Putative Function	Gene in S. suis	S. pneumoniae	S. pyogenes	S. mutans	S. thermophilus	L. lactis	L. plantarum	B. subtilis
Transcriptional control								
First transcriptional regulator	comR (SSU0049)	37.46%	35.93%	43.81%	34.43%	-	-	-
Master regulator	comX (SSU0016)	46.36%	40.00%	43.23%	40.52%	32.71%	30.86%(sigH)*	comK*
DNA uptake-recombination machinery								
Helicase required for DNA uptake	comFA (SSU0393)	66.36%	50.00%	57.87%	52.79%	51.20%	38.95%	37.35%
Membrane DNA-binding receptor	comEA (SSU0394)	47.95%	47.59%	53.41%	59.26%	37.56%	46.34%	37.56%
Competence protein	coiA (SSU1083)	51.60%	45.19%	50.48%	46.01%	42.50%	39.11%	31.91%
Component of the DNA transport	comGC (SSU0128)	70.37%	55.68%	60.23%	60.23%	56.82%	43.37%	49.33%
Competence associated endonuclease	endA (SSU1009)	69.49%	65.47%	65.38%	61.56%		35.29%	
DNA transporter	comFC (SSU0394)	49.08%	40.64%	50.91%	44.09%	45.25%	35.24%	31.28%
Signalling function								
Sensing and regulation		ComD-E	-	-	-	-	-	comA-comP
Peptide export		ComA-B	-	-	-	-	-	comQ
Possible pheromone-processing and peptide transporter								
Pheromone-processing	eep (SSU1754)	63.25%	64.29%	62.29%	65.00%	54.00%	47.73%	37.94%
Oligopeptide binding protein	oppA (SSU1664)	-	-	22.69%	-	32.26%	-	24.14%
		66.82%	49.92%	=	AmiA1	26.97%	28.43%	-
Oligopeptide transporter								
	oppB(SSU1661)		33.44%	35.74%		52.66%		39.69%
	oppC (SSU1660)	32.51%	31.67%	32.16%	32.39%	51.45%	32.89%	33.78%
	oppD (SSU1663)	45.03%	46.03%	47.63%	44.27%	55.11%	46.84%	48.28%
	oppF(SSU1662)	47.73%	47.53%	47.55%	49.79%	60.13%	47.91%	50.78%

Table S1. Conservation of competence genes in streptococci, Lactococcus lactis, Lactobacillus plantarum and Bacillus subtilis