

Table S1. Identified co-different genus associated with RAS, which showed a positive difference equal to or higher than 10% (in terms of relative abundance).

Contributing OTU	NSctrl (n=28)	NSras (n=31)	Sras (n=19)	P1	P2	P3
Acholeplasma	0.157±0.043	0.0087±0.00	0.046±0.018	0.00	0.01	0.06
	4	45	7	1	8	7
Acidaminococcus	0.0004±0.00	0±0	0.0001±0.00	0.02	0.41	0.38
	04		01	4	2	0
Acidibacter	0.0004±0.00	0±0	0±0	0.01	0.08	1.00
	04			1	8	0
Aeromonas	0.0001±0.00	0.0007±0.00	0±0	0.02	0.51	0.00
	01	07		5	8	9
Anaeroglobus	0.0551±0.01	0.0186±0.00	0.0175±0.00	0.01	0.01	0.93
	46	63	38	7	5	5
Anaerovorax	0.0014±0.00	0±0	0.0004±0.00	0.00	0.03	0.02
	11		04	0	1	1
Asteroleplasma	0.0036±0.00	0.0001±0.00	0.0004±0.00	0.00	0.01	0.07
	13	01	03	2	5	3
Bacteroidales	0.2323±0.09	0.0083±0.00	0.0014±0.00	0.00	0.00	0.16
		47	09	4	1	6
Bacteroides	0.0969±0.01	0.0172±0.00	0.022±0.008	0.00	0.00	0.63
	79	55	4	1	1	3

Bilophila	0.0003±0.00	0±0	0±0	0.05	0.15	1.00
	03			1	3	0
Bryobacter	0.0007±0.00	0±0	0±0	0.00	0.01	1.00
	07			1	4	0
Ca.	0.0032±0.00	0.0002±0.00	0.0015±0.00	0.00	0.29	0.00
Endomicrobium	12	02	11	5	4	0
Ca. Tammella	0.0031±0.00	0±0	0.0003±0.00	0.00	0.00	0.05
	1		02	1	7	5
Catonella	0.6601±0.09	0.4024±0.05	0.4044±0.06	0.01	0.03	0.98
	8	46	77	7	8	3
Centipeda	0.184±0.036	0.0831±0.01	0.1057±0.02	0.01	0.08	0.42
	7	83	13	1	6	7
Christensenellacea	0.0025±0.00	0.0003±0.00	0±0	0.04	0.00	0.30
e	14	02		5	2	5
Crenarchaeota	0±0	0.0004±0.00	0±0	0.03	1.00	0.08
		02		2	0	9
Defluviitaleaceae	0.085±0.018	0.026±0.005	0.0326±0.00	0.00	0.01	0.50
	9	2	75	1	6	4
Deinococcus	0.0004±0.00	0.0011±0.00	0±0	0.03	0.08	0.00
	04	11		0	6	1
Desulfobulbus	0.0058±0.00	0.0019±0.00	0.0059±0.00	0.01	0.97	0.16
	12	07	25	0	5	5

Desulfomicrobium	0.0062±0.00	0±0	0.0002±0.00	0.00	0.01	0.14
	36		02	1	9	4
Dialister	0.2031±0.04	0.0612±0.00	0.098±0.02	0.00	0.01	0.09
	11	81		1	9	9
Eggerthia	0.0231±0.00	0.0019±0.00	0.0067±0.00	0.00	0.07	0.33
	79	05	42	1	4	1
Elizabethkingia	0±0	0.0006±0.00	0±0	0.00	1.00	0.01
		04		4	0	6
Elusimicrobia	0.0137±0.00	0.0001±0.00	0.0027±0.00	0.00	0.16	0.08
	84	01	19	3	4	5
Enterococcus	0.0011±0.00	0.0004±0.00	0.0005±0.00	0.03	0.17	0.75
	06	02	04	0	9	8
Ezakiella	0.014±0.004	0.0007±0.00	0.0091±0.00	0.00	0.45	0.03
	2	04	53	1	9	6
Filifactor	0.4198±0.07	0.1159±0.02	0.3909±0.18	0.00	0.90	0.07
	23	42	82	1	1	1
Fretibacterium	0.2809±0.09	0.0685±0.01	0.1636±0.03	0.00	0.31	0.02
	71	54	69	2	4	5
Geobacter	0.0001±0.00	0.0007±0.00	0±0	0.02	0.51	0.00
	01	05		5	8	9
Ignavibacteria	0.0035±0.00	0±0	0.0016±0.00	0.00	0.54	0.00
	26		14	1	3	0

