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LAMPIRAN

LAMPIRAN I. KUISIONER

KUISIONER

Petunjuk Pengisian

1. Isilah titik-titik di bawah ini dan berilah tanda checklist (√) pada salah satu tanda ☐ sesuai dengan jawaban yang menurut Anda benar
2. Bila ada yang kurang dimengerti oleh Bapak/ Ibu, boleh dipertanyakan pada peneliti.

A. DATA UMUM (diisi oleh peneliti)

Kode	
Tanggal Pengambilan sampel	
No Rekam Medik	
Pewawancara	
Tempat Wawancara	
(Khusus kontak) Kode pasien/ Kontak sebagai	

B. DATA DEMOGRAFI RESPONDEN

Nama Pasien	
Jenis Kelamin	☐ Laki-laki ☐ Perempuan
Umur	.... tahun
Alamat	

Telepon	
Status perkawinan	☐ Belum kawin ☐ Kawin ☐ Janda ☐ Duda
Pekerjaan	....
Pendidikan Terakhir	☐ SD ☐ SMP ☐ SMA/ SMK ☐ S1 ☐ S2 ☐ S3 ☐ Tidak sekolah
Berat Badan	.... kg
Tinggi Badan	.... cm
Suku Bangsa	☐ Bugis ☐ Makassar ☐ Mandar ☐ Toraja ☐ Jawa ☐ Tionghoa ☐ Lain-lain : ....
Kondisi Rumah	a. Ventilasi rumah ☐ Ada ☐ Tidak ada b. Sinar matahari yang masuk ke rumah ☐ Cukup (saat siang hari, tidak perlu menyalakan lampu) ☐ Tidak cukup c. Luas rumah: ………………….
Keluarga	a. Jenis Keluarga ☐ Keluarga inti (hanya orang tua dan anak) ☐ Keluarga extenden (orang tua, anak dan lainnya) b. Jumlah anggota keluarga serumah ☐ < 2 orang ☐ 3 orang ☐ 4 orang ☐ 5 orang ☐ > 5 orang e. Jumlah anggota keluarga sekamar

	☐ < 2 orang ☐ 2 orang ☐ > 2 orang

C. RIWAYAT PENYAKIT SAAT INI

Gejala-gejala yang Anda rasakan saat ini	a. Gejala utama : .... b. Gejala lain : ☐ Batuk ☐ Batuk darah ☐ Nyeri dada ☐ Sesak ☐ Demam ☐ Nafsu makan menurun ☐ Berat badan menurun

D. RIWAYAT KONTAK

Riwayat kontak dengan penderita TBC	a. Apakah sebelumnya Anda pernah ada kontak dengan penderita TB/batuk lama? ☐ Ya ☐ Tidak ☐ Tidak tahu Jika ya, dengan siapa? ☐ Orang satu rumah: hubungan keluarga:…………….. ☐ Teman kerja ☐ Tetangga ☐ Teman ☐ Pasien rumah sakit b. Jika orang serumah, berapa lama Anda telah tinggal bersama?

	☐ <6 bulan ☐ 6 bulan atau lebih b. Jika orang serumah, apakah Anda sekamar ? ☐ Ya ☐ Tidak

E. FAKTOR-FAKTOR RESIKO

Riwayat merokok	a. Apakah Anda merokok? ☐ Ya, hingga saat ini ☐ Pernah , saat ini berhenti ☐ Tidak pernah b. Jumlah rokok sehari:
Riwayat minum alkohol	a. Apakah Anda mengkonsumsi alkohol? ☐ Ya ☐ Tidak pernah
Riwayat penggunaan narkoba	a. Apakah Anda pernah menggunakan narkoba sebelumnya? ☐ Ya ☐ Tidak b. Jika Ya, apa nama obatnya? ....
Riwayat Diabetes Mellitus	a. Apakah Anda pernah menderita Diabetes Mellitus (penyakit gula)? ☐ Ya ☐ Tidak ☐ Tidak tahu b. Jika Ya, Kadar gula terakhir? ....

	c. Obat DM yang diminum? ....
Riwayat penggunaan obat-obat imunosupresi, steroid	a. Apakah Anda pernah atau sedang menggunakan obat-obatan jenis imunosupresi atau steroid?? ☐ Ya ☐ Tidak ☐ Tidak tahu Jika Ya, lanjutkan menjawab pertanyaan ini - Nama obat : .... - Alasan minum: .... - Lama minum :.............................
Riwayat HIV	a. Apakah Anda pernah menderita HIV? ☐ Ya ☐ Tidak ☐ Tidak tahu Jika ya, lanjutkan menjawab pertanyaan ini - Kapan didiagnosis? .... - Pernahkah minum obat anti HIV ☐ Ya ☐ Tidak Jika ya, apa nama obatnya? Apakah obat tersebut dibeli? ☐ Ya ☐ Tidak

F. RIWAYAT PENYAKIT LAINNYA

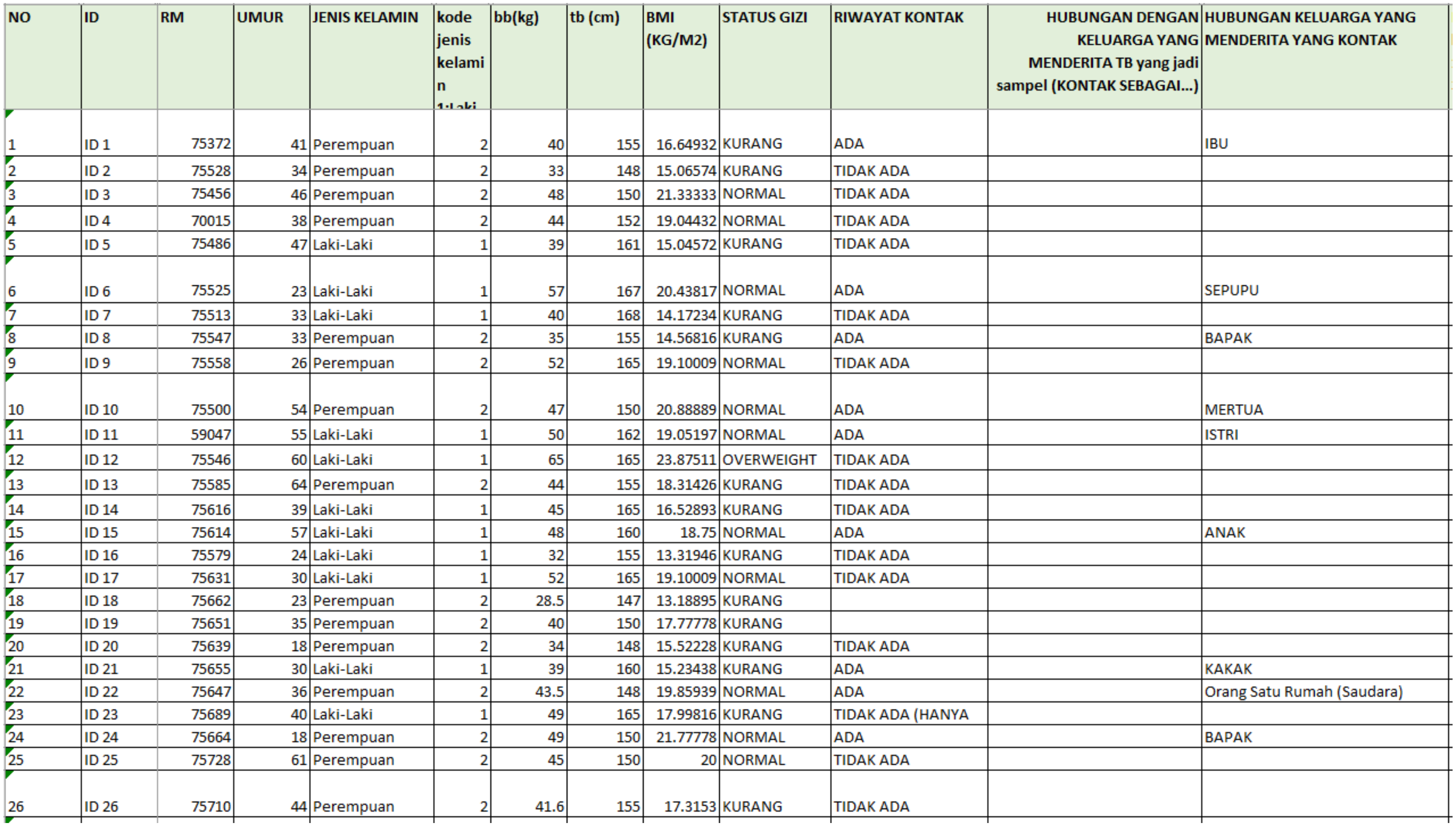
Riwayat penyakit lainnya	- ....

