Contamination Protocol				
	Sequencing Center	BEI		Collaborator
1.	A Sequencing Center identifies a contaminant in a DNA or microbial sample.	 BEI identifies a problem with a sample during their quality control. BEI contacts the collaborator who 	1.	The collaborator identifies a problem with the sample that they sent to BEI or to the Sequencing Center.
2.	The Sequencing Center notifies the collaborator and BEI about the issue and cc's NIH.	2. BEI contacts the collaborator who provided the strain and cc's NIH. NIH forwards the information to the Sequencing Center	2.	The collaborator contacts the Sequencing Center to discuss the issue and develop a draft plan to resolve the issue. The draft plan is communicated
3.	The collaborator proposes a draft plan to the Sequencing Center.	3. The collaborator proposes a plan forward to BEI then the draft plan is communicated to the Sequencing	3	to BEI. If the collaborator initially contacts
4.	The Sequencing Center reviews the draft plan, finalizes the plan with their collaborator and informs NIH.	Center. 4. The Sequencing Center reviews the		NIH, NIH will redirect the collaborator to the Sequencing Center and BEI.
5.	NIH contacts BEI and cc's the Sequencing Center about the contamination and the plan forward	draft plan, finalizes a plan forward with their collaborator and cc's NIH.5. NIH communicates the plan to BEI.	4.	Once a plan is received from the collaborator, BEI or the Sequencing Center will proceed through the same steps as if they had identified the contamination themselves.
6.	BEI will contact the collaborator if a new microbial or DNA sample is needed and destroy the original sample when a new sample is received.	6. BEI will contact the collaborator if a new microbial or DNA sample is needed and destroy the original sample when the new sample is received.		contamination themserves.
7.	If a strain will not be sequenced due to contamination, the Sequencing Center will contact the DACC to update the catalog entry, including why the project was dropped and BEI will destroy the contaminated sample.	7. If a strain will not be sequenced due to contamination, the Sequencing Center will contact the DACC to update the catalog entry, including why the project was dropped and BEI will destroy the contaminated sample.		

Collaborator Synopsis

If you identify a problem (e. g. contamination) with a sample that you contributed to the Human Microbiome Project, please contact both the Sequencing Center that will be sequencing the sample and the Biodefense and Emerging Infections Research Resources Repository (BEI) (if the sample is being deposited there), as soon as possible, so a plan to resolve the problem can be formulated and executed.