

Table 1: Gene symbols in original, unprocessed data (columns 1 to 3) and in the preprocessed data (columns 5 to 7) *shared* by pairs of brain areas. The two *Unique* columns show the number of unique genes measured in each brain area (row). The reductions from the number of unique genes in the original to the preprocessed data result from the elimination of some of the probes that were used to measure gene expression.

	Original				Preprocessed			
	cerebellum	temporal	pons	Unique	cerebellum	temporal	pons	Unique
prefrontal	15285	15406	15233	16676	15273	15387	15214	16667
cerebellum		15300	15339	16687		15286	15327	16683
temporal			15267	16643			15248	16634
pons				16643				16634

Table 2: Gene symbols in original, unprocessed data (columns 1 to 3) and in the preprocessed data (columns 5 to 7) *not shared* by pairs of brain areas. The two *Unique* columns show the number of unique genes measured in each brain area (row). The reductions from the number of unique genes in the original to the preprocessed data result from the elimination of some of the probes that were used to measure gene expression.

	Original				Preprocessed			
	cerebellum	temporal	pons	Unique	cerebellum	temporal	pons	Unique
prefrontal	1391	1270	1443	16676	1394	1280	1453	16667
cerebellum		1387	1348	16687		1397	1356	16683
temporal			1376	16643			1386	16634
pons				16643				16634