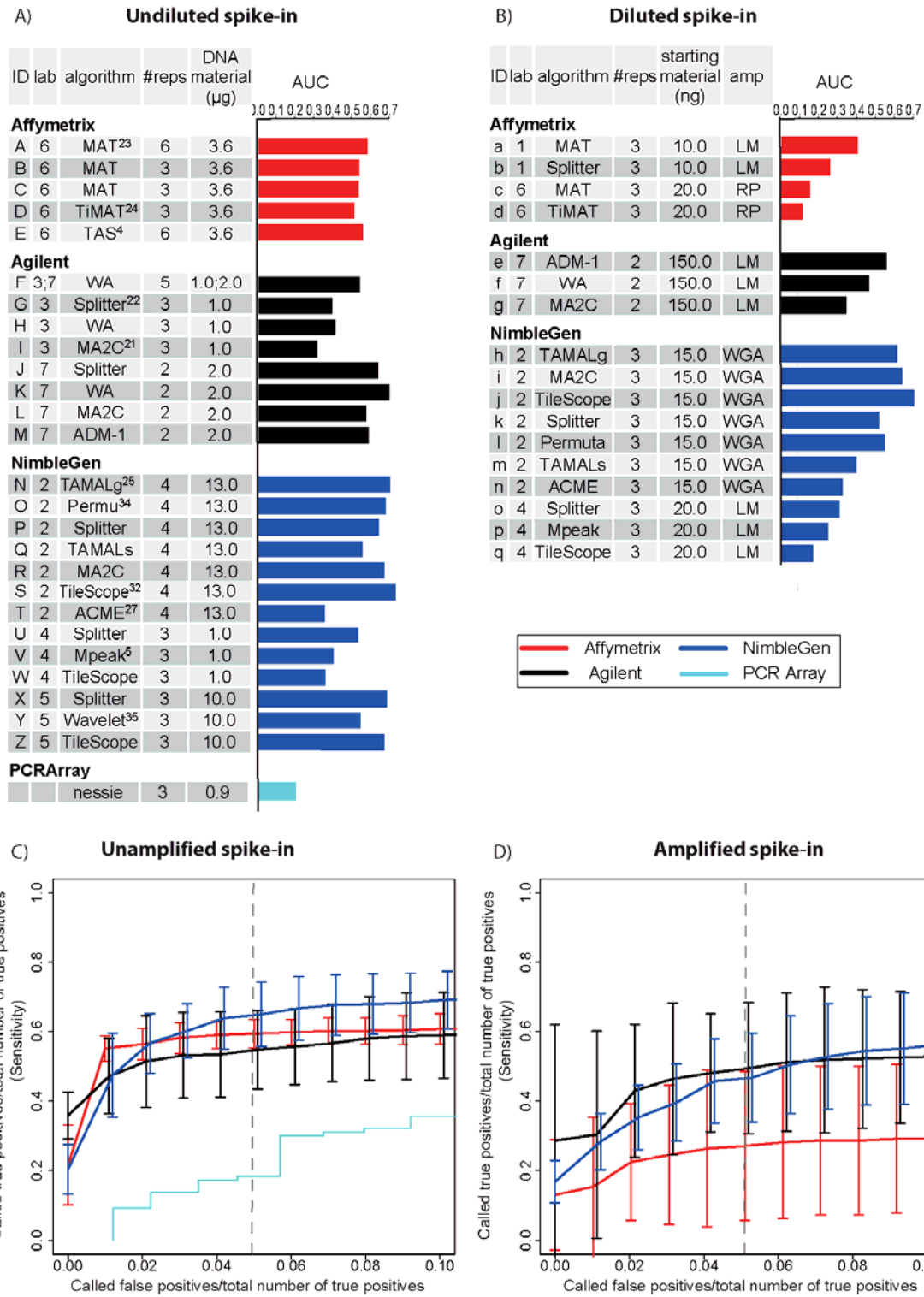


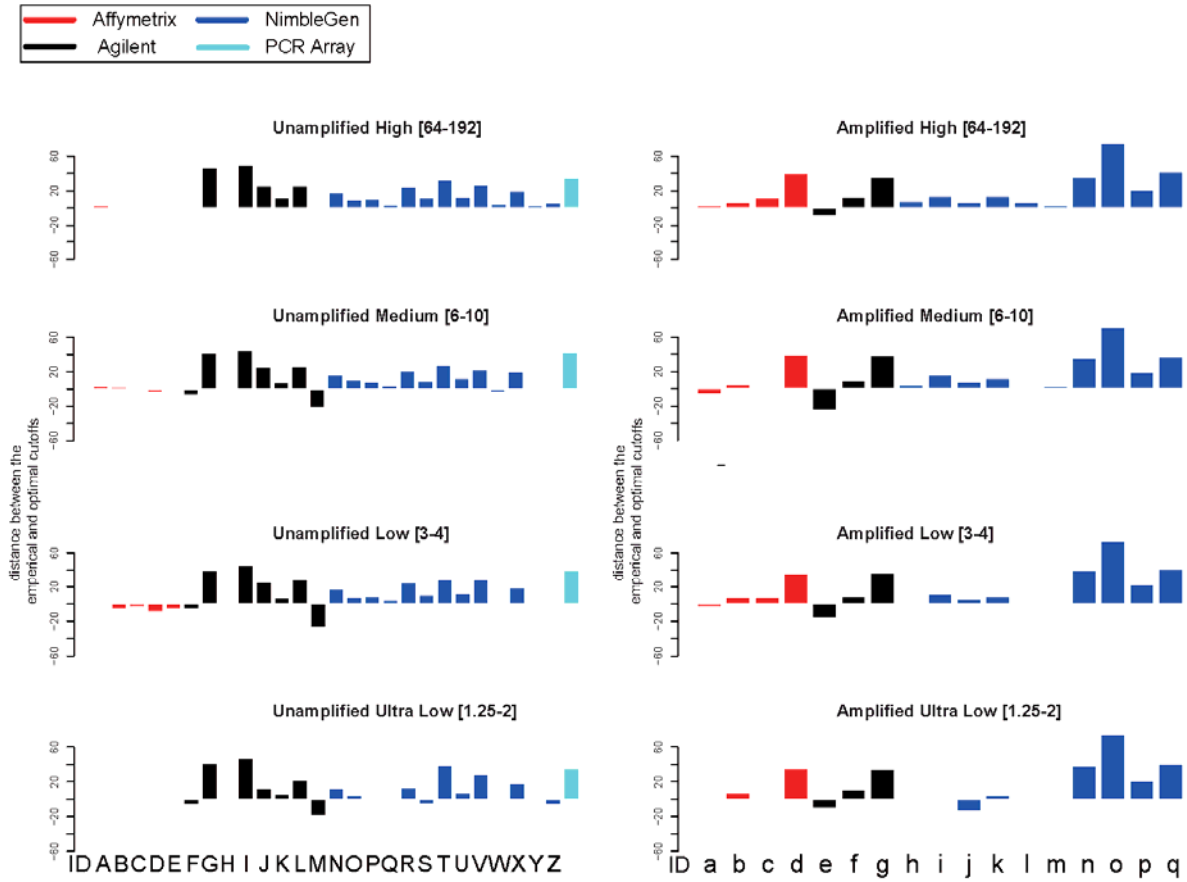
Supplemental Figure 1



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.

Supplemental Figure 2



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/ μ 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/ μ 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.