G. HASIL PEMERIKSAAN YANG SUDAH ADA (diisi oleh peneliti)

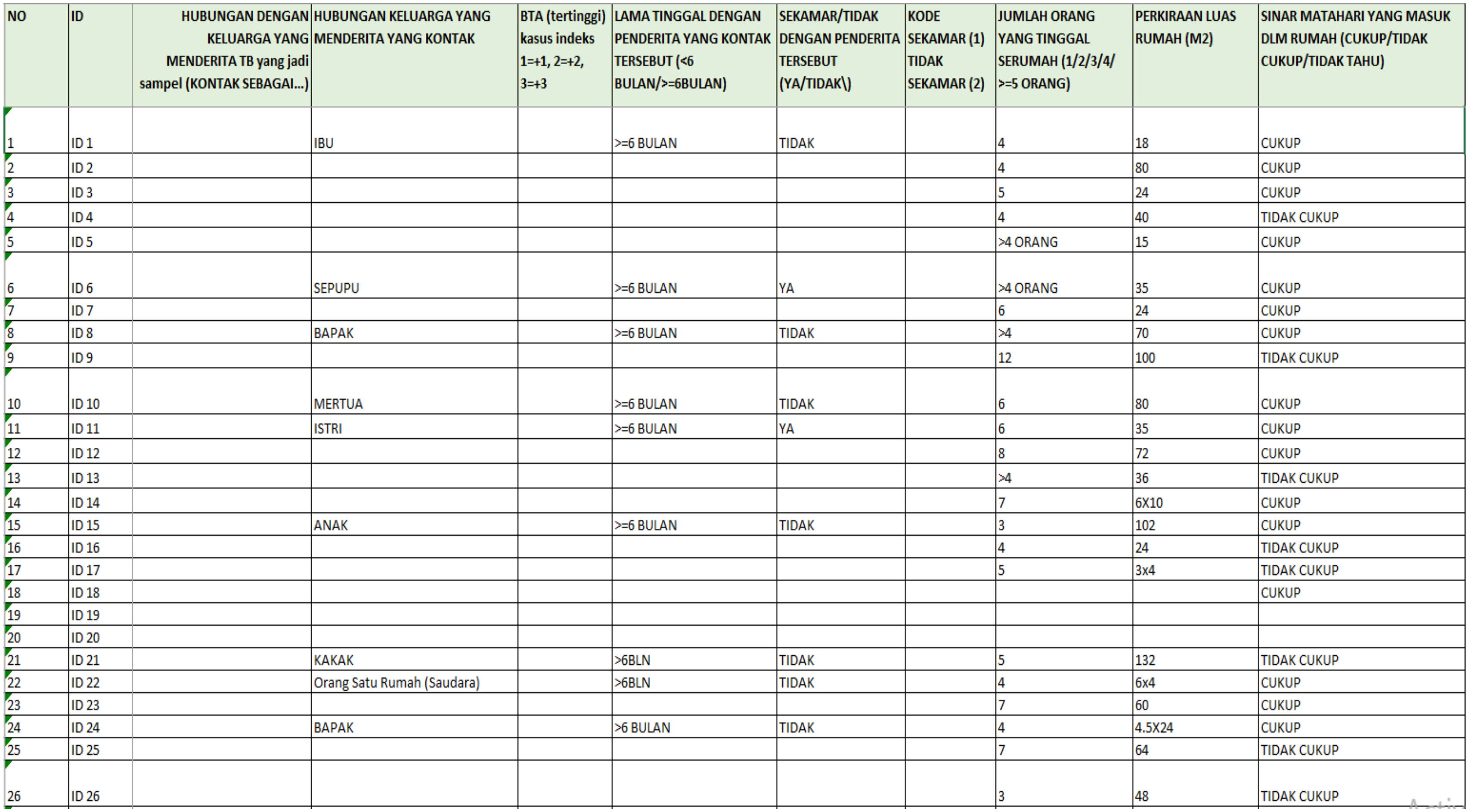
Hasil foto X-Ray thorax (khusus pasien)	

Hasil sputum BTA di tempat ini (khusus pasien)	Sputum 1: Sputum 2: Sputum 3:
Hasil pemeriksaan darah rutin	WBC : ……... Neutrofil: ……….% Limfosit: ………% Monosit: ………% Hb : ………g/dL

