Supplementary Figure 1. Assessment of cross-platform data agreement using CAT plots

Figure 1-a. CAT plots of UniGene (UG) matched normalized $\log_2$ ratios (filtered) for up regulated genes. The list sizes were chosen to be from 10 to 100, with an increment of 5. The platform used for reference is listed at the top of each plot. The color and each line type correspond to a particular platform. The 'blue solid', 'red solid', 'black solid', 'magenta solid', 'green solid', 'blue dash', 'red dash', 'black dash', 'magenta dash', and 'green dash' correspond to 'Affymetrix', 'Amersham', 'Mergen', 'ABI', 'academic cDNA', 'MGH long oligo', 'MWG', 'Agilent', 'Compugen', and 'Operon' platforms, respectively.
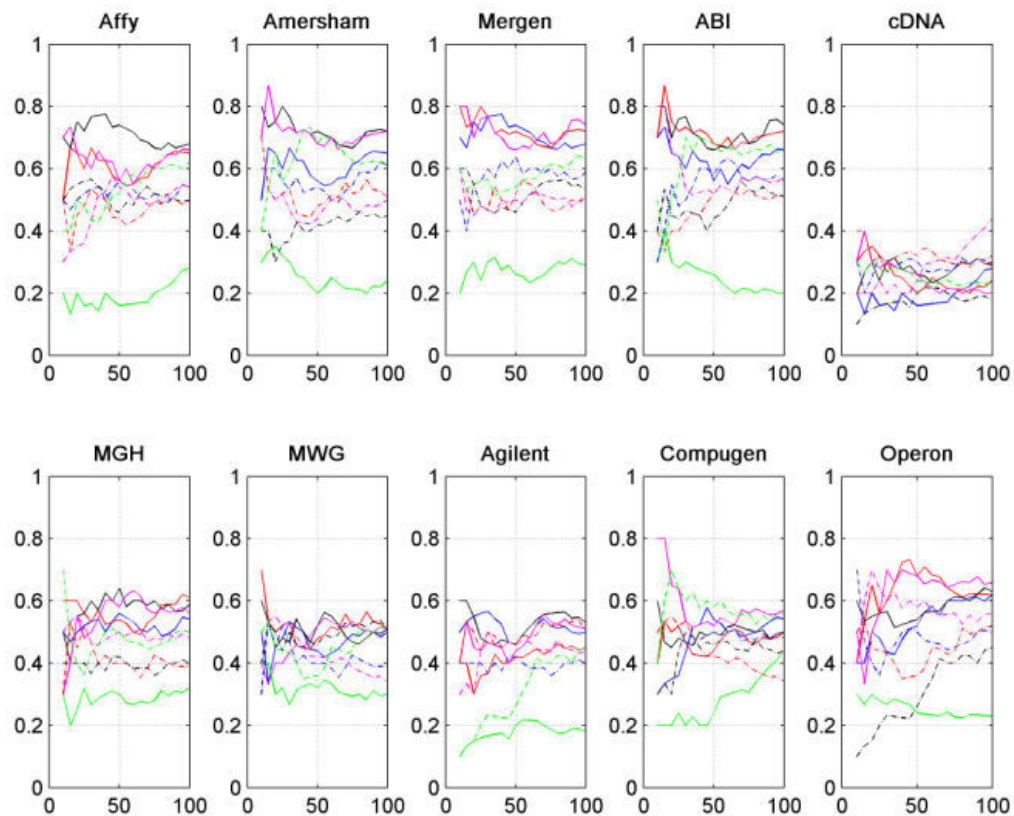
Figure 1-b. CAT plots of UniGene (UG) matched normalized $\log_2$ ratios (filtered) for down regulated genes. The list sizes were chosen to be from 10 to 100, with an increment of 5. The platform used for reference is listed at the top of each plot. The color and each line type correspond to a particular platform. The 'blue solid', 'red solid', 'black solid', 'magenta solid', 'green solid', 'blue dash', 'red dash', 'black dash', 'magenta dash', and 'green dash' correspond to 'Affymetrix', 'Amersham', 'Mergen', 'ABI', 'academic cDNA', 'MGH long oligo', 'MWG', 'Agilent', 'Compugen', and 'Operon' platforms, respectively.
