|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table S1. Genome engineering of cohesin variant mESCs** | | | | | | | | |  |
|  |  | |  | | | | | |  |
| Genotype | Type of edit | sgRNAs delivered (5' to 3') | | Repair templates delivered (5' to 3') | Number of potential off-target locations with: | | |
| 1 mismatch | 2 mismatches | 3 mismatches |
| *Stag1-/- cl1* | In-frame indel | TATATTGACACTGTCGAATC | | none | 0 | 0 | 4 |
| AGGCATACAAGTACCCTTGC | | 0 | 0 | 8 |
| *Stag1-/- cl2* | Frameshift indel | TATATTGACACTGTCGAATC | | 0 | 0 | 4 |
| AGGCATACAAGTACCCTTGC | | 0 | 0 | 8 |
| *Stag2-/- cl1* | Frameshift indel | ACTGTCATTTCACTTCTTAC | | ATACAGTATCATATATGATGAGTACATGATGGATACTGTCATTTTACTTTTGACTGGATTGTCTGACTCCCAAGTCAGAGCATTTCGAC | 0 | 2 | 12 |
|  | | |
| *Stag2-/- cl2* | Frameshift indel | GATTACCCACTTACCATGGC | | CTGTATGTACATTTTTATTTTAGGATAGTGGGGATTACCCACTTGGAGTGTTTGTACATAGATACAGATAAGGCAAGACAGATTCCTTT | 0 | 1 | 5 |  | | |
| GAGTGTTTGTACATAGATAC | | 0 | 0 | 17 |  | | |
| *Stag2V181M* | Valine to Methionine substitution | AGTTCATTGGTGTGTTAGTA | | CTCAGTGGAAGAAGTTCAAGTCCAGCTTCTGTGAGTTCATTGGTATGTTAGTACGACAGTGTCAATACAGTATCATATATGATGAGTAC | 0 | 0 | 14 |  | | |
| *Stag2S202L cl1* | Serine to Leucine substitution | ACTGTCATTTCACTTCTTAC | | ATACAGTATCATATATGATGAGTACATGATGGATACTGTCATTTTACTTTTGACTGGATTGTCTGACTCCCAAGTCAGAGCATTTCGAC | 0 | 2 | 12 |  | | |
|  | | |
| *Stag2S202L cl2* |  | | |
|  | | |
| *Stag2∆164-196 cl1* | In-frame indel | GATTACCCACTTACCATGGC | | CTGTATGTACATTTTTATTTTAGGATAGTGGGGATTACCCACTTGGAGTGTTTGTACATAGATACAGATAAGGCAAGACAGATTCCTTT GTACATTTTTATTTTAGGATAGTGGGGATTACCCACTTACCATGTACAGGTAAGACAAGACAGATTCCTTTAAAGTGGTTGAGACAGAC | 0 | 1 | 5 |  | | |
|  | | |
| *Stag2∆164-196 cl2* | GAGTGTTTGTACATAGATAC | | 0 | 0 | 17 |  | | |
| CCCACTTACCATTACAGGTA | | 0 | 0 | 5 |  | | |
| *Smc1aR96H cl1* | Arginine to Histidine substitution | ACCTACAATGACTCGGGCAA | | GGTCTACTCGGAGGAGGGTGCTGAGGACCGTACATTTGCCCACGTCATTGTAGGTGAGTGAGGCTCAGAAGGCTCGAGGGGTCCAATGA | 0 | 0 | 3 |  | | |
|  | | |
| *Smc1aR96H cl2* |  | | |
|  | | |
| *Smc1aR586W cl1* | Arginine to Tryptohan substitution | AGAAACTCCGGGAGCTGAAG | | AAGATTCTTCACACACAGGTGAAACCTACTGATGAGAAACTCTGGGAGCTGAAGGGCGCCAAGCTAGTGATTGATGTAATTCGTTAT | 0 | 1 | 60 |  | | |
|  | | |
| *Smc1aR586W cl2* |  | | |
|  | | |
| *Smc1aR711W cl1* | Arginine to Tryptohan substitution | TCAGCCGCATTTGAAGCCCG | | GAACTGCGTCAAGTGCAGTCTCAGGCACACGGGCTTCAAATGTGGCTGAAGTACTCACAGAGTGACCTAGAACAGACTAAGACAAGG | 0 | 0 | 3 |  | | |
|  | | |
| *Smc1aR711W cl2* |  | | |
|  | | |
| *Smc1aR816G cl1* | Arginine to Glycine substitution | GAGAATCAGAAGACTCGCTT | | TTCCCCTTTCGTTCTGCAGCTTGGAATTTGAGAATCAGAAGACTGGCCTGGGCATCCAATTGGATTTTGAAAAGAATCAGTTGAAGGAG | 0 | 0 | 9 |  | | |
|  | | |
| *Smc1aR816G cl2* |  | | |
|  | | |