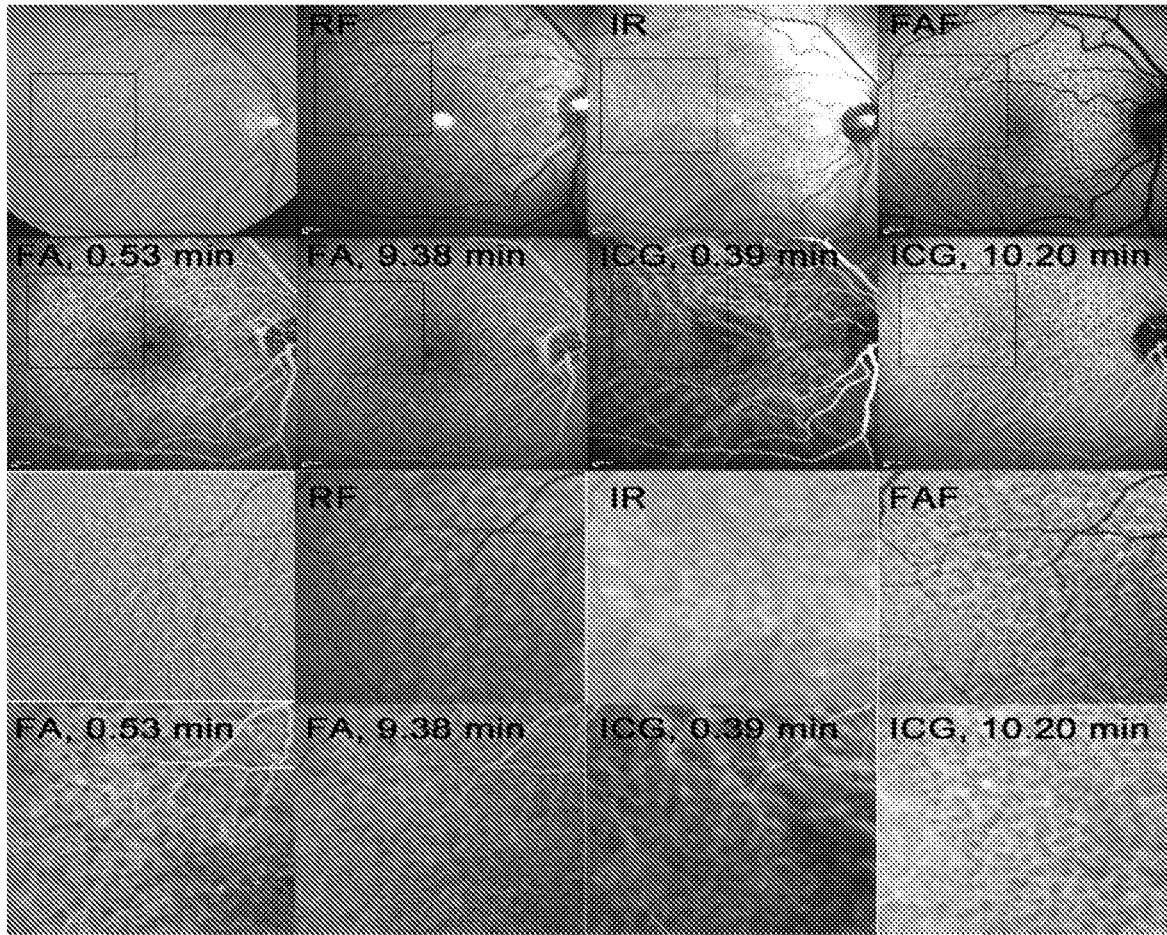


**FIG. 1**

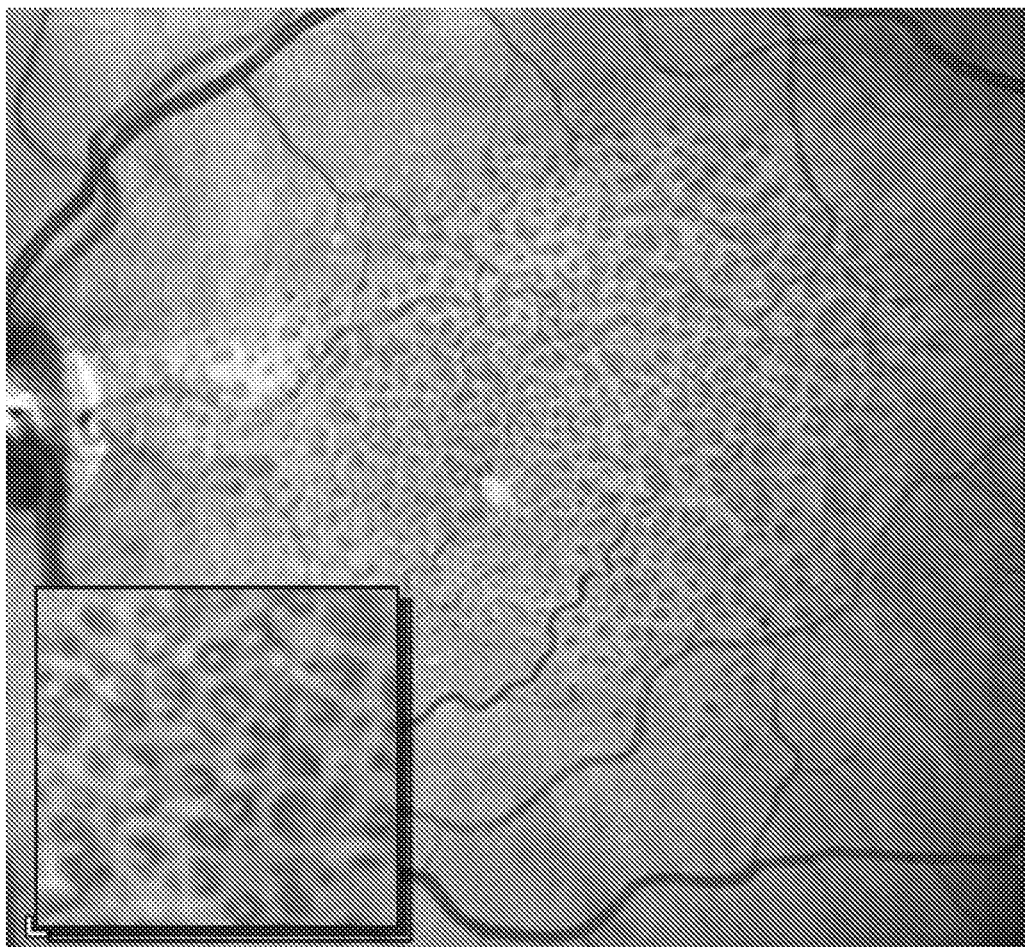


FIG.2

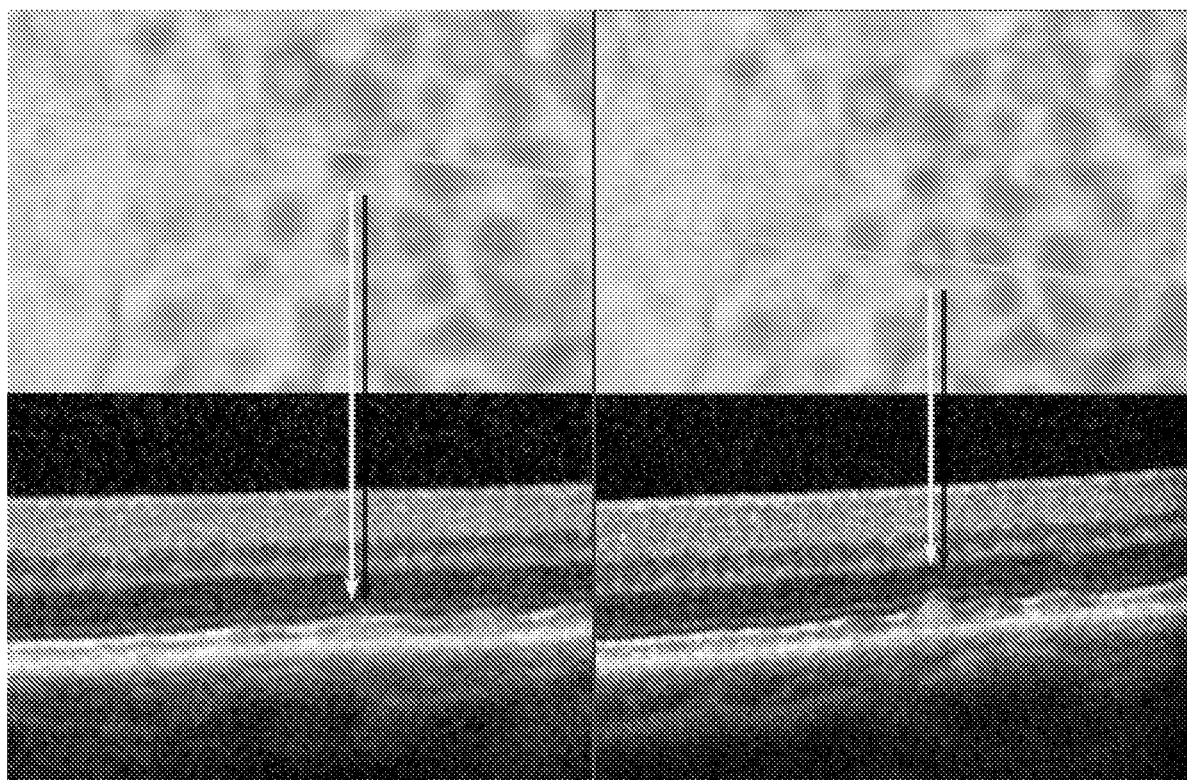


FIG. 3

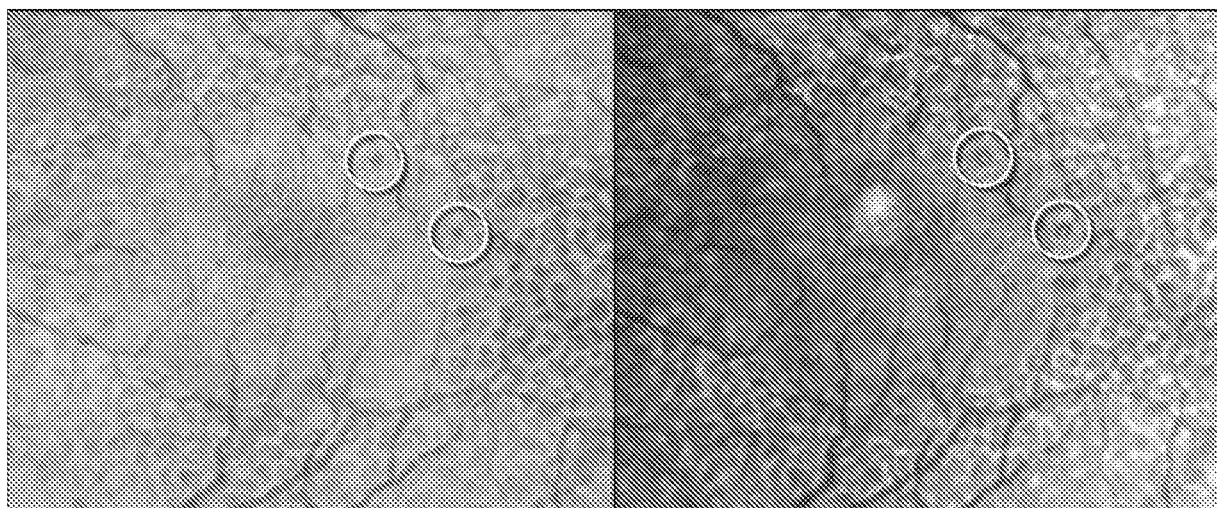


FIG. 4

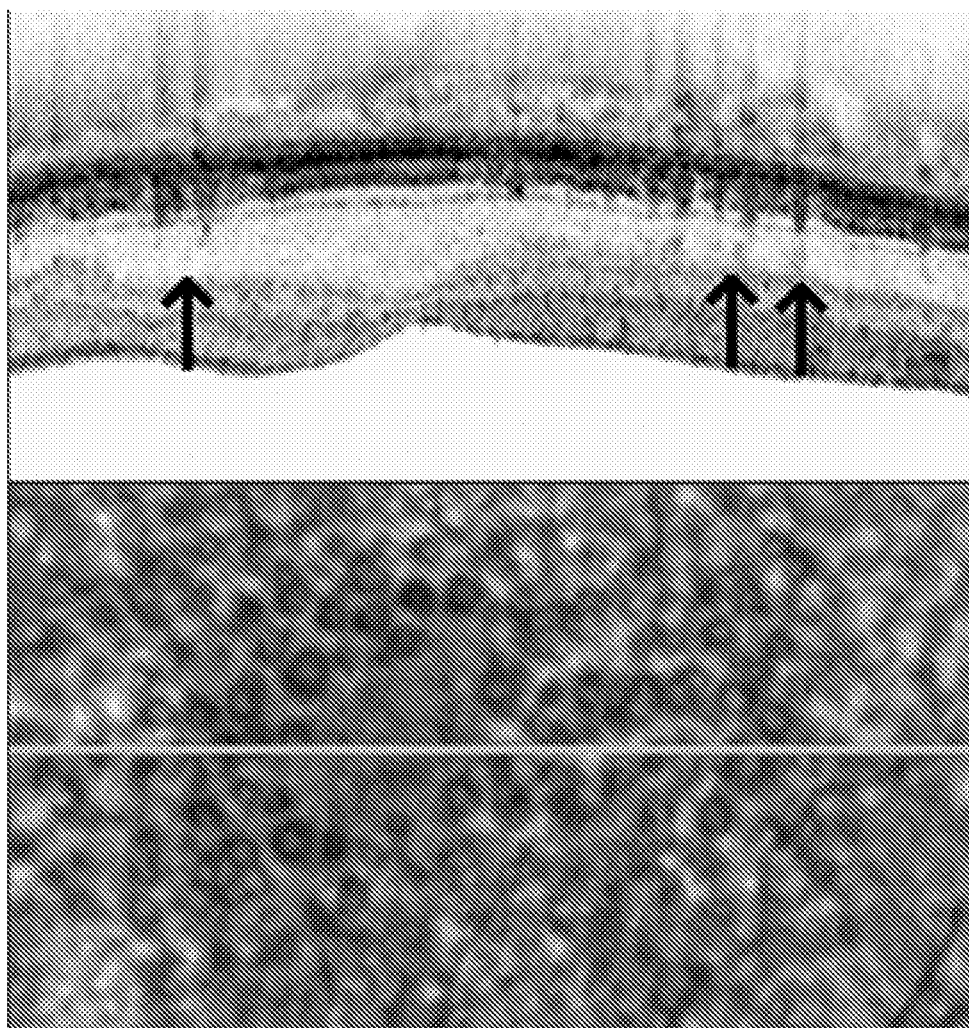
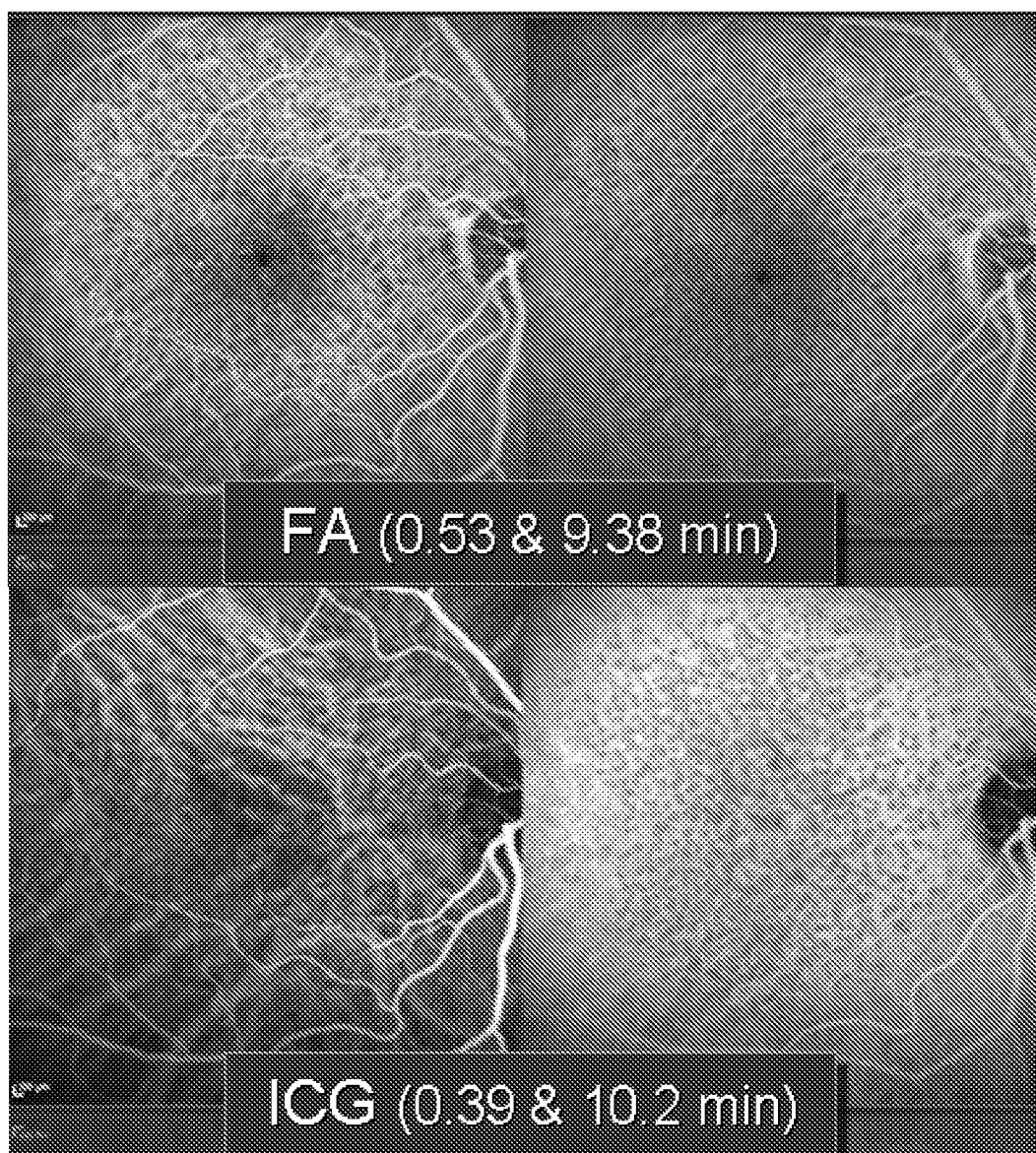