chromosome	start	end	length	fold enrichment
chr20	33764090	33784541	451	1.25
chr20	33510833	33511308	475	1.25
chr22	30176335	30176802	467	1.25
chr19	59358980	59359528	548	1.25
chr19	59629039	59629534	495	1.25
chr16	269384	269384	1	1.25
chr2	118482405	118482935	531	1.25
chr5	56272684	56273202	518	1.25
chr15	41870909	41871378	469	1.25
chr11	64334735	64335175	450	1.25
chr19	59295840	59296345	506	1.5
chr15	199587	200155	468	1.5
chr16	81026	81509	483	1.5
chr11	5227580	5228051	471	1.5
chr7	89679055	89679569	514	1.5
chr7	126346235	126346698	463	1.5
chr2	118426127	118426528	401	1.5
chr13	112378544	112378997	453	1.5
chr21	39598713	39599201	488	1.5
chr5	142323583	142329113	528	1.5
chr5	131337573	131338076	504	2
chr5	132189859	132190397	538	2
chr11	116246154	116246634	480	2
chr22	31177837	31178329	492	2
chr22	30293251	30293759	508	2
chr21	33843373	33843845	472	2
chrX	152690757	152691262	505	2
chrX	153303406	153303948	540	2
chrX	152750948	152751419	471	2
chr19	59568260	59568782	522	2
chr15	41728338	41728763	425	2
chrX	122592347	122592876	529	2
chr5	220127083	220127557	474	3
chr20	33656752	33656823	456	3
chr20	33656850	33656921	471	3
chr20	33716226	33716773	547	3
chr20	33943588	33944112	524	3
chr20	33580786	33581296	510	3
chr20	33992700	33993224	524	3
chr6	41823030	41823494	464	3
chr13	112456969	112457435	466	4
chr13	112487050	112487551	501	4
chr21	39739470	39739957	487	4
chr6	74218638	74219130	494	4
chr6	74227772	74228281	509	4
chr1	147975684	147976181	517	4
chr1	148184608	148185149	541	4
chr1	148039771	148040293	522	4
chr1	148158165	148158660	495	4
chr15	41906083	41906596	513	4
chr19	59989150	59989672	522	6
chr16	142412	142937	525	6
chr16	219369	219873	504	6
chr16	43578	44030	452	6
chr11	5487721	5488219	498	6
chr11	5237338	5237980	642	6
chr7	126827194	126827874	478	6
chr7	126812582	126820250	497	6
chr2	118383013	118383531	518	6
chr2	234545097	234545621	524	6
chrX	153339074	153339524	450	8
chrX	153814670	153815188	518	8
chrX	152731002	152731552	550	8
chr19	59297541	59298014	473	8
chr19	59310790	59311240	450	8
chr19	59396157	59396612	455	8
chr19	59516126	59516605	479	8
chr19	59258267	59258757	490	8
chr19	59651827	59652305	478	8
chr19	59849743	59849715	477	8
chr7	116096977	116097574	597	10
chr7	116155645	116157369	524	10
chr7	115444111	115444629	518	10
chr7	115732907	115733457	550	10
chr5	131920131	131920607	476	10
chr5	132038887	132039322	485	10
chr11	116148836	116149290	454	10
chr22	31520998	31521450	452	10
chr21	34209952	34210443	491	10
chrX	153177342	153177891	549	10
chr15	41877380	41877850	475	64
chr21	33307633	33308183	498	64
chr2	234381112	234383596	458	64
chr7	115520503	115521042	455	64
chr22	31107050	31107555	505	64
chrX	153242627	153243120	493	64
chr19	59320507	59320999	492	64
chr5	142228632	142229129	497	64
chr11	64089726	64089199	463	128
chr6	41766704	41767211	507	128
chr11	116235281	116235785	504	128
chr11	5602340	5602843	503	128
chr2	234372085	234377638	543	128
chr15	41856966	41857494	528	128
chr11	64424979	64425472	495	128
chr2	234381238	234386475	497	128
chr22	30424201	30424719	518	196
chr21	33865608	33866084	476	196

Table S2.

