ERRATUM

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Erratum to: MetCap: A bioinformatics probe design pipeline for large-scale targeted metagenomics

Sandeep K. Kushwaha^{1*}, Lokeshwaran Manoharan¹, Tejashwari Meerupati¹, Katarina Hedlund¹ and Dag Ahren^{1,2}

Erratum

In our article [1], the numbers of probes and sequences for the CAZy dataset in the Additional file 3, table S3 (A) (Table 1 here) have been switched. The corrected table S3 (A) is presented in this erratum.

In the following three parts of our article [1] we would like to correct the numbers for probes and sequences accordingly.

Abstract (Results), page 1

To illustrate the advantage of a targeted metagenome approach, we have generated more than 400,000 probes that match more than 300,000 publicly available sequences related to carbon degradation, and used these probes for targeted sequencing in a soil metagenome study.

Results and discussion, page 6

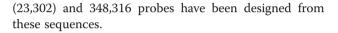
In this study, 306,525 nucleotide sequences were extracted through the pipeline and used as a proof of concept. A list of group-wise collected sequences and generated probes from databases are given as Additional file 3: Table S3. In total, 406,277 unique probes were produced from these extracted nucleotide sequences in this study with the following criteria: length (50mer), GC contents (35-65), melting temperature (55-65), and 3 probes per cluster on 90 % cluster similarity.

Results and discussion, page 8

Among the downloaded sequences (Additional file 3: Table S3), 258,544 sequences belong to the CAZy database from four major families: Glycoside Hydrolase (110,923), Glycosyl Transferases (103,952), Carbohydrate Esterases (13,787), Polysaccharide Lyases (6,580), and an associated module, Carbohydrate binding-modules

* Correspondence: sandeep.kushwaha@biol.lu.se

¹Department of Biology, Lund University, Ecology Building, Lund 223 62, Sweden



Author details

¹Department of Biology, Lund University, Ecology Building, Lund 223 62, Sweden. ²Bioinformatics Infrastructure for Life Sciences (BILS), Department of Biology, Lund University, Ecology Building, Lund 223 62, Sweden.

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GT	7755 57	106687 4663	30802 1082	160	683 51	146087 5859	103952 6580
GH	2754	97488	33643	1457	7382	142724	110923
CE	311	14646	3254	66	9	18286	13787
CBM	439	26910	7424	134	453	35360	23302
Family	Archaea	Bacteria	Eukaryota	Unclassified	Virus	Total probes	Total sequences

Table 1 (A): Family-wise summary of generated probes based on sequences downloaded from CAZy database