Successful Pregnancies after Application of Array-CGH in PGD-Aneuploidy Screening

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Hellani et al; ESHRE 2009

Applications of preimplantation genetic screening (PGS)

PGS has been suggested and used to improve pregnancy rates for the following indications:
Advanced maternal age
Repeated IVF failure
Repeated miscarriage
Testicular sperm extraction
(Kuliev and Verlinsky., 2008; Donoso *et al*., 2006; Gianaroli *et al*., 2005, Caglar *et al*., 2005).

Hellani et al; ESHRE 2009

PGS and chromosomal abnormalities

Although, improvements in IVF outcome after PGS have been observed in multiple case-controlled studies (Munne *et al*., 2007a; Munne *at al*. 2007b) its effectiveness in randomized controlled studies is still limited. One of the main reasons for this limitation is in the FISH technique.

Hellani et al; ESHRE 2009

Background

Aneuploidy is the main cause of recurrent IVF failure (RIF)

Majority of the applications has been done using

FISH Technique

Number of chromosomes assessed varies from 5 to 12

Hellani et al; ESHRE 2009

Rational

Screening the entire set of single cells chromosomes
In patients suffering from RIF using agilent A-CGH
platform

Assess the outcomes in term of pregnancy rate

Hellani et al; ESHRE 2009

Validation of A-CGH technique

	Chr.13		Chr.16		Chr.18		Chr.21		Chr.22		Chr.X/Y
	Trizomy	Monozomy	Trizomy	Monozomy	Trizomy	Monozomy	Trizomy	Monozomy	Trizomy	Monozomy	
of embryos iagnosed by ISH	3	1	2	1	2	1	3	2	2	1	XXY 2
of embryos iagnosed by CGH	2*	1	2	1	2	1	1*	2	1*	1	XXY 1*

- * Discrepancy in the diagnosis observed between the two methods.
- Chr.: Chromosome
-In FISH, one blastomere was used whereas in aCGH two blastomeres were used due to protocol requirements for each method (see materials and methods section).
- Each embryo examined by aCGH had only one chromosome abnormality as detected by FISH.
-Possible reason for discrepancies between the FISH and aCGH is embryo-mosaicism due to the number of blastomeres diagnosed

Hellani et al; ESHRE 2009

Recurrent IVF failure patients selection criteria

A minimum of 7 IVF failures was the main criteria set for patient selection

Hellani et al; ESHRE 2009

PGS steps

Embryos are biopsied on day 3 where two cells are systematically taken

Multiple Displacement Amplification (MDA) was performed on the 2 cells of each embryo, labeled and hybridized agains a normal control DNA

After 20 hours of hybridization slides are washed and scanned using the agilent platform.

Hellani et al; ESHRE 2009

Patient age	# of recurrent IVF failure	# of embryos assessed by Acgh	# of normal embryos detected	# of abnormal embryos detected and type of abnormalities	Pregnancy (heartbeat)	Pregnancy duration
38	10	6	3	E1: Trizomy 18 E2*: Trizomies: 13, 16, 22 E3: Trizomy 20	Yes	Third-trimester
41	11	4	2	E1*: Trizomies: 13, 21; Monozomies: 22, 14 E2: 8q deletion	Yes	Third-trimester
44	9	3	None	E1: Trizomy 15 E2: Monozomy 10 E3: Trizomy 14	NA	Third-trimester
42	10	4	None	E1: Monozomy 17 E2: Trizomy 15 E3: Trizomy 2 E4: Monozomy 10	NA	Third-trimester
34	7	6	4	E1: Monzomy 1 E2: Trizomy 21 E3: Trizomy 15 E4: XXY	Yes	Third-trimester
28	9	6	2	E1: Trizomy 4 E2: Trizomy 16 E3: Monozyomy 12 E4: X0	Yes	Third-trimester
31	7	6	3	E1: Trizomy 16 E2: Trizomy 21 E3: Monozomy 18	No	Third-trimester
32	12	6	2	E1: Duplication 1p E2: Trizomy 13 E3: Monozomy 5 E4: Trizomy 12	Yes	Third-trimester

Hellani et al; ESHRE 2009

Result summary

Number of patients	Transfer performed	Pregnancy
24	19/24 (79%)	13/19 (68%)

Hellani et al; ESHRE 2009

Conclusion

The first clinical application of A-CGH in PGS

The technique is reliable and paves the way for more applications

The discrepancy observed between A-CGH and the FISH is most probably due to the mosaicism mechanism known in the embryos

Hellani et al; ESHRE 2009

Conclusion

Many abnormalities detected by aCGH were missed using the FISH technique.

Abnormalities in chromosomes 1, 2, 4, 5, 8, 10, 12, 14, 15, 17 and 20 in many embryos tested. Such abnormalities could not be detected using the seven probes FISH panel used in our routine PGS.

Hellani et al; ESHRE 2009

Conclusion

The percentage of embryos with those abnormal chromosomes was 60%, when compared to the total number of abnormal embryos.

Therefore, FISH panel for chromosomes 13, 16, 18, 21, 22 and sex chromosomes, could only detect 40% of the chromosomal abnormalities

Hellani et al; ESHRE 2009

Conclusion

The confirmation of aCGH result on the non-transferred embryos by FISH showed the presence of embryos with mosaicism involving more than one chromosome (18%)

The 18% figure should be added to the percentage of biased factor due to missed mosaicism by aCGH (embryo diagnosed as normal and transferred).

Hellani et al; ESHRE 2009

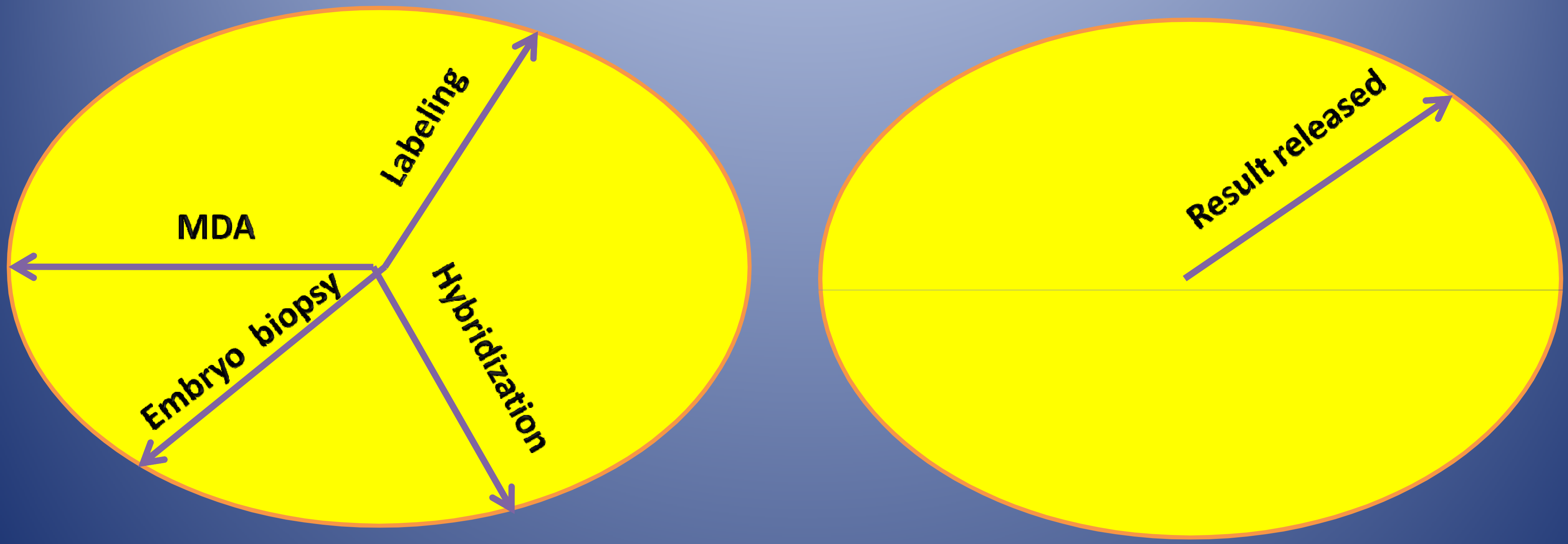
Conclusion

Two cells are systematically diagnosed for each embryo; consequently, mosaicism could not be easily detected which may explain the high percentage of normal embryos (40%) compared with the 25% previously reported (Voullaire *et al*., 2000).

During the aCGH validation and confirmation processes, 25% and 18% of the embryos were mosaics.

Hellani et al; ESHRE 2009

Challenges and possible improvements duration of diagnosis



Hellani et al; ESHRE 2009

Future directions

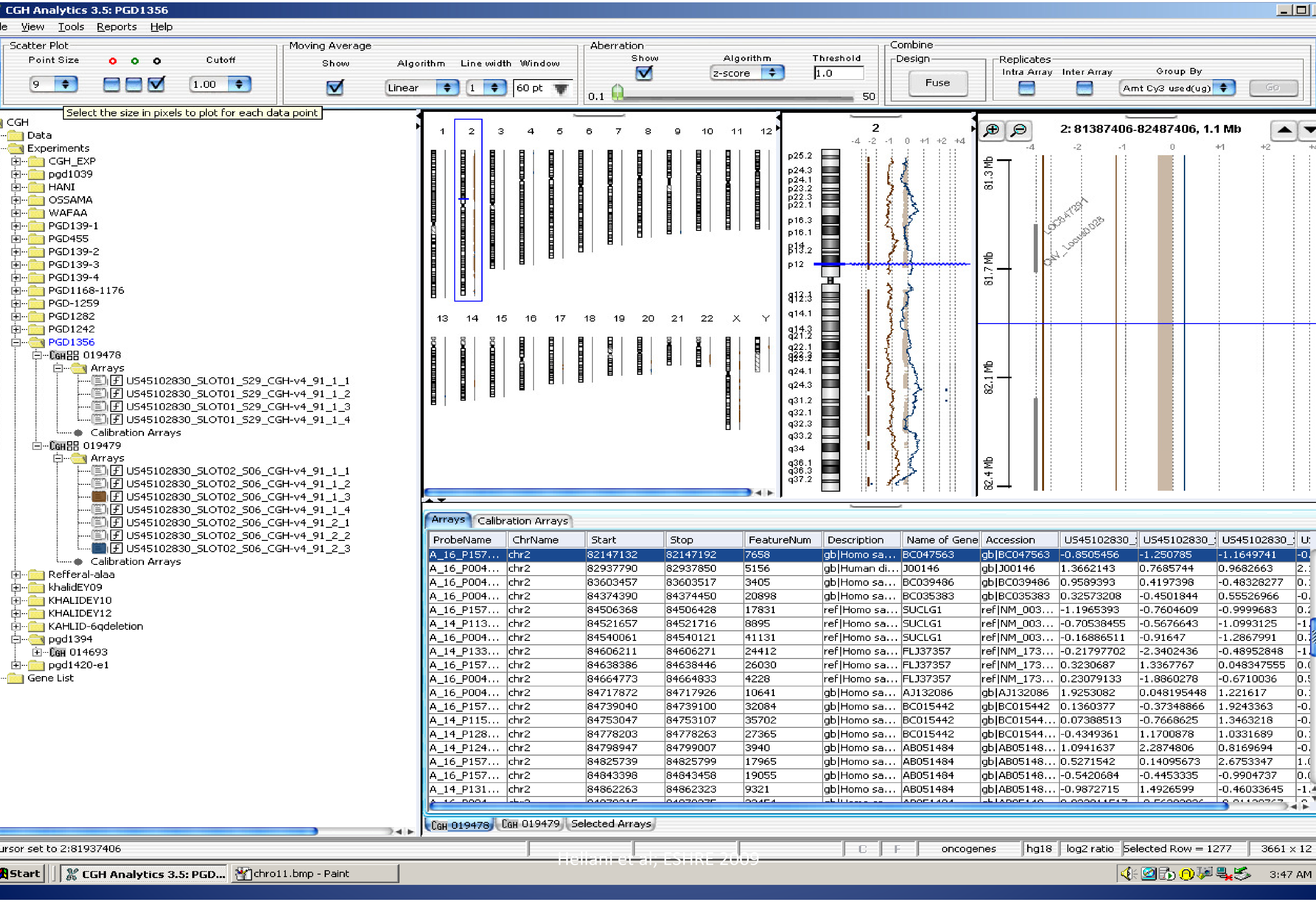
A-CGH and Recurrent miscarriages

Study design: 3 or more miscarriages during the first trimester

Hellani et al; ESHRE 2009

Ten recurrent miscarriages patients
She produced 10 embryos
after PGD, 9 embryos were found abnormal
Abnormalities observed in the following chromosomes:
19, 14, 20, 21, 11, 2, 22
Patient did not get pregnant with single embryo transferred.

