1 **Supplementary information**

2 **Supplementary Figure S1: Microbial composition in individual samples at the phylum**

3 **level.** (A) Fungal and (B) bacterial abundance (%) across DW samples. The low abundant

4 phyla Acidobacteria, Chloroflexi, Cyanobacteria, Spirochaetes, Synergistetes,

5 Verrucomicrobia and other unclassified/unassigned reads are combined in the miniscule

6 'others'. Gap in the dataset refer to samples where sequence data could not be generated.
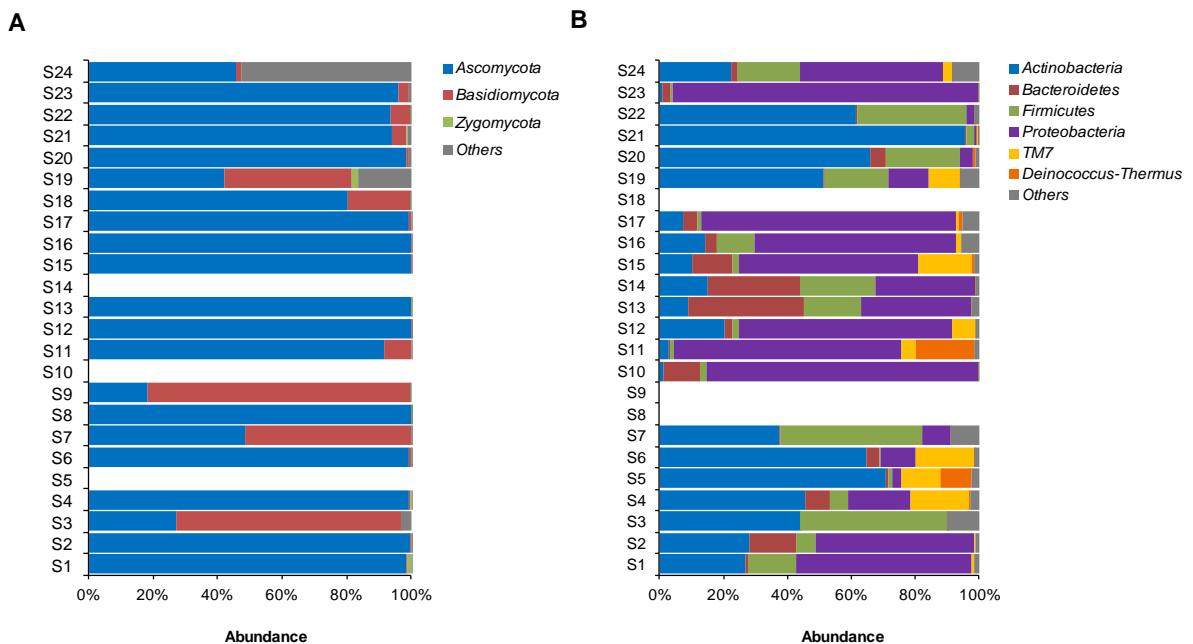
Supplementary Figure S2: Significant co-occurrence and co-exclusion interactions among

bacterial and fungal OTUs in the DWs microbiome. Predicted pairwise interaction network

between the bacterial and fungal OTUs generated from the OTU matrix. The displayed

pairwise co-occurrences appeared in at least 50% of all samples and were dominated by

