



Modulation of the psoriasis-associated microbiome with thermal water at Comano Terme

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Balneology in changing societies, Castel San Pietro Terme, 5th November 2022

Psoriasis & balneotherapy

- Psoriasis (PSO) is an autoimmune condition
- It affects 2-3% of the worldwide population and lacks definitive treatments
- Balneotherapy is a successful adjuvant treatment
- Comano Terme spring water harbors a distinct environmental microbiota
- Lysates from these communities have positive effects *in vitro*

DERMATOLOGIC Therapy

Full Access

Balneotherapy for chronic plaque psoriasis at Comano spa in Trentino, Italy

Anna Peroni, Paolo Gisondi, Mauro Zanoni, Giampiero Girolomoni

Genomic and metagenomic insights into the microbial community of a thermal spring

Renato Pedron, Alfonso Esposito, Irene Bianconi, Edoardo Pasolli, Adrian Tett, Francesco Asnicar, Mario Cristofolini, Nicola Segata & Olivier Jousson

INTERNATIONAL

MEDICAL RESEARCH

Microbiome 7, Article number: 8 (2019) Cite this article

Pre-Clinical Research Report

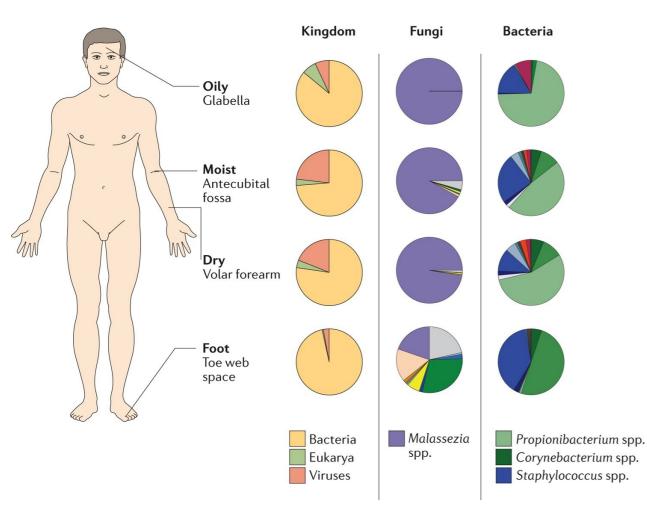
Regenerative effects of spring water-derived bacterial lysates on human skin fibroblast in *in vitro* culture: preliminary results

Giovanni Nicoletti^{1,2,3}, Marco Saler¹, Marco Mario Tresoldi^{1,2}, Angela Faga³, Mattia Benedet⁴ and Mario Cristofolini⁵ of International Medical Research 2019, Vol. 47(11) 5777–5786 © The Author(s) 2019 Article reuse guidelines: sagepub.com/journals.permissions DOI: 10.1177/0300060519880371 journals.sagepub.com/home/imr ©SAGE

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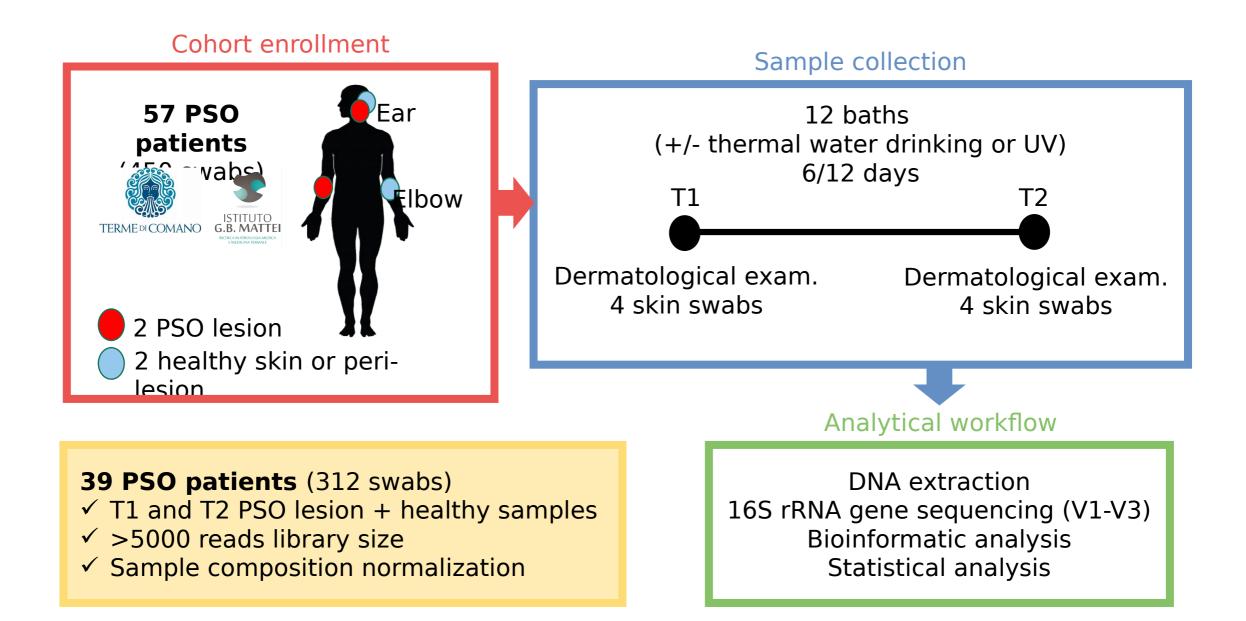
Psoriasis & the skin microbiome



