How to get name and sequence of reads mapped to a particular gene

Hello,

 I am trying to look at some of the actual reads that mapped to a particular gene using the GEUVADIS data set.

For example, lets say I have a bed file for one individual (SAMPLE1.bed) and the gencode annotation file (GENCODE.v12.gtf). I would like the output to be bed file oriented like this:

Mappedread_ID	Mappedread_Chr	Mappedread_start	Mappedread_end	Mappedread_sequence	Gene_ID	Gene_chromosome	Gene_start	Gene_end
HWI-ST:XXXXX	1	15000	15020	ATTTATATGATTTATATAT	ENSG000001234	Chr1	14000	16000

With my limited understanding about flux-capacitor, it seems to me that its main purpose is to generate read counts for each gene and does not return the actual read ID's which mapped to a certain gene.

I managed to do this in bedtools by using the following command, but wasn't sure if bedtools and flux-capacitor are operating in the same fashion.

bedtools intersect -a SAMPLE1.bed -b GENCODE.v12.gtf -wb > output.txt

Is the equivalent to the above possible using flux capacitor ?

Thanks,

Jin