Appendix B: Values permitted for data.type and type in getTCGA function.

Omics-Profile	data.type	type	Description
Gene Expression	mRNA_Array	<u>G450</u>	Microarray, Agilent 244K Custom Gene Expression G4502A-07
	mRNA_Array	U133	Microarray, Affymetrix Human Genome U133A 2.0 Array
	mRNA_Array	Huex	Microarray, Affymetrix Human Exon 1.0 ST Array
	RNASeq	count	RNA-Seq, raw counts
	RNASeq	RPKM	RNA-Seq, normalized counts
	RNASeq2		RNA-Seq second analysis pipeline, RSEM
miRNA expression	miRNA_Array		miRNA array, Agilent 8 x 15K Human miRNA-specific microarray (H-miRNA_8x15K)
	miRNA_Array		miRNA array, Agilent Human miRNA Microarray Rel12.0 (H-miRNA_8x15Kv2- for OV only).
	miRNASeq	count	miRNA-Seq, raw counts
	miRNASeq	rpmmm	miRNA-Seq, reads per million miRNA mapped
Mutation	Mutation	<u>somatic</u>	Somatic non-silent mutations
	Mutation	all	All mutations called
Methylation	Methylation	<u>27K</u>	Illumina Infinium HumanMethylation27 BeadChip
		450K	Illumina Infinium HumanMethylation450 BeadChip
Copy number changes	CNA_SNP		CNA, Affymetrix Genome-Wide Human SNP Array 6.0
	CNV_SNP		CNV, Affymetrix Genome-Wide Human SNP Array 6.0
	CNA_CGH	<u>415K</u>	CNA, Agilent Human Genome CGH Custom Microarray 2x415K
	CNA_CGH	244A	CNA, Agilent Human Genome CGH Microarray 244A

Remark: $\underline{\text{type}}$ that's bold and underlined is the default type for the particular data.type