Since this is a very extensive table, the format and content has not been edited by ActaDV.

**Table SI. Detailed overview of observational studies characterizing the oral and gut microbiology in patients with psoriasis and/or psoriatic arthritis and in healthy controls**

| Study type/ outcome | | Author (year)/ Location | Study type | Sample | Study population/ Severity of disease (psoriasis type) | Age (years) | Men (%) | BMI ($kg/m^{2)}$ | Antipsoriatic treatment/ other restrictions | Method | Main findings | Additional notes |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Observational studies | Oral microbiology | Waldman* (2001) Israel (13) | Case-control | Saliva/ Oral | 50 patients with mild-to-severe psoriasis PASI, mean (SD): 13.5 (12.6) (PQ)<br>50 healthy controls | Patients with psoriasis, mean age: 51 (range 10–82)<br>Healthy controls, mean age: 49 (range 15–70) | 33 (66)<br>27 (54) | NS | NS | Culturing | The prevalence and count of *Candida* species was significantly higher in patients with psoriasis compared with healthy controls (prevalence: 78% vs 50%, $p<0.01$). No association between PASI score and quantity of *Candida* colonies was observed. | No information on treatment, comorbidities, smoking. |
| | | Bedair (2012) Jordan (29) | Case-control | Swab smear oral-rinse/ Oral cavity and lips | 100 mild-to-severe psoriasis patients (NS)<br>100 healthy controls | Patients with psoriasis, mean age±SD: 32±14.8<br>Healthy controls, mean age±SD: 32±14.8/ | 54 (54)<br>54 (54) | NS | All psoriasis treatment was allowed (68% received topical and/or systemic treatment)<br>No antifungal/antibiotics were allowed 2 months prior to study start | Culturing | The prevalence and count of *Candida* species was significantly higher in patients with psoriasis compared with healthy controls (prevalence 69% vs 44%, $p<0.001$, count: 11 vs 5).<br>No significant difference in mean PASI was observed between *Candida* carriers and *Candida*-free patients with psoriasis (9.4±9.8 vs 8.8±8.1, $p=0.73$).<br>Prevalence of *Candida* carriers slightly higher among smokers than non-smokers in psoriasis (NS). Opposite with healthy (NS)<br>No significant difference in prevalence of *Candida* in treated/untreated patients with psoriasis | |
| | | Sarvtin (2014) Iran (11) | Case-control | Swab/Oral | 100 patients with psoriasis,<br>76% had PASI<11,<br>9% had PASI 11–50 | Patients with psoriasis, mean age±SD: 40.5±11.0 | 44 (44)<br>22 (44) | NS | Corticosteroids and antibiotics were not allowed, information on other | Culturing | The prevalence and count of *Candida* species were significantly higher in patients with psoriasis | No information on treatment, smoking. |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | and 15% had PASI> 50<br>(PQ)<br>50 healthy controls | Healthy controls, mean age±SD: 39.9±11.4 | | | treatments not given. | | compared with healthy controls (63% vs 24%) | Diabetes patients were excluded. |
