

CURRICULUM VITAE**Stephen A. Murray, Ph.D.****HOME ADDRESS**

18 Hancock Street
 Bar Harbor, ME 04609
 Office Phone: (207) 288-6857
 Mobile: (207) 801-8411
 Work Email: steve.murray@jax.org
 Home Email: stevemurray7956@gmail.com

EDUCATION

Carleton College, Northfield, MN	B.A.	1989-1993	Biology
Boston University School of Medicine	Ph.D.	1996-2002	Biochemistry (Z-X. Xiao, advisor)
The Jackson Laboratory, Bar Harbor, ME	postdoc	2002-2006	Development (T. Gridley, advisor)

POSITIONS AND APPOINTMENTS

1994-1996	Research Assistant Boston University School of Medicine
2007-2008	Associate Research Scientist The Jackson Laboratory
2008-2014	Research Scientist The Jackson Laboratory
2014-2017	Senior Research Scientist The Jackson Laboratory
2017-present	Associate Professor The Jackson Laboratory
2021-present	Research Associate Professor of Medicine Tufts University School of Medicine
2021-present	Member, Genetics Graduate Program Tufts University School of Medicine

FELLOWSHIPS AND AWARDS

1996-2001	NIH graduate training Fellowship, Boston University of Medicine
2002-2004	Institutional NRSA Postdoctoral fellowship (HD07065) in developmental genetics
2004	Awarded individual NRSA from NIH/NICHHD (declined)
2004-2006	Individual Postdoctoral Fellowship (PF-04-245-010DDC) from the American Cancer Society
2005	Awarded the Renee G. Adelman Cancer Research Fund
2006	Fellowship from the American Cancer Society Midwest Division - Ann's Hope Foundation

PROFESSIONAL ACTIVITIES

The overall goal of this project is to develop genome editing IND-enabling therapeutic strategies, including base and prime editing, for important neurological diseases including Spinal Muscle Atrophy, Friedreich's Ataxia, Huntington's Disease, and Rett Syndrome.

Role: Co-investigator; Lead of Preclinical Mouse Model Core

UM1 OD023222-01 (Braun, **Murray**, White) 7/1/2022 - 6/30/2027 3.00 Calendar
NIH/NHGRI

The Jackson Laboratory Knockout Mouse Production and Phenotyping Project (JAX KOMP2) The Knockout Mouse Phenotyping Program (KOMP2) seeks to create an encyclopedia of gene function for the ~20,000 genes in the mouse and to ultimately create a resource for understanding gene function in humans. The Jackson Laboratory (JAX) KOMP2 Phase 3 Center will contribute to this goal by efficiently generating and characterizing knockout lines and sharing functional data for 600 mouse genes.

Role: Principal Investigator

1 U54 OD030187-02 (**Murray**, Lutz) 9/1/2020 – 8/31/2025 1.80 Calendar
NIH/ORIP

The Jackson Laboratory Center for Precision Genetics

The overarching goal of the JAX Center for Precision Genetics (JCPG) is to integrate the core systems and platforms in place at JAX to create a seamless pipeline to support the model development needs of the clinical genetics community and to advance the development of therapeutic strategies for human disease.

Role: Principal Investigator

INV-0027204 (Braun) 12/1/2021 - 11/30/2024 0.60 Calendar
Bill & Melinda Gates Foundation

The Jackson Laboratory Non-hormonal Contraceptive Model Development Program

To characterize mouse models of fertility and infertility-associated genetic mutations in order to identify novel targets for non-hormonal contraceptive drug discovery.

Role: co-Investigator

2 P30 CA034196-35 (Liu) 4/1/2020 - 3/31/2025 0.60 Calendar
NIH/NCI

Cancer Center Support (CORE) Grant - Cancer Models Development Shared Resource

The Cancer Models Development Resource Shared Resource (CMDR) advises and supports JAX Cancer Center (JAXCC) members in the design, development, and use of advanced mouse models for cancer research, including genetically engineered mouse models (GEMMs), genetically diverse mapping panels, and patient-derived xenograft (PDX) platforms.

Role: Technical Lead

2 R24OD011190-11 (**Murray**, Smith) 8/1/2019 - 7/31/2023 (NCE) 1.20 Calendar
NIH/OD

CRE Driver Strain Resources

Our goal for this proposal also seeks to import an expanded set of Cre driver strains that will fill gaps in our collection and potentially replace critical strains that are confounded by off target activity. Together, these will provide the community with a comprehensive source of Cre driver tool strains and information about them.

Role: Principal Investigator

5 U42 OD026635-05 (**Murray**, Lutz) 9/18/2018 - 7/31/2023 (NCE) 2.40 Calendar
NIH/OD

The Jackson Laboratory Gene Editing Testing Center (JAX-GETC)

The goal of the SCGE program is to improve genome editing technologies to accelerate the translation of this technology into clinical applications and maximize the potential to treat as many diseases as possible.

Role: Principal Investigator

3 U42 OD026635-05S1 (**Murray**, Lutz) 8/1/2022 - 7/31/2023 (NCE) Effort only

NIH/OD

The Jackson Laboratory Gene Editing Testing Center (JAX-GETC)

The goal of this supplement is to test the efficacy of delivery of genome editing cargo in various nanoparticle formulations using Focused Ultrasound in collaboration with Dr. Kam Leong at Columbia University.

3 U42 OD026635-05S2 (**Murray**, Lutz) 8/1/2022 - 7/31/2023 (NCE) Effort only

NIH/OD

The Jackson Laboratory Gene Editing Testing Center (JAX-GETC)

The goal of this supplement is to perform a rigorous comparison of genome editor delivery capacity of various nanoparticle and RNP formulations using a single mode of administration: Convection Enhanced Delivery (CED).

3 U42 OD026635-05S3 (**Murray**, Lutz) 8/1/2022 - 7/31/2023 (NCE) Effort only

NIH/OD

The Jackson Laboratory Gene Editing Testing Center (JAX-GETC)

This supplement to the JAX-GETC will test novel genome editing therapeutic strategies in two models of Charcot-Marie-Tooth Disease, in collaboration with Dr. Rob Burgess at JAX and Bruce Conklin at the Gladstone institute.

3 U42 OD026635-05S4 (**Murray**, Lutz) 8/1/2022 - 7/31/2023 (NCE) Effort only

NIH/OD

The Jackson Laboratory Gene Editing Testing Center (JAX-GETC)

This supplement to the JAX-GETC will test two novel genome editing therapeutic strategies in a model of TTN truncating variant-induced cardiomyopathy, in collaboration with Dr. Travis Hinson at UConn Health/JAX-GM.

COMPLETED RESEARCH SUPPORT

DIF-Orofacial Morphogenesis 01/25/2021 – 07/24/2022 0.60 Calendar

The Jackson Laboratory-Directors Fund

Developmental Systems Genomics of Orofacial Morphogenesis

The overall goal of this DIF proposal is to establish a framework for the use of diversity genetic resources to understand the role of genetic variation in the development of the mammalian secondary palate, addressing the unique challenges of a developmental study and demonstrating the feasibility of developmental systems genomics in the mouse.

Role: Principal Investigator

2 P30 CA034196-35 (Liu) 4/1/2020 - 3/31/2025 0.24 Calendar

NIH/NCI

Cancer Center Support (CORE) Grant - Genome and Single Cell Technologies Shared Resource

The key function of The Jackson Laboratory Cancer Center (JAXCC) Genome and Single Cell Technologies Shared Resource (GSCT) is the provision of genomic technologies to sequence the genomic structures (DNA, RNA, epigenome) and to precisely define the molecular features of individual cells.

Role: Co-Project Lead

5 UM1 OD023222-10, (NCE) (Braun, **Murray**, White) 8/2/2016 - 7/31/2022 4.56 Calendar

NIH/OD

The Jackson Laboratory Knockout Mouse Production and Phenotyping Project (JAX KOMP2)

The specific goal of this project is to expand the JAX KOMP2 Center to produce and phenotype 1,500 novel lines of knockout mice on an isogenic C57BL/6N background, and to share these animal resources and data with the scientific community.

Role: Principal Investigator3 UM1 OD023222-10S1, (NCE) (Braun, **Murray**, White) 9/11/2020 – 7/31/2022 0.01 Calendar

NIH/OD

The goal of the project is to create a second-generation mouse model platform incorporating diverse genetic backgrounds, to characterize the variation in SARS-CoV-2 infection dynamics and the development of clinically-relevant disease.

Role: Principal Investigator

3 UM1 OD023222-10S2 (Braun, **Murray**, White) 8/3/2021 - 7/31/2022 0.01 Calendar

NIH/OD

The Jackson Laboratory Knockout Mouse Production and Phenotyping Project (JAX KOMP2)

The purpose of this request for a funded extension beyond the current project period is to complete the initial goals of creating and phenotyping 1000 lines of KO mice. The Specific Aims of this funded extension are to breed and populate the EAP (Early Adult Pipeline) from the remaining 140 mouse lines to bring our total to 1000 lines.

Role: Principal Investigator

3 UM1 OD023222-10S3 (Braun, **Murray**, White) 8/4/2021 - 7/31/2022 0.01 Calendar

NIH/OD

The Jackson Laboratory Knockout Mouse Production and Phenotyping Project (JAX KOMP2)

This supplement provides funds to generate 25 new homozygous viable gene knockout mouse lines.

Role: Principal Investigator

5 R01 HL142788-04 (Lo, Tsang) 7/1/2018 - 4/30/2022 0.36 Calendar

NIH/NHLBI

Mechanism of LV Hypoplasia in Hypoplastic Left Heart Syndrome

The objective of this proposal is to delineate the cellular, molecular and genetic mechanisms of ventricular hypoplasia in hypoplastic left heart syndrome (HLHS), a congenital defect with marked hypoplasia of the left ventricle that essentially leaves the conceptus with only a single pumping chamber.

Role: Consortium PI

5 U24 HG010423-02 (Dwinell) 1/1/2020 - 11/30/2021 0.01 Calendar

NIH/NHGRI

Dissemination and Coordinating Center for the SCGE Consortium; Development of a GFP-IVS2 Mouse Reporter Strain for PNA-based Genome Editing Detection

The goal is to develop a novel small animal model reporter strain that can be used to evaluate PNA-based gene editing therapies using a splicing strategy to activate the reporter gene.

Role: Consortium PI

5 U24 HG010423-02 (Dwinell) 1/1/2020 - 11/30/2021 0.01 Calendar

NIH/NHGRI

Dissemination and Coordinating Center for the SCGE Consortium; Improved Reporters to Evaluate Base Editor Activity in Mice

The goal of this work is to generate three knockin mouse models to support the use of base editors in therapeutic contexts.

Role: Consortium PI

5 UM1 OD023222-08S3 Braun, **Murray**, White (MPI) 8/1/18-7/31/20 (NCE)

NIH/OD

The Jackson Laboratory Knockout Mouse Production and Phenotyping Project (JAX KOMP2)

This administrative supplement supports a pilot project to generate precision models for novel mutations identified by the Gabriella Miller Kids First program.