chromosome	start	end	length	fold enrichment
chr7	116096027	116096574	547	1.25
chr7	116186845	116187360	524	1.25
chr7	118444111	118444623	518	1.25
chr7	115732007	115732457	550	1.25
chr5	131920131	131920607	476	1.25
chr5	152936837	152937322	485	1.25
chr11	116148836	116149296	460	1.25
chr22	31520958	31521450	452	1.25
chr21	34209952	34210443	491	1.25
chrX	153177342	153177891	549	1.25
chrX	153339074	153339524	450	1.5
chrX	153814670	153815188	518	1.5
chrX	152731007	152731552	550	1.5
chr19	59297441	59298014	473	1.5
chr19	59310790	59311240	450	1.5
chr19	59396157	59396612	455	1.5
chr19	59516128	59516605	479	1.5
chr19	59536967	59537451	484	1.5
chr19	59551192	59551605	478	1.5
chr19	59846743	59847215	472	1.5
chr19	59989150	59989672	522	2
chr16	142412	142937	525	2
chr16	219369	219873	504	2
chr16	43678	44090	452	2
chr11	5487721	5488219	498	2
chr11	5232536	5233080	544	2
chr7	126927131	126927672	478	2
chr7	126619563	126620063	497	2
chr2	118288013	118288531	518	2
chr2	234545027	234545521	524	2
chr13	112456969	112457435	466	3
chr13	112487050	112487551	501	3
chr21	39739470	39739957	487	3
chr6	74218636	74219130	494	3
chr6	74227779	74228281	502	3
chr1	147975664	147976181	517	3
chr1	148184608	148185149	541	3
chr1	148339771	148340293	522	3
chr1	148158168	148158660	495	3
chr15	41936393	41936894	513	3
chr15	41728398	41728763	465	4
chrX	122592347	122592872	529	4
chr2	220127093	220127557	464	4
chr20	33658757	33659223	466	4
chr20	33666850	33667321	471	4
chr20	33716226	33716773	547	4
chr20	33343588	33344112	524	4
chr20	33580788	33581298	510	4
chr20	33592700	33593224	524	4
chr6	41822330	41822894	464	4
chr5	131337572	131338078	504	5
chr5	132189859	132190397	538	5
chr11	116246154	116246634	480	6
chr22	31177837	31178329	492	5
chr22	30293251	30293759	508	5
chr21	33843373	33843845	472	5
chrX	152690757	152691262	505	5
chrX	153303406	153303946	540	5
chrX	152750648	152751119	471	5
chr19	59268560	59269062	502	5
chr19	59285348	59285846	526	5
chr16	195827	200155	458	5
chr16	81026	81509	483	5
chr11	5227580	5228051	471	5
chr7	89679053	89679560	514	5
chr7	126346248	126346696	450	5
chr2	118426127	118426628	501	5
chr13	112575544	112575997	453	5
chr21	39559713	39559201	488	5
chr5	142238582	142239118	536	5
chr20	33744290	33744541	451	10
chr20	33510833	33511308	475	10
chr22	30176345	30176802	457	10
chr19	59358980	59359524	544	10
chr19	59629039	59629534	495	10
chr16	288063	288584	519	10
chr2	118482498	118482938	531	10
chr5	56272694	56273202	518	10
chr15	41870904	41871378	469	10
chr11	64334723	64335175	450	10
chr11	64365756	64366199	483	64
chr6	41766708	41767241	527	64
chr11	116235281	116235785	504	64
chr11	5602540	5602843	503	64
chr2	234372085	234372628	543	64
chr15	41856366	41857494	528	64
chr11	64424979	64425474	495	64
chr22	30424201	30424719	518	64
chr21	33885808	33886084	476	64
chr2	234381928	234382425	497	64
chr15	41877380	41877856	476	128
chr21	39907825	39908182	498	128
chr2	234583112	234583598	486	128
chr7	115520591	115521048	458	128
chr22	31107450	31107553	505	128
chrX	153242627	153243120	493	128
chr19	59320507	59320999	492	128
chr19	59911022	59911510	488	128
chr19	29631724	29632180	456	128
chr5	142228632	142229129	497	128

Table S3.

