## Supplemental Figure 1



Supp\_Fig. 1 Summary performance statistics for spike-in predictions (including that from PCR array).

Due to the low resolution of the PCR array platform as compared to the oligonucleotide platforms, we considered a region to be predicted correctly (true positive) if the single predicted coordinate was less than 1kb away from the spike-in region, instead of within the spike-in region, as shown in Fig. 2. Please see legend of Fig. 2 for details.



## Supp\_Fig. 2 Enrichment-specific E-O distances (including those from PCR array).

The spike-in clones were divided up into 4 levels of enrichment: High fold-change (64-192); Medium fold-change (6-10); Low fold-change (3-4) and Ultra Low fold-change (1.25-2). The E-O distance metrics at various spike-in enrichment levels were shown. Please see legend of Fig. 4 for details.

**Supplemental Table S1.** Genome locations (UCSC hg17; NCBIv34) of plasmid clones used for the "amplified" spike-in mixture. Corresponding fold enrichments over the genomic DNA input are given. This mixture was delivered to participating labs at  $3ng/\mu L$ , which necessitated amplification prior to microarray hybridization.

**Supplemental Table S2.** Genome locations (UCSC hg17; NCBIv34) of plasmid clones used for the "unamplified" spike-in mixture. Corresponding fold enrichments over the genomic DNA input are given. This mixture was delivered to participating labs at  $77ng/\mu L$ , and did not require amplification prior to microarray hybridization.

**Supplemental Table S3.** Critical sequence characteristics for false positive (FP), false negative (FN), and true positive (TP) predictions for each amplified experiment. Included are percentage of nucleotides that are G or C (GC%), percentage of nucleotides that are RepeatMasked (% repeat), percentage of clones that have more than one significant BLAT match, and percentage of nucleotides in simple tandem repeats (% STR). In the true amplified spike-in mixture, 38% of the nucleotides are GC, 28% of the nucleotides are RepeatMasked, 1.7% of the nucleotides are contained within simple tandem repeats, and 11% of the clones have more than one significant BLAT match.

**Supplemental Table S4.** Critical sequence characteristics for false positive (FP), false negative (FN), and true positive (TP) predictions for each unamplified experiment. Included are percentage of nucleotides that are G or C (GC%), percentage of nucleotides that are RepeatMasked (% repeat), percentage of clones that have more than one significant BLAT match, and percentage of nucleotides in simple tandem repeats (% STR). In the true amplified spike-in mixture, 38% of the nucleotides are GC, 28% of the nucleotides are RepeatMasked, 1.1% of the nucleotides are contained within simple tandem repeats, and 11% of the clones have more than one significant BLAT match.

Table S1.