- Infections may cause disease exacerbation
- The skin microbiome
 - Educates the immune system
 - Prevents pathogens colonization

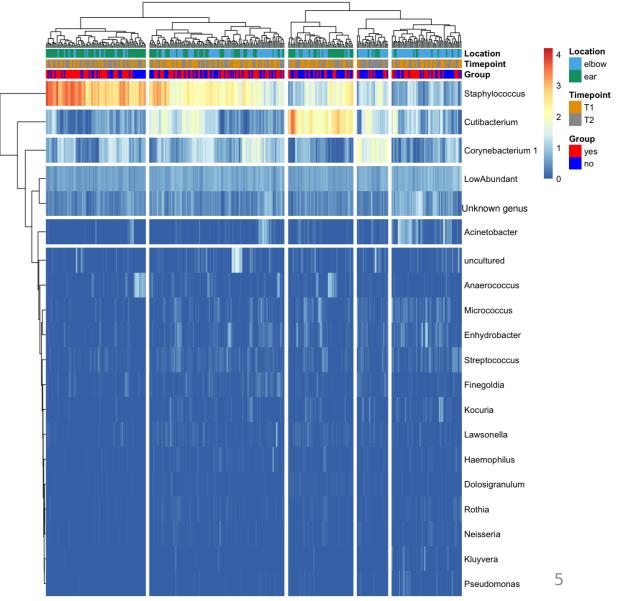
Does balneotherapy affect the skin microbiome in PSO patients?

Byrd, Belkaid & Segre. Nat Rev Microbiol (2018)

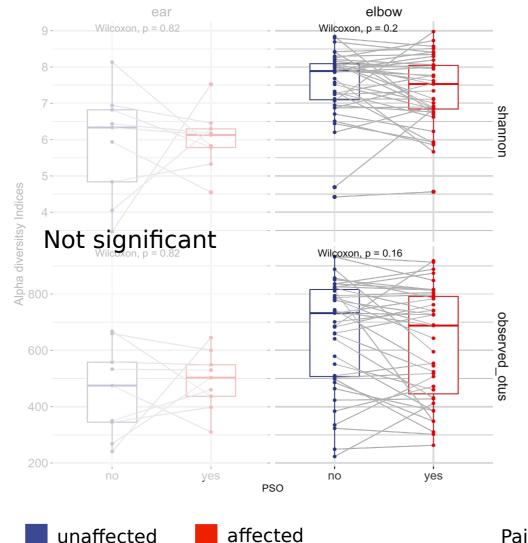


PSO lesions and healthy skin harbour a similar microbiome

- Most abundant bacterial genera are usual skinassociated microbes
- Skin microbiome profiles are similar between healthy skin and PSO lesion

