

MAYUKO FURUTA

Ph.D. (Science)

Personal and Contact Information

Office Address: 10 Discovery Drive, Farmington, CT 06032

Work Phone: +1-(860)422-5489

Work Email: Mayuko.Furuta@jax.org

Place of Birth: Tokyo, Japan

Technical Experience

Research fields

Molecular Biology, Genetics, Cancer Biology, Bioinformatics

Lab works

- Proficient in basic technologies on molecular biology (DNA works, RNA works, protein works, PCR, qPCR, ChIP, EMSA, Western blotting, etc), functional analysis using human cancer cell lines (growth assay, invasion/migration assay, FACS, Immunoprecipitation, Immunostaining) and omics analysis (Chip-based gene expression array, preparation of sequencing libraries such as ChIP-seq, RNA-seq, WGS, WES, Hi-C)
- Experience on mouse models (orthotopic transplantation, subcutaneous implantation of tumor cells)
- Experience on CRISPR-Cas9 genome engineering using cell lines

Computational works

- Basic programming skills (Linux/bash, Perl, R)
- Experience on handling next generation sequencing data (RNA-seq, WGS, exome, targeted capture, Hi-C) analyzed by BWA, SAMtools and in-house programs or Bowtie, Blat and Picard.
- Daily use of SHIROKANE Supercomputer system (Human Genome Center, Tokyo, Japan) to analyze sequencing data.

Language

Japanese - Native

English - Business use; Meetings, Writing manuscripts, Presentations

Academic History

Mar. 2019 - present	Associate Research Scientist , The Jackson Laboratory for Genomic Medicine, CT, USA
Mar. 2017 - Mar. 2019	Postdoctoral Associate , The Jackson Laboratory for Genomic Medicine, CT, USA
Oct. 2012 - Mar. 2017	Research Fellow , Laboratory for Genome Sequencing Analysis, RIKEN Center for Integrative Medical Sciences, Tokyo, Japan, Adviser: Hidewaki Nakagawa, M.D., Ph.D
Apr. 2012 - Sept. 2012	Research Fellow , Japan Society for the Promotion of Science (JSPS), Tokyo, Japan
Apr. 2012 - Sept. 2012	Postdoctoral Training , Department of Molecular Cytogenetics, Medical Research Institute (MRI) Tokyo Medical and Dental University (TMDU), Tokyo, Japan, Adviser: Johji Inazawa, M.D., Ph.D
Mar. 2012	Ph.D. (Science) , Tokyo Medical and Dental University Graduate School of Biomedical Science PhD Program, Tokyo, Japan, Adviser: Johji Inazawa, M.D., Ph.D
Apr. 2011 - Sept. 2012	Research Assistant , Tokyo Medical and Dental University, Tokyo, Japan
Mar. 2009	MSc , Tokyo Medical and Dental University Graduate School of Biomedical Science PhD Program, Tokyo, Japan, Adviser: Johji Inazawa, M.D., Ph.D
Apr. 2008 - Mar. 2009	Research Assistant , Tokyo Medical and Dental University, Tokyo, Japan
Mar. 2007	B.S , Tokyo University of Science, Department of Applied Biological Science, Chiba, Japan, Adviser: Osamu Koiwai, Ph.D.

Other Competitive Scholarships

Mar. 2017- Mar. 2019	JAX Scholar award , The Jackson Laboratory, CT, USA
Apr. 2011 - Mar. 2012	Research Fellowship for Young Scientists , Japan Society for the Promotion of Science (JSPS) Tokyo, Japan
Apr. 2009 - Sept. 2011	Advanced.I.Super Student (AISS) , Global COE program, International Research Center for Molecular Science in Tooth and Bone Diseases Tokyo Medical and Dental University

Honors and Awards

2017	Research award 2017, RIKEN, Japan
2012	Excellent-presentation-Special Award- in AISS workshop, Global COE program, TMDU
2012	3 rd Place Presentation Award, Workshop for Graduate students and Young Scientists, MRI, TMDU
2011	Young Investigator/Scientist Presentation Award, Workshop for Graduate students and Young Scientists, MRI, TMDU
2011	Excellent-presentation-Special Award- in AISS workshop, Global COE program, TMDU
2009	2 nd Place Presentation Award, Workshop for Graduate students and Young Scientists, MRI, TMDU
2008	Research Fellowship for Young Scientists, MRI, TMDU (Direct cost: ¥1,000,000)

Publications

(*1st author papers including equal contribution)

1. Taniguchi H, Fujimoto A, Kono H, **Furuta M**, Fujita M, Nakagawa H.

Loss-of-function mutations in Zn-finger DNA-binding domain of HNF4A cause aberrant transcriptional regulation in liver cancer.

