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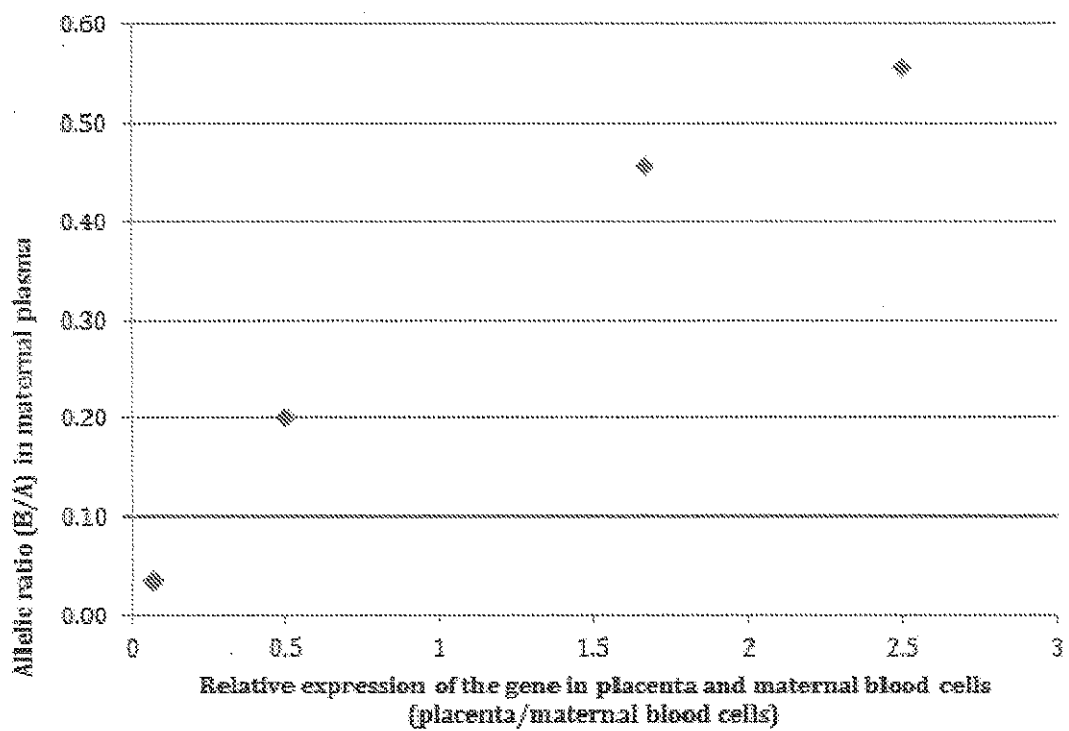


FIG. 1

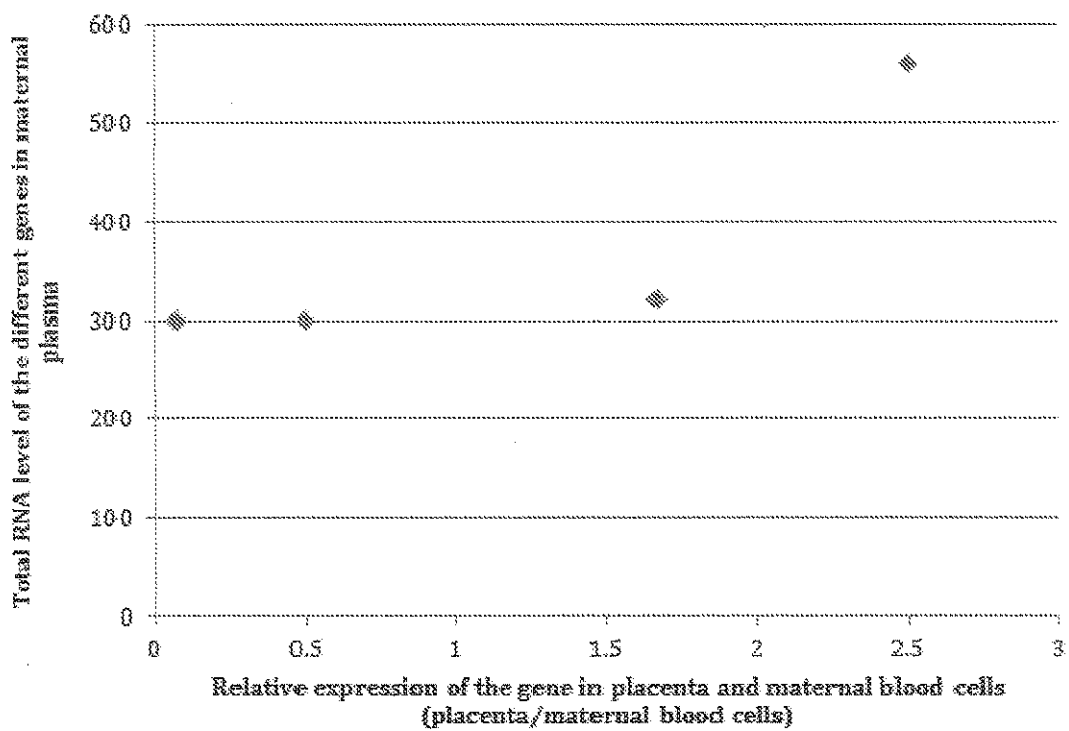


FIG. 2

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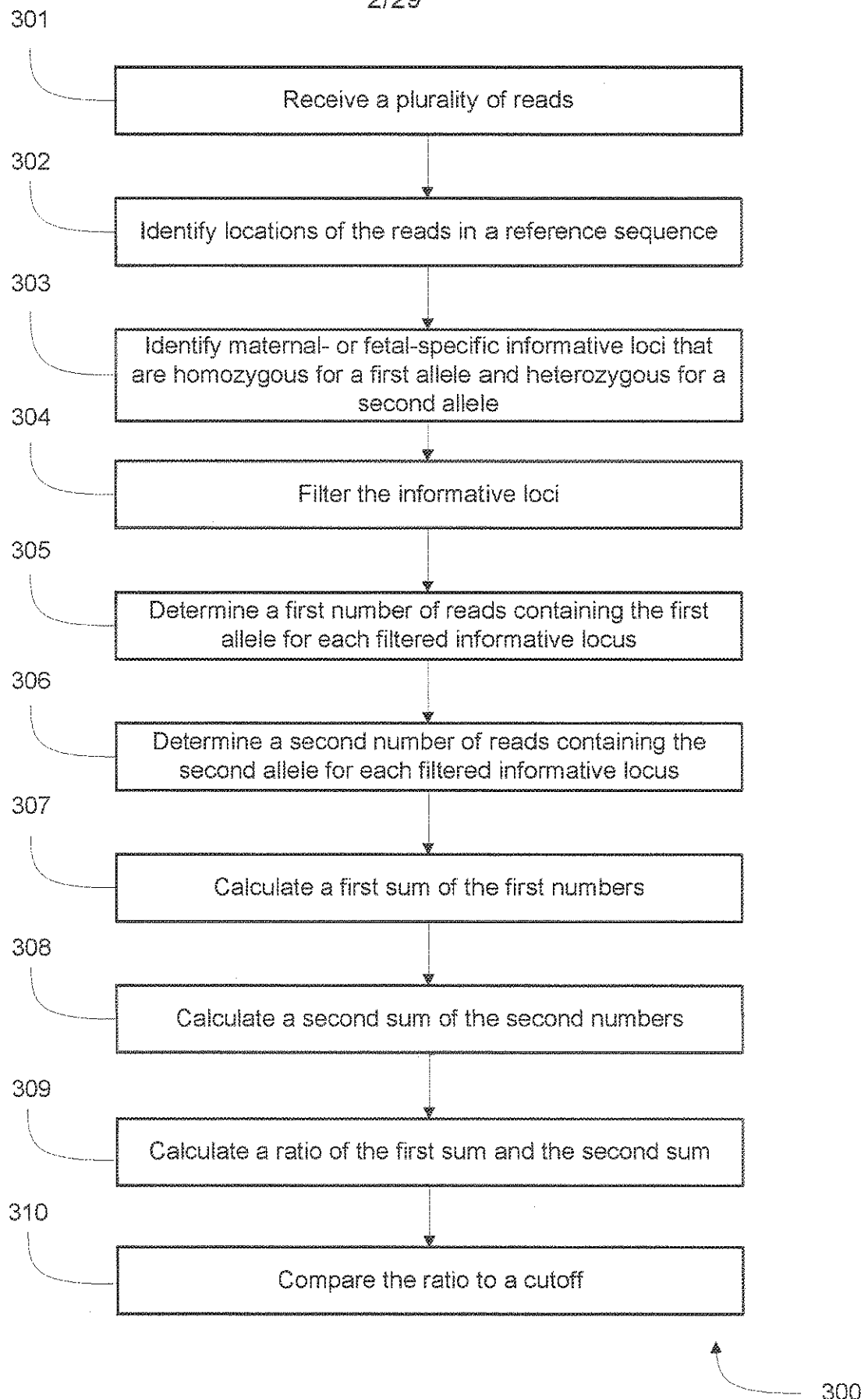


FIG. 3

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Sample type	Sample	Raw reads	Preprocessed ^a reads	(%) ^b	Mappable reads ^c	(%) ^d
Non-pregnant female plasma	CTR081	180,080,810	23,012,332	12.78%	7,708,011	33.50%
	CTR082	132,567,446	20,559,146	15.51%	6,848,249	33.31%
Pre-delivery maternal plasma	M9600P	367,301,939	45,255,199	12.32%	16,849,461	37.23%
	M9549P	597,724,438	151,243,195	25.30%	34,627,313	22.90%
	M9356P	820,742,404	190,030,278	23.15%	14,091,631	7.42%
	M9415P	970,145,241	143,615,377	14.80%	41,517,504	28.91%
Post-delivery maternal plasma	M9356BP	587,698,232	132,012,632	22.46%	7,828,124	5.93%
	M9415BP	853,401,365	101,070,496	11.84%	26,707,674	26.42%
Placenta	N9356	202,711,386	169,500,629	83.62%	160,417,620	94.64%
	N9415	257,219,381	203,094,642	78.96%	193,126,555	95.09%
Maternal blood cells	M9600W	163,832,386	38,707,658	23.63%	11,348,398	29.32%
	M9549W	240,383,043	83,922,150	34.91%	73,117,147	87.12%
	M9356W	208,400,902	60,851,642	29.20%	54,974,158	90.34%
	M9415W	265,636,207	49,943,628	18.80%	42,670,781	85.44%

a. Retained reads after removal of highly repetitive reads.

b. % of the raw reads.

c. See Supplemental Data Table 2B for detailed breakdown.

d. % of the preprocessed reads.

FIG. 4

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Sample type	Sample	Filtered reads ^a	Analyzable reads ^b	Exon (%)	Intron (%)	Intergenic region (%) ^c
Non-pregnant female plasma	CTR081	4,186,990	3,521,021	64.00%	6.47%	29.53%
	CTR082	3,594,966	3,253,283	61.93%	7.29%	30.78%
Pre-delivery maternal plasma	M9600P	7,711,430	9,138,031	64.42%	6.47%	29.10%
	M9549P	20,481,388	14,145,925	41.84%	13.16%	45.00%
	M9356P	1,683,896	12,407,735	56.80%	30.76%	12.45%
	M9415P	23,164,778	18,352,726	53.61%	10.80%	35.59%
Post-delivery maternal plasma	M9356BP	988,066	6,840,058	50.41%	38.15%	11.44%
	M9415BP	15,853,377	10,854,297	50.12%	13.68%	36.19%
Placenta	N9356	3,204,907	157,212,713	31.18%	55.89%	12.93%
	N9415	4,186,711	188,939,844	26.51%	59.59%	13.90%
Maternal blood cells	M9600W	854,869	10,493,529	69.71%	23.50%	6.79%
	M9549W	8,120,655	64,996,492	66.98%	26.67%	6.36%
	M9356W	4,255,081	50,719,077	69.13%	24.70%	6.16%
	M9415W	5,318,314	37,352,467	85.68%	10.74%	3.58%

a. Filtered reads are mostly the nuclear and mitochondrial rRNAs and tRNAs.

b. Analyzable reads = total mappable reads -- filtered reads.

c. % of reads that aligned to regions outside exons and introns of the reference genes.

