**Ivanov A**, Mattei D, Radscheit K, Compagnion A, **Pett J**, Herzel H, Paolicelli R, Piwecka M, Meyer U, **Beule D** (2022). “Analyses of circRNA Expression throughout the Light-Dark Cycle Reveal a Strong Regulation of Cdr1as, Associated with Light Entrainment in the SCN.” *Int J Mol Sci*, *23*. doi:10.3390/ijms232012347 [Link](https://doi.org/10.3390/ijms232012347)

Wirges A, Bunse M, Joedicke J, **Blanc E**, Gudipati V, Moles M, Shiku H, Beule D, Huppa J, Höpken U, Rehm A (2022). “EBAG9 silencing exerts an immune checkpoint function without aggravating adverse effects.” *Mol Ther*, *30*, 3358-3378. doi:10.1016/j.ymthe.2022.07.009 [Link](https://doi.org/10.1016/j.ymthe.2022.07.009)

Hönzke K, **Obermayer B**, Mache C, Fathykova D, Kessler M, Dökel S, Wyler E, Baumgardt M, Löwa A, Hoffmann K, Graff P, Schulze J, Mieth M, Hellwig K, Demir Z, Biere B, Brunotte L, Mecate-Zambrano A, Bushe J, Dohmen M, Hinze C, Elezkurtaj S, Tönnies M, Bauer T, Eggeling S, Tran H, Schneider P, Neudecker J, Rückert J, Schmidt-Ott K, Busch J, Klauschen F, Horst D, Radbruch H, Radke J, Heppner F, Corman V, Niemeyer D, Müller M, Goffinet C, Mothes R, Pascual-Reguant A, Hauser A, **Beule D**, Landthaler M, Ludwig S, Suttorp N, Witzenrath M, Gruber A, Drosten C, Sander L, Wolff T, Hippenstiel S, Hocke A (2022). “Human lungs show limited permissiveness for SARS-CoV-2 due to scarce ACE2 levels but virus-induced expansion of inflammatory macrophages.” *Eur Respir J*, *60*. doi:10.1183/13993003.02725-2021 [Link](https://doi.org/10.1183/13993003.02725-2021)

Freitag K, Sterczyk N, Wendlinger S, **Obermayer B**, Schulz J, Farztdinov V, Mülleder M, Ralser M, Houtman J, Fleck L, Braeuning C, Sansevrino R, Hoffmann C, Milovanovic D, Sigrist S, Conrad T, **Beule D**, Heppner F, Jendrach M (2022). “Spermidine reduces neuroinflammation and soluble amyloid beta in an Alzheimer’s disease mouse model.” *J Neuroinflammation*, *19*, 172. doi:10.1186/s12974-022-02534-7 [Link](https://doi.org/10.1186/s12974-022-02534-7)

Schalbetter S, von AA, Cruz-Ochoa N, Dawson K, **Ivanov A**, Mueller F, Lin H, Amport R, Mildenberger W, Mattei D, **Beule D**, Földy C, Greter M, Notter T, Meyer U (2022). “Adolescence is a sensitive period for prefrontal microglia to act on cognitive development.” *Sci Adv*, *8*, eabi6672. doi:10.1126/sciadv.abi6672 [Link](https://doi.org/10.1126/sciadv.abi6672)

Grunert C, Willimsky G, Peuker C, Rhein S, Hansmann L, Blankenstein T, **Blanc E**, **Beule D**, Keller U, Pezzutto A, Busse A (2022). “Isolation of Neoantigen-Specific Human T Cell Receptors from Different Human and Murine Repertoires.” *Cancers (Basel)*, *14*. doi:10.3390/cancers14071842 [Link](https://doi.org/10.3390/cancers14071842)

Dannebaum R, Suwalski P, Asgharian H, Du ZG, Lin H, **Weiner J**, **Holtgrewe M**, Thibeault C, Müller M, Wang X, Karadeniz Z, Saccomanno J, Doehn J, Hübner R, Hinzmann B, Blüher A, Siemann S, Telman D, Suttorp N, Witzenrath M, Hippenstiel S, Skurk C, Poller W, Sander L, **Beule D**, Kurth F, Guettouche T, Landmesser U, Berka J, Luong K, Pa-COVID SG, Rubelt F, Heidecker B (2022). “Highly multiplexed immune repertoire sequencing links multiple lymphocyte classes with severity of response to COVID-19.” *EClinicalMedicine*, *48*, 101438. doi:10.1016/j.eclinm.2022.101438 [Link](https://doi.org/10.1016/j.eclinm.2022.101438)