Hellani et al; ESHRE 2009



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A_16_P004…	chr2	82937790	82937850	5156	gb|Human di…	J00146	gb|J00146	1.3662143	0.7685744	0.9682663	2.
A_16_P004…	chr2	83603457	83603517	3405	gb|Homo sa…	BC039486	gb|BC039486	0.9589393	0.4197398	-0.48328277	0.
A_16_P004…	chr2	84374390	84374450	20898	gb|Homo sa…	BC035383	gb|BC035383	0.32573208	-0.4501844	0.55526966	-0.
A_16_P157…	chr2	84506368	84506428	17831	ref|Homo sa…	SUCLG1	ref|NM_003…	-1.1965393	-0.7604609	-0.9999683	0.
A_14_P113…	chr2	84521657	84521716	8895	ref|Homo sa…	SUCLG1	ref|NM_003…	-0.70538455	-0.5676643	-1.0993125	-1.
A_16_P004…	chr2	84540061	84540121	41131	ref|Homo sa…	SUCLG1	ref|NM_003…	-0.16886511	-0.91647	-1.2867991	0.
A_14_P133…	chr2	84606211	84606271	24412	ref|Homo sa…	FLJ37357	ref|NM_173…	-0.21797702	-2.3402436	-0.48952848	-1.
A_16_P157…	chr2	84638386	84638446	26030	ref|Homo sa…	FLJ37357	ref|NM_173…	0.3230687	1.3367767	0.048347555	0.0
A_16_P004…	chr2	84664773	84664833	4228	ref|Homo sa…	FLJ37357	ref|NM_173…	0.23079133	-1.8860278	-0.6710036	0.5
A_16_P004…	chr2	84717872	84717926	10641	gb|Homo sa…	AJ132086	gb|AJ132086	1.9253082	0.048195448	1.221617	0.
A_16_P157…	chr2	84739040	84739100	32084	gb|Homo sa…	BC015442	gb|BC015442	0.1360377	-0.37348866	1.9243363	-0.
A_14_P115…	chr2	84753047	84753107	35702	gb|Homo sa…	BC015442	gb|BC01544…	0.07388513	-0.7668625	1.3463218	-0.
A_14_P128…	chr2	84778203	84778263	27365	gb|Homo sa…	BC015442	gb|BC01544…	-0.4349361	1.1700878	1.0331689	0.
A_14_P124…	chr2	84798947	84799007	3940	gb|Homo sa…	AB051484	gb|AB05148…	1.0941637	2.2874806	0.8169694	-0.
A_16_P157…	chr2	84825739	84825799	17965	gb|Homo sa…	AB051484	gb|AB05148…	0.5271542	0.14095673	2.6753347	1.0
A_16_P157…	chr2	84843398	84843458	19055	gb|Homo sa…	AB051484	gb|AB05148…	-0.5420684	-0.4453335	-0.9904737	0.0
A_14_P131…	chr2	84862263	84862323	9321	gb|Homo sa…	AB051484	gb|AB05148…	-0.9872715	1.4926599	-0.46033645	-1.

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oncogenes | hg18 | log2 ratio | Selected Row = 1277 | 3661 x 12

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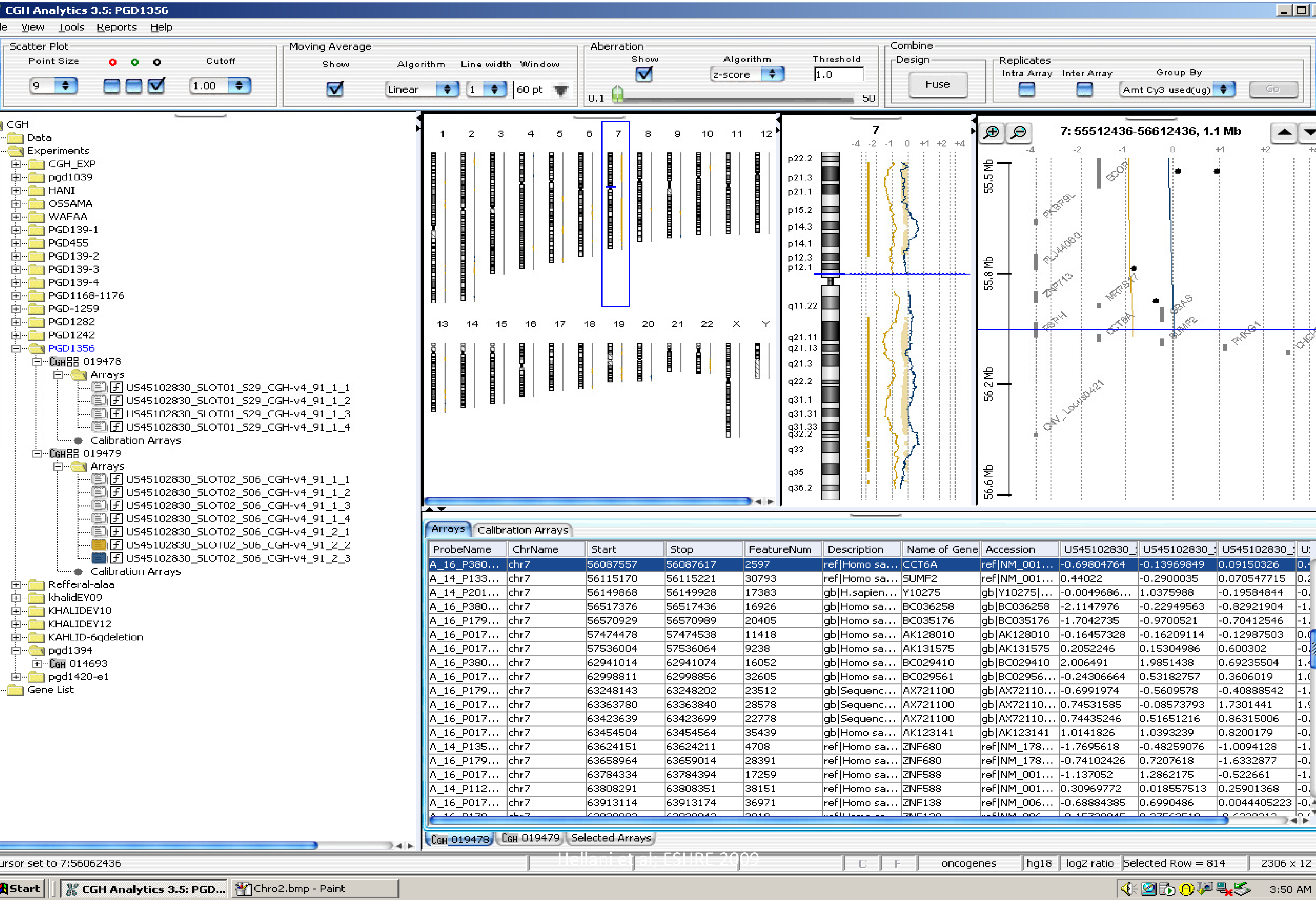

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Group By: Amt Cy3 used(ug)

- CGH
  - Data
  - Experiments
    - CGH_EXP
    - pgd1039
    - HANI
    - OSSAMA
    - WAFAA
    - PGD139-1
    - PGD455
    - PGD139-2
    - PGD139-3
    - PGD139-4
    - PGD1168-1176
    - PGD-1259
    - PGD1282
    - PGD1242
    - PGD1356
      - CGH 019478
        - Arrays
          - US45102830_SLOT01_S29_CGH-v4_91_1_1
          - US45102830_SLOT01_S29_CGH-v4_91_1_2
          - US45102830_SLOT01_S29_CGH-v4_91_1_3
          - US45102830_SLOT01_S29_CGH-v4_91_1_4
        - Calibration Arrays
      - CGH 019479
        - Arrays
          - US45102830_SLOT02_S06_CGH-v4_91_1_1
          - US45102830_SLOT02_S06_CGH-v4_91_1_2
          - US45102830_SLOT02_S06_CGH-v4_91_1_3
          - US45102830_SLOT02_S06_CGH-v4_91_1_4
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          - US45102830_SLOT02_S06_CGH-v4_91_2_2
          - US45102830_SLOT02_S06_CGH-v4_91_2_3
        - Calibration Arrays
    - Refferal-alaa
    - khalidEY09
    - KHALIDEY10
    - KHALIDEY12
    - KAHLID-6qdeletion
    - pgd1394
      - CGH 014693
    - pgd1420-e1
  - Gene List

Arrays | Calibration Arrays

ProbeName	ChrName	Start	Stop	FeatureNum	Description	Name of Gene	Accession	US45102830_	US45102830_	US45102830_	U
A_16_P380...	chr7	56087557	56087617	2597	ref|Homo sa...	CCT6A	ref|NM_001...	-0.69804764	-0.13969849	0.09150326	0.
A_14_P133...	chr7	56115170	56115221	30793	ref|Homo sa...	SUMF2	ref|NM_001...	0.44022	-0.2900035	0.070547715	0.2
A_14_P201...	chr7	56149868	56149928	17383	gb|H.sapien...	Y10275	gb|Y10275|...	-0.0049686...	1.0375988	-0.19584844	-0.
A_16_P380...	chr7	56517376	56517436	16926	gb|Homo sa...	BC036258	gb|BC036258	-2.1147976	-0.22949563	-0.82921904	-1.
A_16_P179...	chr7	56570929	56570989	20405	gb|Homo sa...	BC035176	gb|BC035176	-1.7042735	-0.9700521	-0.70412546	-1.
A_16_P017...	chr7	57474478	57474538	11418	gb|Homo sa...	AK128010	gb|AK128010	-0.16457328	-0.16209114	-0.12987503	0.0
A_16_P017...	chr7	57536004	57536064	9238	gb|Homo sa...	AK131575	gb|AK131575	0.2052246	0.15304986	0.600302	-0.
A_16_P380...	chr7	62941014	62941074	16052	gb|Homo sa...	BC029410	gb|BC029410	2.006491	1.9851438	0.69235504	1.
A_16_P017...	chr7	62998811	62998856	32605	gb|Homo sa...	BC029561	gb|BC02956...	-0.24306664	0.53182757	0.3606019	1.0
A_16_P179...	chr7	63248143	63248202	23512	gb|Sequenc...	AX721100	gb|AX72110...	-0.6991974	-0.5609578	-0.40888542	-1.
A_16_P017...	chr7	63363780	63363840	28578	gb|Sequenc...	AX721100	gb|AX72110...	0.74531585	-0.08573793	1.7301441	1.9
A_16_P017...	chr7	63423639	63423699	22778	gb|Sequenc...	AX721100	gb|AX72110...	0.74435246	0.51651216	0.86315006	-0.
A_16_P017...	chr7	63454504	63454564	35439	gb|Homo sa...	AK123141	gb|AK123141	1.0141826	1.0393239	0.8200179	-0.
A_14_P135...	chr7	63624151	63624211	4708	ref|Homo sa...	ZNF680	ref|NM_178...	-1.7695618	-0.48259076	-1.0094128	-1.
A_16_P179...	chr7	63658964	63659014	28391	ref|Homo sa...	ZNF680	ref|NM_178...	-0.74102426	0.7207618	-1.6332877	-0.
A_16_P017...	chr7	63784334	63784394	17259	ref|Homo sa...	ZNF588	ref|NM_001...	-1.137052	1.2862175	-0.522661	-1.
A_14_P112...	chr7	63808291	63808351	38151	ref|Homo sa...	ZNF588	ref|NM_001...	0.30969772	0.018557513	0.25901368	-0.
A_16_P017...	chr7	63913114	63913174	36971	ref|Homo sa...	ZNF138	ref|NM_006...	-0.68884385	0.6990486	0.0044405223	-0.

