Figure S8. **Cross-Platform Comparisons.** Size comparisons for CNVs inferred by different platforms and methodologies on eight common HapMap samples. For each plot, the estimated size for a CNV annotated by fosmid ESP mapping is shown along the X-axis. Sizes for variants that overlap by any number of nucleotides within the same sample as annotated by Redon et al. (a) which used BAC CGH/Affymetrix 5.0 arrays, McCarroll et al. (b) which used Affymetrix 6.0 arrays, or Cooper et al. (c) which used IlluminaHuman1M BeadChips. The scale is in nucleotides on all three plots. Note that clustering of sizes can be seen, this is a result of the same CNV inferred within multiple samples.

Figure S8 a)

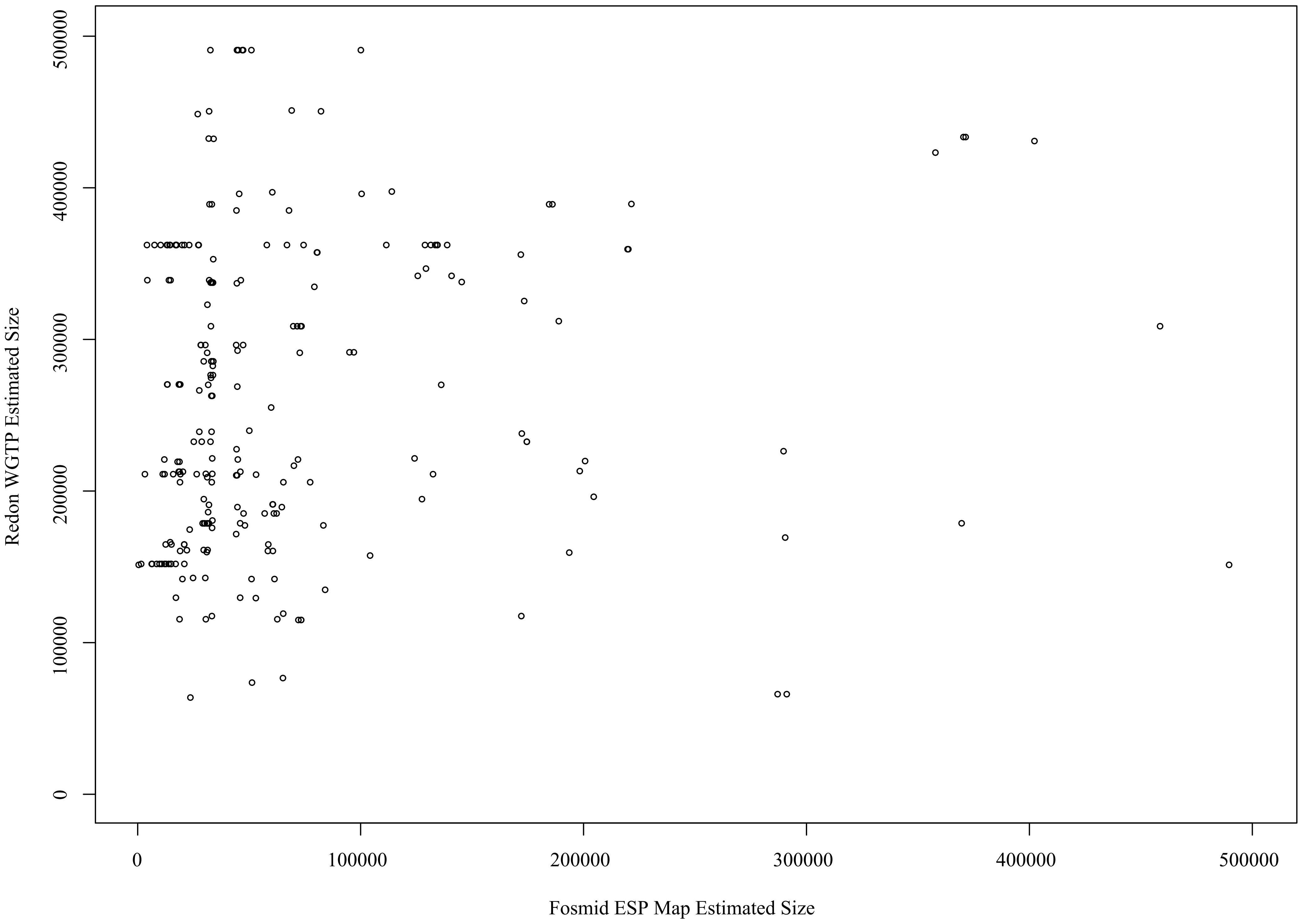
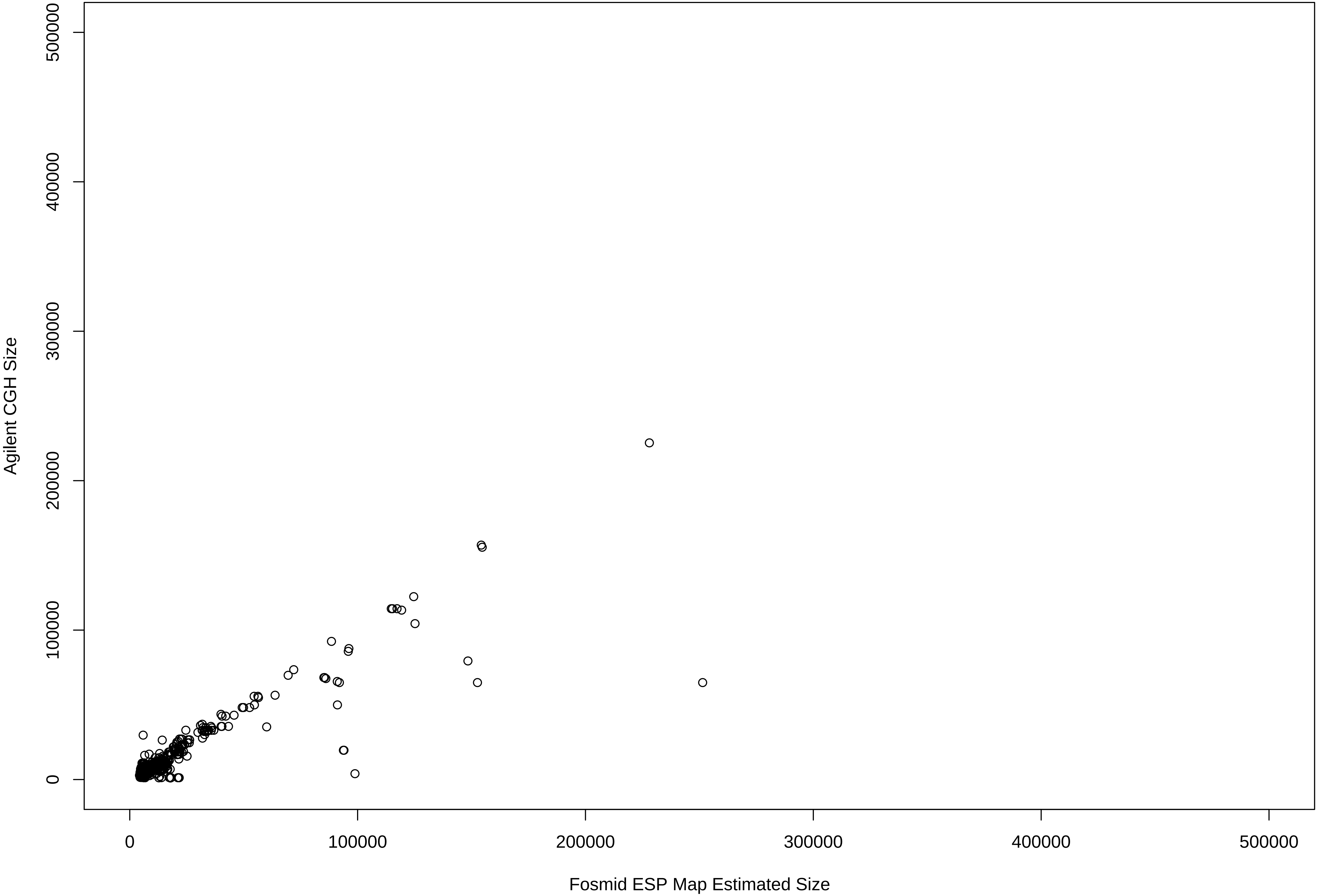