| | | Lesan (2018)<br>Iran<br>(24) | Case - control | Smear /Oral | 70 patients with psoriasis<br>PASI, mean±SD: 13.4±10.8<br>(PQ)<br>70 healthy controls | Patients with psoriasis, mean age±SD: 36.6±2.3<br><br>Healthy controls, mean age±SD: 36.2±1.7 | 35 (50)<br><br><br>35 (50) | NS | All patients had never been treated with systemics.<br>28 (40%) used phototherapy.<br>No antibiotics, antifungals or corticosteroids were allowed within 2 months prior to study start. | Culturing | The prevalence and count of *Candida* species were significantly higher in patients with psoriasis compared with healthy controls 20% vs 2.8%, $p$=0.002). A significant positive association between PASI score and colony count $p$<0.001 | Smokers and patients with other systemic diseases were excluded. |
| | | Belstrøm (2019)<br>Denmark<br>(30) | Case-control | Oral/ Swab and saliva | 27 patients with psoriasis without periodontitis<br>(NS)<br>52 healthy controls | Patients with psoriasis, mean age (range): 55.3 (38–74)<br>Healthy controls, mean age (range): 54.8 (40–80) | 16 (59)<br><br>27 (52) | NS | Antibiotics were not allowed 3 months prior to study start | 16s rRNA (V1-V3), 22 PCR cycles, Illumina Miseq Sequencing | α-diversity/relative abundance (Shannon's Diversity Index): No significance in of predominant genera/species between the groups<br>β-diversity (PCoA): Showed a random distribution within the groups (no clustering)<br>Genera: *Streptococcus, Prevotella, Veillonella* and *Neisseria* were the most dominating in both groups.<br>Species: *Prevotella melalogenica* and *Streptococcus salivarius* were the most dominating in both groups.<br>21 bacterial taxa at various levels differentiated between the groups | Samples taken at least 2 h after tooth hygiene<br>No information on disease severity |
| | Gut microbiology | Buslau (1997)<br>Germany<br>(28) | Case-control | Stool/ NS | 343 patients with psoriasis<br>(mixed)<br><br>50 healthy controls | Patients with psoriasis, mean age: 42<br><br>Healthy controls, mean age: | NS | NS | NS | Culturing | The prevalence of yeast was 68% of patients with psoriasis, and 54% of healthy controls. Strong to massive growth was | No information on disease severity or treatment |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | 29 | | | | | more common in patients with psoriasis compared with healthy<br>*Candida albicans* was the most predominant.<br>*Geotrichum candidum* was seen in 22% of psoriasis and 3% of healthy controls.<br>*Aspergillis* seen in 1% of patients with psoriasis but not in healthy controls. | |
| | | Smith (1997)<br>Scotland<br>(33) | Case-control | Stool/Psoriasis patients: posted samples<br>Healthy controls: delivery to lab 3 h after defaecation | 5 psoriatic arthritis patients<br>(NS)<br>36 healthy controls | Psoriatic arthritis patients, mean age (range): 41 (31–49)<br><br>Healthy controls: NS | 5 (100) | NS | NS | Culturing | Species: The most abundant bacteria isolated from stool was *E.coli* for psoriatic arthritis patients<br>The most abundant bacteria isolated from stool were *E. coli, Enterococci, Klebsiella oxytoca* and *Klebsiella pneumonia* for healthy controls. | No information on disease severity or treatment |
| | | Waldman (2001)<br>Israel<br>(13) | Case-control | Stool/<br>NS | 50 patients with psoriasis<br>PASI, mean±SD: 13.5±12.6<br>(PQ)<br>50 healthy controls | Patients with psoriasis, mean age (range): 51 (10–82)<br><br>Healthy controls, mean age (range): 49 (15–70) | 33 (66)<br><br>27 (54) | NS | NS | Culturing | The prevalence and count of *Candida* species were significantly higher in patients with psoriasis compared with healthy controls (72% vs 46%, $p<0.01$).<br>No association between PASI score and quantity of *Candida* colonies in stool was observed. | No information on treatment, smoking and comorbidities |