FIG. 5

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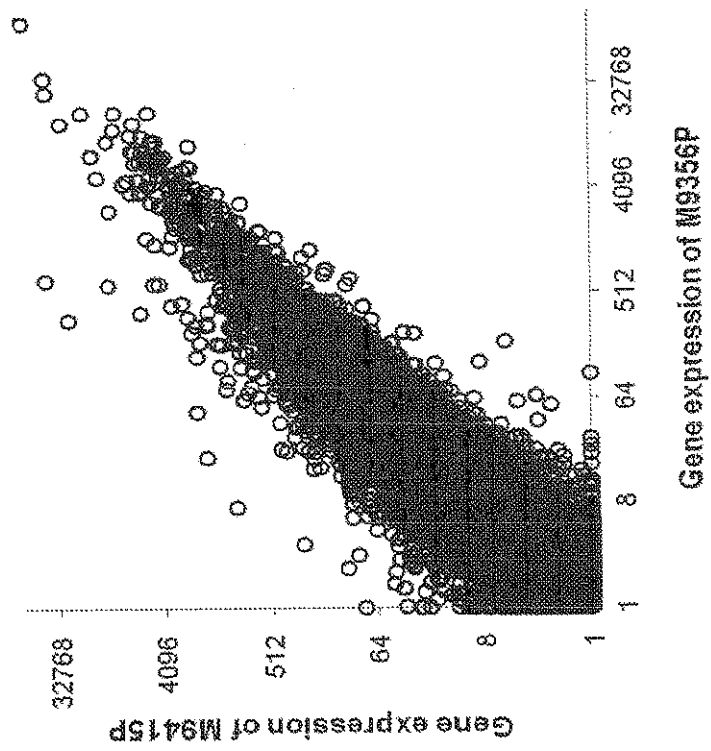


FIG. 6B

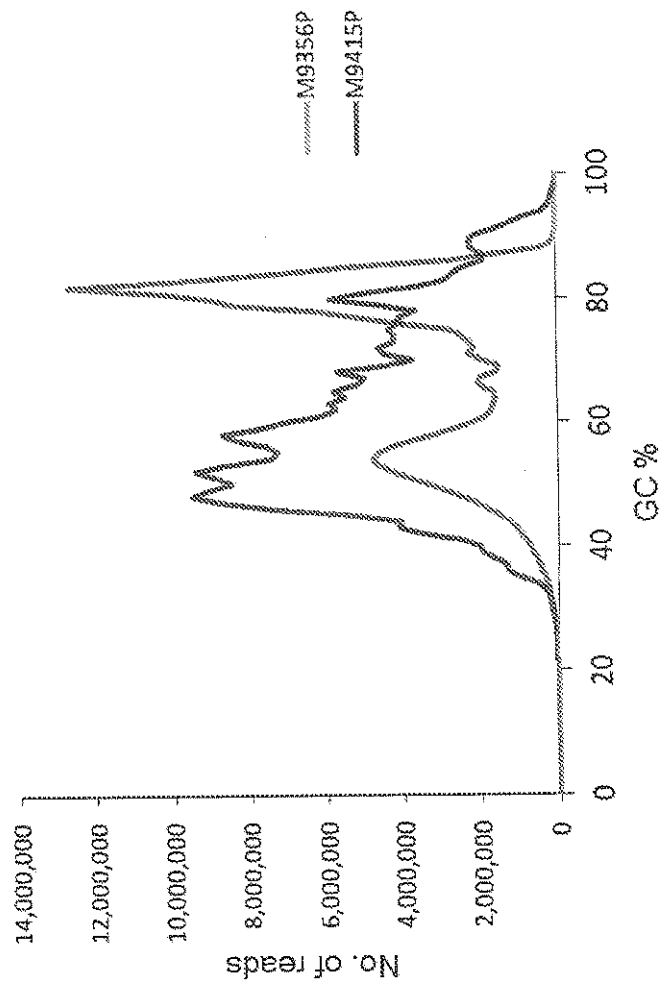


FIG. 6A

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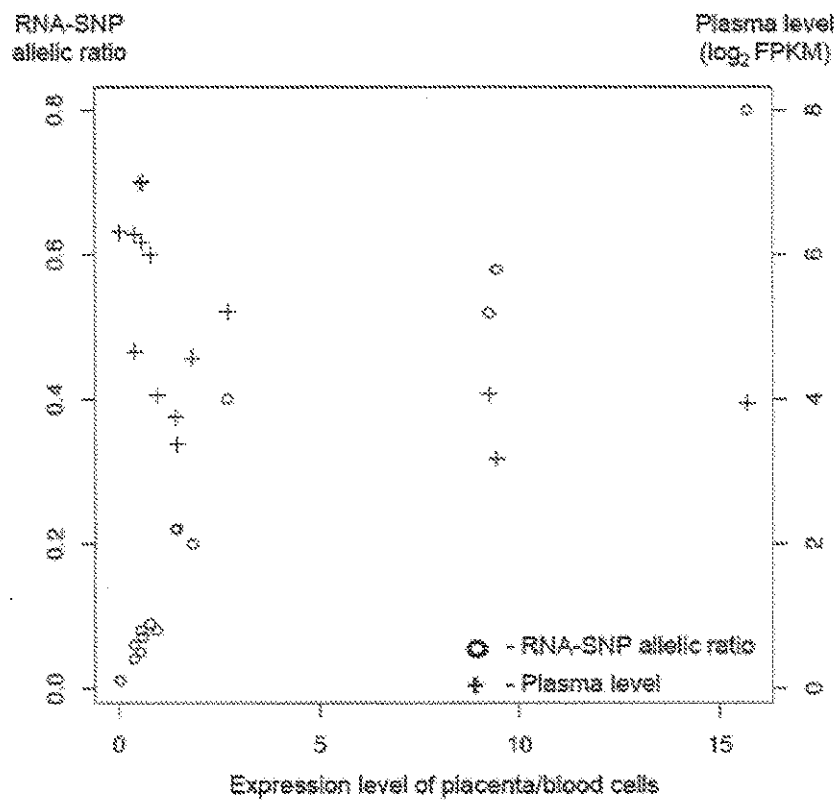


FIG. 7

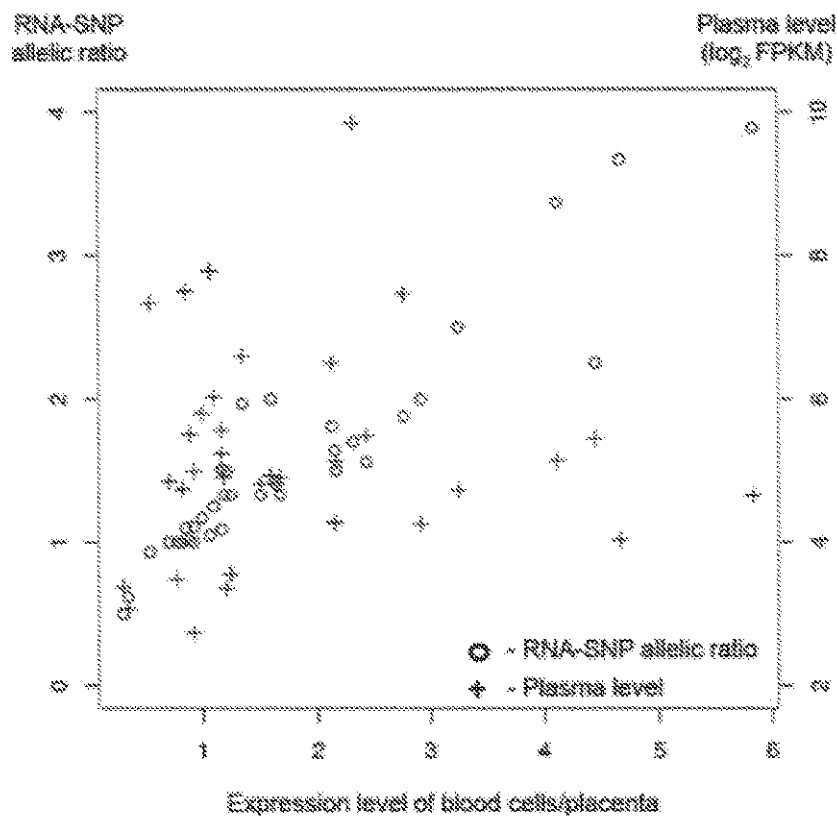


FIG. 8

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Fetal-specific SNP alleles (Maternal: AA, Fetal: AB)	SNPs	Fetal allele/shared allele ratio	Average RNA- SNP ratio per gene	Placenta FPKM	Blood cell FPKM	Fold-difference (Placenta/Blood cell)	Plasma FPKM
AFF1	SNP 7:rs342462	0.28	0.52	149.731	16.1598	9.27	16.7037
	SNP 8:rs342459	1					
	SNP 9:rs10029915	0.29					
SH3BGR2	SNP 13:rs1507	0.07	0.07	24.7477	40.3078	0.61	128.2908
SLC38A1	SNP 3:rs3742058	0.17	0.58	142.8723	15.1123	9.45	9.0209
	SNP 4:rs3742059	1					
PTTG1P	SNP 6:rs873317	0.4	0.4	152.8104	56.4153	2.71	37.1191
GMAP1-GMAP5	SNP 14:rs1046355	0.04	0.04	15.9771	39.9271	0.4	77.4282
	SNP 1:rs3754212	0.01	0.01	11.0084	382.8589	0.03	79.3012
RHOBTB3	SNP 10:rs34896	1	0.8	338.5763	21.5841	15.69	15.4046
	SNP 11:rs34898	0.6					
	SNP 12:rs34899	0.8					
ARHGEF12	SNP 2:rs192719576	0.09	0.09	88.5256	110.1833	0.8	63.7037
TXNRD1	SNP 5:rs11111979	0.2	0.2	65.9309	35.795	1.84	23.6787
HPCAL1	SNP 11:rs2270302	0.06	0.06	17.2498	42.5469	0.41	25.2768
RAB4A	SNP 2:rs15452	0.08	0.08	12.7741	22.2066	0.58	72.2382
PGM2	SNP 13:rs3752683	0.22	0.22	33.0576	23.045	1.43	13.4293
PSMB3	SNP 10:rs228274	0.05	0.05	65.0683	117.5188	0.55	127.3262
ADIPOR2	SNP 4:rs12342	0.08	0.08	18.1942	18.7699	0.97	16.5717
	SNP 5:rs1044471	0.08					
CHFR	SNP 9:rs35011845	0.22	0.22	21.9501	15.0583	1.46	10.3748