Oncotarget. 2018 May 25;9(40):26144-26156

2. **Furuta M***, Tanaka H, Shiraishi Y, Unida T, Imamura M, Fujimoto A, Fujita M, Sasaki-Oku A, Maejima K, Nakano K, Kawakami Y, Arihiro K, Aikata H, Ueno M, Hayami S, Ariizumi SI, Yamamoto M, Gotoh K, Ohdan H, Yamaue H, Miyano S, Chayama K, Nakagawa H

Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers.

Oncotarget. 2018 May 18;9(38):25075-25088

3. Fujita M, Matsubara N, Matsuda I, Maejima K, Oosawa A, Yamano T, Fujimoto A, **Furuta M**, Nakano K, Oku-Sasaki A, Tanaka H, Shiraishi Y, Mateos RN, Nakai K, Miyano S, Tomita N, Hirota S, Ikeuchi H, Nakagawa H.

Genomic landscape of colitis-associated cancer indicates the impact of chronic inflammation and its stratification by mutations in the Wnt signaling.

Oncotarget. 2017 Dec 12;9(1):969-981

4. Wardell CP, Fujita M, Yamada T, Simbolo M, Fassan M, Karlic R, Polak P, Kim J, Hatanaka Y, Maejima K, Lawlor RT, Nakanishi Y, Mitsuhashi T, Fujimoto A, **Furuta M**, Ruzzenente A, Conci S, Oosawa A, Sasaki-Oku A, Nakano K, Tanaka H, Yamamoto Y, Michiaki K, Kawakami Y, Aikata H, Ueno M, Hayami S, Gotoh K, Ariizumi SI, Yamamoto M, Yamaue H, Chayama K, Miyano S, Getz G, Scarpa A, Hirano S, Nakamura T, Nakagawa H.

Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations.

J Hepatol. 2018 May;68(5):959-969

5. **Furuta M***, Ueno M, Fujimoto A, Hayami S, Yasukawa S, Kojima F, Arihiro K, Kawakami Y, Wardell CP, Shiraishi Y, Tanaka H, Nakano K, Maejima K, Sasaki-Oku A, Tokunaga N, Boroevich KA, Abe T, Aikata H, Ohdan H, Goto K, Kubo M, Tsunoda T, Miyano S, Chayama K, Yamaue H, Nakagawa H.

Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors.

J Hepatol. 2017 Feb;66(2):363-373

6. Fujimoto A, **Furuta M***, Totoki Y, Tsunoda T, Kato M, Shiraishi Y, Tanaka H, Taniguchi H, Kawakami Y, Ueno M, Gotoh K, Ariizumi SI, Wardell CP, Hayami S, Nakamura T, Aikata H, Arihiro K, Boroevich KA, Abe T, Nakano K, Maejima K, Sasaki-Oku A, Ohsawa A, Shibuya T, Nakamura H, Hama N, Hosoda F, Arai Y, Ohashi S, Urushidate T, Nagae G, Yamamoto S, Ueda H, Tatsuno K, Ojima H, Hiraoka N, Okusaka T, Kubo M, Marubashi S, Yamada T, Hirano S, Yamamoto M, Ohdan H, Shimada K, Ishikawa O, Yamaue H, Chayama K, Miyano S, Aburatani H, Shibata T, Nakagawa H.

Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer.

Nat Genet. 2016 Apr 11. doi: 10.1038/ng.3547.

7. Nakagawa H, Wardell CP, **Furuta M**, Taniguchi H, **Fujimoto A**.

Cancer whole-genome sequencing: present and future.

Oncogene. 2015 Dec 3;34(49):5943-50. doi: 10.1038/onc.2015.90. Epub 2015 Mar 30. Review.

8. Ono A, Fujimoto A, Yamamoto Y, Akamatsu S, Hiraga N, Imamura M, Kawaoka T, Tsuge M, Abe H, Hayes CN, Miki D, **Furuta M**, Tsunoda T, Miyano S, Kubo M, Aikata H, Ochi H, Kawakami Y, Nakagawa H, and Chayama K.

Circulating tumor DNA analysis for liver cancers and its usefulness as a liquid biopsy.

Cell Mol Gastroenterol Hepatol 1: 516-534 (2015)

9. Fujimoto A, **Furuta M***, Shiraishi Y, Gotoh K, Kawakami Y, Arihiro K, Nakamura T, Ueno M, Ariizumi S, Nguyen HH, Shigemizu D, Abe T, Boroevich KA, Nakano K, Sasaki A, Kitada R, Maejima K, Yamamoto Y, Tanaka H, Shibuya T, Shibata T, Ojima H, Shimada K, Hayami S, Shigekawa Y, Aikata H, Ohdan H, Marubashi S, Yamada T, Kubo M, Hirano S, Ishikawa O, Yamamoto M, Yamaue H, Chayama K, Miyano S, Tsunoda T, Nakagawa H.

Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity.

Nat Commun. 2015 Jan 30;6:6120.

10. Shiraishi Y, Fujimoto A, **Furuta M**, Tanaka H, Chiba K, Boroevich KA, Abe T, Kawakami Y, Ueno M, Gotoh K, Ariizumi S, Shibuya T, Nakano K, Sasaki A, Maejima K, Kitada R, Hayami S, Shigekawa Y, Marubashi S, Yamada T, Kubo M, Ishikawa O, Aikata H, Arihiro K, Ohdan H, Yamamoto M, Yamaue H, Chayama K, Tsunoda T, Miyano S, Nakagawa H.

Integrated analysis of whole genome and transcriptome sequencing reveals diverse transcriptomic aberrations driven by somatic genomic changes in liver cancers.

PLoS One. 2014 Dec 19;9(12):e114263.

11. Shigemizu D, Fujimoto A, Akiyama S, Abe T, Nakano K, Boroevich KA, Yamamoto Y, **Furuta M**, Kubo M, Nakagawa H, Tsunoda T.

A practical method to detect SNVs and indels from whole genome and exome sequencing data.

Sci Rep. 2013;3:2161.

12. **Furuta M***, Kozaki K, Tanimoto K, Tanaka S, Arie S, Shimamura T, Niida A, Miyano S, Inazawa J.

The tumor-suppressive miR-497-195 cluster targets multiple cell-cycle regulators in hepatocellular carcinoma.

PLoS One. 2013;8(3):e60155.

13. Endo H, Muramatsu T, **Furuta M**, Uzawa N, Pimkhaokham A, Amagasa T, Inazawa J, Kozaki K.

Potential of tumor-suppressive miR-596 targeting LGALS3BP as a therapeutic agent in oral cancer.

Carcinogenesis. 2013 Mar;34(3):560-9.

14. Matsumura S, Imoto I, Kozaki KI, Matsui T, Muramatsu T, **Furuta M**, Tanaka S, Sakamoto M, Arie S, Inazawa J.

Integrative Array-Based Approach Identifies MZB1 as a Frequently Methylated Putative Tumor Suppressor in Hepatocellular Carcinoma.

Clin. Cancer Res. 2012 May 31.

15. Tsuruta T, Kozaki K, Uesugi A, **Furuta M**, Hirasawa A, Imoto I, Susumu N, Aoki D, Inazawa J.

miR-152 is a tumor suppressor microRNA that is silenced by DNA hypermethylation in endometrial cancer.

Cancer Res. 2011 Oct 15;71(20):6450-62. Epub 2011 Aug 25.

16. Uesugi A, Kozaki K, Tsuruta T, **Furuta M**, Morita K, Imoto I, Omura K, Inazawa J.

The tumor suppressive microRNA miR-218 targets the mTOR component Rictor and inhibits AKT phosphorylation in oral cancer.

Cancer Res. 2011 Sep 1;71(17):5765-78. Epub 2011 Jul 27.

17. **Furuta M***, Kozaki KI, Tanaka S, Arie S, Imoto I, Inazawa J.

miR-124 and miR-203 are epigenetically silenced tumor-suppressive microRNAs in hepatocellular carcinoma

Carcinogenesis. 2010 May; 31(5): 766-76.

18. Uesugi A, Kozaki K, Tsuruta T, **Furuta M**, Morita K, Imoto I, Omura K, Inazawa J.

The tumor suppressive microRNA *miR-218* targets the mTOR component Rictor and inhibits AKT phosphorylation in oral cancer.

Cancer Res. 2011 Sep 1;71(17):5765-78.

International presentations

Invited presentations (1)

2011 Invited speaker for young scientist section, International Scientific Coordination Network, Groupement de Recherche "France-Japan-Cancer", Montpellier, France

Oral presentations (3)

1. **Mayuko Furuta**, Akihiro Fujimoto, Masaki Ueno, Shinya Hayami, Yoshi-iku Kawakami, Kunihito Gotoh, Tatsuhiko Tsunoda, Satoru Miyano, Hideki Ohdan, Kazuaki Chayama, Hiroki Yamaue, and Hidewaki Nakagawa

Genome sequencing analysis of multiple liver cancer nodules for the determination of causal events for multi-occurrence

74th Annual Meeting of the Japanese Cancer Association; 2015 October 8-10, Nagoya, Japan

2. **Mayuko Furuta**, Ha Hai Nguyen, Akihiro Fujimoto, Yuichi Shiraishi, Satoru Miyano, Tatsuhiko Tsunoda, Hidewaki Nakagawa

The consequence of AT-rich interacting domain 2 (ARID2) depletion in hepatocellular carcinoma (HCC)

72nd Annual Meeting of the Japanese Cancer Association; 2013 October 3-5, Yokohama, Japan

3. **Mayuko Furuta**, Ken-ichi Kozaki, Shinji Tanaka, Shigeki Arai, Issei Imoto, Johji Inazawa

Functional genomics-assisted approach identifies candidates for tumor-suppressive microRNAs in hepatocellular carcinoma.

