

QASIM AYUB

<http://www.sanger.ac.uk/people/directory/ayub-qasim>

ORCID ID: 0000-0003-3291-0917

Associate Professor Genomics
Director Genomics Facility
Monash University Malaysia
47500 Bandar Sunway
Selangor Darul Ehsan, Malaysia

Phone: +60-3-5514 6106
E-mail: qasim.ayub@monash.edu

EDUCATION

01/1987-12/1991 Ph.D. in Biological Sciences (Immunology)
Department of Biological Sciences
University of North Texas, Denton, USA

Prevention of endotoxic shock in mice using anti-tumor necrosis factor-alpha monoclonal antibody.

Graduated with honors (G.P.A. 4.0)
Doctoral work, travel and stay fully funded (Grant #391-MOST-002/87)

03/1980-07/1985 Bachelor of Medicine; Bachelor of Surgery (M.B;B.S.)
Khyber Medical College, University of Peshawar, Peshawar, Pakistan

RESEARCH & EMPLOYMENT

September, 2017 – Present **Associate Professor & Director Genomics Facility**
School of Science, Monash University Malaysia

Duties, responsibilities and achievements:

- Teaching, research and development of the genomics facility and bioinformatics.

May, 2008 – August 2017 **Research Associate and Staff Scientist**
Human Evolution Team (Team 19),
Genome Research Limited,
The Wellcome Trust Sanger Institute

Duties, responsibilities and achievements:

- Developed a method that can be used to universally test for positive selection and adaptation signals in different gene sets and populations using whole-genome sequencing data.
- Member of Analysis Group of The 1000 Genomes, HGDP-CEPH and Eastern Gorilla Sequencing Projects.
- Supervision of visitors and Sanger Ph.D. students, including input into their project design.
- External advisor for Ph.D. student at Department of Archaeology and Anthropology, University of Cambridge.
- Published > 20 papers in last 5 years including several on South Asian populations as first or corresponding author.
- Responsible for the team's wet lab and health and safety.

July, 2003- April, 2008

Visiting Professor

Institute of Biotechnology and Genetic Engineering (KIBGE),
University of Karachi, Pakistan.

Duties and responsibilities:

- Assisted in setting up this facility.
- Research co-supervisor of two doctoral students.

December, 1992 - April, 2007

Biomedical & Genetic Engineering Division Laboratories,
(Renamed "Institute of Biomedical and Genetic Engineering" in July 2007)
Government of Pakistan, Islamabad, Pakistan.

Deputy Director

May, 2001-April, 2007

Principal Scientific Officer

July, 1998 - April, 2007

Assistant Director

July, 1993 - May, 2001

Senior Scientific Officer

December, 1992 – June, 1993

Duties and responsibilities:

Administrative:

- Articulated goals, mission and vision of the laboratory's research programs.
- Oversight for compliance issues related to research and bioethics.
- Preparation and submission of grant proposals.
- Developed and coordinated research projects on human population genetics.
- Supervised a group of 10 researchers and technicians.
- Established the denaturing high performance liquid chromatography technique.
- Established lymphoblastoid cell lines of several indigenous populations of Pakistan. This is acknowledged internationally as a major Pakistani contribution (Science 2002, 296:261-262).

Teaching:

- Lectured on Human Molecular Biology, Bioinformatics and Biostatistics.
- Use of Genome Browsers and Statistical Package for Social Sciences.
- Trained new recruits and visitors in molecular biology and tissue culture.

June, 1990 – October, 1991

Research Fellow

The Cancer Center at Wadley Institutes of Molecular Medicine
9000 Harry Hines Boulevard, Dallas, Texas 75235, U.S.A.