Role: **Principal Investigator**

5 UM1 OD023222-09S1 Braun, **Murray**, White (MPI) 8/1/18-7/31/20 (NCE)

NIH/OD

The Jackson Laboratory Knockout Mouse Production and Phenotyping Project (JAX KOMP2)
This administrative supplement supports a pilot project to establish F0 mutagenesis and phenotyping for highly constrained genes predicted to be essential.

Role: **Principal Investigator**

3U42 OD026635-02S1 **Murray**, Lutz (MPI)

8/1/19-7/31/20 (NCE)

NIH/OD

AAV Tropism Supplement

The goal of this supplement is to systematically test the tropism of a panel of AAV serotypes in mice to establish a data resource for the SCGE and the scientific community.

Role: **Principal Investigator**

1R21 OD024941 **Murray** (MPI)

02/13/18-12/31/20 (NCE)

NIH/OD

Rapid In Vivo Modeling of Developmental Disorders

The goal of this project is to optimize CRISPR/Cas9 mutagenesis for direct phenotyping of F0 embryos and to apply this platform to specific human developmental diseases that would benefit from a direct F0 approach.

Role: **Principal Investigator**

DIF18-SM

9/18/18-2/29/20

JAX internal – Director Innovation Fund

Establishing the JAX High-throughput phenotyping pipeline (HTP)

The goal of this project is to develop a data analysis and visualization infrastructure using the Mouse Phenome Database framework for the data from the current KOMP2 pipeline to allow the pipeline to be extended to other project types.

Role: **Principal Investigator**

2 P30 CA034196 Liu (PI)

07/01/14-06/30/20

NIH/NCI

Cancer Center Support (Core) Grant – Cancer Models Development Resource

The CMDR provides JAX Cancer Center (JAXCC) investigators access to existing cancer models and supports development of new mouse models tailored to specific cancer research questions of importance to the Cancer Center.

Role: **Co-Project Leader**

5 UM1 OD023222-08S4 Braun, **Murray**, White (MPI)

8/1/18-7/31/19 (NCE)

NIH/OD

The Jackson Laboratory Knockout Mouse Production and Phenotyping Project (JAX KOMP2)

This administrative supplement supports a pilot project to generate microbiome profiles for all KOMP2 Centers.

Role: **Principal Investigator**

5 U42 OD011185 **Murray**, Taft Jr (PI)

09/07/11-07/31/17

NIH/OD

High Throughput Production and Cryopreservation of Knockout Mice-The objective of this project is to generate over 800 well-characterized knockout (KO) strains of mice over five years and deliver cohorts to the JAX KOMP2 Phenotyping Center.

Role: **Principal Investigator**

3 U54 HG006332-03S1 Braun, Svenson (PI)

08/01/13-07/31/16

NIH/NHGRI

The Jackson Laboratory KOMP2 Phenotyping Center - Administrative Supplement: Embryo Phenotyping

This proposal aims to expand the scope of the KOMP2 Program to include embryonic lethal phenotypes that are not only important for understand gene function, but are also key models of human birth defects.

Role: Co-Investigator

5 R24 OD011190-03S1 **Murray**, Eppig (PI) 09/05/13-08/31/15
NIH/OD

Cre Driver Strain Resources: EUCCOMMTOOLS Supplement

The goal of this supplemental project is to generate and characterize 10-15 new cre driver strains in collaboration with EUCCOMMTOOLS

Role: **Principal Investigator**

5 U42 OD011185-04S1 **Murray**, Taft Jr (PI) 08/01/14-07/31/15
NIH/OD

High Throughput Production and Cryopreservation of Knockout Mice-Administrative Supplement.

Develop technology and test feasibility of scaled production of knockout mice using CRISPR technology.

Role: **Principle Investigator**

5 U42 OD011185-05S1 **Murray**, Taft Jr (PI) 08/01/15-07/31/16
NIH/OD

High Throughput Production and Cryopreservation of Knockout Mice-Administrative Supplement.

Generate 100 KO models using CRISPR/Cas9

Role: **Principle Investigator**

5 U01 DE020052 **Murray** (PI) 09/21/09-04/30/14
NIH/NIDCR

Technology Project: Genetic Tools and Resources for Orofacial Clefting Research

The overall goal of this project is to facilitate orofacial clefting research by generating new mouse genetic tools and by providing a repository of mouse strains critical for clefting research community.

Role: **Principal Investigator**

5 U01 DE020052-04S1 **Murray** (PI) 8/15/2012-04/30/2014
NIH/NIDCR

Technology Project: Genetic Tools and Resources for Orofacial Clefting Research

The goal of this Competitive Revision is to identify, characterize and discover the causative gene(s) for spontaneous and induced models of craniofacial dysmorphology, and provide new models to the scientific community.

Role: **Principal Investigator**

3 P30 CA034196-28S3 Liu (PI) 09/21/09-04/30/14
NIH/NCI

Cancer Center Support (Core) Grant - Cell Biology/Microinjection

This service provides resources and techniques to scientists at The Jackson Laboratory for their transgenic mouse and tissue culture experiments, particularly for embryonic stem cells.

Role: **Project Leader**

5 R03 DE019451 **Murray** (PI) 8/15/2012-04/30/2014
NIH/NIDCR

Genetic Characterization of a Novel Model of Cleft Palate

The overall goal of this project is to develop a novel ENU-induced mouse model of cleft palate. The two Aims of this project are to 1) To genetically map and identify the specific gene that underlies the *clfp4* mutation and 2) To define the developmental defects in *clfp4* mice.

Role: **Principal Investigator**

5 R21 RR026117 **Murray** (PI) 09/07/09-08/31/12
NIH/NCRR

Enhancing the Utility of Cre Driver Lines Through Expanded Characterization

This project seeks to improve the value of the JAX Cre Repository by performing comprehensive characterization of Cre strains. The Aims are to 1) To develop and validate an expanded set of standardized protocols for comprehensive and high-throughput characterization of Cre driver line functionality; and 2) To systematically characterize the functionality of a panel of Cre mouse lines and provide the data to the scientific community.

Role: **Principal Investigator**

PEER-REVIEWED PUBLICATIONS

1. Gacheru, S.N., Thomas, K.M., **Murray, S.A.**, Csiszar, K., Smith-Mungo, L.I., and Kagan, H.M. (1997). Transcriptional and post-transcriptional control of lysyl oxidase expression in vascular smooth muscle cells: effects of TGF-beta 1 and serum deprivation. *J Cell Biochem* 65, 395-407. PubMed PMID: 9138095.
2. Gallo-Hendriks, E., **Murray, S.A.**, Vonderhaar, B.K., and Xiao, Z.X. (2001). Vanadate disrupts mammary gland development in whole organ culture. *Dev Dyn* 222, 354-367. PubMed PMID: 11747071.
3. You, H., Zheng, H., **Murray, S.A.**, Yu, Q., Uchida, T., Fan, D., and Xiao, Z.X. (2002). IGF-1 induces Pin1 expression in promoting cell cycle S-phase entry. *J Cell Biochem* 84, 211-216. PubMed PMID: 11787050.
4. Zheng, H., You, H., Zhou, X.Z., **Murray, S.A.**, Uchida, T., Wulf, G., Gu, L., Tang, X., Lu, K.P., and Xiao, Z.X. (2002). The prolyl isomerase Pin1 is a regulator of p53 in genotoxic response. *Nature* 419, 849-853. PubMed PMID: 12397361.
5. Gu, L., Ying, H., Zheng, H., **Murray, S.A.**, and Xiao, Z.X. (2003). The MDM2 RING finger is required for cell cycle-dependent regulation of its protein expression. *FEBS Lett* 544, 218-222. PubMed PMID: 12782320.
6. Gu, L., Zheng, H., **Murray, S.A.**, Ying, H., and Jim Xiao, Z.X. (2003). Deregulation of Cdc2 kinase induces caspase-3 activation and apoptosis. *Biochem Biophys Res Commun* 302, 384-391. PubMed PMID: 12604359.
7. **Murray, S.A.**, Zheng, H., Gu, L., and Jim Xiao, Z.X. (2003). IGF-1 activates p21 to inhibit UV-induced cell death. *Oncogene* 22, 1703-1711. PubMed PMID: 12642873.
8. Collin, G.B., Cyr, E., Bronson, R., Marshall, J.D., Gifford, E.J., Hicks, W., **Murray, S.A.**, Zheng, Q.Y., Smith, R.S., Nishina, P.M., and Naggert, J.K. (2005). Alms1-disrupted mice recapitulate human Alstrom syndrome. *Hum Mol Genet* 14, 2323-2333. PubMed PMID: 16000322; PMCID: PMC2862911.
9. **Murray, S.A.**, Yang, S., Demicco, E., Ying, H., Sherr, D.H., Hafer, L.J., Rogers, A.E., Sonenshein, G.E., and Xiao, Z.X. (2005). Increased expression of MDM2, cyclin D1, and p27Kip1 in carcinogen-induced rat mammary tumors. *J Cell Biochem* 95, 875-884. PubMed PMID: 15844214.
10. **Murray, S.A.**, Carver, E.A., and Gridley, T. (2006). Generation of a Snail1 (Snai1) conditional null allele. *Genesis* 44, 7-11. PubMed PMID: 16397867.
11. **Murray, S.A.**, and Gridley, T. (2006). Snail1 gene function during early embryo patterning in mice. *Cell Cycle* 5, 2566-2570. PubMed PMID: 17106264.
12. **Murray, S.A.**, and Gridley, T. (2006). Snail family genes are required for left-right asymmetry determination, but not neural crest formation, in mice. *Proc Natl Acad Sci U S A* 103, 10300-10304. PubMed PMID: 16801545; PMCID: PMC1502452.