Kocuria	0.0008±0.00	0±0	0±0	0.00	0.00	1.00
	05			0	4	0
Lachnoanaerobaculum	0.2657±0.02	0.41±0.062	0.3901±0.06	0.03	0.08	0.82
	93		42	2	9	6
Lactococcus	0.0014±0.00	0.0006±0.00	0±0	0.03	0.00	0.01
	06	03		7	0	6
Lentimicrobiaceae	0.1711±0.04	0.0502±0.00	0.0749±0.02	0.00	0.07	0.41
	68	91	46	4	1	2
Leptotrichia	1.7866±0.22	3.9499±0.82	2.7362±0.46	0.00	0.08	0.23
	49	34	72	4	0	7
Lysobacter	0.0015±0.00	0.0006±0.00	0.0007±0.00	0.02	0.07	1.00
	07	03	05	5	5	0
Microbacterium	0.0005±0.00	0.0001±0.00	0±0	0.03	0.04	1.00
	04	01		1	7	0
Moraxella	0.5556±0.21	0.1133±0.07	0.008±0.005	0.03	0.00	0.11
	06	22	8	9	2	5
Morganella	0.0048±0.00	0±0	0±0	0.00	0.02	1.00
	3			1	3	0
Moryella	0.0079±0.00	0.0013±0.00	0.002±0.000	0.00	0.00	0.24
	13	04	9	1	1	5
Mycoplasma	0.1001±0.02	0.0374±0.00	0.0517±0.01	0.00	0.05	0.34
	12	78	37	6	9	4

Nitrospiraceae	0.001±0.000	0.0001±0.00	0±0	0.00	0.00	1.00
	9	01		1	1	0
Paracoccus	0.001±0.000	0.0003±0.00	0.0008±0.00	0.01	0.65	0.11
	4	02	06	6	8	7
Parascardovia	0±0	0.0008±0.00	0±0	0.00	1.00	0.00
		05		1	0	5
Parvimonas	0.2109±0.04	0.0965±0.01	0.115±0.023	0.00	0.04	0.52
	29	54		2	3	7
Pelospora	0.0077±0.00	0.0004±0.00	0.0043±0.00	0.00	0.47	0.31
	28	03	35	1	1	9
Phocaeicola	0.0241±0.00	0.005±0.001	0.0161±0.00	0.00	0.37	0.04
	36		71	1	9	8
Porphyromonas	6.5812±0.49	4.3845±0.59	4.6934±0.81	0.00	0.04	0.76
	88	54	42	6	6	9
Propionivibrio	0.0022±0.00	0.0003±0.00	0.001±0.000	0.03	0.24	0.05
	09	02	6	1	2	4
Pseudoramibacter	0.0059±0.00	0.0019±0.00	0.0031±0.00	0.02	0.12	0.48
	15	1	11	1	1	4
Pyramidobacter	0.0057±0.00	0.0009±0.00	0.0005±0.00	0.00	0.00	0.35
	15	04	03	4	2	1
Ralstonia	0.0016±0.00	0.0007±0.00	0.0026±0.00	0.02	0.50	0.15
	08	03	12	0	1	0