FIG. 5

**FIG. 6**

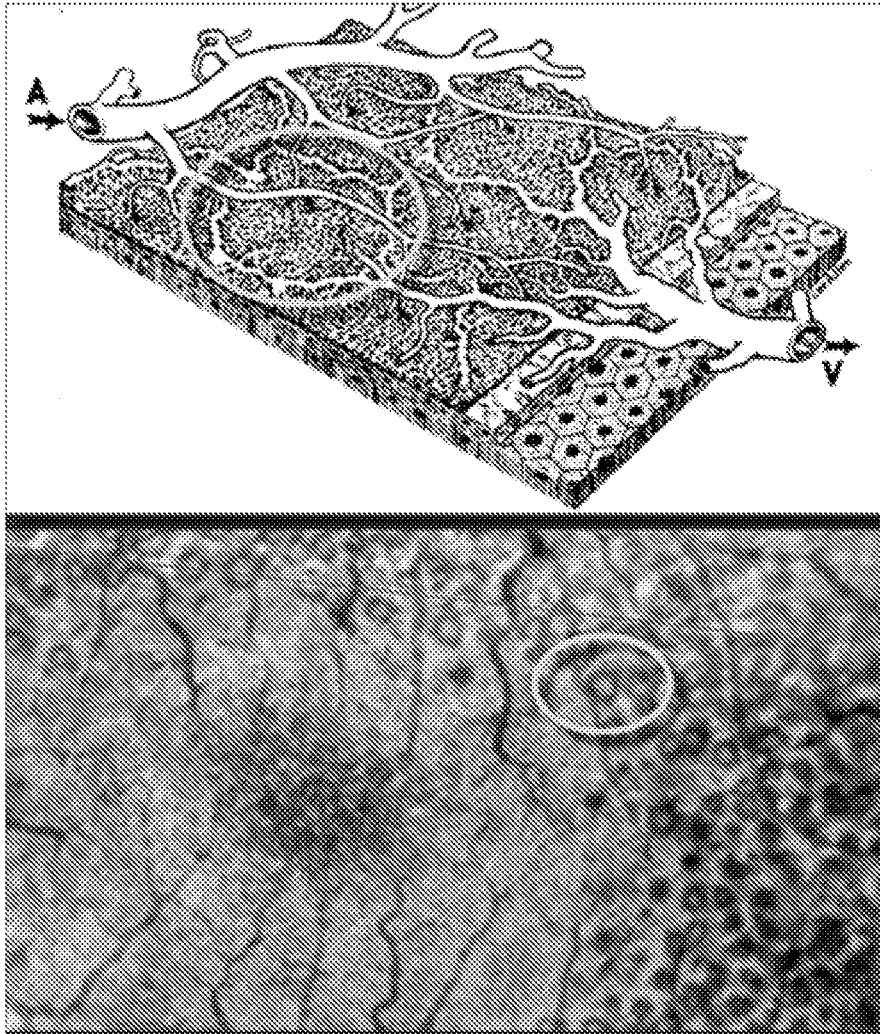


FIG. 7

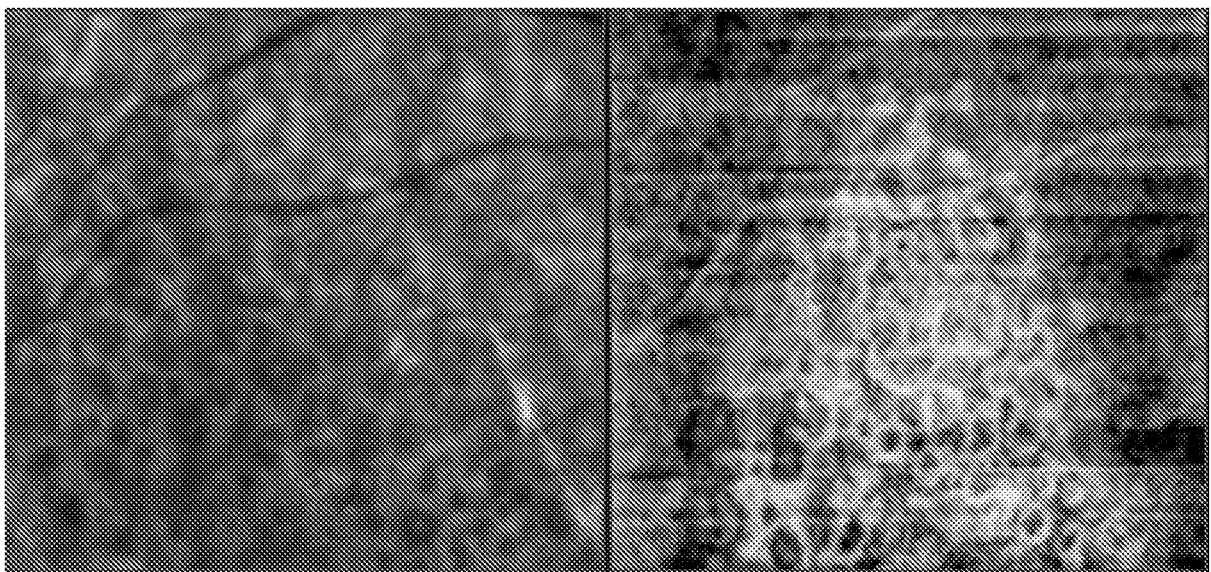


FIG. 8

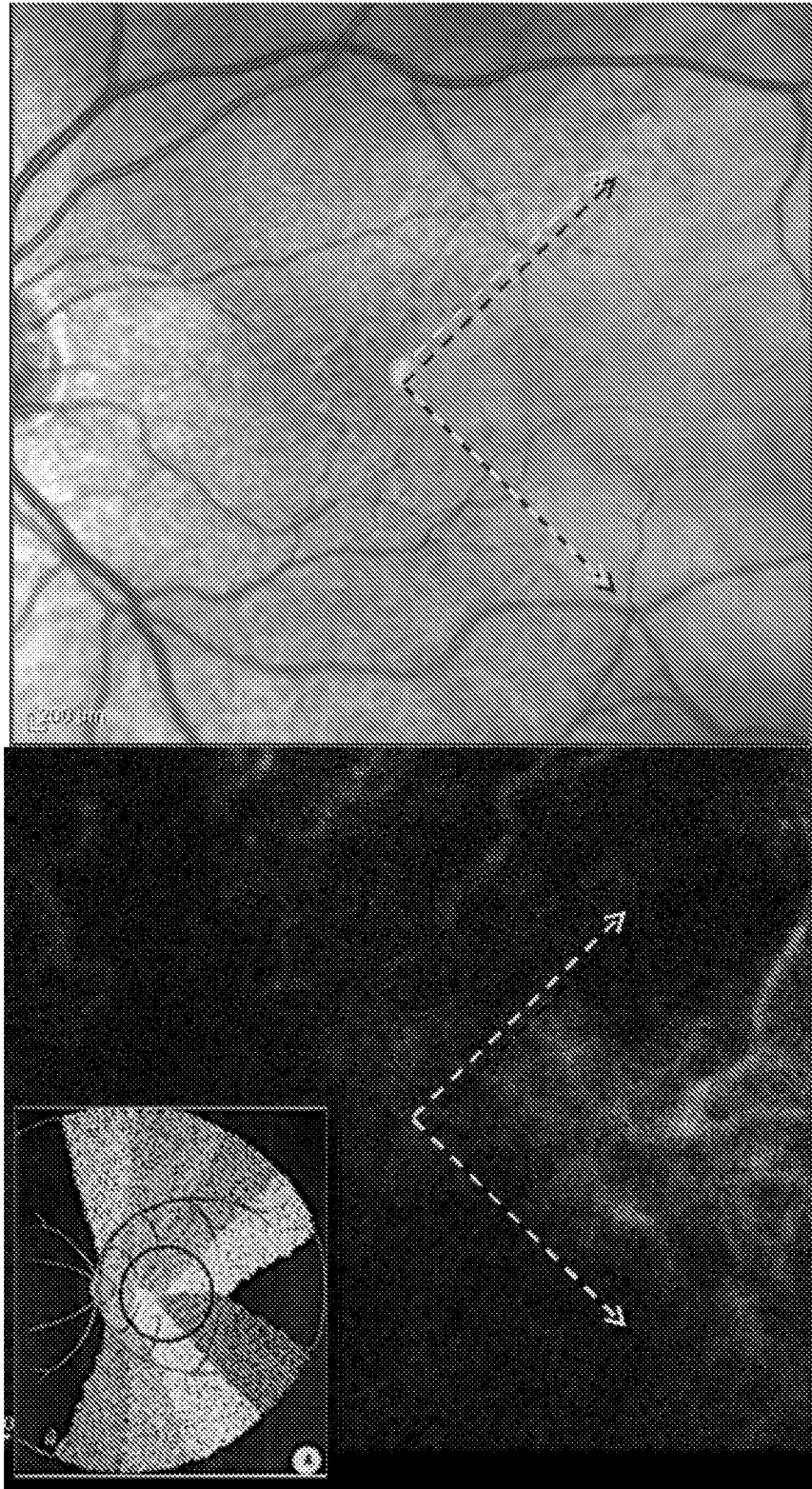


FIG. 9

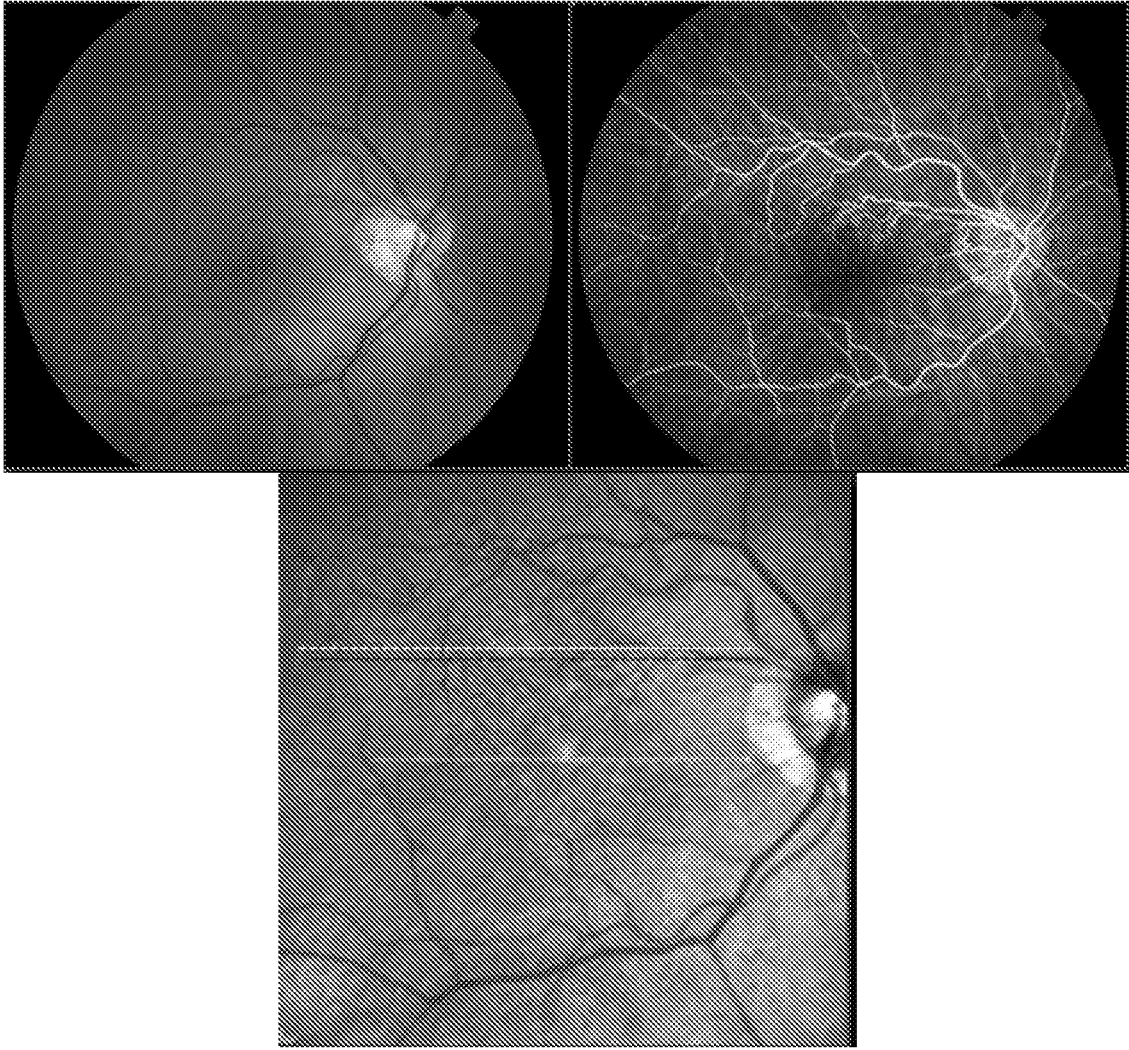


FIG. 10