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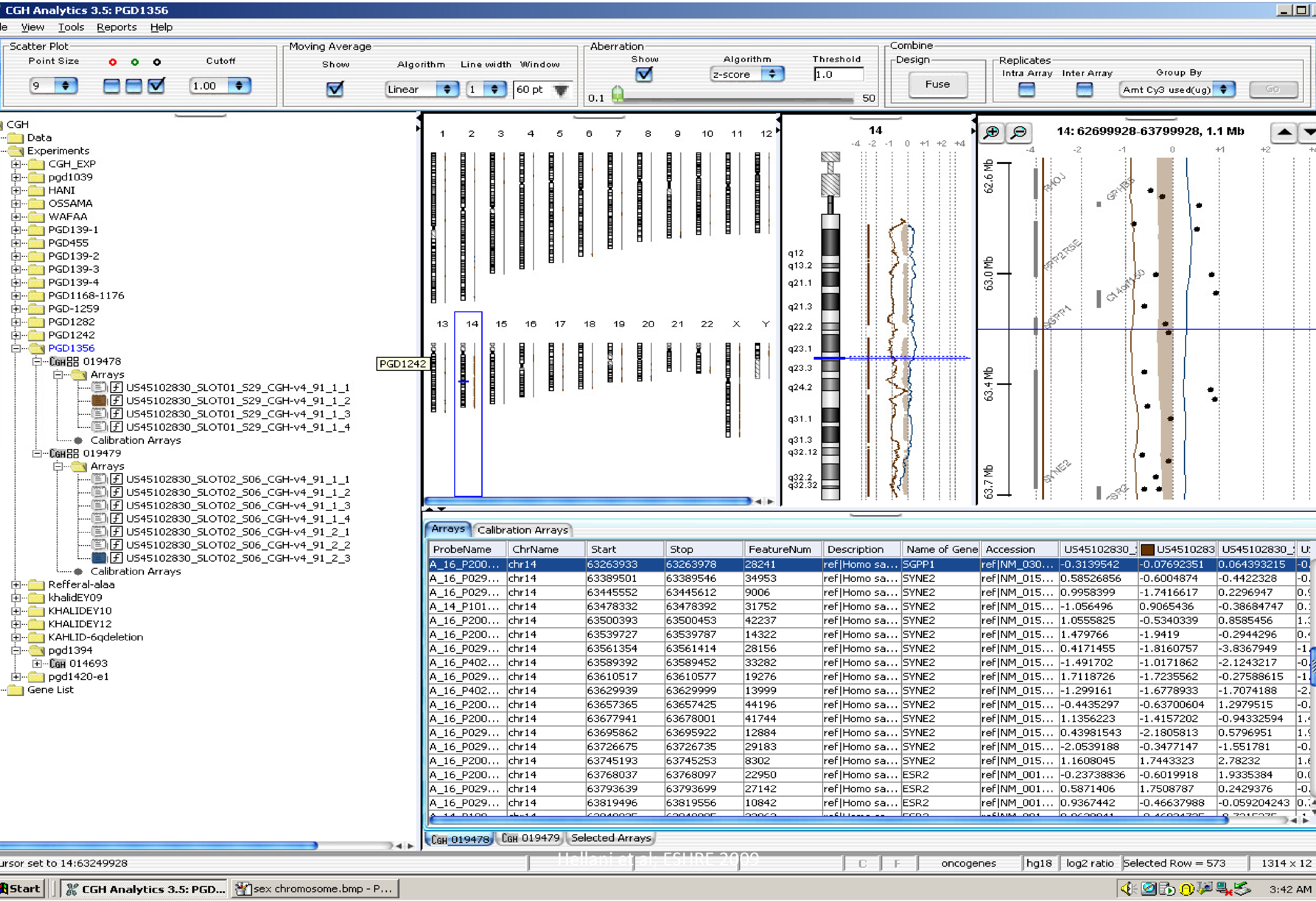
Hellani et al, ESHRE 2009



CGH Analytics 3.5: PGD1356

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Aberration
Show ☑
Algorithm z-score
Threshold 1.0

Combine
Design Fuse
Replicates Intra Array Inter Array
Group By Amt Cy3 used(ug)

CGH
- Data
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  - CGH_EXP
  - pgd1039
  - HANI
  - OSSAMA
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  - PGD139-1
  - PGD455
  - PGD139-2
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  - PGD-1259
  - PGD1282
  - PGD1242
  - PGD1356
    - CGH 019478
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        - US45102830_SLOT01_S29_CGH-v4_91_1_3
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  - pgd1420-e1
- Gene List

Arrays | Calibration Arrays

ProbeName	ChrName	Start	Stop	FeatureNum	Description	Name of Gene	Accession	US45102830_	US4510283	US45102830_
A_16_P200...	chr14	63263933	63263978	28241	ref|Homo sa...	SGPP1	ref|NM_030...	-0.3139542	-0.07692351	0.064393215
A_16_P029...	chr14	63389501	63389546	34953	ref|Homo sa...	SYNE2	ref|NM_015...	0.58526856	-0.6004874	-0.4422328
A_16_P029...	chr14	63445552	63445612	9006	ref|Homo sa...	SYNE2	ref|NM_015...	0.9958399	-1.7416617	0.2296947
A_14_P101...	chr14	63478332	63478392	31752	ref|Homo sa...	SYNE2	ref|NM_015...	-1.056496	0.9065436	-0.38684747
A_16_P200...	chr14	63500393	63500453	42237	ref|Homo sa...	SYNE2	ref|NM_015...	1.0555825	-0.5340339	0.8585456
A_16_P200...	chr14	63539727	63539787	14322	ref|Homo sa...	SYNE2	ref|NM_015...	1.479766	-1.9419	-0.2944296
A_16_P029...	chr14	63561354	63561414	28156	ref|Homo sa...	SYNE2	ref|NM_015...	0.4171455	-1.8160757	-3.8367949
A_16_P402...	chr14	63589392	63589452	33282	ref|Homo sa...	SYNE2	ref|NM_015...	-1.491702	-1.0171862	-2.1243217
A_16_P029...	chr14	63610517	63610577	19276	ref|Homo sa...	SYNE2	ref|NM_015...	1.7118726	-1.7235562	-0.27588615
A_16_P402...	chr14	63629939	63629999	13999	ref|Homo sa...	SYNE2	ref|NM_015...	-1.299161	-1.6778933	-1.7074188
A_16_P200...	chr14	63657365	63657425	44196	ref|Homo sa...	SYNE2	ref|NM_015...	-0.4435297	-0.63700604	1.2979515
A_16_P200...	chr14	63677941	63678001	41744	ref|Homo sa...	SYNE2	ref|NM_015...	1.1356223	-1.4157202	-0.94332594
A_16_P029...	chr14	63695862	63695922	12884	ref|Homo sa...	SYNE2	ref|NM_015...	0.43981543	-2.1805813	0.5796951
A_16_P029...	chr14	63726675	63726735	29183	ref|Homo sa...	SYNE2	ref|NM_015...	-2.0539188	-0.3477147	-1.551781
A_16_P200...	chr14	63745193	63745253	8302	ref|Homo sa...	SYNE2	ref|NM_015...	1.1608045	1.7443323	2.78232
A_16_P200...	chr14	63768037	63768097	22950	ref|Homo sa...	ESR2	ref|NM_001...	-0.23738836	-0.6019918	1.9335384
A_16_P029...	chr14	63793639	63793699	27142	ref|Homo sa...	ESR2	ref|NM_001...	0.5871406	1.7508787	0.2429376
A_16_P029...	chr14	63819496	63819556	10842	ref|Homo sa...	ESR2	ref|NM_001...	0.9367442	-0.46637988	-0.059204243

CGH 019478 | CGH 019479 | Selected Arrays

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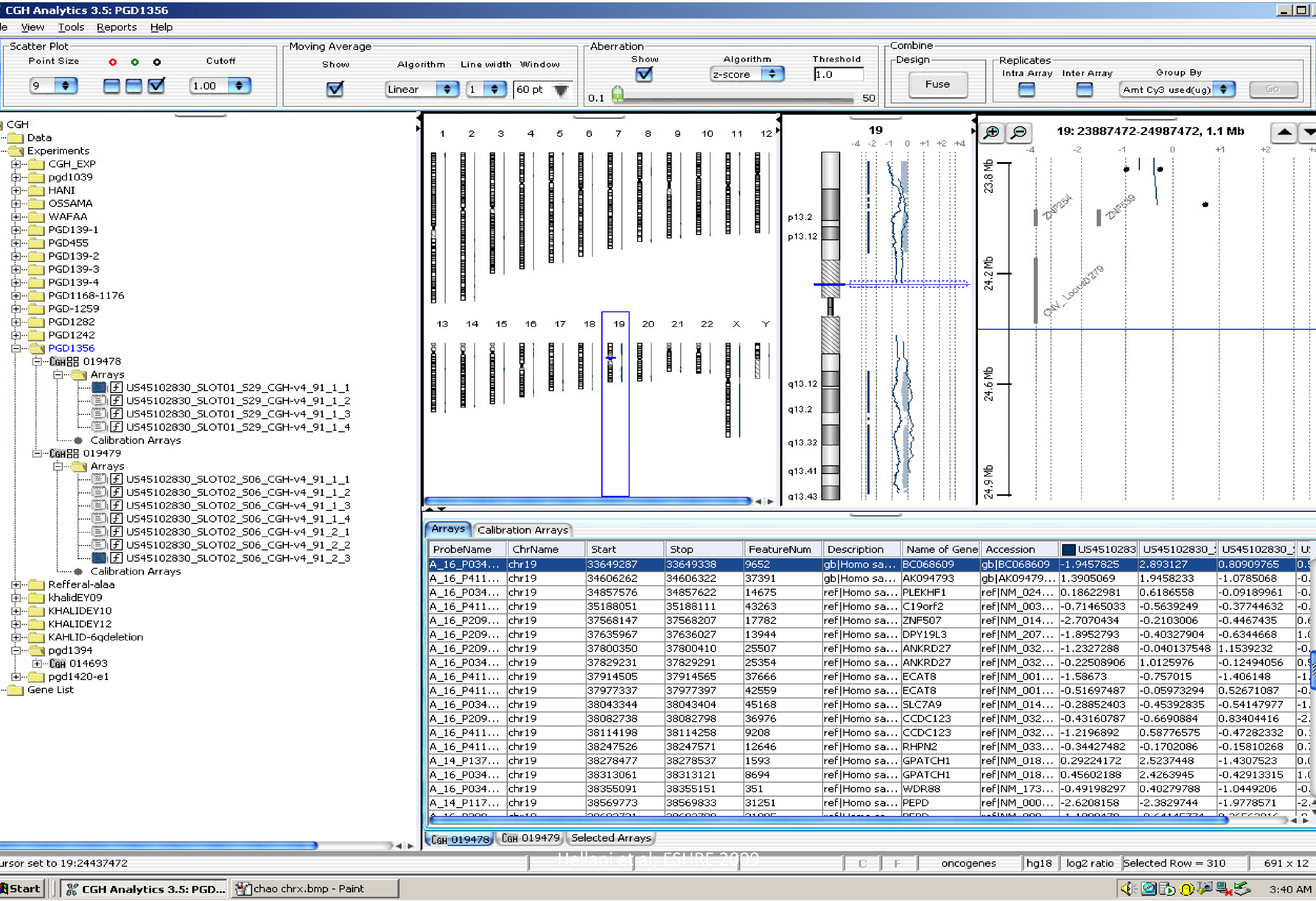

- CGH
  - Data
  - Experiments
    - CGH_EXP
    - pgd1039
    - HANI
    - OSSAMA
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    - PGD455
    - PGD139-2
    - PGD139-3
    - PGD139-4
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    - PGD-1259
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          - US45102830_SLOT02_S06_CGH-v4_91_2_1
          - US45102830_SLOT02_S06_CGH-v4_91_2_2
          - US45102830_SLOT02_S06_CGH-v4_91_2_3
        - Calibration Arrays
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    - pgd1420-e1
  - Gene List