Rhodospirillales	0.0055±0.00	0.0001±0.00	0.0018±0.00	0.00	0.08	0.00
	19	01	1	2	2	0
Rickettsiales	0.0001±0.00	0.0017±0.00	0.0002±0.00	0.00	1.00	0.00
	01	15	02	0	0	0
Rikenellaceae	0.1195±0.02	0.0205±0.00	0.0675±0.02	0.00	0.09	0.03
	32	51	12	1	9	3
Roseburia	0.0759±0.01	0.0076±0.00	0.042±0.015	0.00	0.07	0.00
	24	21	1	1	8	7
Rothia	0.2585±0.04	0.6597±0.16	0.4548±0.13	0.00	0.20	0.32
	23	13	16	6	7	5
Sediminispirochaet a	0.0058±0.00	0.0001±0.00	0.0012±0.00	0.00	0.11	0.00
	26	01	12	4	8	0
Shuttleworthia	0.0137±0.00	0.0033±0.00	0.0059±0.00	0.00	0.05	0.30
	35	12	21	3	1	1
Sneathia	0±0	0.0006±0.00	0.0019±0.00	0.00	0.00	0.00
		06	11	4	0	7
Sphaerochaeta	0.0027±0.00	0.0003±0.00	0.0003±0.00	0.01	0.02	1.00
	13	02	02	9	3	0
Spirochaetaceae	2.2324±0.26	0.5967±0.09	1.0848±0.22	0.00	0.00	0.05
	93	03	17	1	4	1
Spirochaetes	0.0013±0.00	0±0	0±0	0.00	0.00	1.00
	1			0	0	0

Steroidobacter	0.0006±0.00	0±0	0±0	0.00	0.02	1.00
	06			3	5	0
Succiniclasticum	0.0012±0.00	0±0	0.0001±0.00	0.00	0.00	0.38
	06		01	0	2	0
Terrimonas	0.0004±0.00	0±0	0±0	0.02	0.08	1.00
	03			4	6	0
Veillonella	4.4598±0.84	7.1675±0.75	8.1253±1.56	0.01	0.04	0.55
	22	94	18	9	8	1
Weissella	0.0016±0.00	0.0003±0.00	0.0004±0.00	0.00	0.01	0.48
	05	01	03	0	3	9
Wolinella	0.0169±0.00	0.0009±0.00	0.003±0.001	0.00	0.00	0.08
	35	04	1	1	1	6
Xanthomonas	0±0	0.0004±0.00	0.0001±0.00	0.03	0.40	0.26
		02	01	2	4	4

NSctrl, non-smoker/healthy; NSras, non-smoker/Recurrent aphthous stomatitis; Sras, smoker/ recurrent aphthous stomatitis. P1-value, NSctrl vs. NSras; P2-value, NSctrl vs. Sras; P3-value, NSras vs. Sras.

Table S2. Identified co-different species associated with RAS, which showed a positive difference equal to or higher than 10% (in terms of relative abundance).

Contributing OTU	NSctrl (n=28)	NSras (n=31)	Sras (n=19)	P1	P2	P3
Acholeplasma_sp_KDA-feline;	0.0056± 0.0021	0.0003± 0.0003	0.0008± 0.0005	0.0 05	0.0 16	0.2 32
Acholeplasmatales_bacterium_cani ne_oral_taxon_172;	0.0392± 0.0152	0.0015± 0.001	0.0298± 0.0144	0.0 01	0.6 69	0.0 07
Actinomyces_sp_oral_taxon_414;	0.0027± 0.0009	0.0005± 0.0002	0.0013± 0.0009	0.0 13	0.2 82	0.0 32
Actinomyces_weissii;	0.0008± 0.0006	0.0002± 0.0002	0.0001± 0.0001	0.0 29	0.0 35	1.0 00
Aeromonas_veronii;	0.0001± 0.0001	0.0007± 0.0007	0±0	0.0 25	0.5 18	0.0 09
Aggregatibacter_segnis;	0.555±0. 1131	0.1483± 0.0313	0.1518± 0.0529	0.0 01	0.0 03	0.9 65
Alphaproteobacteria_bacterium_ca nine_oral_taxon_081;	0.0055± 0.0019	0.0001± 0.0001	0.0018± 0.001	0.0 04	0.0 92	0.0 00
Bacteroidales_genomosp_P1;	0.025±0. 0141	0.0007± 0.0004	0.0042± 0.0031	0.0 01	0.0 65	0.2 71
Bacteroidales_genomosp_P4_oral_ clone_MB2_G17;	0.1665± 0.0468	0.0437± 0.0084	0.0681± 0.0242	0.0 03	0.0 63	0.3 98