13. Howell, G.R., Shindo, M., **Murray, S.**, Gridley, T., Wilson, L.A., and Schimenti, J.C. (2007). Mutation of a ubiquitously expressed mouse transmembrane protein (Tapt1) causes specific skeletal homeotic transformations. *Genetics* 175, 699-707. PubMed PMID: 17151244; PMCID: PMC1800629.
14. **Murray, S.A.**, Oram, K.F., and Gridley, T. (2007). Multiple functions of Snail family genes during palate development in mice. *Development* 134, 1789-1797. PubMed PMID: 17376812.
15. Escriva, M., Peiro, S., Herranz, N., Villagrasa, P., Dave, N., Montserrat-Sentis, B., **Murray, S.A.**, Franci, C., Gridley, T., Virtanen, I., and Garcia de Herreros, A. (2008). Repression of PTEN phosphatase by Snail1 transcriptional factor during gamma radiation-induced apoptosis. *Mol Cell Biol* 28, 1528-1540. PubMed PMID: 18172008; PMCID: PMC2258777.
16. **Murray, S.A.**, Morgan, J.L., Kane, C., Sharma, Y., Heffner, C.S., Lake, J., and Donahue, L.R. (2010). Mouse gestation length is genetically determined. *PLoS One* 5, e12418. PubMed PMID: 20811634; PMCID: PMC2928290.
17. Varlakhanova, N.V., Cotterman, R.F., deVries, W.N., Morgan, J., Donahue, L.R., **Murray, S.**, Knowles, B.B., and Knoepfler, P.S. (2010). myc maintains embryonic stem cell pluripotency and self-renewal. *Differentiation* 80, 9-19. PubMed PMID: 20537458; PMCID: PMC2916696.
18. Besnard, V., Wert, S.E., Ikegami, M., Xu, Y., Heffner, C., **Murray, S.A.**, Donahue, L.R., and Whitsett, J.A. (2011). Maternal synchronization of gestational length and lung maturation. *PLoS One* 6, e26682. PubMed PMID: 22096492; PMCID: PMC3212521.
19. Fairfield, H., Gilbert, G.J., Barter, M., Corrigan, R.R., Curtain, M., Ding, Y., D'Ascenzo, M., Gerhardt, D.J., He, C., Huang, W., Richmond, T., Rowe, L., Probst, F.J., Bergstrom, D.E., **Murray, S.A.**, Bult, C., Richardson, J., Kile, B.T., Gut, I., Hager, J., Sigurdsson, S., Mauceli, E., Di Palma, F., Lindblad-Toh, K., Cunningham, M.L., Cox, T.C., Justice, M.J., Spector, M.S., Lowe, S.W., Albert, T., Donahue, L.R., Jeddloh, J., Shendure, J., and Reinholdt, L.G. (2011). Mutation discovery in mice by whole exome sequencing. *Genome Biol* 12, R86. PubMed PMID: 21917142; PMCID: PMC3308049.
20. Hochheiser, H., Aronow, B.J., Artinger, K., Beaty, T.H., Brinkley, J.F., Chai, Y., Clouthier, D., Cunningham, M.L., Dixon, M., Donahue, L.R., Fraser, S.E., Hallgrimsson, B., Iwata, J., Klein, O., Marazita, M.L., Murray, J.C., Murray, S., de Villena, F.P., Postlethwait, J., Potter, S., Shapiro, L., Spritz, R., Visel, A., Weinberg, S.M., and Trainor, P.A. (2011). The FaceBase Consortium: a comprehensive program to facilitate craniofacial research. *Dev Biol* 355, 175-182. PubMed PMID: 21458441; PMCID: PMC3440302.
- *21. **Murray, S.A.** (2011). Mouse resources for craniofacial research. *Genesis* 49, 190-199. PubMed PMID: 21309071; PMCID: PMC3610317.
- *22. Heffner, C.S., Herbert Pratt, C., Babiuk, R.P., Sharma, Y., Rockwood, S.F., Donahue, L.R., Eppig, J.T., and **Murray, S.A.** (2012). Supporting conditional mouse mutagenesis with a comprehensive cre characterization resource. *Nat Commun* 3, 1218. PubMed PMID: 23169059; PMCID: PMC3514490.
- *23. **Murray, S.A.**, Eppig, J.T., Smedley, D., Simpson, E.M., and Rosenthal, N. (2012). Beyond knockouts: cre resources for conditional mutagenesis. *Mamm Genome* 23, 587-599. PubMed PMID: 22926223; PMCID: PMC3655717.
24. Xu, Y., Wang, Y., Besnard, V., Ikegami, M., Wert, S.E., Heffner, C., **Murray, S.A.**, Donahue, L.R., and Whitsett, J.A. (2012). Transcriptional programs controlling perinatal lung maturation. *PLoS One* 7, e37046. PubMed PMID: 22916088; PMCID: PMC3423373.

25. Adams, D., Baldock, R., Bhattacharya, S., Copp, A.J., Dickinson, M., Greene, N.D., Henkelman, M., Justice, M., Mohun, T., **Murray, S.A.**, Pauws, E., Raess, M., Rossant, J., Weaver, T., and West, D. (2013). Bloomsbury report on mouse embryo phenotyping: recommendations from the IMPC workshop on embryonic lethal screening. *Dis Model Mech* 6, 571-579. PubMed PMID: 23519032; PMCID: PMC3634642.
26. Taft, R.A., Low, B.E., Byers, S.L., **Murray, S.A.**, Kutny, P., and Wiles, M.V. (2013). The perfect host: a mouse host embryo facilitating more efficient germ line transmission of genetically modified embryonic stem cells. *PLoS One* 8, e67826. PubMed PMID: 23844102; PMCID: PMC3699516.
27. Hopkins, J., Hwang, G., Jacob, J., Sapp, N., Bedigian, R., Oka, K., Overbeek, P., **Murray, S.**, and Jordan, P.W. (2014). Meiosis-specific cohesin component, Stag3 is essential for maintaining centromere chromatid cohesion, and required for DNA repair and synapsis between homologous chromosomes. *PLoS Genet* 10, e1004413. PubMed PMID: 24992337; PMCID: PMC4081007.
- *28. Curtain, M., Heffner, C.S., Maddox, D.M., Gudis, P., Donahue, L.R., and **Murray, S.A.** (2015). A novel allele of *Alx4* results in reduced *Fgf10* expression and failure of eyelid fusion in mice. *Mamm Genome* 26, 173-180. PubMed PMID: 25673119; PMCID: PMC4482110.
- *29. Davisson, M.T., Cook, S.A., Akeson, E.C., Liu, D., Heffner, C., Gudis, P., Fairfield, H., and **Murray, S.A.** (2015). Kidney adysplasia and variable hydronephrosis, a new mutation affecting the odd-skipped related 1 gene in the mouse, causes variable defects in kidney development and hydronephrosis. *Am J Physiol Renal Physiol* 308, F1335-1342. PubMed PMID: 25834070; PMCID: PMC4469887.
30. Fairfield, H., Srivastava, A., Ananda, G., Liu, R., Kircher, M., Lakshminarayana, A., Harris, B.S., Karst, S.Y., Dionne, L.A., Kane, C.C., Curtain, M., Berry, M.L., Ward-Bailey, P.F., Greenstein, I., Byers, C., Czechanski, A., Sharp, J., Palmer, K., Gudis, P., Martin, W., Tadenev, A., Bogdanik, L., Pratt, C.H., Chang, B., Schroeder, D.G., Cox, G.A., Cliften, P., Milbrandt, J., **Murray, S.**, Burgess, R., Bergstrom, D.E., Donahue, L.R., Hamamy, H., Masri, A., Santoni, F.A., Makrythanasis, P., Antonarakis, S.E., Shendure, J., and Reinholdt, L.G. (2015). Exome sequencing reveals pathogenic mutations in 91 strains of mice with Mendelian disorders. *Genome Res* 25, 948-957. PubMed PMID: 25917818; PMCID: PMC4484392.
31. Guimier, A., Gabriel, G.C., Bajolle, F., Tsang, M., Liu, H., Noll, A., Schwartz, M., El Malti, R., Smith, L.D., Klena, N.T., Jimenez, G., Miller, N.A., Oufadem, M., Moreau de Bellaing, A., Yagi, H., Saunders, C.J., Baker, C.N., Di Filippo, S., Peterson, K.A., Thiffault, I., Bole-Feysot, C., Cooley, L.D., Farrow, E.G., Masson, C., Schoen, P., Deleuze, J.F., Nitschke, P., Lyonnet, S., de Pontual, L., **Murray, S.A.**, Bonnet, D., Kingsmore, S.F., Amiel, J., Bouvagnet, P., Lo, C.W., and Gordon, C.T. (2015). MMP21 is mutated in human heterotaxy and is required for normal left-right asymmetry in vertebrates. *Nat Genet* 47, 1260-1263. PubMed PMID: 26437028; PMCID: PMC5620017.
32. Lloyd, K.C., Meehan, T., Beaudet, A., **Murray, S.**, Svenson, K., McKerlie, C., West, D., Morse, I., Parkinson, H., Brown, S., Mallon, A.M., and Moore, M. (2015). Precision medicine: Look to the mice. *Science* 349, 390. PubMed PMID: 26206923; PMCID: PMC4960978.
33. Sundberg, J.P., Dadras, S.S., Silva, K.A., Kennedy, V.E., **Murray, S.A.**, Denegre, J.M., Schofield, P.N., King, L.E., Jr., Wiles, M.V., and Pratt, C.H. (2015). Excavating the Genome: Large-Scale Mutagenesis Screening for the Discovery of New Mouse Models. *J Investig Dermatol Symp Proc* 17, 27-29. PubMed PMID: 26551941; PMCID: PMC4734626.
- *34. Dickinson, M.E., Flenniken, A.M., Ji, X., Teboul, L., Wong, M.D., White, J.K., Meehan, T.F., Weninger, W.J., Westerberg, H., Adissu, H., Baker, C.N., Bower, L., Brown, J.M., Caddle, L.B., Chiani, F., Clary, D., Cleak, J., Daly, M.J., Denegre, J.M., Doe, B., Dolan, M.E., Edie, S.M., Fuchs, H., Gailus-Durner, V., Galli, A., Gambadoro, A., Gallegos, J., Guo, S., Horner, N.R., Hsu, C.W., Johnson, S.J., Kalaga, S.,