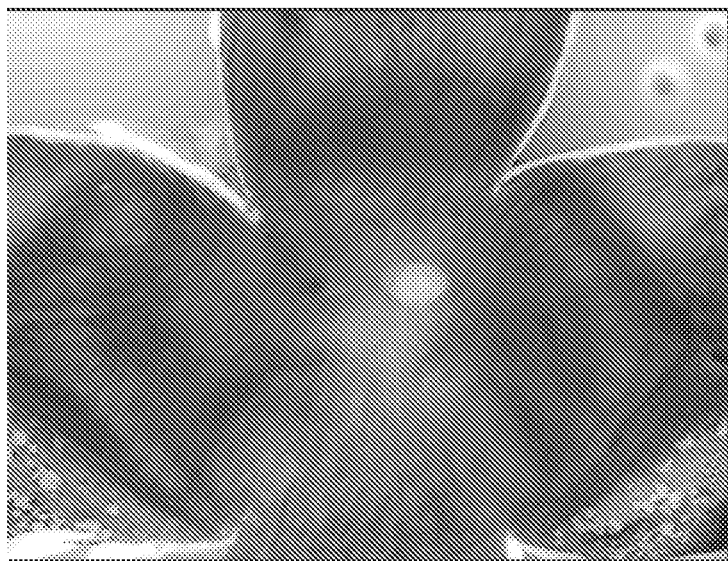


FIG. 11

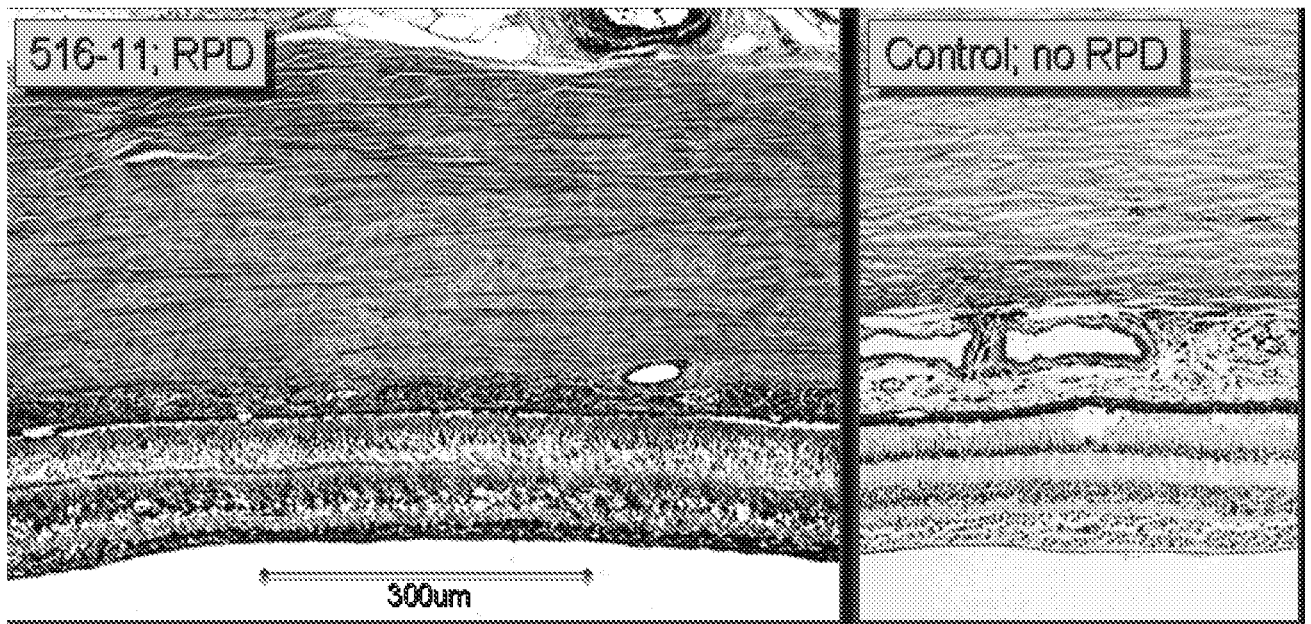


FIG. 12

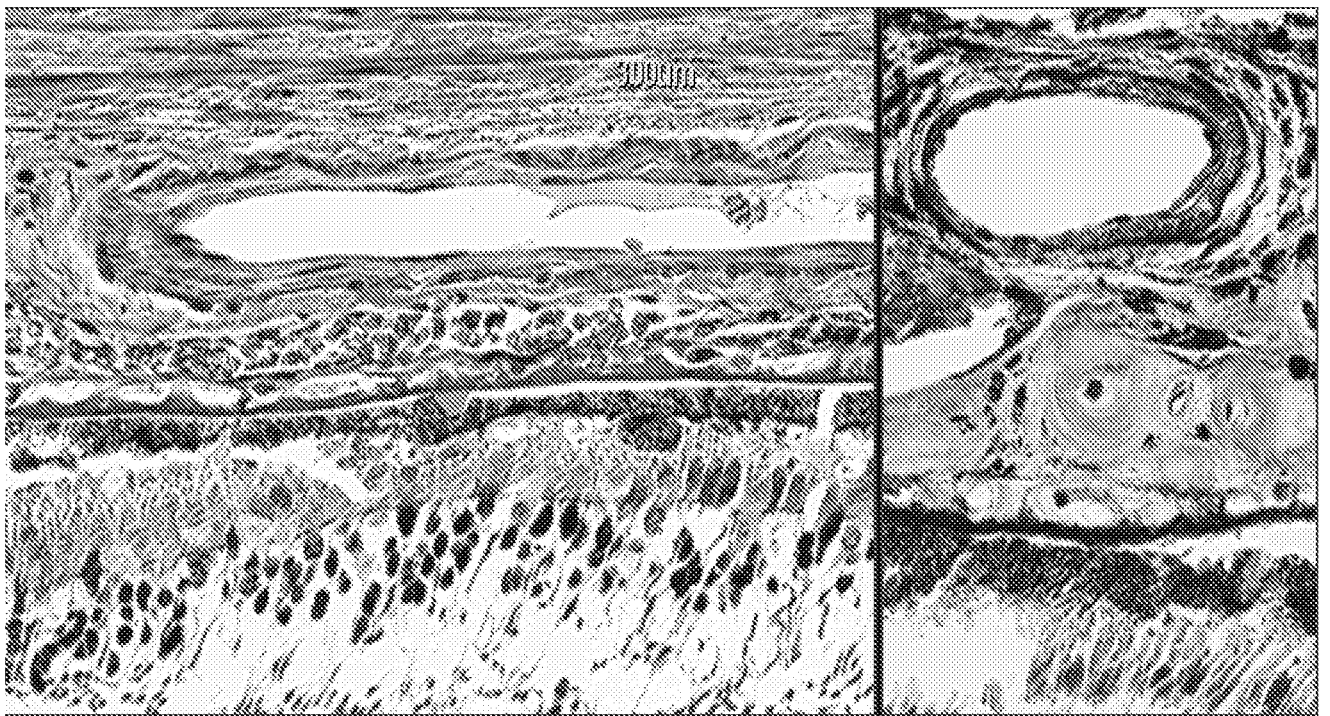
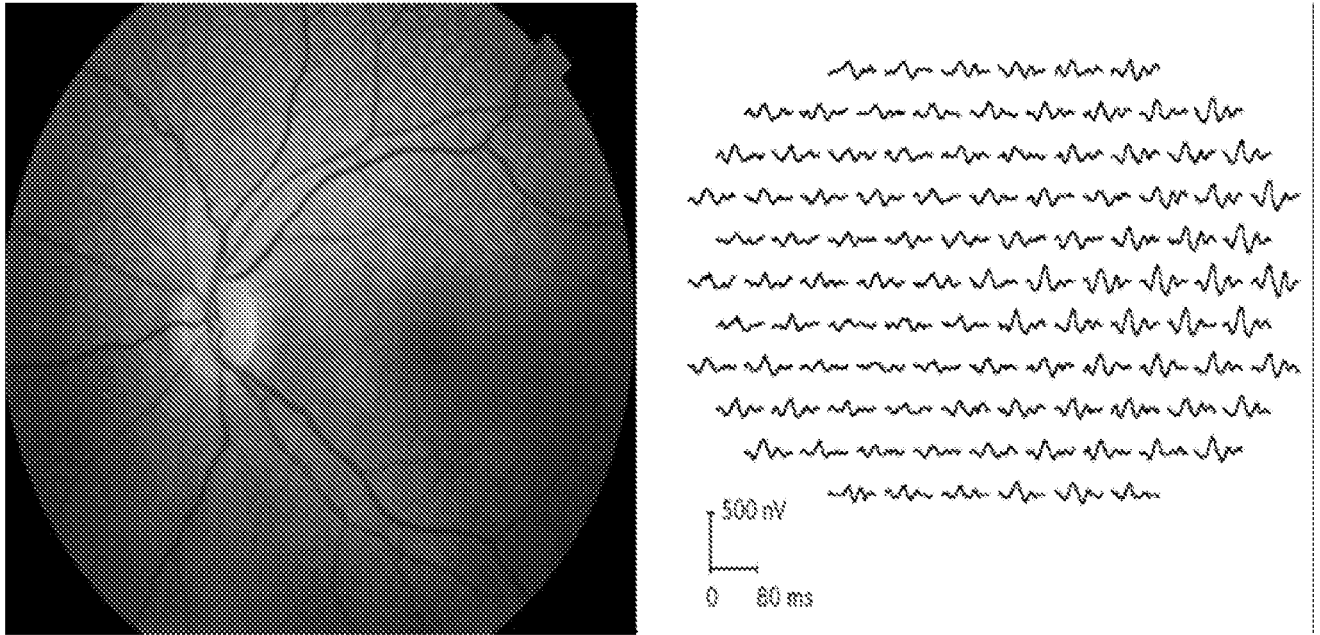
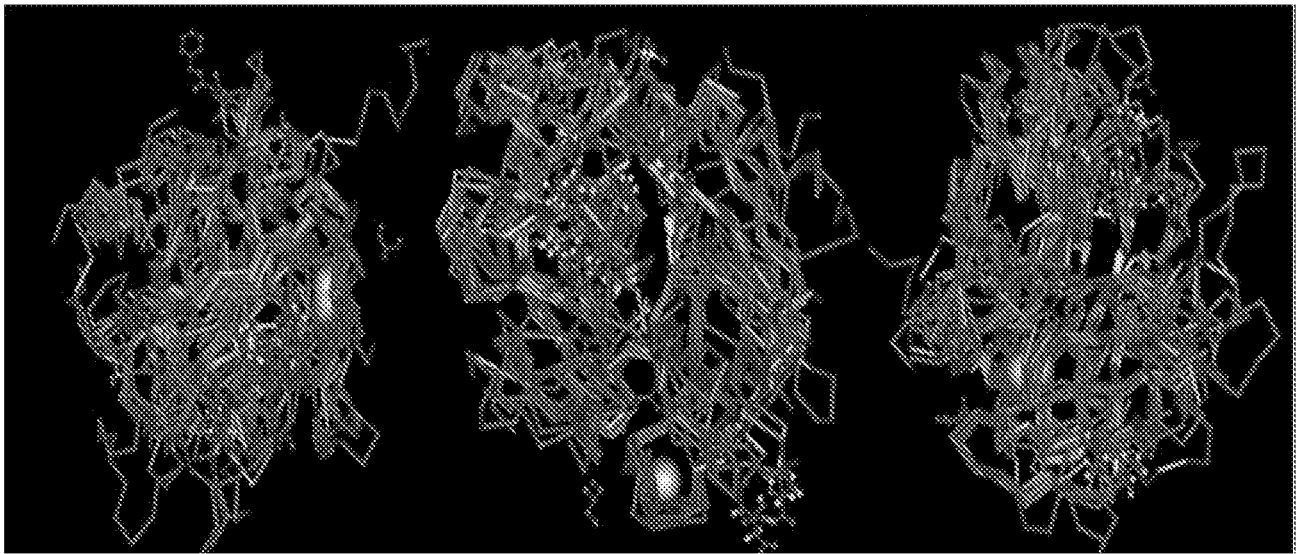