Bacteroidales_oral_clone_MCE7_164;	0.0592±	0.0131±	0.0531±	0.0	0.8	0.0
	0.0136	0.0034	0.0186	01	11	40
Bacteroides_coprocola;	0.0004±	0±0	0±0	0.0	0.0	1.0
	0.0002			11	88	00
Bacteroidia_bacterium_canine_oral_taxon_041;	0.0286±	0.0066±	0.0103±	0.0	0.0	0.2
	0.0062	0.0023	0.0022	02	01	76
Bacteroidia_bacterium_feline_oral_taxon_115;	0.0067±	0.0001±	0±0	0.0	0.0	0.5
	0.0031	0.0001		02	02	29
Bacteroidia_bacterium_feline_oral_taxon_141;	0.2323±	0.0083±	0.0014±	0.0	0.0	0.1
	0.09	0.0047	0.0009	02	04	62
Butyrivibrio_sp_Marseille-P2984;	0.0011±	0.0003±	0±0	0.0	0.0	0.1
	0.0005	0.0001		23	01	64
Butyrivibrio_sp_oral_clone_DA074;	0.0019±	0.0004±	0.0001±	0.0	0.0	0.2
	0.0007	0.0002	0.0001	00	00	64
Campylobacter_gracilis;	0.0586±	0.0274±	0.0443±	0.0	0.3	0.0
	0.0133	0.0043	0.0087	37	88	92
Capnocytophaga_ochracea;	0.0865±	0.0536±	0.086±0.	0.0	0.9	0.1
	0.0118	0.0077	019	29	81	23
Catonella_morbi;	0.094±0.	0.0136±	0.0218±	0.0	0.0	0.2
	0225	0.0032	0.0055	01	02	18
Cercis_gigantea;	0.0319±	0.0121±	0.0261±	0.0	0.7	0.5
	0.008	0.0034	0.0163	36	89	04

Chlorobi_bacterium_canine_oral_t	0.0035±	0±0	0.0016±	0.0	0.5	0.0
axon_046;	0.0026		0.0014	01	44	00
Clostridiales_bacterium_canine_or	0.0025±	0.0003±	0±0	0.0	0.0	0.3
al_taxon_028;	0.0014	0.0002		41	01	05
Clostridium_disporicum;	0.0027±	0±0	0±0	0.0	0.0	1.0
	0.0016			01	12	00
Deinococcus_geothermalis;	0±0	0.0011±	0±0	0.0	1.0	0.0
		0.0011		00	00	01
Desulfomicrobium_orale;	0.0062±	0±0	0.0002±	0.0	0.0	0.1
	0.0036		0.0002	01	18	44
Dialister_pneumosintes;	0.0714±	0.0197±	0.0313±	0.0	0.0	0.1
	0.0151	0.0037	0.0063	01	24	12
Eubacterium_minutum;	0.0016±	0.0004±	0.0028±	0.0	0.8	0.3
	0.0005	0.0002	0.0023	02	27	54
Eubacterium_nodatum;	0.0815±	0.0221±	0.0443±	0.0	0.1	0.1
	0.0179	0.0054	0.0139	01	20	49
Eubacterium_sp_oral_clone_FX02	0.0009±	0±0	0.0009±	0.0	1.0	0.0
8;	0.0004		0.0009	00	00	00
Firmicutes_bacterium_canine_oral	0.0013±	0±0	0±0	0.0	0.0	1.0
_taxon_309;	0.001			00	00	00
Fusobacterium_mortiferum;	0.0007±	0±0	0±0	0.0	0.0	1.0
	0.0004			01	07	00