chromocomo	ctaut	and	longth	fold enrichment			
chr20	33784090	33784541	451	1.25			
dhr20	33510833	33511308	475	1.25			
chr22 chr19	30176345	30176802	457	1.25			
chr19	59629039	59629534	495	1.25			
chr16	288065	288584	519	1.25			
chr2	118482405	118482936	531	1.25			
dor15	41870909	41871378	- <u>110</u> - 469	1.25			
chr11	64334725	64335175	450	1.25			
dpc1.9	59295840	59296346	506	1.5			
chr16	199687	200155	468	1.5			
chr11	5227580	5228051	471	1.5			
chr7	89679055	89679569	514	1.5			
chr7	126346246	126346696	450	1.5			
cnrz chr13	118426127	112575997	453	1.5			
chr21	39558713	39559201	468	1.5			
chr5	142328582	142329118	536	1.5			
chr5 chr5	131337572	131338076	538				
dhr11	116246154	116246534	480	2			
dhr22	31177837	31178329	492	2			
chr22	30293251	30293759	508	2			
chrX	152690757	152691262	97.4 505	2			
chrX	153303406	153303946	540	2			
chrX	152750948	152751419	471	2			
chr19 chr15	59568260 41758568	41709760	<u>522</u>	2			
chrX	122592347	122592876	529	3			
chr2	220127093	220127557	464	3			
<u>dr20</u>	33658757	33659223	456	3			
ioni20 dhr20	33056850	33667321	4/1 547	3			
chr20	33343588	33344112	524	3			
chr20	33580786	33581296	510	3			
chr20	33592700	33593224	524	3			
chro chr13	41823030	112457435	404	3			
chr13	112487050	112487551	501	4			
chr21	39739470	39739957	487	4			
chr6	74218636	74219130	494	4			
chr1	147975664	147976181		4			
chr1	148184608	148185149	541	4			
chr1	148039771	148040293	522	4			
chrii chrii 5	41906083	41906596	495 513	4			
chr19	59989150	59989672	522	6			
chr16	142412	142937	525	6			
chr16	219369	219873	504	6			
chr11	5487721	5488219	498	6			
chr11	5232536	5233080	544	6			
chr7	126827194	126827572	478	6			
chr2	118288013	118288531	- 497 - 518	5			
chr2	234545097	234545621	524	5			
dhrX	153339074	153339524	450	8			
onrX chrV	153814670	153815188	518	8			
chr19	<u>592975</u> 41	<u>592980</u> 14	473	8			
chr19	59310790	59311240	450	8			
chr19 Ichr19	59396157	59396612	455	8			
dr19	59258967	59259457	490	8			
dr19	59651827	59652305	478	8			
dhr19	59846743	59847215	472	8			
onr7 chr7	116186845	116096574	524	10			
dhr7	115444111	115444629	518	10			
chr7	115732907	115733457	550	10			
chr5 chr5	131920131	131920607	476	10			
chr11	116148836	116149290	454	10			
chr22	31520998	31521450	452	10			
chr21	34209952	34210443	491	10			
diră chr15	41877380	41877856	- <u>549</u> - 476	1U 64			
dhr21	33907685	33908183	498	64			
chr2	234383112	234383598	486	64			
dhr7 chr22	115520593	115521048	455	64 64			
chrX	153242627	153243120	493	64			
chr19	59320507	59320999	492	64			
chr5	142228632	142229129	497	64			
chró	64085736 41766704	41767211	463	128			
chr11	116235281	116235785	504	128			
dhr11	5602340	5602843	503	128			
chr2	234372085	234372628	543	128			
dr15	41856966 64474979	64425494	- <u>228</u> - 495	128			
dhr2	234381928	234382425	497	128			
dhr22	30424201	30424719	518	196			
chr21	33885608	33886084	476	196			

Table S2.