FIG. 9

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Maternal-specific SNP alleles (Maternal: AB, Fetal: AA)	SNPs	Maternal allele/shared allele ratio	Average RNA-SNP ratio per gene	Placenta FPKM	Blood cell FPKM	Fold-difference (Blood cell/Placenta)	Plasma FPKM
AKAP10	SNP 18:rs2108978	1.33	1.33	22.414	18.1324	1.24	11.7168
EIF252	SNP 37:rs4911406	1.25	1.25	39.3008	35.9748	1.09	65.1988
JHDM2D	SNP 51:rs76676651	1.4	1.4	43.0656	26.1836	1.64	28.1734
	SNP 5:rs11022079	0.5	0.5	10.735	36.1867	0.3	10.3945
USP47	SNP 6:rs148238084	0.5					
PPP4R2	SNP 40:rs61188513	1.09	1.09	80.3628	69.563	1.16	47.4149
	SNP 15:rs4779520	0.78	1.64	22.9283	10.6869	2.15	19.3486
KLF13	SNP 16:rs6493629	2.5					
FAM107B	SNP 4:rs11259151	2	2	24.1087	15.1776	1.59	30.5864
APOL2	SNP 39:rs132759	1.33	1.33	17.9996	12.0226	1.5	28.1601
	SNP 10:rs2389910	1.56	1.11	27.2282	29.7396	0.92	31.7672
RAP2A	SNP 11:rs12873919	0.67					
	SNP 1:rs117963129	4	3.37	48.3896	11.7589	4.11	35.3443
	SNP 2:rs1055184	5					
RIT1	SNP 3:rs493446	1.12					
STK17A	SNP 48:rs56286238	1.33	1.33	61.0052	36.447	1.67	30.0074
	SNP 23:rs14031	0.5	0.62	11.0432	32.3155	0.34	8.3988
C19orf63	SNP 24:rs1045246	0.75					
SMERK1	SNP 14:rs10135595	2	1	27.1212	33.0441	0.82	26.2366
	SNP 42:rs3797341	1.5	1.02	26.837	30.3427	0.88	45.4491
	SNP 43:rs3203922	0.78					
TNFAIP8	SNP 44:rs1045242	0.79					
CPEB4	SNP 46:rs12659398	1	1	28.4523	40.5723	0.7	28.802
PTPRJ	SNP 7:rs117902837	2	2	59.7568	20.5437	2.91	19.0642
RPL36	SNP 22:rs3810220	1.7	1.7	152.2501	65.9528	2.31	921.8925
	SNP 25:rs1137288	1.62	1.88	114.7107	41.6213	2.76	176.8333
	SNP 26:rs3087895	2.17					
	SNP 27:rs3768670	1.86					
YPEL5	SNP 28:rs3768671	1.86					
	SNP 53:rs114261839	1	1.33	51.7974	43.9599	1.18	30.1847
	SNP 54:rs208753	1.4					
	SNP 55:rs17635381	2.27					
PCM1	SNP 56:rs6991775	0.67					
UBR2	SNP 47:rs6916713	2.25	2.25	102.9892	23.2007	4.44	43.5569
	SNP 32:rs3747	1.22	1.97	50.467	37.5349	1.34	96.8859
	SNP 33:rs9579	2.17					
	SNP 34:rs3088214	2.89					
TNS1	SNP 35:rs1063281	1.62					
EIF4A1	SNP 17:rs1057086	0.93	0.93	70.1974	132.2932	0.53	161.6599
BACH1	SNP 38:rs15092	2.5	2.5	112.4409	34.6219	3.25	26.4284
	SNP 49:rs6850	1.11	1.05	66.7742	62.9202	1.06	220.7639
PPIA	SNP 50:rs6904	1					
TMX1	SNP 12:rs7160810	1	1	11.8758	12.8978	0.92	6.7127
ANKRD44	SNP 29:rs3731569	3.67	3.67	65.5013	14.0504	4.66	16.412
	SNP 57:rs3398	0.33	1.51	43.1289	37.048	1.16	37.6685
ZFAND5	SNP 58:rs959	2.69					
	SNP 19:rs12327477	0.67	3.89	171.6269	29.4281	5.83	25.153
	SNP 20:rs2304859	7					
SMCHD1	SNP 21:rs7238459	4					
NR3C1	SNP 45:rs6191	1	1	28.0561	36.5516	0.77	11.2138
CRNKL1	SNP 36:rs2255255	1.5	1.5	15.8244	13.148	1.2	10.1897
CALM1	SNP 13:rs5871	1.1	1.1	76.0647	89.0949	0.85	181.3474
FDFT1	SNP 52:rs79708434	1.56	1.56	83.9629	34.6215	2.43	44.9826
	SNP 30:rs1051677	1	1.17	74.6452	75.2029	0.99	55.8144
XRCC5	SNP 31:rs2440	1.33					
	SNP 8:rs3741380	2.75	1.81	29.7293	14.0146	2.12	90.3776
EHBP1L1	SNP 9:rs6591182	0.88					
OPA1	SNP 41:rs7643844	1.5	1.5	49.1647	22.7367	2.16	34.8335

FIG. 10

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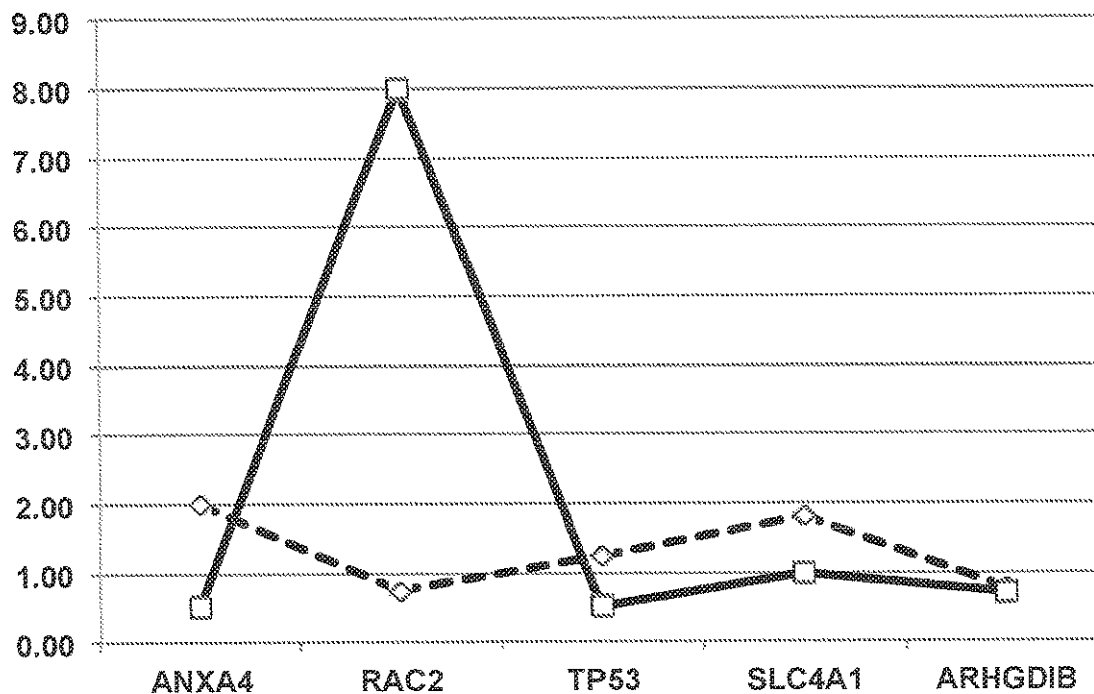
RNA-SNP
allelic ratio

FIG. 11A

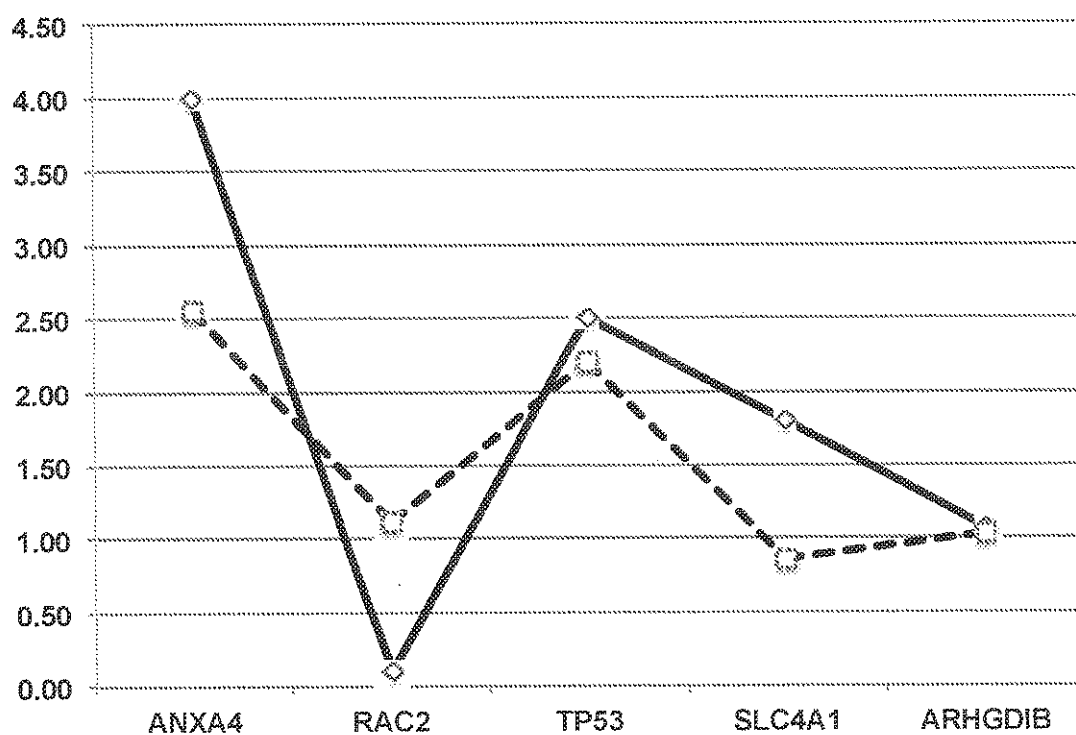
Fold-
differences

FIG. 11B

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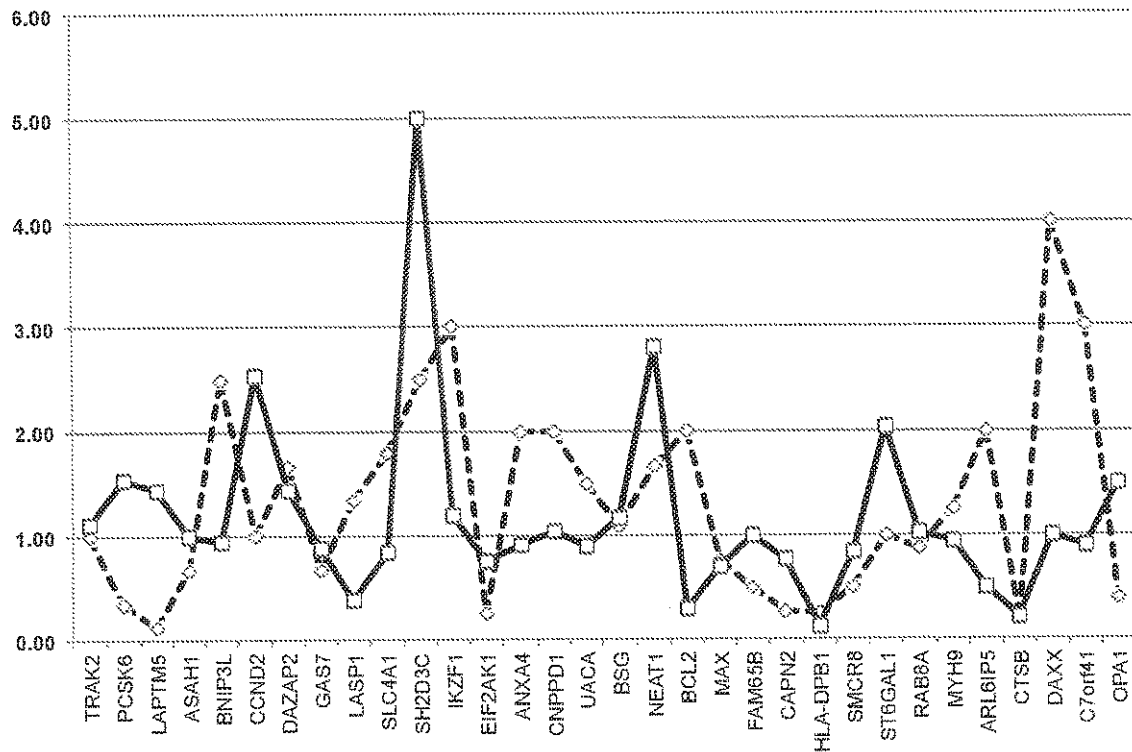
RNA-SNP
allelic ratio

