

Supplementary Information

Effect of Target Length on Specificity and Sensitivity of Oligonucleotide Microarrays: A Comparison between Dendrimer and Modified PCR based Labelling Methods

Abdullah Gibriel^{*,1,2}

¹Biochemistry and Molecular Biology Department, Faculty of Pharmacy, Ahram Canadian University (ACU)

²Institute of Molecular, Cell and Systems Biology, College of Medical, Veterinary and Life Sciences, University of Glasgow, Glasgow, United Kingdom

Table S1. Percentage of identity between all unique reporter (UR) sequences.

	UR10	UR11	UR13	UR14	UR15	UR16	UR17	UR18
UR10	100%	65%	65%	65%	65%	57%	57%	48%
UR11	65%	100%	61%	65%	70%	65%	39%	52%
UR13	65%	61%	100%	61%	61%	57%	48%	35%
UR14	65%	65%	61%	100%	57%	57%	35%	48%
UR15	65%	70%	61%	57%	100%	74%	35%	39%
UR16	57%	65%	57%	57%	74%	100%	48%	57%
UR17	57%	39%	48%	35%	35%	48%	100%	52%
UR18	48%	52%	35%	48%	39%	57%	52%	100%

Fig. (S2). Multiple Homology alignment for all unique reporter (UR) sequences: Identical nucleotides are highlighted in grey while conserved ones are highlighted in red. Mismatched nucleotides are not highlighted.

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UR10  GG T CT G AG CG A A AT GT GT GG A G G
UR11  C G ACT A AG C C G AT T GT GT GG A C C
UR13  G G AT T G AG C G G A C G G T G T A A A C G
UR14  G G ACT T AG C G G ACT G T T T G A G G C
UR15  G G ACT G C T A C G ACT G T GT GG A C G
UR16  C A ACC T C T C G G ACT G T GT GG A C G
UR17  G A T A A T AG C G A C G G C A G T GG A C G
UR18  C G T C C T A T C G T C G T C T G T G C T C C

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Table S3. Degree of cross reactivity for each of the eight full length transcripts, labelled with the dendrimer technology, against all UR captures. Cross reactivity is represented by relative percentage of mean signal-background.

	UR10 probe	UR11 probe	UR13 probe	UR14 probe	UR15 probe	UR16 probe	UR17 probe	UR18 probe
UR10 capture	100%	1.5%	24.5%	23.5%	3.7%	17.3%	69%	333.3%
UR11 capture	10.4%	100%	42%	23.5%	2.8%	21.8%	28.8%	205%
UR13 capture	2.5%	0.3%	100%	6%	1.2%	7.8%	5.3%	18.5%
UR14 capture	4.8%	0.5%	8.4%	100%	6.3%	18.8%	12.5%	56%
UR15 capture	6%	0.8%	13.9%	12.6%	100%	16.5%	13.3%	85.3%
UR16 capture	6.7%	0.4%	9.2%	9.1%	1.8%	100%	9.8%	49%
UR17 capture	9.6%	0.9%	18.2%	18.5%	4.3%	40.1%	100%	92%
UR18 capture	41.8%	0.9%	4.7%	4.4%	1%	9.3%	22.5%	100%

Table S4. Degree of cross reactivity for each of the eight 330 bases transcripts, labelled with the dendrimer technology, against all UR captures. Cross reactivity is represented by relative percentage of mean signal-background.

	UR10 probe	UR11 probe	UR13 probe	UR14 probe	UR15 probe	UR16 probe	UR17 probe	UR18 probe
UR10 capture	100%	179.1%	950.7%	128.9%	128.9%	111.9%	40.2%	29.2%
UR11 capture	67.6%	100%	2844.8%	115.6%	100%	53.5%	40.2%	28.2%
UR13 capture	8.7%	3.7%	100%	15%	3.4%	4.8%	4.7%	22.2%
UR14 capture	69.3%	42.2%	1892.5%	100%	57.8%	109%	46.9%	120%
UR15 capture	171.3%	130.9%	2149%	118.5%	100%	98.1%	75.9%	140.8%
UR16 capture	37.9%	35.8%	3180.7%	141.7%	130%	100%	58.7%	113.7%
UR17 capture	32.2%	20.8%	1974.3%	52.9%	50%	77.9%	100%	89.7%
UR18 capture	50.4%	40.4%	1926.1%	138.5%	53.8%	129.4%	80.8%	100%

Table S5. Degree of cross reactivity for each of the eight 120 bases transcripts, generated by the modified PCR based labelling method, against all UR captures. Cross reactivity is represented by relative percentage of mean signal-background.

	UR10 probe	UR11 probe	UR13 probe	UR14 probe	UR15 probe	UR16 probe	UR17 probe	UR18 probe
UR10 capture	100%	7%	5.4%	3%	1%	7.3%	5.3%	3.3%
UR11 capture	5.6%	100%	6.6%	4.6%	3%	5.5%	4.2%	4.5%
UR13 capture	4.7%	8.7%	100%	6.9%	4%	5.1%	6.4%	7.9%
UR14 capture	9.6%	8%	6.2%	100%	3%	6.1%	6.8%	6.7%
UR15 capture	3.5%	5.6%	5%	3.4%	100%	8.4%	5.3%	5.2%
UR16 capture	3.5%	6.7%	5%	2.9%	3%	100%	4.6%	5%
UR17 capture	4.3%	6.3%	5.3%	3.6%	3%	7.5%	100%	4%
UR18 capture	3.2%	5.5%	5.8%	3.1%	3%	7.1%	9.4%	100%