chromosome	start	end	length	fold enrichment		
chr7	116096027	116096574	547	1.25		
chr7	116186845	116137369	524	1.25		
chr7	115732007	115733457	518	1.25		
chr5	131920131	131920607	476	1.25		
chr5	132036837	132037322	485	1.25		
chr11	116148836	116149290	454	1.25		
chr22	31520998	31521450	452	1.25		
<u>chr21</u>	153177342	153177891	5491	1.25		
chrX	153339074	153339524	450	1.5		
chrX	153814670	153815188	S18	1.5		
ehrX	152731002	152731552	550	1.5		
chr19	59297541	59298014	47.3	1.5		
chr19	59310790	59311240	450	1.5		
chr19	59516126	59516605	479	1.5		
chr19	59258967	59259457	490	1.5		
chr19	59651827	59652305	478	1.5		
chr19	59846743	59847215	47.2	1.5		
chr19	59989150	59989672	522	2		
chrib shatC	142412	142937	525			
chr16	219369	21967.5	204 //50	2		
chr11	5487721	5438219	498	2		
chr11	5232536	5233080	544	2		
chr7	126827194	126827672	478	2		
chr7	126819563	126820060	497	2		
chr2	118288013	118288531	518	2		
chr2	234545097	234545621	524	2		
chr13 chr13	112456969	11245/435	466	3		
chr21	39739470	39739957	487	3		
chró	74218636	74219130	494	3		
chr6	74227779	74228281	502	3		
chr.1	147975664	147976181	517	3		
chr1	148184608	148185149	541	<u> </u>		
chr1	148039771	148040293	522	<u></u>		
chr1	148158165	148158660	495	<u> </u>		
chr15	41906063	41900395		4		
chrX	122592347	122592876	529	4		
chr2	220127093	220127557	464	4		
chr20	33658757	33659223	466	4		
shr20	33666850	33667321	47.i	4		
chr20	33716226	33716773	547	4		
chr20 chr20	33343588	33344112	524	4		
chr20	33592700	33593224	524	4		
chr6	41823030	41823494	464	4		
chr5	131337572	131338076	504	6		
chr5	132189859	132190397	538	ő		
chr11	116246154	116246634	480	6		
<u>chr22</u> chr22	30293251	311783259	492 509	6		
chr21	33843373	33843845	47.2	6		
chrX	152690757	152691262	505	6		
chrX	153303406	153303946	540	6		
chrX	152750948	152751419	471	6		
chr19	59568260	59568782	522	6		
chr19 chr16		50006045		• •		
chr16	59295840	59296346	505	8		
	59295840 199687 81026	59296346 200155 81509	505 468 483	8		
chr11	59295840 199687 81026 5227580	59296346 200155 81509 5228051	506 468 483 471	8 8 8 8		
chr11 chr7	59295840 199687 81026 5227580 89679055	59296348 200155 81509 5228051 89679569	505 468 483 471 514	8 8 8 8 8		
chr11 chr7 chr7	59295840 199687 81026 5227580 89679055 126346246	59296348 200155 81509 5228051 89679569 126346696	505 468 483 471 514 450	8 8 8 8 8 8 8		
chr11 chr7 shr7 chr2	59295840 199687 81026 5227580 89679055 126346246 118426127	59296348 200155 81509 5228051 89679569 126346696 118426528	505 468 483 471 514 450 501	8 8 8 8 8 8 8 8 8 8		
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chr11 chr7 chr7 chr2 chr2 chr20	59295441 199687 81026 5227580 82672055 12653462464 115426127 115425127 11542558713 32558713 32558713 325585810 3351033 2017 6245 59358840 59629039 288055 118482405 566272684 41870592 564234725 564234725 56425255	59296246 200155 81509 5226051 59679569 13626628 113426628 113426528 113426528 113426528 1134229113 23724541 23724541 23724541 23724541 23724541 23724541 23724541 23724541 23725524 23755524 23755524 23755524 23755524 23755524 23755524 23755524 23755524 23755524 23755524 237555524 237555524 237555524 237555524 237555524 237555524 2375555524 2375555554 2375555554 2375555554 23755555554 237555555554 237555555555555555555555555555555555555	208 468 432 471 450 501 453 453 453 453 455 451 475 451 475 519 519 519 519 519 519 519 519 519 51	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		
chr11 chr7 chr7 chr7 chr2 chr3 chr20	52/95/44 199627 81025 52/27580 89679055 12575544 3255871 12575544 3255871 12575544 3255871 12575544 32754020 33510833 23754020 33510833 23754020 235582400 2355824000 235582400000000000000000000000000000000000	59296246 200155 81509 52280511 59679550 126346696 113426692 11342652 11342652 11342652 11342652 11342652 11342652 11342652 20176802 201776802 2017777777777777777777777777777777777	208 483 471 453 471 453 451 453 485 556 455 455 455 455 455 519 519 531 556 455 519 531 556 455 519 531 556 455 556 455 556 455 556 455 556 557 557 557 557 557 557 557 557 5	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		
chr11           chr2           chr2           chr3           chr4           chr3           chr4           chr3           chr4           chr3           chr4           chr3           chr4           chr3           chr4	59295441 199827 81025 5227580 89679055 118425127 112575544 118425127 112575544 118425127 1142228552 1142228552 1142228552 1142228552 1142228552 11525544 11525284 116228520 288055 11526724 116272664 11677676 11777676 1177767676 117776767676767676767676767676767676767	59296345 200155 3220615 3220615 3220615 3220615 132426636 113426636 113426636 113426636 13255201 33555201 33555201 3355520 3355520 335552 335552 335552 3355254 3455254 3455254 3455254 3455254 3455254 3455254 3455254 3455254 3455254 3455254 3455254 34552554 3455254 345555554 345555554 3455555554 3455555554 3455555555	2002 463 471 514 453 471 514 453 453 453 453 454 455 544 455 519 533 559 459 5519 5519 5519 5519 5519 5519 5	8         8           8         8           8         8           8         8           8         8           9         9           10         10           10         10           10         10           10         10           10         10           10         64           64         64           64         64		
chr11           chr7           chr7           chr7           chr7           chr7           chr7           chr13           chr13           chr20           chr11           chr20           chr21           chr20           chr11           chr20	52/95/44/ 199827 81026 52/27880 89879055 126346246 118426127 1275544 39559713 2017 6245 33510833 2017 6245 33510833 2017 6245 33524080 20382840 50622039 228305 5642082736 41262704 41267092 6403736 54082538 41265704 41265704 41267092 6403736 41265728 4126728 4126778 412678	59296346 200155 31509 5220615 12024 120344660 118424633 11275307 11275307 11275307 11275307 11275307 11275307 11263521 1305524 2855554 2855554 2855554 2855554 2855554 2855554 285555555555	505 468 483 471 514 453 501 501 453 456 535 455 455 455 455 455 455 455 455 455	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 10 10 10 10 10 10 10 10 10 10 10 4 64 64 64		
chr11 chr7 chr7 chr7 chr2 chr20 chr21 chr20	59295441 199827 81025 5227580 89679055 125346545 118425127 112275544 92559713 1422225852 337544020 33510633 30176345 59629039 228305 59629039 228305 228305 564234725 54434725 544354725 544557264 41765704 41765704 116525281 5562240 234372085	59296345 200155 3220615 5220615 5220615 18527550 18527650 18527650 18527650 18527650 1842955 1842955 1842956 1842956 1842956 1842956 2017680 2017680 2017680 2017680 2017680 2017680 201760 200	502           463           471           483           471           514           450           514           450           451           452           453           453           453           453           454           455           512           513           514           450           452           513           514           450           450           507           502           503	8         8           8         8           8         8           8         8           9         8           9         8           9         10           10         10           10         10           10         10           10         4           64         64           64         64           64         64           64         64		
