Table -1 Remapping array elements designed against OLIV prediction set (see http://intramural.niddk.nih.gov/research/nimble/description.txt), or Release 4.2.1for *D. mel*.

spp	total probes	GLEANR # probes[1,2]	GLEANR % probes	GLEANR # genes[3]	GLEANR % genes	CAF1 # probes[1,2]	CAF1 % probes	GLEANR nonCAF1 # probes	GLEANR nonCAF1 % probes
D.mel	148,763	147,506	99	13,427	98	125,836	85	21,948	15
D.sim	186,701	113,557	61	11,945	70	119,960	64	13,565	7
D.yak	190,097	136,367	72	13,389	71	146,538	77	17,051	9
D.ana	173,102	124,732	72	14,209	63	128,306	74	15,508	9
D.pse	190,109	163,407	86	12,471	72	159,829	84	19,575	10
D.moj	190,904	146,838	77	12,181	69	154,079	81	14,856	8
D.vir	187,293	149,943	80	12,440	70	150,393	80	15,936	9

[1] Perfect Probe-(Annotation or Assembly) matches only. Duplicate mappings removed.
[2] Release 4.3 for *D.mel*
[3] >2 probes per gene