FIG. 13

**FIG. 14****FIG. 15**

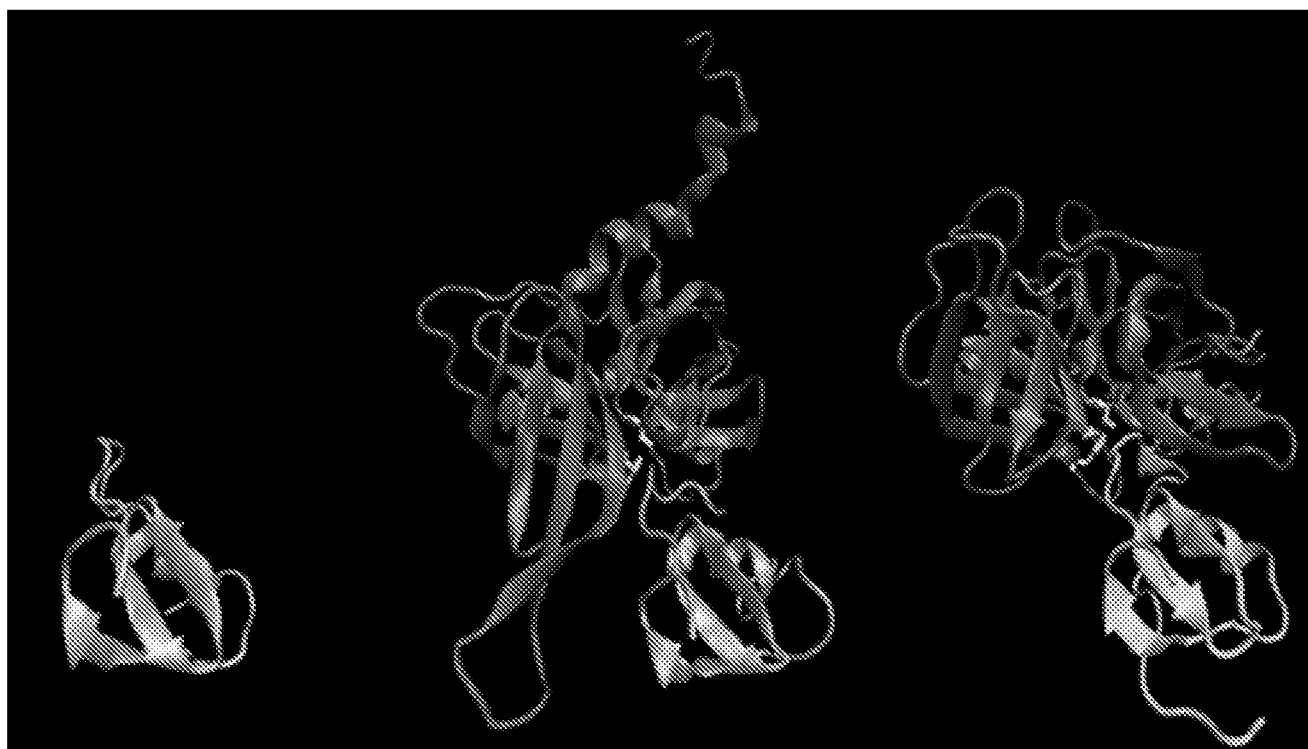


FIG. 16

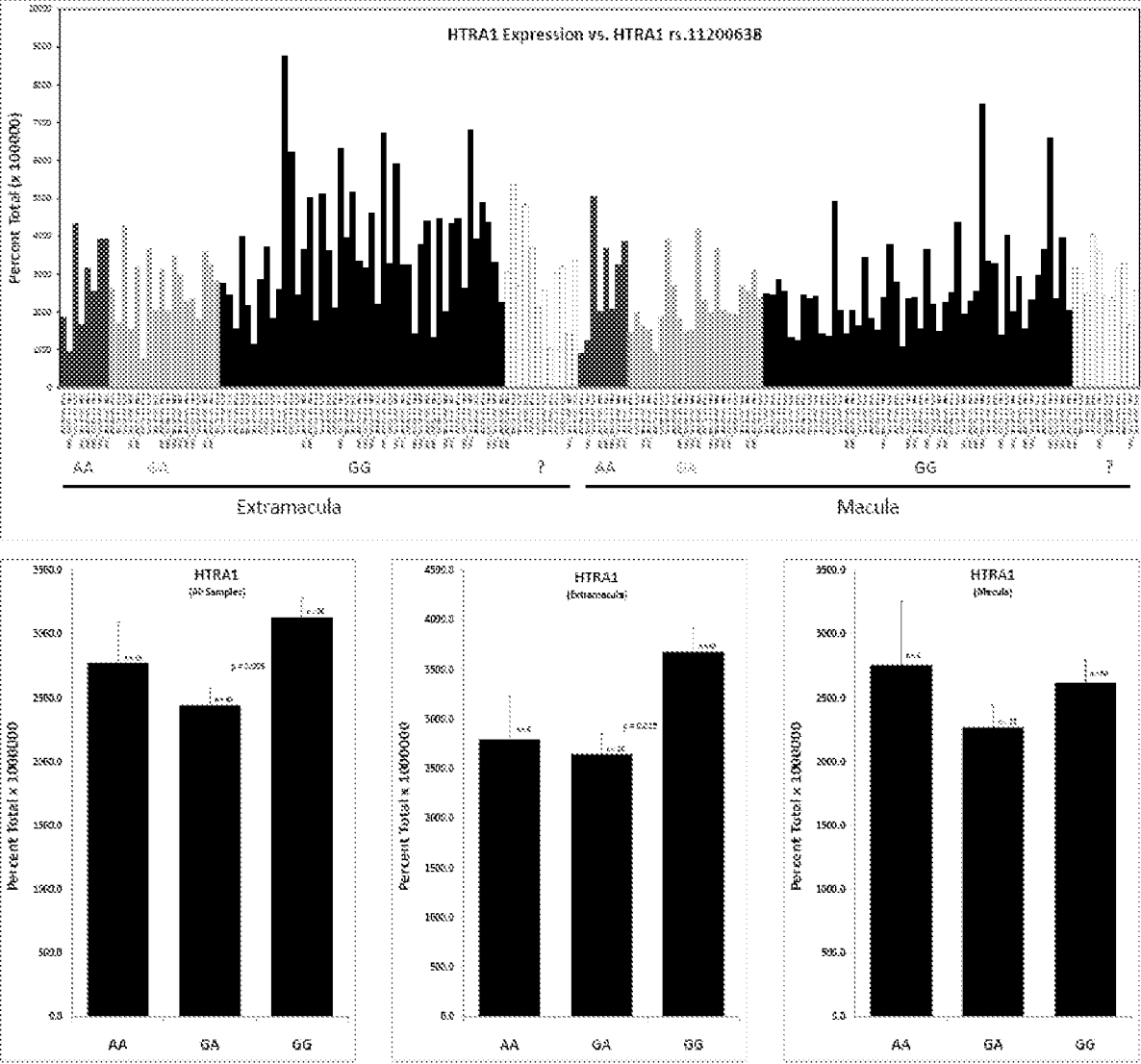


FIG. 17

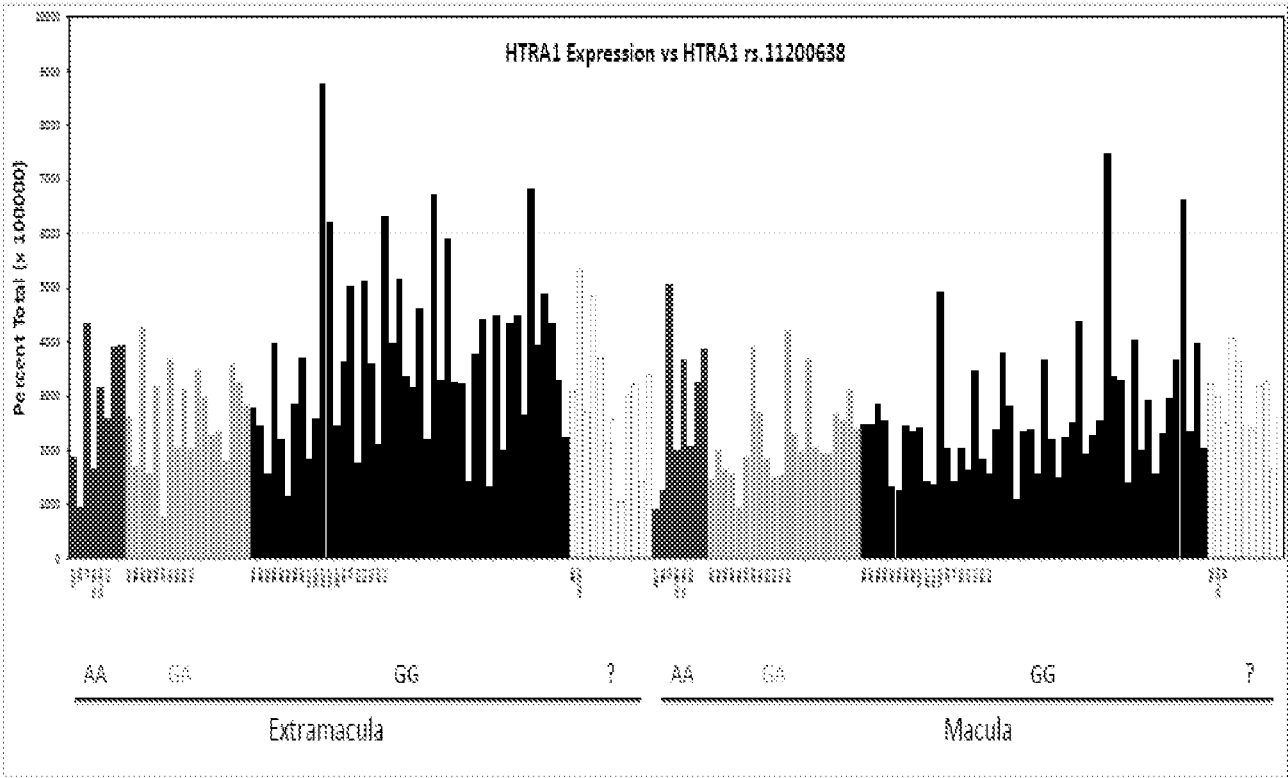


FIG. 18

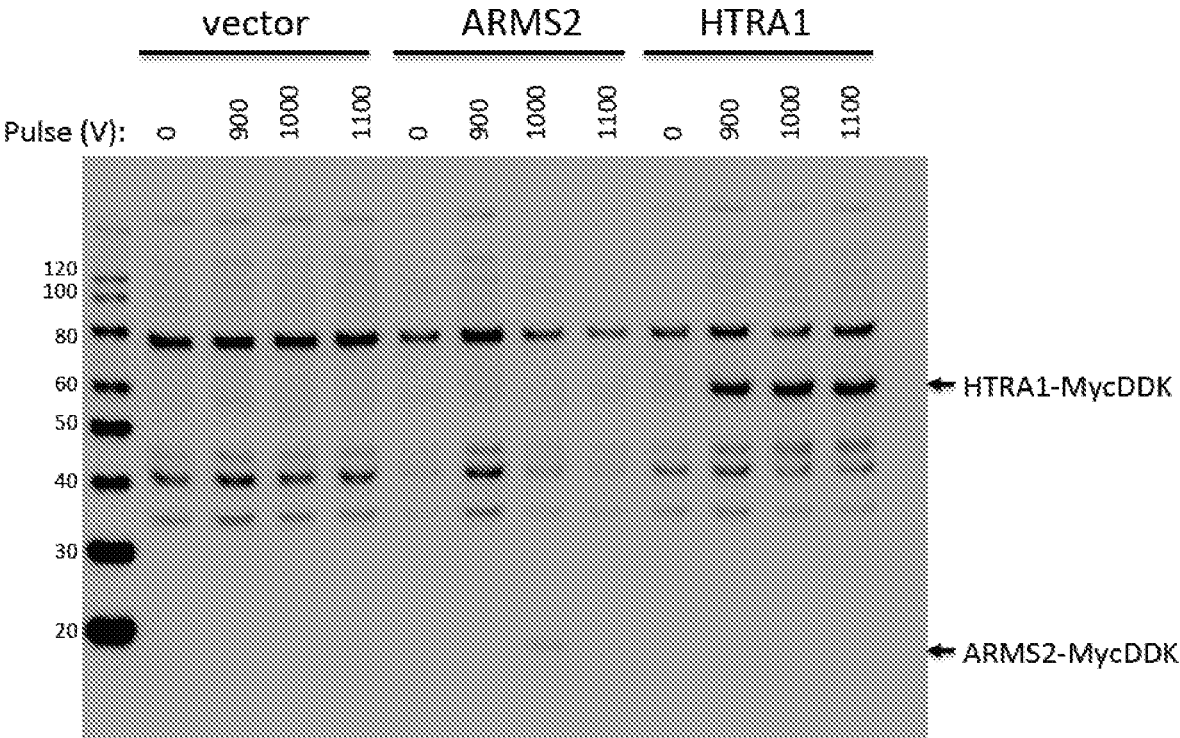


FIG. 19

Western blots showing reactivity of HTRA1 subdomain specific antibodies

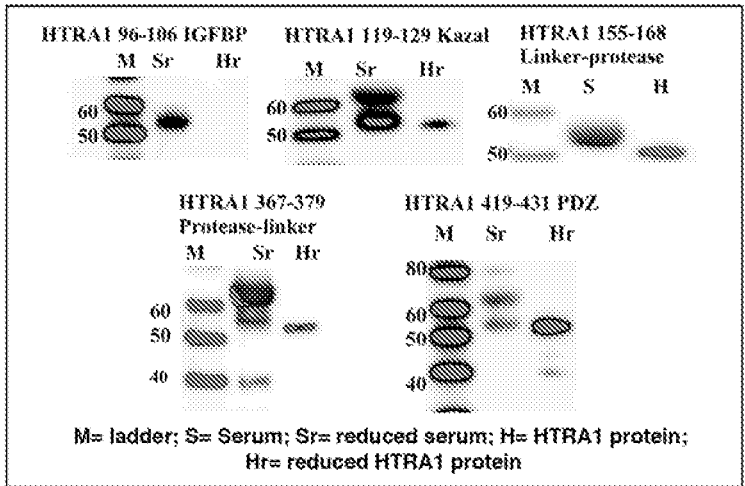


FIG. 20

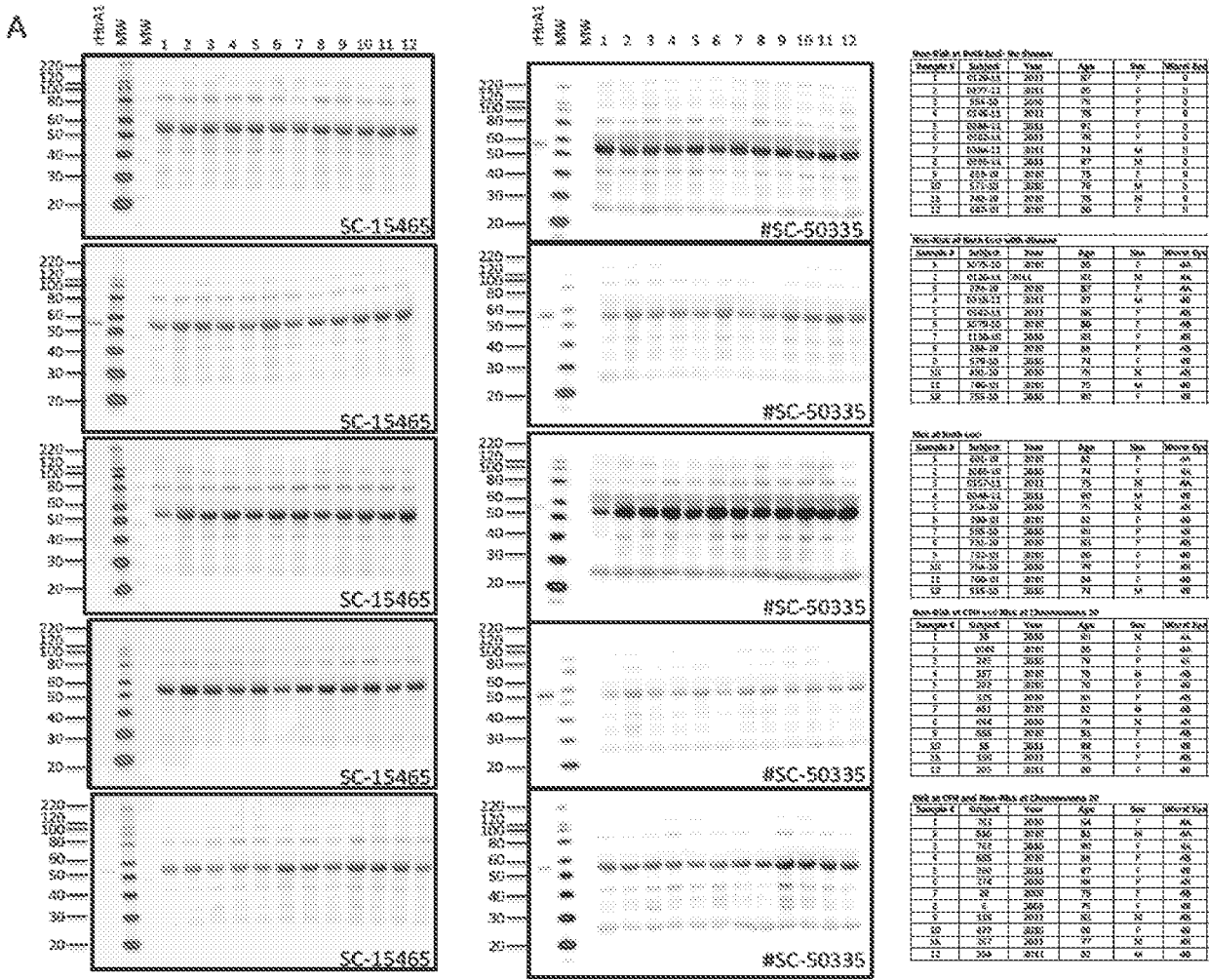


FIG. 21 A

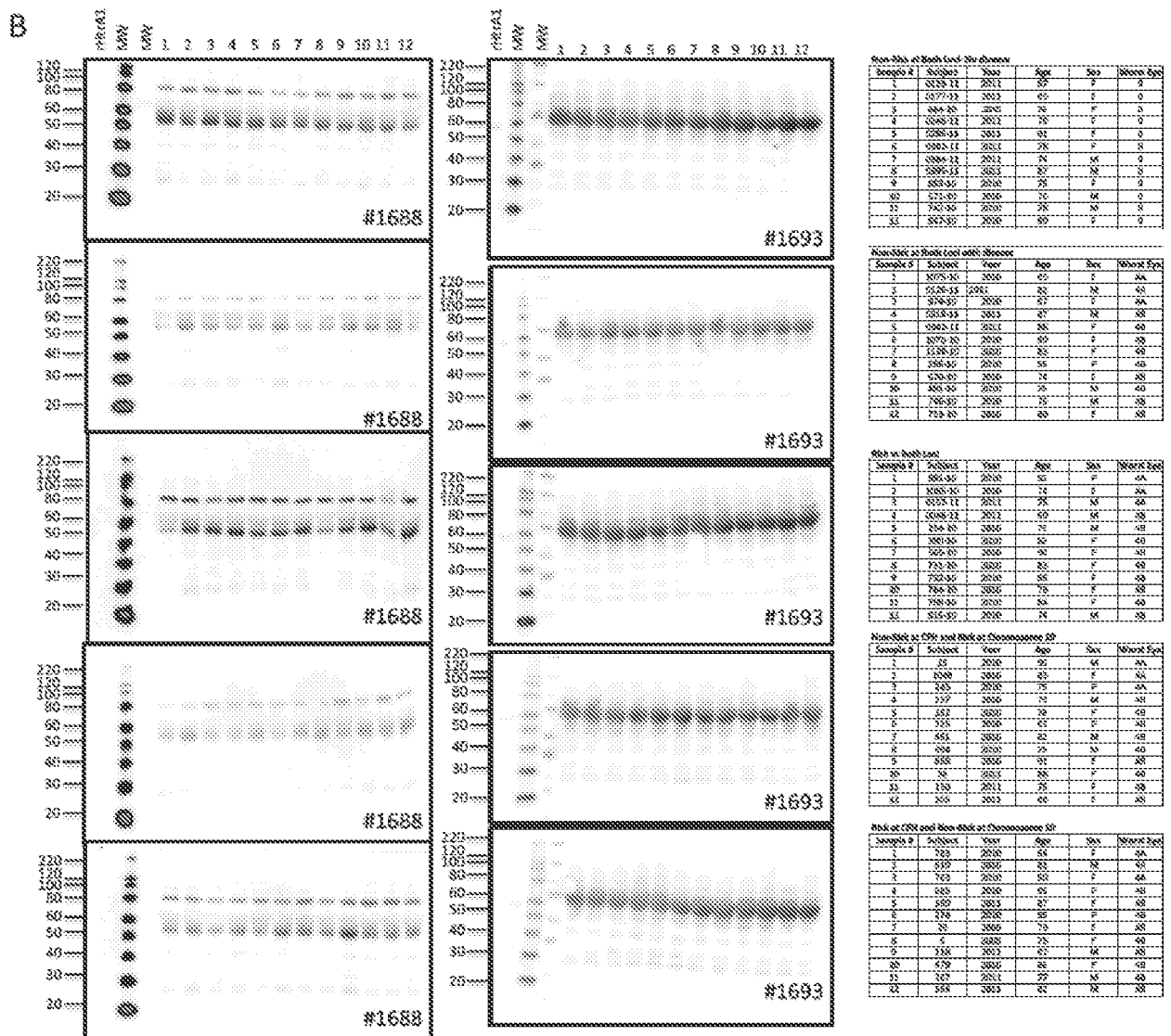


FIG. 21 B

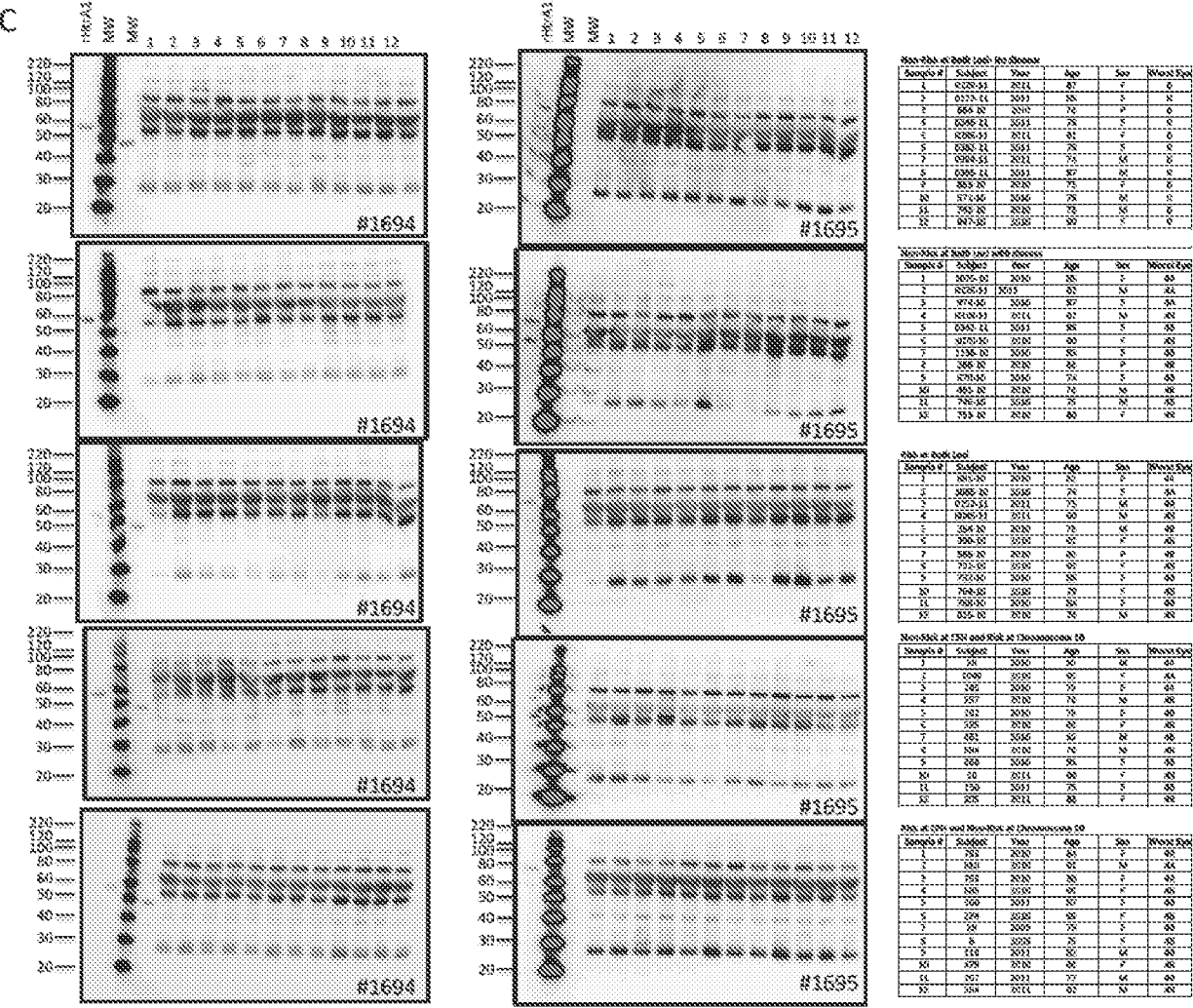


FIG. 21 C