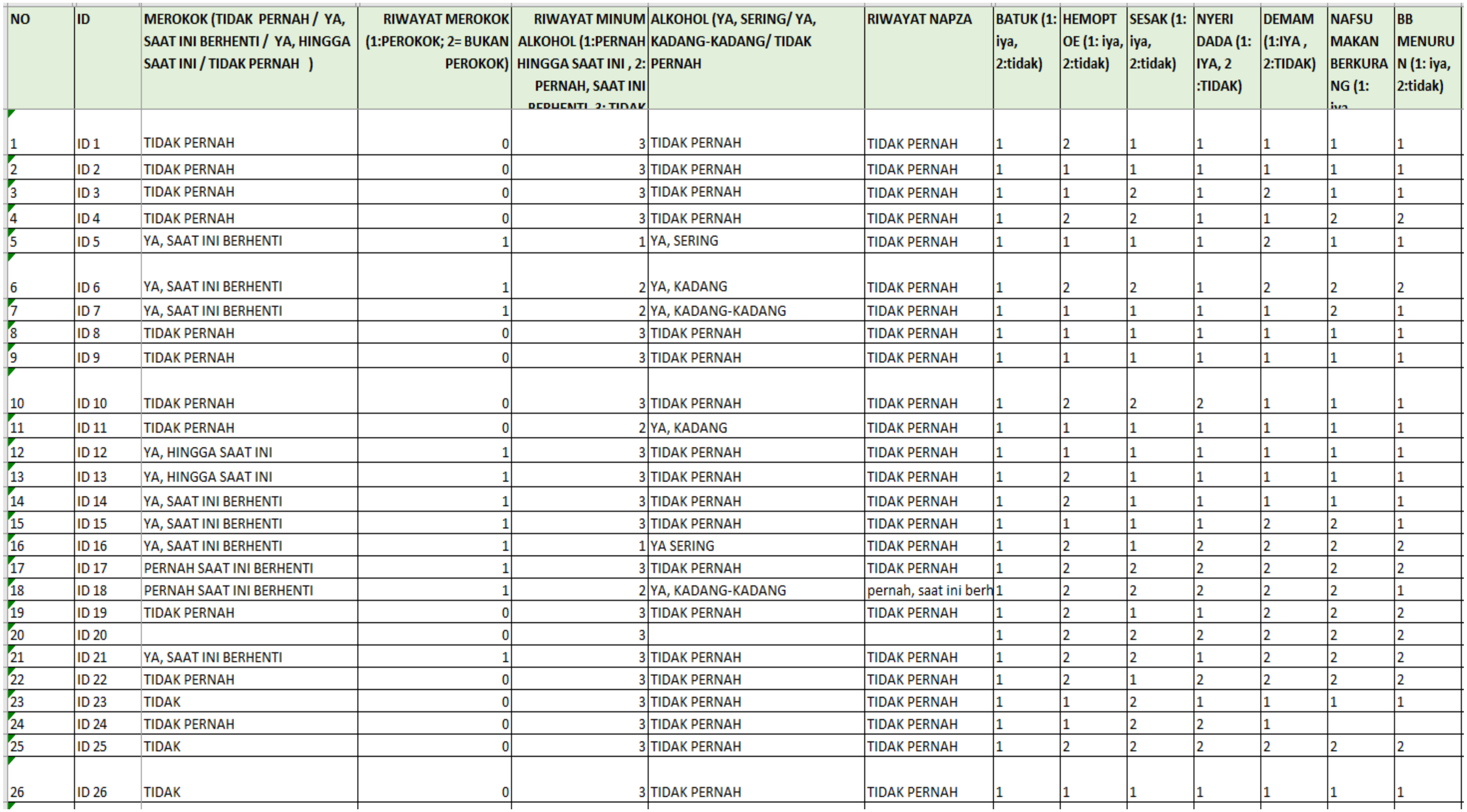
LAMPIRAN 2. DATA SAMPEL



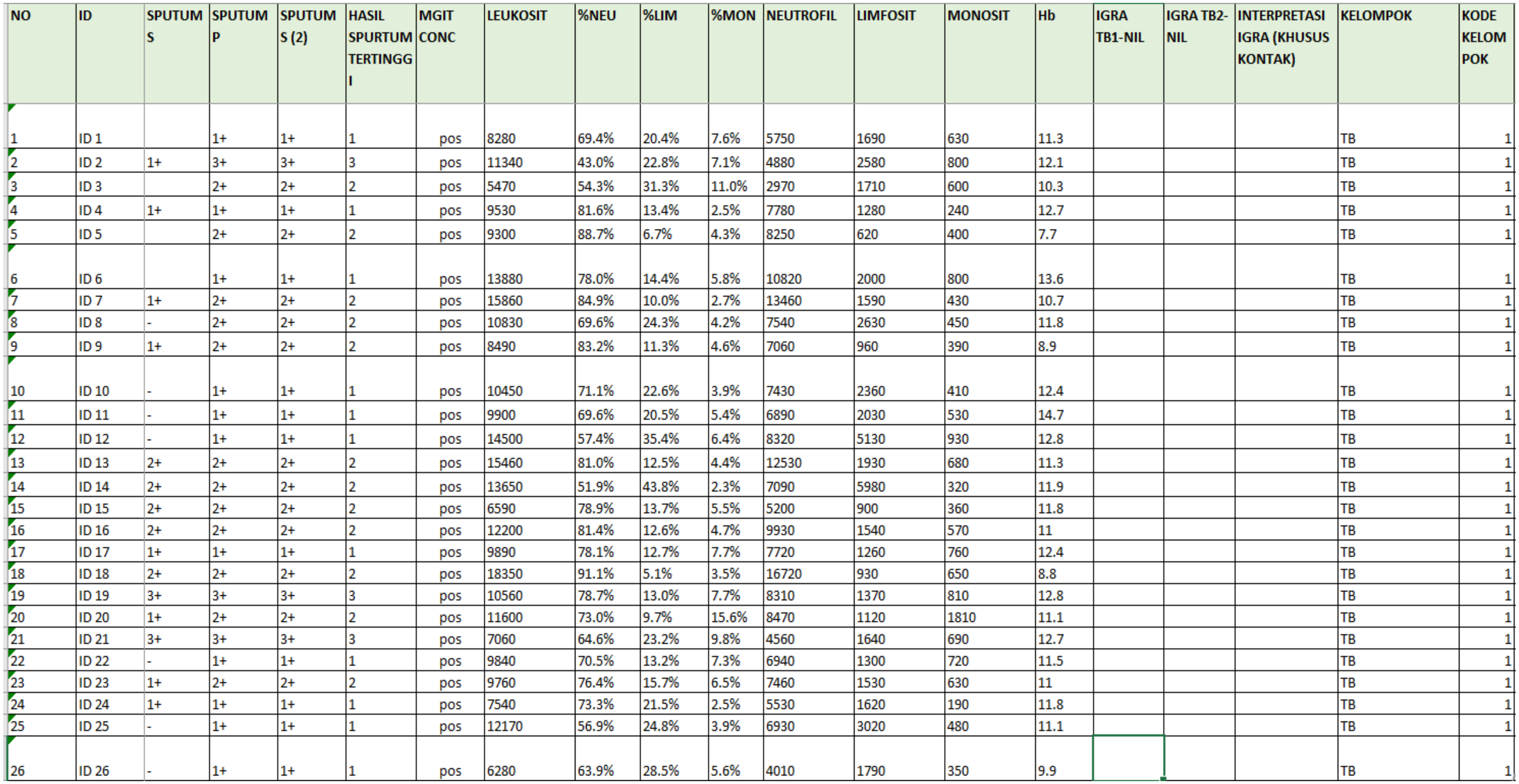
NO	ID	RM	UMUR	JENIS KELAMIN	kode jenis kelamin 1:Laki	bb(kg)	tb (cm)	BMI (KG/M2)	STATUS GIZI	RIWAYAT KONTAK	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK
1	ID 1	75372	41	Perempuan	2	40	155	16.64932	KURANG	ADA		IBU
2	ID 2	75528	34	Perempuan	2	33	148	15.06574	KURANG	TIDAK ADA		
3	ID 3	75456	46	Perempuan	2	48	150	21.33333	NORMAL	TIDAK ADA		
4	ID 4	70015	38	Perempuan	2	44	152	19.04432	NORMAL	TIDAK ADA		
5	ID 5	75486	47	Laki-Laki	1	39	161	15.04572	KURANG	TIDAK ADA		
6	ID 6	75525	23	Laki-Laki	1	57	167	20.43817	NORMAL	ADA		SEPUPU
7	ID 7	75513	33	Laki-Laki	1	40	168	14.17234	KURANG	TIDAK ADA		
8	ID 8	75547	33	Perempuan	2	35	155	14.56816	KURANG	ADA		BAPAK
9	ID 9	75558	26	Perempuan	2	52	165	19.10009	NORMAL	TIDAK ADA		
10	ID 10	75500	54	Perempuan	2	47	150	20.88889	NORMAL	ADA		MERTUA
11	ID 11	59047	55	Laki-Laki	1	50	162	19.05197	NORMAL	ADA		ISTRI
12	ID 12	75546	60	Laki-Laki	1	65	165	23.87511	OVERWEIGHT	TIDAK ADA		
13	ID 13	75585	64	Perempuan	2	44	155	18.31426	KURANG	TIDAK ADA		
14	ID 14	75616	39	Laki-Laki	1	45	165	16.52893	KURANG	TIDAK ADA		
15	ID 15	75614	57	Laki-Laki	1	48	160	18.75	NORMAL	ADA		ANAK
16	ID 16	75579	24	Laki-Laki	1	32	155	13.31946	KURANG	TIDAK ADA		
17	ID 17	75631	30	Laki-Laki	1	52	165	19.10009	NORMAL	TIDAK ADA		
18	ID 18	75662	23	Perempuan	2	28.5	147	13.18895	KURANG			
19	ID 19	75651	35	Perempuan	2	40	150	17.77778	KURANG			
20	ID 20	75639	18	Perempuan	2	34	148	15.52228	KURANG	TIDAK ADA		
21	ID 21	75655	30	Laki-Laki	1	39	160	15.23438	KURANG	ADA		KAKAK
22	ID 22	75647	36	Perempuan	2	43.5	148	19.85939	NORMAL	ADA		Orang Satu Rumah (Saudara)
23	ID 23	75689	40	Laki-Laki	1	49	165	17.99816	KURANG	TIDAK ADA (HANYA		
24	ID 24	75664	18	Perempuan	2	49	150	21.77778	NORMAL	ADA		BAPAK
25	ID 25	75728	61	Perempuan	2	45	150	20	NORMAL	TIDAK ADA		
26	ID 26	75710	44	Perempuan	2	41.6	155	17.3153	KURANG	TIDAK ADA		



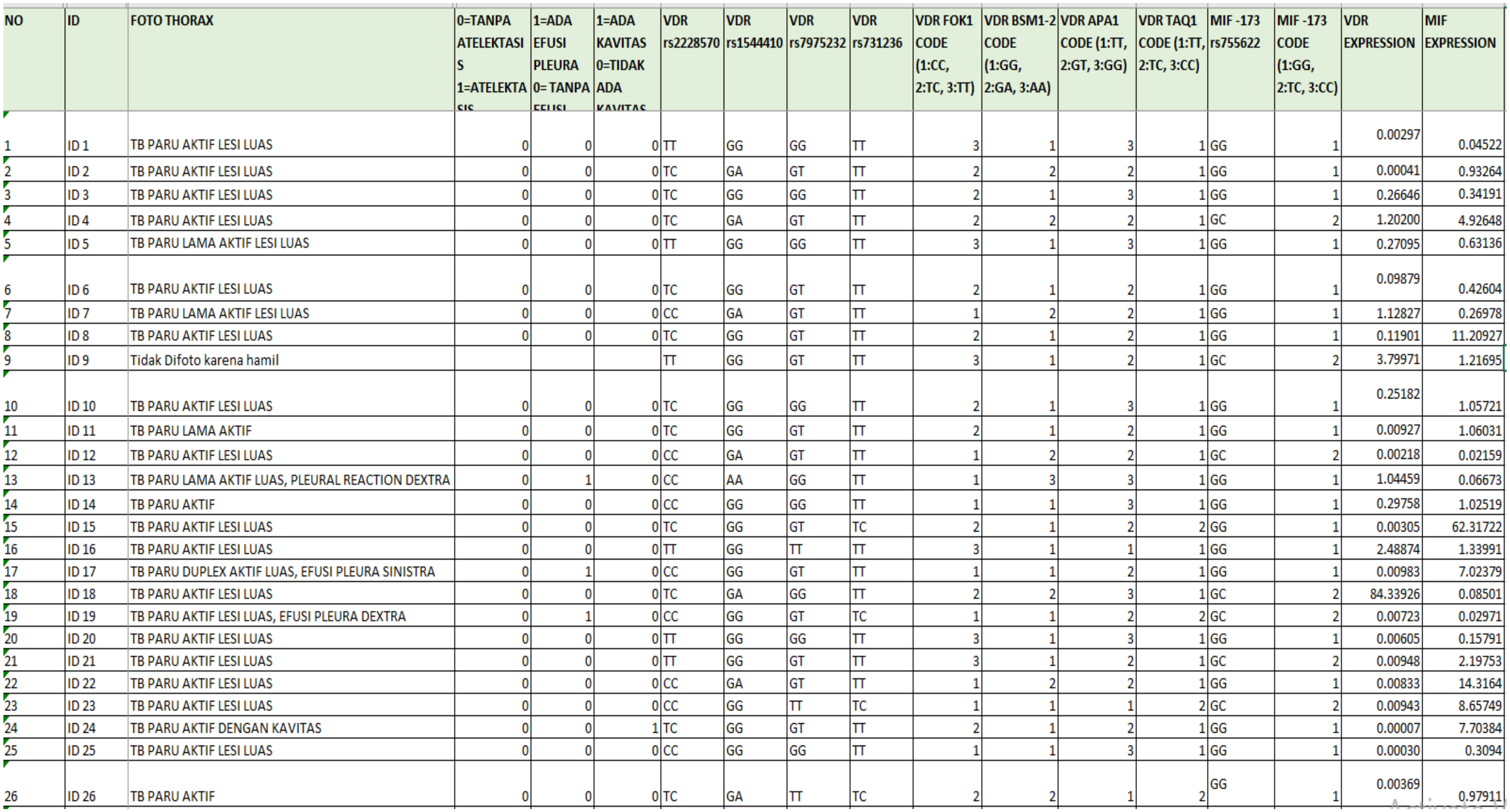
NO	ID	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK	BTA (tertinggi) kasus indeks 1=+1, 2=+2, 3=+3	LAMA TINGGAL DENGAN PENDERITA YANG KONTAK TERSEBUT (<6 BULAN/>=6BULAN)	SEKAMAR/TIDAK DENGAN PENDERITA TERSEBUT (YA/TIDAK\)	KODE SEKAMAR (1) TIDAK SEKAMAR (2)	JUMLAH ORANG YANG TINGGAL SERUMAH (1/2/3/4/ >=5 ORANG)	PERKIRAAN LUAS RUMAH (M2)	SINAR MATAHARI YANG MASUK DLM RUMAH (CUKUP/TIDAK CUKUP/TIDAK TAHU)
1	ID 1		IBU		>=6 BULAN	TIDAK		4	18	CUKUP
2	ID 2							4	80	CUKUP
3	ID 3							5	24	CUKUP
4	ID 4							4	40	TIDAK CUKUP
5	ID 5							>4 ORANG	15	CUKUP
6	ID 6		SEPUPU		>=6 BULAN	YA		>4 ORANG	35	CUKUP
7	ID 7							6	24	CUKUP
8	ID 8		BAPAK		>=6 BULAN	TIDAK		>4	70	CUKUP
9	ID 9							12	100	TIDAK CUKUP
10	ID 10		MERTUA		>=6 BULAN	TIDAK		6	80	CUKUP
11	ID 11		ISTRI		>=6 BULAN	YA		6	35	CUKUP
12	ID 12							8	72	CUKUP
13	ID 13							>4	36	TIDAK CUKUP
14	ID 14							7	6X10	CUKUP
15	ID 15		ANAK		>=6 BULAN	TIDAK		3	102	CUKUP
16	ID 16							4	24	TIDAK CUKUP
17	ID 17							5	3x4	TIDAK CUKUP
18	ID 18									CUKUP
19	ID 19									
20	ID 20									
21	ID 21		KAKAK		>6BLN	TIDAK		5	132	TIDAK CUKUP
22	ID 22		Orang Satu Rumah (Saudara)		>6BLN	TIDAK		4	6x4	CUKUP
23	ID 23							7	60	CUKUP
24	ID 24		BAPAK		>6 BULAN	TIDAK		4	4.5X24	CUKUP
25	ID 25							7	64	TIDAK CUKUP
26	ID 26							3	48	TIDAK CUKUP