| | | Codoner (2014)<br>Spain<br>(12) | Case-control | Stool/ (immediately frozen at –80°C) | 52 patients with psoriasis<br>PASI, mean±SD: 13.3±3.3<br>(PQ)<br>52 healthy controls | Patients with psoriasis, mean age±SD: 41.2±14.4<br><br>Control were age- and sex-matched | 25 (48.1) | NS | Systemic psoriasis treatment were not allowed 3 months prior to study start<br>Systemic antibiotics were not allowed 2 weeks prior to study start | 16sRNA (V3-V4), Illumina Miseq Sequencing | α-diversity (Shannon's diversity): Significantly higher in patients with psoriasis compared with healthy controls.<br>β-diversity (PCA): Differences were observed between patients with psoriasis compared with healthy | Matched from Microbiome project |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | controls, but some healthy clustered in the psoriasis group<br>Phylum (PSO): ↓ Bacteroidetes<br>Genera (PSO):↑ *Faecalibacterium*, ↓ *Bacteroides*<br>↑ *Akkermansia*, ↑ *Ruminococcus* | |
| | | Scher (2015)<br>USA (NY)<br>(14) | Case-control | Stool/ Received max 24 h after production | 15 patients with psoriasis<br>PASI, mean±SD: 6.3±(SD NS) (NS)<br>16 patients with psoriatic arthritis<br>DAS28, mean±SD: 4.8±(not given)<br>17 healthy controls | 39.4 (median 37)<br><br>46.2 (median 40)<br><br>42.2 (median 39) | 7 (47)<br><br>7 (44)<br><br>6 (36) | NS | No systemic antibiotics 3 months prior to study start<br>Extreme diet<br>PsA: DMARD naïve, biologic-naïve<br>No IBD | 16s rRNA (V1-V2)<br>454 pyrosequencing | α-diversity (Shannon's diversity): Significantly lower in patients with psoriasis compared with healthy controls.<br>β-diversity (PCA): Significant clustering between groups<br>Phylum (PSO+PSA): ↓ Bacteroidetes, ↑ Firmicutes<br>Genera (PSO): ↓ *Coprobacillus (PSO),* ↓ *Parabacteroides vs healthy*<br>Genera (PSA): ↓ *Akkermansia (PSA), Ruminococcus (PSA),* and *Pseudobutyrivibrio (PSA) vs healthy*<br><br>Species (PSO+PsA): ↓ *Coprococcus* species | 6 psoriatic arthritis patients treated with methotrexate, all treated with NSAID |
| | | Eppinga (2016)<br>Netherlands<br>(27) | Case-control | Stool/ Mail (stored at –80°C within 48 h | 29 patients with psoriasis (60% had PASI<10) (mixed)<br>33 healthy controls | 45±14.0<br><br>41±14.9 | 12 (41)<br><br>10 (30) | Patients with psoriasis, mean BMI±SD: (–DMF) 27.7±4.4<br>Healthy controls, mean BMI±SD: 24.6±4.9 | No antibiotics 8 weeks prior to study start | 16S rRNA qPCR, 40 cycles, | *F. prausnitzii* significantly lower in patients with psoriasis compared with healthy controls<br>E. coli abundance significantly higher in patients with psoriasis compared with healthy controls | Registration of diet<br>All types of psoriasis including ppp<br>BMI overweight in psoriasis group not in controls (NS)<br>Treated patients 60% PASI below 10 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Eppinga (2017) Netherlands (15) | Case-control | Stool/ Mail (stored at –80°C within 48 h | 30 untreated patients with psoriasis<br>64% had PASI<10 (mixed)<br><br>28 treated patients with psoriasis (dimethylfumarate), *n*=28<br>80% had PASI<10 (mixed)<br><br>32 healthy controls | 