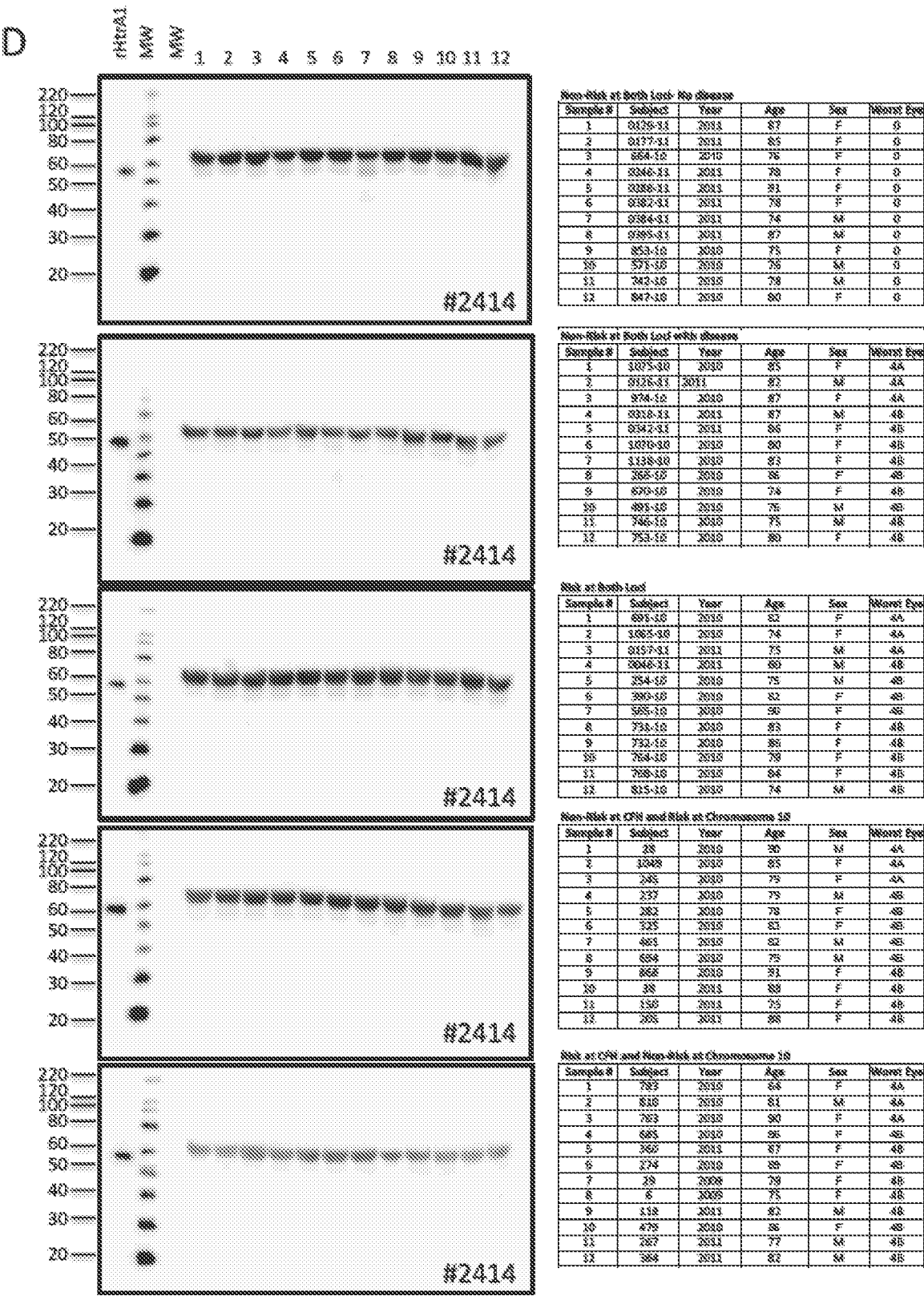
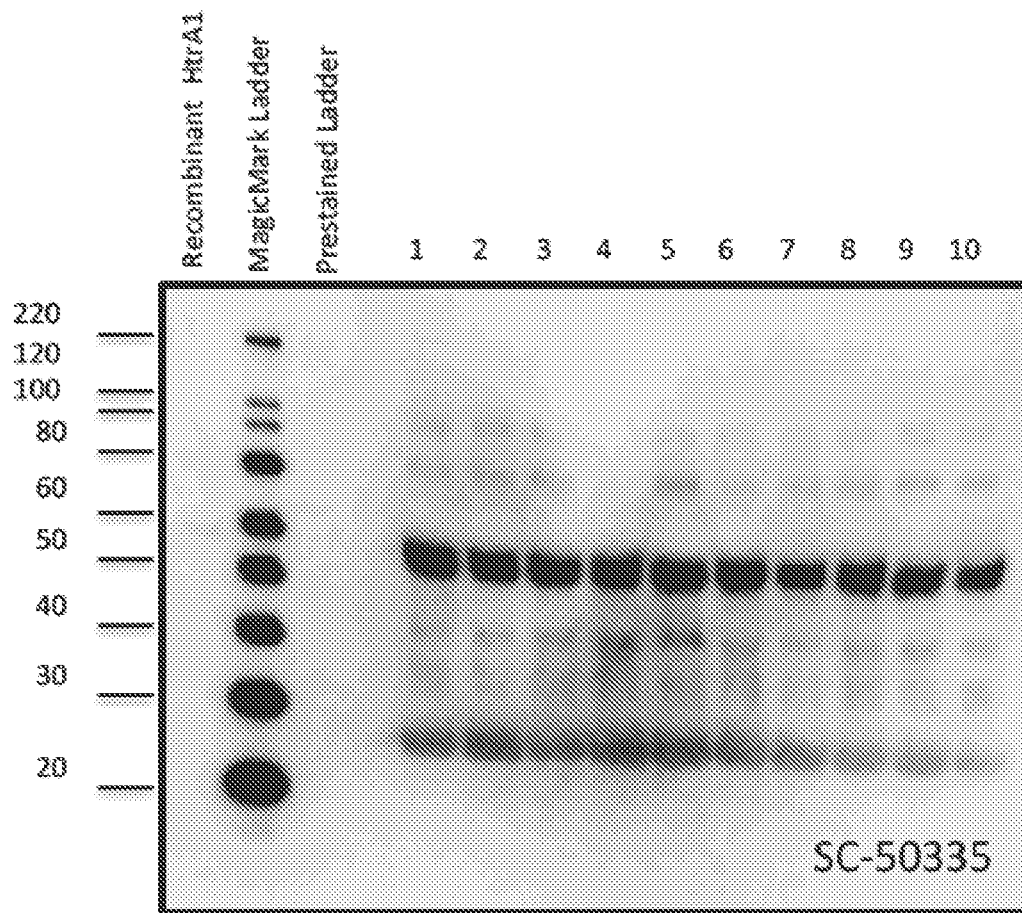


FIG. 21 D



Lane #	Sample #	Subject	Year	Age	Sex	Worst Eye	Genotype at chromo 1 and 10
1	A 11	742-10	2010	78	M	O	no risk
2	A 12	847-10	2010	80	F	O	no risk
3	B 23	746-10	2010	75	M	4B	no risk
4	B 24	753-10	2010	80	F	4B	no risk
5	C 35	768-10	2010	84	F	4B	risk at both loci
6	C 36	815-10	2010	74	M	4B	risk at both loci
7	D 47	150	2011	75	F	4B	risk at 10 only
8	D 48	205	2011	88	F	4B	risk at 10 only
9	E 59	267	2011	77	M	4B	risk at 1 only
10	E 60	364	2011	82	M	4B	risk at 1 only