FIG. 12A

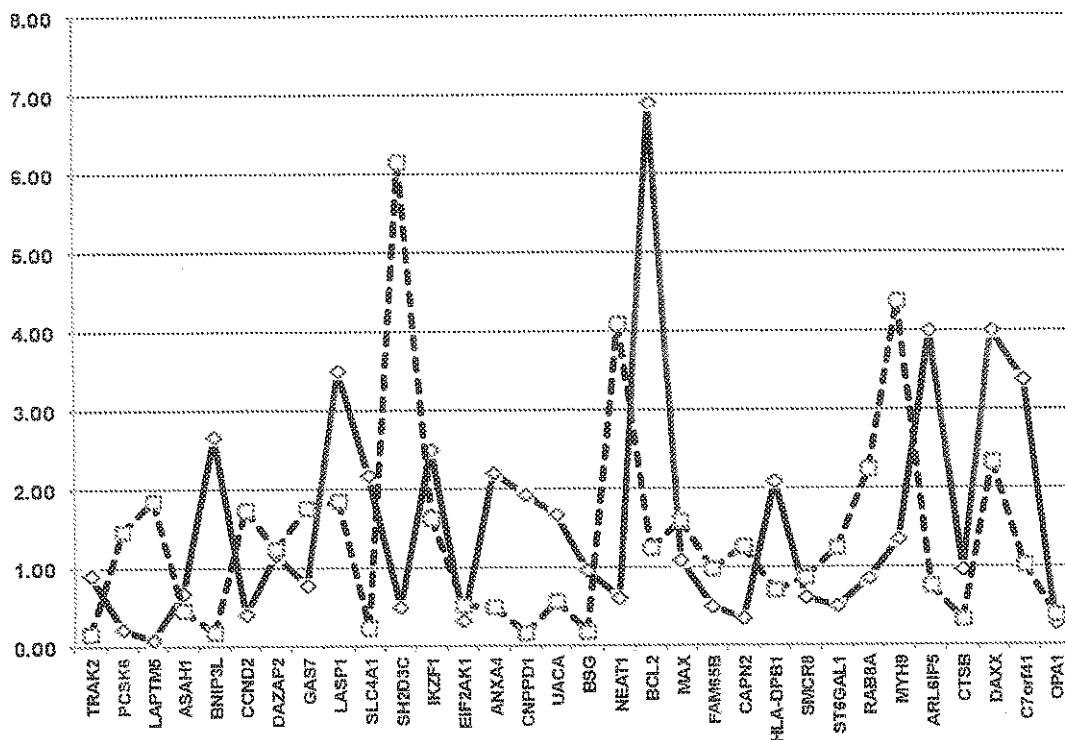
Fold-
differences

FIG. 12B

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Maternal-specific SNP alleles (Maternal:AB, Fetal: AA)	5641 (PEI) (GA: 36 6/7)		7171 (Normal) (GA: 38 8/7)		Average RNA-SNP ratio per gene	Fold-changes of RNA-SNP ratio for each gene (5641 vs 7171)	Expression level in the plasma		Fold-changes of FPKM (5641 vs 7171)
	SNPs	Maternal allele/shared allele ratio	SNPs	Maternal allele/shared allele ratio			5641 FPKM	7171 FPKM	
ANXA4	SNP 1:kp0882337	2	2 SNP 9:rs6546548	0.5	0.5	4	12.1379	4.7565	2.55185356
RAC2	SNP 3:rs8672	0.75	SNP 8:rs2239774	8	8	0.08275	319.973	268.0231	1.118928255
TP53	SNP 2:rs17879353	0.5	SNP 4:rs1042522	0.5	0.5	2.5	28.9503	13.1548	2.200749414
SLC4A1	SNP 5:rs5035	1.8	SNP 7:rs2072081	1	1	1.8	165.1352	192.3307	0.853500317
ARHGAP1B	SNP 6:kp0666929	0.76	SNP 6:kp0666929	0.71	0.71	1.070422535	665.6615	640.9633	1.038532939

FIG. 13

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Maternal-specific SNP alleles (Maternal: AB, Paternal: AA)	5641 (PET) (GA: 35 6/7)			9356 (Normal) (GA: 37 2/7)			Fold-changes of RNA- SNP ratio for each gene (5641 vs 7171)	Expression level in the placenta		
	SNPs	Maternal allele/shared allele ratio	Average RNA- SNP ratio per gene	SNPs	Maternal allele/shared allele ratio	Average RNA- SNP ratio per gene		5641 PPKM	9356 PPKM	Fold-changes of PPKM (5641 vs 7171)
TRAK2	SNP 2.kgp14544935	1	1	SNP 62.rs11616520 SNP 63.rs3761656 SNP 64.rs13622344	0.6 1.47 1.04	1.11	0.900900501	85.0691	818.1783	0.153728125
PCSK5	SNP 26.kgp2626205	0.33	0.33	SNP 46.rs1562220	1.54	1.54	0.214285714	22.3438	15.3949	1.451376755
LAPTM5	SNP 7.kgp15703050	0.12	0.12	SNP 36.rs8048	1.43	1.43	0.083818564	212.9864	117.3578	1.83866158
ASAH1	SNP 3.kgp3689333	0.67	0.67	SNP 62.rs7152182	1	1	0.67	35.6956	78.8371	0.452776675
BNP3L	SNP 5.rs17310285	2.5	2.5	SNP 5.rs17310285 SNP 66.rs1642862	1.09 0.78	0.94	2.659574469	139.8633	793.6419	0.178210609
CCND2	SNP 11.rs1048806	1	1	SNP 11.rs1048806 SNP 42.rs2217625	1.07 4	2.54	0.393700787	39.8564	22.9748	1.738118478
DAZAP2	SNP 25.kgp1918624	1.67	1.67	SNP 43.rs1549487	1.43	1.43	1.487832168	104.3778	84.1193	1.248830682
GAS7	SNP 31.rs2240739	0.67	0.67	SNP 46.rs14583 SNP 56.rs1658888	0.25 1.5	0.82	0.791363636	12.6931	7.2272	1.758295661
LAMP1	SNP 25.kgp2609974	1.33	1.33	SNP 53.rs11639846	0.36	0.36	3.5	72.976	38.5819	1.843670971
SLC4A1	SNP 4.rs9026	1.8	1.8	SNP 64.rs13368786	0.83	0.83	2.188674599	165.1352	728.2616	0.223770222
SH2D3C	SNP 17.rs14028	2.5	2.5	SNP 67.rs35011876	5	5	0.5	31.7735	5.1872	6.198878754
IKZF1	SNP 21.kgp3628738	3	3	SNP 82.rs72644708 SNP 83.rs72644705	1.6 0.8	1.2	2.5	45.9371	28.2684	1.625933686
EF2AK1	SNP 22.rs2839	0.25	0.25	SNP 76.rs2640 SNP 92.rs2836	0.8 0.71	0.76	0.333333333	68.0985	133.8252	0.517166803
ANKA1	SNP 1.kgp8682237	2	2	SNP 61.rs2228203 SNP 66.rs112136	0.61 1.1	0.81	2.167802158	12.1378	24.8466	0.4884742
CNPPD1	SNP 8.rs1043156	2	2	SNP 66.rs112136 SNP 66.rs1127102 SNP 66.rs1043160 SNP 67.rs1127101	1.06 1.36 0.61	1.04	1.023076923	26.7431	163.7143	0.163352255
UACA	SNP 16.rs334085	1.5	1.5	SNP 16.rs334085 SNP 47.rs4776523 SNP 47.rs4776525	1.6 0.2 0.2	0.9	1.888656667	12.9841	23.1721	0.580333332
BSG	SNP 10.rs2228864	1.1	1.1	SNP 65.rs4662 SNP 67.rs8637 SNP 68.rs8759	1.2 1.32 0.96	1.16	0.948275862	151.0873	867.8964	0.174084488
NEAT1	SNP 32.rs680413	1.67	1.67	SNP 32.rs680413 SNP 41.rs2228865	1.12 4.6	2.81	0.59430665	83.9749	20.5134	4.093680728
BCI2	SNP 36.rs1564483	2	2	SNP 66.rs1127102 SNP 66.rs1127102	0.29 1.06	0.29	6.898951724	13.8146	11.001	1.237605672
MAAX	SNP 15.rs4902359	0.75	0.75	SNP 44.rs4902357 SNP 45.rs1557649 SNP 46.rs1557646 SNP 18.rs4902356	0.62 0.75 0.74 0.64	0.69	1.08956522	186.4524	117.3962	1.58381624
FAM65B	SNP 12.rs12183109	0.5	0.5	SNP 77.rs11285	1	1	0.5	38.0914	39.9277	0.969956534
CAPN2	SNP 6.rs17588 SNP 13.kgp4535923	0.33 0.2	0.27	SNP 36.rs378383 SNP 6.rs17588 SNP 40.rs10661	0.62 0.48 0.93	0.77	0.359549351	59.5279	47.4986	1.253258855
HLA-DPB1	SNP 27.kgp4559778	0.25	0.25	SNP 76.rs41158014	0.12	0.12	2.053333333	62.8314	99.6788	0.682918939
SMCR8	SNP 35.rs3629956	0.5	0.5	SNP 51.rs1563832 SNP 52.rs921865	1 0.67	0.83	0.602408638	4.3801	5.1191	0.855805665
STB GAL1	SNP 19.rs2284749	1	1	SNP 19.rs2284749 SNP 75.rs4688848 SNP 76.rs1801380 SNP 76.rs75735	1.27 4.5 4.5 0.4	2.64	0.480196078	15.0179	12.2028	1.230892958
RAB5A	SNP 6.rs3745314 SNP 26.rs1772795 SNP 50.rs1040994 SNP 37.rs1643346	0.71 1.33 0.44 1	0.87	SNP 66.rs3745313 SNP 66.rs3745314 SNP 26.rs1772795 SNP 37.rs1043346 SNP 60.rs1643347	1.86 0.82 1.17 0.36 0.78	1.02	0.852841176	150.8067	67.5592	2.232215598
MYH9	SNP 28.kgp7015884	1.25	1.25	SNP 66.rs2461 SNP 66.rs7078 SNP 70.rs12107 SNP 71.rs1108787	1.35 0.46 0.47 1.38	0.93	1.344886022	547.5622	125.4471	4.36044708
ARL6IP5	SNP 35.rs7038	2	2	SNP 72.rs6005086	0.5	0.5	4	67.8305	77.8226	0.743194848
CTSB	SNP 34.kgp8442325	0.2	0.2	SNP 84.rs138489258	0.21	0.21	0.952380952	40.7536	124.8545	0.326411143
DAXX	SNP 23.rs1058231	4	4	SNP 23.rs1058231	1	1	4	33.1412	14.2532	2.325176101
C7orf41	SNP 15.rs2110394	3	3	SNP 80.rs704829 SNP 81.rs3760689	0.67 1.11	0.89	3.370786517	87.1367	86.8271	1.003565707
OPAT	SNP 14.kgp7301324 SNP 24.kgp8804495	0.4 0.4	0.4	SNP 76.rs7643844	1.5	1.5	0.266666667	13.0804	34.8355	0.375612078

FIG. 14

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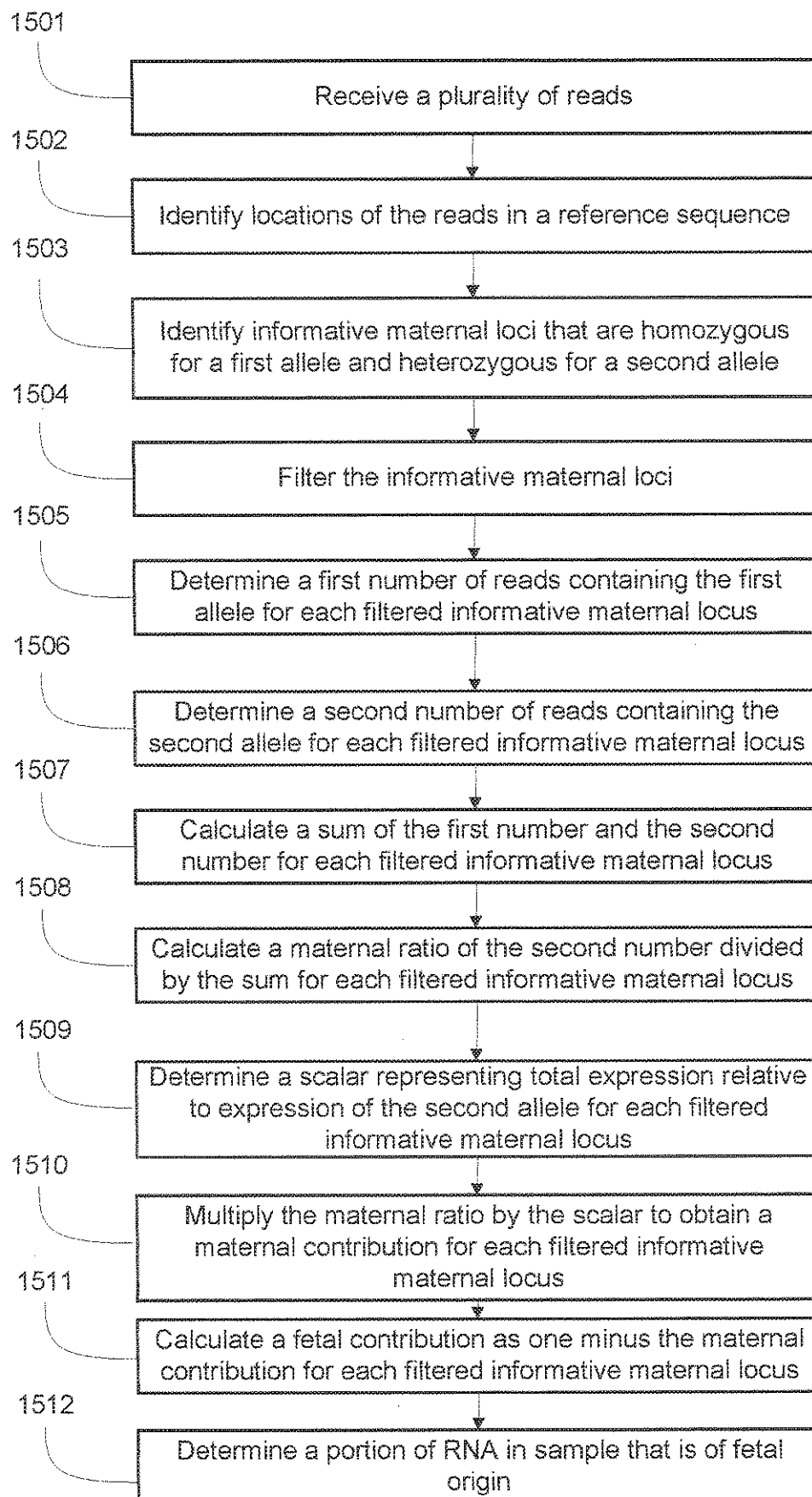


