

Predicted secondary metabolite biosynthetic gene clusters (smBGCs) in *H. alvei* A23BA genome.

smBGC	Type	Location	Locus tags of genes	Predicted gene product of core biosynthetic gene(s)	Most similar known gene cluster/ MIBiG ID	Similarity
1	Siderophore	648,007 – 659,842 (11,836 nucleotides)	ctg1_571 – ctg1_580	lucA/lucC family siderophore biosynthesis protein	Desferrioxamine E / BGC0001572	75%
2	Thiopeptide	1,642,170 – 1,668,688 (26,519 nucleotides)	ctg1_1477 – ctg1_1495	Pyruvate formate lyase 1-activating protein; YcaO-like family protein	O-antigen / BGC0000781	14%
3	Homoserine lactone	2,511,420 – 2,532,067 (20,648 nucleotides)	ctg1_2268 – ctg1_2293	Acyl-homoserine-lactone synthase	-	-
4	Beta- lactone	3,748,962 – 3,774,466 (25,505 nucleotides)	ctg1_3390 – ctg1_3408	Long-chain fatty acid-CoA ligase; 2- isopropylmalate synthase	-	-