Duties and responsibilities:

- Execution and reporting of several on-going phase I and II clinical research protocols being conducted at the institute under the supervision of Professor Amanullah Khan. These related to the evaluation of monoclonal antibodies, cytokines and platinum compounds in advanced malignancies.
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JOURNAL REFEREE:

Reviewed numerous papers for several journals of international repute over the past decade, including the following:

American Journal of Human Genetics (2015); American Journal of Physical Anthropology (2006, 2008, 2009, 2014 - 2016); Annals of Human Genetics (2017); Biology Direct (2010); BMC Medical Genetics (2011); European Journal of Human Genetics (2009, 2010, 2011, 2015); Forensic Science International: Genetics (2013, 2014); Genome Biology and Evolution (2014); Genomics (2016); Human Genetics (2015 - 2017); International Journal of Sociology and Anthropology, IJSA (2010); Journal of Human Genetics (2011, 2013, 2014, 2015); Journal of Medical Genetics (2009); Journal of Molecular and Genetic Medicine (2010); Journal of Postgraduate Medical Institute, JPMI (2011); Molecular Biology and Evolution (2015); Nature Communications (2016); PLoS Genetics (2013); PLoS One (2013 - 2016); Theoretical Biology and Medical Modelling (2017)

TECHNICAL REVIEW:

1. The Human Variome Project (<http://www.humanvariomeproject.org/>)
International Scientific Advisory Committee Member
2. Shifa Tameer-e-Millat University, Islamabad, Pakistan
Member Graduate Studies and Research Management Council
3. American Society of Human Genetics 9th, 10th, 11th and 2018 DNA Day Essay Contest Judge.
4. Panel referee for the Organization of Islamic Countries (OIC) Standing Committee on Scientific and Technological Cooperation (COMSTECH) Best Young Researcher Award.

FUNDING AGENCIES GRANT SUPERVISION

- 1 Higher Education Commission, Government of Pakistan, Islamabad, Pakistan.
List of Approved Ph.D. Supervisor in Biological Sciences
Grant Review Committee
 - 2 Pakistan Council for Science and Technology, Islamabad, Pakistan.
Grants Review Committee
 - 3 Third World Academy of Sciences, Trieste, Italy.
Research Grant Reviews
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GRANTS & AWARDS:

2008 – 2017	Wellcome Trust Core Grants to Wellcome Trust Sanger Institute [WT077009 and 098051]
2006	President of Pakistan's Medal of Excellence in Science (Tamgha-i-Imtiaz, T.I.).
2006	Research Support Grant for Active Scientists and Technologists, Pakistan Science Foundation, Islamabad, Pakistan.
1999 - 2001	Wellcome Trust Research Assistant, [CRIG No.053584/Z/98/Z] Department of Biochemistry, University of Oxford, Oxford OX1 3QU, UK.
1996 - 1997	Post-doctoral Fellowship in Molecular Pathology, International Centre for Genetic Engineering and Biotechnology, Padriciano I-34012, Trieste, Italy.
1987 - 1990	Thomas Jefferson Fellowship, United States Agency for International Development and the Ministry of Science & Technology, Government of Pakistan. [Grant #391-MOST-002/87].

TEACHING WORKSHOPS, TRAINING COURSES AND CONFERENCES - ORGANIZED:

1. Research Methods Workshop: The UCSC Genome Browser. Monash University Malaysia, Bandar Sunway, Malaysia, March 19, 2018.
2. Research Methods Workshop: Introduction to Ensembl. Monash University Malaysia, Bandar Sunway, Malaysia, February 26, 2018.
3. Introduction to Bio-Linux and High-throughput Genomics. Monash University Malaysia, Bandar Sunway, Malaysia, November 20-21, 2017.
4. Dr. S. Qasim Mehdi Memorial Symposium: Human Population and Disease Genomics. COMSTECH Secretariat, Islamabad, Pakistan, April 10-12, 2017.
5. Ensembl Workshop. National Research Centre, Cairo, Egypt, November 21-23, 2016.
6. Data Mining with Ensembl. In 41st International Nathiagali Summer College on Physics and Contemporary Needs: Computational Biology Session, Islamabad, Pakistan, July 25, 2016.
7. COMSTECH-SIUT Workshop on Bioinformatics: ENSEMBL Database Mining and Whole Genome Sequencing Analyses, Islamabad (December 16-18) and Karachi (December 20-22), Pakistan, 2014.
8. Bioinformatics: Database Mining and High Throughput Genomic Analyses Workshops. Islamabad (March 19-21) and Karachi (March 22-24), Pakistan, 2012.