- Keith, L.C., Lanoue, L., Lawson, T.N., Lek, M., Mark, M., Marschall, S., Mason, J., McElwee, M.L., Newbigging, S., Nutter, L.M., Peterson, K.A., Ramirez-Solis, R., Rowland, D.J., Ryder, E., Samocha, K.E., Seavitt, J.R., Selloum, M., Szoke-Kovacs, Z., Tamura, M., Trainor, A.G., Tudose, I., Wakana, S., Warren, J., Wendling, O., West, D.B., Wong, L., Yoshiki, A., International Mouse Phenotyping, C., Jackson, L., Infrastructure Nationale Phenomin, I.C.d.I.S., Charles River, L., Harwell, M.R.C., Toronto Centre for, P., Wellcome Trust Sanger, I., Center, R.B., MacArthur, D.G., Tocchini-Valentini, G.P., Gao, X., Flicek, P., Bradley, A., Skarnes, W.C., Justice, M.J., Parkinson, H.E., Moore, M., Wells, S., Braun, R.E., Svenson, K.L., de Angelis, M.H., Herault, Y., Mohun, T., Mallon, A.M., Henkelman, R.M., Brown, S.D., Adams, D.J., Lloyd, K.C., McKerlie, C., Beaudet, A.L., Bucan, M., and **Murray, S.A.** (2016). High-throughput discovery of novel developmental phenotypes. *Nature* 537, 508-514. PubMed PMID: 27626380; PMCID: PMC5295821.
35. Leduc, M.S., Niu, Z., Bi, W., Zhu, W., Miloslavskaya, I., Chiang, T., Streff, H., Seavitt, J.R., **Murray, S.A.**, Eng, C., Chan, A., Yang, Y., and Lalani, S.R. (2016). CRIPT exonic deletion and a novel missense mutation in a female with short stature, dysmorphic features, microcephaly, and pigmentary abnormalities. *Am J Med Genet A* 170, 2206-2211. PubMed PMID: 27250922; PMCID: PMC5725961.
- *36. Palmer, K., Fairfield, H., Borgeia, S., Curtain, M., Hassan, M.G., Dionne, L., Yong Karst, S., Coombs, H., Bronson, R.T., Reinholdt, L.G., Bergstrom, D.E., Donahue, L.R., Cox, T.C., and **Murray, S.A.** (2016). Discovery and characterization of spontaneous mouse models of craniofacial dysmorphology. *Dev Biol* 415, 216-227. PubMed PMID: 26234751; PMCID: PMC4733616.
- *37. Shaheen, R., Anazi, S., Ben-Omran, T., Seidahmed, M.Z., Caddle, L.B., Palmer, K., Ali, R., Alshidi, T., Hagos, S., Goodwin, L., Hashem, M., Wakil, S.M., Abouelhoda, M., Colak, D., **Murray, S.A.**, and Alkuraya, F.S. (2016). Mutations in SMG9, Encoding an Essential Component of Nonsense-Mediated Decay Machinery, Cause a Multiple Congenital Anomaly Syndrome in Humans and Mice. *Am J Hum Genet* 98, 643-652. PubMed PMID: 27018474; PMCID: PMC4833216.
38. Ward, A., Hopkins, J., McKay, M., **Murray, S.**, and Jordan, P.W. (2016). Genetic Interactions Between the Meiosis-Specific Cohesin Components, STAG3, REC8, and RAD21L. *G3 (Bethesda)* 6, 1713-1724. PubMed PMID: 27172213; PMCID: PMC4889667.
39. Bowl, M.R., Simon, M.M., Ingham, N.J., Greenaway, S., Santos, L., Cater, H., Taylor, S., Mason, J., Kurbatova, N., Pearson, S., Bower, L.R., Clary, D.A., Meziane, H., Reilly, P., Minowa, O., Kelsey, L., International Mouse Phenotyping, C., Tocchini-Valentini, G.P., Gao, X., Bradley, A., Skarnes, W.C., Moore, M., Beaudet, A.L., Justice, M.J., Seavitt, J., Dickinson, M.E., Wurst, W., de Angelis, M.H., Herault, Y., Wakana, S., Nutter, L.M.J., Flenniken, A.M., McKerlie, C., **Murray, S.A.**, Svenson, K.L., Braun, R.E., West, D.B., Lloyd, K.C.K., Adams, D.J., White, J., Karp, N., Flicek, P., Smedley, D., Meehan, T.F., Parkinson, H.E., Teboul, L.M., Wells, S., Steel, K.P., Mallon, A.M., and Brown, S.D.M. (2017). A large scale hearing loss screen reveals an extensive unexplored genetic landscape for auditory dysfunction. *Nat Commun* 8, 886. PubMed PMID: 29026089; PMCID: PMC5638796.
40. Brophy, P.D., Rasmussen, M., Parida, M., Bonde, G., Darbro, B.W., Hong, X., Clarke, J.C., Peterson, K.A., Denegre, J., Schneider, M., Sussman, C.R., Sunde, L., Lildballe, D.L., Hertz, J.M., Cornell, R.A., **Murray, S.A.**, and Manak, J.R. (2017). A Gene Implicated in Activation of Retinoic Acid Receptor Targets Is a Novel Renal Agenesis Gene in Humans. *Genetics* 207, 215-228. PubMed PMID: 28739660; PMCID: PMC5586373.
41. Furtado, M.B., Wilmanns, J.C., Chandran, A., Perera, J., Hon, O., Biben, C., Willow, T.J., Nim, H.T., Kaur, G., Simonds, S., Wu, Q., Williams, D., Salimova, E., Plachta, N., Denegre, J.M., **Murray, S.A.**, Fatkin, D., Cowley, M., Pearson, J.T., Kaye, D., Ramialison, M., Harvey, R.P., Rosenthal, N.A., and Costa, M.W. (2017). Point mutations in murine Nkx2-5 phenocopy human congenital heart disease and induce pathogenic Wnt signaling. *JCI Insight* 2, e88271. PubMed PMID: 28352650; PMCID: PMC5358496 exists.

42. Karp, N.A., Mason, J., Beaudet, A.L., Benjamini, Y., Bower, L., Braun, R.E., Brown, S.D.M., Chesler, E.J., Dickinson, M.E., Flenniken, A.M., Fuchs, H., Angelis, M.H., Gao, X., Guo, S., Greenaway, S., Heller, R., Herault, Y., Justice, M.J., Kurbatova, N., Lelliott, C.J., Lloyd, K.C.K., Mallon, A.M., Mank, J.E., Masuya, H., McKerlie, C., Meehan, T.F., Mott, R.F., **Murray, S.A.**, Parkinson, H., Ramirez-Solis, R., Santos, L., Seavitt, J.R., Smedley, D., Sorg, T., Speak, A.O., Steel, K.P., Svenson, K.L., International Mouse Phenotyping, C., Wakana, S., West, D., Wells, S., Westerberg, H., Yaacoby, S., and White, J.K. (2017). Prevalence of sexual dimorphism in mammalian phenotypic traits. *Nat Commun* 8, 15475. PubMed PMID: 28650954; PMCID: PMC5490203.
43. Liu, E.T., Bolcun-Filas, E., Grass, D.S., Lutz, C., **Murray, S.**, Shultz, L., and Rosenthal, N. (2017). Of mice and CRISPR: The post-CRISPR future of the mouse as a model system for the human condition. *EMBO Rep* 18, 187-193. PubMed PMID: 28119373; PMCID: PMC5286389.
44. Liu, X., Yagi, H., Saeed, S., Bais, A.S., Gabriel, G.C., Chen, Z., Peterson, K.A., Li, Y., Schwartz, M.C., Reynolds, W.T., Saydmohammed, M., Gibbs, B., Wu, Y., Devine, W., Chatterjee, B., Klena, N.T., Kostka, D., de Mesy Bentley, K.L., Ganapathiraju, M.K., Dexheimer, P., Leatherbury, L., Khalifa, O., Bhagat, A., Zahid, M., Pu, W., Watkins, S., Grossfeld, P., **Murray, S.A.**, Porter, G.A., Jr., Tsang, M., Martin, L.J., Benson, D.W., Aronow, B.J., and Lo, C.W. (2017). The complex genetics of hypoplastic left heart syndrome. *Nat Genet* 49, 1152-1159. PubMed PMID: 28530678; PMCID: PMC5737968.
45. Meehan, T.F., Conte, N., West, D.B., Jacobsen, J.O., Mason, J., Warren, J., Chen, C.K., Tudose, I., Relac, M., Matthews, P., Karp, N., Santos, L., Fiegel, T., Ring, N., Westerberg, H., Greenaway, S., Sneddon, D., Morgan, H., Codner, G.F., Stewart, M.E., Brown, J., Horner, N., International Mouse Phenotyping, C., Haendel, M., Washington, N., Mungall, C.J., Reynolds, C.L., Gallegos, J., Gailus-Durner, V., Sorg, T., Pavlovic, G., Bower, L.R., Moore, M., Morse, I., Gao, X., Tocchini-Valentini, G.P., Obata, Y., Cho, S.Y., Seong, J.K., Seavitt, J., Beaudet, A.L., Dickinson, M.E., Herault, Y., Wurst, W., de Angelis, M.H., Lloyd, K.C.K., Flenniken, A.M., Nutter, L.M.J., Newbigging, S., McKerlie, C., Justice, M.J., **Murray, S.A.**, Svenson, K.L., Braun, R.E., White, J.K., Bradley, A., Flicek, P., Wells, S., Skarnes, W.C., Adams, D.J., Parkinson, H., Mallon, A.M., Brown, S.D.M., and Smedley, D. (2017). Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. *Nat Genet* 49, 1231-1238. PubMed PMID: 28650483; PMCID: PMC5546242.
46. Paul, B.J., Palmer, K., Sharp, J.C., Pratt, C.H., **Murray, S.A.**, and Dunnwald, M. (2017). ARHGAP29 Mutation Is Associated with Abnormal Oral Epithelial Adhesions. *J Dent Res* 96, 1298-1305. PubMed PMID: 28817352; PMCID: PMC5613885.
- *47. Peterson, K.A., Beane, G.L., Goodwin, L.O., Kutny, P.M., Reinholdt, L.G., and **Murray, S.A.** (2017). CRISPRtools: a flexible computational platform for performing CRISPR/Cas9 experiments in the mouse. *Mamm Genome* 28, 283-290. PubMed PMID: 28280930; PMCID: PMC5591755.
48. Samuelov, L., Li, Q., Bochner, R., Najor, N.A., Albrecht, L., Malchin, N., Goldsmith, T., Grafi-Cohen, M., Vodo, D., Fainberg, G., Meilik, B., Goldberg, I., Warshauer, E., Rogers, T., Edie, S., Ishida-Yamamoto, A., Burzenski, L., Erez, N., **Murray, S.A.**, Irvine, A.D., Shultz, L., Green, K.J., Uitto, J., Sprecher, E., and Sarig, O. (2017). SVEP1 plays a crucial role in epidermal differentiation. *Exp Dermatol* 26, 423-430. PubMed PMID: 27892606; PMCID: PMC5543306.
49. Seidel, K., Marangoni, P., Tang, C., Houshmand, B., Du, W., Maas, R.L., **Murray, S.**, Oldham, M.C., and Klein, O.D. (2017). Resolving stem and progenitor cells in the adult mouse incisor through gene co-expression analysis. *Elife* 6. PubMed PMID: 28475038; PMCID: PMC5419740.
50. Snyder, E.M., McCarty, C., Mehalow, A., Svenson, K.L., **Murray, S.A.**, Korstanje, R., and Braun, R.E. (2017). APOBEC1 complementation factor (A1CF) is dispensable for C-to-U RNA editing in vivo. *RNA* 23, 457-465. PubMed PMID: 28069890; PMCID: PMC5340909.

