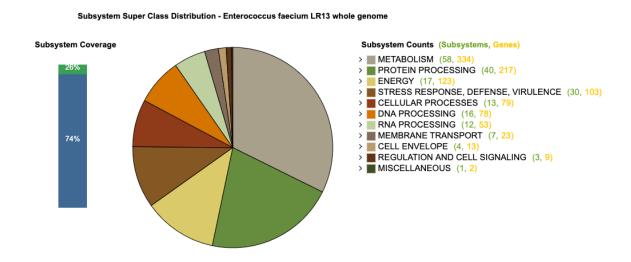
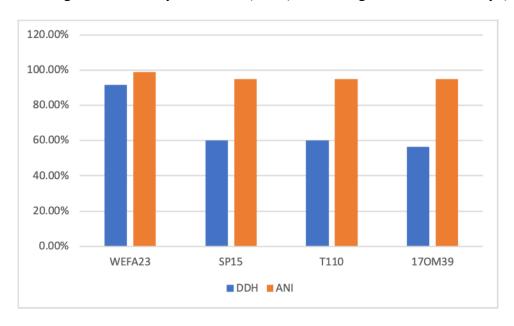
Supplementary Fig 1: Overview of subsystem-based analysis to annotate *Enterococcus faecium* LR13 genome. The whole-genome sequence of the strain LR13 was annotated using PATRIC RASTtk server.



Supplementary Fig 2: 10 prophage regions have been predicted in complete genome using PHAST server, of which 3 regions were intact (Red), 6 regions were incomplete (grey) and 1 regions were questionable (green).

Region	Region Length	Completeness	Score	# Total Proteins	Region Position	Most Common Phage	GC %	Details	
NODE_14_length_67016_cov_7.921451									
1	66Kb	intact	150	75	155-66211 ①	PHAGE_Aeromo_AS_gz_NC_042019(71)	41.00%	Show ①	
				NODE_18_lei	ngth_51843_cov_570.8	305181			
2	42.8Kb	intact	100	63	8203-51076 ①	PHAGE_Lister_B025_NC_009812(5)	34.36%	Show ①	
	NODE_19_length_51673_cov_380.136561								
3	33.4Kb	intact	120	51	10766-44203 ①	PHAGE_Bacill_BCJA1c_NC_006557(10)	36.76%	Show ①	
				NODE_20_length_49166_cov_8.829045					
4	49Kb	incomplete	60	76	145-49166 ①	PHAGE_Aeromo_AS_gz_NC_042019(63)	41.80%	Show ①	
				NODE_28_I	ength_28821_cov_8.72	21229			
5	28.1Kb	incomplete	50	62	3-28141 ①	PHAGE_Aeromo_Aes012_NC_020879(43)	41.23%	Show ①	
				NODE_29_le	ength_21725_cov_3.28	3444			
6	20.4Kb	incomplete	50	26	2-20415 ①	PHAGE_Salmon_38_NC_029042(10)	45.49%	Show ①	
				NODE_34_le	NODE_34_length_16032_cov_9.050517				
7	15.8Kb	questionable	80	29	1-15845 ①	PHAGE_Aeromo_AesO12_NC_020879(23)	41.53%	Show ①	
				NODE_35_l	NODE_35_length_15953_cov_2.945641				
8	15.7Kb	incomplete	60	26	1-15707 ①	PHAGE_Salmon_38_NC_029042(10)	45.64%	Show ①	
				NODE_39_I	NODE_39_length_12292_cov_2.912321				
9	11.2Kb	incomplete	60	17	1048-12290 ①	PHAGE_Escher_EP75_NC_049433(13)	44.71%	Show ①	
	NODE_48_length_8117_cov_3.381716								
10	8.1Kb	incomplete	30	19	8-8115 ①	PHAGE_Salmon_heyday_NC_049500(7)	43.60%	Show ①	

Supplementary Fig. 3: Pan-genomic comparison of *E. faecium* LR13 with other probiotic strains using DNA-DNA Hybridization (DDH) and average nucleotide identity (ANI)



Supplementary Fig 4: Overall COG representation of core, accessory and unique present in LR13, WEFA23, T110, 170M39 and SP15 probiotic strains