positive correlations.
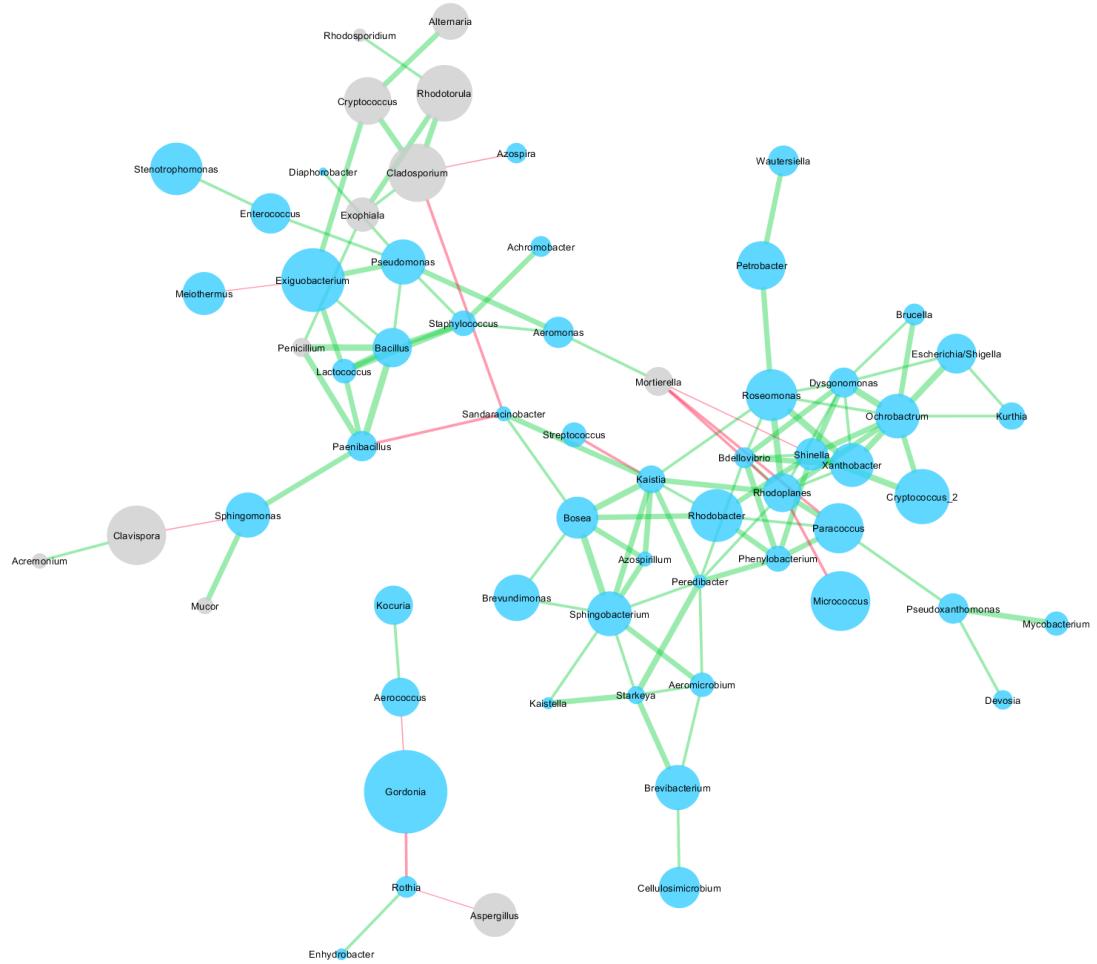
13 **Supplementary Table S1:** Summary table of 16S rRNA gene and ITS gene based amplicon

14 profiles obtained. **'**No reads' indicates samples where sequences reads could not be generated.

15 SRR represents the SRA accession numbers obtained after deposition of raw reads to NCBI

16 database.