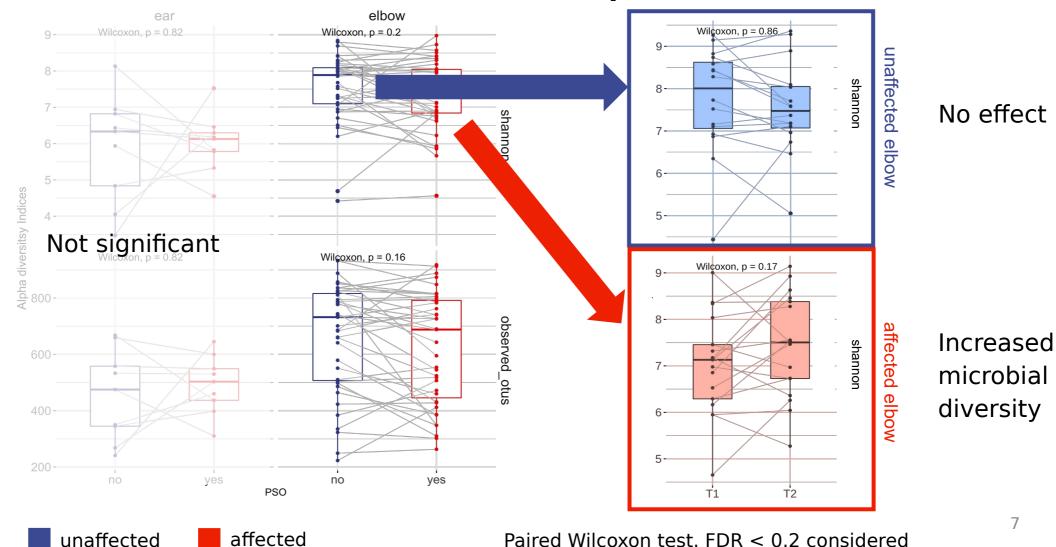


PSO is associated with lower microbial diversity...



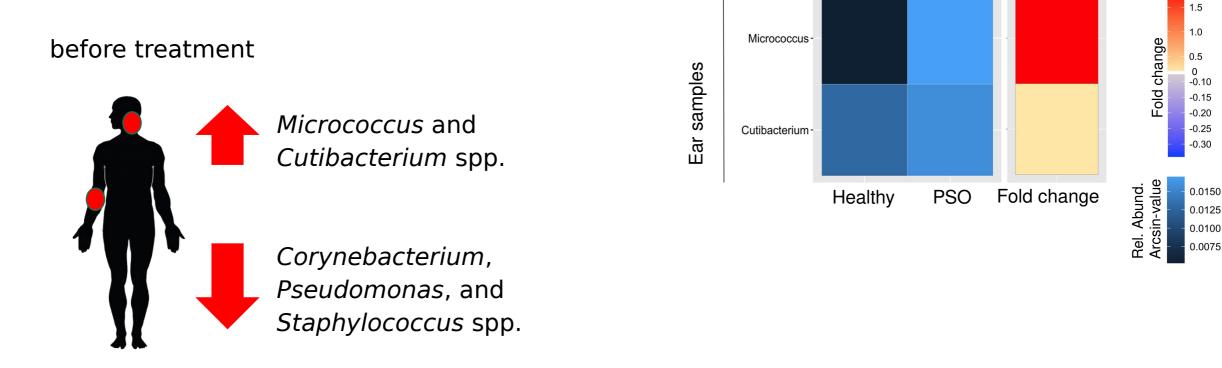
- Alpha diversity is a measure of microbial community complexity in a sample
- Lowered alpha-diversity is associated with chronic and inflammatory diseases
- Before treatment, lower alpha diversity on elbow
 PSO lesions

...that can be improved by thermal water treatments in PSO patients



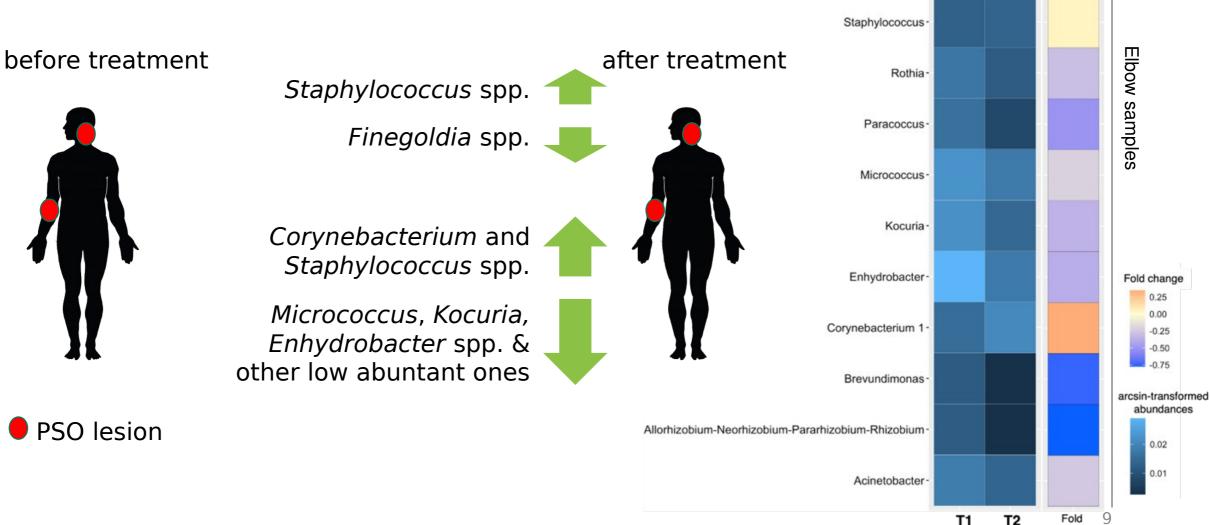
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Some bacterial genera are differentially abundant on PSO lesions