46.1±13.9<br><br>42.7±14.1<br><br>42.6±14.1 | 12 (40)<br><br>14 (50)<br><br>12 (37.5) | Patients with psoriasis, mean BMI±SD: (–DMF) 27.8±5.3 (+DMF) 27.2±4.5<br><br>Healthy controls, mean BMI±SD: 25.3±4.8 | No antibiotics 8 weeks prior to study start<br>Age 18–74<br><br>7% used other systemic treatment | 16S rRNA qPCR, 40 cycles | *Saccharomyces cerevisiae* significantly lower in patients with psoriasis compared with healthy controls<br>*Saccharomyces cerevisiae* significantly higher in treated patients with psoriasis compared with untreated psoriasis. Similar to healthy controls. | No baseline data (before treatment) for treated group<br>BMI overweight in pso group not in controls (NS)<br>No IBD<br>Higher prevalence of smokers in pso groups (S)<br>Mixed psoriasis (p.vulgaris, guttat, PPP) |
| | | Tan (2018) China (25) | Case-control | Stool/ Stored at –80°C within 1 h | 14 patients with psoriasis (PASI median 27.0, range not given) (PQ)<br>14 healthy controls (including family members, not specified number/relation) | 47.5±4.7<br><br>40.4±2.5 | 10 (71%)<br><br>8 (57%) | Patients with psoriasis, mean BMI±SD: 24.2±1.2<br><br>Healthy controls, mean BMI±SD: 22.4±0.6 | No anti-inflammatory treatment | 16s RNA (V4), 30 cycles, Illumina Miseq Sequencing | α-diversity: (Chao/ACE): No significant difference, but psoriasis group showed slight decreased diversity.<br>70% OTUs were shared, 118 and 135 OTUs were individual to the groups.<br>β-diversity: Slightly separated groups<br>Phylum level (PSO): ↓*Verrucomicrobia*, ↓ *Tenericutes*<br>Class: ↓ *Mollicutes*, ↓ *Verrucomicrobiae*<br>Order: ↓ *Verrucomicrobiales*, ↓ RF39<br>Family level: *Bacteridaceae* and *Enterococcaceae* was increased in patients with psoriasis<br>Genus level: ↓ *Akkermansia*, ↑ *Enterococcus* and ↑ *Bacteroides*<br>Species (PSO); ↓ *Akkermansia* | Mixed controls including family members<br>No description of wash-out period of anti-inflammatory drugs.<br>No autoimmune comorbidities |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | *muciniphila*, ↑ *Clostridium citroniae* | |
| | | Hidalgo-Cantabrana (2019) Spain (16) | Case-control | Stool/ Sterile container, stored immediately at –20°C | 19 patients with psoriasis (mean PASI 12.2±6.1) (NS)<br>20 healthy controls | 49±11.0<br>43±11.0 | 12 (63%)<br>5 (25%) | NS | No antibiotics or systemic anti-psoriasic treatment 3 months prior to study start | 16s rRNA (V2-V3), Ion 16S Metagenomics Kit | α-diversity (Chao1/whisker/Shannon's diversity): Significant lower diversity in patients with psoriasis<br>β-diversity (PCoA): Significant clustering<br>Phylum (PSO): ↓ Bacteroidetes, ↓ Proteobacteria, ↑ Actinobacteria, ↑ Firmicutes<br>Family:↑(*Bifidobacteriaceae, Coriobacteriaceae, Lachnospiraceae, Clostridiales* Family XIII, *Eggerthellaceae, Peptostreptococcaceae, Ruminococcaceae* and *Erysipelotrichaceae)*<br>↓*(Bacteroidaceae, Barnesiellaceae, Prevotellaceae, Tannerellaceae, Burkholderiaceae, Rikenellaceae, Lactobacillaceae, Streptococcaceae, Desulfovibrionaceae, Veillonellaceae, Marinifilaceae, Victivallaceae* and *Pasteurellaceae)*<br>Genus level: ↑ *Bifidobacterium, Blautia, Collinsella, Slackia*<br>↓ *Bacteroides, Parabacteroides, Barnesiella, Alistipes, Paraprevotella* | Same geographical area |