NO	ID	MEROKOK (TIDAK PERNAH / YA, SAAT INI BERHENTI / YA, HINGGA SAAT INI / TIDAK PERNAH)	RIWAYAT MEROKOK (1:PEROKOK; 2= BUKAN PEROKOK)	RIWAYAT MINUM ALKOHOL (1:PERNAH HINGGA SAAT INI , 2: PERNAH, SAAT INI	ALKOHOL (YA, SERING/ YA, KADANG-KADANG/ TIDAK PERNAH	RIWAYAT NAPZA	BATUK (1: iya, 2:tidak)	HEMOPTOE (1: iya, 2:tidak)	SESAK (1: iya, 2:tidak)	NYERI DADA (1: IYA, 2 :TIDAK)	DEMAM (1:IYA , 2:TIDAK)	NAFSU MAKAN BERKURANG (1:	BB MENURUN (1: iya, 2:tidak)
1	ID 1	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	1	1
2	ID 2	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
3	ID 3	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	2	1	2	1	1
4	ID 4	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	1	1	2	2
5	ID 5	YA, SAAT INI BERHENTI	1	1	YA, SERING	TIDAK PERNAH	1	1	1	1	2	1	1
6	ID 6	YA, SAAT INI BERHENTI	1	2	YA, KADANG	TIDAK PERNAH	1	2	2	1	2	2	2
7	ID 7	YA, SAAT INI BERHENTI	1	2	YA, KADANG-KADANG	TIDAK PERNAH	1	1	1	1	1	2	1
8	ID 8	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
9	ID 9	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
10	ID 10	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	2	1	1	1
11	ID 11	TIDAK PERNAH	0	2	YA, KADANG	TIDAK PERNAH	1	1	1	1	1	1	1
12	ID 12	YA, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
13	ID 13	YA, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	1	1
14	ID 14	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	1	1
15	ID 15	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	2	2	1
16	ID 16	YA, SAAT INI BERHENTI	1	1	YA SERING	TIDAK PERNAH	1	2	1	2	2	2	2
17	ID 17	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	2	2	2	2
18	ID 18	PERNAH SAAT INI BERHENTI	1	2	YA, KADANG-KADANG	pernah, saat ini berh	1	2	2	2	2	2	1
19	ID 19	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	2	2	2
20	ID 20		0	3			1	2	2	2	2	2	2
21	ID 21	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	1	2	2	2
22	ID 22	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	2	2	2	2
23	ID 23	TIDAK	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	2	1	1	1	1
24	ID 24	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	2	2	1		
25	ID 25	TIDAK	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	2	2	2	2
26	ID 26	TIDAK	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1

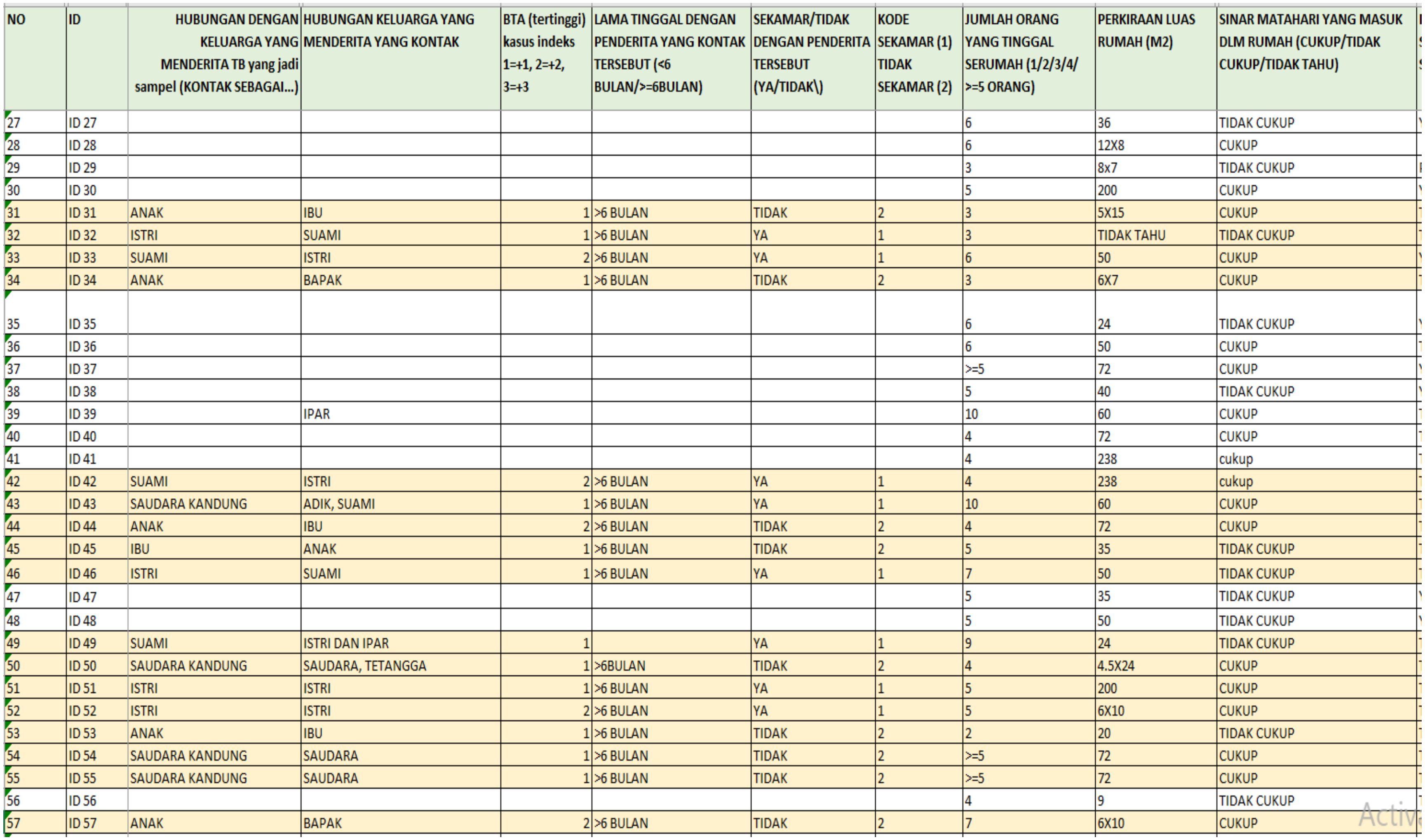


NO	ID	SPUTUM S	SPUTUM P	SPUTUM S (2)	HASIL SPURTUM TERTINGGI	MGIT CONC	LEUKOSIT	%NEU	%LIM	%MON	NEUTROFIL	LIMFOSIT	MONOSIT	Hb	IGRA TB1-NIL	IGRA TB2-NIL	INTERPRETASI IGRA (KHUSUS KONTAK)	KELOMPOK	KODE KELOMPOK
1	ID 1		1+	1+	1	pos	8280	69.4%	20.4%	7.6%	5750	1690	630	11.3				TB	1
2	ID 2	1+	3+	3+	3	pos	11340	43.0%	22.8%	7.1%	4880	2580	800	12.1				TB	1
3	ID 3		2+	2+	2	pos	5470	54.3%	31.3%	11.0%	2970	1710	600	10.3				TB	1
4	ID 4	1+	1+	1+	1	pos	9530	81.6%	13.4%	2.5%	7780	1280	240	12.7				TB	1
5	ID 5		2+	2+	2	pos	9300	88.7%	6.7%	4.3%	8250	620	400	7.7				TB	1
6	ID 6		1+	1+	1	pos	13880	78.0%	14.4%	5.8%	10820	2000	800	13.6				TB	1
7	ID 7	1+	2+	2+	2	pos	15860	84.9%	10.0%	2.7%	13460	1590	430	10.7				TB	1
8	ID 8	-	2+	2+	2	pos	10830	69.6%	24.3%	4.2%	7540	2630	450	11.8				TB	1
9	ID 9	1+	2+	2+	2	pos	8490	83.2%	11.3%	4.6%	7060	960	390	8.9				TB	1
10	ID 10	-	1+	1+	1	pos	10450	71.1%	22.6%	3.9%	7430	2360	410	12.4				TB	1
11	ID 11	-	1+	1+	1	pos	9900	69.6%	20.5%	5.4%	6890	2030	530	14.7				TB	1
12	ID 12	-	1+	1+	1	pos	14500	57.4%	35.4%	6.4%	8320	5130	930	12.8				TB	1
13	ID 13	2+	2+	2+	2	pos	15460	81.0%	12.5%	4.4%	12530	1930	680	11.3				TB	1
14	ID 14	2+	2+	2+	2	pos	13650	51.9%	43.8%	2.3%	7090	5980	320	11.9				TB	1
15	ID 15	2+	2+	2+	2	pos	6590	78.9%	13.7%	5.5%	5200	900	360	11.8				TB	1
16	ID 16	2+	2+	2+	2	pos	12200	81.4%	12.6%	4.7%	9930	1540	570	11				TB	1
17	ID 17	1+	1+	1+	1	pos	9890	78.1%	12.7%	7.7%	7720	1260	760	12.4				TB	1
18	ID 18	2+	2+	2+	2	pos	18350	91.1%	5.1%	3.5%	16720	930	650	8.8				TB	1
19	ID 19	3+	3+	3+	3	pos	10560	78.7%	13.0%	7.7%	8310	1370	810	12.8				TB	1
20	ID 20	1+	2+	2+	2	pos	11600	73.0%	9.7%	15.6%	8470	1120	1810	11.1				TB	1
21	ID 21	3+	3+	3+	3	pos	7060	64.6%	23.2%	9.8%	4560	1640	690	12.7				TB	1
22	ID 22	-	1+	1+	1	pos	9840	70.5%	13.2%	7.3%	6940	1300	720	11.5				TB	1
23	ID 23	1+	2+	2+	2	pos	9760	76.4%	15.7%	6.5%	7460	1530	630	11				TB	1
24	ID 24	1+	1+	1+	1	pos	7540	73.3%	21.5%	2.5%	5530	1620	190	11.8				TB	1
25	ID 25	-	1+	1+	1	pos	12170	56.9%	24.8%	3.9%	6930	3020	480	11.1				TB	1
26	ID 26	-	1+	1+	1	pos	6280	63.9%	28.5%	5.6%	4010	1790	350	9.9				TB	1