51. Sundberg, J.P., Dadras, S.S., Silva, K.A., Kennedy, V.E., Garland, G., **Murray, S.A.**, Sundberg, B.A., Schofield, P.N., and Pratt, C.H. (2017). Systematic screening for skin, hair, and nail abnormalities in a large-scale knockout mouse program. *PLoS One* 12, e0180682. PubMed PMID: 28700664; PMCID: PMC5503261.
52. Teboul, L., **Murray, S.A.**, and Nolan, P.M. (2017). Phenotyping first-generation genome editing mutants: a new standard? *Mamm Genome* 28, 377-382. PubMed PMID: 28756587; PMCID: PMC5569115.
53. Moore, B.A., Leonard, B.C., Sebbag, L., Edwards, S.G., Cooper, A., Imai, D.M., Straiton, E., Santos, L., Reilly, C., Griffey, S.M., Bower, L., Clary, D., Mason, J., Roux, M.J., Meziane, H., Herault, Y., International Mouse Phenotyping, C., McKerlie, C., Flenniken, A.M., Nutter, L.M.J., Berberovic, Z., Owen, C., Newbigging, S., Adissu, H., Eskandarian, M., Hsu, C.W., Kalaga, S., Udensi, U., Asomugha, C., Bohat, R., Gallegos, J.J., Seavitt, J.R., Heaney, J.D., Beaudet, A.L., Dickinson, M.E., Justice, M.J., Philip, V., Kumar, V., Svenson, K.L., Braun, R.E., Wells, S., Cater, H., Stewart, M., Clementson-Mobbs, S., Joynson, R., Gao, X., Suzuki, T., Wakana, S., Smedley, D., Seong, J.K., Tocchini-Valentini, G., Moore, M., Fletcher, C., Karp, N., Ramirez-Solis, R., White, J.K., de Angelis, M.H., Wurst, W., Thomasy, S.M., Flicek, P., Parkinson, H., Brown, S.D.M., Meehan, T.F., Nishina, P.M., **Murray, S.A.**, Krebs, M.P., Mallon, A.M., Lloyd, K.C.K., Murphy, C.J., and Moshiri, A. (2018). Identification of genes required for eye development by high-throughput screening of mouse knockouts. *Commun Biol* 1, 236. PubMed PMID: 30588515; PMCID: PMC6303268.
54. Munoz-Fuentes, V., Cacheiro, P., Meehan, T.F., Aguilar-Pimentel, J.A., Brown, S.D.M., Flenniken, A.M., Flicek, P., Galli, A., Mashhadi, H.H., Hrabe de Angelis, M., Kim, J.K., Lloyd, K.C.K., McKerlie, C., Morgan, H., **Murray, S.A.**, Nutter, L.M.J., Reilly, P.T., Seavitt, J.R., Seong, J.K., Simon, M., Wardle-Jones, H., Mallon, A.M., Smedley, D., Parkinson, H.E., and consortium, I. (2018). The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of the mammalian genome that informs conservation. *Conserv Genet* 19, 995-1005. PubMed PMID: 30100824; PMCID: PMC6061128.
55. Nutter, L.M.J., Heaney, J.D., Lloyd, K.C.K., **Murray, S.A.**, Seavitt, J.R., Skarnes, W.C., Teboul, L., Brown, S.D.M., and Moore, M. (2018). Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". *Nat Methods* 15, 235-236. PubMed PMID: 29600991.
56. Percival, C.J., Green, R., Roseman, C.C., Gatti, D.M., Morgan, J.L., **Murray, S.A.**, Donahue, L.R., Mayeux, J.M., Pollard, K.M., Hua, K., Pomp, D., Marcucio, R., and Hallgrimsson, B. (2018). Developmental constraint through negative pleiotropy in the zygomatic arch. *Evodevo* 9, 3. PubMed PMID: 29423138; PMCID: PMC5787316.
57. Rozman, J., Rathkolb, B., Oestereich, M.A., Schutt, C., Ravindranath, A.C., Leuchtenberger, S., Sharma, S., Kistler, M., Willershauser, M., Brommage, R., Meehan, T.F., Mason, J., Haselimashhadi, H., Consortium, I., Hough, T., Mallon, A.M., Wells, S., Santos, L., Lelliott, C.J., White, J.K., Sorg, T., Champy, M.F., Bower, L.R., Reynolds, C.L., Flenniken, A.M., **Murray, S.A.**, Nutter, L.M.J., Svenson, K.L., West, D., Tocchini-Valentini, G.P., Beaudet, A.L., Bosch, F., Braun, R.B., Dobbie, M.S., Gao, X., Herault, Y., Moshiri, A., Moore, B.A., Kent Lloyd, K.C., McKerlie, C., Masuya, H., Tanaka, N., Flicek, P., Parkinson, H.E., Sedlacek, R., Seong, J.K., Wang, C.L., Moore, M., Brown, S.D., Tschop, M.H., Wurst, W., Klingenspor, M., Wolf, E., Beckers, J., Machicao, F., Peter, A., Staiger, H., Haring, H.U., Grallert, H., Campillos, M., Maier, H., Fuchs, H., Gailus-Durner, V., Werner, T., and Hrabe de Angelis, M. (2018). Identification of genetic elements in metabolism by high-throughput mouse phenotyping. *Nat Commun* 9, 288. PubMed PMID: 29348434; PMCID: PMC5773596.
58. Sundberg, J.P., Shen, T., Fiehn, O., Rice, R.H., Silva, K.A., Kennedy, V.E., Gott, N.E., Dionne, L.A., Bechtold, L.S., **Murray, S.A.**, Kuiper, R., and Pratt, C.H. (2018). Sebaceous gland abnormalities in fatty acyl CoA reductase 2 (Far2) null mice result in primary cicatricial alopecia. *PLoS One* 13, e0205775. PubMed PMID: 30372477; PMCID: PMC6205590 following competing interests: JPS, KAS, and VEK

have or had research contracts with Biocon, Takeda, Theravance, and Curadim and JPS is a consultant for Bioniz all of which have no relevance to this project. This does not alter our adherence to PLOS ONE policies on sharing data and materials. TS, NEG, LAD, LSB, OF, RK, SAM, RHR, and CHP state no conflicts of interest.

59. Yagi, H., Liu, X., Gabriel, G.C., Wu, Y., Peterson, K., **Murray, S.A.**, Aronow, B.J., Martin, L.J., Benson, D.W., and Lo, C.W. (2018). The Genetic Landscape of Hypoplastic Left Heart Syndrome. *Pediatr Cardiol* 39, 1069-1081. PubMed PMID: 29569026; PMCID: PMC8565805.
60. Geuther, B.Q., Deats, S.P., Fox, K.J., **Murray, S.A.**, Braun, R.E., White, J.K., Chesler, E.J., Lutz, C.M., and Kumar, V. (2019). Robust mouse tracking in complex environments using neural networks. *Commun Biol* 2, 124. PubMed PMID: 30937403; PMCID: PMC6440983.
- *61. Goodwin, L.O., Splinter, E., Davis, T.L., Urban, R., He, H., Braun, R.E., Chesler, E.J., Kumar, V., van Min, M., Ndukum, J., Philip, V.M., Reinholdt, L.G., Svenson, K., White, J.K., Sasner, M., Lutz, C., and **Murray, S.A.** (2019). Large-scale discovery of mouse transgenic integration sites reveals frequent structural variation and insertional mutagenesis. *Genome Res* 29, 494-505. PubMed PMID: 30659012; PMCID: PMC6396414.
62. Brown, H.M., **Murray, S.A.**, Northrup, H., Au, K.S., and Niswander, L.A. (2020). Snx3 is important for mammalian neural tube closure via its role in canonical and non-canonical WNT signaling. *Development* 147. PubMed PMID: 33214242; PMCID: PMC7687862.
63. Cacheiro, P., Munoz-Fuentes, V., **Murray, S.A.**, Dickinson, M.E., Bucan, M., Nutter, L.M.J., Peterson, K.A., Haselimashhadi, H., Flenniken, A.M., Morgan, H., Westerberg, H., Konopka, T., Hsu, C.W., Christiansen, A., Lanza, D.G., Beaudet, A.L., Heaney, J.D., Fuchs, H., Gailus-Durner, V., Sorg, T., Prochazka, J., Novosadova, V., Lelliott, C.J., Wardle-Jones, H., Wells, S., Teboul, L., Cater, H., Stewart, M., Hough, T., Wurst, W., Sedlacek, R., Adams, D.J., Seavitt, J.R., Tocchini-Valentini, G., Mammano, F., Braun, R.E., McKerlie, C., Heralut, Y., de Angelis, M.H., Mallon, A.M., Lloyd, K.C.K., Brown, S.D.M., Parkinson, H., Meehan, T.F., Smedley, D., Genomics England Research, C., and International Mouse Phenotyping, C. (2020). Human and mouse essentiality screens as a resource for disease gene discovery. *Nat Commun* 11, 655. PubMed PMID: 32005800; PMCID: PMC6994715.
64. Katz, D.C., Aponte, J.D., Liu, W., Green, R.M., Mayeux, J.M., Pollard, K.M., Pomp, D., Munger, S.C., **Murray, S.A.**, Roseman, C.C., Percival, C.J., Cheverud, J., Marcucio, R.S., and Hallgrimsson, B. (2020). Facial shape and allometry quantitative trait locus intervals in the Diversity Outbred mouse are enriched for known skeletal and facial development genes. *PLoS One* 15, e0233377. PubMed PMID: 32502155; PMCID: PMC7274373.
65. Lloyd, K.C.K., Adams, D.J., Baynam, G., Beaudet, A.L., Bosch, F., Boycott, K.M., Braun, R.E., Caulfield, M., Cohn, R., Dickinson, M.E., Dobbie, M.S., Flenniken, A.M., Flicek, P., Galande, S., Gao, X., Grobler, A., Heaney, J.D., Heralut, Y., de Angelis, M.H., Lupski, J.R., Lyonnet, S., Mallon, A.M., Mammano, F., MacRae, C.A., McInnes, R., McKerlie, C., Meehan, T.F., **Murray, S.A.**, Nutter, L.M.J., Obata, Y., Parkinson, H., Pepper, M.S., Sedlacek, R., Seong, J.K., Shiroishi, T., Smedley, D., Tocchini-Valentini, G., Valle, D., Wang, C.L., Wells, S., White, J., Wurst, W., Xu, Y., and Brown, S.D.M. (2020). The Deep Genome Project. *Genome Biol* 21, 18. PubMed PMID: 32008577; PMCID: PMC6996159.
66. Ngan, C.Y., Wong, C.H., Tjong, H., Wang, W., Goldfeder, R.L., Choi, C., He, H., Gong, L., Lin, J., Urban, B., Chow, J., Li, M., Lim, J., Philip, V., **Murray, S.A.**, Wang, H., and Wei, C.L. (2020). Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. *Nat Genet* 52, 264-272. PubMed PMID: 32094912; PMCID: PMC7869692.
67. Swan, A.L., Schutt, C., Rozman, J., Del Mar Muniz Moreno, M., Brandmaier, S., Simon, M., Leuchtenberger, S., Griffiths, M., Brommage, R., Keski-Valko, P., Grallert, H., Werner, T., Teperino,