Horak P, Griffith M, Danos A, Pitel B, Madhavan S, Liu X, Chow C, Williams H, Carmody L, Barrow-Laing L, Rieke D, Kreutzfeldt S, Stenzinger A, Tamborero D, **Benary M**, Rajagopal P, Ida C, Lesmana H, Satgunaseelan L, Merker J, Tolstorukov M, Campregher P, Warner J, Rao S, Natesan M, Shen H, Venstrom J, Roy S, Tao K, Kanagal-Shamanna R, Xu X, Ritter D, Pagel K, Krysiak K, Dubuc A, Akkari Y, Li X, Lee J, King I, Raca G, Wagner A, Li M, Plon S, Kulkarni S, Griffith O, Chakravarty D, Sonkin D (2022). “Standards for the classification of pathogenicity of somatic variants in cancer (oncogenicity): Joint recommendations of Clinical Genome Resource (ClinGen), Cancer Genomics Consortium (CGC), and Variant Interpretation for Cancer Consortium (VICC).” *Genet Med*, *24*, 986-998. doi:10.1016/j.gim.2022.01.001 [Link](https://doi.org/10.1016/j.gim.2022.01.001)

**Weiner J**, **Obermayer B**, **Beule D** (2022). “Venn Diagrams May Indicate Erroneous Statistical Reasoning in Transcriptomics.” *Front Genet*, *13*, 818683. doi:10.3389/fgene.2022.818683 [Link](https://doi.org/10.3389/fgene.2022.818683)

Gloaguen Y, Kirwan J, **Beule D** (2022). “Deep Learning-Assisted Peak Curation for Large-Scale LC-MS Metabolomics.” *Anal Chem*, *94*, 4930-4937. doi:10.1021/acs.analchem.1c02220 [Link](https://doi.org/10.1021/acs.analchem.1c02220)

Chopra A, Mueller R, **Weiner J**3, Rosowski J, Dommisch H, Grohmann E, Schaefer A (2022). “BACH1 Binding Links the Genetic Risk for Severe Periodontitis with ST8SIA1.” *J Dent Res*, *101*, 93-101. doi:10.1177/00220345211017510 [Link](https://doi.org/10.1177/00220345211017510)

Bischoff P, Trinks A, Wiederspahn J, **Obermayer B**, **Pett J**, Jurmeister P, Elsner A, Dziodzio T, Rückert J, Neudecker J, Falk C, **Beule D**, Sers C, Morkel M, Horst D, Klauschen F, Blüthgen N (2022). “The single-cell transcriptional landscape of lung carcinoid tumors.” *Int J Cancer*, *150*, 2058-2071. doi:10.1002/ijc.33995 [Link](https://doi.org/10.1002/ijc.33995)

Georg P, Astaburuaga-García R, Bonaguro L, Brumhard S, Michalick L, Lippert L, Kostevc T, Gäbel C, Schneider M, Streitz M, Demichev V, Gemünd I, Barone M, Tober-Lau P, Helbig E, Hillus D, Petrov L, Stein J, Dey H, Paclik D, Iwert C, Mülleder M, Aulakh S, Djudjaj S, Bülow R, Mei H, Schulz A, Thiel A, Hippenstiel S, Saliba A, Eils R, Lehmann I, Mall M, Stricker S, Röhmel J, Corman V, **Beule D**, Wyler E, Landthaler M, **Obermayer B**, von SS, Boor P, Demir M, Wesselmann H, Suttorp N, Uhrig A, Müller-Redetzky H, Nattermann J, Kuebler W, Meisel C, Ralser M, Schultze J, Aschenbrenner A, Thibeault C, Kurth F, Sander L, Blüthgen N, Sawitzki B, PA-COVID-19 SG (2022). “Complement activation induces excessive T cell cytotoxicity in severe COVID-19.” *Cell*, *185*(3), 493-512.e25. ISSN 0092-8674, doi:10.1016/j.cell.2021.12.040 [Link](https://doi.org/10.1016/j.cell.2021.12.040)