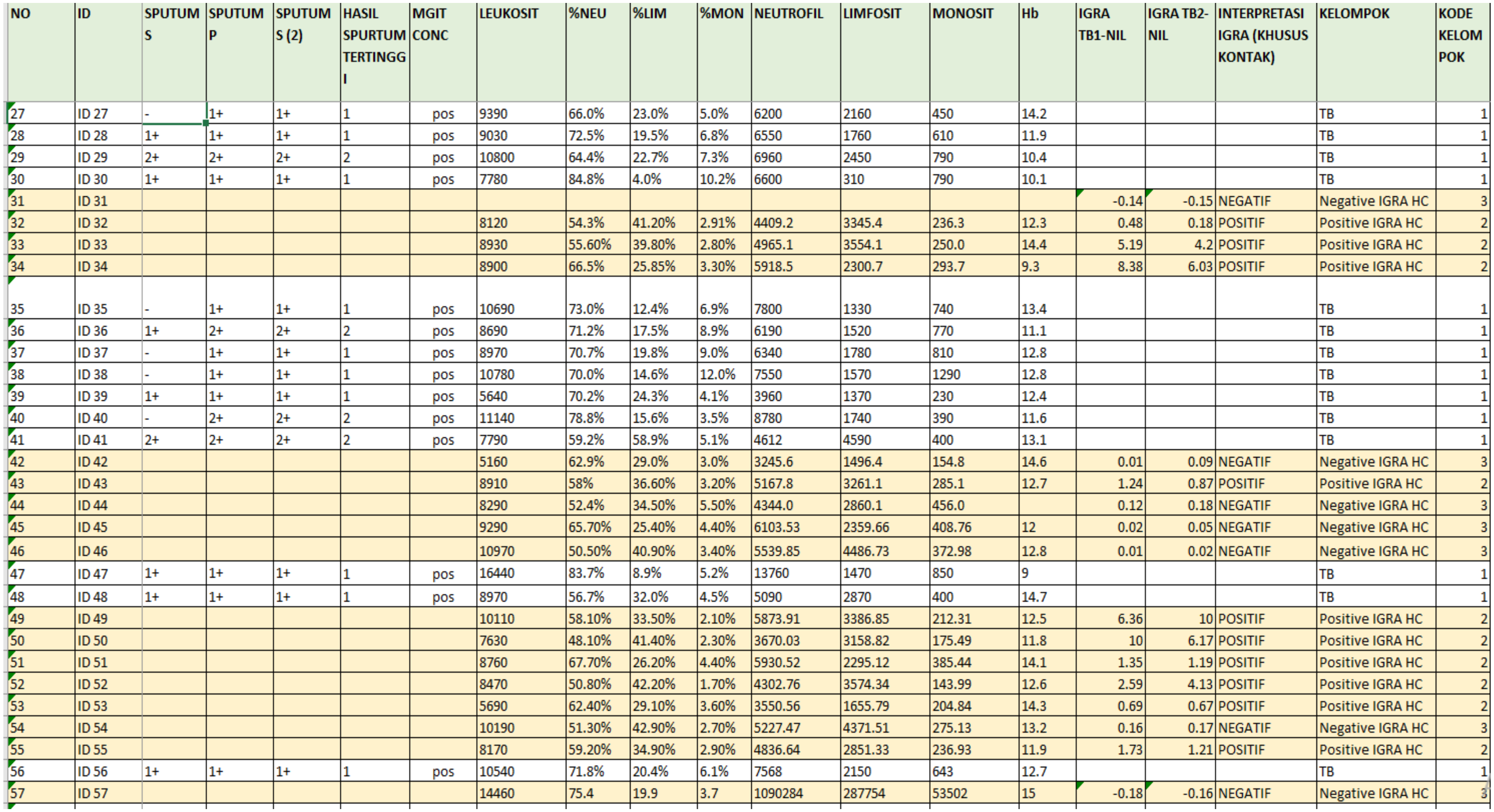
NO	ID	FOTO THORAX	0=TANPA ATELEKTASIS 1=ATELEKTASIS	1=ADA EFUSI PLEURA 0= TANPA EFUSI	1=ADA KAVITAS 0=TIDAK ADA KAVITAS	VDR rs2228570	VDR rs1544410	VDR rs7975232	VDR rs731236	VDR FOK1 CODE (1:CC, 2:TC, 3:TT)	VDR BSM1-2 CODE (1:GG, 2:GA, 3:AA)	VDR APA1 CODE (1:TT, 2:GT, 3:GG)	VDR TAQ1 CODE (1:TT, 2:TC, 3:CC)	MIF -173 rs755622	MIF -173 CODE (1:GG, 2:TC, 3:CC)	VDR EXPRESSION	MIF EXPRESSION
1	ID 1	TB PARU AKTIF LESI LUAS	0	0	0	TT	GG	GG	TT	3	1	3	1	GG	1	0.00297	0.04522
2	ID 2	TB PARU AKTIF LESI LUAS	0	0	0	TC	GA	GT	TT	2	2	2	1	GG	1	0.00041	0.93264
3	ID 3	TB PARU AKTIF LESI LUAS	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	0.26646	0.34191
4	ID 4	TB PARU AKTIF LESI LUAS	0	0	0	TC	GA	GT	TT	2	2	2	1	GC	2	1.20200	4.92648
5	ID 5	TB PARU LAMA AKTIF LESI LUAS	0	0	0	TT	GG	GG	TT	3	1	3	1	GG	1	0.27095	0.63136
6	ID 6	TB PARU AKTIF LESI LUAS	0	0	0	TC	GG	GT	TT	2	1	2	1	GG	1	0.09879	0.42604
7	ID 7	TB PARU LAMA AKTIF LESI LUAS	0	0	0	CC	GA	GT	TT	1	2	2	1	GG	1	1.12827	0.26978
8	ID 8	TB PARU AKTIF LESI LUAS	0	0	0	TC	GG	GT	TT	2	1	2	1	GG	1	0.11901	11.20927
9	ID 9	Tidak Difoto karena hamil				TT	GG	GT	TT	3	1	2	1	GC	2	3.79971	1.21695
10	ID 10	TB PARU AKTIF LESI LUAS	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	0.25182	1.05721
11	ID 11	TB PARU LAMA AKTIF	0	0	0	TC	GG	GT	TT	2	1	2	1	GG	1	0.00927	1.06031
12	ID 12	TB PARU AKTIF LESI LUAS	0	0	0	CC	GA	GT	TT	1	2	2	1	GC	2	0.00218	0.02159
13	ID 13	TB PARU LAMA AKTIF LUAS, PLEURAL REACTION DEXTRA	0	1	0	CC	AA	GG	TT	1	3	3	1	GG	1	1.04459	0.06673
14	ID 14	TB PARU AKTIF	0	0	0	CC	GG	GG	TT	1	1	3	1	GG	1	0.29758	1.02519
15	ID 15	TB PARU AKTIF LESI LUAS	0	0	0	TC	GG	GT	TC	2	1	2	2	GG	1	0.00305	62.31722
16	ID 16	TB PARU AKTIF LESI LUAS	0	0	0	TT	GG	TT	TT	3	1	1	1	GG	1	2.48874	1.33991
17	ID 17	TB PARU DUPLEX AKTIF LUAS, EFUSI PLEURA SINISTRA	0	1	0	CC	GG	GT	TT	1	1	2	1	GG	1	0.00983	7.02379
18	ID 18	TB PARU AKTIF LESI LUAS	0	0	0	TC	GA	GG	TT	2	2	3	1	GC	2	84.33926	0.08501
19	ID 19	TB PARU AKTIF LESI LUAS, EFUSI PLEURA DEXTRA	0	1	0	CC	GG	GT	TC	1	1	2	2	GC	2	0.00723	0.02971
20	ID 20	TB PARU AKTIF LESI LUAS	0	0	0	TT	GG	GG	TT	3	1	3	1	GG	1	0.00605	0.15791
21	ID 21	TB PARU AKTIF LESI LUAS	0	0	0	TT	GG	GT	TT	3	1	2	1	GC	2	0.00948	2.19753
22	ID 22	TB PARU AKTIF LESI LUAS	0	0	0	CC	GA	GT	TT	1	2	2	1	GG	1	0.00833	14.3164
23	ID 23	TB PARU AKTIF LESI LUAS	0	0	0	CC	GG	TT	TC	1	1	1	2	GC	2	0.00943	8.65749
24	ID 24	TB PARU AKTIF DENGAN KAVITAS	0	0	1	TC	GG	GT	TT	2	1	2	1	GG	1	0.00007	7.70384
25	ID 25	TB PARU AKTIF LESI LUAS	0	0	0	CC	GG	GG	TT	1	1	3	1	GG	1	0.00030	0.3094
26	ID 26	TB PARU AKTIF	0	0	0	TC	GA	TT	TC	2	2	1	2	GG	1	0.00369	0.97911