- R., Becker, L., Miller, G., Moshiri, A., Seavitt, J.R., Cissell, D.D., Meehan, T.F., Acar, E.F., Lelliott, C.J., Flenniken, A.M., Champy, M.F., Sorg, T., Ayadi, A., Braun, R.E., Cater, H., Dickinson, M.E., Flicek, P., Gallegos, J., Ghirardello, E.J., Heaney, J.D., Jacquot, S., Lally, C., Logan, J.G., Teboul, L., Mason, J., Spielmann, N., McKerlie, C., **Murray, S.A.**, Nutter, L.M.J., Odfalk, K.F., Parkinson, H., Prochazka, J., Reynolds, C.L., Selloum, M., Spoutil, F., Svenson, K.L., Vales, T.S., Wells, S.E., White, J.K., Sedlacek, R., Wurst, W., Lloyd, K.C.K., Croucher, P.I., Fuchs, H., Williams, G.R., Bassett, J.H.D., Gailus-Durner, V., Herault, Y., Mallon, A.M., Brown, S.D.M., Mayer-Kuckuk, P., Hrabe de Angelis, M., and Consortium, I. (2020). Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. *PLoS Genet* 16, e1009190. PubMed PMID: 33370286; PMCID: PMC7822523.
68. Wotton, J.M., Peterson, E., Anderson, L., **Murray, S.A.**, Braun, R.E., Chesler, E.J., White, J.K., and Kumar, V. (2020). Machine learning-based automated phenotyping of inflammatory nocifensive behavior in mice. *Mol Pain* 16, 1744806920958596. PubMed PMID: 32955381; PMCID: PMC7509709.
69. Aponte, J.D., Katz, D.C., Roth, D.M., Vidal-Garcia, M., Liu, W., Andrade, F., Roseman, C.C., **Murray, S.A.**, Cheverud, J., Graf, D., Marcucio, R.S., and Hallgrimsson, B. (2021). Relating multivariate shapes to genescapes using phenotype-biological process associations for craniofacial shape. *Elife* 10. PubMed PMID: 34779766; PMCID: PMC8631940.
- *70. Birling, M.C., Yoshiki, A., Adams, D.J., Ayabe, S., Beaudet, A.L., Bottomley, J., Bradley, A., Brown, S.D.M., Burger, A., Bushell, W., Chiani, F., Chin, H.G., Christou, S., Codner, G.F., DeMayo, F.J., Dickinson, M.E., Doe, B., Donahue, L.R., Fray, M.D., Gambadoro, A., Gao, X., Gertsenstein, M., Gomez-Segura, A., Goodwin, L.O., Heaney, J.D., Herault, Y., de Angelis, M.H., Jiang, S.T., Justice, M.J., Kasperek, P., King, R.E., Kuhn, R., Lee, H., Lee, Y.J., Liu, Z., Lloyd, K.C.K., Lorenzo, I., Mallon, A.M., McKerlie, C., Meehan, T.F., Fuentes, V.M., Newman, S., Nutter, L.M.J., Oh, G.T., Pavlovic, G., Ramirez-Solis, R., Rosen, B., Ryder, E.J., Santos, L.A., Schick, J., Seavitt, J.R., Sedlacek, R., Seisenberger, C., Seong, J.K., Skarnes, W.C., Sorg, T., Steel, K.P., Tamura, M., Tocchini-Valentini, G.P., Wang, C.L., Wardle-Jones, H., Wattenhofer-Donze, M., Wells, S., Wiles, M.V., Willis, B.J., Wood, J.A., Wurst, W., Xu, Y., International Mouse Phenotyping, C., Teboul, L., and **Murray, S.A.** (2021). A resource of targeted mutant mouse lines for 5,061 genes. *Nat Genet* 53, 416-419. PubMed PMID: 33833456; PMCID: PMC8397259.
71. Elrick, H., Peterson, K.A., Wood, J.A., Lanza, D.G., Acar, E.F., Teboul, L., Ryder, E.J., Ayabe, S., Birling, M.-C., Caulder, A., Chiani, F., Codner, G.F., Doe, B., Duddy, G., Gambadoro, A., Gertsenstein, M., Gomez-Segura, A., Goodwin, L.O., Ju, C., Kasperek, P., King, R., Lee, D., Lee, H., Lintott, L.G., Liu, Z., Lorenzo, I., Mackenzie, M., Marschall, S., Matthews, P., Ruhe, M., Santos, L., Seavitt, J.R., Seisenberger, C., Wardle-Jones, H., Willis, B.J., Zhang, J., Zhao, J., Zhou, F., Adams, D.J., Bradley, A., Braun, R.E., DeMayo, F.J., Dickinson, M.E., Gao, X., Héraul, Y., Hrabě de Angelis, M., Lloyd, K.C.K., Mallon, A.-M., Mammano, F., McKerlie, C., Meehan, T., Parkinson, H., Ramirez-Solis, R., Sedlacek, R., Seong, J.K., Skarnes, W.C., Smedley, D., Tamura, M., Wells, S., White, J.K., Wurst, W., Yoshiki, A., Consortium, I.M.P., **Murray, S.A.**, Heaney, J.D., and Nutter, L.M.J. (2021). The production of 4,182 mouse lines identifies experimental and biological variables impacting Cas9-mediated mutant mouse line production. *bioRxiv*.
72. Foxworth, N., Wells, J., Ocaña-Lopez, S., Muller, S., Denegre, J., Palmer, K., McGee, T., Memishian, W., **Murray, S.**, Donahoe, P., Bult, C., and Loscertales, M. (2021). The extracellular matrix gene, *Svep1*, orchestrates airway patterning and the transition from lung branching morphogenesis to alveolar maturation in the mouse. *bioRxiv. Under Review at Nature Comms*
73. Hines, T.J., Lutz, C., **Murray, S.A.**, and Burgess, R.W. (2021). An Integrated Approach to Studying Rare Neuromuscular Diseases Using Animal and Human Cell-Based Models. *Front Cell Dev Biol* 9, 801819. PubMed PMID: 35047510; PMCID: PMC8762301.

74. Paul, B.J., Palmer, K.J., Rhea, L., Carlson, M., Sharp, J.C., Pratt, C.H., **Murray, S.A.**, and Dunnwald, M. (2021). The Mafb cleft-associated variant H131Q is not required for palatogenesis in the mouse. *Dev Dyn* 250, 1463-1476. PubMed PMID: 33715275.
75. Peterson, K.A., Khalouei, S., Wood, J.A., Lanza, D.G., Lintott, L.G., Willis, B.J., Seavitt, J.R., Hanafi, N., Braun, R.E., Dickinson, M.E., White, J.K., Lloyd, K.C.K., Heaney, J.D., **Murray, S.A.**, Ramani, A., and Nutter, L.M.J. (2021). Whole genome analysis for 163 guide RNAs in Cas9 edited mice reveals minimal off-target activity. *bioRxiv*.
76. Saha, K., Sontheimer, E.J., Brooks, P.J., Dwinell, M.R., Gersbach, C.A., Liu, D.R., **Murray, S.A.**, Tsai, S.Q., Wilson, R.C., Anderson, D.G., Asokan, A., Banfield, J.F., Bankiewicz, K.S., Bao, G., Bulte, J.W.M., Bursac, N., Campbell, J.M., Carlson, D.F., Chaikof, E.L., Chen, Z.Y., Cheng, R.H., Clark, K.J., Curiel, D.T., Dahlman, J.E., Deverman, B.E., Dickinson, M.E., Doudna, J.A., Ekker, S.C., Emborg, M.E., Feng, G., Freedman, B.S., Gamm, D.M., Gao, G., Ghiran, I.C., Glazer, P.M., Gong, S., Heaney, J.D., Hennebold, J.D., Hinson, J.T., Khvorova, A., Kiani, S., Lagor, W.R., Lam, K.S., Leong, K.W., Levine, J.E., Lewis, J.A., Lutz, C.M., Ly, D.H., Maragh, S., McCray, P.B., Jr., McDevitt, T.C., Mirochnitchenko, O., Morizane, R., Murthy, N., Prather, R.S., Ronald, J.A., Roy, S., Roy, S., Sabbisetti, V., Saltzman, W.M., Santangelo, P.J., Segal, D.J., Shimoyama, M., Skala, M.C., Tarantal, A.F., Tilton, J.C., Truskey, G.A., Vandsburger, M., Watts, J.K., Wells, K.D., Wolfe, S.A., Xu, Q., Xue, W., Yi, G., Zhou, J., and Consortium, S. (2021). The NIH Somatic Cell Genome Editing program. *Nature* 592, 195-204. PubMed PMID: 33828315; PMCID: PMC8026397.
77. Wellard, S.R., Zhang, Y., Shults, C., Zhao, X., McKay, M., **Murray, S.A.**, and Jordan, P.W. (2021). Overlapping roles for PLK1 and Aurora A during meiotic centrosome biogenesis in mouse spermatocytes. *EMBO Rep* 22, e51023. PubMed PMID: 33615678; PMCID: PMC8024899.
78. Cacheiro, P., Westerberg, C.H., Mager, J., Dickinson, M.E., Nutter, L.M.J., Munoz-Fuentes, V., Hsu, C.W., Van den Veyver, I.B., Flenniken, A.M., McKelvie, C., Murray, S.A., Teboul, L., Heaney, J.D., Lloyd, K.C.K., Lanoue, L., Braun, R.E., White, J.K., Creighton, A.K., Laurin, V., Guo, R., Qu, D., Wells, S., Cleak, J., Bunton-Stasyshyn, R., Stewart, M., Harrison, J., Mason, J., Haseli Mashhadi, H., Parkinson, H., Mallon, A.M., International Mouse Phenotyping, C., Genomics England Research, C., and Smedley, D. (2022). Mendelian gene identification through mouse embryo viability screening. *Genome Med* 14, 119. PubMed PMID: 36229886; PMCID: PMC9563108.
79. Devine, J., Vidal-Garcia, M., Liu, W., Neves, A., Lo Vercio, L.D., Green, R.M., Richbourg, H.A., Marchini, M., Unger, C.M., Nickle, A.C., Radford, B., Young, N.M., Gonzalez, P.N., Schuler, R.E., Bugacov, A., Rolian, C., Percival, C.J., Williams, T., Niswander, L., Calof, A.L., Lander, A.D., Visel, A., Jirik, F.R., Cheverud, J.M., Klein, O.D., Birnbaum, R.Y., Merrill, A.E., Ackermann, R.R., Graf, D., Hemberger, M., Dean, W., Forkert, N.D., **Murray, S.A.**, Westerberg, H., Marcucio, R.S., and Hallgrímsson, B. (2022). MusMorph, a database of standardized mouse morphology data for morphometric meta-analyses. *Sci Data* 9, 230. PubMed PMID: 35614082.
80. Spielmann, N., Miller, G., Oprea, T.I., Hsu, C.-W., Fobo, G., Frishman, G., Montrone, C., Haseli Mashhadi, H., Mason, J., Munoz Fuentes, V., Leuchtenberger, S., Ruepp, A., Wagner, M., Westphal, D.S., Wolf, C., Görlach, A., Sanz-Moreno, A., Cho, Y.-L., Teperino, R., Brandmaier, S., Sharma, S., Galter, I.R., Östereich, M.A., Zapf, L., Mayer-Kuckuk, P., Rozman, J., Teboul, L., Bunton-Stasyshyn, R.K.A., Cater, H., Stewart, M., Christou, S., Westerberg, H., Willett, A.M., Wotton, J.M., Roper, W.B., Christiansen, A.E., Ward, C.S., Heaney, J.D., Reynolds, C.L., Prochazka, J., Bower, L., Clary, D., Selloum, M., Bou About, G., Wendling, O., Jacobs, H., Leblanc, S., Meziane, H., Sorg, T., Audain, E., Gilly, A., Rayner, N.W., Aguilar-Pimentel, J.A., Becker, L., Garrett, L., Hölter, S.M., Amarie, O.V., Calzada-Wack, J., Klein-Rodewald, T., da Silva-Buttkus, P., Lengger, C., Stoeger, C., Gerlini, R., Rathkolb, B., Mayr, D., Seavitt, J., Gaspero, A., Green, J.R., Garza, A., Bohat, R., Wong, L., McElwee, M.L., Kalaga, S., Rasmussen, T.L., Lorenzo, I., Lanza, D.G., Samaco, R.C., Veeraragaven, S., Gallegos, J.J., Kašpárek, P., Petrezsélyová, S., King, R., Johnson, S., Cleak, J., Szcoe-Kovacs, Z.,