9. Regional Training of the Trainers: WHO Workshop on Bioinformatics Methods and Software Handling, Cairo, Egypt, May 11-15, 2008.
10. First Human Genome Diversity Workshop, Islamabad, Pakistan, October 9-14, 2000.
11. Advanced Immunology Course for post-graduate medical students, Quaid-i-Azam Postgraduate Medical College, Pakistan Institute of Medical Sciences, Islamabad, Pakistan, April 1 to May 15, 1995. The course was part of their preparation for the FCPS Part I examination in Basic Medical Sciences, a mandatory requirement for the Fellowship of the College of Physicians and Surgeons, Pakistan.

PROFESSIONAL SOCIETIES AND COLLEGE MEMBERSHIPS:

University of Cambridge, Affiliated Postdoctoral Member at Clare Hall (2012 - 2017)
 University of North Texas Alumni Association (NT Exes ID#10160307)
 The American Society for Human Genetics (Membership Number:74924)
 The Human Genome Organization (Membership Number HUGO-00740)
 The Human Variome Project
 Pakistan Medical and Dental Council (PMDC; Registration Number 3048-N)
 Phi Kappa Phi Honor Society
 Global Alliance for Genomics and Health (GA4GH)

PUBLIC ENGAGEMENT:

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| 2013 – 2017 | Contributing writer to the Wellcome Trust Sanger Institute Blog. |
| 2009 – 2017 | Tour Leader Wellcome Trust Sanger Institute and volunteer at the Wellcome Trust Sanger Institute presentation during the Cambridge Science Festivals (2009, 2012, 2013, 2016 and 2017). |
| 2013 | <ul style="list-style-type: none"> • Interacted with artist Katie Paterson during her residency at the Wellcome Trust Sanger Institute as part of <i>Art in Global Health</i>, a Wellcome Collection project, that led to the creation of the award winning “Fossil Necklace” (https://www.youtube.com/watch?v=FuFWroMHUd8). • Presenter at the Wellcome Trust Sanger Institute stall “Beyond the Genome” at the Royal Society Summer Science Exhibition 2013, London. (http://sse.royalsociety.org/2013/exhibits/beyond-the-genome/). |
| 2009 | Contributed to an episode of the television series on The History Channel “Ancients Behaving Badly: Genghis Khan”, Blink Films. |
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SELECTED INVITED PRESENTATIONS:

1. Population sub-structure and high altitude adaptation in the Himalayas, Codon Genomics, Seri Kembangan, Malaysia (2018).
2. Setting up a research lab. In Aspiring Leaders in Science Workshop, Wellcome Sanger Institute, Wellcome Genome Campus, Hinxton (2018).
3. Next generation sequencing, Human genomic variation and Population and evolutionary genomics. In 41st International Nathiagali Summer College on Physics and Contemporary Needs: Computational Biology Session, Islamabad, Pakistan (2016).
4. High altitude adaptation in the Himalayan populations. Clare Hall Graduate Conference University of Cambridge, Cambridge, UK (2016).
5. The Kalash genetic isolate from Pakistan. Clare Hall, University of Cambridge, Cambridge, UK (2015).
6. "All that glitters is not gold" - Positive selection in recent human evolutionary history. IRIBHM - Université Libre de Bruxelles, Campus Erasme, Brussels, Belgium (2015).
7. The Hazaras from Pakistan and the genetic legacy of the Mongols. Centre of Development Studies, University of Cambridge, Cambridge, UK (2014).
8. Pakistan: An ethnolinguistic and genetic perspective. In Migrations and Transfers in Prehistory: Asian and Oceanic Ethnolinguistic Phylogeography, University of Bern, Switzerland (2014)
9. Genetic variation in Pakistan: Influence of geography, ethnicity and language. In 16th PGMI Symposium, Department of Medical Oncology, Post Graduate Medical Institute (PGMI), Lady Reading Hospital, Peshawar, Pakistan (2011).
10. Next-generation sequencing and the era of personal Y genomes. In Beyond the Genome: The True Gene Count, Human Evolution and Disease Genomics, Harvard Medical School, Boston, Massachusetts, USA. (2010).
11. Genetic variation in Pakistan: Influence of geography, ethnicity and language. In European School of Genetic Medicine Course in Genomic and Cultural Evolution of Humans, Bologna, Italy. (2010).
12. Pathogenesis of rheumatic heart disease: a systems biology approach. In 20th Annual Conference, Pakistan Cardiac Society, Rawalpindi, Pakistan. (2007).
13. Association of *ADRB1* polymorphism with heart failure in Pakistan. In World Health Updates, Basic Sciences, Karachi, Pakistan. (2007).
14. Genetics of heart failure in Pakistan. In 19th Annual Conference, Pakistan Cardiac Society, Islamabad, Pakistan. (2006).

QASIM AYUB COMPLETE LIST OF PUBLICATIONS
ORCID ID 0000-0003-3291-0917
Scopus Author ID: 6602356251

PEER REVIEWED PUBLICATIONS AS CORRESPONDING AUTHOR:

1. Chaubey G, **Q Ayub**, N Rai, S Prakash, V Mushrif-Tripathy, M Mezzavilla, AK Pathak, R Tamang, S Firasat, M Reidla, M Karmin, DS Rani, AG Reddy, J Parik, E Metspalu, S Rootsi, K Dalal, S Khaliq, SQ Mehdi, L Singh, M Metspalu, T Kivisild, C Tyler-Smith, R Villems and K Thangaraj. "Like sugar in milk": reconstructing the genetic history of the Parsi population. *Genome Biol* 18:110 (2017). PMID: 28615043.
2. Pagani L, V Colonna, C Tyler-Smith and **Q Ayub**. An ethnolinguistic and genetic perspective on the origins of the Dravidian-speaking Brahui in Pakistan. *Man In India* 97:267-278 (2017). PMID:28381901.
3. Hackinger S, T Kraaijenbrink, Y Xue, M Mezzavilla, Asan, G van Driem, MA Jobling, P de Knijff, C Tyler-Smith and **Q Ayub**. Wide distribution and altitude correlation of an archaic high-altitude-adaptive *EPAS1* haplotype in the Himalayas. *Hum Genet* 135:393-402 (2016). PMID: 26883865.
4. **Ayub Q**, M Mezzavilla, L Pagani, M Haber, A Mohyuddin, S Khaliq, SQ Mehdi and C Tyler-Smith. Response to Hellenthal *et al.* *Am J Hum Genet* 98:398-399 (2016). PMID: 26849117.
5. Arciero E, SA Biagini, Y Chen, Y Xue, D Luiselli, C Tyler-Smith, L Pagani and **Q Ayub**. Genes regulated by vitamin D in bone cells are positively selected in East Asians. *PLoS One* 10:e0146072 (2015). PMID: 26719974.
6. Shah SS, A Mohyuddin, V Colonna, SQ Mehdi and **Q Ayub**. Monoamine oxidase A gene polymorphisms and self reported aggressive behaviour in a Pakistani ethnic group. *J Pak Med Assoc* 65:818-824 (2015). PMID: 26228323.
7. **Ayub Q**, M Mezzavilla, L Pagani, M Haber, A Mohyuddin, S Khaliq, SQ Mehdi and C Tyler-Smith. The Kalash genetic isolate: Ancient divergence, drift, and selection. *Am J Hum Genet* 96:775-783 (2015). PMID: 25937445.
8. **Ayub Q**, B Yngvadottir, Y Chen, Y Xue, M Hu, SC Vernes, SE Fisher and C Tyler-Smith. FOXP2 targets show evidence of positive selection in European populations. *Am J Hum Genet* 92:696-706 (2013). PMID: 23602712.
9. **Ayub Q**. Male lineages in the Himalayan foothills: A commentary on Y-chromosome haplogroup diversity in the sub-Himalayan Terai and Duars populations of East India. *J Hum Genet* 56:813-814 (2011). PMID: 21975650.
10. Firasat S, S Khaliq, A Mohyuddin, M Papaioannou, C Tyler-Smith, PA Underhill and **Q Ayub**. Y-chromosomal evidence for a limited Greek contribution to the Pathan population of Pakistan. *Eur J Hum Genet* 15:121-126 (2007). PMID: 17047675.