Fusobacterium_sp_B57-13;	0.0006±	0±0	0±0	0.0	0.0	1.0
	0.0004			03	25	00
Geobacter_soli;	0.0001±	0.0007±	0±0	0.0	0.5	0.0
	0.0001	0.0005		25	18	09
Haemophilus_parainfluenzae;	0.653±0.	1.1606±	1.1557±	0.0	0.0	0.9
	1175	0.2292	0.2604	50	97	91
Ileibacterium_massiliense;	0.0006±	0±0	0±0	0.0	0.0	1.0
	0.0004			03	25	00
Kingella_denitrificans;	0.1289±	0.0655±	0.1066±	0.0	0.6	0.3
	0.0268	0.0141	0.0395	48	63	46
Kocuria_kristinae;	0.0008±	0±0	0±0	0.0	0.0	1.0
	0.0005			00	04	00
Lachnoanaerobaculum_sp_OBRC5	0.0041±	0.0109±	0.0069±	0.0	0.2	0.2
-5;	0.0014	0.0029	0.002	30	61	86
Lachnospiraceae_bacterium_feline	0.0759±	0.0076±	0.042±0.	0.0	0.0	0.0
_oral_taxon_021;	0.0124	0.0021	0.0151	01	79	04
Lachnospiraceae_oral_clone_MCE	0.0079±	0.0011±	0.002±0.	0.0	0.0	0.1
9_173;	0.0013	0.0004	0.0009	01	04	17
Lachnospiraceae_oral_clone_MCE	0.0062±	0.0025±	0.0053±	0.0	0.7	0.2
9_31;	0.0014	0.0009	0.0021	35	45	93
Leptotrichia_sp_oral_clone_EI013;	0.0525±	0.8182±	0.2931±	0.0	0.0	0.2
	0.02	0.3924	0.0987	23	18	82

Leptotrichia_sp_oral_clone_EX10	0.01±0.0	0.0024±	0.0074±	0.0	0.5	0.1
3;	031	0.0007	0.0029	12	84	27
Leptotrichia_sp_oral_clone_FP036	0.1017±	0.5087±	0.3562±	0.0	0.0	0.4
;	0.0309	0.1695	0.0755	08	04	41
Leptotrichia_sp_oral_taxon_847;	0.0146±	0.004±0.	0.0032±	0.0	0.0	0.6
	0.0046	0013	0.001	27	13	63
Moraxella_lacunata;	0.5534±	0.113±0.	0.008±0.	0.0	0.0	0.1
	0.2097	0721	0058	36	05	24
Mycoplasma_spermatophilum;	0.0001±	0.0009±	0±0	0.0	0.5	0.0
	0.0001	0.0008		05	18	02
Mycoplasmataceae_genomosp_P1	0.0813±	0.004±0.	0.0149±	0.0	0.0	0.5
_oral_clone_MB1_G23;	0.0362	0022	0.0123	19	75	95
Neisseria_flava;	1.9255±	0.6857±	1.0526±	0.0	0.1	0.3
	0.4719	0.1148	0.3635	17	56	85
Nitrospira_japonica;	0.0009±	0.0001±	0±0	0.0	0.0	1.0
	0.0008	0.0001		01	02	00
Olsenella_uli;	0.0016±	0.0003±	0.0008±	0.0	0.0	0.1
	0.0005	0.0001	0.0005	00	88	17
Oribacterium_sp_oral_taxon_102;	0.0173±	0.0031±	0.0065±	0.0	0.0	0.3
	0.0043	0.0009	0.0032	01	70	62
Peptostreptococcus_sp_oral_clone	0.0042±	0.0012±	0.0004±	0.0	0.0	0.0
_AP24;	0.0015	0.0004	0.0003	34	02	77

