Sanger sequencing of PCR products amplifying the SDHC promoter region from bisulfite-treated DNA. 13 of the total 16 CpGs are highlighted. No methylation was detected in the patient’s blood and normal adrenal tissue, low-level methylation (<5-10%) was measured in the adenoma. For PGL1 and PGL2, methylation was estimated at 40-50% and 70-80%, respectively, for CpG 1, 3 and 7 to 13. CpG 2 was 20-25% methylated in PGL1 and PGL2, CpG 4-6 were 25% methylated in PGL1 and 50-75% in PGL2.
Hierarchical clustering of pheochromocytomas/paragangliomas based on expression data for genes hypermethylated and downregulated in tumors with SDHx mutations. PGL1 of patient 52 clusters with tumors harboring the CpG island methylator phenotype (CIMP).