	Bacterial Richness				Fungal Richness		
Samples	OTUs	Counts	SRR	Samples	OTUs	Counts	SRR
S1	97	12056	*3335213*	**S1**	26	4536	*3354512*
S2	104	14880	*3279031*	**S2**	30	47413	*3354513*
S3	35	13294	*3335242*	**S3**	64	52407	*3354514*
S4	105	11086	*3343755*	**S4**	32	53664	*3354515*
S5	56	4812	*3343756*	**S5**	No reads	No reads	No reads
S6	104	8872	*3343757*	**S6**	43	9514	*3354535*
S7	112	5790	*3343758*	**S7**	26	28574	*3354573*
S8	No reads	No reads	No reads	**S8**	22	37174	*3354574*
S9	No reads	No reads	No reads	**S9**	60	24041	*3354575*
S10	115	17912	*3343759*	**S10**	No reads	No reads	No reads
S11	55	1511	*3343760*	**S11**	33	14060	*3354576*
S12	60	961	*3343761*	**S12**	26	19847	*3354577*
S13	104	14995	*3343763*	**S13**	28	9602	*3354578*
S14	96	6661	*3343796*	**S14**	No reads	No reads	No reads
S15	107	9683	*3343797*	**S15**	15	10340	*3354579*
S16	50	127	*3343798*	**S16**	20	3520	*3354580*
S17	107	3580	*3343799*	**S17**	18	3601	*3354581*
S18	No reads	No reads	No reads	**S18**	30	2162	*3354582*
S19	95	24429	*3343800*	**S19**	104	4372	*3354583*
S20	29	100	*3343802*	**S20**	25	660	*3354584*
S21	71	8529	*3343803*	**S21**	45	891	*3354585*
S22	110	26115	*3343805*	**S22**	27	472	*3354587*
S23	92	15960	*3343810*	**S23**	30	436	*3354588*
S24	150	13036	*3335236*	**S24**	40	49511	*3354600*

Supplementary Table S2: Dishwasher alpha diversity summary post rarefaction of sequence counts. **'NA'** indicates samples in which sequences reads were not generated.

	Bacterial Diversity				Fungal Diversity		
Samples	*Richness Taxa_S*	*Shannon_H*	*Chao-1*	**Samples**	Richness Taxa_S	Shannon_H	Chao-1
S1	69	2.7	78	**S1**	10	0.7633	11
S2	75	2.9	82	**S2**	5	0.32	5
S3	18	1.2	19	**S3**	16	1.658	16
S4	75	2.2	103	**S4**	10	0.9061	12
S5	48	1.7	54	**S5**	NA	NA	NA
S6	72	2.0	83	**S6**	13	1.441	16
S7	87	2.7	108	**S7**	3	0.03494	4
S8	NA	NA	NA	**S8**	19	1.601	24
S9	NA	NA	NA	**S9**	NA	NA	NA
S10	78	2.4	92	**S10**	15	1.655	17
S11	-	-	-	**S11**	7	0.3897	9
S12	-	-	-	**S12**	8	0.8721	8
S13	68	2.5	79	**S13**	NA	NA	NA
S14	73	2.8	103	**S14**	4	0.697	4
S15	84	3.0	105	**S15**	10	1.039	25
S16	-	-	-	**S16**	7	0.261	10
S17	-	-	-	**S17**	12	1.632	14
S18	NA	NA	NA	**S18**	42	2.714	46
S19	51	2.2	62	**S19**	14	0.8477	16
S20	-	-	-	**S20**	26	1.481	32
S21	50	2.0	55	**S21**	21	2.483	23
S22	59	2.2	74	**S22**	26	1.276	30
S23	57	1.3	83	**S23**	22	1.669	31
S24	110	3.6	133	**S24**	10	0.7633	11

19 **Supplementary Table S3:** Summary of p-values from pairwise comparisons on bacterial
20 alpha diversity indices using Wilcoxon-Mann-Whitney.

Chao-1	Year	0-4	5-7	Freq	1-3	7	WH	MS	SH	MH
	0-4	-	0.43	1-3	-	0.56	MS	-	0.55	0.31
	5-7	0.43	-	7	0.56	-	SH	0.55	-	0.62
	8	0.47	0.21	14	0.99	0.70	MH	0.31	0.62	-
							H	0.27	0.49	0.72
Shannon_H	Year	0-4	5-7	Freq	1-3	7	WH	MS	SH	MH
	0-4	-	0.52	1-3	-	0.16	MS	-	0.35	0.07
	5-7	0.52	-	7	0.16	-	SH	0.35	-	0.28
	8	0.37	0.22	14	0.63	0.16	MH	0.07	0.28	-
							H	0.28	0.71	0.66
Richness	Year	0-4	5-7	Freq	1-3	7	WH	MS	SH	MH
	0-4	-	0.41	1-3	-	0.28	MS	-	0.42	0.24
	5-7	0.41	-	7	0.28	-	SH	0.42	-	0.67
	8	0.30	0.13	14	0.99	0.46	MH	0.24	0.67	-
							H	0.20	0.46	0.65