Codner, G., Mackenzie, M., Caulder, A., Kenyon, J., Gardiner, W., Phelps, H., Hancock, R., Norris, C., Moore, M.A., Seluke, A.M., Urban, R., Kane, C., Goodwin, L.O., Peterson, K.A., McKay, M., Cook, J.J., Lowy, J.P., McFarland, M., Wood, J.A., Willis, B.J., Tolentino, H., Tolentino, T., Schuchbauer, M., Salazar, J., Johnson, J., Munson, R., Ayadi, A., Pavlovic, G., Birling, M.-C., Jacquot, S., Ali-Hadji, D., Charles, P., Andre, P., Champy, M.-F., Riet, F., Vukobradovic, I., Berberovic, Z., Qu, D., Guo, R., D'Souza, A., Huang, Z., Camilleri, S., Ganguly, M., Adissu, H., Eskandarian, M., Shang, X., Duffin, K., Xu, C., Robertson, K., Laurin, V., Lan, Q., Sleep, G., Creighton, A., Lintott, L., Gertsenstein, M., Pereira, M., Tondat, S., Patel, A., Cruz, M., Bezginov, A., Miller, D., Hy, W., Yoshiki, A., Tanaka, N., Tamura, M., Liu, Z., Ermakova, O., Ferrara, A., Fruscoloni, P., Seisenberger, C., Bürger, A., Giesert, F., Ambrose, J.C., Arumu gam, P., Bevers, R., Bleda, M., Boardman-Pretty, F., Boustred, C.R., Brittain, H., Caulfield, M.J., Chan, G.C., Fowler, T., Giess, A., Hamblin, A., Henderson, S., Hubbard, T.J.P., Jackson, R., Jones, L.J., Kasperaviciute, D., Kayikci, M., Kousathanas, A., Lahnstein, L., Leigh, S.E.A., Leong, I.U.S., Lopez, F.J., Maleady-Crowe, F., McEntagart, M., Minneci, F., Moutsianas, L., Mueller, M., Murugaesu, N., Need, A.C., O'Donovan, P., Odhams, C.A., Patch, C., Perez-Gil, D., Pereira, M.B., Pullinger, J., Rahim, T., Rendon, A., Rogers, T., Savage, K., Sawant, K., Scott, R.H., Siddiq, A., Sieghart, A., Smith, S.C., Sosinsky, A., Stuckey, A., Tanguy, M., Taylor-Tavares, A.L., Thomas, E.R.A., Thompson, S.R., Tucci, A., Welland, M.J., Williams, E., Witkowska, K., Wood, S.M., Hitz, M.-P., Zeggini, E., Wolf, E., Sedlacek, R., **Murray, S.A.**, Svenson, K.L., Braun, R.E., White, J.K., Kelsey, L., Gao, X., Shiroishi, T., Xu, Y., Seong, J.K., Mammano, F., Tocchini-Valentini, G.P., Beaudet, A.L., Meehan, T.F., Parkinson, H., Smedley, D., Mallon, A.-M., Wells, S.E., Grallert, H., Wurst, W., Marschall, S., Fuchs, H., Brown, S.D.M., Flenniken, A.M., Nutter, L.M.J., McKerlie, C., Herault, Y., Lloyd, K.C.K., Dickinson, M.E., Gailus-Durner, V., Hrabe de Angelis, M., consortium, I., and Genomics England Research, C. (2022). Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. *Nature Cardiovascular Research* 1, 157-173.

81. Gridley, T., and **Murray, S.A.** (2022). Mouse mutagenesis and phenotyping to generate models of development and disease. *Curr Top Dev Biol* 148, 1-12. PubMed PMID: 35461561.
82. Kanai, S.M., Heffner, C., Cox, T.C., Cunningham, M.L., Perez, F.A., Bauer, A.M., Reigan, P., Carter, C., **Murray, S.A.**, and Clouthier, D.E. (2022). Auriculocondylar syndrome 2 results from the dominant-negative action of PLCB4 variants. *Dis Model Mech* 15. PubMed PMID: 35284927; PMCID: PMC9066496.
83. Perry, M.N., Smith, C.M., Onda, H., Ringwald, M., **Murray, S.A.**, and Smith, C.L. (2022). Annotated expression and activity data for murine recombinase alleles and transgenes: the CrePortal resource. *Mamm Genome* 33, 55-65. PubMed PMID: 34482425; PMCID: PMC8913597.
- *84. Peterson, K.A., and **Murray, S.A.** (2022). Progress towards completing the mutant mouse null resource. *Mamm Genome* 33, 123-134. PubMed PMID: 34698892; PMCID: PMC8913489.
85. Qiu, C., Cao, J., Martin, B.K., Li, T., Welsh, I.C., Srivatsan, S., Huang, X., Calderon, D., Noble, W.S., Disteche, C.M., **Murray, S.A.**, Spielmann, M., Moens, C.B., Trapnell, C., and Shendure, J. (2022). Systematic reconstruction of cellular trajectories across mouse embryogenesis. *Nat Genet* 54, 328-341. PubMed PMID: 35288709; PMCID: PMC8920898.
86. Teekakirikul, P., Zhu, W., Xu, X., Young, C.B., Tan, T., Smith, A.M., Wang, C., Peterson, K.A., Gabriel, G.C., Ho, S., Sheng, Y., Moreau de Bellaing, A., Sonnenberg, D.A., Lin, J.H., Fotiou, E., Tenin, G., Wang, M.X., Wu, Y.L., Feinstein, T., Devine, W., Gou, H., Bais, A.S., Glennon, B.J., Zahid, M., Wong, T.C., Ahmad, F., Rynkiewicz, M.J., Lehman, W.J., Keavney, B., Alastalo, T.P., Freckmann, M.L., Orwig, K., **Murray, S.**, Ware, S.M., Zhao, H., Feingold, B., and Lo, C.W. (2022). Genetic resiliency associated with dominant lethal TPM1 mutation causing atrial septal defect with high heritability. *Cell Rep Med* 3, 100501. PubMed PMID: 35243414; PMCID: PMC8861813.

87. Wotton, J.M., Peterson, E., Flenniken, A.M., Bains, R.S., Veeraragavan, S., Bower, L.R., Bubier, J.A., Parisien, M., Bezginov, A., Haselimashhadi, H., Mason, J., Moore, M.A., Stewart, M.E., Clary, D.A., Delbarre, D.J., Anderson, L.C., D'Souza, A., Goodwin, L.O., Harrison, M.E., Huang, Z., McKay, M., Qu, D., Santos, L., Srinivasan, S., Urban, R., Vukobradovic, I., Ward, C.S., Willett, A.M., Braun, R.E., Brown, S.D.M., Dickinson, M.E., Heaney, J.D., Kumar, V., Lloyd, K.C.K., Mallon, A.M., McKerlie, C., **Murray, S.A.**, Nutter, L.M.J., Parkinson, H., Seavitt, J.R., Wells, S., Samaco, R.C., Chesler, E.J., Smedley, D., Diatchenko, L., Baumbauer, K.M., Young, E.E., Bonin, R.P., Mandillo, S., White, J.K., and International Mouse Phenotyping, C. (2022). Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. *Pain* 163, 1139-1157. PubMed PMID: 35552317; PMCID: PMC9100450.
88. Mark, P.R., **Murray, S.A.**, Yang, T., Eby, A., Lai, A., Lu, D., Zieba, J., Rajasekaran, S., VanSickle, E.A., Rossetti, L.Z., Guidugli, L., Watkins, K., Wright, M.S., Bupp, C.P., and Prokop, J.W. (2022). Autosomal recessive LRP1-related syndrome featuring cardiopulmonary dysfunction, bone dysmorphology, and corneal clouding. *Cold Spring Harb Mol Case Stud* 8. PubMed PMID: 36307211.
89. Lao, Y.H., Ji, R., Zhou, J.K., Snow, K.J., Kwon, N., Saville, E., He, S., Chauhan, S., Chi, C.W., Datta, M.S., Zhang, H., Quek, C.H., Cai, S.S., Li, M., Gaitan, Y., Bechtel, L., Wu, S.Y., Lutz, C.M., Tomer, R., **Murray, S.A.**, Chavez, A., Konofagou, E.E., and Leong, K.W. (2023). Focused ultrasound-mediated brain genome editing. *Proc Natl Acad Sci U S A* 120, e2302910120. PubMed PMID: 37579143; PMCID: PMC10450663.
- *90. Luzzio, A., Edie, S., Palmer, K., Caddle, L.B., Urban, R., Goodwin, L.O., Welsh, I.C., Reinholdt, L.G., Bergstrom, D.E., Cox, T.C., Donahue, L.R., and **Murray, S.A.** (2023). The spontaneous mouse mutant low set ears (Lse) is caused by tandem duplication of Fgf3 and Fgf4. *Mamm Genome* 34, 453-463. PubMed PMID: 37341808.
91. Metzger, J.M., Wang, Y., Neuman, S.S., Snow, K.J., **Murray, S.A.**, Lutz, C.M., Bondarenko, V., Felton, J., Gimse, K., Xie, R., Li, D., Zhao, Y., Flowers, M.T., Simmons, H.A., Roy, S., Saha, K., Levine, J.E., Emborg, M.E., and Gong, S. (2023). Efficient in vivo neuronal genome editing in the mouse brain using nanocapsules containing CRISPR-Cas9 ribonucleoproteins. *Biomaterials* 293, 121959. PubMed PMID: 36527789; PMCID: PMC9868115.
92. Peterson, K.A., Khalouei, S., Hanafi, N., Wood, J.A., Lanza, D.G., Lintott, L.G., Willis, B.J., Seavitt, J.R., Braun, R.E., Dickinson, M.E., White, J.K., Lloyd, K.C.K., Heaney, J.D., **Murray, S.A.**, Ramani, A., and Nutter, L.M.J. (2023). Whole genome analysis for 163 gRNAs in Cas9-edited mice reveals minimal off-target activity. *Commun Biol* 6, 626. PubMed PMID: 37301944; PMCID: PMC10257658.
93. Qiu, C., Martin, B.K., Welsh, I.C., Daza, R.M., Le, T.M., Huang, X., Nichols, E.K., Taylor, M.L., Fulton, O., Oa Day, D.R., Gomes, A.R., Ilcisin, S., Srivatsan, S., Deng, X., Disteche, C.M., Noble, W.S., Hamazaki, N., Moens, C.B., Kimelman, D., Cao, J., Schier, A.F., Spielmann, M., **Murray, S.A.**, Trapnell, C., and Shendure, J. (2023). A single-cell transcriptional timelapse of mouse embryonic development, from gastrula to pup. *bioRxiv*. PubMed PMID: 37066300; PMCID: PMC10104014. (*will likely be accepted to Nature this month*)
94. Wang, L., Heffner, C., Vong, K.I., Barrows, C., Ha, Y.J., Lee, S., Lara-Gonzalez, P., Jhamb, I., Van Der Meer, D., Loughnan, R., Parker, N., Sievert, D., Mittal, S., Issa, M.Y., Andreassen, O.A., Dale, A., Dobyons, W.B., Zaki, M.S., **Murray, S.A.**, and Gleeson, J.G. (2023). TMEM161B modulates radial glial scaffolding in neocortical development. *Proc Natl Acad Sci U S A* 120, e2209983120. PubMed PMID: 36669109.
96. Elliott, K.H., Balchand, S.K., Bonatto Paese, C.L., Chang, C.F., Yang, Y., Brown, K.M., Rasicci, D.T., He, H., Thorner, K., Chaturvedi, P., **Murray, S.A.**, Chen, J., Porollo, A., Peterson, K.A., and Brugmann,

S.A. (2023). Identification of a heterogeneous and dynamic cilium during embryonic development and cell differentiation. *Development* 150. PubMed PMID: 36971348; PMCID: PMC10163354.

