Species	System	PMID where applicable	Additional information about the system	Total number of sites targeted	Optimal restriction enzyme combination	Optimal theoretical size range (in bp)	% max *Score*	*NF* /1000	*Enrichment Value* (*EV*)	*Cost Reduction Factor* (*CRF*)	*Robustness* (*R*)
Homo sapiens	Exon-intron boundaries		DNA methylation has been shown to affect alternative splicing. Therefore, we focused on targeting CpGs close to canonical splicing sites.	26211	(BsiSI OR MspI) AND (SbfI OR SdaI OR Sse8387I)	80_500	25.4	772.23	2.06446811	53.32	0.94704403
Homo sapiens	Horvath epigenetic clock	24138928	The Horvath epigenetic clock is the best predictor of biological age available in humans. We have attempted to target the 353 CpG sites that are used in the model in order to reduce the cost associated with the assay.	353	(BsiSI OR MspI) AND (BspQI OR LguI OR SapI)	60_160	27.57	442.456	3.65771916	93.06	0.91305072
Homo sapiens	Imprinted loci	26769960	Genomic imprinting is an epigenetic phenomenon that results in gene expression occuring in a parent-of-origin fashion. We have attempted to target Cs in CpG context that are found within the canonical human imprints.	2810	(BmeT110I OR BsoBI) AND (BsaWI)	60_540	25.12	336.88	2.67867053	122.23	0.98085689
Homo sapiens	Placental imprinted loci	26769960	Genomic imprinting is an epigenetic phenomenon that results in gene expression occuring in a parent-of-origin fashion. However, until recently many extraembryonic imprints were still unknown. We have targetted Cs in CpG context that are found within these novel human placental imprints.	7591	(BsaWI) AND (BssAI)	60_540	26.41	107.248	1.72827483	383.94	0.93382453
Homo sapiens	CTCF sites	26257180	CTCF is an important architectural protein that helps to organise chromatin domains. Since its binding has been shown to be dependent on DNA methylation in some of its recognition sequences, we have targeted the CpG sites within these regions of the genome.	2000	(BmeT110I OR BsoBI) AND (BssAI)	40_360	25.5	314.079	2.78946872	131.1	0.88798165
Mus musculus	iPSCs demethylated	28147265	iPSC reprogramming in mouse is characterised by global changes in DNA methylation. Sites that tend to undergo demethylation faster than the genome average tend to be within ESC-Super Enhancers. We targetted the Cs in CpG context in these regions, as they are interesting for the reprogramming field.	1449	(BmeT110I OR BsoBI) AND (BsiSI OR MspI)	80_980	25.19	974.05	3.42628839	37.31	0.96792238
Mus musculus	iPSCs maintained	28147265	iPSC reprogramming in mouse is characterised by global changes in DNA methylation. Sites that tend to be resistant to the genome-wide demethylation tend to be within Intercisernal A-particle containing regions. We targetted the Cs in CpG context in these regions, as they are interesting for the reprogramming field.	3896	(BmeT110I OR BsoBI) AND (BsiSI OR MspI)	80_560	25.85	690.088	2.835875	52.66	0.94227711
Mus musculus	NRF1 sites	26675734	NRF1 is a transcription factor whose binding to the DNA is dependent on the methylation status of its recognition sequences. We have tried to enrich for those CpG sites that overlap with *in vivo* NRF1 binding sites.	17018	(BmeT110I OR BsoBI) AND (PaeI OR SphI)	20_760	25.04	445.36	2.01909776	81.6	0.99634045
Arabidopsis thaliana	CHG sites	27419873	Non-CpG methylation is an important epigenetic modification in plants. In this study a huge number of regions containing non-CpG methylation were found to vary between different Arabidopsis accessions in the 1001 Epigenomes Project. We targetted Cs in non-CpG context within these non-CpG DMRs.	21801	(AanI OR PsiI) AND (Csp6I OR CviQI)	100_520	25.05	165.313	1.48095531	9.65	0.94999336