| | | Huang (2019) China (17) | Case-control | Stool/ stored at –80°C within 30 min | 35 patients with psoriasis (12 with severe psoriasis) (mixed)<br>27 healthy controls | 52.1±3.0<br>52.9±1.5 | 22 (63%)<br>16 (59%) | NS | No antibiotics/probiotics within 1 month | 16s rRNA (V4-V5) Illumina Miseq Sequencing | α-diversity (Chao/ACE): lower richness in PSO<br>Shannon/Simpson: no significance in diversity<br>β-diversity (PCoA): significant separation of | No info ongoing treatment<br>No metabolic disease<br>Mixed psoriasis (p.vulgaris, |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | communities between groups<br>Phylum: No differences between subtypes, but significant difference in abundance.<br>(PSO) ↓ Firmicutes (59% healthy vs 46% PSO), p 0.026)<br>↑ Bacteroidetes (12% healthy vs 37% PSO), p>0.0001),<br>↓ Proteobacteriae (23% healthy vs 15% pso), NS,<br>↓ Actinobacteriae (5% healthy vs 2% pso, NS)<br>Genus (PSO): ↑ (*Bacillus, Bacteroides, Sutterella, Lactococcus, Lachnospiraceae_UCG004, Lachnospira, Mitochondria_norank, Cyanobacteria_norank,* and *Parabacteroides*)<br>↓ (*Thermus, Streptococcus, Rothia, Granulicatella, Gordonibacter, Allobaculum, and Carnobacterium*)<br>Severe state of PSO differs from mild PSO at genus level | erythroderm, PPP) |
| | | Shapiro (2019)<br>Israel<br>(31) | Case-control | Stool/<br>Up to 72 h at –20°C, then –80°C | 24 patients with psoriasis<br>(NS)<br>22 healthy controls | 52.7±11.6<br><br><br>43.9±12.7 | | Patients with psoriasis, mean BMI±SD: 27.5±3.4<br>Healthy controls, mean BMI±SD: 25±2.9 | No systemic antibiotics 3 months prior to study start | 16s rRNA (V4)<br>Illumina Miseq Sequencing | α-diversity (Shannon's index): No difference<br>β-diversity: Significant difference<br>Phylum (Pso):<br>↑Firmicutes, Actinobacteria<br>↓ Bacteroidetes, Proteobacteria<br>(no change after correction for age/sex/BMI) | Patients with diabetes, biologic treatment also included. |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | Genus (pso): ↑*Blautia*, ↑ *Faecalibacterium*<br>↓ *Prevotella*<br>Species (pso): ↑ *Ruminoccocus gnavus*, ↑*Dorea formicigenerans*, ↑ *Collinsella aerofaciens*<br>↓ *Prevotella copri* | |
| | | Chen (2019) Taiwan (18) | Case-control | Stool/ posted in cooler-bags, then –80°C | 32 patients with psoriasis (*n*=4 history of PSA)<br>PASI<10: 19 (59.4%) (PQ)<br>64 healthy controls | 52.8±12.6<br><br><br><br>44.2±10.8 | | Patients with psoriasis, BMI<25: 19 (59.4%) BMI≥25: 13 (40.6%) Healthy controls, BMI<25: 36 (56.4%) BMI≥25: 28 (43.8%) | 20 /62.5%) used biologics/DMARDs, 8 (25%) used phototherapy<br><br>No antibiotics/PPI within 1 month before study start | 16s rRNA (V3-V4) Illumina Miseq Sequencing | α-diversity (Chao1, Shannon's diversity): No difference between groups<br>β-diversity: Significant difference between treated, untreated and controls<br>Significant difference between patients with psoriasis and healthy controls in group with BMI<25, not among BMI≥25.<br>At OTU level significant difference between those using biologics vs biologic-naïve.<br>Both groups:<br>Phylum level (PSO + controls): dominated by: Bacteroidetes, Firmicutes<br>Proteobacteriae, Bacteroidetes, Firmicutes<br>PSO: ↓ Bacteroidetes, ↑ Firmicutes<br>Family level (PSO + controls): dominated by *Bacteroidaceae, Prevotellaceae, Ruminococcaceae, Veillonellaceae and Lacnospiraceae*<br>PSO: ↓ *Prevotellaceae, Ruminococcaceae,* | Erythroderma/PPP excluded (1 patients with diabetes included in each group) |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | ↑ *Veillonellaceae and Lacnospiraceae*<br>Genus (PSO): ↑ *Ruminococcus, Megasphaera, Dialister*<br>↓ *Sutterella, Paraprevotella*<br>Covariates: sex, PASI score, phototherapy, arthritis, diet, alcohol, smoking did not affect abundance profile among group of psoriasis and controls. | |