11. Mansoor A, K Mazhar, S Khaliq, A Hameed, S Rehman, S Siddiqi, M Papaioannou, LL Cavalli-Sforza, SQ Mehdi and **Q Ayub**. Investigation of the Greek ancestry of populations from northern Pakistan. *Hum Genet* 114:484-490 (2004). PMID: 14986106.

PEER REVIEWED PUBLICATIONS AS FIRST AUTHOR:

1. **Ayub Q**, L Moutsianas, Y Chen, K Panoutsopoulou, V Colonna, L Pagani, I Prokopenko, GR Ritchie, C Tyler-Smith, MI McCarthy, E Zeggini and Y Xue. Revisiting the thrifty gene hypothesis via 65 loci associated with susceptibility to type 2 diabetes. *Am J Hum Genet* 94:176-185 (2014). PMID: 24412096.
2. **Ayub Q**, Y Xue and C Tyler-Smith. Genomic triumph meets clinical reality. *Genome Biol* 14:307 (2013). PMID: 23714135.
3. **Ayub Q** and C Tyler-Smith. Genetic variation in South Asia: assessing the influences of geography, language and ethnicity for understanding history and disease risk. *Brief Funct Genomic Proteomic* 8:395-404 (2009). PMID: 19535507.
4. Shah SS, **Q Ayub**, S. Firasat, F. Kaiser and SQ Mehdi. Y haplogroups and aggressive behavior in a Pakistani ethnic group. *Aggress Behav* 35:68-74 (2009). PMID: 18942110.
5. Mohyuddin A, **Q Ayub**, PA Underhill, C Tyler-Smith and SQ Mehdi. Detection of novel Y SNPs provides further insights into Y chromosomal variation in Pakistan. *J Hum Genet* 51:375-378 (2006). PMID: 16470330.
6. **Ayub Q**, A Mansoor, M Ismail, S Khaliq, A Mohyuddin, A Hameed, K Mazhar, S Rehman, S Siddiqi, M Papaioannou, A Piazza, LL Cavalli-Sforza and SQ Mehdi. Reconstruction of human evolutionary tree using polymorphic autosomal microsatellites. *Am J Phys Anthropol* 122:259-268 (2003). PMID: 14533184.
7. **Ayub Q**, A Mohyuddin, R Qamar, K Mazhar, T Zerjal, SQ Mehdi and C Tyler-Smith. Identification and characterisation of novel human Y-chromosomal microsatellites from sequence database information. *Nucleic Acids Res* 28:e8 (2000). PMID: 10606676.