21 **Supplementary Table S4:** Summary of p-values from pairwise comparisons on fungal alpha
22 diversity indices using Wilcoxon-Mann-Whitney (* $p \le 0.05$)

Chao-1	Year	0-4	5-7	Freq	0-6	WH	MS	SH	MH
	0-4	-	0.72	7-14	0.20	MS	-	0.19	0.27
	5-7	0.72	-			SH	0.19	-	0.71
	8	0.91	0.82			MH	0.27	0.71	-
						H	0.19	0.01*	0.02*
Shannon_H	Year	0-4	5-7	Freq	0-6	WH	MS	SH	MH
	0-4	-	0.04*	7-14	0.31	MS	-	0.28	0.64
	5-7	0.04*	-			SH	0.28	-	0.38
	8	0.84				MH	0.64	0.38	-
						H	0.02*	0.0009*	0.003*
Richness	Year	0-4	5-7	Freq	0-6	WH	MS	SH	MH
	0-4	-	0.56	7-14	0.4	MS	-	0.33	0.25
	5-7	0.56	-			SH	0.33	-	0.85
	8	0.98	0.60			MH	0.25	0.85	-
						H	0.05*	0.01*	0.01*

23 **Supplementary Table S5:** Summary from redundancy based ANOVA analysis done using
24 each of the factors (999 permutations). The composition of the bacterial community was
25 significantly affected by the factors 'years of use' and 'frequency' of DWs. The composition
26 of fungal community was significantly affected by years of use, frequency of use and tap
27 water hardness. df: degrees of freedom; F: ratio of the between groups variance and within
28 groups variance; p: p-values. Star indicates the level of significance of each factor: '*' p <
29 0.05.

Source	Factors	df	Variance (%)	F	p
Bacteria Diversity	Years (0-4y, 5-7y and 8y)	2	23.44	1.34	0.047*
	Temperature (≥65°C, ≤60°C)	1	9.63	1.11	0.299
	Frequency of use (1-3, 7 and 14)	2	27.21	1.55	0.022*
	Water Hardness (H,MH,SH and MS)	3	24.00	0.91	0.660
Fungi Diversity	Years (0-4y, 5-7y and 8y)	2	9.47	1.32	0.043 *
	Temperature (≥65°C, ≤60°C)	1	4.04	1.12	0.280
	Frequency of use (0-7 and 14)	1	5.78	1.61	0.034 *
	Water Hardness (H,MH,SH and MS)	3	18.87	1.76	0.017 *

30 **Supplementary Table S6**: PERMANOVA based on Bray-Curtis dissimilarity index and
31 dishwasher conditions using 999 permutations. The analyses were executed using the vegan
32 package for R software. df: degrees of freedom; R^2: coefficient of determination; p: p-values.
33 Star indicates the level of significance of each factor: '*' p < 0.05.

Source	Factors	df	R^2	p
Bacteria Diversity	Years of use	2	0.11	0.186
	Temperature	1	0.05	0.386
	Water hardness	3	0.13	0.519
	Frequency of use	2	0.14	0.045*
	Residuals	12	0.56	
Fungi Diversity	Years of use	2	0.10	0.200
	Temperature	1	0.06	0.135
	Water Hardness	3	0.17	0.018*
	Frequency of use	1	0.09	0.127
	Residuals	13	0.58	