95. Yagi, H., Cui, C., Saydmohammed, M., Gabriel, G., Baker, C., Devine, W., Wu, Y., Lin, J.H., Malek, M., Bais, A., **Murray, S.**, Aronow, B., Tsang, M., Kostka, D., and Lo, C.W. (2023). Spatial transcriptome profiling uncovers metabolic regulation of left-right patterning. *bioRxiv*. PubMed PMID: 37131609; PMCID: PMC10153223.

* Corresponding author

INVITED AND SYMPOSIUM PLATFORM PRESENTATIONS (SINCE 2011)

- 2011 Wadsworth Genetic Diseases in Children Conference, New York, NY (invited)
 2011 North American Cystic Fibrosis Conference-Genetic Modifiers Workshop, Anaheim, CA (invited)
 2011 KOMP2 kickoff/IMPC meeting, Washington DC (invited)
 2011 InfraCOMP/IMPC meeting, Munich Germany (invited)
 2012 Mouse as an Instrument for Ear Research IV, Bar Harbor, ME (invited)
 2012 JAX-UCONN Symposium (invited)
 2012 Gordon Research Conference-Craniofacial Morphogenesis, Ventura, CA (abstract selected)
 2012 26th International Mammalian Genome Conference, St. Petersburg, FL (abstract selected)
 2012 InfraCOMP/IMPC meeting on Embryonic Lethal Phenotyping, Bloomsbury, London, UK (co-organizer and speaker)
 2012 KOMP2/IMPC joint annual meeting, Bethesda, MD (invited)
 2013 KOMP2/IMPC joint annual meeting, Galveston, TX (invited)
 2013 NHLBI Animal models of lung disease workshop, Bethesda, MD (invited)
 2013 IMPC Phenotyping Workshop, Toronto, ON (invited)
 2013 EUCOMMTOOLS/IMPC meeting, Rome, IT (invited)
 2014 Guest seminar, Maine Medical Research Institute, Scarborough, ME (invited)
 2014 Guest seminar, JAX Genomic Medicine, Farmington, CT (invited)
 2014 Transgenic Technology 2014, Edinburgh, UK (invited)
 2014 28th International Mammalian Genome Conference, Bar Harbor, ME (abstract-selected)
 2014 Tenth Comparative Medicine Resource Director's Meeting, Bethesda, MD (invited)
 2014 Guest seminar, Seoul National University, Seoul RK (invited)
 2014 IMPC meeting, Barcelona SP (invited)
 2014 5th Biannual March of Dimes/Burroughs Wellcome Fund Preventing Prematurity Symposium (invited)
 2015 IMPC meeting, Seoul RK (invited)
 2016 Transgenic Technology 2016, Prague, CZ (invited session chair)
 2016 Guest seminar, University of South Carolina, Columbia, SC (invited)
 2016 IMPC meeting, Strasbourg FR (invited)
 2016 Guest seminar, Regeneron Pharmaceuticals, Tarrytown, NY (invited)
 2016 The Allied Genetics Conference, Orlando FL (abstract selected)
 2016 Eleventh Comparative Medicine Resource Director's Meeting, Bethesda, MD (invited)
 2016 Mouse as an Instrument for Ear Research VI, Bar Harbor, ME (invited)
 2017 Guest seminar, PreventionGenetics, Marshfield, WI (invited)
 2017 IMPC meeting, Nanjing, China (invited)
 2017 Guest Webinar, Ambry Genetics (invited)
 2017 Mutant Mouse Resource & Research Centers annual meeting, Farmington, CT (invited)
 2017 Workshop on Phenotyping Mouse Models of Lung Disease, Bar Harbor, ME (invited)
 2018 IACUC 2018, Columbus, OH (invited)
 2018 IMPC meeting, Toronto, CA (invited)
 2018 12th Comparative Medicine Resource Directors Meeting, Rockville, MD (invited)
 2018 NHGRI Genome Sequencing Program (GSP) meeting, Bethesda, MD (invited)
 2018 Mouse as an Instrument for Ear Research VII, Bar Harbor, ME (invited)
 2019 Guest Seminar, Cincinnati Children's Hospital Medical Center (invited)

- 2019 NHLBI TopMED workshop (invited)
 2019 Society for Craniofacial Genetics and Developmental Biology, Houston, TX (invited plenary)
 2019 IMPC meeting, NIH Stakeholder meeting, Washington, DC (invited)
 2020 Guest Seminar, Case Western Reserve University (invited)
 2020 IMPC meeting, virtual (invited)
 2020 JAX Scientific Services Open Day, Bar Harbor, ME (invited)
 2021 Fetal-seq Consortium Meeting, virtual (invited)
 2021 Guest Seminar, NIEHS, virtual (invited)
 2021 American Society for Human Genetics, virtual (invited speaker)
 2022 Genome Writers Guild, virtual (invited speaker)
 2022 PACS1 4th Annual Scientific Conference, New York, NY (invited speaker)
 2023 Rare Disease Research Forum, Farmington CT (invited speaker)
 2023 NICDH Council poster presentation for Kids First program
 2023 IMPC Oxford (invited speaker)
 2023 PACS1 5th Annual Scientific Conference, New York, NY (invited speaker)

TEACHING AND EDUCATION

- 1997-1998 Lecturer, Early Medical School Selection Program (EMSSP) basic biochemistry course, Boston University School of Medicine, Boston, MA
 2005-2010 Biology course guest lectures, College of the Atlantic, Bar Harbor, ME
 2011 20st Short Course on Experimental Models of Human Cancer, Bar Harbor, ME (instructor)
 2012 21nd Short Course on Experimental Models of Human Cancer, Bar Harbor, ME (instructor)
 2013 22rd Short Course on Experimental Models of Human Cancer, Bar Harbor, ME (instructor)
 2015 Jackson Laboratory CRISPR/Cas9 workshop, Bar Harbor, ME (instructor)
 2015 24rd Short Course on Experimental Models of Human Cancer, Bar Harbor, ME (instructor)
 2016 Workshop on Neurogenetic Tools: Using Mouse Models to Study Human Disease (instructor)
 2016 25th Short Course on Experimental Models of Human Cancer, Bar Harbor, ME (instructor)
 2016 Jackson Laboratory CRISPR/Cas9 workshop, Bar Harbor, ME (instructor)
 2017 21st Century Mouse Genetics Course, Bar Harbor, ME (instructor)
 2018 Workshop on Neurogenetic Tools, Bar Harbor, ME (instructor)
 2018 Course Instructor, Mammalian Genetics II (Tufts Genetics course)
 2018 Course Instructor, Mammalian Genetics I ((Tufts Genetics course)
 2018 21st Century Mouse Genetics Course, Bar Harbor, ME (instructor)
 2019 Co-Course Director, Mammalian Genetics (Tufts Genetics course)
 2020 Co-Course Director, Mammalian Genetics (Tufts Genetics course)
 2021 Advanced Human Genetics Course lecture or models of disease (Harvard Medical School Genetics Training Program; instructor)
 2021 Course Instructor, CSHL Mouse Engineering Virtual Minicourse (instructor)
 2021 Course Instructor, Mammalian Genetics (Tufts Genetics course)
 2022 Course Instructor, Mammalian Genetics (Tufts Genetics course)
 2023 Advanced Human Genetics Course lecture or models of disease (Harvard Medical School Genetics Training Program; instructor)
 2023 CSHL mouse development course (Instructor)

MENTORING

- 2006 Susan Lin, The Jackson Laboratory Summer Student Program
 2007 Stephanie Siegmund, The Jackson Laboratory Summer Student Program
 2009 Katelyn DeNegre, The Jackson Laboratory Summer Student Program
 2012-2014 Jocelyn Sharp, University of Maine, Master of Science thesis
 2013 Olivia Katz, The Jackson Laboratory Summer Student Program
 2014-2018 Sarah Edie, Postdoctoral Fellow
 2014-2016 Candice Baker, Postdoctoral Fellow
 2015-2016 William Miller, high school intern

2015-2016 Kevin Elk, high school intern
2016 Madison Luck, summer intern
2017 Amelia Meles, The Jackson Laboratory Summer Student Program
2017-2023 Nicholas Tolman – Tufts Ph.D. Thesis Committee
2018 Ali Ladha, The Jackson Laboratory Summer Student Program
2018 Cesar Gonzales, Post-baccalaureate intern
2019-2021 Alana Luzzio, Research Intern
2019 Ben Clauss, Tufts Genetics rotation
2019 Haley Fortin, Tufts Genetics rotation
2019 Logan Schwartz, Tufts qualifying exam committee (Chair)
2019 Zach Kulstad, Carleton College Externship
2019 Astrid Petropolous, Carleton College Externship
2019 Ayano Ishimura, high school intern
2020 Elli Hartig, Tufts qualifying exam committee (Chair)
2020-2022 Luke Parsely – Tufts Ph.D. Thesis Committee
2020- Haley Fortin – Tufts Ph.D. Thesis Committee
2020- Eric Bogenschutz, Postdoctoral Fellow
2021- Sherrea Brown, Tufts Ph.D. Student
2022 Tess Kelly, The Jackson Laboratory Summer Student Program
2023 Aria Hossein, The Jackson Laboratory Summer Student Program
2023 Sig Reinholdt, MDI high school intern
2023- Shawn David, UMaine Ph.D. Thesis Committee
2023- Arad Bustan, Tufts Ph.D. Thesis Committee