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| **CRITERIA TO REPORT ON FOR ALL RESEARCH ANIMALS** | | | |
| **Genetic background** | **Genetic background description including Strain/breed/stock type** | Official name of species, strain, and sub-strain, as applicable, of the animal. Alternatively, for farm animals, indicate breed https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi Describe type of breeding for strain/stock/breed using species standard wording.  For example, in rodent: outbred, inbred, hybrid, congenic, documented mixed or non-documented genetic background. For example, in zebrafish: specify which wildtype background (AB, TU, TL); if mixed background, provide a clear explanation of the breeding scheme and estimation of percentage of each background. | **🞎** |
| **Breeding scheme and stability program (only relevant for rodents)** | Specify breeding schemes used to maintain stock and generate experimental animals. Include the genotype of the parents when possible. This is particularly important to trace the origin of sex chromosomes in congenic strains.  *Specify breeding strategy to maintain genetic quality of the colony; indicate known family tree.* | **🞎** |
| **Source of animals** | Name origin of strain(s). Name supplier or repository or other origin of animals used in the experiment. | **🞎** |
| **International nomenclature** | Name strain according to internationally agreed standard when available. *Use research resource identifier (RRID) when applicable.* | **🞎** |
| **Strain or stock identifier** | Show unique identifier of strain or stock used by the supplier or the repository. | **🞎** |
| **Genetic background validation** | Indicate if, when (at what breeding generation) and how the genetic background was verified (i.e., sequencing, SNP (single-nucleotide polymorphism) panel, STR panel, genetic testing chip panel). | **🞎** |
| **ADDITIONAL CRITERIA TO REPORT ON FOR ANIMALS WITH GENETIC ALTERATION** | | | |
|  | **Name of mutant allele** | Detail the shorthand used in article, and official nomenclature. Use unique identifier (e.g. MGI ID) when applicable. | **🞎** |
|  | **Allele type** | Specify the method of model creation: naturally occurring allele/gene targeting/genome editing/additive transgenesis/chemical or physical mutagenesis/viral insertion/site-specific recombination/transposition. | **🞎** |
|  | **Intended and observed consequence of mutagenesis** | *Detail whether allele is a frameshift, deletion, coding or non-coding variant, overexpression, conditional allele, humanization, reporter, structural variation. Detail new gene product if known.* | **🞎** |
| **Genetic alteration** | **Model summary description** | Provide a short summary of genetic modification and background used for establishing genetic alteration. | **🞎** |
|  | **DNA sequence** | Provide access to the sequence of the genetic modification: targeting vector, donor template or vector for transgenesis. If employed in the mutagenesis process, provide the sequence of donor (e.g., targeting vector, oligodeoxynucleotide, transgene or template sequence used for mutagenesis; DNA or prime editing guide). *Annotate genomic sequences with corresponding genome assembly version and coordinates. Use universal format; i.e., .fasta or .gb. Annotate features.* | **🞎** |
|  | **Allele schematic** | Consider presenting a map of the genetic modification. | **🞎** |
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|  | **Material availability/source of materials** | Describe how to access available materials (plasmids, mutant cells, animals and/or germplasm).  *RRID and/or repository identifier.* | **🞎** |
|  | **Obvious phenotype and welfare concern** | Specify salient phenotypes, such as issues with viability and/or fertility, or immunodeficiency. Describe the severity of the associated phenotype. If necessary, include any requirement to mitigate welfare concerns. Include publication, archive or database reference if available.  *For mice, consider SHIRPA (SmithKline Beecham/Harwell/Imperial College/Royal London Hospital/phenotype assessment) description.* | **🞎** |
|  | **Initial reference** | Detail whether report is the initial description of mutant and/or mention initial publication of materials. | **🞎** |
| **Genetic alteration** | **Genotyping assay** | Describe assay and sequence of primers used for genotyping of established colony. | **🞎** |
|  | **Enzyme and other reagents used for genome engineering** | Describe enzymes (nuclease, recombinase) if used to generate mutation including number and sequence of guide(s) for ribonucleoproteins if relevant. Detail reagents. | **🞎** |
|  | **Validation of allele sequence** | *If done, describe how the region of interest was validated.* | **🞎** |
|  | **Validation of allele structure** | *If done, describe the precise method used for validation of chromosomal or allele structure, and the outcome.* | **🞎** |
|  | **Validation to exclude additional integration of mobilized sequence** | *If done, describe the method and outcome of analyzing the material for additional integrations of donor templates45 or reintegration of deleted segments.* | **🞎** |
|  | **Evaluation of potential off-target activity** | *Genome editing off-target is defined as a genomic position and/or nucleic acid sequence distinct from the target. If done, describe the method, selection criteria and outcome of off-target analysis.* | **🞎** |