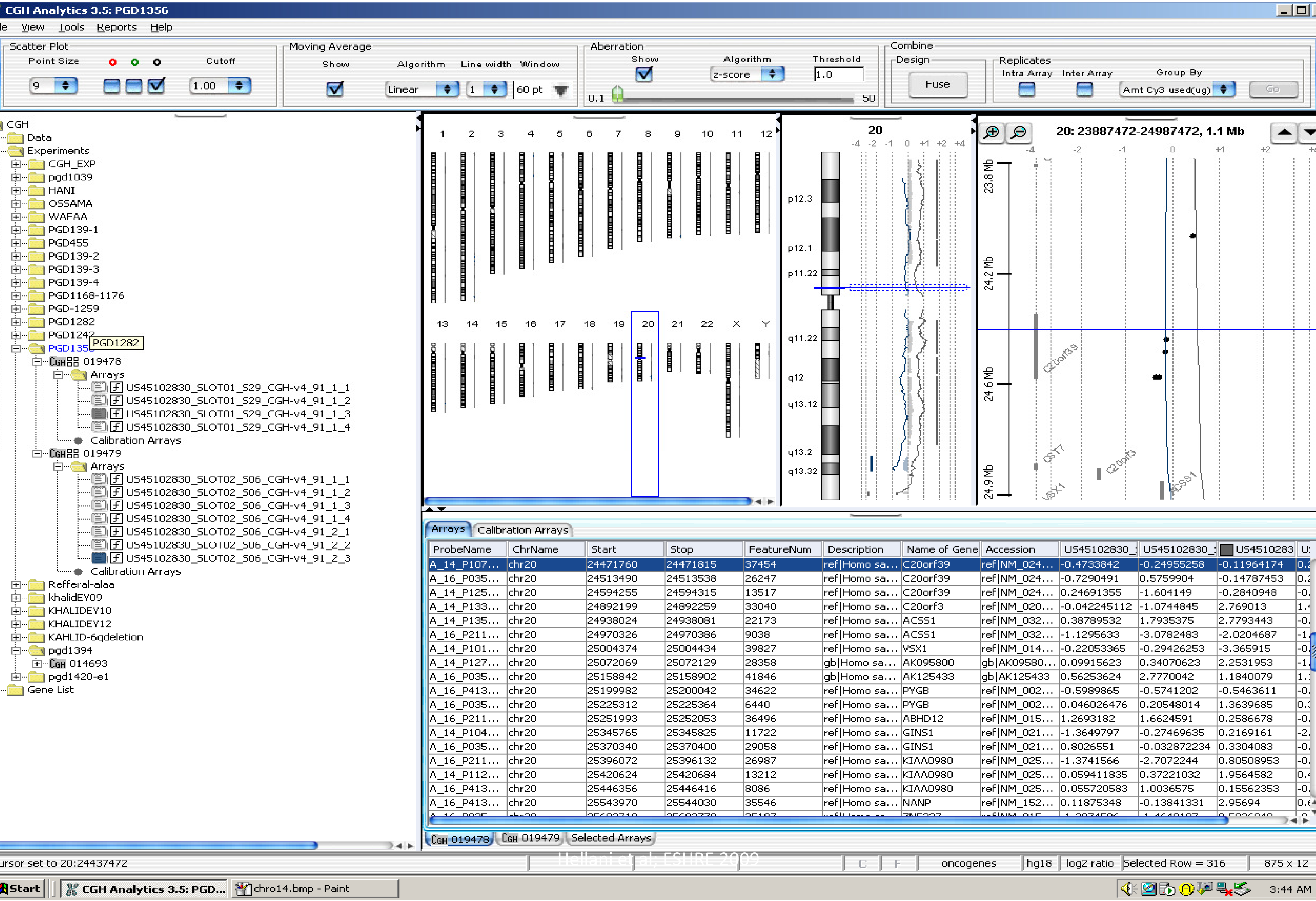
Arrays | Calibration Arrays

ProbeName	ChrName	Start	Stop	FeatureNum	Description	Name of Gene	Accession	■ US45102830	US45102830_:	US45102830_:	U:
A_16_P034...	chr19	33649287	33649338	9652	gb|Homo sa...	BC068609	gb|BC068609	-1.9457825	2.893127	0.80909765	0.5
A_16_P411...	chr19	34606262	34606322	37391	gb|Homo sa...	AK094793	gb|AK09479...	1.3905069	1.9458233	-1.0785068	-0.
A_16_P034...	chr19	34857576	34857622	14675	ref|Homo sa...	PLEKHF1	ref|NM_024...	0.18622981	0.6186558	-0.09189961	-0.
A_16_P411...	chr19	35188051	35188111	43263	ref|Homo sa...	C19orf2	ref|NM_003...	-0.71465033	-0.5639249	-0.37744632	-0.
A_16_P209...	chr19	37568147	37568207	17782	ref|Homo sa...	ZNF507	ref|NM_014...	-2.7070434	-0.2103006	-0.4467435	0.6
A_16_P209...	chr19	37635967	37636027	13944	ref|Homo sa...	DPY19L3	ref|NM_207...	-1.8952793	-0.40327904	-0.6344668	1.0
A_16_P209...	chr19	37800350	37800410	25507	ref|Homo sa...	ANKRD27	ref|NM_032...	-1.2327288	-0.040137548	1.1539232	-0.
A_16_P034...	chr19	37829231	37829291	25354	ref|Homo sa...	ANKRD27	ref|NM_032...	-0.22508906	1.0125976	-0.12494056	0.5
A_16_P411...	chr19	37914505	37914565	37666	ref|Homo sa...	ECAT8	ref|NM_001...	-1.58673	-0.757015	-1.406148	-1.
A_16_P411...	chr19	37977337	37977397	42559	ref|Homo sa...	ECAT8	ref|NM_001...	-0.51697487	-0.05973294	0.52671087	-0.
A_16_P034...	chr19	38043344	38043404	45168	ref|Homo sa...	SLC7A9	ref|NM_014...	-0.28852403	-0.45392835	-0.54147977	-1.
A_16_P209...	chr19	38082738	38082798	36976	ref|Homo sa...	CCDC123	ref|NM_032...	-0.43160787	-0.6690884	0.83404416	-2.
A_16_P411...	chr19	38114198	38114258	9208	ref|Homo sa...	CCDC123	ref|NM_032...	-1.2196892	0.58776575	-0.47282332	0.
A_16_P411...	chr19	38247526	38247571	12646	ref|Homo sa...	RHPN2	ref|NM_033...	-0.34427482	-0.1702086	-0.15810268	0.
A_14_P137...	chr19	38278477	38278537	1593	ref|Homo sa...	GPATCH1	ref|NM_018...	0.29224172	2.5237448	-1.4307523	0.0
A_16_P034...	chr19	38313061	38313121	8694	ref|Homo sa...	GPATCH1	ref|NM_018...	0.45602188	2.4263945	-0.42913315	1.0
A_16_P034...	chr19	38355091	38355151	351	ref|Homo sa...	WDR88	ref|NM_173...	-0.49198297	0.40279788	-1.0449206	-0.
A_14_P117...	chr19	38569773	38569833	31251	ref|Homo sa...	PEPD	ref|NM_000...	-2.6208158	-2.3829744	-1.9778571	-2.

CGH 019478 | CGH 019479 | Selected Arrays

ursor set to 19:24437472 | C | F | oncogenes | hg18 | log2 ratio | Selected Row = 310 | 691 x 12

Hellani et al, ESHRE 2009



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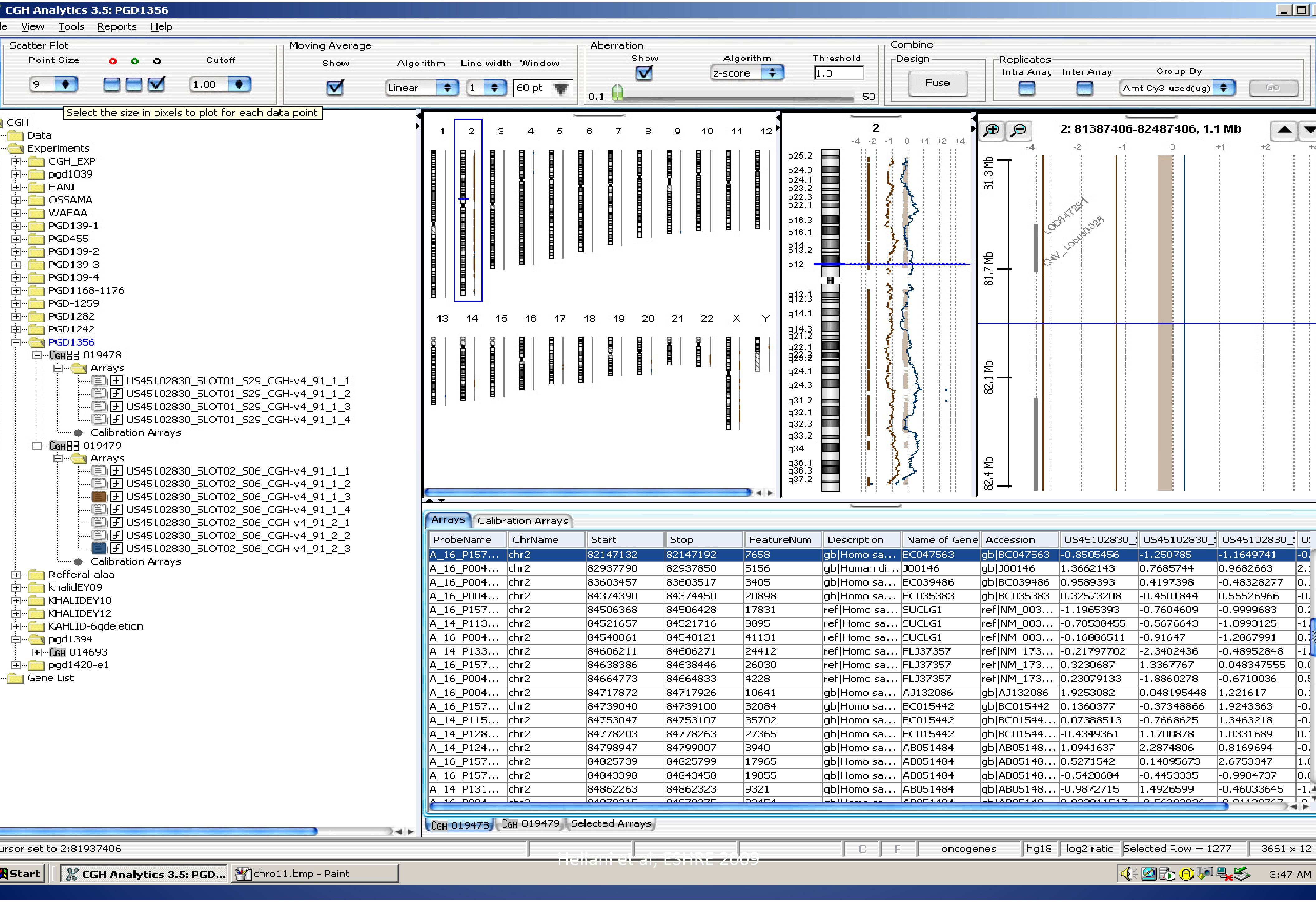
A_14_P107...	chr20	24471760	24471815	37454	ref|Homo sa...	C20orf39	ref|NM_024...	-0.4733842	-0.24955258	-0.11964174	0.2
A_16_P035...	chr20	24513490	24513538	26247	ref|Homo sa...	C20orf39	ref|NM_024...	-0.7290491	0.5759904	-0.14787453	0.2
A_14_P125...	chr20	24594255	24594315	13517	ref|Homo sa...	C20orf39	ref|NM_024...	0.24691355	-1.604149	-0.2840948	-0.
A_14_P133...	chr20	24892199	24892259	33040	ref|Homo sa...	C20orf3	ref|NM_020...	-0.042245112	-1.0744845	2.769013	1.
A_14_P135...	chr20	24938024	24938081	22173	ref|Homo sa...	ACSS1	ref|NM_032...	0.38789532	1.7935375	2.7793443	-0.
A_16_P211...	chr20	24970326	24970386	9038	ref|Homo sa...	ACSS1	ref|NM_032...	-1.1295633	-3.0782483	-2.0204687	-1.
A_14_P101...	chr20	25004374	25004434	39827	ref|Homo sa...	VSX1	ref|NM_014...	-0.22053365	-0.29426253	-3.365915	-0.
A_14_P127...	chr20	25072069	25072129	28358	gb|Homo sa...	AK095800	gb|AK09580...	0.09915623	0.34070623	2.2531953	-1.
A_16_P035...	chr20	25158842	25158902	41846	gb|Homo sa...	AK125433	gb|AK125433	0.56253624	2.7770042	1.1840079	1.
A_16_P413...	chr20	25199982	25200042	34622	ref|Homo sa...	PYGB	ref|NM_002...	-0.5989865	-0.5741202	-0.5463611	-0.
A_16_P035...	chr20	25225312	25225364	6440	ref|Homo sa...	PYGB	ref|NM_002...	0.046026476	0.20548014	1.3639685	0.
A_16_P211...	chr20	25251993	25252053	36496	ref|Homo sa...	ABHD12	ref|NM_015...	1.2693182	1.6624591	0.2586678	-0.
A_14_P104...	chr20	25345765	25345825	11722	ref|Homo sa...	GINS1	ref|NM_021...	-1.3649797	-0.27469635	0.2169161	-2.
A_16_P035...	chr20	25370340	25370400	29058	ref|Homo sa...	GINS1	ref|NM_021...	0.8026551	-0.032872234	0.3304083	-0.
A_16_P211...	chr20	25396072	25396132	26987	ref|Homo sa...	KIAA0980	ref|NM_025...	-1.3741566	-2.7072244	0.80508953	-0.
A_14_P112...	chr20	25420624	25420684	13212	ref|Homo sa...	KIAA0980	ref|NM_025...	0.059411835	0.37221032	1.9564582	0.
A_16_P413...	chr20	25446356	25446416	8086	ref|Homo sa...	KIAA0980	ref|NM_025...	0.055720583	1.0036575	0.15562353	-0.
A_16_P413...	chr20	25543970	25544030	35546	ref|Homo sa...	NANP	ref|NM_152...	0.11875348	-0.13841331	2.95694	0.6