NO	ID	RM	UMUR	JENIS KELAMIN	kode jenis kelamin 1:Laki	bb(kg)	tb (cm)	BMI (KG/M2)	STATUS GIZI	RIWAYAT KONTAK	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK	BTA (tertinggi) kasus indeks 1=+1, 2=+2, 3=+3
27	ID 27	75720	35	Laki-Laki	1	47	160	18.35938	KURANG	TIDAK ADA			
28	ID 28	75832	16	Perempuan	2	40	158	16.02307	KURANG	TIDAK ADA			
29	ID 29	75831	58	Laki-Laki	1	35	160	13.67188	KURANG	TIDAK ADA			
30	ID 30	75923	62	Laki-Laki	1	58	167	20.79673	NORMAL	TIDAK ADA			
31	ID 31		38	Perempuan	2	65	160	25.39063	OBESE CLASS I	ADA	ANAK	IBU	1
32	ID 32		70	Perempuan	2	60	145	28.53746	OBESE CLASS I	ADA	ISTRI	SUAMI	1
33	ID 33		24	Laki-Laki	1	70	160	27.34375	OBESE CLASS I	ADA	SUAMI	ISTRI	2
34	ID 34		18	Perempuan	2	50	160	19.53125	NORMAL	ADA	ANAK	BAPAK	1
35	ID 35	76116	61	Laki-Laki	1	61	165	22.40588	NORMAL	TIDAK ADA			
36	ID 36	76108	24	Perempuan	2	52	156	21.36752	NORMAL	TIDAK ADA			
37	ID 37	76208	30	Laki-Laki	1	45	162	17.14678	KURANG	TIDAK ADA			
38	ID 38	76308	55	Laki-Laki	1	48	165	17.63085	KURANG	TIDAK ADA			
39	ID 39	76426	18	Perempuan	2	48	157	19.47341	NORMAL	ADA		IPAR	
40	ID 40	76443	53	Perempuan	2	41	155	17.06556	KURANG	TIDAK ADA			
41	ID 41	76436	56	Perempuan	2	50	155	20.81165	NORMAL	TIDAK ADA			
42	ID 42		58	Laki-Laki	1	72	170	24.91349	OVERWEIGHT	ADA	SUAMI	ISTRI	2
43	ID 43		23	Perempuan	2	55	155	22.89282	NORMAL	ADA	SAUDARA KANDUNG	ADIK, SUAMI	1
44	ID 44		26	Laki-Laki	1	90	170	31.14187	OBESE CLAS II	ADA	ANAK	IBU	2
45	ID 45		54	Perempuan	2	40	150	17.77778	KURANG	ADA	IBU	ANAK	1
46	ID 46		39	Perempuan	2	85	154	35.84078	OBESE CLAS II	ADA	ISTRI	SUAMI	1
47	ID 47	76621	23	Laki-Laki	1	45	167	16.13539	KURANG	TIDAK ADA			
48	ID 48	76625	44	Laki-Laki	1	76	166	27.5802	OBESE CLASS I	TIDAK ADA			
49	ID 49		22	Laki-Laki	2	51	164	18.96193	NORMAL	ADA	SUAMI	ISTRI DAN IPAR	1
50	ID 50		44	Perempuan	2	55	149	24.77366	OVERWEIGHT	ADA	SAUDARA KANDUNG	SAUDARA, TETANGGA	1
51	ID 51		69	Perempuan	2	45	15	2000	OBESE CLAS II	ADA	ISTRI	ISTRI	1
52	ID 52		33	Perempuan	2	65	157	26.37024	OBESE CLASS I	ADA	ISTRI	ISTRI	2
53	ID 53		24	Laki-Laki	1	53	168	18.77834	NORMAL	ADA	ANAK	IBU	1
54	ID 54		33	Perempuan	2	82	153	35.02926	OBESE CLAS II	ADA	SAUDARA KANDUNG	SAUDARA	1
55	ID 55		25	Perempuan	2	63	160	24.60938	OVERWEIGHT	ADA	SAUDARA KANDUNG	SAUDARA	1
56	ID 56	76714	45	Perempuan	2	45	152	19.47715	NORMAL	TIDAK ADA			

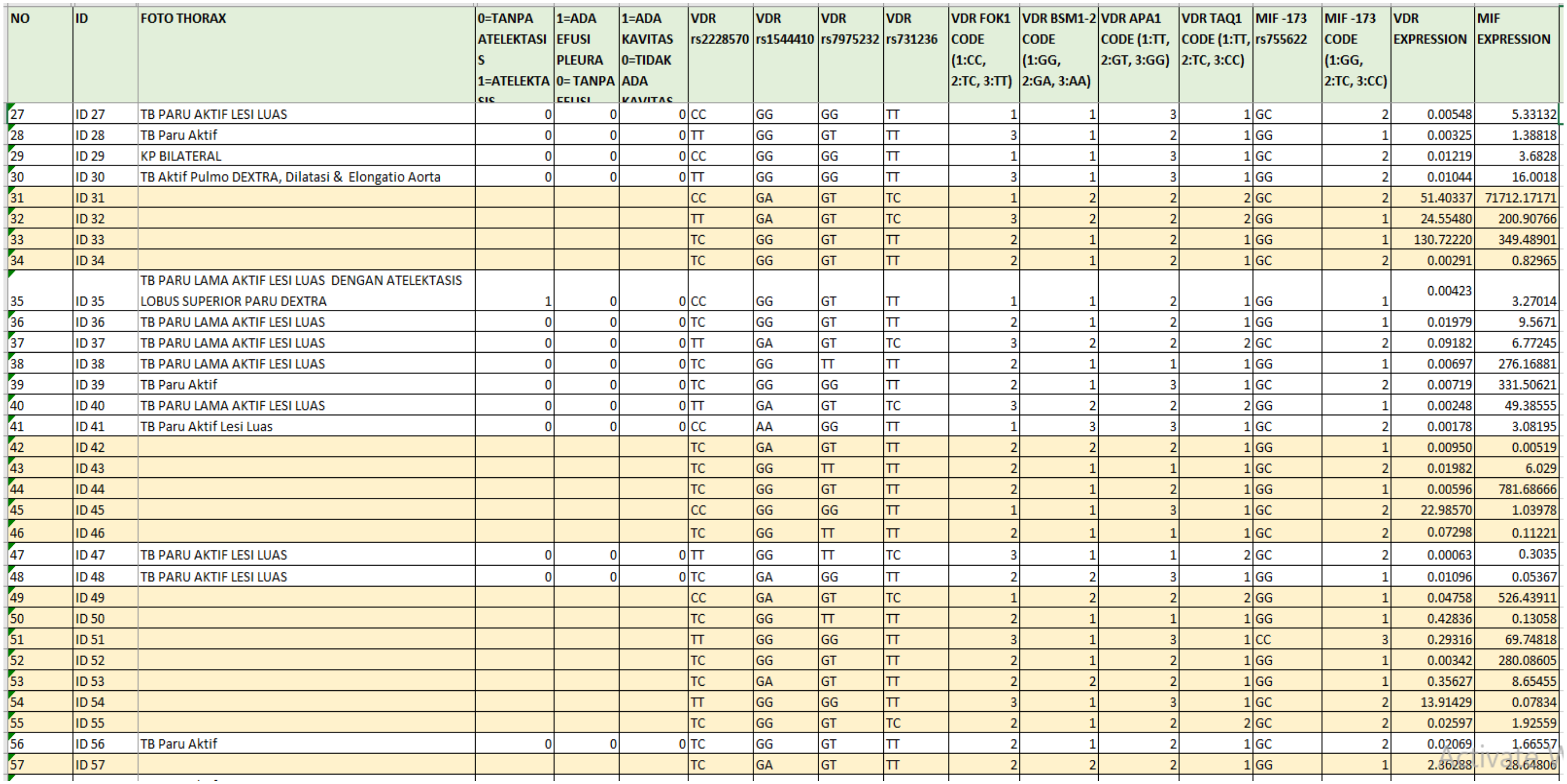


NO	ID	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK	BTA (tertinggi) kasus indeks 1=+1, 2=+2, 3=+3	LAMA TINGGAL DENGAN PENDERITA YANG KONTAK TERSEBUT (<6 BULAN/>=6BULAN)	SEKAMAR/TIDAK DENGAN PENDERITA TERSEBUT (YA/TIDAK\)	KODE SEKAMAR (1) TIDAK SEKAMAR (2)	JUMLAH ORANG YANG TINGGAL SERUMAH (1/2/3/4/ >=5 ORANG)	PERKIRAAN LUAS RUMAH (M2)	SINAR MATAHARI YANG MASUK DLM RUMAH (CUKUP/TIDAK CUKUP/TIDAK TAHU)
27	ID 27							6	36	TIDAK CUKUP
28	ID 28							6	12X8	CUKUP
29	ID 29							3	8x7	TIDAK CUKUP
30	ID 30							5	200	CUKUP
31	ID 31	ANAK	IBU	1	>6 BULAN	TIDAK	2	3	5X15	CUKUP
32	ID 32	ISTRI	SUAMI	1	>6 BULAN	YA	1	3	TIDAK TAHU	TIDAK CUKUP
33	ID 33	SUAMI	ISTRI	2	>6 BULAN	YA	1	6	50	CUKUP
34	ID 34	ANAK	BAPAK	1	>6 BULAN	TIDAK	2	3	6X7	CUKUP
35	ID 35							6	24	TIDAK CUKUP
36	ID 36							6	50	CUKUP
37	ID 37							>=5	72	CUKUP
38	ID 38							5	40	TIDAK CUKUP
39	ID 39		IPAR					10	60	CUKUP
40	ID 40							4	72	CUKUP
41	ID 41							4	238	cukup
42	ID 42	SUAMI	ISTRI	2	>6 BULAN	YA	1	4	238	cukup
43	ID 43	SAUDARA KANDUNG	ADIK, SUAMI	1	>6 BULAN	YA	1	10	60	CUKUP
44	ID 44	ANAK	IBU	2	>6 BULAN	TIDAK	2	4	72	CUKUP
45	ID 45	IBU	ANAK	1	>6 BULAN	TIDAK	2	5	35	TIDAK CUKUP
46	ID 46	ISTRI	SUAMI	1	>6 BULAN	YA	1	7	50	TIDAK CUKUP
47	ID 47							5	35	TIDAK CUKUP
48	ID 48							5	50	TIDAK CUKUP
49	ID 49	SUAMI	ISTRI DAN IPAR	1		YA	1	9	24	TIDAK CUKUP
50	ID 50	SAUDARA KANDUNG	SAUDARA, TETANGGA	1	>6BULAN	TIDAK	2	4	4.5X24	CUKUP
51	ID 51	ISTRI	ISTRI	1	>6 BULAN	YA	1	5	200	CUKUP
52	ID 52	ISTRI	ISTRI	2	>6 BULAN	YA	1	5	6X10	CUKUP
53	ID 53	ANAK	IBU	1	>6 BULAN	TIDAK	2	2	20	TIDAK CUKUP
54	ID 54	SAUDARA KANDUNG	SAUDARA	1	>6 BULAN	TIDAK	2	>=5	72	CUKUP
55	ID 55	SAUDARA KANDUNG	SAUDARA	1	>6 BULAN	TIDAK	2	>=5	72	CUKUP
56	ID 56							4	9	TIDAK CUKUP
57	ID 57	ANAK	BAPAK	2	>6 BULAN	TIDAK	2	7	6X10	CUKUP