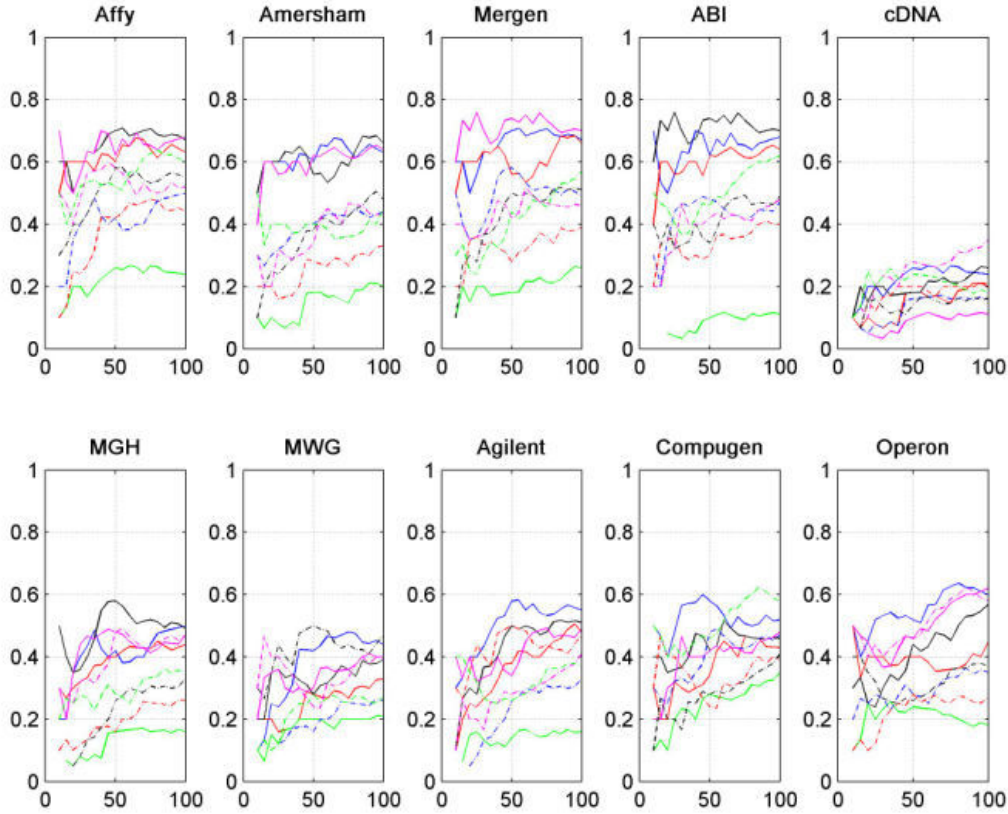
Figure 1-c. CAT plots of LocusLink identifier (LL) matched normalized $\log_2$ ratios (filtered) for up regulated genes. The list sizes were chosen to be from 10 to 100, with an increment of 5. The platform used for reference is listed at the top of each plot. The color and each line type correspond to a particular platform. The 'blue solid', 'red solid', 'black solid', 'magenta solid', 'green solid', 'blue dash', 'red dash', 'black dash', 'magenta dash', and 'green dash' correspond to 'Affymetrix', 'Amersham', 'Mergen', 'ABI', 'academic cDNA', 'MGH long oligo', 'MWG', 'Agilent', 'Compugen', and 'Operon' platforms, respectively.