FIG. 22

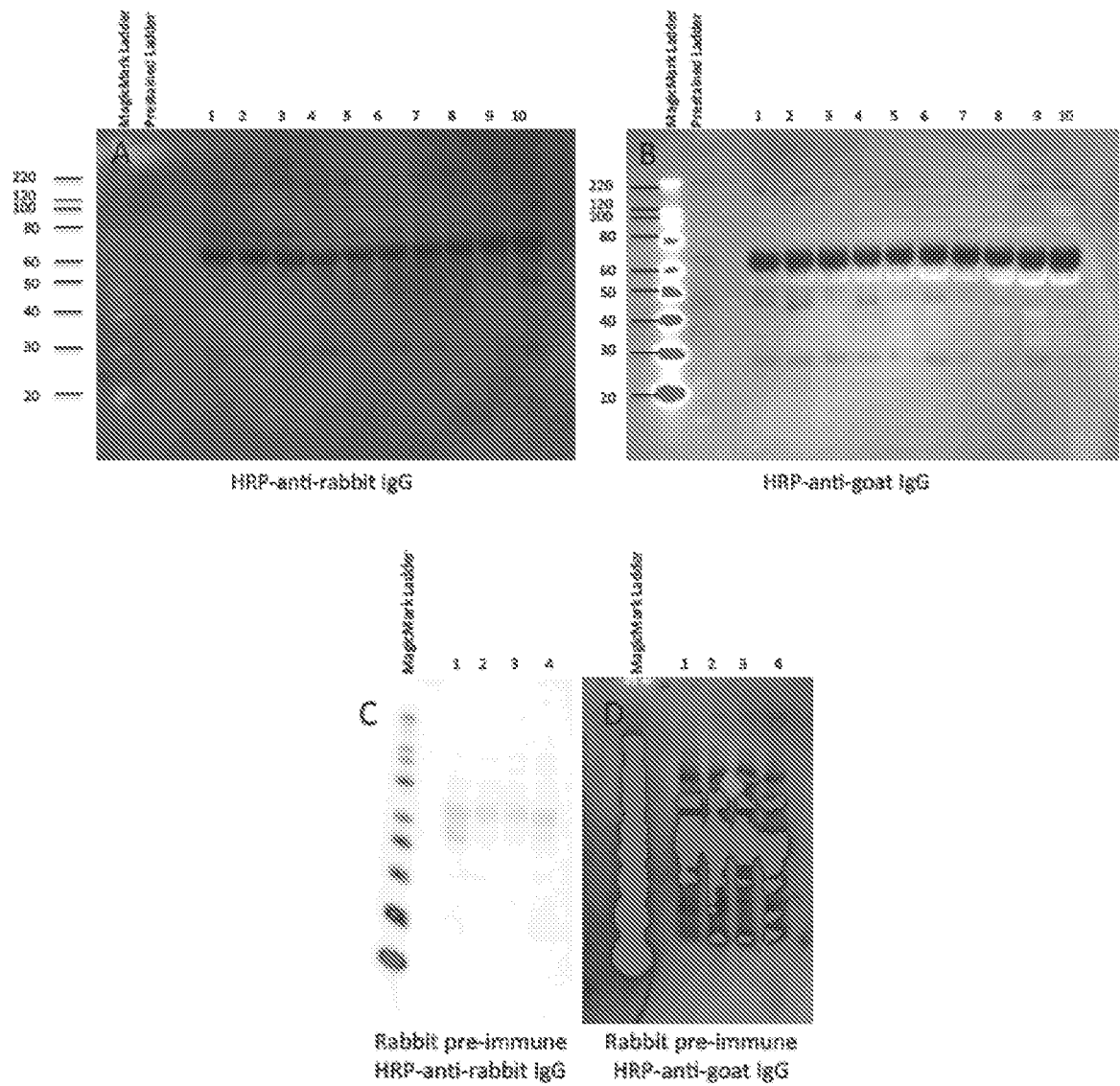


FIG. 23

Retina/RPE Extracts

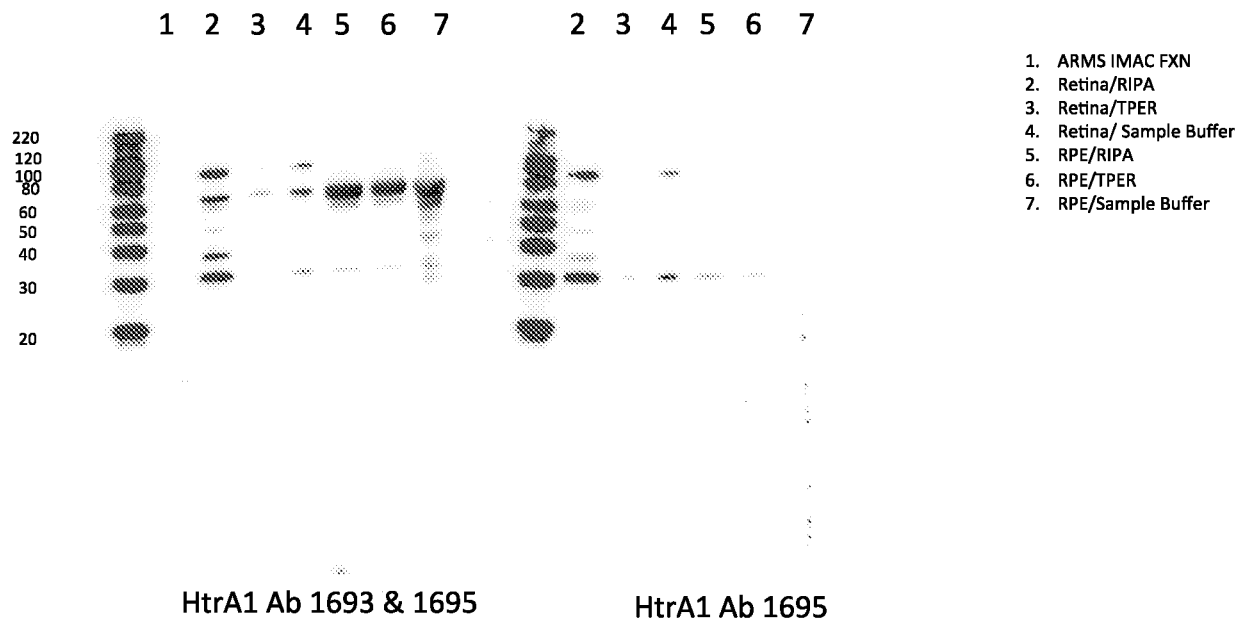


FIG. 24A

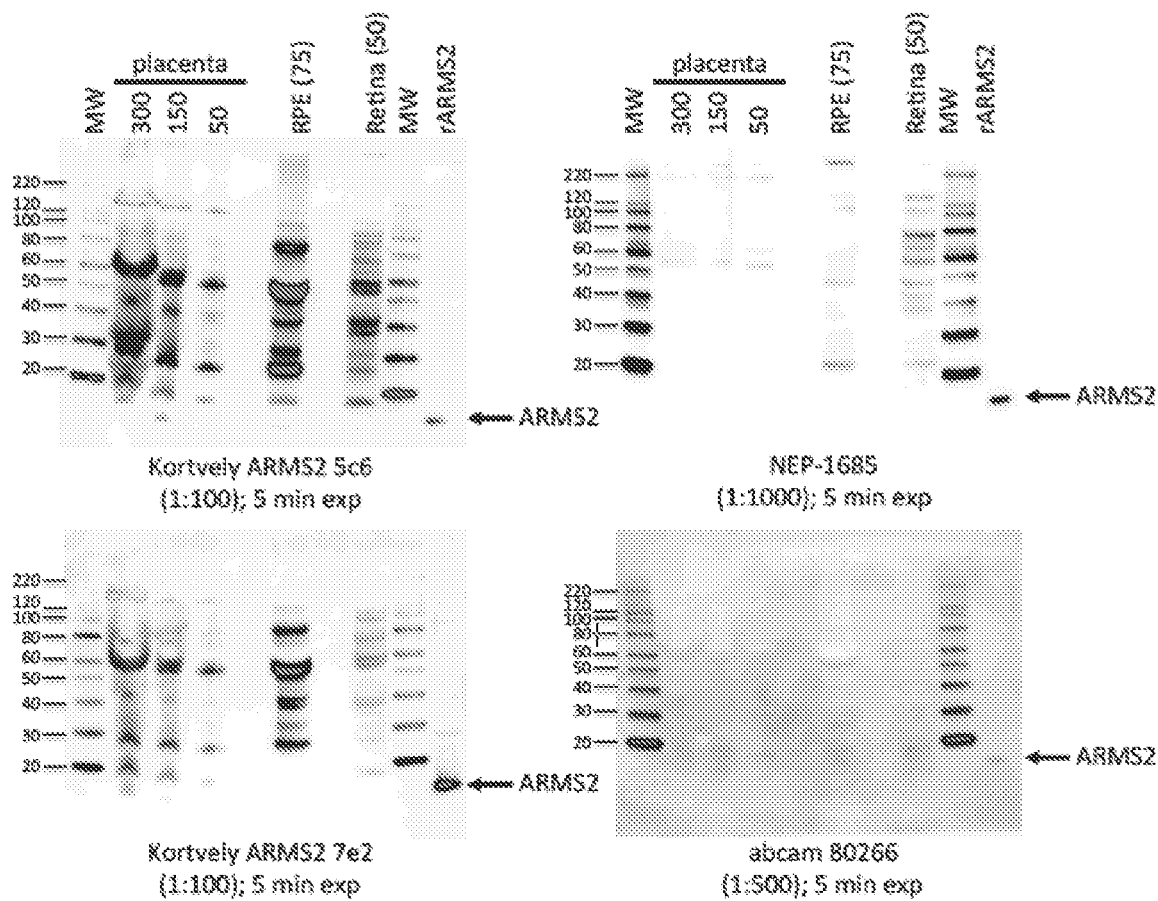
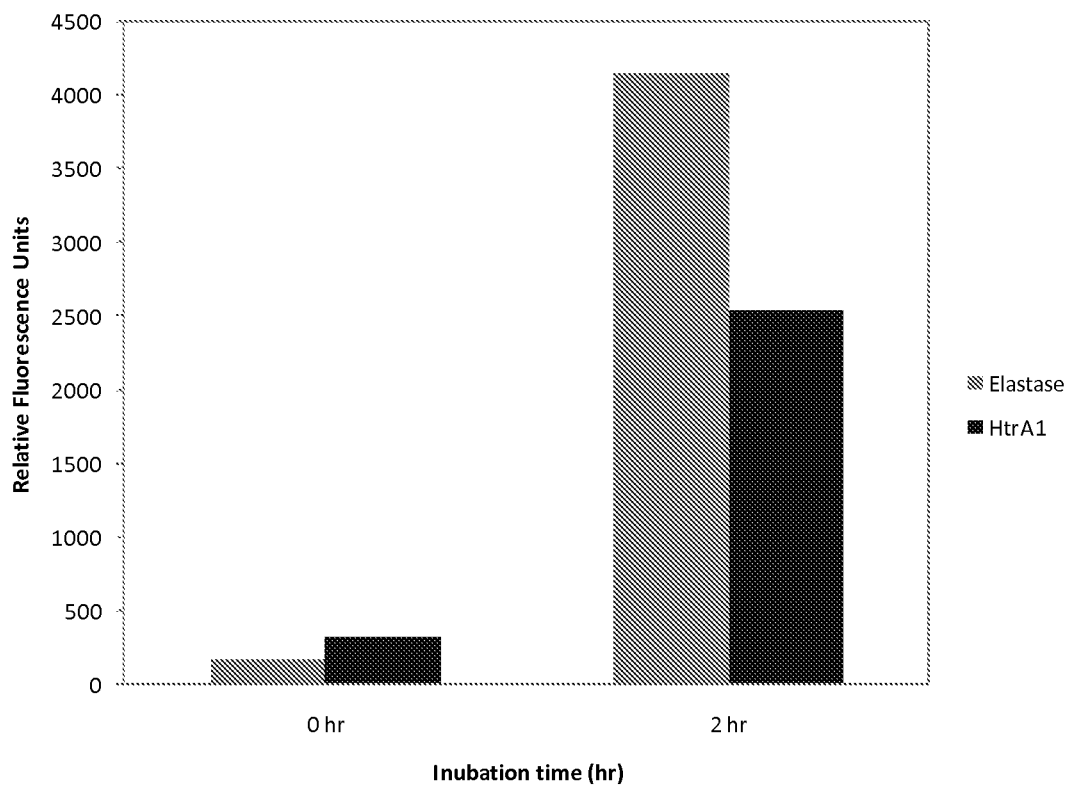
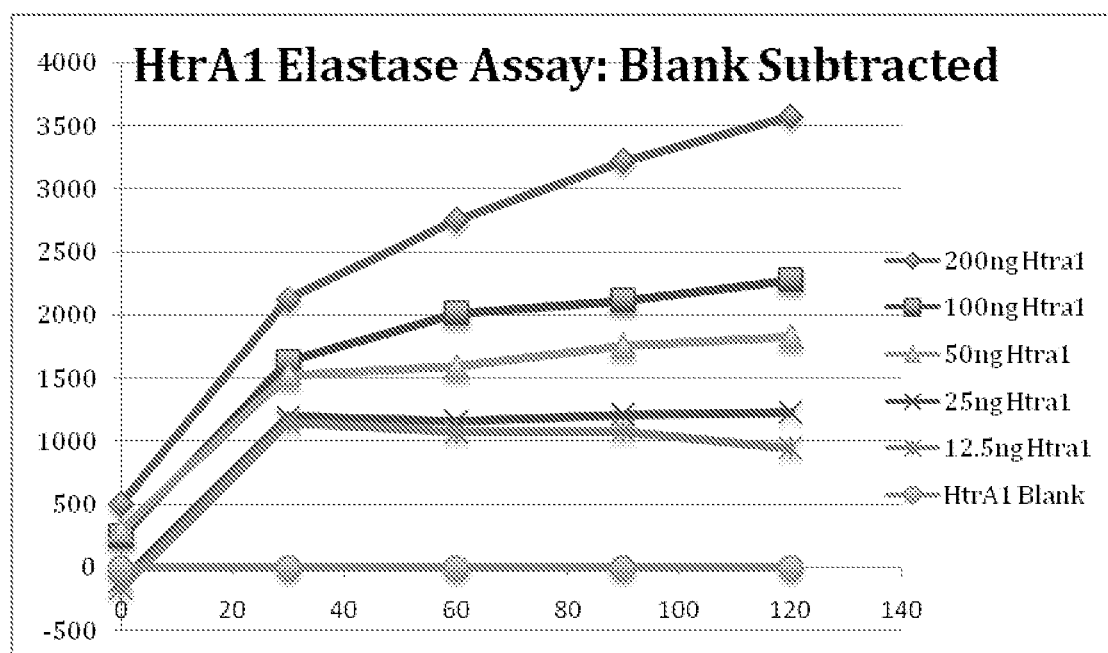