CONTRIBUTING AUTHOR IN CONSORTIUM PAPERS:

1. Jota MS, DR Lacerda, JR Sandoval, PPR Vieira, D Ohasi, JE Santos-Júnior, O Acosta, C Cuellar, S Revollo, C Paz-y-Miño, R Fujita, GA Vallejo, TG Schurr, EM Tarazona-Santos, SDJ Pena, **Q Ayub**, C Tyler-Smith, FR Santos and The Genographic Consortium. New native South American Y chromosome lineages. *J Hum Genet* 61:593-603 (2016). PMID: 27030145 & 27453507.
2. Poznik GD, Y Xue, FL Mendez, TF Willems, A Massaia, MAW Sayres, **Q Ayub**, SA McCarthy, A Narechania, S Kashin, Y Chen, R Banerjee, JL Rodriguez-Flores, M Cerezo, H Shao, M Gymrek, A Malhotra, S Louzada, R Desalle, GRS Ritchie, E Cerveira, TW Fitzgerald, E Garrison, A Marcketta, D Mittelman, M Romanovitch, C Zhang, X Zheng-Bradley, GR Abecasis, SA McCarroll, P Flicek, PA Underhill, L Coin, DR Zerbino, F Yang, C Lee, L Clarke, A Auton, Y Erlich, RE Handsaker, The 1000 Genomes Project Consortium, CD Bustamante and C Tyler-Smith. Punctuated bursts in human male

- demography inferred from 1,244 worldwide Y-chromosome sequences. *Nat Genet* 48:593-599 (2016). PMID: 27111036.
3. **The 1000 Genomes Project Consortium.** A global reference for human genetic variation. *Nature* 526:68-74 (2015). PMID: 26432245.
 4. Colonna V, **Q Ayub**, Y Chen, L Pagani, P Luisi, M Pybus, E Garrison, Y Xue, C Tyler-Smith and The 1000 Genomes Project Consortium. Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. *Genome Biol* 15:R88 (2014). PMID: 24980144.
 5. Xue Y, Y Chen, **Q Ayub**, N Huang, EV Ball, M Mort, AD Phillips, K Shaw, PD Stenson, DN Cooper, C Tyler-Smith and 1000 Genomes Project Consortium. Deleterious- and disease-allele prevalence in healthy individuals: Insights from current predictions, mutation databases, and population-scale resequencing. *Am J Hum Genet* 91:1022-1032 (2012). PMID: 23217326.
 6. **The 1000 Genomes Project Consortium.** An integrated map of genetic variation from 1,092 human genomes. *Nature* 491:56-65 (2012). PMID: 23128226.
 7. MacArthur DG, S Balasubramanian, A Frankish, N Huang, J Morris, K Walter, L Jostins, L Habegger, JK Pickrell, SB Montgomery, CA Albers, ZD Zhang, DF Conrad, G Lunter, H Zheng, **Q Ayub**, MA DePristo, E Banks, M Hu, RE Handsaker, J Rosenfeld, M Fromer, M Jin, XJ Mu, E Khurana, K Ye, M Kay, GI Saunders, M-M Suner, T Hunt, IHA Barnes, C Amid, DR Carvalho-Silva, AH Bignell, C Snow, B Yngvadottir, S Bumpstead, DN Cooper, Y Xue, IG Romero, 1000 Genomes Project Consortium, J Wang, Y Li, RA Gibbs, SA McCarroll, ET Dermitzakis, JK Pritchard, JC Barrett, J Harrow, ME Hurles, MB Gerstein and C Tyler-Smith. A systematic survey of loss-of-function variants in human protein-coding genes. *Science* 335:823-828 (2012). PMID: 22344438.
 8. **The 1000 Genomes Project Consortium.** A map of human genome variation from population-scale sequencing. *Nature* 467:1061-1073 (2010). PMID: 20981092.

