S10 Table. OTU overlaps between/among technical replicates at different sequencing depth [b]

# of Sequences Resampled [c]	With singletons			Without singletons		
	# of Total OTU	OTUs overlap		# of Total OTU	OTUs overlap	
		Between	Among		Between	Among
160000	24745	**0.4391**	**0.3045**	14399	**0.6650**	**0.5257**
150000	24088	**0.4386**	**0.3039**	14362	**0.6553**	**0.5150**
120000	21862	**0.4331**	**0.2970**	14018	**0.6130**	**0.4685**
100000	20129	**0.4263**	**0.2902**	13647	**0.5875**	**0.4413**
80000	18158	**0.4222**	**0.2862**	13018	**0.5544**	**0.4054**
60000	15813	**0.4163**	**0.2793**	12141	**0.5173**	**0.3678**
50000	14615	**0.4073**	**0.2707**	11366	**0.5040**	**0.3554**
30000	11341	**0.3896**	**0.2529**	9510	**0.4541**	**0.3068**
20000	9328	**0.3668**	**0.2311**	8087	**0.4161**	**0.2686**
10000	6531	**0.3199**	**0.1877**	5953	**0.3528**	**0.2110**
5000	4309	**0.2873**	**0.1592**	4098	**0.2985**	**0.1635**
2000	2501	**0.2067**	**0.1004**	2339	**0.2262**	**0.1116**
1000	1540	**0.1641**	**0.0708**	1514	**0.1706**	**0.0740**
500	892	**0.1281**	**0.0493**	899	**0.1378**	**0.0534**
200	437	**0.0813**	**0.0275**	429	**0.0863**	**0.0256**
100	230	**0.0688**	**0.0261**	239	**0.0527**	**0.0167**

[a] Jaccard overlap, not considering sequence abundances of OTUs.

[b] One soil sample were tagged three times and deep sequenced. More than 160,000 sequences were obtained for each tagged PCR library.

[c] Sequence resampling was done after OTUs were generated.