Balneotherapy restores PSO skin microbiome composition



Ear

samples

change

means

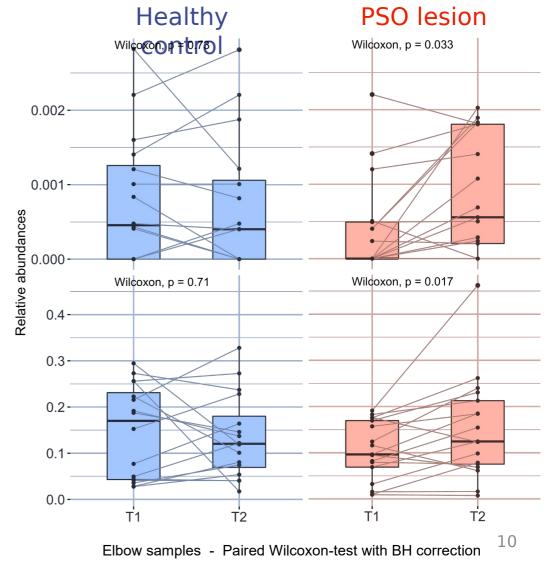
Staphylococcus

Finegoldia

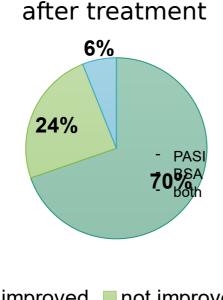
S. epidermidis abundance increases after balneotherapy

- Increased S. epidermidis abundance on PSO lesions after balneotherapy
- No significant difference in healthy control samples

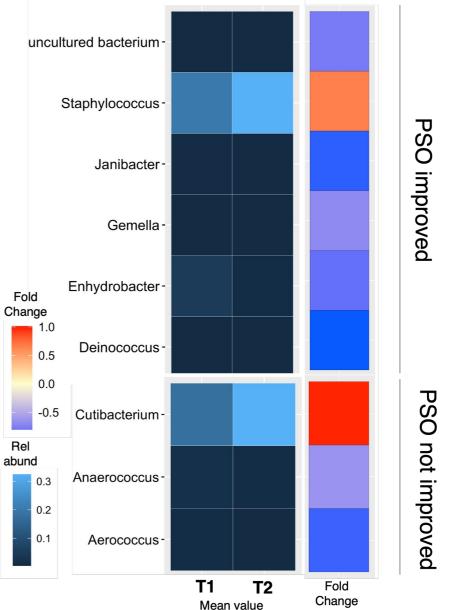
Balneotherapy may restore a healthy-like microbiome on the skin affected by PSO