| | | Yeh (2019)<br>Taiwan<br>(19) | Case-control | Stool/ sterile rectal swab, then in DNA stabilizer (–20°C), then to laboratory for analyses | 24 patients with psoriasis (secukinumab), Mean PASI 16.6±6.0 (NS)<br>10 patients with psoriasis (ustekinumab), Mean PASI 12.1±3.9 (NS)<br>Healthy controls, *n*=12 | 51.0±12.0<br>48.4±12.7<br>48.8±13.3 | 19 (9.5%)<br>6 (60%)<br>10 (83.3%) | Patients with psoriasis, mean BMI±SD: (secukinumab) 27.4±5.6 (ustekinumab) 26.3±6.9 Healthy controls, mean BMI±SD: 27.8±3.4 | No antibiotics, oral corticosteroids, systemic anti-psoriatic drugs within 1 month before study start | 16s rRNA (V3-V4) Illumina Miseq Sequencing | α-diversity: No significant difference between treated groups<br>β-diversity (PCoA): Significant alterations of microbiome at 6 months in secukinumab group but not in ustekinumab group. | BMI matched 27.4±5.6 vs 26.3±6.9 vs 27.8±3.4 *p*=0.62<br>Number of participants with diabetes: 5 (21%), 2 (20%), 2 (17%) |
| | | Manasson (2020)<br>USA (NY)<br>(32) | Case-control | Stool/ NS | 15 patients with psoriatic arthritis (all had psoriasis, mean PASI 2.1±2.3), Tender joint count, mean±SD (range) 5.5±6.6 (0–22) Swollen joint count, mean±SD (range)# 3.6±2.9 (0–11) Healthy controls, *n*=15 | 38.9±9.5 (22–53) Age, sex, ethnicity matched | 11 (73) | Patients with psoriasis, BMI±SD: 26.8 (+TNF-i) Healthy controls, NS | Biologic-naïve (93.3%) or brief exposure (6.7%)>1 year ago. No info of antibiotics | 16s rRNA (V4 region), Illumina Miseq Sequencing/Fungal: ITS1 region | PsA<br>Order: ↑ *Clostridiales*, ↑*Erysipelotrichiales*<br>↓ *Bacteroidaldes*<br>(no further comparisons for untreated groups) | PsA/SpA (all had Pso) BMI 26.8 (6.0)<br>BMI for controls NS<br>Additional treatment NS |
| | | Dei-Cas (2020)<br>Argentina<br>(20) | Case-control | Stool/ Sterile bacteriostatic buffer tube | 55 patients with psoriasis (various forms), *n*=55 PASI 9.9±7.2 | Patients with psoriasis, mean age±SD: 44.8±16.9 | 28 (50.9)<br>11 (42.3) | Patients with psoriasis, mean | No systemic anti-psoriatic treatment including phototherapy and | 16s rRNA (V3-V4) | α-diversity (Chao1 index): no significant difference between | BMI matched (29.6±5.5 vs 28.1±5.2, not significant) |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | (PQ)<br>27 healthy controls (clinic staff) | Healthy controls, mean age±SD: 48.7±18.8 | | BMI±SD: 29.6±5.5<br>Healthy controls, mean BMI±SD: 28.1±5.2 | antibiotics 3 months prior to study start | Illumina Miseq Sequencing | patients with psoriasis and controls<br>β-diversity: Significant (weighted Unifrac analyses)/not significant (non-weighted Unifrac analyses)<br>Phylum: No differences between subtypes, but difference in abundance.<br>(PSO) ↓ Bacteroidetes (47.1% pso vs 59.9% healthy),<br>↑Firmicutes, (44.6% pso vs 33% healthy)<br>↑ Proteobacteriae (5.4% pso vs 4.2% healthy)<br>Actinobacteriae (0.8% pso vs0.8% healthy)<br>Genus (pso): ↑*Blautia,* ↑ *Faecalibacterium*<br>↓ *Paraprevotella,* ↓ *Bacteroides*<br>No significant changes in gut microbiota associated with change in age, weight and BMI<br>Mild vs moderate-to-severe psoriasis (PASI≥10)<br>Moderate to severe psoriasis had lower biodiversity than mild. | Number of participants with diabetes: 9 (16.6%)<br>Psoriatic arthritis and IBD patients were excluded. |