Zinnall U, Milek M, Minia I, Vieira-Vieira C, Müller S, Mastrobuoni G, Hazapis O, Del GS, Schwefel D, Bley N, Voigt F, Chao J, Kempa S, Hüttelmaier S, Selbach M, Landthaler M (2022). “HDLBP binds ER-targeted mRNAs by multivalent interactions to promote protein synthesis of transmembrane and secreted proteins.” *Nat Commun*, *13*(1), 2727. doi:10.1038/s41467-022-30322-7 [Link](https://doi.org/10.1038/s41467-022-30322-7)

Dörr D, **Obermayer B**, **Weiner J**, Zimmermann K, Anania C, Wagner L, Lyras E, Sapozhnikova V, Lara-Astiaso D, Prósper F, Lang R, Lupiáñez D, **Beule D**, Höpken U, Leutz A, Mildner A (2022). “C/EBPβ regulates lipid metabolism and Pparg isoform 2 expression in alveolar macrophages.” *Sci Immunol*, *7*(75), eabj0140. doi:10.1126/sciimmunol.abj0140 [Link](https://doi.org/10.1126/sciimmunol.abj0140)

Kedziora S, **Obermayer B**, Sugulle M, Herse F, Kräker K, Haase N, Langmia I, Müller D, Staff A, **Beule D**, Dechend R (2022). “Placental Transcriptome Profiling in Subtypes of Diabetic Pregnancies Is Strongly Confounded by Fetal Sex.” *Int J Mol Sci*, *23*(23). ISSN 1422-0067, doi:10.3390/ijms232315388 [Link](https://doi.org/10.3390/ijms232315388)

Pennitz P, Kirsten H, Wyler E, Goekeri C, **Obermayer B**, Heinz GA, Mashreghi MF, Trimpert J, Landthaler M, Suttorp N, Hocke AC, Hippenstiel S, Tönnies M, Scholz M, Kuebler WM, Witzenrath M, Hoenzke K, Nouailles G (2022). “Integrational approaches for cross-species analysis of lung pathologies at single-cell resolution.” *Pneumologie*, *76*(S 01), FV 285. FV 285.

Hoffmann K, **Obermayer B**, Hönzke K, Fatykhova D, Demir Z, Löwa A, Alves L, Wyler E, Lopez-Rodriguez E, Mieth M, Baumgardt M, Hoppe J, Firsching T, Tönnies M, Bauer T, Eggeling S, Tran H, Schneider P, Neudecker J, Rückert J, Gruber A, Ochs M, Landthaler M, **Beule D**, Suttorp N, Hippenstiel S, Hocke A, Kessler M (2022). “Human alveolar progenitors generate dual lineage bronchioalveolar organoids.” *Commun Biol*, *5*(1), 875. ISSN 2399-3642, doi:10.1038/s42003-022-03828-5 [Link](https://doi.org/10.1038/s42003-022-03828-5)

Neitzel H, Varon R, Chughtai S, Dartsch J, Dutrannoy-Tönsing V, Nürnberg P, Nürnberg G, Schweiger M, Digweed M, Hildebrand G, Hackmann K, **Holtgrewe M**, Sarioglu N, Schulze B, Horn D, Sperling K (2022). “Transmission ratio distortion of mutations in the master regulator of centriole biogenesis PLK4.” *Hum Genet*, *141*(11), 1785-1794. doi:10.1007/s00439-022-02461-w [Link](https://doi.org/10.1007/s00439-022-02461-w)

Foddis M, Blumenau S, **Holtgrewe M**, Paquette K, Westra K, Alonso I, Macario M, Morgadinho A, Velon A, Santo G, Santana I, Mönkäre S, Kuuluvainen L, Schleutker J, Pöyhönen M, Myllykangas L, Pavlovic A, Kostic V, Dobricic V, Lohmann E, Hanagasi H, Santos M, Guven G, Bilgic B, Bras J, **Beule D**, Dirnagl U, Guerreiro R, Sassi C (2022). “TREX1 p.A129fs and p.Y305C variants in a large multi-ethnic cohort of CADASIL-like unrelated patients.” doi:10.1016/j.neurobiolaging.2022.11.013 [Link](https://doi.org/10.1016/j.neurobiolaging.2022.11.013)

