

Supplemental Materials

Supplemental Table 1 – Metadata of Samples

| Sample ID | Start Date | Start Location | | End Date | End Location | | Middle Location | |
|-----------|------------|----------------|-------|----------|--------------|--------|-----------------|--------|
| # | dd.mm | Lat. | Long. | dd.mm | Lat. | Long. | Lat. | Long. |
| 1 | 07.04 | 35.467 | 26.4 | 08.04 | 33.27 | 29.83 | 34.367 | 28.117 |
| 2 | 08.04 | 33.267 | 29.83 | 09.04 | 33.55 | 34.05 | 33.408 | 31.941 |
| 3 | 09.04 | 33.55 | 34.05 | 10.04 | 33.68 | 32.15 | 33.617 | 33.1 |
| 4 | 10.04 | 33.68 | 32.15 | 11.04 | 33.58 | 28.733 | 33.63 | 30.44 |
| 5 | 11.04 | 33.58 | 28.73 | 12.04 | 34.48 | 24.317 | 34.03 | 26.525 |
| 6 | 12.04 | 34.48 | 24.32 | 13.04 | 35.467 | 21.95 | 34.98 | 23.13 |
| 7 | 13.04 | 35.467 | 21.95 | 14.04 | 35.15 | 18.7 | 35.31 | 20.325 |
| 8 | 14.04 | 35.15 | 18.7 | 15.04 | 36.5 | 19 | 35.825 | 18.85 |
| 9 | 18.04 | 37.32 | 17.2 | 19.04 | 38.5 | 12.67 | 37.91 | 14.93 |
| 10 | 19.04 | 38.5 | 12.67 | 20.04 | 40.13 | 11.23 | 39.317 | 11.95 |
| 11 | 20.04 | 40.13 | 11.23 | 21.04 | 38.5 | 8.2 | 39.317 | 9.717 |
| 12 | 21.04 | 38.5 | 8.2 | 22.04 | 38.45 | 4.5 | 38.475 | 6.35 |
| 13 | 22.04 | 38.45 | 4.5 | 23.04 | 37.9 | 1 | 38.175 | 2.75 |
| 14 | 23.04 | 37.83 | 1.75 | 24.04 | 36.4 | 1.7 | 37.12 | 1.725 |
| 15 | 24.04 | 36.4 | 1.7 | 25.04 | 35.98 | -5.38 | 36.19 | -1.84 |
| 16 | 25.04 | 35.98 | -5.38 | 26.04 | 36.68 | -8.5 | 36.33 | -6.94 |

Supplemental Table 2 – Detailed Description of Common Bacteria

| Family | Genus | Gram Stain | Oxygen Requirement | Spore Forming | Habitat | Previously found airborne | Indoor or Outdoor | Location | Source | Citation | Description reference |
|--------------------|-----------------|------------|-----------------------|---------------|--|---------------------------|-------------------|--|--------------------|---|-------------------------------------|
| Unassigned | Unassigned | Variable | Variable | NA | NA | NA | | NA | NA | NA | NA |
| Corynebacteriaceae | Corynebacterium | + | Variable | N | Variable, includes animal microbiota, soil, water, plants, and food products | Y | Both | Eastern Mediterranean; Mali; Indoor; Beijing | Sahar, Sahar/Sahel | Griffin et al., 2007; Kellogg et al., 2005; Hwang et al., 2016; Fang et al., 2007; Dybwad et al., 2012 Barberan et al., 2015; Hwang et al., 2016; Bertolini et al., 2013; DeLeon-Rodriguez et al., 2013; Robertson et al., 2013 Adams et al., 2015; Cuthbertson et al., 2017; Pearce et al., 2010 | Bernard, 2012; Alberto et al., 2017 |
| Bifidobacteriaceae | Bifidobacterium | + | Anaerobic | N | Animal and human microbiota | Y | Both | Indoor dust; Beijing; Milan; NYC Subways | | Bertolini et al., 2013; DeLeon-Rodriguez et al., 2013; Robertson et al., 2013 Adams et al., 2015; Cuthbertson et al., 2017; Pearce et al., 2010 | O'Callaghan & van Sinderen, 2016 |
| Weeksellaceae | Cloacibacterium | - | Facultative Anaerobic | N | Aquatic | Y | Both | Indoor; Chicago IL, USA; Antarctica; Arctic | | Cuthbertson et al., 2017; Pearce et al., 2010 | Allen et al., 2006 |

| | | | | | | | | | | | | |
|-------------------|-------------------|----------|-----------------------|----------|------------------------------|---|---------|--|---------------|---|--|--|
| Chitinophagaceae | Sediminibacterium | - | Aerobic | N | Freshwater; Soil | N | - | | | | | Kang et al., 2014; Qu and Yuan, 2008 |
| Bacillaceae | Bacillus | + | Facultative Anaerobic | Y; U | Soil | Y | Outdoor | Washington D.C | n/a | Be et al., 2015 | | Su and Xu, 2014 |
| Paenibacillaceae | Ammoniphilus | Variable | Aerobic | Y | Plant roots, resin fragments | Y | Both | France; Beijing | | Cao et al., 2014; Brudan et al., 2009 | | Zaitsev et al., 1998; Rainey et al., 2015; Lin et al., 2015; |
| Planococcaceae | Unassigned | Variable | Variable | Variable | Variable | Y | Outdoor | Israel; Milan | N.Africa | Mazar et al., 2016; Bertolini et al., 2013 | | Shivaji et al., 2014 |
| Staphylococcaceae | Staphylococcus | + | Facultative Anaerobic | N | Variable | Y | Both | Japan, Slovenia; Norway; France; Beijing | Asian deserts | Maki et al., 2018; Mulec et al., 2017; Fang et al., 2007; Barberan et al., 2015; Dybwad et al., 2012; Martin-Sanchez et al., 2014 | | G_tz et al., 2006 |