Phocaecicola_abscessus;	0.0241±	0.005±0.	0.0161±	0.0	0.3	0.0
	0.0036	001	0.0071	01	17	35
Porphyromonas_endodontalis;	0.9003±	0.4519±	1.2803±	0.0	0.3	0.0
	0.0837	0.0849	0.4042	01	69	62
Porphyromonas_gingivalis;	1.6934±	0.616±0.	0.6692±	0.0	0.0	0.8
	0.2798	1522	0.2682	02	10	86
Porphyromonas_sp_oral_clone_HF	0.0223±	0.005±0.	0.0071±	0.0	0.1	0.7
001;	0.0102	0018	0.0043	32	51	09
Prevotella_baroniae;	0.1064±	0.0333±	0.0483±	0.0	0.0	0.3
	0.0206	0.0096	0.0117	01	16	72
Prevotella_buccae;	0.018±0.	0.0058±	0.0095±	0.0	0.0	0.2
	0032	0.0013	0.003	01	59	75
Prevotella_denticola;	0.2363±	0.0472±	0.1351±	0.0	0.3	0.1
	0.0644	0.0087	0.066	01	55	67
Prevotella_disiens;	0.0001±	0.001±0.	0.0003±	0.0	0.3	0.0
	0.0001	0009	0.0003	01	10	87
Prevotella_enoeca;	0.0228±	0.0093±	0.0174±	0.0	0.4	0.1
	0.0042	0.002	0.0046	03	13	09
Prevotella_genomosp_C2;	0.0362±	0.0171±	0.0182±	0.0	0.0	0.8
	0.0078	0.004	0.0039	25	48	44
Prevotella_genomosp_P6;	0.3194±	0.1664±	0.1299±	0.0	0.0	0.3
	0.0457	0.0282	0.0197	10	02	22

Prevotella_heparinolytica;	0.0603±	0.0101±	0.0113±	0.0	0.0	0.9
	0.0168	0.0045	0.0062	01	07	02
Prevotella_intermedia;	0.7991±	0.3185±	0.4838±	0.0	0.1	0.3
	0.1355	0.0685	0.1382	04	00	17
Prevotella_loescheii;	0.1401±	0.0634±	0.0567±	0.0	0.0	0.7
	0.0274	0.0137	0.0172	08	05	69
Prevotella_maculosa;	0.0167±	0.0066±	0.0108±	0.0	0.1	0.0
	0.0034	0.0011	0.0023	01	72	96
Prevotella_marshii;	0.0223±	0.0087±	0.0105±	0.0	0.0	0.7
	0.0043	0.0035	0.0027	13	16	95
Prevotella_multiformis;	0.0694±	0.0053±	0.0303±	0.0	0.3	0.0
	0.0333	0.0026	0.0133	02	43	60
Prevotella_oris;	0.4923±	0.3017±	0.5928±	0.0	0.6	0.1
	0.0615	0.0487	0.1686	14	13	08
Prevotella_saccharolytica;	0.0266±	0.0138±	0.0155±	0.0	0.0	0.6
	0.0049	0.0024	0.0027	13	35	31
Prevotella_shahii;	0.2698±	0.6049±	0.3227±	0.0	0.8	0.2
	0.0489	0.1452	0.1606	08	60	03
Prevotella_sp;	0.0042±	0.0007±	0.001±0.	0.0	0.0	0.4
	0.0011	0.0003	0005	03	14	80
Prevotella_sp_oral_clone_DA058;	1.0405±	0.144±0.	0.3167±	0.0	0.0	0.1
	0.2423	0653	0.0952	01	02	51

Prevotella_sp_oral_clone_P4PB_8	0.051±0.	0.1124±	0.1197±	0.0	0.0	0.8
3_P2;	0086	0.0207	0.0297	06	29	20
Prevotella_zoogeoformans;	0.0091±	0.0001±	0.0083±	0.0	0.9	0.1
	0.0043	0.0001	0.0057	09	01	56
Pseudoramibacter_alactolyticus;	0.0059±	0.0019±	0.0031±	0.0	0.1	0.4
	0.0015	0.001	0.0011	30	57	25
Pyramidobacter_piscolens;	0.0057±	0.0007±	0.0005±	0.0	0.0	0.7
	0.0015	0.0003	0.0003	01	01	98
Rothia_aeria;	0.0007±	0.0038±	0.0035±	0.0	0.3	0.9
	0.0003	0.0017	0.0025	50	16	45
Shuttleworthia_satelles;	0.0096±	0.0029±	0.004±0.	0.0	0.0	0.5
	0.0027	0.0012	0013	23	82	40
Sneathia_amnii;	0±0	0.0006±	0.0019±	0.0	0.0	0.0
		0.0006	0.0011	04	00	07
Spirochaeta_sp_canine_oral_taxon	0.0058±	0.0001±	0.0012±	0.0	0.1	0.0
_314;	0.0026	0.0001	0.0012	01	10	00
Spirochaeta_sp_canine_oral_taxon	0.0013±	0.0003±	0.0002±	0.0	0.0	0.7
_379;	0.0005	0.0002	0.0002	05	08	16
Synergistetes_bacterium_oral_taxo	0.0544±	0.0137±	0.0395±	0.0	0.6	0.0
n_363;	0.0186	0.0031	0.0081	02	66	06
Syntrophomonadaceae_genomosp_	0.0077±	0.0004±	0.0043±	0.0	0.4	0.3
P1;	0.0028	0.0003	0.0035	01	84	15