chr11           shr7           shr7           shr7           shr8           shr11           shr12           shr11	52/95/40 199827 81026 52/27880 89827955 16346246 118426127 112275544 39255711 142228582 37264020 33510333 30176245 59358930 59358930 59358930 59358930 59258930	59296345 200155 31596 5522651 55675550 183246696 118426628 11842673 25555201 25555201 25555201 25555201 2555520 25075202 5555524 285554 20178502 20	2002 4683 471 51,4 453 471 53,4 453 453 455 455 455 544 475 544 475 544 475 544 475 544 475 544 469 450 533 551 551 551 552 563 564 553 5543 5543	0         0           8         8           8         8           8         8           8         8           9         10           10         10           10         10           10         10           10         64           64         64           64         64           64         64           64         64           64         64           64         64		
chr11           chr2           chr2           chr2           chr2           chr2           chr2           chr20           chr21           chr21           chr21           chr21           chr21           chr21           chr11           chr11           chr21           chr12           chr13           chr14           chr15           chr11           chr15           chr14           chr15           chr11	52/95441 199687 81025 52/27880 89679055 126346246 118825127 1275544 32558713 14253258713 14253258713 23784090 33510833 20176345 539529039 228265 539529039 228265 5495272634 418770929 64035735 6403242420 740224201 75022420 7502420 7502420 7502420 7502420 7502420 7502420 7502420 7502420 7502420 7502420 7502420 7502420 7502420 7502420 7502420 75045 7505	59296346 200155 21596 12529615 126424636 116424636 116424636 116424636 116424636 116424636 1164242413 2555201 42329118 3251234 285582 13642521 235552 201763 2017632 2017632 2	502           468           482           481           481           514           501           453           482           483           501           453           453           453           453           451           452           544           455           518           459           450           452           453           507           504           502           513           502           503           503           504           505           507           504           503           503           503           504           505           518           459           528           528           518	8         8           8         8           8         8           8         8           8         8           9         10           10         10           10         10           10         10           10         10           10         64           64         64           64         64           64         64           64         64           64         64           64         64		
chr11           shr7           shr7           shr7           shr7           shr7           shr7           shr8           shr16           shr16           shr11           shr11           shr11           shr11           shr12           shr11           shr12           shr11           shr11           shr11           shr11           shr11           shr11           shr11           shr11           shr11	59(9544) 199827 81025 5227580 89679055 125346246 1182251571 1423258571 1423258571 1423258571 1423258571 1423258571 1423258571 1423258571 1423258571 1423258571 1423258571 14232584 156222684 41765704 156222684 41765704 156222684 41765704 1550266 64324725 5642535 564224975 33385506 64424975 33385506 564224975 33385508 56508 56508 56508 56508 56508 56508 56608 56	59296345 200155 3220615 3220615 3220615 3220615 322061 18426636 118426636 33555201 33555201 33555201 33555201 3355520 33552520 335252 335252 335252 335252 335252 335252 335252 335252 335252 335252 335252 335252 335252 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 3355552 33555552 33555552 33555552 3355555555	2002 463 471 514 453 471 514 453 453 453 453 454 455 544 455 519 533 544 459 519 533 559 507 507 507 504 459 459 459 459 459 459 459 459 507 507 504 495 514 495 514 405 519 519 519 519 519 519 519 519 519 51	8         8           8         8           8         8           8         8           9         9           10         10           10         10           10         10           10         64           64         64           64         64           64         64           64         64           64         64           64         64           64         64           64         64		
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chr11           chr7           chr3           chr13           chr13           chr13           chr13           chr13           chr13           chr13           chr13           chr30           chr30           chr19           chr19           chr16           chr19           chr16           chr17           chr18           chr14           chr2           chr15           chr11           chr14           chr2           chr11           chr11           chr2           chr11           chr2           chr11           chr2           chr11           chr2           chr2           chr15           chr2           chr2	5929544 199687 81025 5227580 89679055 112575544 112575544 12527554 12527554 12527554 12527554 12527554 12527554 12527554 12527554 12527554 12527554 12527554 12527554 1252755 41256705 412577575 412577575 412577575 412577575 41257757575 412577575 4125775757575 41257757575757575757	59296345 200155 21596 220251 2526051 2526051 2526051 2527650 2527650 2527650 2527650 2527625 2555200 255520 2555000 2555000 2555000 2555000 255500000000	50:           463           47:           47:           51:4           450:           50:           50:           50:           50:           50:           50:           483           47:           451           47:           452           51:           51:           51:           51:           51:           450           450           507           502           503           502           503           502           503           503           503           503           503           503           503           503           503           503           504           505           507           502           503           504           505           518           476           476           476 </td <td><math display="block">\begin{array}{c} 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ </math></td>	$\begin{array}{c} 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ $		
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Table	S3.

