

Ain_RyC-MR95	A	T	C	C	G	T	T	G	A	T	C	A	A	A	T	T	T	G	A	G	G	T	T	T	G	A	G	A	G	A	T	A	T	G	T	A	A	A	T	T	C	A	A	A	G	G	A	T	A	A	T	C	A	A	A	C
Asp_D21	A	T	C	C	G	T	T	G	A	T	C	A	A	A	T	T	T	G	A	G	G	T	T	T	G	A	G	A	G	A	T	A	T	G	T	A	A	A	T	T	C	A	A	A	G	G	A	T	A	A	T	C	A	A	A	C
Bbi_S17	A	G	G	A	A	T	C	C	T	T	A	A	G	G	C	T	A	T	C	G	G	T	T	T	C	A	G	A	T	G	C	C	T	G	T	C	A	G	A	T	C	A	A	T	G	A	C	T	T	T	G	A	C	C	A	C
Bca_FSLF6-1037	A	C	A	A	A	A	T	C	G	A	C	G	C	A	T	T	T	G	A	G	G	T	T	T	A	G	A	G	C	T	G	T	G	T	T	A	A	A	T	T	G	A	A	T	G	G	T	A	T	T	A	A	A	A	C	
Bfi_16/4	G	T	T	G	G	A	A	A	T	T	T	G	G	A	T	T	T	G	A	C	G	T	T	T	A	G	T	A	C	C	C	G	G	G	A	A	A	A	T	T	A	A	G	T	G	A	T	T	G	G	A	A	A	A	C	
Bpe_CAG:437	T	T	T	G	G	A	T	A	A	C	A	T	G	A	T	T	T	G	G	T	A	T	T	T	A	G	T	A	C	C	T	G	A	A	C	A	A	A	T	T	A	C	G	T	G	A	C	T	G	T	A	A	A	A	C	
Bsp_AC2005	T	T	T	A	T	C	A	T	A	C	T	A	T	A	T	T	T	G	G	T	G	T	T	T	A	G	T	A	C	C	T	A	G	A	G	A	A	A	T	T	A	A	G	T	G	A	T	T	A	G	A	A	A	A	C	
Bth_DSM20171	A	C	A	A	A	A	T	T	T	C	A	T	T	G	T	T	T	G	A	G	G	T	T	T	A	G	A	G	C	T	G	T	G	T	T	A	A	A	T	T	G	A	A	T	G	G	T	A	T	T	A	A	A	A	C	
Cgl_PW2	G	A	G	A	A	G	A	T	T	T	T	G	A	T	C	C	A	A	T	G	G	T	T	T	T	G	G	A	G	C	A	G	T	G	T	C	G	T	T	C	T	G	A	C	T	G	G	T	A	A	T	C	C	A	A	C
Cla_DSM_14151	A	T	G	G	C	T	C	T	C	T	A	A	A	A	T	T	T	G	A	G	G	T	T	T	A	G	A	C	C	A	G	T	G	T	A	A	T	T	T	T	A	G	A	G	A	G	T	A	G	T	A	A	A	A	C	
Cma_M35/04/3	T	T	T	A	A	A	T	A	T	T	A	C	A	A	T	T	T	A	A	G	G	T	T	C	T	T	G	T	A	C	T	T	T	C	T	A	G	A	T	T	T	T	C	A	T	A	T	T	A	G	T	A	A	A	A	C
Cmi_DSM15897	A	T	T	G	G	A	T	T	T	T	T	G	A	A	T	T	T	G	A	G	G	T	T	T	A	G	G	G	T	T	A	T	G	T	T	A	T	T	T	T	G	A	A	C	T	G	A	A	T	T	A	A	A	A	C	
Csp_CAG:230	C	G	A	T	T	A	T	A	T	T	T	G	A	A	T	T	T	G	A	T	A	T	T	T	A	G	T	A	C	C	T	G	A	A	A	G	A	A	T	T	G	A	G	T	T	A	T	C	G	T	A	A	A	A	C	
Csp_ZWU0011	T	A	C	G	T	T	A	T	A	A	T	G	A	A	A	T	T	G	A	C	A	T	T	T	G	G	T	A	C	T	C	T	C	G	C	A	T	C	T	T	T	T	T	G	G	T	A	T	A	A	G	G	A	A	A	C
Dlo_AGR2136	C	G	G	C	G	A	G	A	A	C	C	G	G	A	T	T	T	G	A	G	G	T	T	T	G	A	G	A	G	T	C	T	T	G	T	T	A	A	T	A	C	G	G	A	A	G	G	A	T	T	T	T	A	A	A	C
Edo_DSM3991	T	A	T	G	T	T	A	A	A	A	T	A	T	G	T	T	T	G	A	G	G	T	T	T	T	G	T	T	A	C	C	A	T	A	T	G	G	A	T	T	T	T	T	G	C	T	A	G	A	T	T	A	A	G	A	C
Efa_1141733	G	G	A	A	A	A	A	T	T	T	T	T	T	C	T	G	C	G	A	G	G	T	T	T	A	G	A	G	C	T	A	T	G	C	T	G	A	T	T	T	G	A	A	T	G	C	T	T	C	C	A	A	A	A	C	
Efa_D32_1	G	A	A	A	A	A	A	A	T	A	A	T	T	C	T	C	C	G	A	G	G	T	T	T	A	G	A	G	T	C	A	T	G	T	T	G	T	T	T	A	G	A	A	T	G	G	T	A	C	C	A	A	A	A	C	
Efa_OG1RF_1	G	A	A	A	A	A	A	A	T	A	A	T	T	C	T	C	C	G	A	G	G	T	T	T	A	G	A	G	T	C	A	T	G	T	T	G	T	T	T	A	G	A	A	T	G	G	T	A	C	C	A	A	A	A	C	
Efa_TX0012	T	T	T	C	A	A	A	T	T	T	T	A	A	A	T	T	T	G	A	G	G	T	T	T	T	G	T	A	C	T	C	T	C	A	A	T	A	A	T	T	T	C	T	T	A	T	C	A	G	T	A	A	A	A	C	
Efa_TX0012_2	T	T	T	C	A	A	A	T	T	T	T	A	A	A	T	T	T	G	A	G	G	T	T	T	T	G	T	A	C	T	C	T	C	A	A	T	A	A	T	T	T	C	T	T	A	T	C	A	G	T	A	A	A	A	C	
Eit_DSM15952	A	G	A	T	A	A	A	A	A	T	A	T	C	T	G	C	G	A	G	G	T	T	T	T	A	G	A	G	C	T	A	T	G	T	T	G	A	A	T	C	G	A	A	T	G	C	T	T	C	C	A	A	A	A	C	
Emu_QU25_DNA	G	A	A	A	A	A	A	T	T	T	T	T	T	C	T	A	C	G	A	G	G	T	T	T	A	G	A	G	C	T	A	T	G	T	T	G	A	A	T	T	G	A	A	T	G	C	T	T	C	C	A	A	A	A	C	
Eph_ATCCBAA-412	A	G	A	A	A	G	A	A	A	A	T	G	G	C	T	G	C	G	A	G	G	T	T	T	A	G	A	G	C	C	A	T	G	T	T	G	A	A	T	T	G	A	A	T	G	C	T	T	C	C	A	A	A	A	C	

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