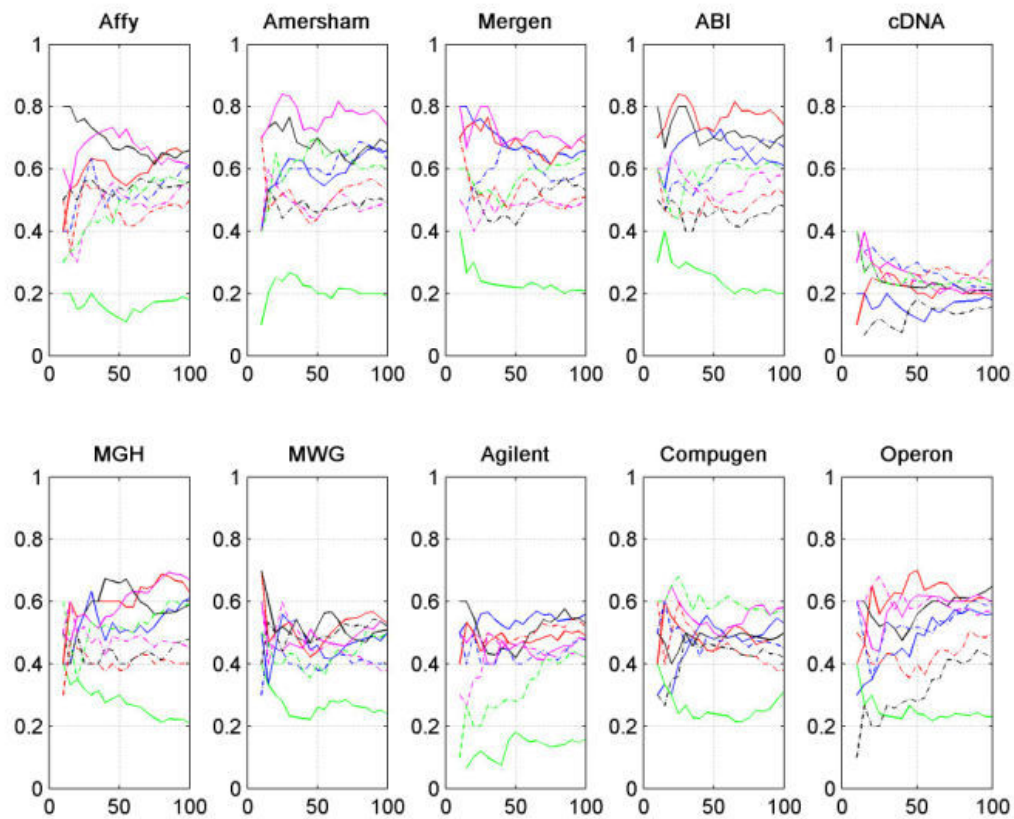
Figure 1-d. CAT plots of LocusLink identifier (LL) matched normalized $\log_2$ ratios (filtered) for down regulated genes. The list sizes were chosen to be from 10 to 100, with an increment of 5. The platform used for reference is listed at the top of each plot. The color and each line type correspond to a particular platform. The 'blue solid', 'red solid', 'black solid', 'magenta solid', 'green solid', 'blue dash', 'red dash', 'black dash', 'magenta dash', and 'green dash' correspond to 'Affymetrix', 'Amersham', 'Mergen', 'ABI', 'academic cDNA', 'MGH long oligo', 'MWG', 'Agilent', 'Compugen', and 'Operon' platforms, respectively.
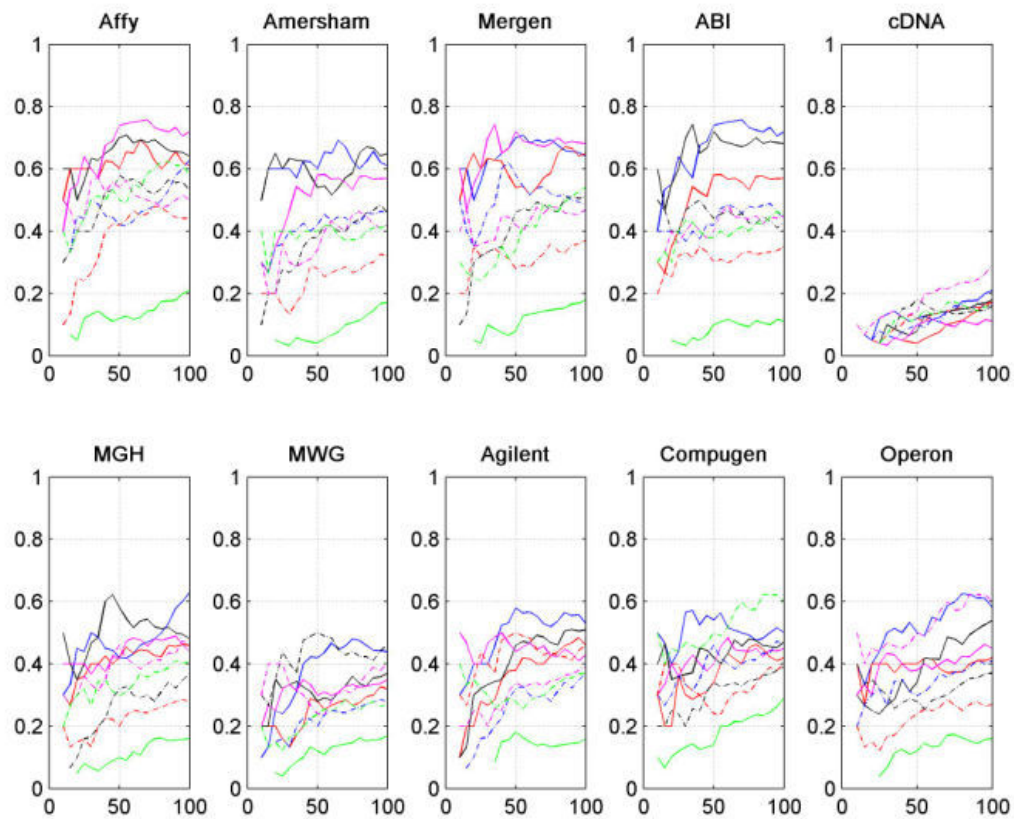
Figure 1-e. CAT plots of RefSeq identifier (RS) matched normalized $\log_2$ ratios (filtered) for up regulated genes. The list sizes were chosen to be from 10 to 100, with an increment