ID	Lab	Algorithm	#Reps	FP fraction redund by blat:	instances FP	FN%GC	FP%GC	TP%GC	FN%repeat	FP%repeat	TP%repeat	FN%STR	FP%STR	TP%STR
а	1	MAT	3	0.20000	15	0.38660	0.22222	0.47637	0.27590	0.37900	0.06048	0.00400	0.29196	0.18500
b	1	Splitter	з	0.14285	14	0.52933	0.47854	0.42695	0.01692	0.12918	0.10133	0.09837	0.13687	0.02470
c	7	MAT	3	0.06411	107	0.52700	0.40895	0.42974	0.01682	0.07659	0.10133	0.11895	0.05735	0.00000
d	7	TIMAT	3	0.10843	83	0.37010	0.17857	0.39617	0.28799	0.38784	0.06124	0.00550	0.28292	0.07235
e	8	ADM-1	z	0.00000	7	0.38859	0.00000	0.27581	0.29213	0.37347	0.34204	0.00624	0.27276	0.00000
ſ	9	WA	z	0.03351	1.79	0.34831	0.31643	0.39152	0.31827	0.11164	0.27211	0.02507	0.00738	0.01370
g	8	MA2C	2	0.06928	112	0.54394	0.25278	0.44785	0.00000	ü.47755	0.08680	0.14914	0.02025	0.01673
h	3	TAMALQ	3	0.15306	98	0.60950	0.46560	0.45463	0.10654	0.11094	0.04383	0.00000	0.07450	0.07930
I	3	MA2C	3	0.09322	118	0.61817	0.32361	0.45271	0.00000	0.36596	0.06751	0.23653	0.03037	0.02674
)	3	TileScope	3	0.05976	86	0.61817	0.39418	0.45271	0.00000	0.26274	0.06751	0.23653	0.01038	0.02674
k	3	Spiitter	3	0.11702	94	NA	0.48329	0.48279	NA	0.10241	0.05523	NA	0.01668	0.06488
1	3	Permuta	3	0.75000	s	0.41217	0.22222	0.43671	0.23805	0.32427	0.06274	0.02172	0.37576	0.11097
m	3	TAMALS	3	0.08571	35	0.60950	0.50574	0.45463	0.10654	0.08561	0.04383	0.00000	0.00332	0.07930
n	3	ACME	3	0.10891	101	NA	0.46295	0.48279	NA	0.12694	0.05523	NA	0.06073	0.06488
0	5	Splitter	3	0.24347	1.15	0.52415	0.48964	0.45916	0.02523	0.08091	0.07238	0.12622	0.21575	0.02983
р	5	Mpeak	3	0.35164	91	0.40852	0.14130	0.44350	0.24949	0.36468	0.03588	0.01140	0.30851	0.11996
q	5	TileScope	3	0.33333	105	0.53215	0.38684	0.42355	0.05233	0.22749	0.05871	0.09837	0.17143	0.02470