Boschann F, Moreno D, Mensah M, Sczakiel H, Skipalova K, **Holtgrewe M**, Mundlos S, Fischer-Zirnsak B (2022). “Xq27.1 palindrome mediated interchromosomal insertion likely causes familial congenital bilateral laryngeal abductor paralysis (Plott syndrome).” *J Hum Genet*, *67*(7), 405-410. doi:10.1038/s10038-022-01018-z [Link](https://doi.org/10.1038/s10038-022-01018-z)

Seidel F, Laser K, Klingel K, Dartsch J, Theisen S, Pickardt T, Holtgrewe M, Gärtner A, Berger F, **Beule D**, Milting H, Schubert S, Klaassen S, Kühnisch J (2022). “Pathogenic Variants in Cardiomyopathy Disorder Genes Underlie Pediatric Myocarditis-Further Impact of Heterozygous Immune Disorder Gene Variants?” *J Cardiovasc Dev Dis*, *9*(7), 216. doi:10.3390/jcdd9070216 [Link](https://doi.org/10.3390/jcdd9070216)

May V, Koch L, Fischer-Zirnsak B, Horn D, Gehle P, Kornak U, **Beule D**, **Holtgrewe M** (2022). “ClearCNV: CNV calling from NGS panel data in the presence of ambiguity and noise.” *Bioinformatics*, *38*(16), 3871-3876. doi:10.1093/bioinformatics/btac418 [Link](https://doi.org/10.1093/bioinformatics/btac418)

Schöpflin R, Melo U, Moeinzadeh H, Heller D, Laupert V, Hertzberg J, **Holtgrewe M**, Alavi N, Klever M, Jungnitsch J, Comak E, Türkmen S, Horn D, Duffourd Y, Faivre L, Callier P, Sanlaville D, Zuffardi O, Tenconi R, Kurtas N, Giglio S, Prager B, Latos-Bielenska A, Vogel I, Bugge M, Tommerup N, Spielmann M, Vitobello A, Kalscheuer V, Vingron M, Mundlos S (2022). “Integration of Hi-C with short and long-read genome sequencing reveals the structure of germline rearranged genomes.” *Nat Commun*, *13*(1), 6470. doi:10.1038/s41467-022-34053-7 [Link](https://doi.org/10.1038/s41467-022-34053-7)

Rieke D, de BT, Horak P, Lamping M, **Benary M**, Jelas I, Rüter G, Berger J, Zettwitz M, Kagelmann N, Kind A, Fabian F, **Beule D**, Glimm H, Brors B, Stenzinger A, Fröhling S, Keilholz U (2022). “Feasibility and outcome of reproducible clinical interpretation of high-dimensional molecular data: a comparison of two molecular tumor boards.” *BMC Med*, *20*, 367. ISSN 17417015, doi:10.1186/s12916-022-02560-5 [Link](https://doi.org/10.1186/s12916-022-02560-5)

Richter G, Wagner G, Reichenmiller K, Staufenbiel I, Martins O, Löscher B, **Holtgrewe M**, Jepsen S, Dommisch H, Schaefer A (2022). “Exome Sequencing of 5 Families with Severe Early-Onset Periodontitis.” *J Dent Res*, *101*(2), 151-157. doi:10.1177/00220345211029266 [Link](https://doi.org/10.1177/00220345211029266)

Coutelier M, **Holtgrewe M**, Jäger M, Flöttman R, Mensah M, Spielmann M, Krawitz P, Horn D, **Beule D**, Mundlos S (2022). “Combining callers improves the detection of copy number variants from whole-genome sequencing.” *Eur J Hum Genet*, *30*(2), 178-186. doi:10.1038/s41431-021-00983-x [Link](https://doi.org/10.1038/s41431-021-00983-x)

Vogt G, Verheyen S, Schwartzmann S, Ehmke N, Potratz C, Schwerin-Nagel A, Plecko B, **Holtgrewe M**, Seelow D, Blatterer J, Speicher M, Kornak U, Horn D, Mundlos S, Fischer-Zirnsak B, Boschann F (2022). “Biallelic truncating variants in ATP9A cause a novel neurodevelopmental disorder involving postnatal microcephaly and failure to thrive.” *J Med Genet*, *59*(7), 662-668. doi:10.1136/jmedgenet-2021-107843 [Link](https://doi.org/10.1136/jmedgenet-2021-107843)