Redon WGTP Estimated Size
0
100000
200000
300000
400000
500000
Fosmid ESP Map Estimated Size
0
100000
200000
300000
400000
500000

Figure S8 b)



Agilent CGH Size
0
100000
200000
300000
400000
500000
Fosmid ESP Map Estimated Size
0
100000
200000
300000
400000
500000

Figure S8 c)

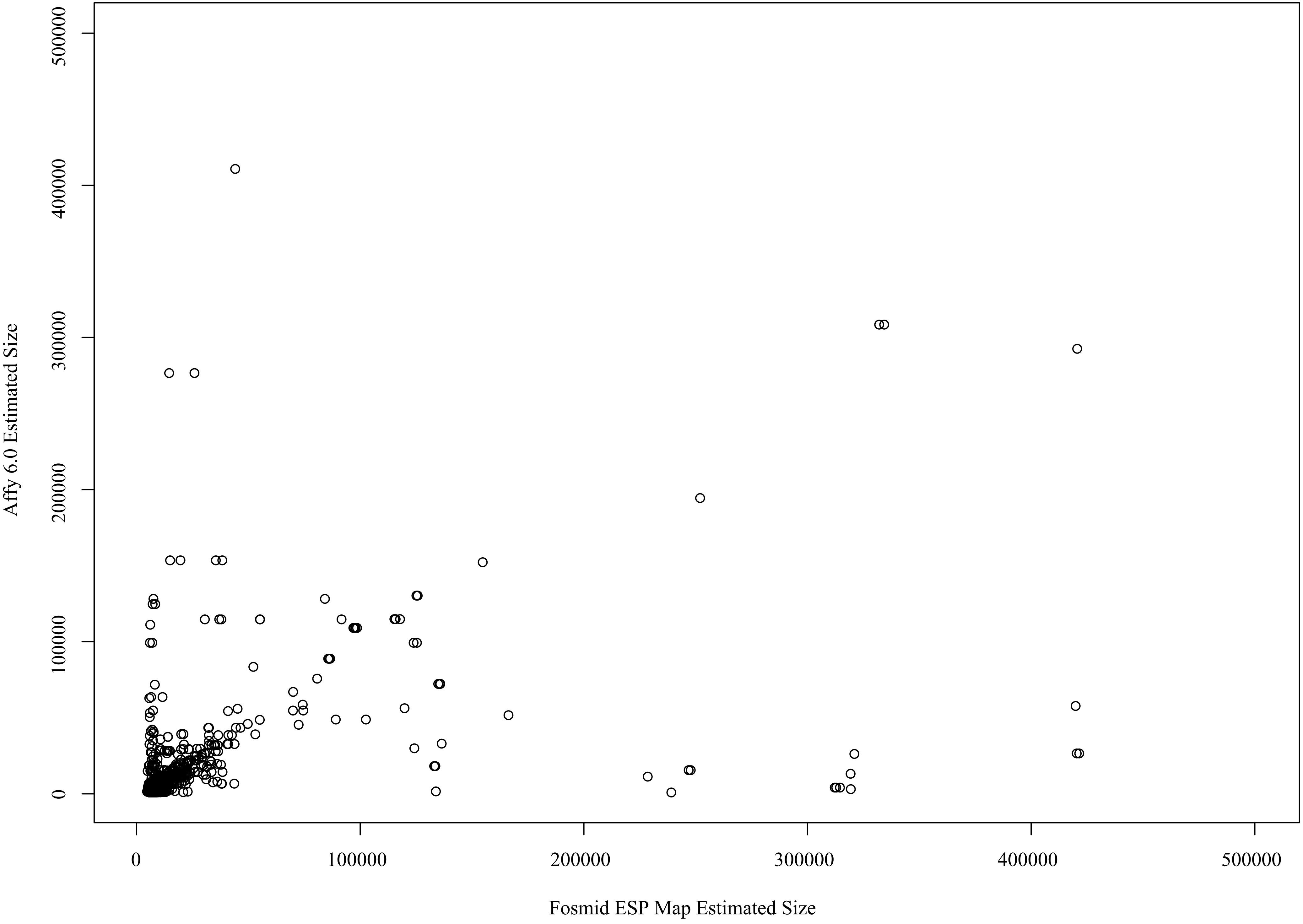