| | | | | | | | | | | | |
|-----------------------|----------------|-------------|-------------|-------------|--|---|---------|---------------------------|--------------------|-----------------------------------|--|
| Turicibacteraceae | Turicibacter | + | Anaerobic | N | Animal and human microbiota | Y | Outdoor | Beijing | n.a | Cao et al., 2014 | Bosshard et al., 2002 |
| Clostridiaceae | Caloramator | + | Anaerobic | Variable | Thermal environments | Y | Outdoor | Beijing | | Cao et al., 2014 | Seyfried et al., 2002 |
| Clostridiaceae | Clostridium | + | Anaerobic | Y | Variable, includes human microbiota, animal microbiota, and plant microbiota | Y | Outdoor | Israel | Clear days | Gat et al., 2017 | Wiegel et al., 2006 |
| Clostridiaceae | SMB53 | Not defined | Not defined | Not defined | Gut microbe | N | | | | | Hsieh Y-H. et al., 2016 |
| Peptostreptococcaceae | Unassigned | Variable | Anaerobic | N | Variable, includes human microbiota, manure, soil, and sediments, and deep sea vents | Y | Indoor | Denmark | Indoor | Vestergaard et al., 2018 | Rosenberg et al., 2013; Galperin et al., 2016; |
| Veillonellaceae | Unassigned | - | Variable | N | Variable, includes beer spoilage, animal and human microbiota | N | | | | | Marchandin et al., 2014 |
| Bradyrhizobiaceae | Bradyrhizobium | - | Aerobic | N | Soil, plant roots | Y | Outdoor | Beijing; Washington DC | Urban | Cao et al., 2014; Be et al., 2015 | Marcondes de Souza et al., 2014 |
| Rhodobacteraceae | Paracoccus | - | Aerobic | N | Soil | Y | Outdoor | Atlantic Ocean; US Virgin | Sahar, Sahar/Sahel | Griffin et al., 2006; 2007; | Urakami et al., 1990; |

| | | | | | | | | | | | |
|--------------------|---------------|---|-----------------------|---|--|---|---------|---------------------------------------|-----------------------------|--|--|
| Comamonadaceae | Unassigned | - | Variable | N | Variable, includes aquatic, soil, animal microbiome | Y | Outdoor | Islands; Mali Japan, European Alps | Asian deserts; Sahara/Sahel | Kellogg et al., 2004 Maki et al., 2018; Meola et al., 2015 Cao et al., 2014; Byung Cheol Cho & Chung Yeon Hwang 2011 | Kelly et al., 2006 Willems et al., 1991; Willems 2014 Mikhailov et al., 2006 |
| Alteromonadaceae | Alteromonas | - | Aerobic | N | Marine | Y | Outdoor | Beijing, East Sea | | | |
| Enterobacteriaceae | Unassigned | - | Facultative Anaerobic | N | Variable, includes aquatic, terrestrial, animal microbiota (prokaryotes) | Y | Outdoor | Japan | | Maki et al., 2018 | Octavia and Lan, 2014 |
| Enterobacteriaceae | Erwinia | - | Facultative Anaerobic | N | Plant microbiome | Y | Outdoor | Greater Mexico city | | Garcia-Mena et al., 2016 | Kado, 2006 |
| Enterobacteriaceae | Escherichia | - | Facultative Anaerobic | N | Human microbiota | Y | Both | Spain, Mexico City | | Sanz et al., 2005; Santos-Burgoa and Rosas, 2015 | Janda 2006; Welch 2006 Bouvet and Grimont, 1986 |
| Moraxellaceae | Acinetobacter | - | Aerobic | N | Human microbiota | N | | | | | |

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|-------------------|---------------|---|-----------------------|---|---------------------------------------|---|---------|--|--|---|
| Moraxellaceae | Enhydrobacter | - | Facultative Anaerobic | N | Eutrophic lake, human microbiome | Y | Both | Beijing, Norway (underground subway station), Hong Kong (subway station) | Cao et al., 2014; Dybwad et al., 2012; Marcus et al., 2014 | Staley et al., 1987 |
| Salinisphaeraceae | Salinisphaera | - | Aerobic | N | Hypersaline environments | Y | Outdoor | Beijing | Cao et al., 2014 | Crespo-Medina et al., 2009; Vetriani et al., 2014 |
| Vibrionaceae | Vibrio | - | Facultative Anaerobic | N | Aquatic, some species human pathogens | Y | Outdoor | Beijing | Cao et al., 2014; Fang et al., 2007 | Madigan and Martinko, 2005 |
| Sinobacteraceae | Unassigned | - | Aerobic | N | Soil | N | | - | | Zhou et al., 2008 |

Supplemental Figure 1 – Backward trajectories constructed using NOAA HYSPLIT MODEL for each sample.

