

Additional file 2: peaks obtained from two groups

	Total peaks^a	Peak mean length	Peak Median Length	Peak Total Length	Peak Covered Size In Genome
Abnormal cloned piglets	146809	1276.06	1104	187337580	8.28%
Normal cloned piglets	145564	1321.13	1145	192308374	8.50%

^apeak is the enrichment region where the reads was aligned to the same position in the genome