FIG. 24B

**FIG. 25****FIG. 26**

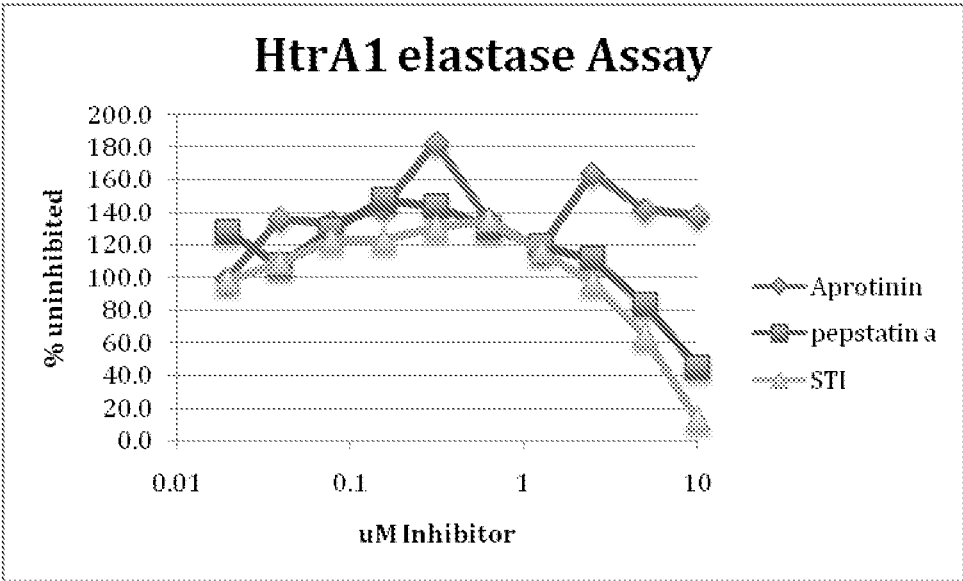


FIG. 27



FIG. 28

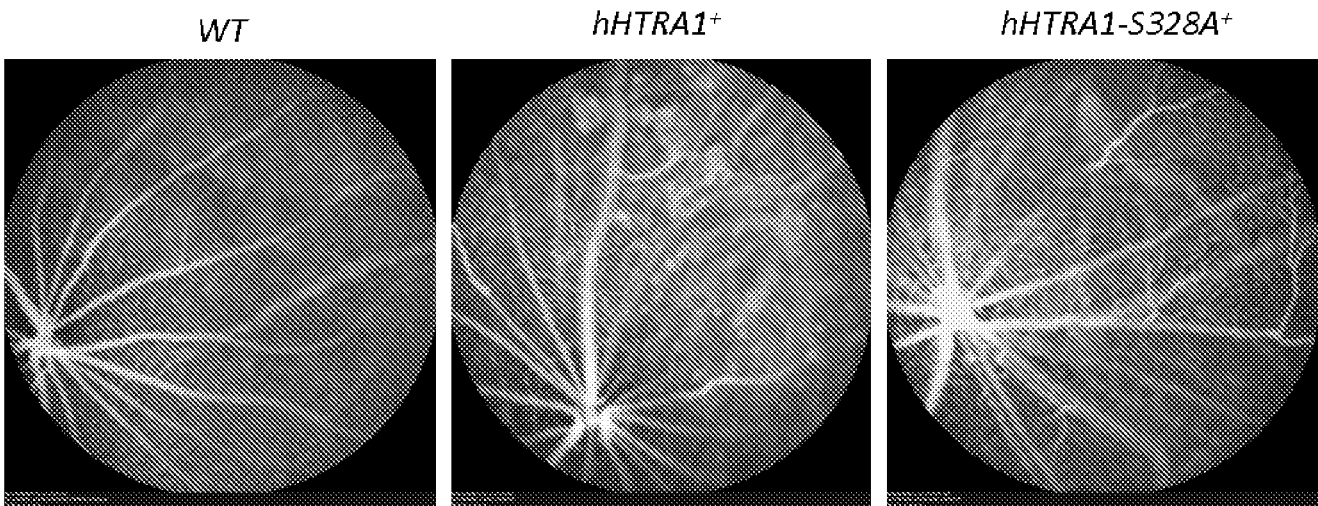


FIG. 29

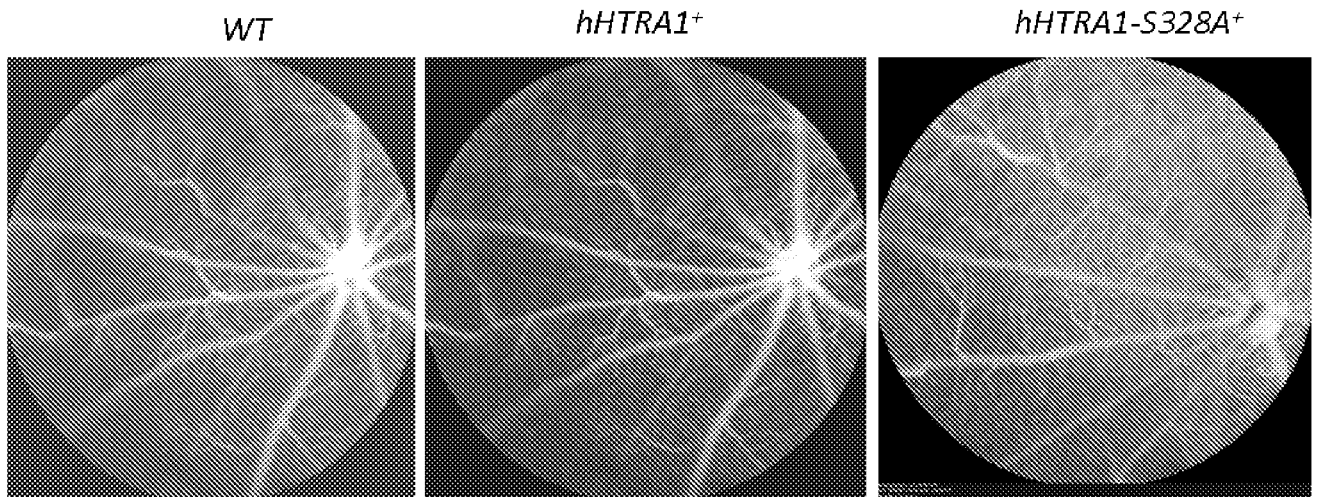


FIG. 30

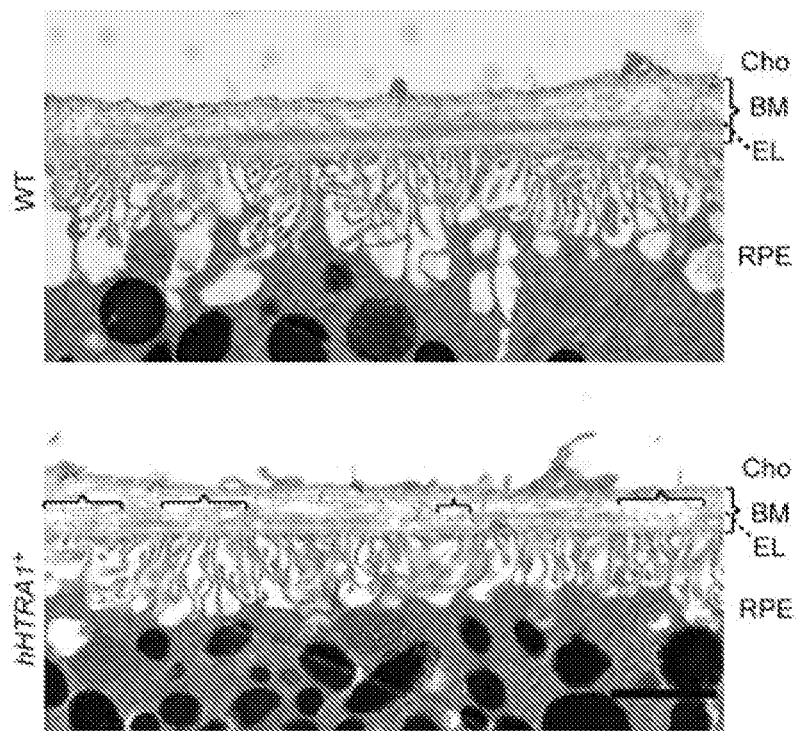


FIG. 31

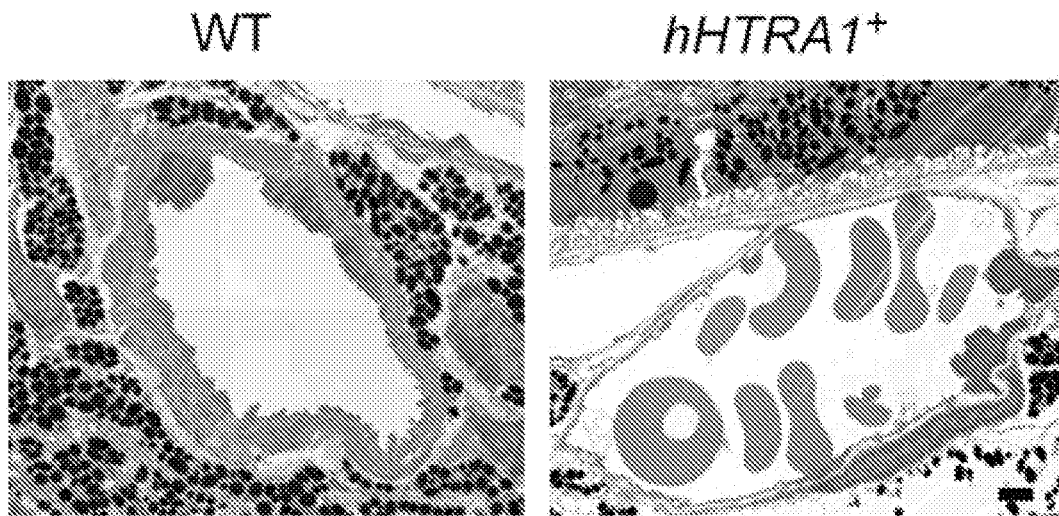


FIG. 32

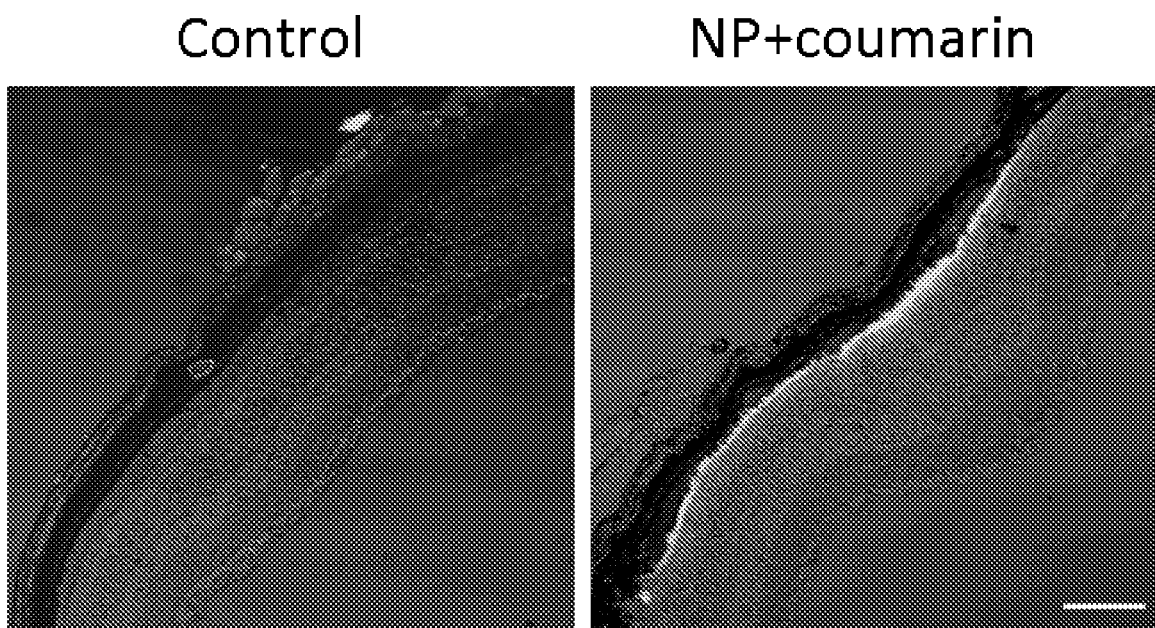


FIG. 33

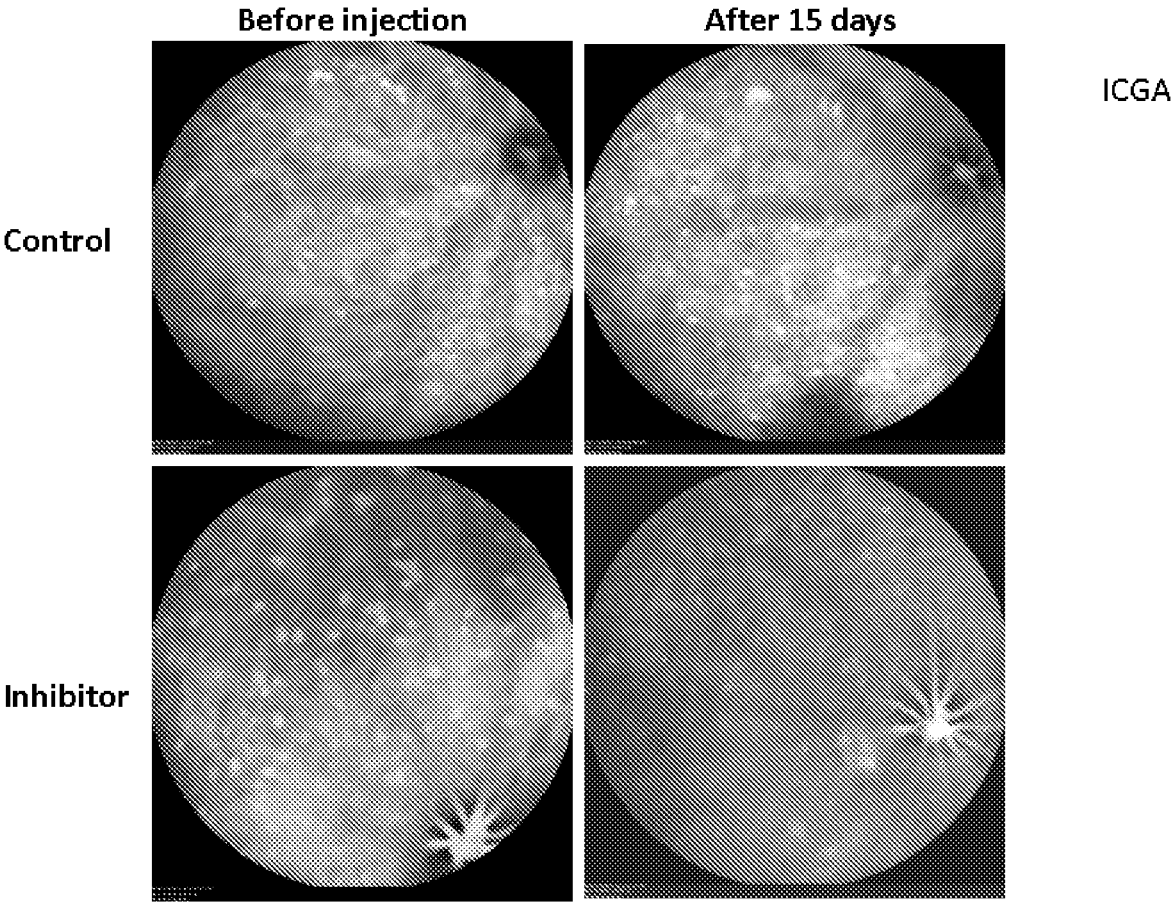


FIG. 34

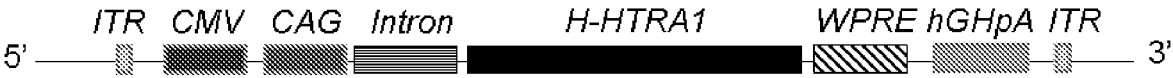


FIG. 35

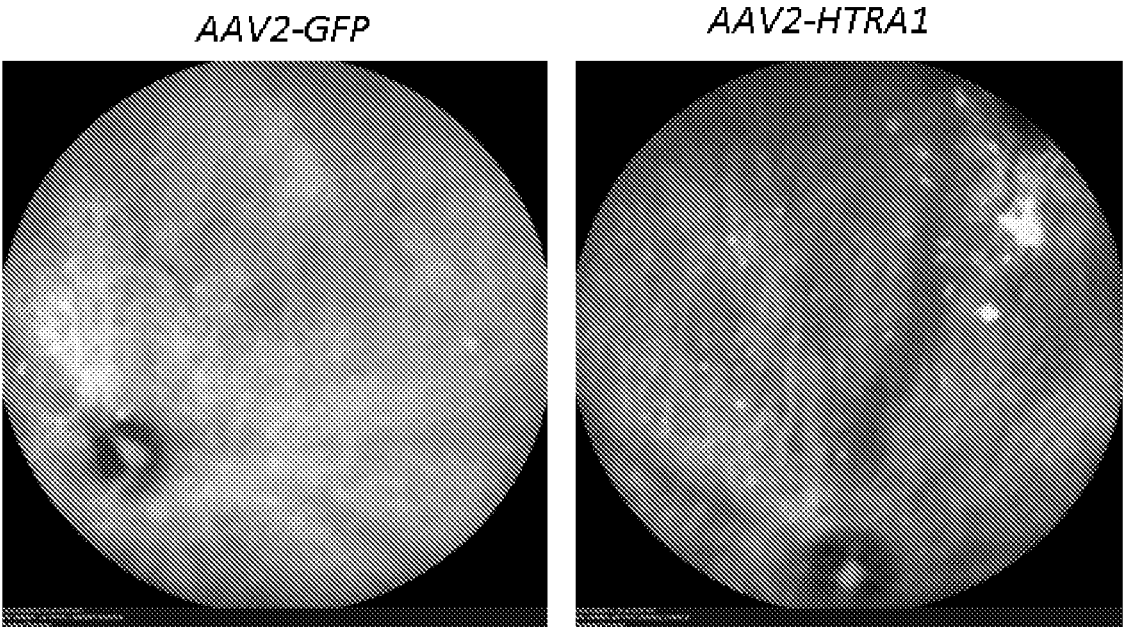


FIG. 36

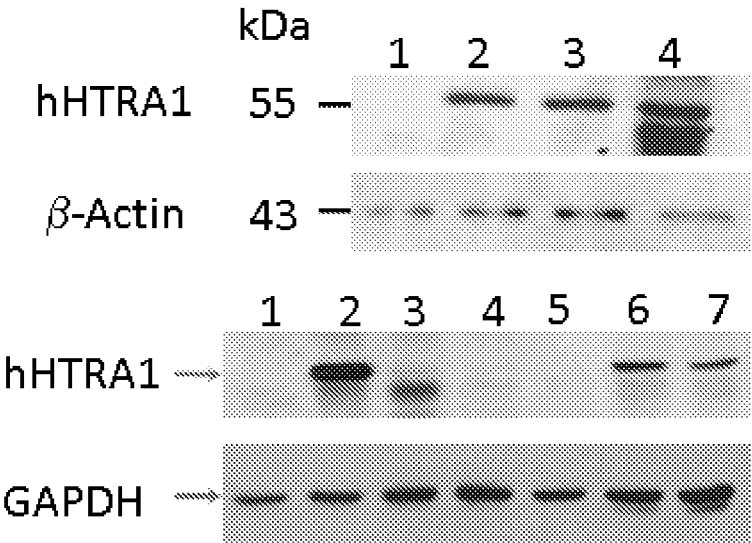


FIG. 37

Chr10/Chr1 Diplotypes

rs10490924/rs1061170

Phenotype	Total Genotyped	TTCC (risk/risk)	TTTT (risk/nr)	GGCC (nr/risk)	GGTT (nr/nr)	GTCT (het/het)	TTCT (risk/het)	GGCT (nr/het)	GTCC (het/risk)	GTTT (het/nr)
ACL Yes	377	22 5.8%	16 4.2%	43 11.4%	24 6.4%	86 22.8%	38 10.1%	59 15.6%	54 14.3%	35 9.3%
ACL No	406	11 2.7%	9 2.2%	53 13.1%	60 14.8%	78 19.2%	21 5.2%	89 21.9%	46 11.3%	39 9.6%