CONTRIBUTING AUTHOR IN OTHER PEER REVIEWED PUBLICATIONS:

1. Arciero E, T Kraaijenbrink, Asan, M Haber, M Mezzavilla, **Q Ayub**, W Wang, Z Pingcuo, H Yang, J Wang, MA Jobling, G van Driem, Y Xue, P de Knijff and C Tyler-Smith. Demographic history and genetic adaptation in the Himalayan region inferred from genome-wide SNP genotypes of 49 populations. *Mol Biol Evol* 35:1916-1933 (2018). PMID: 29796643.
2. Szpak M, M Mezzavilla, **Q Ayub**, Y Chen, Y Xue, C Tyler-Smith. *FineMAV*: prioritizing candidate genetic variants driving local adaptations in human populations. *Genome Biol* 19:5 (2018). PMID: 29343290.
3. Shi W, A Massaia, S Louzada, R Banerjee, P Hallast, Y Chen, A Bergström, Y Gu, S Leonard, MA Quail, **Q Ayub**, F Yang, C Tyler-Smith and Y Xue. Copy number variation arising from gene conversion on the human Y chromosome. *Hum Genet* 137:73-83 (2018). PMID: 29209947.

4. Pagani L, S Bose, **Q Ayub** and C Tyler-Smith. Kayasthas of Bengal legends, genealogies and genetics. *Economic and Political Weekly* LII(47):44-53 (2017).
5. Laso-Jadart R, C Harmant, H Quach, N Zidane, C Tyler-Smith, Q Mehdi, **Q Ayub**, L Quintana-Murci and E Patin. The genetic legacy of the Indian Ocean slave trade: Recent admixture and post-admixture selection in the Makranis of Pakistan. *Am J Hum Genet* 101:977-984 (2017). PMID: 29129317.
6. Xue Y, M Mezzavilla, M Haber, S McCarthy, Y Chen, V Narasimhan, A Gilly, **Q Ayub**, V Colonna, L Southam, C Finan, A Massaia, H Chheda, P Palta, G Ritchie, J Asimit, G Dedoussis, P Gasparini, A Palotie, S Ripatti, N Soranzo, D Toniolo, JF Wilson, R Durbin, C Tyler-Smith and E Zeggini. Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. *Nat Commun* 8:15927 (2017). PMID: 28643794.
7. Pagani L, DJ Lawson, E Jagoda, A Mörseburg, A Eriksson, M Mitt, F Clemente, G Hudjashov, M DeGiorgio, L Saag, JD Wall, A Cardona, R Mägi, MAW Sayres, S Kaewert, C Inchley, CL Scheib, M Järve, M Karmin, GS Jacobs, T Antao, FM Iliescu, A Kushniarevich, **Q Ayub**, C Tyler-Smith, Y Xue, B Yunusbayev, K Tambets, CB Mallick, L Saag, E Pocheshkhova, G Andriadze, C Muller, MC Westaway, DM Lambert, G Zoraqi, S Turdikulova, D Dalimova, Z Sabitov, GNN Sultana, J Lachance, S Tishkoff, K Momynaliev, J Isakova, LD Damba, M Gubina, P Nymadawa, I Evseeva, L Atramentova, O Utevska, F-X Ricaut, N Brucato, H Sudoyo, T Letellier, MP Cox, NA Barashkov, V Škaro, L Mulahasanovic, D Primorac, H Sahakyan, M Mormina, CA Eichstaedt, DV Lichman, S Abdullah, G Chaubey, JTS Wee, E Mihailov, A Karunas, S Litvinov, R Khusainova, N Ekomasova, V Akhmetova, I Khidiyatova, D Marjanović, L Yepiskoposyan, DM Behar, E Balanovska, A Metspalu, M Derenko, B Malyarchuk, M Voevoda, SA Fedorova, LP Osipova, MM Lahr, P Gerbault, M Leavesley, AB Migliano, M Petraglia, O Balanovsky, EK Khusnutdinova, E Metspalu, MG Thomas, A Manica, R Nielsen, R Villems, E Willerslev, T Kivisild and M Metspalu. Genomic analyses inform on migration events during the peopling of Eurasia. *Nature* 538:238-242 (2016). PMID: 27654910.
8. Boattini A, S Sarno, C Bini, V Pesci, C Barbieri, S De Fanti, A Quagliariello, L Pagani, **Q Ayub**, G Ferri, D Pettener, D Luiselli and S Pelotti. Mutation rates and discriminating power for 13 rapidly-mutating Y-STRs between related and unrelated individuals. *PLoS One* 11:e0165678 (2016). PMID: 27802306.
9. Bergström A, N Nagle, Y Chen, S McCarthy, MO Pollard, **Q Ayub**, S Wilcox, L Wilcox, RA van Oorschot, P McAllister, L Williams, Y Xue, RJ Mitchell and C Tyler-Smith C. Deep roots for aboriginal Australian Y chromosomes. *Curr Biol* 26:809-813 (2016). PMID: 26923783.
10. Espinosa JRF, **Q Ayub**, Y Chen, Y Xue and C Tyler-Smith. Structural variation on the human Y chromosome from population-scale resequencing. *Croat Med J* 56:194-207 (2015). PMID: 26088844.