ursor set to 20:24437472

C F oncogenes hg18 log2 ratio Selected Row = 316 875 x 12

Hellani et al, ESHRE 2009



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Group By: Amt Cy3 used(ug)

Select the size in pixels to plot for each data point

- CGH
  - Data
  - Experiments
    - CGH_EXP
    - pgd1039
    - HANI
    - OSSAMA
    - WAFAA
    - PGD139-1
    - PGD455
    - PGD139-2
    - PGD139-3
    - PGD139-4
    - PGD1168-1176
    - PGD-1259
    - PGD1282
    - PGD1242
    - PGD1356
      - CGH 019478
        - Arrays
          - US45102830_SLOT01_S29_CGH-v4_91_1_1
          - US45102830_SLOT01_S29_CGH-v4_91_1_2
          - US45102830_SLOT01_S29_CGH-v4_91_1_3
          - US45102830_SLOT01_S29_CGH-v4_91_1_4
        - Calibration Arrays
      - CGH 019479
        - Arrays
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          - US45102830_SLOT02_S06_CGH-v4_91_1_2
          - US45102830_SLOT02_S06_CGH-v4_91_1_3
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          - US45102830_SLOT02_S06_CGH-v4_91_2_2
          - US45102830_SLOT02_S06_CGH-v4_91_2_3
        - Calibration Arrays
    - Refferal-alaa
    - khalidEY09
    - KHALIDEY10
    - KHALIDEY12
    - KAHLID-6qdeletion
    - pgd1394
      - CGH 014693
    - pgd1420-e1
  - Gene List

ProbeName	ChrName	Start	Stop	FeatureNum	Description	Name of Gene	Accession	US45102830_	US45102830_	US45102830_	U:
A_16_P157...	chr2	82147132	82147192	7658	gb|Homo sa...	BC047563	gb|BC047563	-0.8505456	-1.250785	-1.1649741	-0.
A_16_P004...	chr2	82937790	82937850	5156	gb|Human di...	J00146	gb|J00146	1.3662143	0.7685744	0.9682663	2.
A_16_P004...	chr2	83603457	83603517	3405	gb|Homo sa...	BC039486	gb|BC039486	0.9589393	0.4197398	-0.48328277	0.
A_16_P004...	chr2	84374390	84374450	20898	gb|Homo sa...	BC035383	gb|BC035383	0.32573208	-0.4501844	0.55526966	-0.
A_16_P157...	chr2	84506368	84506428	17831	ref|Homo sa...	SUCLG1	ref|NM_003...	-1.1965393	-0.7604609	-0.9999683	0.
A_14_P113...	chr2	84521657	84521716	8895	ref|Homo sa...	SUCLG1	ref|NM_003...	-0.70538455	-0.5676643	-1.0993125	-1.
A_16_P004...	chr2	84540061	84540121	41131	ref|Homo sa...	SUCLG1	ref|NM_003...	-0.16886511	-0.91647	-1.2867991	0.
A_14_P133...	chr2	84606211	84606271	24412	ref|Homo sa...	FLJ37357	ref|NM_173...	-0.21797702	-2.3402436	-0.48952848	-1.
A_16_P157...	chr2	84638386	84638446	26030	ref|Homo sa...	FLJ37357	ref|NM_173...	0.3230687	1.3367767	0.048347555	0.0
A_16_P004...	chr2	84664773	84664833	4228	ref|Homo sa...	FLJ37357	ref|NM_173...	0.23079133	-1.8860278	-0.6710036	0.5
A_16_P004...	chr2	84717872	84717926	10641	gb|Homo sa...	AJ132086	gb|AJ132086	1.9253082	0.048195448	1.221617	0.
A_16_P157...	chr2	84739040	84739100	32084	gb|Homo sa...	BC015442	gb|BC015442	0.1360377	-0.37348866	1.9243363	-0.
A_14_P115...	chr2	84753047	84753107	35702	gb|Homo sa...	BC015442	gb|BC01544...	0.07388513	-0.7668625	1.3463218	-0.
A_14_P128...	chr2	84778203	84778263	27365	gb|Homo sa...	BC015442	gb|BC01544...	-0.4349361	1.1700878	1.0331689	0.
A_14_P124...	chr2	84798947	84799007	3940	gb|Homo sa...	AB051484	gb|AB05148...	1.0941637	2.2874806	0.8169694	-0.
A_16_P157...	chr2	84825739	84825799	17965	gb|Homo sa...	AB051484	gb|AB05148...	0.5271542	0.14095673	2.6753347	1.0
A_16_P157...	chr2	84843398	84843458	19055	gb|Homo sa...	AB051484	gb|AB05148...	-0.5420684	-0.4453335	-0.9904737	0.0
A_14_P131...	chr2	84862263	84862323	9321	gb|Homo sa...	AB051484	gb|AB05148...	-0.9872715	1.4926599	-0.46033645	-1.

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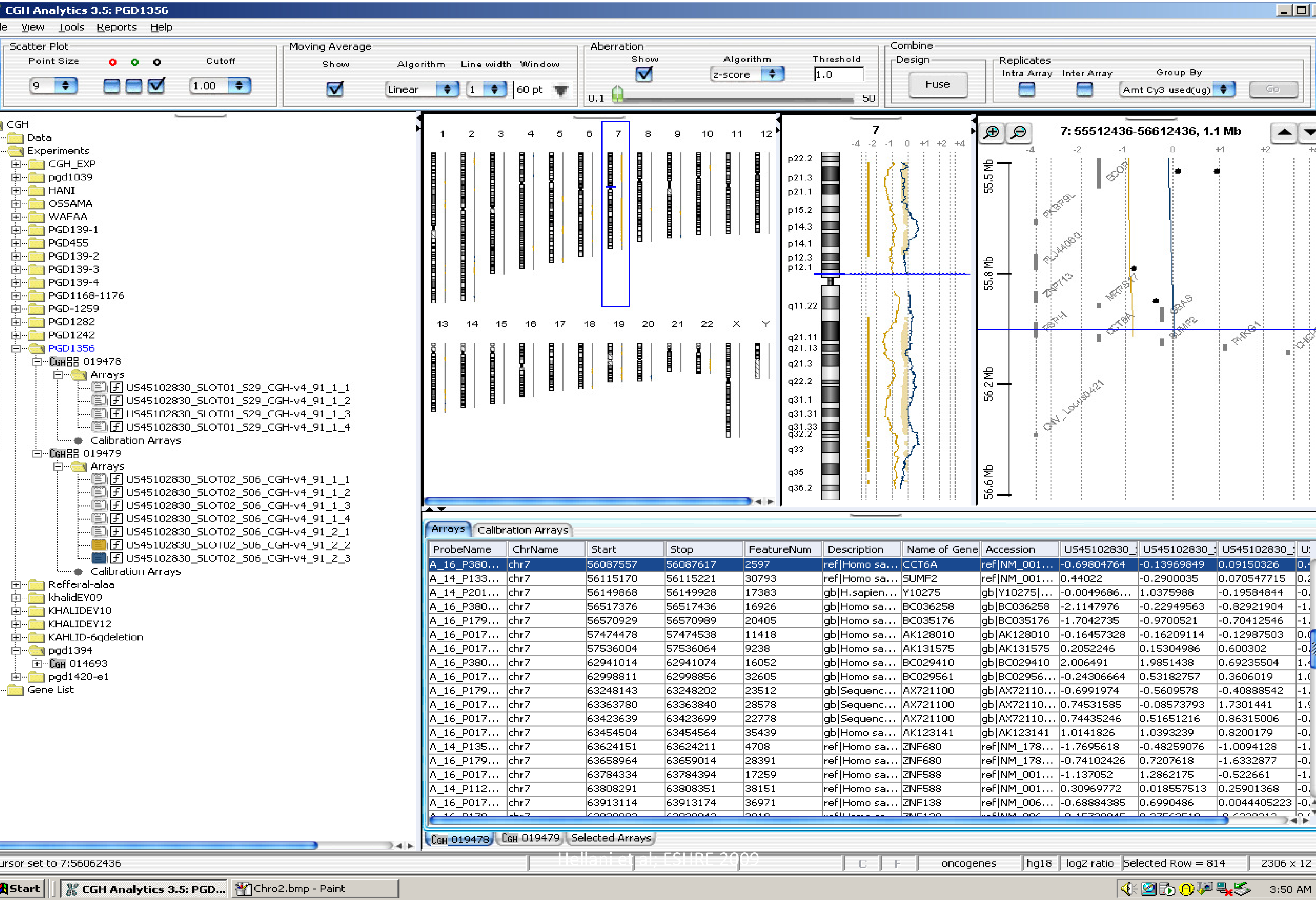

- CGH
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    - PGD455
    - PGD139-2
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    - PGD139-4
    - PGD1168-1176
    - PGD-1259
    - PGD1282
    - PGD1242
    - PGD1356
      - CGH 019478
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          - US45102830_SLOT01_S29_CGH-v4_91_1_2
          - US45102830_SLOT01_S29_CGH-v4_91_1_3
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          - US45102830_SLOT02_S06_CGH-v4_91_1_3
          - US45102830_SLOT02_S06_CGH-v4_91_1_4
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          - US45102830_SLOT02_S06_CGH-v4_91_2_2
          - US45102830_SLOT02_S06_CGH-v4_91_2_3
        - Calibration Arrays
    - Refferal-alaa
    - khalidEY09
    - KHALIDEY10
    - KHALIDEY12
    - KAHLID-6qdeletion
    - pgd1394
      - CGH 014693
    - pgd1420-e1
  - Gene List