FIG. 15

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	Early pregnancy		Late pregnancy	
	no. of SNPs	no. of genes ^a	no. of SNPs	no. of genes
<i>Fetal-specific SNP alleles (fetus=AB, mother=AA):</i>				
Total informative SNPs/genes	16,051	6,714	20,643	7,788
SNPs/genes after ASE filtering	NA ^b		19,463	7,581
Transcripts in maternal plasma	4,470	2,647 (39.43%) ^c	7,114	3,813 (48.96%)
Fetal contribution (total)	109	98 (3.70%) ^d	504	430 (11.28%)
High fetal contribution	25	24 (0.91%) ^e	112	96 (2.52%)
<i>Maternal-specific SNP alleles (fetus=AA, mother=AB):</i>				
Total informative SNPs/genes	15,962	6,753	19,833	7,761
SNPs/genes after ASE filtering	NA		19,343	7,656
Transcripts in maternal plasma	4,414	2,654 (39.30%)	6,995	3,717 (47.89%)
Maternal contribution (total)	3,156	2,041 (76.90%)	5,023	2,911 (78.32%)
High maternal contribution	1,634	1,130 (42.58%)	3,002	1,895 (50.98%)

a. Number of genes that contained informative SNPs.

b. Allele-specific expression (ASE) filtering was not performed for early pregnancy samples.

c. % of total informative genes that was present in maternal plasma.

d. % of maternal plasma transcripts contributed by fetus.

e. % of maternal plasma transcripts contributed highly by fetus.

FIG. 16

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	Late pregnancy	
	no. of SNPs	no. of genes ^a
<i>Fetal-specific SNP alleles (fetus=AB, mother=AA):</i>		
Total informative SNPs/genes	20,643	7,788
Transcripts in maternal plasma	7,303	3,839 (49.29%) ^b
Fetal contribution (total)	581	485 (12.63%) ^c
High fetal contribution	132	111 (2.89%) ^d
<i>Maternal-specific SNP alleles (fetus=AA, mother=AB):</i>		
Total informative SNPs/genes	19,833	7,761
Transcripts in maternal plasma	7,365	3,829 (49.34%)
Maternal contribution (total)	5,326	3,014 (78.72%)
High maternal contribution	3,321	1,986 (51.87%)

a. Number of genes that contained informative SNPs.

b. % of total informative genes that was present in maternal plasma.

c. % of maternal plasma transcripts contributed by fetus.

d. % of maternal plasma transcripts contributed highly by fetus.

FIG. 17

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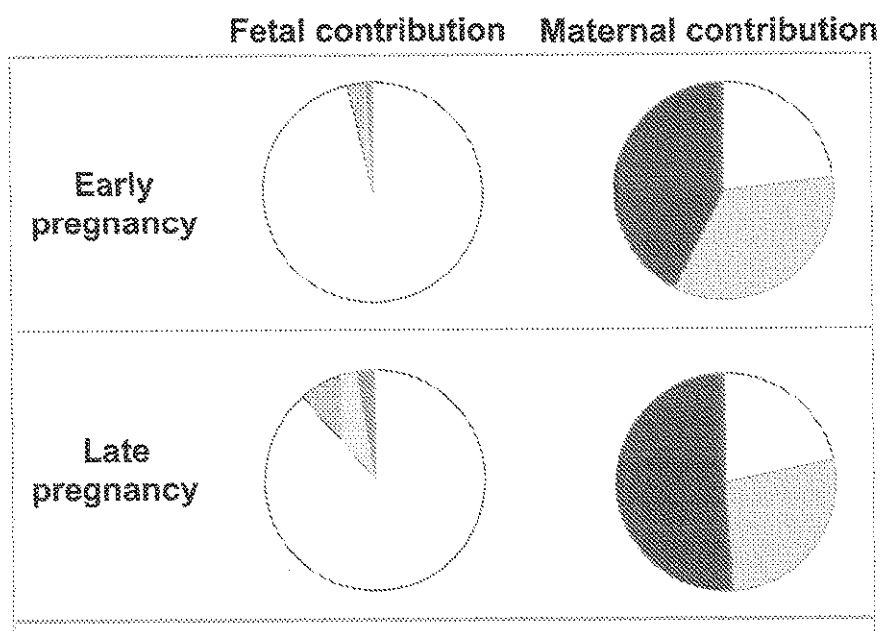


FIG. 18A

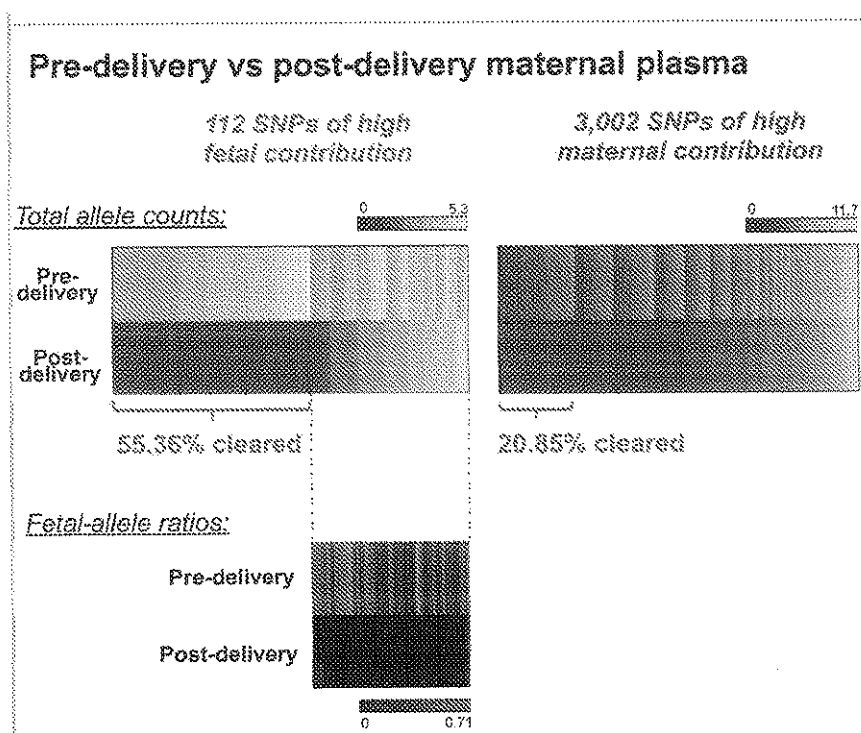


FIG. 18B

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GNAS (SNP locus: rs7121)	Genotyping	A-allele count (shared allele)	B-allele count (Maternal-specific)	Fractional maternal contribution, $M = \frac{2 \times \text{Maternal allele}}{\text{Maternal} + \text{Fetal allele}}$	Fractional fetal contribution, $F = 1 - M$	FPKM	% change in fractional fetal contribution vs control	% change in fractional maternal contribution vs control
7171 (Control)	Mother: AB, Fetus: AA	7	6	0.92	0.08	310.3		
GNAS (SNP locus: rs7121)	Genotyping	A-allele count (shared allele)	B-allele count (Fetal-specific)	Fractional fetal contribution, $F = \frac{2 \times \text{Fetal allele}}{\text{Maternal} + \text{Fetal allele}}$	Fractional maternal contribution, $M = 1 - F$	FPKM	% change in fractional fetal contribution vs control	% change in fractional maternal contribution vs control
5841 (PET)	Mother: AA, Fetus: AB	81	4	0.09	0.91	376.2	$(0.91 - 0.92) / 0.92 \times 100 = -1.09\%$	$(0.09 - 0.08) / 0.08 \times 100 = +12.5\%$

