

**Table 9. Strict analysis of Severe (SE) vs. Mild (MI)**

Seed-motifs	Number of contigs	Number of isolates represented	SE		MI	Motifs of PfEMP1s of in vitro propagated parasites	Seed id	P	Skew
			SE	MI					
S1-EPGKQH	10	11	9	2		R29	Contig1134_18_23	0,048	0,600
S2-EDLEKK	28	30	21	9		FCR3S1.2	Contig1239_53_58	0,038	0,340
S3-ALNRQE	54	55	37	18		R29, Var0	Contig722_67_72	0,014	0,290
M1-AYVLQS	4	4	0	4			Contig1170_103_108	0,048	-1,000
M2-TCGVKG	4	4	0	4			Contig1418_111_116	0,046	-1,000
M3-TCDDDN	18	18	5	13			Contig1361_114_119	0,020	-0,500
M4-DSIKTH	34	34	11	23		MCvar1o2, FCR3S1.2	Contig1361_1_6	0,007	-0,410
M5-QICTVL	207	227	115	112		FCR3S1.2, r29, var0, Mcvar1o2, M284S2	Contig1081_20_25	0,022	-0,050

Amino-acid motifs found present in assembled *var*-contigs translated into amino-acids of fresh isolates obtained from Ugandan children as a function of disease severity (severe vs. mild; SE vs. MI). See also M&M. The analysis was strict ie. only motifs from the same alignment region of DBL1alpha were considered.