ProbeName	ChrName	Start	Stop	FeatureNum	Description	Name of Gene	Accession	US45102830_	US45102830_	US45102830_	U:
A_16_P380...	chr7	56087557	56087617	2597	ref|Homo sa...	CCT6A	ref|NM_001...	-0.69804764	-0.13969849	0.09150326	0.
A_14_P133...	chr7	56115170	56115221	30793	ref|Homo sa...	SUMF2	ref|NM_001...	0.44022	-0.2900035	0.070547715	0.2
A_14_P201...	chr7	56149868	56149928	17383	gb|H.sapien...	Y10275	gb|Y10275|...	-0.0049686...	1.0375988	-0.19584844	-0.
A_16_P380...	chr7	56517376	56517436	16926	gb|Homo sa...	BC036258	gb|BC036258	-2.1147976	-0.22949563	-0.82921904	-1.
A_16_P179...	chr7	56570929	56570989	20405	gb|Homo sa...	BC035176	gb|BC035176	-1.7042735	-0.9700521	-0.70412546	-1.
A_16_P017...	chr7	57474478	57474538	11418	gb|Homo sa...	AK128010	gb|AK128010	-0.16457328	-0.16209114	-0.12987503	0.0
A_16_P017...	chr7	57536004	57536064	9238	gb|Homo sa...	AK131575	gb|AK131575	0.2052246	0.15304986	0.600302	-0.
A_16_P380...	chr7	62941014	62941074	16052	gb|Homo sa...	BC029410	gb|BC029410	2.006491	1.9851438	0.69235504	1.
A_16_P017...	chr7	62998811	62998856	32605	gb|Homo sa...	BC029561	gb|BC02956...	-0.24306664	0.53182757	0.3606019	1.0
A_16_P179...	chr7	63248143	63248202	23512	gb|Sequenc...	AX721100	gb|AX72110...	-0.6991974	-0.5609578	-0.40888542	-1.
A_16_P017...	chr7	63363780	63363840	28578	gb|Sequenc...	AX721100	gb|AX72110...	0.74531585	-0.08573793	1.7301441	1.
A_16_P017...	chr7	63423639	63423699	22778	gb|Sequenc...	AX721100	gb|AX72110...	0.74435246	0.51651216	0.86315006	-0.
A_16_P017...	chr7	63454504	63454564	35439	gb|Homo sa...	AK123141	gb|AK123141	1.0141826	1.0393239	0.8200179	-0.
A_14_P135...	chr7	63624151	63624211	4708	ref|Homo sa...	ZNF680	ref|NM_178...	-1.7695618	-0.48259076	-1.0094128	-1.
A_16_P179...	chr7	63658964	63659014	28391	ref|Homo sa...	ZNF680	ref|NM_178...	-0.74102426	0.7207618	-1.6332877	-0.
A_16_P017...	chr7	63784334	63784394	17259	ref|Homo sa...	ZNF588	ref|NM_001...	-1.137052	1.2862175	-0.522661	-1.
A_14_P112...	chr7	63808291	63808351	38151	ref|Homo sa...	ZNF588	ref|NM_001...	0.30969772	0.018557513	0.25901368	-0.
A_16_P017...	chr7	63913114	63913174	36971	ref|Homo sa...	ZNF138	ref|NM_006...	-0.68884385	0.6990486	0.0044405223	-0.

ursor set to 7:56062436 | C | F | oncogenes | hg18 | log2 ratio | Selected Row = 814 | 2306 x 12

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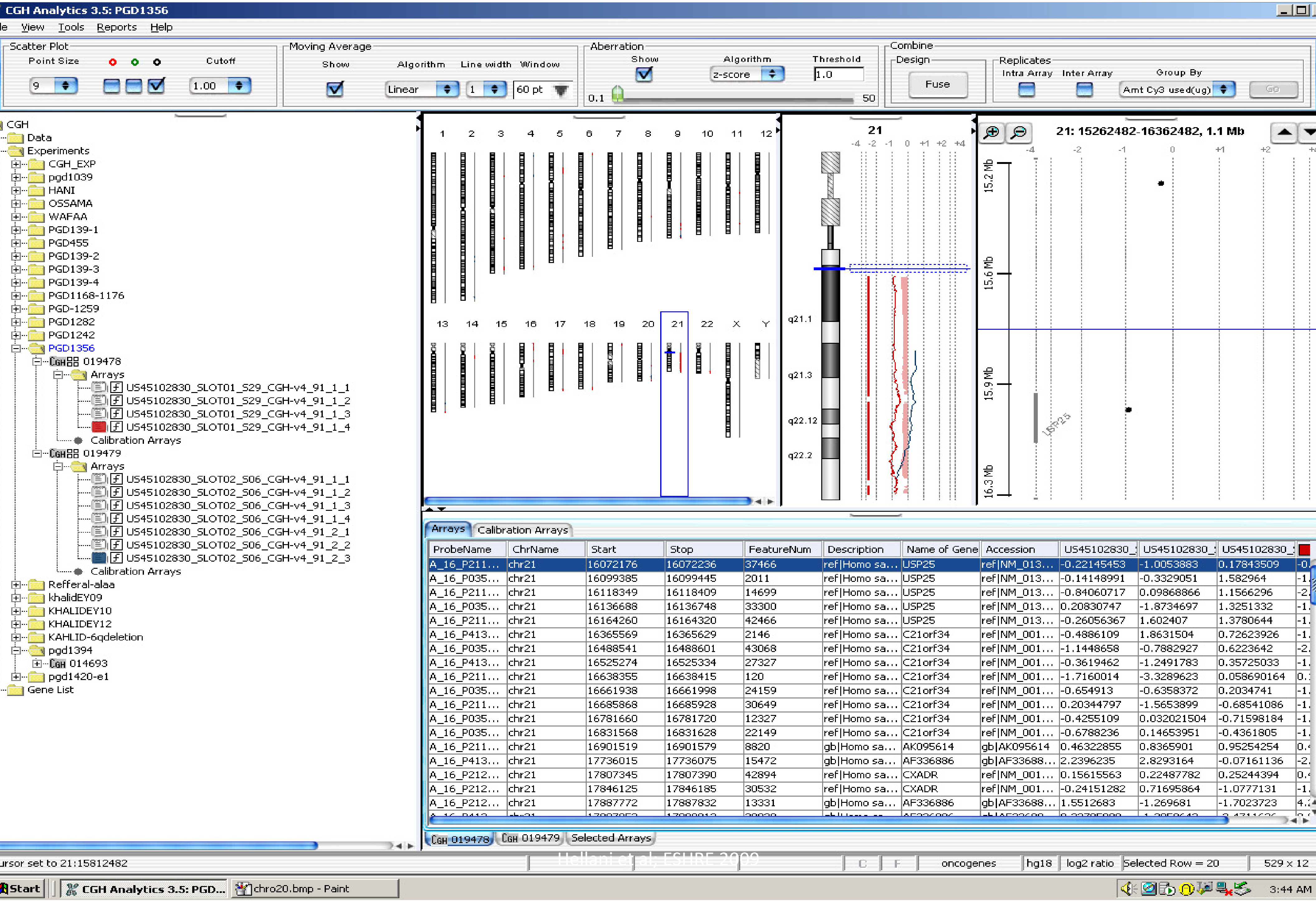

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Line width: 1
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Algorithm: z-score
Threshold: 1.0
Group By: Amt Cy3 used(ug)

- CGH
  - Data
  - Experiments
    - CGH_EXP
    - pgd1039
    - HANI
    - OSSAMA
    - WAFAA
    - PGD139-1
    - PGD455
    - PGD139-2
    - PGD139-3
    - PGD139-4
    - PGD1168-1176
    - PGD-1259
    - PGD1282
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    - PGD1356
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          - US45102830_SLOT01_S29_CGH-v4_91_1_3
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        - Calibration Arrays
      - CGH 019479
        - Arrays
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          - US45102830_SLOT02_S06_CGH-v4_91_2_2
          - US45102830_SLOT02_S06_CGH-v4_91_2_3
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    - Refferal-alaa
    - khalidEY09
    - KHALIDEY10
    - KHALIDEY12
    - KAHLID-6qdeletion
    - pgd1394
      - CGH 014693
    - pgd1420-e1
  - Gene List

Arrays | Calibration Arrays

ProbeName	ChrName	Start	Stop	FeatureNum	Description	Name of Gene	Accession	US45102830_	US45102830_	US45102830_	🟥
A_16_P211...	chr21	16072176	16072236	37466	ref|Homo sa...	USP25	ref|NM_013...	-0.22145453	-1.0053883	0.17843509	-0.
A_16_P035...	chr21	16099385	16099445	2011	ref|Homo sa...	USP25	ref|NM_013...	-0.14148991	-0.3329051	1.582964	-1.
A_16_P211...	chr21	16118349	16118409	14699	ref|Homo sa...	USP25	ref|NM_013...	-0.84060717	0.09868866	1.1566296	-2.
A_16_P035...	chr21	16136688	16136748	33300	ref|Homo sa...	USP25	ref|NM_013...	0.20830747	-1.8734697	1.3251332	-1.
A_16_P211...	chr21	16164260	16164320	42466	ref|Homo sa...	USP25	ref|NM_013...	-0.26056367	1.602407	1.3780644	-1.
A_16_P413...	chr21	16365569	16365629	2146	ref|Homo sa...	C21orf34	ref|NM_001...	-0.4886109	1.8631504	0.72623926	-1.
A_16_P035...	chr21	16488541	16488601	43068	ref|Homo sa...	C21orf34	ref|NM_001...	-1.1448658	-0.7882927	0.6223642	-2.
A_16_P413...	chr21	16525274	16525334	27327	ref|Homo sa...	C21orf34	ref|NM_001...	-0.3619462	-1.2491783	0.35725033	-1.
A_16_P211...	chr21	16638355	16638415	120	ref|Homo sa...	C21orf34	ref|NM_001...	-1.7160014	-3.3289623	0.058690164	0.
A_16_P035...	chr21	16661938	16661998	24159	ref|Homo sa...	C21orf34	ref|NM_001...	-0.654913	-0.6358372	0.2034741	-1.
A_16_P211...	chr21	16685868	16685928	30649	ref|Homo sa...	C21orf34	ref|NM_001...	0.20344797	-1.5653899	-0.68541086	-1.
A_16_P035...	chr21	16781660	16781720	12327	ref|Homo sa...	C21orf34	ref|NM_001...	-0.4255109	0.032021504	-0.71598184	-1.
A_16_P035...	chr21	16831568	16831628	22149	ref|Homo sa...	C21orf34	ref|NM_001...	-0.6788236	0.14653951	-0.4361805	-1.
A_16_P211...	chr21	16901519	16901579	8820	gb|Homo sa...	AK095614	gb|AK095614	0.46322855	0.8365901	0.95254254	0.
A_16_P413...	chr21	17736015	17736075	15472	gb|Homo sa...	AF336886	gb|AF33688...	2.2396235	2.8293164	-0.07161136	-2.
A_16_P212...	chr21	17807345	17807390	42894	ref|Homo sa...	CXADR	ref|NM_001...	0.15615563	0.22487782	0.25244394	0.
A_16_P212...	chr21	17846125	17846185	30532	ref|Homo sa...	CXADR	ref|NM_001...	-0.24151282	0.71695864	-1.0777131	-1.
A_16_P212...	chr21	17887772	17887832	13331	gb|Homo sa...	AF336886	gb|AF33688...	1.5512683	-1.269681	-1.7023723	4.