70th Annual Meeting of the Japanese Cancer Association; 2011 October 3-5, Nagoya, Japan

Poster presentations (6)

1. Francesca Menghi, **Mayuko Furuta**, Floris Barthel¹, Vinod Yadav¹, Ming Tang², Bo Ji³, Gregory Carter³, Jos Jonkers⁴, Roeland Verhaak¹, Ralph Scully⁵ and Edison T. Liu

Understanding the genesis and oncogenic consequences of tandem duplicator phenotypes in human cancers

Human Genome Meeting 2018; 2018 March 11-15, Yokohama, Japan

2. **Mayuko Furuta**, Akihiro Fujimoto, Masaki Ueno, Shinya Hayami, Yoshi-iku Kawakami, Kunihito Gotoh, Tatsuhiko Tsunoda, Satoru Miyano, Hideki Ohdan, Kazuaki Chayama, Hiroki Yamaue, Hidewaki Nakagawa.

Whole genome sequencing analysis of multiple liver cancer nodules for determination of causal events for multi-occurrence.

106th American Association for Cancer Research Annual Meeting; 2015 April 18-22, Philadelphia, Pennsylvania (Abstract: #2970)

3. **Mayuko Furuta**, Akihiro Fujimoto, Yuichi Shiraishi, Satoru Miyano, Tatsuhiko Tsunoda, Hidewaki Nakagawa.

Genome-wide profiling of somatic mutations in liver cancers revealed significantly mutated genes and non-coding regions in liver cancers.

105th American Association for Cancer Research Annual Meeting; 2014 April 5-9, San Diego, California (Abstract:#5177)

4. **Mayuko Furuta**, Ha H. Nguyen, Akihiro Fujimoto, Yuichi Shiraishi, Satoru Miyano, Tatsuhiko Tsunoda, Hidewaki Nakagawa.

Genome-wide integrative analysis for the determination of the consequence of AT-rich interacting domain 2 (ARID2) depletion in hepatocellular carcinoma.

104th American Association for Cancer Research Annual Meeting; 2013 April 6-10, Washington, DC (Abstract:#5200)

5. **Furuta M**, Kozaki KI, Tanaka S, Ariei S, Imoto I, Inazawa J.

Functional genomics-assisted approach identifies candidates for tumor-suppressive microRNAs in hepatocellular carcinoma.

102nd American Association for Cancer Research Annual Meeting; 2011 April 2-6, Orland, Florida (Abstract:11-A-4582)

6 **Mayuko Furuta**, Ken-ichi Kozaki, Shinji Tanaka, Shigeki Ariei, Issei Imoto, Johji Inazawa.

miR-124 and miR-203 are epigenetically silenced tumor-suppressive microRNAs in hepatocellular carcinoma.

101th American Association for Cancer Research Annual Meeting; 2010 April 17-21, Washington, DC (Abstract:#2080)

Research Supports

2017-2019 **JAX Scholar Award, The Jackson Laboratory**

JAX Scholar stipend (JAX postdoc scale + 15%) for two years, One-time budget: \$10,000

2015 - 2017 **JSPS, Grant-in-Aid for Young Scientists (B), Japan**

Role: PI, Annual direct cost: ¥4,030,000

Identification of genomic features of multiple liver cancer nodules for the determination of causal events for multi-occurrence using whole genome sequencing analysis.

2013 - 2015 **JSPS, Grant-in-Aid for Young Scientists (B), Japan**

Role: PI, Annual direct cost: ¥4,030,000

Determination of the consequence of a chromatin regulator, AT-rich interacting domain 2 (ARID2), depletion in hepatocellular carcinoma.

2011 - 2013 **JSPS, Grant-in-Aid for JSPS Fellows, Japan**

Role: PI, Annual direct cost: ¥1,300,000

Identification of tumor-suppressive microRNAs that have potential as a therapeutics for HCC and determined their role during hepatocarcinogenesis.

2009 - 2010 **Research Fellowship for Young Scientists**, Medical Research Institute, Tokyo Medical and Dental University

Direct cost: ¥1,000,000

Screening of tumor-suppressive microRNAs silenced by DNA hepermethylation in hepatocellular carcinoma