of 5. The platform used for reference is listed at the top of each plot. The color and each line type correspond to a particular platform. The 'blue solid', 'red solid', 'black solid', 'magenta solid', 'green solid', 'blue dash', 'red dash', 'black dash', 'magenta dash', and 'green dash' correspond to 'Affymetrix', 'Amersham', 'Mergen', 'ABI', 'academic cDNA', 'MGH long oligo', 'MWG', 'Agilent', 'Compugen', and 'Operon' platforms, respectively.
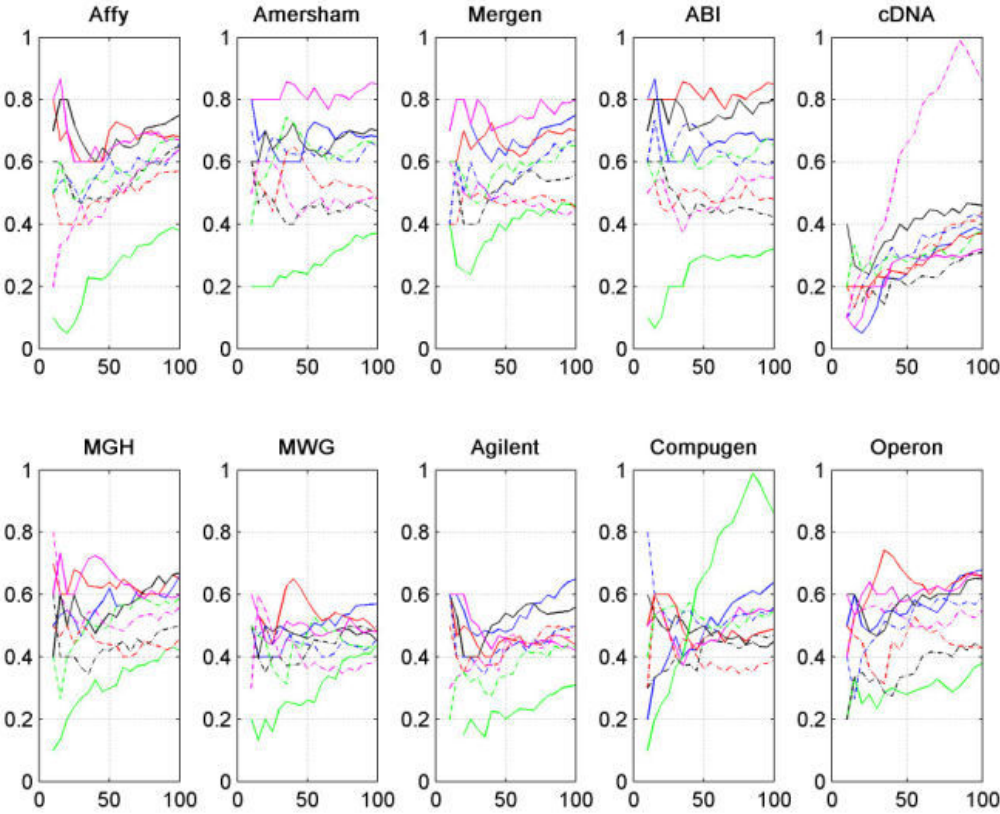
Figure 1-f. CAT plots of RefSeq identifier (RS) matched normalized log$_2$ ratios (filtered) for down regulated genes. The list sizes were chosen to be from 10 to 100, with an increment of 5. The platform used for reference is listed at the top of each plot. The color and each line type correspond to a particular platform. The 'blue solid', 'red solid', 'black solid', 'magenta solid', 'green solid', 'blue dash', 