CGH 019478 | CGH 019479 | Selected Arrays

ursor set to 21:15812482 | C | F | oncogenes | hg18 | log2 ratio | Selected Row = 20 | 529 x 12

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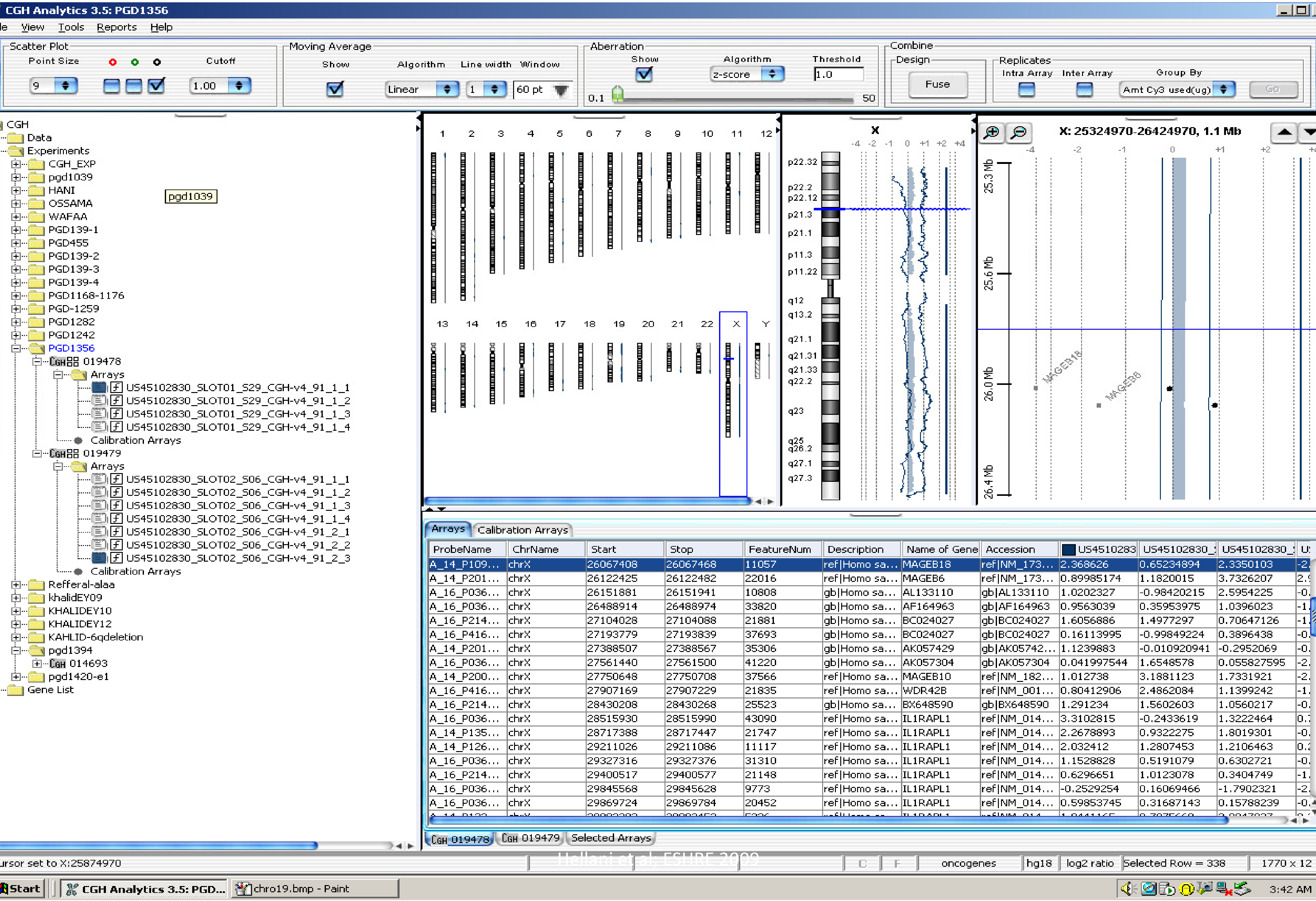

- CGH
  - Data
  - Experiments
    - CGH_EXP
    - pgd1039
    - HANI
    - OSSAMA
    - WAFAA
    - PGD139-1
    - PGD455
    - PGD139-2
    - PGD139-3
    - PGD139-4
    - PGD1168-1176
    - PGD-1259
    - PGD1282
    - PGD1242
    - PGD1356
      - CGH 019478
        - Arrays
          - US45102830_SLOT01_S29_CGH-v4_91_1_1
          - US45102830_SLOT01_S29_CGH-v4_91_1_2
          - US45102830_SLOT01_S29_CGH-v4_91_1_3
          - US45102830_SLOT01_S29_CGH-v4_91_1_4
        - Calibration Arrays
      - CGH 019479
        - Arrays
          - US45102830_SLOT02_S06_CGH-v4_91_1_1
          - US45102830_SLOT02_S06_CGH-v4_91_1_2
          - US45102830_SLOT02_S06_CGH-v4_91_1_3
          - US45102830_SLOT02_S06_CGH-v4_91_1_4
          - US45102830_SLOT02_S06_CGH-v4_91_2_1
          - US45102830_SLOT02_S06_CGH-v4_91_2_2
          - US45102830_SLOT02_S06_CGH-v4_91_2_3
        - Calibration Arrays
    - Refferal-alaa
    - khalidEY09
    - KHALIDEY10
    - KHALIDEY12
    - KAHLID-6qdeletion
    - pgd1394
      - CGH 014693
    - pgd1420-e1
  - Gene List

Arrays | Calibration Arrays

ProbeName	ChrName	Start	Stop	FeatureNum	Description	Name of Gene	Accession	US4510283	US45102830_	US45102830_	U
A_14_P109...	chrX	26067408	26067468	11057	ref|Homo sa...	MAGEB18	ref|NM_173...	2.368626	0.65234894	2.3350103	-2.
A_14_P201...	chrX	26122425	26122482	22016	ref|Homo sa...	MAGEB6	ref|NM_173...	0.89985174	1.1820015	3.7326207	2.
A_16_P036...	chrX	26151881	26151941	10808	gb|Homo sa...	AL133110	gb|AL133110	1.0202327	-0.98420215	2.5954225	-0.
A_16_P036...	chrX	26488914	26488974	33820	gb|Homo sa...	AF164963	gb|AF164963	0.9563039	0.35953975	1.0396023	-1.
A_16_P214...	chrX	27104028	27104088	21881	gb|Homo sa...	BC024027	gb|BC024027	1.6056886	1.4977297	0.70647126	-1.
A_16_P416...	chrX	27193779	27193839	37693	gb|Homo sa...	BC024027	gb|BC024027	0.16113995	-0.99849224	0.3896438	-0.
A_14_P201...	chrX	27388507	27388567	35306	gb|Homo sa...	AK057429	gb|AK05742...	1.1239883	-0.010920941	-0.2952069	-0.
A_16_P036...	chrX	27561440	27561500	41220	gb|Homo sa...	AK057304	gb|AK057304	0.041997544	1.6548578	0.055827595	-2.
A_14_P200...	chrX	27750648	27750708	37566	ref|Homo sa...	MAGEB10	ref|NM_182...	1.012738	3.1881123	1.7331921	-2.
A_16_P416...	chrX	27907169	27907229	21835	ref|Homo sa...	WDR42B	ref|NM_001...	0.80412906	2.4862084	1.1399242	-1.
A_16_P214...	chrX	28430208	28430268	25523	gb|Homo sa...	BX648590	gb|BX648590	1.291234	1.5602603	1.0560217	-0.
A_16_P036...	chrX	28515930	28515990	43090	ref|Homo sa...	IL1RAPL1	ref|NM_014...	3.3102815	-0.2433619	1.3222464	0.
A_14_P135...	chrX	28717388	28717447	21747	ref|Homo sa...	IL1RAPL1	ref|NM_014...	2.2678893	0.9322275	1.8019301	-0.
A_14_P126...	chrX	29211026	29211086	11117	ref|Homo sa...	IL1RAPL1	ref|NM_014...	2.032412	1.2807453	1.2106463	0.
A_16_P036...	chrX	29327316	29327376	31310	ref|Homo sa...	IL1RAPL1	ref|NM_014...	1.1528828	0.5191079	0.6302721	-0.
A_16_P214...	chrX	29400517	29400577	21148	ref|Homo sa...	IL1RAPL1	ref|NM_014...	0.6296651	1.0123078	0.3404749	-1.
A_16_P036...	chrX	29845568	29845628	9773	ref|Homo sa...	IL1RAPL1	ref|NM_014...	-0.2529254	0.16069466	-1.7902321	-2.
A_16_P036...	chrX	29869724	29869784	20452	ref|Homo sa...	IL1RAPL1	ref|NM_014...	0.59853745	0.31687143	0.15788239	-0.

CGH 019478 | CGH 019479 | Selected Arrays

ursor set to X:25874970 | C | F | oncogenes | hg18 | log2 ratio | Selected Row = 338 | 1770 x 12

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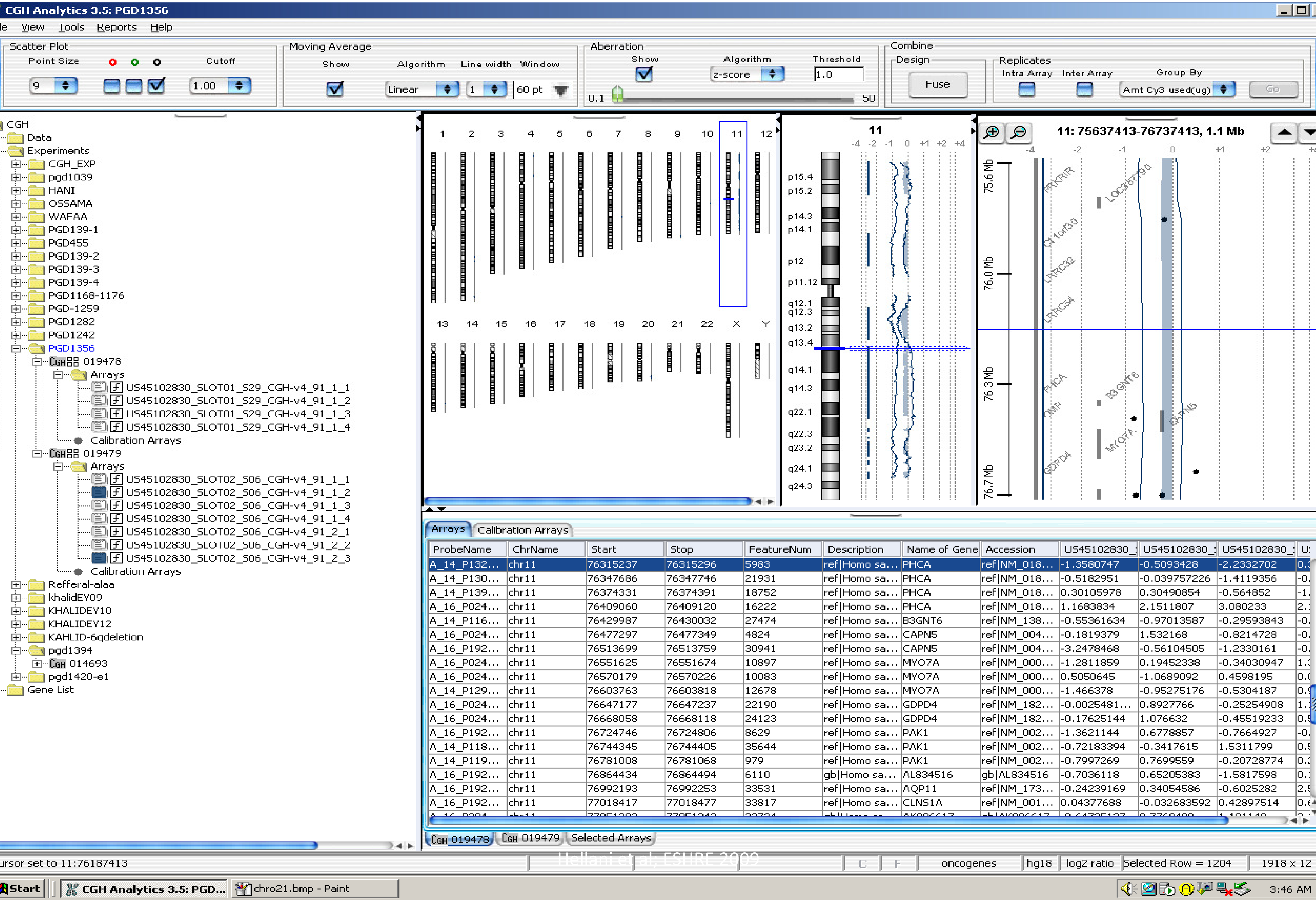
Start | CGH Analytics 3.5: PGD... | chro19.bmp - Paint | 3:42 AM



Scatter Plot: Point Size 9; Cutoff 1.00

Moving Average: Show ☑; Algorithm Linear; Line width 1; Window 60 pt

Aberration: Show ☑; Algorithm z-score; Threshold 1.0; 0.1 – 50

Combine: Design; Replicates: Intra Array ☐; Inter Array ☐; Group By Amt Cy3 used(ug)