11. Wei W, TW Fitzgerald, **Q Ayub**, A Massaia, BH Smith, AF Dominiczak, AD Morris, DJ Porteous, ME Hurles, C Tyler-Smith, and Y Xue. Copy number variation in the human Y chromosome in the UK population. *Hum Genet* 134:789-801 (2015). PMID: 25957587 & 25986439.
12. Xue Y, J Prado-Martinez, PH Sudmant, V Narasimhan, **Q Ayub**, M Szpak, P Frandsen, Y Chen, B Yngvadottir, DN Cooper, M de Manuel, J Hernandez-Rodriguez, I Lobon, HR Siegismund, L Pagani, MA Quail, C Hvilsom, A Mudakikwa, EE Eichler, MR Cranfield, T Marques-Bonet, C Tyler-Smith and A Scally. Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. *Science* 348:242-245 (2015). PMID: 25859046.
13. Karmin M, L Saag, M Vicente, MAW Sayres, M Järve, UG Talas, S Rootsi, A-M Ilumäe, R Mägi, M Mitt, L Pagani, T Puurand, Z Faltyskova, F Clemente, A Cardona, E Metspalu, H Sahakyan, B Yunusbayev, G Hudjashov, M DeGiorgio, E-L Loogväli, C Eichstaedt, M Eelmets, G Chaubey, K Tambets, S Litvinov, M Mormina, Y Xue, **Q Ayub**, G Zoraqi, TS Korneliussen, F Akhatova, J Lachance, S Tishkoff, K Momynaliev, F-X Ricaut, P Kusuma, H Razafindrazaka, D Pierron, MP Cox, GNN Sultana, R Willerslev, C Muller, M Westaway, D Lambert, V Skaro, L Kovacevic, S Turdikulova, D Dalimova, R Khusainova, N Trofimova, V Akhmetova, I Khidiyatova, DV Lichman, J Isakova, E Pocheshkhova, Z Sabitov, NA Barashkov, P Nymadawa, E Mihailov, JWT Seng, I Evseeva, AB Migliano, S Abdullah, G Andriadze, D Primorac, L Atramentova, O Utevska, L Yepiskoposyan, D Marjanovic, A Kushniarevich, DM Behar, C Gilissen, L Vissers, JA Veltman, E Balanovska, M Derenko, B Malyarchuk, A Metspalu, S Fedorova, A Eriksson, A Manica, FL Mendez, TM Karafet, KR Veeramah, N Bradman, MF Hammer, LP Osipova, O Balanovsky, EK Khusnutdinova, K Johnsen, M Remm, MG Thomas, C Tyler-Smith, PA Underhill, E Willerslev, R Nielsen, M Metspalu, R Villems and T Kivisild. A recent bottleneck of Y chromosome diversity coincides with a global change in culture. *Genome Res* 25:459-466 (2015). PMID: 25770088.
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