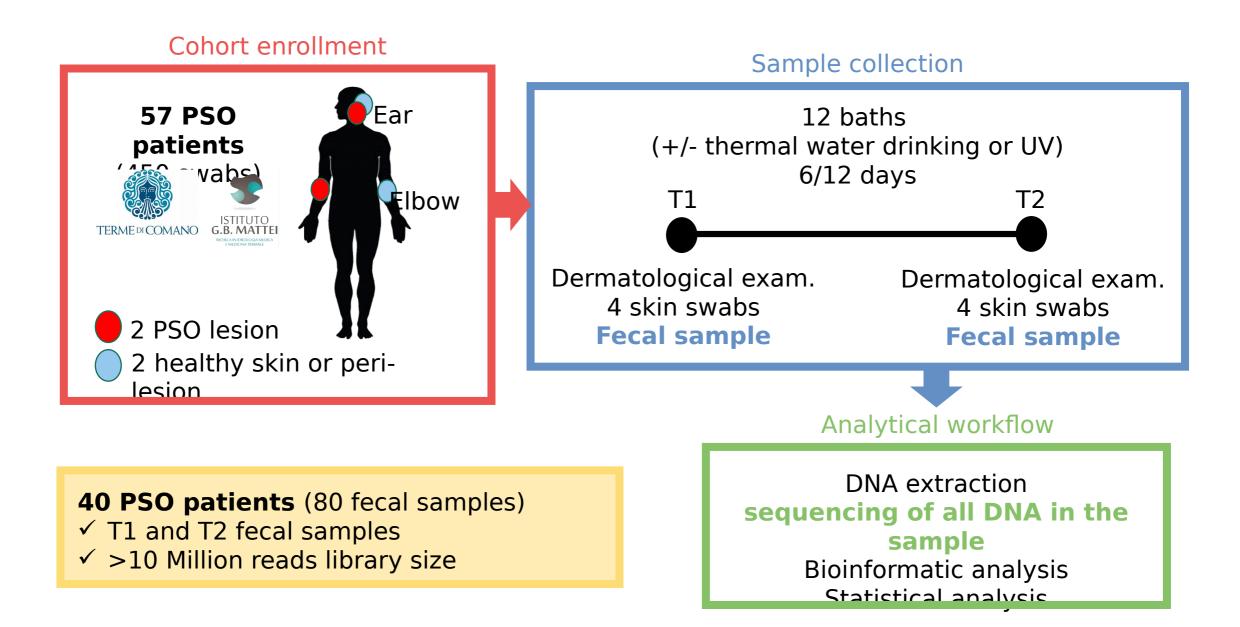
Are microbial genera associated with improvement?



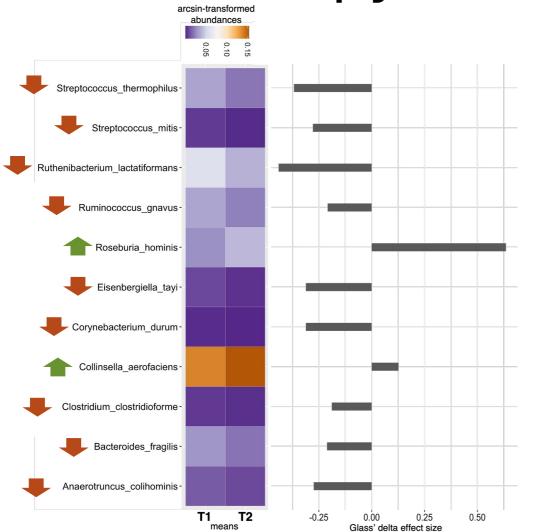
improvednot improvedNA



11



Fecal microbiome changes with balneotherapy



Species <u>decreased</u> after balneotherapy are linked with poor metabolic health

Species increased after balneotherapy are associated with good metabolic health

Balneotherapy might ameliorate the metabolic syndrome associated with psoriasis

Conclusions

- PSO lesions and healthy skin harbour a similar microbiome
- PSO is associated with lower microbial diversity, improved by balneotherapy
- Some bacterial genera are differentially abundant on lesions, restored by balneotherapy
- Changes in the abundance of some genera are associated with PSO improvement
- Balneotherapy is linked with a metabolically healthy composition of the gut microbiome

Take home messages:

Balneotherapy may restore a healthy-like microbiome on the skin affected by PSO Balneotherapy might ameliorate the metabolic syndrome associated with psoriasis

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Thank you for Your attention

The Laboratory of Computational Metagenomics



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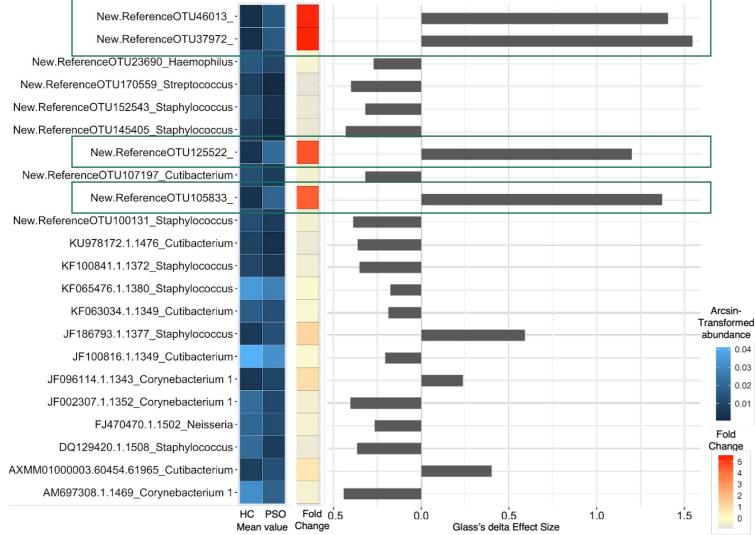


Possiamo definire la composizione di un »microbioma sano»?