'red dash', 'black dash', 'magenta dash', and 'green dash' correspond to 'Affymetrix', 'Amersham', 'Mergen', 'ABI', 'academic cDNA', 'MGH long oligo', 'MWG', 'Agilent', 'Compugen', and 'Operon' platforms, respectively.
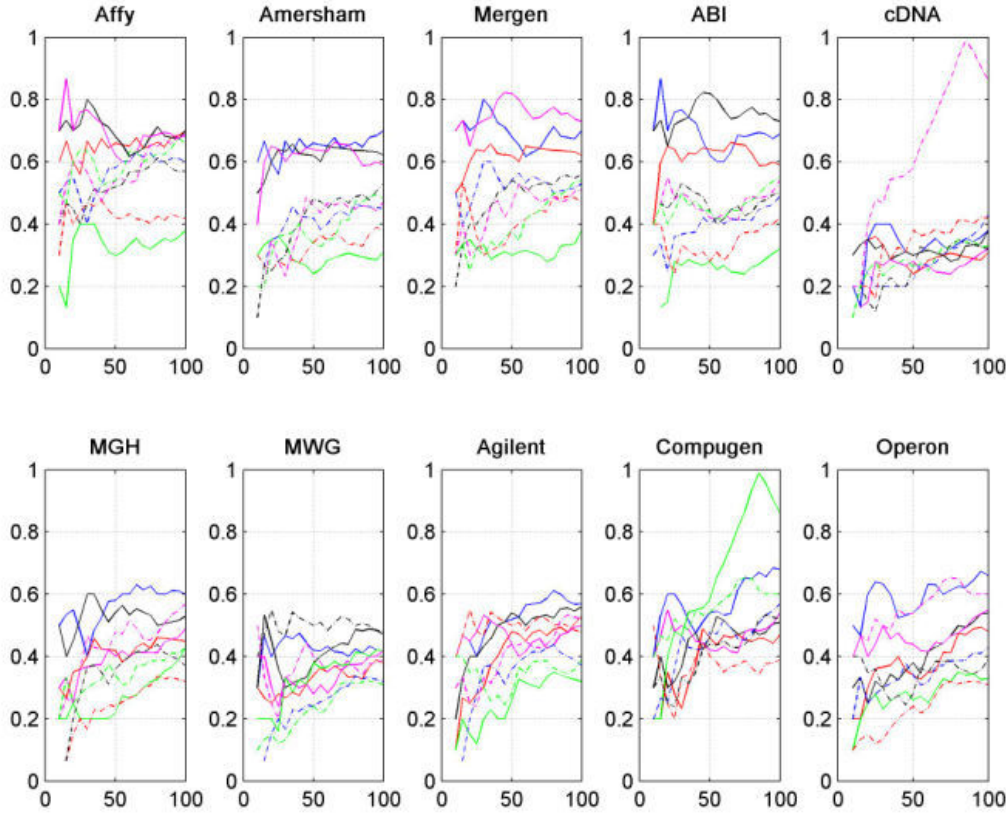
Figure 1-g. CAT plots of RefSeq exon position (RSEXON) matched normalized $\log_2$ ratios (filtered) for up regulated genes. The list sizes were chosen to be from 10 to 100, with an increment of 5. The platform used for reference is listed at the top of each plot. The color and each line type correspond to a particular platform. The 'blue solid', 'red solid', 'black solid', 'magenta solid', 'green solid', 'blue dash', 'red dash', 'black dash', 'magenta dash', and 'green dash' correspond to 'Affymetrix', 'Amersham', 'Mergen', 'ABI', 'academic cDNA', 'MGH long oligo', 'MWG', 'Agilent', 'Compugen', and 'Operon' platforms, respectively.