| | | Yegorov (2020) Kazkhstan (21) | Case-control | Stool/ Stored at –80°C within 2 h | 14 patients with psoriasis (various forms),<br>median (IQR) PASI 11.4 (6.7–16.4)<br>7 healthy controls | Patients with psoriasis, median age (IQR): 34.5 (31.0–37.8)<br>Healthy controls, median age (IQR): 33.0 (31.3–34.0) | 10 (50.0)<br><br><br>11 (55.0) | Patients with psoriasis, median BMI (IQR) 24.8 (21.4–28.7)<br>Healthy controls, median | No antibiotics 3 months prior to study start | 16s rRNA (V1-V3) Illumina Miseq Sequencing | α-diversity (Chao1 index): no significant difference between patients with psoriasis and controls<br>Phylum: No differences in Firmicutes/Bacteroidetes ratio<br>Family (PSO): ↓ *Lacnospiraceae*<br>↑*Ruminococcaceae* | Same geographical area, BMI- and ethnicity matched<br>No information on treatment<br>Other skin conditions, psoriatic arthritis and IBD |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | BMI (IQR) 23.9 (18.6–32.7) | | | Genus (PSO): ↑ *Faecalibacterium* ↓ *Oscillibactor* | patients were excluded |
| | | Zhang (2021) China (22) | Case-control | Stool/ Immediately Stored at –80°C | 30 patients with psoriasis (mixed) NS 30 healthy controls | Patients with psoriasis, mean age±SD: 43.2±13.8 Healthy controls, mean age±SD: 43.2±13.2 | 20 (66.6) 20 (66.6) | NS | No antibiotics 1 month prior to study start | 16sRNA (V3-V4) HiSeq platform | α-diversity (Chao1 index, Shannon's diversity): no significant difference between patients with psoriasis and controls β-diversity (PCoA): significant separation of communities between patients with psoriasis and controls 465 OTU's were shared, 102 OTU's and 68 OTU's were specific to the healthy and psoriasis group, respectively Family (PSO): ↑ Veillonellaceae, ↑ *Ruminococcaceae* Genus (PSO): ↑ *Faecalibacterim*, ↑ *Megamonas* | No information on treatment. Patients with other autoimmune diseases, cancer or infections were excluded |
| | | Wang (2021) China (23) | Case-control | Stool/stored at –80°C (not further specified) | 20 patients with psoriasis (plaque) PASI>6 20 healthy controls | Patients with psoriasis, 48.8 (not further specified) Healthy controls, 47.5 (not further specified) | 15 (75) 15 (75) | NS NS | No anti-psoriatic treatment or antibiotics 1 month prior to study start | 16sRNA (V4) Ion5s platform | α-diversity: (Chao/ACE, Shannons's/Simpsons diversity): No significant difference, but psoriasis group showed slight decreased diversity. β-diversity (PCoA): Significant separation of communities between patients with psoriasis and controls Genus (PSO): ↑ *Megamonas* ↓ *Rombutsia* | Patients with gastrointestinal disease and food allergy excluded |

NS: not specified, PSO: psoriasis, PQ: plaque-type psoriasis, PPP: pustulosis palmoplantaris, PsA: psoriatic arthritis, BMI: body mass index. PCoA: principal coordinates analysis, PCA: principal component analysis.