ID	Lab	Algorithm	#Reps	FP fraction reduced by blat:	instances FP	FN%GC	FP%GC	TP%GC	FN%repeat	FP%repeat	TP%repeat	FN%STR	FP%STR	TP%STR
a	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	3	0.14285	14	0.52923	0.47854	0.42695	0.01682	0.12918	0.10133	0.09837	0.13687	0.02470
c	7	MAT	3	0.08411	107	0.52700	0.40895	0.42974	0.01682	0.07059	0.10133	0.11095	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-L	2	0.00000	7	0.38859	0.00000	0.27581	0.29213	0.37347	0.34204	0.00624	0.27275	0.00000
f	8	WA	2	0.03951	179	0.34821	0.31643	0.39152	0.31827	0.11164	0.27211	0.02507	0.00738	0.01370
g	8	MA2C	2	0.09920	112	0.54394	0.25278	0.44795	0.00000	0.47755	0.08680	0.14914	0.02025	0.01673
h	3	TAMALg	3	0.15306	98	0.60950	0.46560	0.45463	0.10654	0.11094	0.04383	0.00000	0.07480	0.07930
i	3	MA2C	3	0.09322	118	0.61917	0.32361	0.45271	0.00000	0.36596	0.06751	0.23653	0.03037	0.02674
j	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	Splitter	3	0.11702	94	NA	0.48329	0.48279	NA	0.10241	0.05523	NA	0.01668	0.06488
l	3	Permuta	3	0.75000	5	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
o	5	Splitter	3	0.24347	115	0.52415	0.40964	0.45916	0.02523	0.00091	0.07230	0.12622	0.21575	0.02903
p	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	0.23749	0.05871	0.09837	0.17143	0.02470

Table S4.

ID	Lab	Algorithm	#Reps	FP fraction reduced 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	55	0.44598	0.31250	0.35123	0.22825	0.07680	0.30976	0.00943	0.01513	0.02241
B	7	MAT	3	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	0.01273	0.00631	0.01360
D	7	TIMAT	3	0.16220	37	0.42864	0.35179	0.35238	0.25458	0.08386	0.30250	0.01245	0.01113	0.01960
E	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	0.34659	0.36855	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	0.00965	0.01784	0.02570
H	4	WA	3	0.07777	160	0.41297	0.36247	0.33815	0.25877	0.03243	0.31810	0.01617	0.00811	0.02113
I	4	MA2C	3	0.14285	49	0.43346	0.18567	0.31407	0.24421	0.57174	0.33602	0.01760	0.00806	0.01913
J	8	Splitter	2	0.34615	26	0.44920	0.33464	0.36134	0.19011	0.08135	0.31164	0.01009	0.16436	0.02070
K	8	WA	2	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	144	0.50476	0.22645	0.35971	0.16015	0.52448	0.30765	0.01392	0.10146	0.01947
M	8	ADM-L	2	0.07690	13	0.42904	0.29442	0.36030	0.21680	0.22672	0.30400	0.02962	0.07765	0.01235
N	3	TAMALg	4	0.36842	19	0.35098	0.46070	0.38576	0.33231	0.15895	0.27373	0.01091	0.21485	0.01976
O	3	Permuta	4	0.54550	13	0.37759	0.52011	0.38273	0.32472	0.05970	0.27143	0.00908	0.33330	0.01938
P	3	Splitter	4	0.54550	13	0.38802	0.50621	0.37544	0.27742	0.06532	0.29328	0.01324	0.05256	0.01822
Q	3	TAMALs	4	0.25000	4	0.34054	0.53532	0.41749	0.36658	0.05920	0.22116	0.02002	0.40000	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	0.48706	0.38430	0.27603	0.11692	0.28194	0.01254	0.00000	0.01877
T	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	3	0.14285	14	0.45437	0.37031	0.33041	0.23149	0.07396	0.32496	0.00973	0.18325	0.02317
V	5	Mpeak	3	0.25000	148	0.41447	0.41150	0.36574	0.28702	0.05072	0.28812	0.01764	0.09046	0.01675
W	5	TileScope	3	0.10638	47	0.42332	0.27653	0.33630	0.27031	0.20685	0.29819	0.01713	0.05903	0.01948
X	5	Splitter	3	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	0.03000	4	0.44802	0.42040	0.34067	0.22566	0.21194	0.32113	0.01209	0.08259	0.02169
Z	6	TileScope	3	0.06330	12	0.44656	0.43458	0.36439	0.24157	0.11770	0.29049	0.00948	0.00000	0.01905