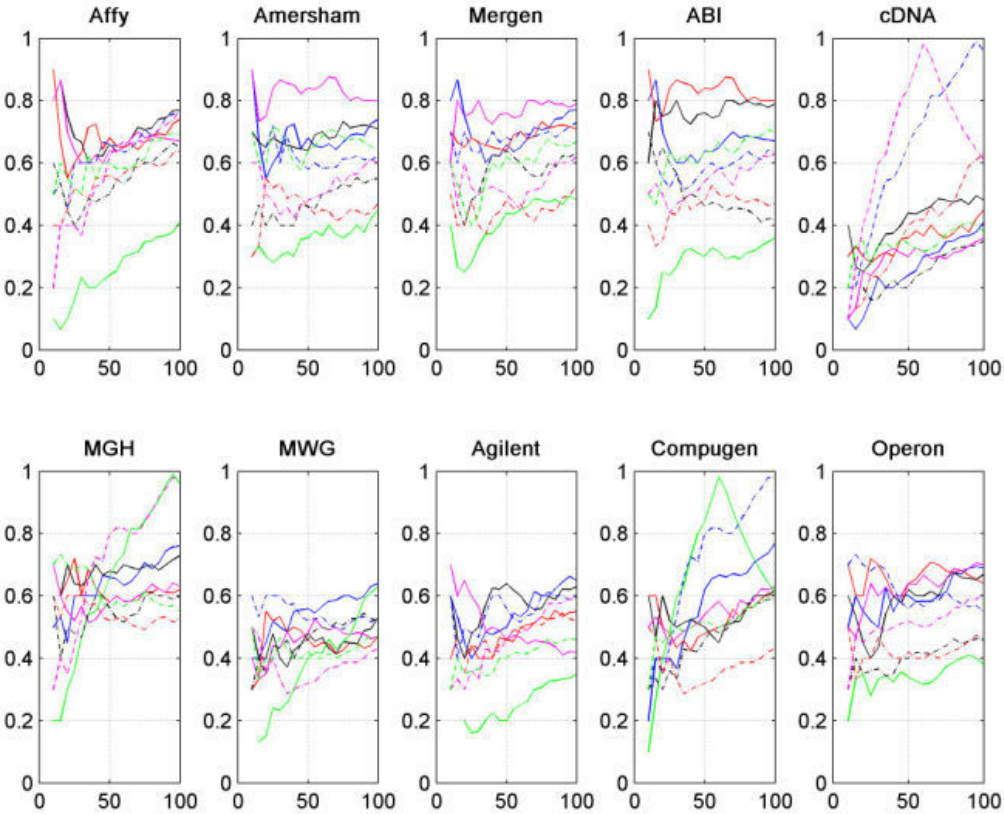
Figure 1-h. CAT plots of RefSeq exon position (RSEXON) matched normalized $\log_2$ ratios (filtered) for down regulated genes. The list sizes were chosen to be from 10 to 100, with an increment of 5. The platform used for reference is listed at the top of each plot. The color and each line type correspond to a particular platform. The 'blue solid', 'red solid', 'black solid', 'magenta solid', 'green solid', 'blue dash', 'red dash', 'black dash', 'magenta dash', and 'green dash' correspond to 'Affymetrix', 'Amersham', 'Mergen', 'ABI', 'academic cDNA', 'MGH long oligo', 'MWG', 'Agilent', 'Compugen', and 'Operon' platforms, respectively.