Tannerella_forsythia;	0.145±0.	0.0682±	0.0954±	0.0	0.2	0.3
	0316	0.0146	0.0257	27	17	82
Tissierella_sp_feline_oral_taxon_0	0.014±0.	0.0007±	0.0088±	0.0	0.4	0.0
25;	0042	0.0004	0.0053	01	80	36
Treponema_denticola;	0.2083±	0.0593±	0.0907±	0.0	0.0	0.3
	0.0348	0.019	0.0256	01	06	57
Treponema_genomosp_P4_oral_cl	0.035±0.	0.0015±	0.0023±	0.0	0.0	0.6
one_MB2_G19;	014	0.0012	0.0016	03	05	58
Treponema_medium;	0.3073±	0.1058±	0.1839±	0.0	0.0	0.1
	0.0343	0.0189	0.0461	01	36	35
Treponema_parvum;	0.0029±	0.0005±	0.0014±	0.0	0.0	0.0
	0.0008	0.0002	0.0005	01	95	19
Treponema_refringens;	0.0161±	0.0638±	0.0333±	0.0	0.1	0.3
	0.0038	0.0272	0.0103	21	48	61
Treponema_sp_3:G:BB003;	0.0347±	0.0075±	0.0081±	0.0	0.0	0.8
	0.0082	0.003	0.0027	03	05	91
Treponema_sp_5:22:BH022;	0.1107±	0.0042±	0.0297±	0.0	0.1	0.4
	0.0466	0.0034	0.0246	15	42	03
Treponema_sp_5:C:AT040;	0.1703±	0.0254±	0.0605±	0.0	0.0	0.0
	0.0716	0.009	0.015	03	48	44
Treponema_sp_9:A:D01;	0.0072±	0.0011±	0.0036±	0.0	0.0	0.0
	0.0016	0.0004	0.0011	02	73	50

Treponema_sp_canine_oral_taxon	0.0183±	0.0032±	0.0081±	0.0	0.0	0.0
_201;	0.003	0.001	0.0022	01	12	56
Treponema_sp_I:C:BA223;	0.0115±	0±0	0.0015±	0.0	0.0	0.0
	0.0041		0.0011	01	30	00
Treponema_sp_I:V:AU076;	0.0453±	0.0034±	0.0069±	0.0	0.0	0.1
	0.012	0.0014	0.002	01	01	85
Treponema_sp_II:I:C53;	0.0177±	0.0013±	0.0022±	0.0	0.0	0.5
	0.0077	0.0009	0.001	05	15	74
Treponema_sp_oral_taxon_271;	0.004±0.	0.0001±	0.0009±	0.0	0.0	0.0
	0012	0.0001	0.0005	01	19	03
Treponema_vincentii;	0.01±0.0	0.0042±	0.0042±	0.0	0.0	0.9
	012	0.0013	0.001	01	02	77
Veillonellaceae_bacterium_oral_taxon_131;	0.0018±	0.0002±	0.0004±	0.0	0.0	0.4
	0.001	0.0002	0.0003	00	04	38
Wolinella_sp_feline_oral_taxon_098;	0.0169±	0.0009±	0.003±0.	0.0	0.0	0.0
	0.0035	0.0004	0011	01	01	74

NSctrl, non-smoker/healthy; NSras, non-smoker/Recurrent aphthous stomatitis; Sras, smoker/ recurrent aphthous stomatitis. P1-value, NSctrl vs. NSras; P2-value, NSctrl vs. Sras; P3-value, NSras vs. Sras.