11: 75637413-76737413, 1.1 Mb

ProbeName	ChrName	Start	Stop	FeatureNum	Description	Name of Gene	Accession	US45102830_	US45102830_	US45102830_
A_14_P132...	chr11	76315237	76315296	5983	ref|Homo sa...	PHCA	ref|NM_018...	-1.3580747	-0.5093428	-2.2332702
A_14_P130...	chr11	76347686	76347746	21931	ref|Homo sa...	PHCA	ref|NM_018...	-0.5182951	-0.039757226	-1.4119356
A_14_P139...	chr11	76374331	76374391	18752	ref|Homo sa...	PHCA	ref|NM_018...	0.30105978	0.30490854	-0.564852
A_16_P024...	chr11	76409060	76409120	16222	ref|Homo sa...	PHCA	ref|NM_018...	1.1683834	2.1511807	3.080233
A_14_P116...	chr11	76429987	76430032	27474	ref|Homo sa...	B3GNT6	ref|NM_138...	-0.55361634	-0.97013587	-0.29593843
A_16_P024...	chr11	76477297	76477349	4824	ref|Homo sa...	CAPN5	ref|NM_004...	-0.1819379	1.532168	-0.8214728
A_16_P192...	chr11	76513699	76513759	30941	ref|Homo sa...	CAPN5	ref|NM_004...	-3.2478468	-0.56104505	-1.2330161
A_16_P024...	chr11	76551625	76551674	10897	ref|Homo sa...	MYO7A	ref|NM_000...	-1.2811859	0.19452338	-0.34030947
A_16_P024...	chr11	76570179	76570226	10083	ref|Homo sa...	MYO7A	ref|NM_000...	0.5050645	-1.0689092	0.4598195
A_14_P129...	chr11	76603763	76603818	12678	ref|Homo sa...	MYO7A	ref|NM_000...	-1.466378	-0.95275176	-0.5304187
A_16_P024...	chr11	76647177	76647237	22190	ref|Homo sa...	GDPD4	ref|NM_182...	-0.0025481...	0.8927766	-0.25254908
A_16_P024...	chr11	76668058	76668118	24123	ref|Homo sa...	GDPD4	ref|NM_182...	-0.17625144	1.076632	-0.45519233
A_16_P192...	chr11	76724746	76724806	8629	ref|Homo sa...	PAK1	ref|NM_002...	-1.3621144	0.6778857	-0.7664927
A_14_P118...	chr11	76744345	76744405	35644	ref|Homo sa...	PAK1	ref|NM_002...	-0.72183394	-0.3417615	1.5311799
A_14_P119...	chr11	76781008	76781068	979	ref|Homo sa...	PAK1	ref|NM_002...	-0.7997269	0.7699559	-0.20728774
A_16_P192...	chr11	76864434	76864494	6110	gb|Homo sa...	AL834516	gb|AL834516	-0.7036118	0.65205383	-1.5817598
A_16_P192...	chr11	76992193	76992253	33531	ref|Homo sa...	AQP11	ref|NM_173...	-0.24239169	0.34054586	-0.6025282
A_16_P192...	chr11	77018417	77018477	33817	ref|Homo sa...	CLNS1A	ref|NM_001...	0.04377688	-0.032683592	0.42897514

ursor set to 11:76187413 | C | F | oncogenes | hg18 | log2 ratio | Selected Row = 1204 | 1918 x 12

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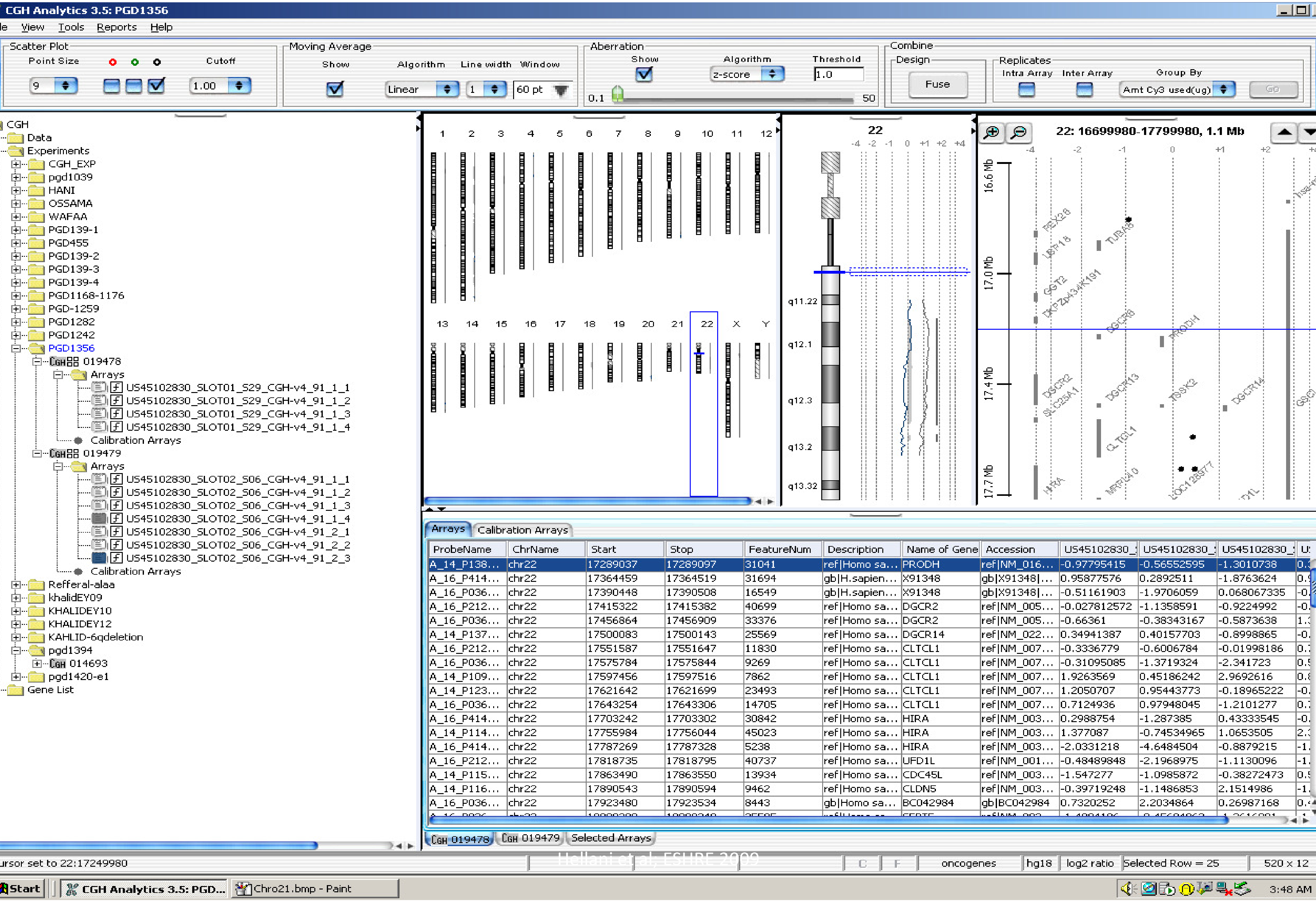

Scatter Plot: Point Size 9; ○ ○ ○ ☐ ☐ ☑; Cutoff 1.00

Moving Average: Show ☑; Algorithm Linear; Line width 1; Window 60 pt

Aberration: Show ☑; Algorithm z-score; Threshold 1.0; 0.1 — 50

Combine: Design; Replicates: Intra Array ☐; Inter Array ☐; Group By Amt Cy3 used(ug)

- CGH
  - Data
  - Experiments
    - CGH_EXP
    - pgd1039
    - HANI
    - OSSAMA
    - WAFAA
    - PGD139-1
    - PGD455
    - PGD139-2
    - PGD139-3
    - PGD139-4
    - PGD1168-1176
    - PGD-1259
    - PGD1282
    - PGD1242
    - PGD1356
      - CGH 019478
        - Arrays
          - US45102830_SLOT01_S29_CGH-v4_91_1_1
          - US45102830_SLOT01_S29_CGH-v4_91_1_2
          - US45102830_SLOT01_S29_CGH-v4_91_1_3
          - US45102830_SLOT01_S29_CGH-v4_91_1_4
        - Calibration Arrays
      - CGH 019479
        - Arrays
          - US45102830_SLOT02_S06_CGH-v4_91_1_1
          - US45102830_SLOT02_S06_CGH-v4_91_1_2
          - US45102830_SLOT02_S06_CGH-v4_91_1_3
          - US45102830_SLOT02_S06_CGH-v4_91_1_4
          - US45102830_SLOT02_S06_CGH-v4_91_2_1
          - US45102830_SLOT02_S06_CGH-v4_91_2_2
          - US45102830_SLOT02_S06_CGH-v4_91_2_3
        - Calibration Arrays
    - Refferal-alaa
    - khalidEY09
    - KHALIDEY10
    - KHALIDEY12
    - KAHLID-6qdeletion
    - pgd1394
      - CGH 014693
    - pgd1420-e1
  - Gene List

Arrays | Calibration Arrays

ProbeName	ChrName	Start	Stop	FeatureNum	Description	Name of Gene	Accession	US45102830_	US45102830_	US45102830_
A_14_P138...	chr22	17289037	17289097	31041	ref|Homo sa...	PRODH	ref|NM_016...	-0.97795415	-0.56552595	-1.3010738
A_16_P414...	chr22	17364459	17364519	31694	gb|H.sapien...	X91348	gb|X91348|...	0.95877576	0.2892511	-1.8763624
A_16_P036...	chr22	17390448	17390508	16549	gb|H.sapien...	X91348	gb|X91348|...	-0.51161903	-1.9706059	0.068067335
A_16_P212...	chr22	17415322	17415382	40699	ref|Homo sa...	DGCR2	ref|NM_005...	-0.027812572	-1.1358591	-0.9224992
A_16_P036...	chr22	17456864	17456909	33376	ref|Homo sa...	DGCR2	ref|NM_005...	-0.66361	-0.38343167	-0.5873638
A_14_P137...	chr22	17500083	17500143	25569	ref|Homo sa...	DGCR14	ref|NM_022...	0.34941387	0.40157703	-0.8998865
A_16_P212...	chr22	17551587	17551647	11830	ref|Homo sa...	CLTCL1	ref|NM_007...	-0.3336779	-0.6006784	-0.01998186
A_16_P036...	chr22	17575784	17575844	9269	ref|Homo sa...	CLTCL1	ref|NM_007...	-0.31095085	-1.3719324	-2.341723
A_14_P109...	chr22	17597456	17597516	7862	ref|Homo sa...	CLTCL1	ref|NM_007...	1.9263569	0.45186242	2.9692616
A_14_P123...	chr22	17621642	17621699	23493	ref|Homo sa...	CLTCL1	ref|NM_007...	1.2050707	0.95443773	-0.18965222
A_16_P036...	chr22	17643254	17643306	14705	ref|Homo sa...	CLTCL1	ref|NM_007...	0.7124936	0.97948045	-1.2101277
A_16_P414...	chr22	17703242	17703302	30842	ref|Homo sa...	HIRA	ref|NM_003...	0.2988754	-1.287385	0.43333545
A_14_P114...	chr22	17755984	17756044	45023	ref|Homo sa...	HIRA	ref|NM_003...	1.377087	-0.74534965	1.0653505
A_16_P414...	chr22	17787269	17787328	5238	ref|Homo sa...	HIRA	ref|NM_003...	-2.0331218	-4.6484504	-0.8879215
A_16_P212...	chr22	17818735	17818795	40737	ref|Homo sa...	UFD1L	ref|NM_001...	-0.48489848	-2.1968975	-1.1130096
A_14_P115...	chr22	17863490	17863550	13934	ref|Homo sa...	CDC45L	ref|NM_003...	-1.547277	-1.0985872	-0.38272473
A_14_P116...	chr22	17890543	17890594	9462	ref|Homo sa...	CLDN5	ref|NM_003...	-0.39719248	-1.1486853	2.1514986
A_16_P036...	chr22	17923480	17923534	8443	gb|Homo sa...	BC042984	gb|BC042984	0.7320252	2.2034864	0.26987168

CGH 019478 | CGH 019479 | Selected Arrays

ursor set to 22:17249980 | C | F | oncogenes | hg18 | log2 ratio | Selected Row = 25 | 520 x 12

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Agilent slides used

8x15 k format: Customized array for our laboratory
4x4 k format: Generic and commercially available

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Conclusion

In conclusion, aCGH can be used routinely in PGD with a potential of high successful pregnancy rate and had superior efficiency over the seven probes FISH panel. Agilent technology made it more convenient with the possibility of screening more than one embryo using one slide.

More cases should be performed in order to define more Accurately the importance of A-CGH in IVF recurrent Failures And recurrent miscarriages

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