Average Positive													N	ega	ativ	/e					Prevalence (%)	
	142.5	149	168	158	172		162					170	163		154					_	99.1	Ruthenibacterium lactatiformans
	167.9		174	165	173	167	175	165		176	173	166	173	170	173	175	170	171	169	174	92.9	Flavonifractor plautii
	142.3	173	161	168	176		159			156		175	152								91.7	Clostridium leptum
	152.9	162	169		154		154	163				173	159	163	166				163		67.1	Escherichia coli
	152.3		154		153		152			151		161		160	161				161	161	66.5	Collinsella intestinalis
	154.4	159			151		160			171			169	162			167			167	64.3	Clostridium sp CAG 58
	154.6		163				171			160		167	164	167		174				166	61.7	Eggerthella lenta
	164.9		176	152		170		170			174		175	175	169			169	170	173	50.5	Anaerotruncus colihominis
	167.0		170		158	168	176	169			172		176	176		169		176	174		50.1	Clostridium bolteae
	160.3			174		169		167		175		165	166		160		161			170	43.7	Clostridium spiroforme
	159.8		165			174		168			176		172	174				175			43.3	Ruminococcus gnavus
	163.6		173			175		176		169	170	174	171	171		167			171	172	41.2	Clostridium innocuum
	153.5		157		139		145			164					153			174		165	28.6	Blautia hydrogenotrophica
	165.8		172			173		173		159			174							171	27.6	Clostridium symbiosum
	161.0	160	164		141	176		175		168		164	170	172		168		170		100 No. 100 No. 100	26.7	Clostridium bolteae CAG 59
	27.7		10			20	18			22		14	14		13		8		7	31	99.5	Faecalibacterium prausnitzii
	20.9		8	-	8	2	8	3		19	16	6	20	10	5				5	26	92.5	Eubacterium eligens
	12.2	9	5	2	4		1			2		11	4	7	7		15	6	6	3	89.3	Oscillibacter sp 57 20
	31.5		14	6			7						32		10	1	14		11	29	82.9	Romboutsia ilealis
	10.1	6	15	1	12	4	2	2		4		23	3	6	1	5	5	19	1	5	54.6	Haemophilus parainfluenzae
	9.7	7	2			6	3	5		3	4	3	1	1	2	2	6	5	4	1	51.3	Firmicutes bacterium CAG 95
	20.5	10	13			1	14	1		28		5	10	5	11	11	27	~	10	9	50.0	Oscillibacter sp PC13
	25.0	13		9		40	21		•	18		19	28		14	8	3	21	18	34	46.8	Veillonella dispar Roseburia sp CAG 182
	14.6		3	3	3 14	13	4	21	2	14	11	8	5	11	4		23		2	15	41.3	Veillonella atypica
	32.9	10	4		14 5	25 14	34 22	19		25		24	10	28	42		2	20	46 8	20 28	40.5	Clostridium sp CAG 167
	20.0 27.3	12 14	4	12	5 11	14	22	19		7 11		24	19 33	28	6 17	19	13 1	28	8 14	28 19	38.5	Veillonella infantium
	27.3	14	12	7	2	11	12	9		23		1	29	25	17	19	10	20	14	19	38.2	Bifidobacterium animalis
	26.9	4	12	'	4	27	6	20		9		22	6	23	9	6	35		13	38	36.0	Prevotella copri
	24.4 14.0	8	23			8	5	8	1	6	2	28	2	3	3	7	22		3	17	34.3	Firmicutes bacterium CAG 170
Validation Coho		0	23		_	0	5	0	1	0	2	20	2	3	3	1	22		3	_		1
n=100	·										1		8								0 50 10	JU
11=100		X	aMED	HFD	Ψ	HDL-D	PUFA/FA	6h	ASCVD	Visceral fat	ġ.	uPDI	ЦG	VLDL-D	GlycA	2h	2h	6h	6h	6h		2 2 2
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PSO lesions show increased abundance of unknown taxa



Further thermal treatments affect