*chr10: T=risk, chr1: C=risk (e.g. GGCC=chr10 homo non-risk, chr1 homo risk)

% of ACL cohort

4.2%

3.2%

12.3%

10.7%

20.9%

7.5%

18.9%

12.8%

9.5%

Normalized ACL

1.384615

1.32973

0.93029

0.59341

1.08912

1.337679

0.82796

1.121538

0.98233

Normalized ACL rank

1

3

7

9

5

2

8

4

6

ACL	chr10	chr1	risk alleles
1	TT	CC	4
2	TT	CT	3
3	TT	TT	2
4	GT	CC	3
5	GT	CT	2
6	GT	TT	1
7	GG	CC	2
8	GG	CT	1
9	GG	TT	0

FIG. 38

Gene Region	Name	Assoc Allele	Case,Control Ratio Counts	Case,Control Freqs	Chi square	P value
CFH-F13B	rs35928059	A	734:22, 783:29	0.971, 0.964	0.544	0.4607
CFH-F13B	rs3753394	T	202:554, 214:610	0.267, 0.260	0.114	0.7357
CFH-F13B	rs551397	C	657:103, 678:148	0.864, 0.821	5.661	0.0173
CFH-F13B	rs800292	G	653:103, 678:148	0.864, 0.821	5.451	0.0196
CFH-F13B	rs16840419	A	709:51, 741:85	0.933, 0.897	6.471	0.011
CFH-F13B	rs3766404	T	699:55, 733:85	0.927, 0.896	4.638	0.0313
CFH-F13B	rs16840422	C	700:56, 743:85	0.926, 0.897	3.981	0.046
CFH-F13B	rs1061147	A	426:334, 417:411	0.561, 0.504	5.152	0.0232
CFH-F13B	rs1329421	A	425:331, 416:410	0.562, 0.504	5.432	0.0198
CFH-F13B	rs10801554	C	418:326, 408:404	0.562, 0.502	5.494	0.0191
CFH-F13B	rs1061170	C	425:335, 416:410	0.559, 0.504	4.909	0.0267
CFH-F13B	rs12124794	A	666:92, 689:135	0.879, 0.836	5.792	0.0161
CFH-F13B	rs6695321	T	520:236, 559:269	0.688, 0.675	0.294	0.5877
CFH-F13B	rs2274700	G	587:169, 576:248	0.776, 0.699	12.166	5.00E-04
CFH-F13B	rs3753395	A	588:170, 581:249	0.776, 0.700	11.696	6.00E-04
CFH-F13B	rs393955	C	449:309, 443:381	0.592, 0.538	4.808	0.0283
CFH-F13B	rs3753396	G	139:617, 133:695	0.184, 0.161	1.5	0.2207
CFH-F13B	rs403846	A	446:310, 444:382	0.590, 0.538	4.407	0.0358
CFH-F13B	rs1410996	G	585:169, 577:249	0.776, 0.699	12.11	5.00E-04
CFH-F13B	rs12144939	G	686:72, 717:111	0.905, 0.866	5.918	0.015
CFH-F13B	rs2284664	C	659:97, 690:136	0.872, 0.835	4.151	0.0416
CFH-F13B	rs35292876	T	14:746, 8:818	0.018, 0.010	2.208	0.1373
CFH-F13B	rs1065489	T	141:619, 135:693	0.186, 0.163	1.395	0.2376
CFH-F13B	rs11582939	T	140:618, 136:692	0.185, 0.164	1.151	0.2834
CFH-F13B	mrd_3876	G	9:751, 7:821	0.012, 0.008	0.456	0.4995
CFH-F13B	mrd_3877	T	14:744, 6:816	0.018, 0.007	3.937	0.0472
CFH-F13B	rs7546940	A	114:638, 111:707	0.152, 0.136	0.807	0.3691
CFH-F13B	rs12406509	G	17:737, 15:807	0.023, 0.018	0.365	0.5456
CFH-F13B	rs1409153	C	432:318, 422:402	0.576, 0.512	6.452	0.0111
CFH-F13B	rs12066959	G	633:119, 671:151	0.842, 0.816	1.79	0.1809
CFH-F13B	mrd_3902	T	18:730, 17:799	0.024, 0.021	0.186	0.6661
CFH-F13B	rs3828032	G	589:165, 630:196	0.781, 0.763	0.762	0.3828
CFH-F13B	mrd_3905	G	613:143, 664:160	0.811, 0.806	0.064	0.8001
CFH-F13B	mrd_3906	G	609:143, 660:160	0.810, 0.805	0.062	0.8032
CFH-F13B	rs6702340	G	714:40, 763:53	0.947, 0.935	0.996	0.3183
CFH-F13B	rs9427662	T	719:39, 773:55	0.949, 0.934	1.591	0.2071
CFH-F13B	rs3748557	T	612:146, 656:166	0.807, 0.798	0.217	0.6415

FIG. 39 A

Gene Region	Name	Assoc Allele	Case,Control Ratio Counts	Case,Control Freqs	Chi square	P value
CFH-F13B	rs12097550	A	11:747, 10:816	0.015, 0.012	0.175	0.6759
CFH-F13B	rs1750311	C	569:185, 605:223	0.755, 0.731	1.184	0.2765
CFH-F13B	rs10922153	G	488:266, 489:339	0.647, 0.591	5.36	0.0206
CFH-F13B	rs698859	T	337:421, 350:478	0.445, 0.423	0.772	0.3796
CFH-F13B	rs5998	A	374:380, 401:425	0.496, 0.485	0.176	0.6752
CFH-F13B	rs2990510	G	299:457, 310:518	0.396, 0.374	0.744	0.3884
CFH-F13B	rs10801586	C	680:80, 710:116	0.895, 0.860	4.521	0.0335
CFH-F13B	rs5991	A	5:745, 5:823	0.007, 0.006	0.025	0.8752
CFH-F13B	rs17514281	C	5:737, 3:815	0.007, 0.004	0.719	0.3964
CFH-F13B	rs5997	C	710:40, 774:52	0.947, 0.937	0.662	0.4159
CFH-F13B	rs1615413	A	379:379, 402:424	0.500, 0.487	0.28	0.5964
CFH-F13B	rs6003	T	713:39, 763:53	0.948, 0.935	1.214	0.2705
CFH-F13B	rs1412631	C	720:40, 772:52	0.947, 0.937	0.793	0.3732
CFH-F13B	rs6428380	C	714:40, 770:52	0.947, 0.937	0.746	0.3878
C2	rs9332739	G	735:23, 798:26	0.970, 0.968	0.019	0.8896
C2	rs547154	G	725:35, 774:56	0.954, 0.933	3.373	0.0663
CFB	rs4151667	A	23:719, 22:788	0.031, 0.027	0.202	0.6527
PLEHKA1	rs12571218	A	681:41, 695:45	0.943, 0.939	0.107	0.7437
PLEHKA1	rs4565845	C	165:577, 122:626	0.222, 0.163	8.414	0.0037
PLEHKA1	rs4751890	T	518:218, 484:262	0.704, 0.649	5.12	0.0237
PLEHKA1	rs10082476	A	598:146, 577:171	0.804, 0.771	2.336	0.1264
PLEHKA1	rs10887148	C	634:108, 621:127	0.854, 0.830	1.647	0.1994
PLEHKA1	rs11200616	G	2:738, 2:746	0.003, 0.003	0	0.9914
PLEHKA1	rs11200617	T	2:740, 2:744	0.003, 0.003	0	0.9957
PLEHKA1	rs10887149	G	554:182, 526:218	0.753, 0.707	3.923	0.0476
PLEHKA1	rs11200621	G	131:611, 111:635	0.177, 0.149	2.104	0.1469
PLEHKA1	rs10510110	C	462:276, 387:357	0.626, 0.520	16.966	3.80E-05
intergenic	rs4752695	G	681:61, 650:96	0.918, 0.871	8.514	0.0035
intergenic	rs2223089	G	690:50, 691:55	0.932, 0.926	0.215	0.6432
ARMS2 R38X	rs2736911	C	674:66, 651:95	0.911, 0.873	5.599	0.018
ARMS2 A69S	rs10490924	T	325:417, 224:520	0.438, 0.301	29.901	4.55E-08
ARMS2	rs17623531	C	667:63, 642:102	0.914, 0.863	9.564	0.002
intergenic	rs2014307	G	514:230, 490:260	0.691, 0.653	2.386	0.1224
HTRA1 prom.	rs11200638	A	321:417, 239:501	0.435, 0.323	19.691	9.10E-06

FIG. 39 B

Gene Region	Name	Assoc Allele	Case,Control Ratio Counts	Case,Control Freqs	Chi square	P value
HTRA1 prom.	rs2672598	C	454:288, 393:349	0.612, 0.530	10.235	0.0014
HTRA1	rs12571363	C	686:58, 688:62	0.922, 0.917	0.112	0.7377
HTRA1	rs12259258	G	9:733, 9:739	0.012, 0.012	0	0.9863
HTRA1	rs2736914	G	669:75, 648:100	0.899, 0.866	3.896	0.0484
HTRA1	rs2672591	T	443:295, 382:362	0.600, 0.513	11.319	8.00E-04
HTRA1	rs4752699	G	666:72, 636:110	0.902, 0.853	8.582	0.0034
HTRA1	rs2672590	A	615:125, 588:156	0.831, 0.790	4.015	0.0451
HTRA1	rs7093894	C	665:77, 631:119	0.896, 0.841	9.849	0.0017
HTRA1	rs2672588	T	600:138, 555:189	0.813, 0.746	9.683	0.0019
HTRA1	rs2672587	G	315:419, 226:514	0.429, 0.305	24.29	8.28E-07
HTRA1	rs4237540	A	470:272, 428:322	0.633, 0.571	6.13	0.0133
HTRA1	rs2736917	A	646:96, 623:125	0.871, 0.833	4.198	0.0405
HTRA1	rs2284668	T	619:123, 599:145	0.834, 0.805	2.132	0.1443
HTRA1	rs2253755	G	325:419, 259:491	0.437, 0.345	13.132	3.00E-04
HTRA1	rs2300431	G	585:159, 551:193	0.786, 0.741	4.302	0.0381
HTRA1	rs2268346	G	706:36, 701:49	0.951, 0.935	1.963	0.1612
HTRA1	rs736962	G	15:723, 15:731	0.020, 0.020	0.001	0.9762
HTRA1	rs2736923	A	678:66, 665:85	0.911, 0.887	2.493	0.1144
HTRA1	rs11200655	C	689:51, 677:67	0.931, 0.910	2.264	0.1324
HTRA1	rs876790	T	609:133, 573:165	0.821, 0.776	4.522	0.0335
HTRA1	rs2250804	C	334:408, 263:483	0.450, 0.353	14.746	1.00E-04
HTRA1	rs2268356	C	416:322, 360:386	0.564, 0.483	9.784	0.0018
C3	rs2230199	C	569:189, 617:209	0.751, 0.747	0.029	0.8658
APOE	rs429358	T	661:77, 679:111	0.896, 0.859	4.626	0.0315
APOE	rs7412	C	687:53, 728:66	0.928, 0.917	0.708	0.4001

FIG. 39 C

PLEKHA1-HTRA1 Haplotype												Case, Control Ratio Counts	Case, Control Freqs	Chi Square	P Value										
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	C	T	A	C	A	C	G	A	C	T	C	C	0.108	103.2	572.2	551.1	605.7	0.153	0.083	15.402	0.8396			
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	C	A	C	T	C	0.063	59.3	617.2	33.1	627.8	0.066	0.050	6.913	0.0365		
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	T	G	A	C	T	C	0.058	47.1	628.4	37.6	623.3	0.070	0.057	0.933	0.334	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	C	A	C	A	A	T	G	C	C	A	C	T	T	0.048	29.2	646.3	40.5	620.4	0.043	0.061	2.211	0.137		
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	C	G	A	C	A	A	T	G	C	A	G	A	C	T	0.031	17.8	657.7	26.7	634.1	0.026	0.040	2.071	0.1501	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	C	A	C	T	T	0.028	26.2	649.3	15.0	645.9	0.039	0.023	2.889	0.0892		
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	C	G	A	C	A	A	T	G	C	A	C	A	C	T	0.028	18.6	656.9	21.9	638.9	0.028	0.033	0.368	0.5441	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	C	G	A	C	A	A	T	G	C	A	C	A	C	T	0.027	17.0	658.5	22.3	638.5	0.025	0.034	0.879	0.3466	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	A	T	G	A	C	0.023	12.9	662.5	20.1	640.8	0.019	0.030	1.747	0.1862	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	A	T	G	A	C	0.019	12.2	663.3	16.2	644.7	0.018	0.024	0.659	0.417	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	A	T	G	A	C	0.018	12.7	662.8	13.9	647.0	0.019	0.021	0.083	0.7758	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	C	T	A	C	A	C	G	A	C	A	T	G	A	C	0.017	15.3	660.2	10.2	650.7	0.023	0.015	0.949	0.33	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	G	A	C	T	T	0.017	13.6	661.9	11.5	649.4	0.020	0.017	0.14	0.7085	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	G	A	C	C	T	0.017	13.8	661.7	11.1	649.8	0.020	0.017	0.256	0.6131	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	C	A	C	A	A	T	G	C	C	A	C	A	C	T	0.016	8.8	666.7	15.1	645.8	0.013	0.023	1.833	0.1758	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	T	C	A	T	C	0.016	8.2	667.3	15.4	645.5	0.012	0.023	2.394	0.1218	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	G	A	C	G	A	C	G	A	C	T	G	C	C	A	C	0.016	8.5	667.0	14.3	646.6	0.013	0.022	1.647	0.1993	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	T	C	G	A	C	0.015	9.5	666.0	12.9	648.0	0.014	0.019	0.605	0.4365	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	C	A	T	C	A	C	0.015	13.9	661.6	8.4	652.5	0.021	0.013	1.288	0.2565	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	C	T	A	C	A	C	G	A	C	T	C	A	C	C	0.015	11.0	664.5	11.2	649.7	0.016	0.017	0.008	0.9307	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	T	C	A	T	C	0.014	12.6	662.8	8.4	652.5	0.019	0.013	0.791	0.3739	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	C	T	C	G	A	0.013	6.6	668.9	11.7	649.1	0.010	0.018	1.583	0.2084	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	G	A	C	G	A	C	G	A	C	T	G	C	C	A	T	0.012	11.7	663.8	5.4	655.5	0.017	0.008	2.201	0.138	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	G	A	C	G	A	C	G	A	C	T	G	C	C	A	T	0.012	6.8	668.7	10.1	650.8	0.010	0.015	0.705	0.401	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	A	C	T	C	A	C	0.011	10.7	664.8	6.0	654.8	0.016	0.009	1.197	0.2739	
AATACGACGAGCTCGACCACTGACTGAAATGGGAATCC	A	T	A	C	A	C	G	A	C	C	T	C	G	A	C	0.011	6.6	668.9	9.9	651.0	0.010	0.015	0.757	0.3944	

Cases are individuals with aberrant chorionicapillaris lobules, while controls are individuals without aberrant chorionicapillaris lobules

*Cases are individuals with aberrant choriocapillaris lobules, while controls are individuals without aberrant choriocapillaris lobules

FIG. 40

FIG. 41

APOE Haplotypes										
ApoE Hap	rs429358	rs7412	Freq.	Case, Control Ratio	Counts	Case, Control Freqs	Chi Square	P Value		
E3	T	C	0.799	609.7 : 130.3	618.0 : 178.0	0.824, 0.776	5.406	0.0201		
E4	C	C	0.123	77.3 : 662.7	111.8 : 684.2	0.104, 0.140	4.614	0.0317		
E2	T	T	0.078	53.0 : 687.0	66.2 : 729.8	0.072, 0.083	0.711	0.3993		

FIG. 42