGTACTGAATGAATTGTAATCTTGGTCAGACATCGTATGGCATTCCTCAACCCGCAAAGAGAAGTCAATCGCGCAGATATTGTAATTGTTCTCTGCGCGTATGGCCAATTGGCATGGGCTGCCTGCTAACCTTTCCCTGCCTACGCATATTTTATATGAACAGGGTGCGCGGACAAAAGAGGGAAACTAGTGGCCTGCTACCCGAGAAAGAGAGAAATGCAACGTTTAATAAACCGATGACGAGCAGGCAACGTGCCCCTTCCGATTTGAATGGCGTTTCAAAATCAGAGTCAGACTTTCTGCGAAGATAGTTTTTGTAAGCGCTTCGAGGGCAATGGAATCCTAAAATGATCAATTTTAATGAAATCGGGATGTAATGTAGGTAGAAATCTAGATCTACGTAGAACCAGGAACTATGTTCTGTGGCTACTAACGATTTTGCAATTTTACATTATACTTTGTTTGTGAGTTTCAGGAAACTTGTGAATTCG | CS568 | ER587 |
| *Cel X site 2* | *Cel* X site 2 insertion of *Cbr rex-5* | Figure 5 | GTCGAACACGTACATGACGACTGCTTAAAAGTTGAAAATTTCCCATATCCGTTTCTCATTTTATGTAGTCTCTTTCAGGTAGTTTTTCGAAAGAACCGCCCAAATTTTGAACTAGACTTGAAAATATTTTCGCGCGTTTAAAAACTTCATTTACTCAGAGTTACATCTTTCAACTTTACGAAGAAAGCATATGAAAGCGTTTTCACGTCTCGTTTCTCTAAATCTCCATTTCCATTTTTGATCCTTTCTCGTGCGGATTTTCTCAACGCCCAAAGAAGTGAAAAATATTTCTTTGAAAAAGAAAAATAGACATTGACGGAGGACAATTATTTTAGAGAAAAACCAACTAACTCTACGAAAAGGTTATATAGGCAAGCATATCAAAAATCAGATTTACATCAAAATTGCAGAACAAAAGCAGAGAAAATCTGGTTCAACGGGATGCCAAGAATTTTCTCTATGTGGGTTTTCAGTTTCTTAAAAGGGATCAACTTCAAATATTATAGAAACCATTTGAGCTTTTAACTTTTCCATAATTGGTCATTGAAAGTTTGCTTGATTATTAAAAATCAAAAACCAAATGACTTTCTTGTACGGCTTTCATTCCGTCAG AACCCTAATGAAAATATAGAATTTATAAAAGTACATTTATTAGGTTGGAAGAAAAGTAACTGTCCACTGTGGCTACTAACGATTTTGCAATTTTACATTATACTTTGTTTGTGAGTTTCAGGAAACTTGTGAATTCG | CS568 | ER588 |