Table 3 Relative fractions of COG groups within the functionally annotated genes for the six genera

COG groups	*Bifidobacterium*		*Lactobacillus*		*Lactococcus*		*Leuconostoc*		*Enterococcus*		*Streptococcus*	
	Pan (%)	Core (%)	Pan (%)	Core (%)	Pan (%)	Core (%)	Pan (%)	Core (%)	Pan (%)	Core (%)	Pan (%)	Core (%)
Information storage	30.0	33.9	34.0	49.1 ↑↑	50.5	30.4 ↓↓	28.1	31.0	26.6	33.8 ↑	34.7	42.6 ↑↑
Cellular process, signalling	21.9	20.2	22.7	20.3	17.1	19.1	19.1	20.0	24.4	18.9 ↓	26.3	20.3 ↓
Metabolism	48.1	45.9	44.3	30.6 ↓↓	32.2	50.6 ↑↑	52.7	49.1	50.0	47.8	39.2	36.9

All percentages are expressed as the fraction of all COG classes C to V. The arrows indicate significant shifts between the pan-genome genes and core genes for a given genus. Percentages do not always add up to 100% due to rounding effects