Table S4.

ю	Lab	Algorithm	#Reps	FP fraction redund by blat:	instances FP	FN%GC	FP%GC	TP%GC	FN %repeat	FP%repeat	TP%repeat	FN%STR	FP%STR	TP%STR
A	7	MAT	6	0.03529	85	0.44598	0.31250	0.35123	0.22828	0.07680	0.30976	0.00943	0.01513	0.02241
В	7	MAT	з	0.11220	98	0.42450	0.31956	0.35630	0.26455	0.05636	0.29490	0.00724	0.00925	0.02275
C	7	MAT	3	0.01754	57	0.42833	0.31790	0.35290	0.25284	0.07463	0.30260	0.01279	0.00631	0.01960
D	7	TIMAT	3	0.16220	37	0.42864	0.35179	0.35236	0.25458	0.08366	0.30250	0.01246	0.01113	0.01960
ε	7	TAS	6	0.10710	28	0.42327	0.27372	0.35909	0.26357	0.22868	0.29453	0.00959	0.01218	0.02292
F	4;8	WA	5	0.10869	46	0.39806	0.34689	0.36858	0.27515	0.03574	0.29040	0.00731	0.00237	0.02685
G	4	Splitter	3	0.04294	163	0.44024	0.30649	0.32447	0.23763	0.11469	0.33139	0.00966	0.01784	0.02570
н	4	WA	3	0.07777	180	0.41297	0.36247	0.33815	0.25877	0.03243	0.31810	0.01617	0.00811	0.02113
Ι	4	MA2C	3	0.14285	49	0.43246	0.18667	0.31407	0.24421	0.57174	0.33602	0.01760	0.00806	0.01913
J	6	Splitter	2	0.34615	26	0.44920	0.53464	0.36134	0.19011	0.08135	0.31164	0.01009	0.16436	0.02070
К	8	WA	z	0.05714	105	0.44079	0.38888	0.36765	0.21566	0.06669	0.29965	0.00817	0.00750	0.02062
L	8	MA2C	2	0.27777	14-4	0.50476	0.226.45	0.35971	0.16015	0.52448	0.30765	0.01392	0.10146	0.01947
м	8	ADM-1	z	0.07690	13	0.43904	0.29442	0.36030	0.21680	0.22672	0.38400	0.02962	0.07765	0.01235
N	З	TAMALg	4	0.36842	19	0.36098	0.46070	0.38576	0.33231	0.15895	0.27373	0.01091	0.21455	0.01976
0	з	Permuta	4	0.54550	13	0.37759	0.52011	0.38273	0.32472	0.05970	0.27143	0.00905	0.33330	0.01938
P	3	Splitter	4	0.54550	13	0.38802	0.50621	0.37544	0.27742	0.06592	0.29328	0.01324	0.05286	0.01822
Q	Ę	TAM AL S	4	0.25000	4	0.34054	0 53532	0.41249	0.36658	0.05920	0.22116	0.02002	<u>6 40000</u>	0.01693
R	3	MA2C	4	0.18421	190	0.41315	0.25584	0.37634	0.17114	0.48885	0.29565	0.05913	0.16117	0.01945
s	3	TileScope	4	0.14285	14	0.36636	0.487.06	0.38430	0.27603	0.11692	0.28194	0.01294	0.00000	0.01877
Ŧ	3	ACME	4	0.37037	27	0.33107	0.52043	0.38779	0.35059	0.07907	0.27542	0.00698	0.22805	0.01965
U	5	Splitter	з	0.14286	14	0.45437	0.37031	0.33041	0.23149	0.07396	0.32496	0.00973	0.18325	0.02317
V	s	Mpeak	3	0.25000	148	0.41447	0.41150	0.36374	0.28702	0.05072	0.28812	0.01764	0.09046	0.01675
W	S	TileScope	3	0.10535	47	0.42332	0.27653	0.33630	0.27031	0.28695	0.29819	0.01713	0.05903	0.01948
X	6	Splitter	з	0.09524	21	0.42218	0.49435	0.36722	0.27110	0.06943	0.29453	0.01195	0.11284	0.01912
Y	6	Wavelet	3	0.00000	4	0.44802	0.42040	0.34067	0.22566	0.21194	0.32113	0.01208	0.08259	0.02169
Z	6	TileScope	з	0.08330	12	0.44686	0.43458	0.36439	0.24157	0.11770	0.29049	0.00948	0.00000	0.01908