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## Identification Of Porcine And Turkey SNPs By High Parallel Sequencing On A Solexa Sequencing Platform

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Turkey and porcine SNPs were identified by massive parallel sequencing using a Solexa Genome Analyzer 1G system (Illumina) in pools of DNA. Due to the different status of availability of genomic sequences two different strategies were used for the two species. In turkey, with limited genomic sequences available, identification of SNPs is achieved by specifically isolating a 4000 bp fraction of restriction enzyme digested DNA from a pool of 6 individuals. In pigs, sequencing of the genome is in progress and therefore we directly isolated a 200 bp fraction of restriction enzyme digested DNA obtained from 5 individuals. The porcine sequences are directly aligned with the available reference sequences, whereas in poultry small sequence contigs are build using the SSAKE and VELVET assembly programs.
For each species we have produced around 20 million sequences, 36 bp in size. In turkey this represents an estimated 4% of the genome whereas in pigs the data represents 1 to 2 % of the genome. In both cases this amounts to a 15 fold coverage of the sequenced regions. Theoretically, this resource could provide 20,000-30,000 SNPs. Because a pool of DNA from 5 to 6 individuals is used the method is targeted at SNPs with high minor allele frequencies