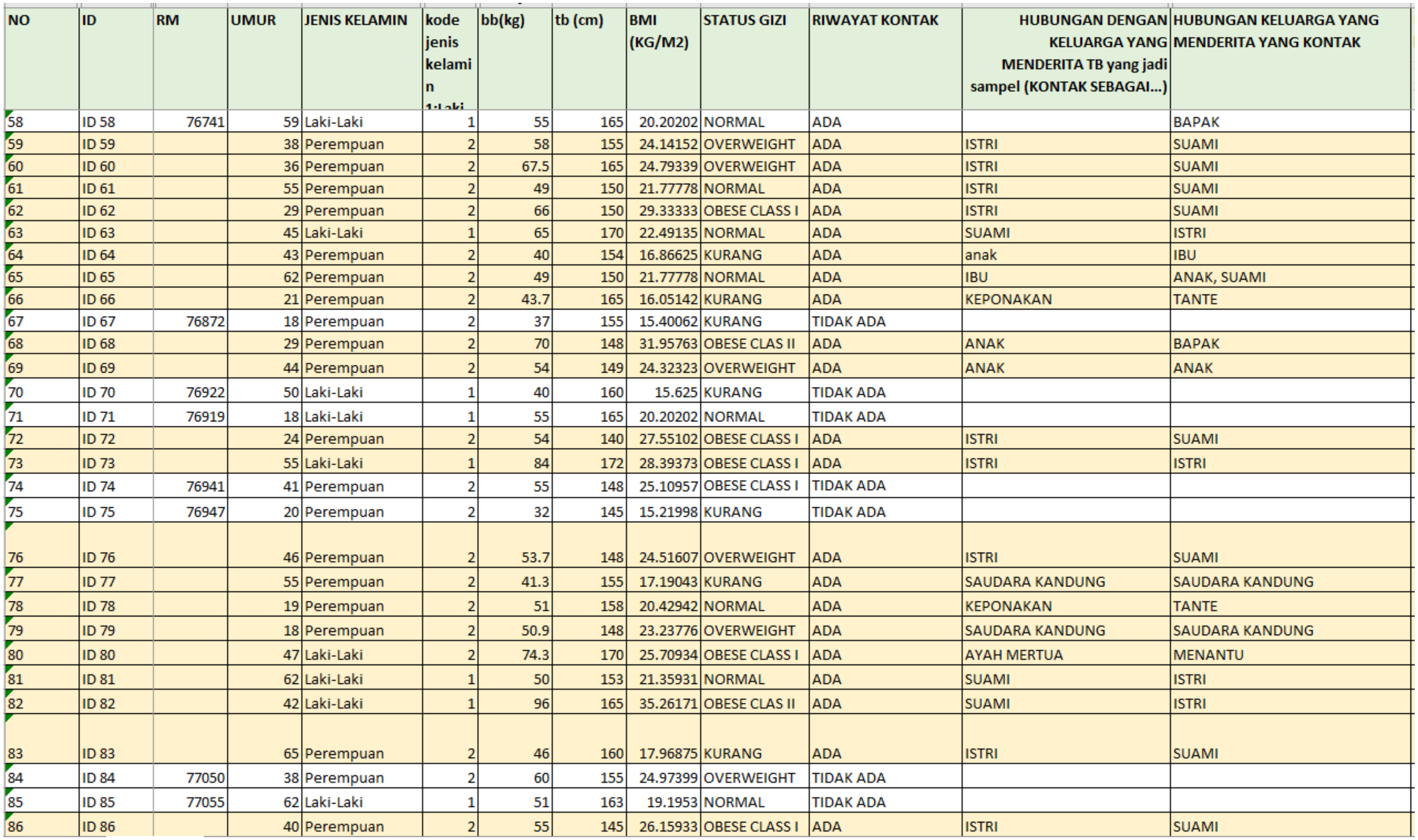
NO	ID	MEROKOK (TIDAK PERNAH / YA, SAAT INI BERHENTI / YA, HINGGA SAAT INI / TIDAK PERNAH)	RIWAYAT MEROKOK (1:PEROKOK; 2= BUKAN PEROKOK)	RIWAYAT MINUM ALKOHOL (1:PERNAH HINGGA SAAT INI , 2: PERNAH, SAAT INI BERHENTI, 3: TIDAK	ALKOHOL (YA, SERING/ YA, KADANG-KADANG/ TIDAK PERNAH	RIWAYAT NAPZA	BATUK (1: iya, 2:tidak)	HEMOPTOE (1: iya, 2:tidak)	SESAK (1: iya, 2:tidak)	NYERI DADA (1: IYA, 2 :TIDAK)	DEMAM (1:IYA , 2:TIDAK)	NAFSU MAKAN BERKURANG (1: iya	BB MENURUN (1: iya, 2:tidak)
27	ID 27	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH		1	2	1	1	2	2	2
28	ID 28		0	3			1	1	1	2	2	2	1
29	ID 29	PERNAH, HINGGA SAAT INI	1	2	YA, KADANG-KADANG	TIDAK PERNAH	1	2	2	2	2	1	1
30	ID 30	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	2	1	1
31	ID 31	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
32	ID 32	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
33	ID 33	YA, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
34	ID 34	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
35	ID 35	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	2	1	2	2
36	ID 36	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
37	ID 37	YA, SAAT INI BERHENTI	1	2	YA, KADANG	TIDAK PERNAH	1	1	1	1	1	1	1
38	ID 38	YA, SAAT INI BERHENTI	1	2	TIDAK PERNAH	TIDAK PERNAH	1	1	2	1	1	1	1
39	ID 39	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	2	1	1
40	ID 40	TIDAK PERNAH	0	3	TIDAK PERNAH		1	2	2	2	1	1	1
41	ID 41	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	2	1	1	1
42	ID 42	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
43	ID 43	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
44	ID 44	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
45	ID 45	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
46	ID 46	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
47	ID 47	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	1	2
48	ID 48	YA, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	2	2	2	2
49	ID 49	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
50	ID 50	TIDAK PERNAH	0	3	YA, KADANG-KADANG, SUDAH BERI	TIDAK PERNAH	2	2	2	2	2	2	2
51	ID 51	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
52	ID 52	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
53	ID 53	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
54	ID 54	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
55	ID 55	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
56	ID 56	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	2	2	1