FIG. 19

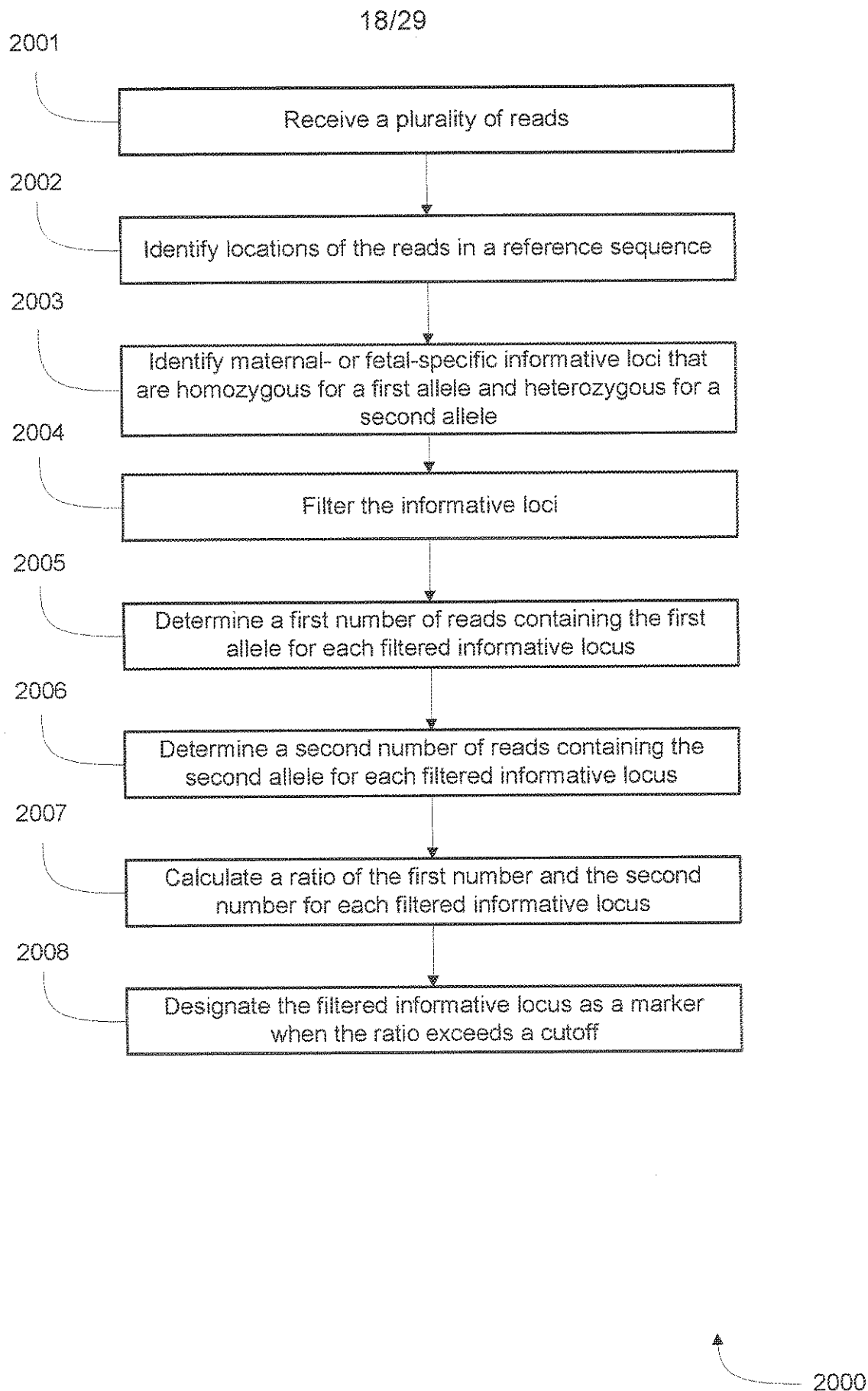


FIG. 20

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Gene	Case 9356			Case 9416			Remark (references)
	Pre-delivery plasma (transcript level)	Post-delivery plasma (transcript level)	Fold-change	Pre-delivery plasma (transcript level)	Post-delivery plasma (transcript level)	Fold-change	
CSH1	1391.00	17.68	78.78	798.21	1.13	704.89	a (1)
KISS1	433.89	8.25	52.56	147.36	7.26	20.29	a (2)
STAT1	227.34	104.49	2.18	275.22	85.30	3.23	b
CGA	270.02	6.98	38.67	134.19	1.00	134.19	
CSH2	136.04	3.89	34.96	185.78	2.74	67.84	
TFFI2	216.09	15.11	14.30	85.16	3.55	24.02	a (2)
GBP1	99.47	45.89	2.17	153.00	63.58	2.41	b
PLAC4	177.67	1.03	172.41	69.32	1.00	69.32	a (3)
HSD17B1	140.14	5.94	23.58	93.76	25.56	3.67	b
CSHL1	140.57	1.00	140.57	66.97	1.00	66.97	a (4)
KRT8	86.47	23.42	3.69	76.78	13.28	5.78	c
KRT18	86.76	25.92	3.35	64.11	20.27	3.16	b
HPGD	87.76	38.45	2.28	39.05	13.36	2.92	d
GADD45G	48.62	20.75	2.35	73.22	23.37	3.13	b
LGALS14	56.55	1.00	56.55	62.88	1.00	62.88	
HSD3B1	60.62	3.51	17.28	48.26	1.00	48.26	
KRT19	77.95	24.04	3.24	30.71	3.52	8.71	
SERPINE1	37.39	15.29	2.45	60.99	12.71	4.79	a (5)
GDF15	62.32	3.68	16.92	33.52	12.10	2.77	
CYP19A1	70.84	4.90	14.47	18.65	1.00	18.65	
PSG4	36.10	1.45	24.89	47.82	1.00	47.82	
PSG3	53.00	1.00	53.00	23.03	1.00	23.03	
CRYAB	15.46	1.00	15.46	58.22	4.50	12.93	
HSPB8	35.57	6.62	5.37	36.79	13.47	2.73	
PKIB	45.08	8.79	5.13	26.12	8.09	3.23	
PGF	44.72	5.40	8.29	24.94	3.80	6.57	
CYP11A1	40.77	3.64	11.20	28.04	1.71	16.41	
PSG5	42.56	1.00	42.56	25.66	1.00	25.66	
PSG1	37.70	1.49	25.29	28.17	1.00	28.17	
PAPPA	40.90	5.91	6.92	20.03	1.00	20.03	a (6)
ADAM12	44.48	4.01	11.09	15.16	1.00	15.16	a (7)
PSG2	29.16	1.00	29.16	29.95	1.00	29.95	
VGLL3	34.80	1.98	17.54	20.36	1.80	11.34	
KRT7	27.20	10.39	2.62	26.54	9.75	2.72	
TMEM54	32.99	5.94	5.56	18.70	5.22	3.58	
PRKCZ	28.22	10.05	2.81	23.12	8.76	2.64	
SDC1	30.62	2.62	11.68	17.43	1.84	9.45	
LGALS13	32.32	1.00	32.32	15.60	1.00	15.60	
EFHD1	15.55	2.80	5.56	30.55	3.94	7.76	
CAPN6	23.18	1.64	14.14	22.90	1.00	22.90	
XAGE3	25.08	2.59	9.67	13.08	1.00	13.08	
EBI3	18.79	6.48	2.90	17.96	7.30	2.46	
GH2	19.16	1.00	19.16	17.22	1.00	17.22	a (7)
PAGE4	28.89	2.99	9.67	6.28	1.00	6.28	

FIG. 21

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Gene	Case 3356			Case 9415			Remark (references)
	Pre-delivery plasma (transcript level)	Post-delivery plasma (transcript level)	Fold-change	Pre-delivery plasma (transcript level)	Post-delivery plasma (transcript level)	Fold-change	
ALPP	19.62	1.54	12.73	14.03	1.00	14.03	
INHSA	18.99	2.71	7.01	14.51	4.29	3.38	a (5)
LOC100505658	17.53	1.00	17.53	15.65	1.00	15.65	
FBLN1	10.12	2.12	4.76	20.01	1.28	15.62	
SEMA3B	16.06	2.52	6.38	12.90	1.00	12.90	
GPC3	18.22	1.00	18.22	10.12	1.00	10.12	
PLAC2	19.86	1.99	9.96	8.04	1.97	4.09	
PSG9	7.10	1.00	7.10	20.32	1.00	20.32	a (8)
FN1	17.30	6.57	2.63	9.72	3.81	2.55	
NOS3	10.01	3.45	2.90	16.07	7.08	2.27	
LOC100506655	12.29	1.00	12.29	13.53	1.00	13.53	
PSG11	19.48	1.83	10.63	5.77	1.00	5.77	
SPTLC3	19.82	1.00	19.82	4.99	1.00	4.99	
EXPH5	12.58	4.48	2.81	12.09	2.24	5.40	
HSPA2	12.86	5.85	2.20	11.40	4.87	2.34	
PSG8	10.66	1.00	10.66	13.38	1.00	13.38	
PLAC1	17.08	1.00	17.08	6.60	1.00	6.60	a (3)
TACC2	5.93	1.81	3.89	16.24	1.64	9.89	
PRPF40B	8.27	3.98	2.08	12.53	5.32	2.36	
LOC388946	12.97	1.00	12.97	7.71	1.00	7.71	
SERPINE2	13.48	1.36	9.91	6.86	1.44	4.77	a (9)
CRH	15.40	1.00	15.40	4.75	1.00	4.75	a (10)
GBP1P1	6.35	1.19	5.32	13.04	5.04	2.59	
CLDN4	12.50	1.00	12.50	6.45	2.84	2.27	
C2orf72	11.14	3.29	3.38	7.26	1.74	4.18	
PAPPA2	10.92	1.53	7.13	7.48	1.00	7.48	
HIST2H3A	14.75	7.27	2.03	2.44	1.02	2.39	
HIST2H3C	14.75	7.27	2.03	2.44	1.02	2.39	
TCL6	12.92	1.00	12.92	3.93	1.00	3.93	
MFSD2A	8.09	3.35	2.42	8.72	1.60	5.72	
ZFAT-AS1	9.10	3.14	2.90	7.25	3.31	2.19	
INSL4	13.90	2.40	5.80	2.01	1.00	2.01	
DHRG2	12.24	6.11	2.00	3.30	1.00	3.30	
HES2	11.03	3.11	3.54	4.50	1.46	3.08	
WLS	11.06	4.77	2.32	4.40	1.66	2.63	
PLCXD3	10.49	3.62	2.90	4.88	2.01	2.43	
LOC100505483	5.40	1.00	5.40	9.39	2.62	3.58	
C1orf130	11.60	1.85	6.28	2.48	1.00	2.48	
FOSB	3.02	1.00	3.02	10.65	4.94	2.16	
GCM1	5.93	1.60	3.71	6.94	1.00	6.94	a (8)
TRPV6	9.31	1.00	9.31	3.41	1.00	3.41	
TFAP2A	4.02	1.00	4.02	8.59	1.46	5.87	
MMP11	10.08	1.96	5.16	2.46	1.00	2.46	
TUSC3	9.90	2.66	3.73	2.55	1.00	2.55	
HMGCR	7.15	2.25	3.18	5.13	2.26	2.27	

FIG. 21 cont.

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Gene	Case 9356			Case 9415			Remark (references)
	Pre-delivery plasma (transcript level)	Post-delivery plasma (transcript level)	Fold-change	Pre-delivery plasma (transcript level)	Post-delivery plasma (transcript level)	Fold-change	
CCK	7.08	1.00	7.08	4.98	1.00	4.98	
LOC100129935	6.56	1.61	5.32	3.38	1.00	3.38	
C8orf39	4.02	1.00	4.02	7.86	2.93	2.69	
GLDN	9.39	1.00	9.39	2.44	1.00	2.44	
PGAP3	6.10	2.19	2.78	4.84	2.32	2.09	
MSX2P1	3.63	1.00	3.63	6.87	3.36	2.05	
GH1	4.33	1.00	4.33	5.02	1.00	6.02	
SVEP1	7.79	2.98	2.61	2.26	1.00	2.26	
PPP1R32	2.78	1.00	2.78	7.24	1.35	5.37	
PSC8	5.01	1.00	5.01	4.94	1.00	4.94	
ENDOU	7.24	2.40	3.02	2.27	1.00	2.27	
ECFR	6.83	1.00	6.83	2.54	1.00	2.54	
DUSP4	5.24	1.61	3.26	4.13	1.41	2.92	
PHYHPL	5.53	1.00	5.53	3.48	1.39	2.51	
CTSF	6.01	1.00	6.01	2.77	1.03	2.69	
TRIM29	3.54	1.00	3.54	5.13	1.00	5.13	
RCN3	3.07	1.00	3.07	5.34	1.12	4.77	
SPRE2	5.93	2.27	2.61	2.48	1.00	2.48	
LOC100216001	4.60	1.06	4.35	3.55	1.49	2.39	
FAM178A	5.76	2.10	2.74	2.36	1.00	2.36	
SCN	5.18	1.00	5.18	2.82	1.00	2.82	
ZNF500	2.41	1.00	2.41	5.52	2.23	2.47	
PRR16	2.83	1.00	2.83	4.91	1.18	4.18	
LOC100128054	4.55	1.05	4.35	3.08	1.00	3.08	
OLR1	4.53	1.17	3.87	2.71	1.00	2.71	
SLC30A2	5.18	1.00	5.18	2.00	1.00	2.00	
LOC285972	3.48	1.00	3.48	3.84	1.02	3.68	
HESX1	4.25	1.26	3.38	2.64	1.00	2.64	
TMEM139	4.61	1.00	4.61	2.25	1.00	2.25	
ZNF727	3.82	1.00	3.82	2.58	1.24	2.09	
TNFSF19	4.04	1.39	2.90	2.34	1.00	2.34	
EFS	3.88	1.00	3.88	2.38	1.00	2.38	
TMD4	2.08	1.00	2.08	3.62	1.51	2.39	
ALDH3B2	2.91	1.00	2.91	2.76	1.00	2.76	
KRT81	2.61	1.00	2.61	2.92	1.00	2.92	
MUC15	2.94	1.00	2.94	2.19	1.00	2.19	
PRSS8	2.20	1.00	2.20	2.87	1.00	2.87	
SH2D5	2.41	1.00	2.41	2.42	1.00	2.42	
LOC728175	2.28	1.00	2.28	2.31	1.10	2.09	
GRHL2	2.45	1.00	2.45	2.13	1.00	2.13	
PABPN1L	2.18	1.00	2.18	2.37	1.00	2.37	
CORO8	2.08	1.00	2.08	2.07	1.00	2.07	

Remark:

- Transcripts previously reported to be pregnancy-associated in maternal plasma
- Transcripts newly identified in this study by maternal plasma RNA-seq and validated by real-time RT-PCR (Supplemental Data Fig. 6)
- KRT8 mRNA was not studied by real-time RT-PCR as the detection assay cannot be designed
- Real-time RT-PCR result showed that maternal plasma *HPGD* mRNA did not show clearance pattern after delivery (Supplemental Data Fig. 6)

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- Ng EKO, Leung TN, Tsui NBY, Lau TK, Panesar NS, Chiu RWK, Lo YMD. Clin Chem 2003;49:727-31.

FIG. 21 cont.