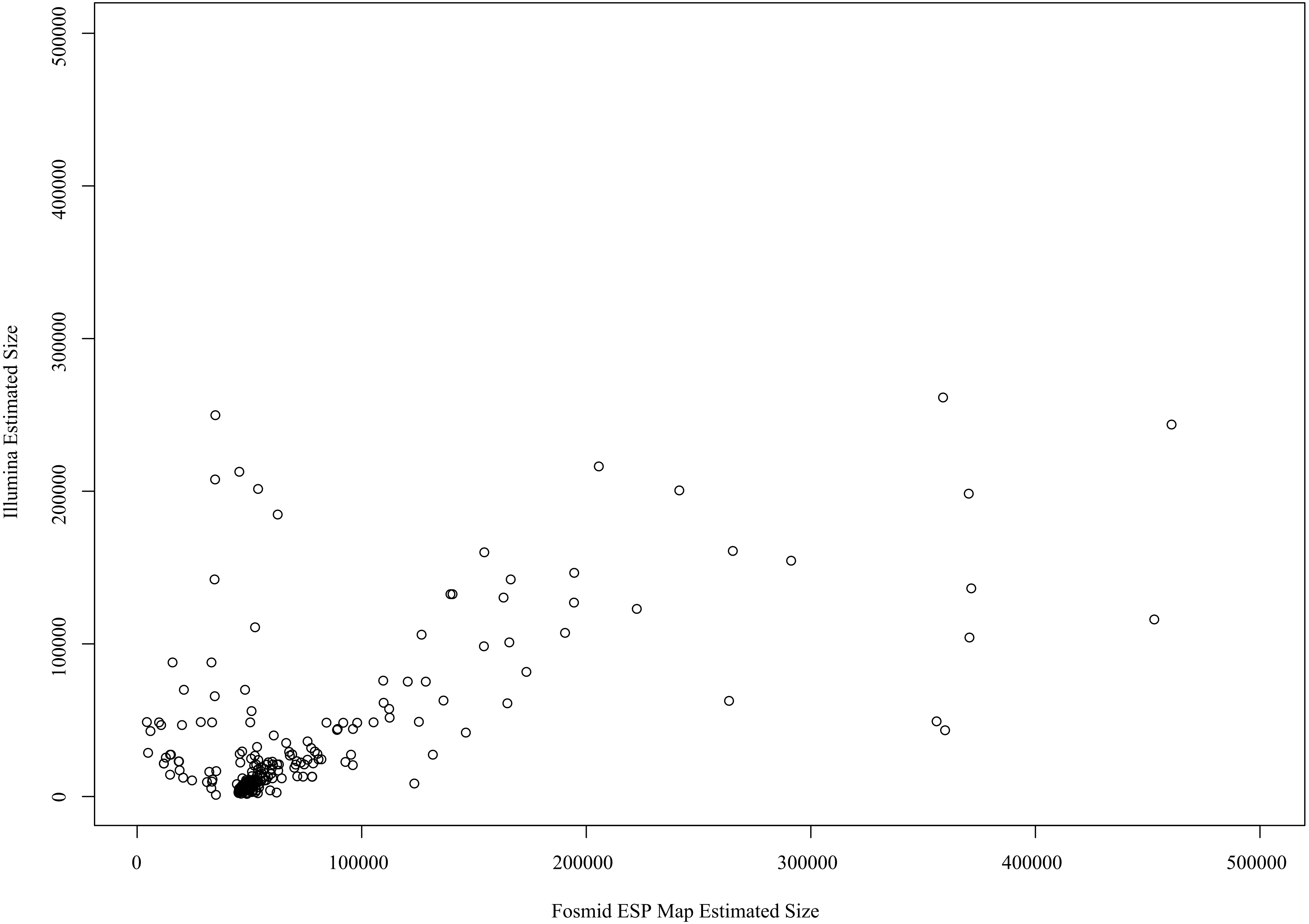

Affy 6.0 Estimated Size
0
100000
200000
300000
400000
500000
Fosmid ESP Map Estimated Size
0
100000
200000
300000
400000
500000

Figure S8 d)


Illumina Estimated Size
0
100000
200000
300000
400000
500000
0
100000
200000
300000
400000
500000
Fosmid ESP Map Estimated Size