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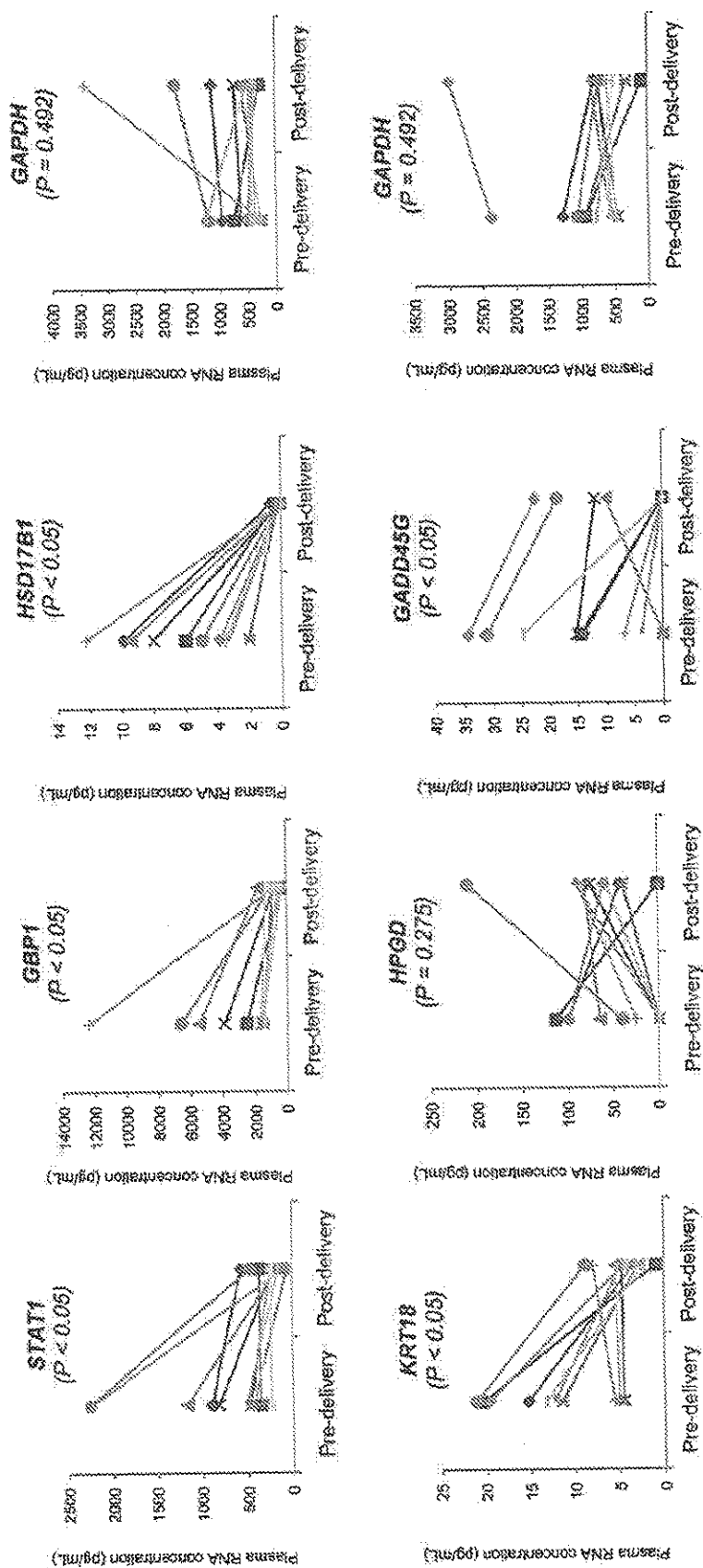


FIG. 22

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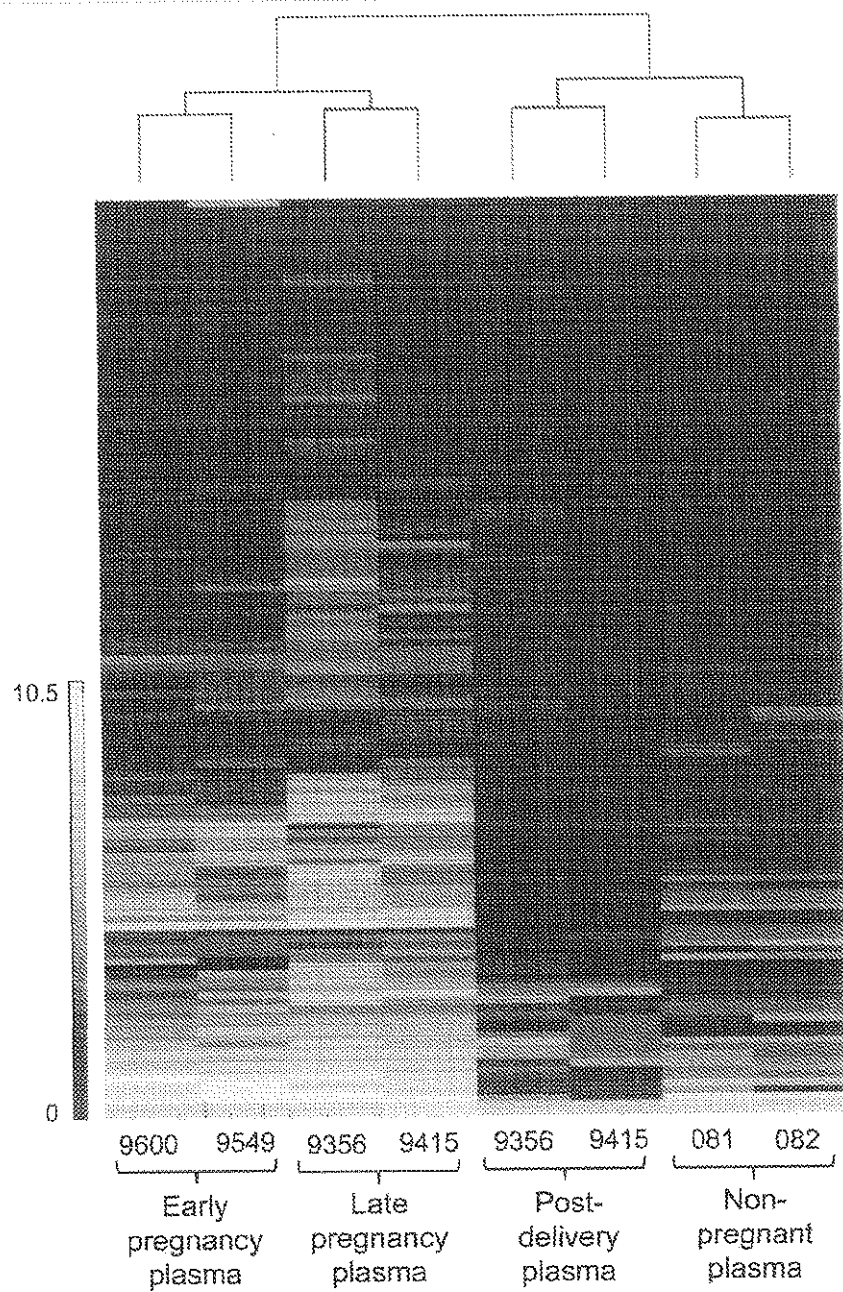


FIG. 23

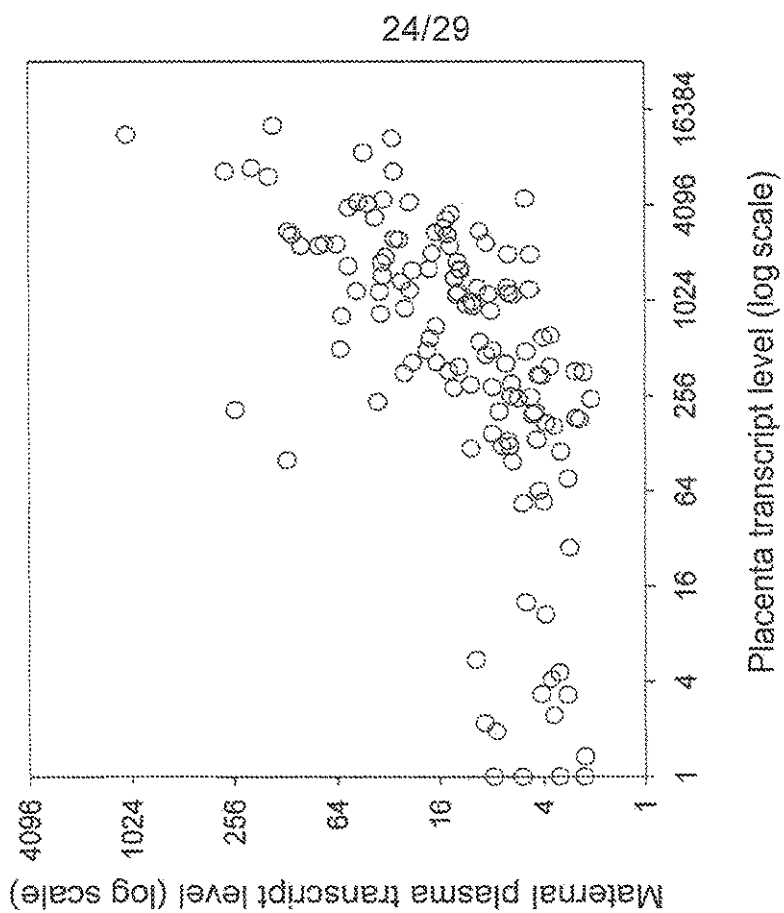


FIG. 24B

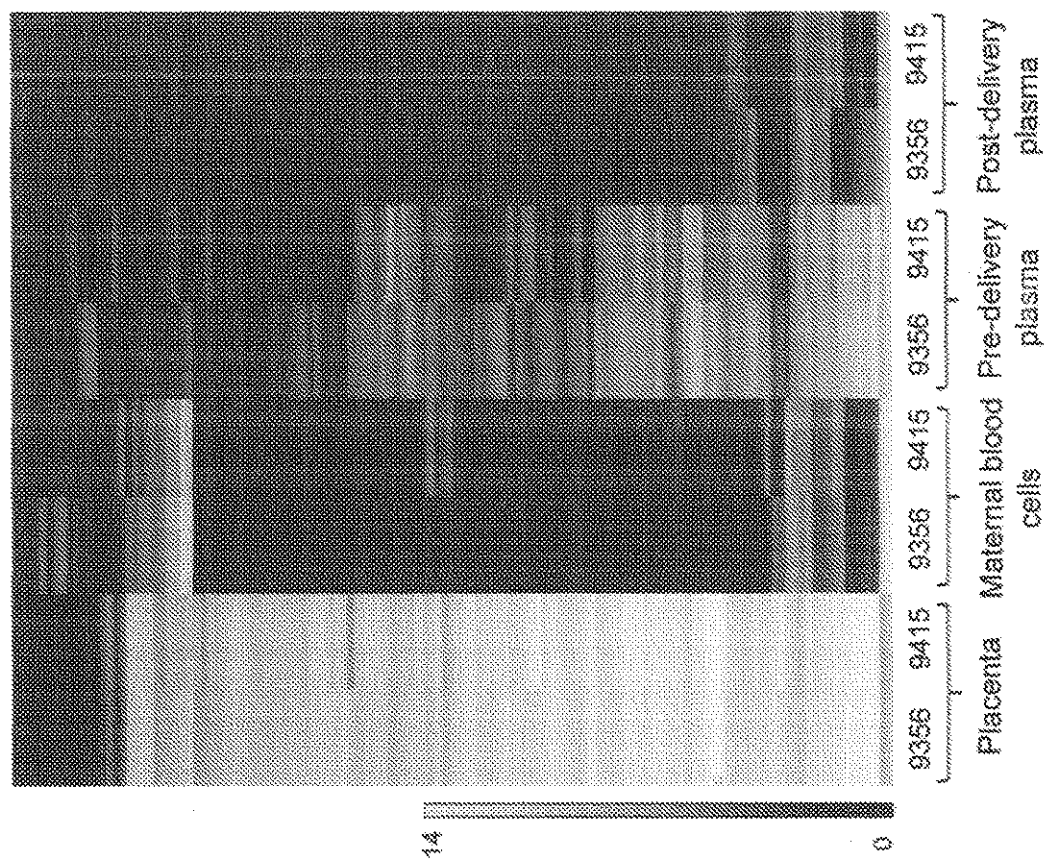
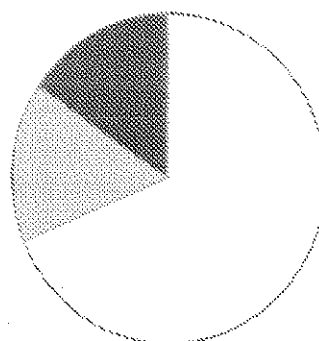
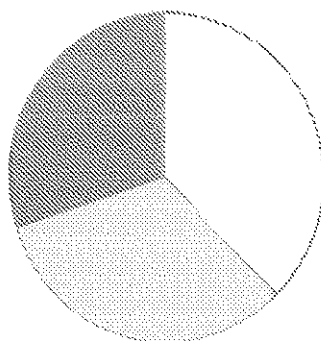


FIG. 24A

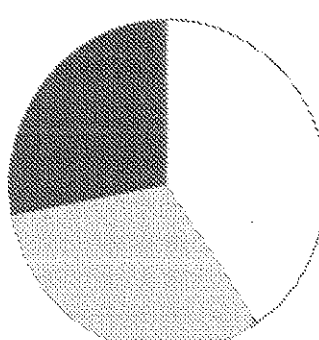
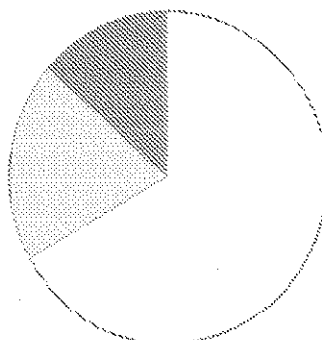
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Fetal contribution Maternal contribution

**Plasma-based
identification**
(131 transcripts)



**Tissue-based
identification**
(798 transcripts)



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RNAs	Preeclampsia	Normal	RNAs	Preeclampsia	Normal
ADAM9	26.78	11.26	LY6E	84.52	31.38
AGBL5	144.47	65.14	MEIS1	79.49	18.77
APOBR	64.12	26.31	MLH3	150.61	36.10
APOL2	59.24	29.05	MYADM	51.11	16.60
APP	212.58	84.93	NCF1	107.35	41.90
ASAH1	167.14	47.38	NCF1B	34.80	9.41
ATP5I	23.85	9.20	NDUFA1	20.73	7.36
ATP6V0E1	60.73	20.56	NES	176.78	58.83
B2M	1765.75	654.19	NFAM1	49.17	17.91
BCAP31	42.85	14.86	NGFRAP1	106.72	19.52
BRK1	91.46	41.63	NPTN	80.63	29.97
C12orf76	16.97	4.56	NT5C3	173.39	65.34
C19orf59	22.94	6.42	OST4	404.86	100.63
C19orf79	13.22	3.00	PARK7	97.39	40.79
C1orf151-NBL1	25.89	11.19	PARP10	52.41	19.75
C21orf7	308.80	83.41	PDGFA	55.19	24.29
C7orf53	8.04	0.73	PF4	680.43	208.45
CARD16	85.90	29.13	PGRMC1	332.76	78.90
CD97	59.09	28.74	PRIC285	72.34	20.44
CEBPD	147.37	44.30	PSMB9	73.17	34.36
CTSA	341.67	138.37	RAB32	51.90	25.20
CYB5R1	25.14	10.12	RABAC1	25.10	7.80
DDX11L10	38.97	7.34	RBX1	36.44	15.06
DUSP1	168.06	30.57	RNF213	316.69	147.00
DYNLRB1	166.30	59.63	RPPH1	242.37	63.73
EMP3	99.80	39.75	S100P	48.92	14.31
ENKUR	64.87	15.45	S1PR3	9.45	1.41
GALM	31.68	5.09	SAT1	213.55	100.86
GDI1	91.22	41.05	SEPT3	14.54	6.35
HIST1H2AC	271.60	72.77	SERF2	310.66	144.79
HIST1H3H	131.91	40.96	SHISA5	141.53	59.85
HIST1H4A	20.40	5.53	SIGLEC1	18.55	3.32
HIST1H4B	25.44	5.58	SIGLEC14	10.79	0.95
HIST1H4E	74.16	26.59	SNN	348.09	171.73
HIST1H4H	69.35	18.31	SOD2	569.41	229.85
HIST1H4L	20.99	6.89	SPARC	914.92	286.17
HLA-C	417.81	203.10	TIMP1	76.27	27.68
HLA-L	11.78	3.90	TMEM140	121.93	29.08
HRC	14.87	0.16	TMEM185A	36.93	12.09
HSPA1A	37.29	14.90	TMEM50A	139.68	32.72
IFI6	171.27	18.29	TRIM22	135.78	58.79
ISG20	86.19	23.09	TSC22D3	330.23	108.27
JAM3	121.57	52.31	UBE2L6	171.88	63.40
KLF6	127.12	62.64	VKORC1L1	63.06	25.17
LEPR	43.19	17.71	VTRNA1-1	7.23	0.08
LEPROT	70.13	34.38	YIF1B	36.33	16.96
LILRA5	31.45	11.05	YPEL3	150.75	73.23
LOC146336	13.75	4.89	YWHAH	236.85	116.18
LRRC32	102.05	34.23	ZNF485	15.35	6.38

FIG. 26

PAPPA SNP rsid	DNA genotype		Placenta		Maternal blood cells		Pre-delivery maternal plasma		Post-delivery maternal plasma	
	Fetus	Mother	A	G	A	G	A	G	A	G
rs386088	GA	AA	2421	2164	0	0	16	21	0	0

FIG. 27

H19 SNP rsid	DNA genotype		Placenta		Maternal blood cells		Pre-delivery maternal plasma		Post-delivery maternal plasma	
	Fetus	Mother	Shared	Maternal-specific	Shared	Maternal-specific	Shared	Maternal-specific	Shared	Maternal-specific
rs2839698 ^a	AA	AG	3418 (A)	10 (G)	0 (A)	0 (G)	246 (A)	1679 (G)	0 (A)	808 (G)
rs2839701	GG	CG	4959 (G)	8 (C)	0 (G)	0 (C)	33 (G)	219 (C)	1 (G)	78 (C)
rs2839702	CC	AC	4996 (C)	8 (A)	0 (C)	0 (A)	38 (C)	233 (A)	2 (C)	92 (A)
rs3741219	GG	AG	2255 (G)	15 (A)	0 (G)	0 (A)	17 (G)	158 (A)	0 (G)	96 (A)

a: The shared A-allele was imprinted while the maternal-specific G-allele was transcribed. Details of the methylation status are shown in Supplemental Data Fig 5.

FIG. 28

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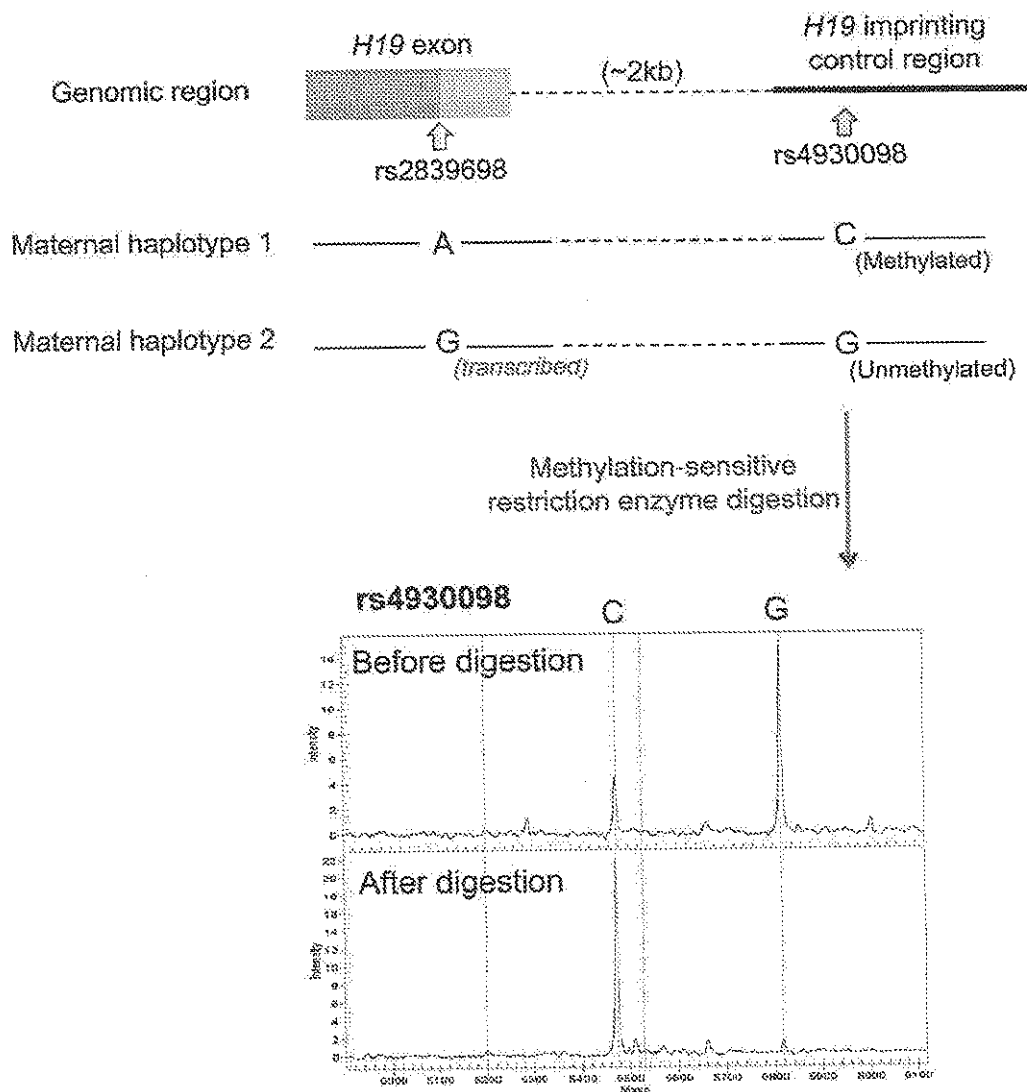


FIG. 29

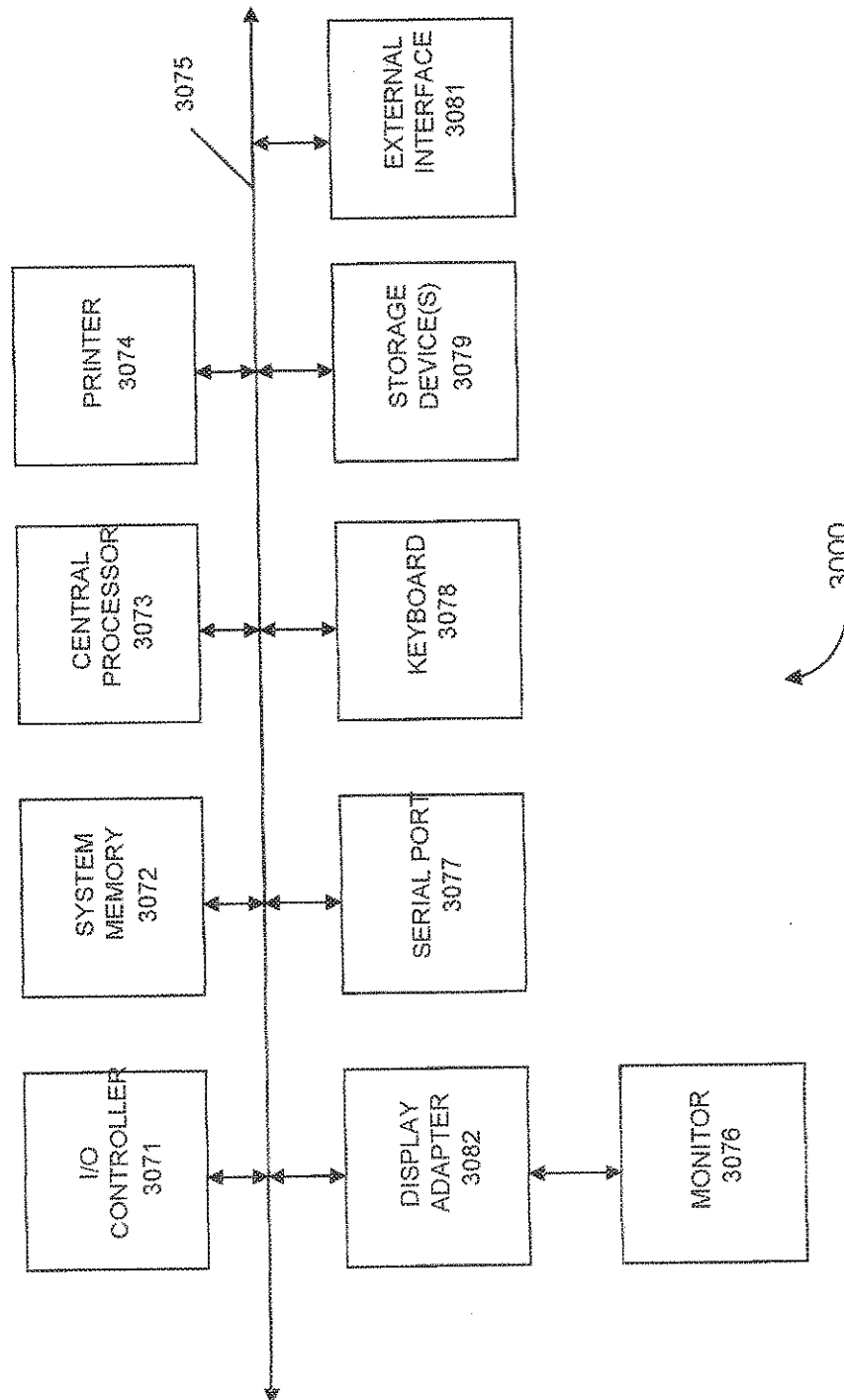


FIG. 30