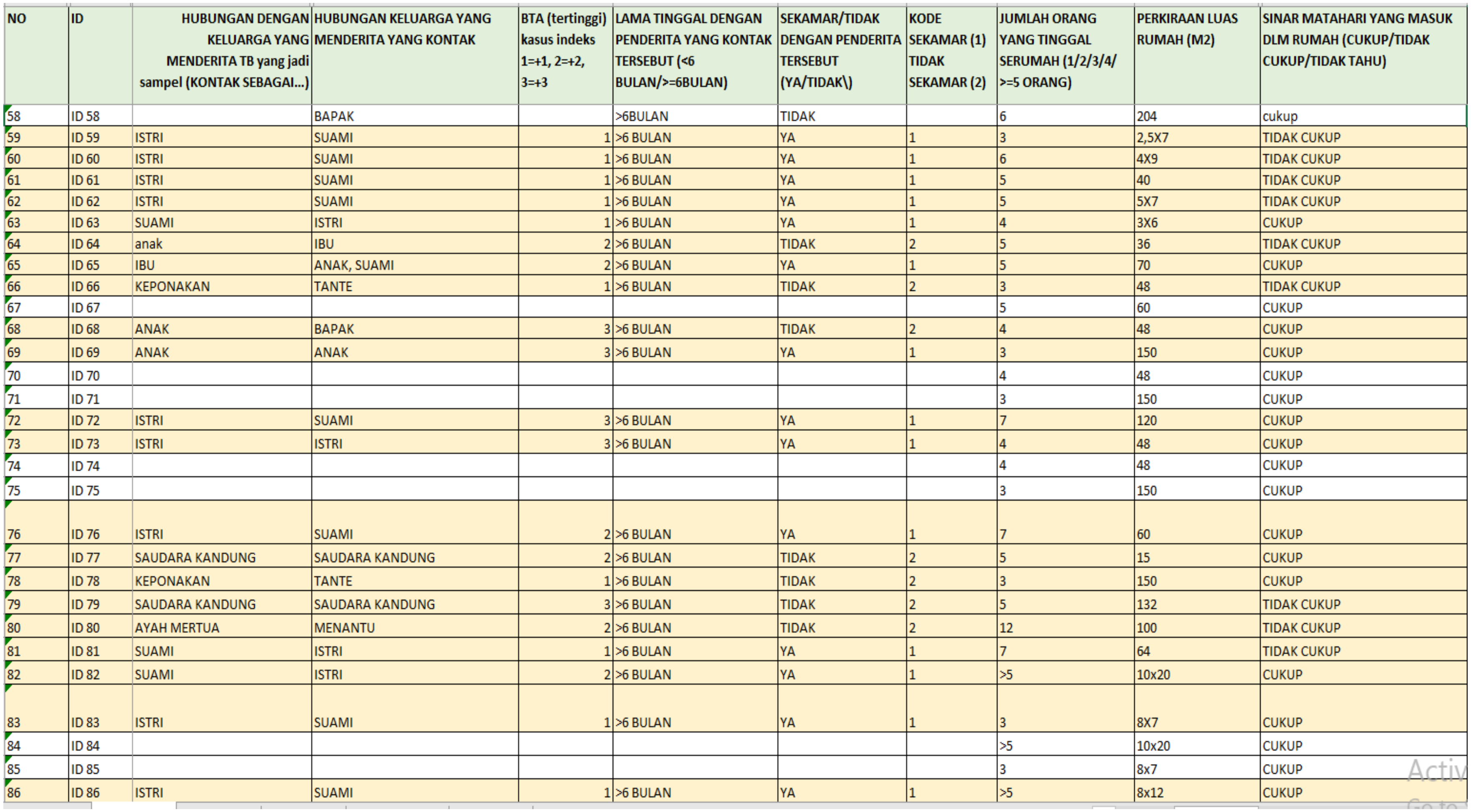
NO	ID	SPUTUM S	SPUTUM P	SPUTUM S (2)	HASIL SPURTUM TERTINGGI	MGIT CONC	LEUKOSIT	%NEU	%LIM	%MON	NEUTROFIL	LIMFOSIT	MONOSIT	Hb	IGRA TB1-NIL	IGRA TB2-NIL	INTERPRETASI IGRA (KHUSUS KONTAK)	KELOMPOK	KODE KELOMPOK
27	ID 27	-	1+	1+	1	pos	9390	66.0%	23.0%	5.0%	6200	2160	450	14.2				TB	1
28	ID 28	1+	1+	1+	1	pos	9030	72.5%	19.5%	6.8%	6550	1760	610	11.9				TB	1
29	ID 29	2+	2+	2+	2	pos	10800	64.4%	22.7%	7.3%	6960	2450	790	10.4				TB	1
30	ID 30	1+	1+	1+	1	pos	7780	84.8%	4.0%	10.2%	6600	310	790	10.1				TB	1
31	ID 31														-0.14	-0.15	NEGATIF	Negative IGRA HC	3
32	ID 32						8120	54.3%	41.20%	2.91%	4409.2	3345.4	236.3	12.3	0.48	0.18	POSITIF	Positive IGRA HC	2
33	ID 33						8930	55.60%	39.80%	2.80%	4965.1	3554.1	250.0	14.4	5.19	4.2	POSITIF	Positive IGRA HC	2
34	ID 34						8900	66.5%	25.85%	3.30%	5918.5	2300.7	293.7	9.3	8.38	6.03	POSITIF	Positive IGRA HC	2
35	ID 35	-	1+	1+	1	pos	10690	73.0%	12.4%	6.9%	7800	1330	740	13.4				TB	1
36	ID 36	1+	2+	2+	2	pos	8690	71.2%	17.5%	8.9%	6190	1520	770	11.1				TB	1
37	ID 37	-	1+	1+	1	pos	8970	70.7%	19.8%	9.0%	6340	1780	810	12.8				TB	1
38	ID 38	-	1+	1+	1	pos	10780	70.0%	14.6%	12.0%	7550	1570	1290	12.8				TB	1
39	ID 39	1+	1+	1+	1	pos	5640	70.2%	24.3%	4.1%	3960	1370	230	12.4				TB	1
40	ID 40	-	2+	2+	2	pos	11140	78.8%	15.6%	3.5%	8780	1740	390	11.6				TB	1
41	ID 41	2+	2+	2+	2	pos	7790	59.2%	58.9%	5.1%	4612	4590	400	13.1				TB	1
42	ID 42						5160	62.9%	29.0%	3.0%	3245.6	1496.4	154.8	14.6	0.01	0.09	NEGATIF	Negative IGRA HC	3
43	ID 43						8910	58%	36.60%	3.20%	5167.8	3261.1	285.1	12.7	1.24	0.87	POSITIF	Positive IGRA HC	2
44	ID 44						8290	52.4%	34.50%	5.50%	4344.0	2860.1	456.0		0.12	0.18	NEGATIF	Negative IGRA HC	3
45	ID 45						9290	65.70%	25.40%	4.40%	6103.53	2359.66	408.76	12	0.02	0.05	NEGATIF	Negative IGRA HC	3
46	ID 46						10970	50.50%	40.90%	3.40%	5539.85	4486.73	372.98	12.8	0.01	0.02	NEGATIF	Negative IGRA HC	3
47	ID 47	1+	1+	1+	1	pos	16440	83.7%	8.9%	5.2%	13760	1470	850	9				TB	1
48	ID 48	1+	1+	1+	1	pos	8970	56.7%	32.0%	4.5%	5090	2870	400	14.7				TB	1
49	ID 49						10110	58.10%	33.50%	2.10%	5873.91	3386.85	212.31	12.5	6.36	10	POSITIF	Positive IGRA HC	2
50	ID 50						7630	48.10%	41.40%	2.30%	3670.03	3158.82	175.49	11.8	10	6.17	POSITIF	Positive IGRA HC	2
51	ID 51						8760	67.70%	26.20%	4.40%	5930.52	2295.12	385.44	14.1	1.35	1.19	POSITIF	Positive IGRA HC	2
52	ID 52						8470	50.80%	42.20%	1.70%	4302.76	3574.34	143.99	12.6	2.59	4.13	POSITIF	Positive IGRA HC	2
53	ID 53						5690	62.40%	29.10%	3.60%	3550.56	1655.79	204.84	14.3	0.69	0.67	POSITIF	Positive IGRA HC	2
54	ID 54						10190	51.30%	42.90%	2.70%	5227.47	4371.51	275.13	13.2	0.16	0.17	NEGATIF	Negative IGRA HC	3
55	ID 55						8170	59.20%	34.90%	2.90%	4836.64	2851.33	236.93	11.9	1.73	1.21	POSITIF	Positive IGRA HC	2
56	ID 56	1+	1+	1+	1	pos	10540	71.8%	20.4%	6.1%	7568	2150	643	12.7				TB	1
57	ID 57						14460	75.4	19.9	3.7	1090284	287754	53502	15	-0.18	-0.16	NEGATIF	Negative IGRA HC	3



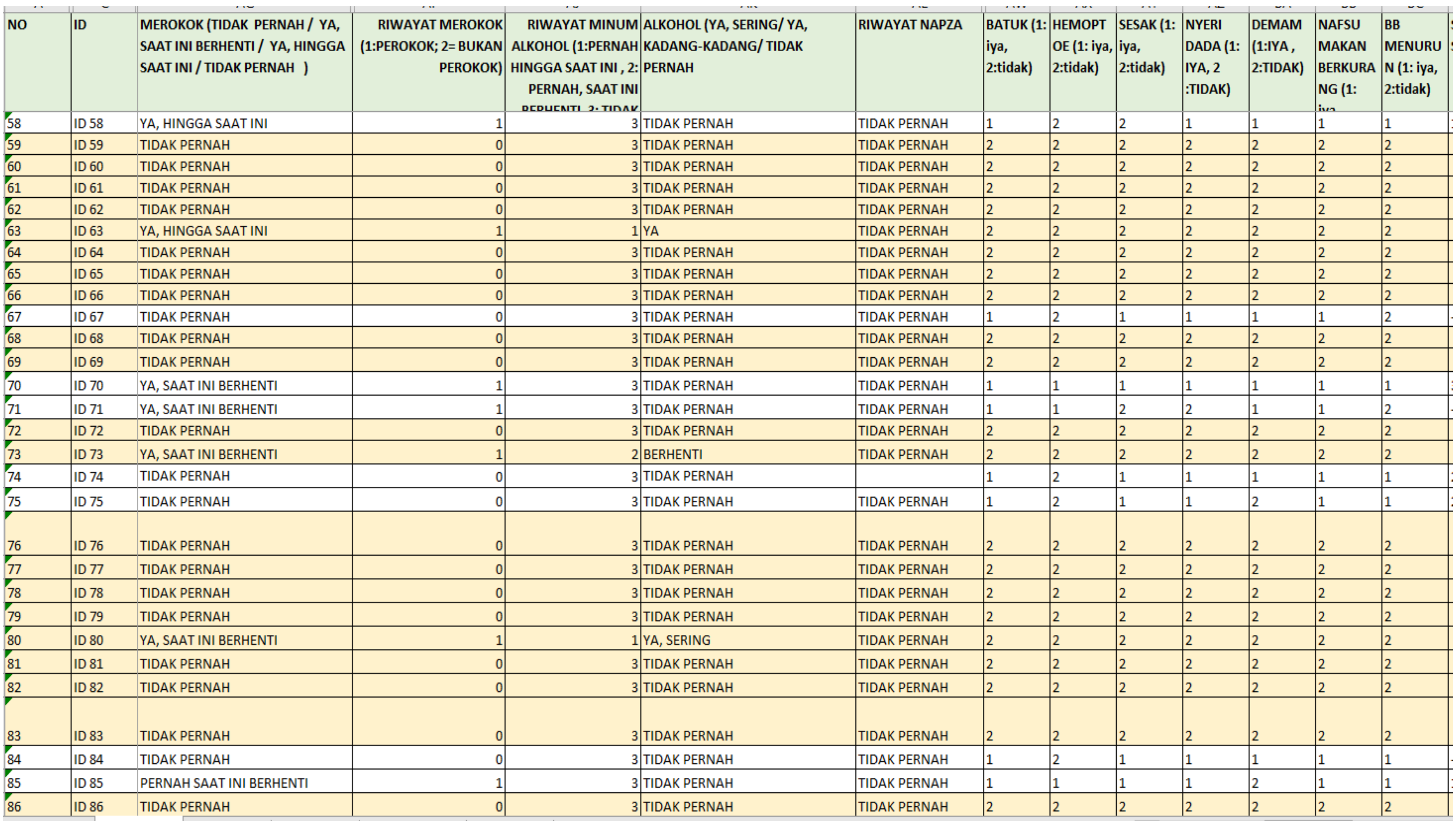
NO	ID	FOTO THORAX	0=TANPA ATELEKTASIS 1=ATELEKTASIS	1=ADA EFUSI PLEURA 0= TANPA EFUSI	1=ADA KAVITAS 0=TIDAK ADA KAVITAS	VDR rs2228570	VDR rs1544410	VDR rs7975232	VDR rs731236	VDR FOK1 CODE (1:CC, 2:TC, 3:TT)	VDR BSM1-2 CODE (1:GG, 2:GA, 3:AA)	VDR APA1 CODE (1:TT, 2:GT, 3:GG)	VDR TAQ1 CODE (1:TT, 2:TC, 3:CC)	MIF -173 rs755622	MIF -173 CODE (1:GG, 2:TC, 3:CC)	VDR EXPRESSION	MIF EXPRESSION
27	ID 27	TB PARU AKTIF LESI LUAS	0	0	0	CC	GG	GG	TT	1	1	3	1	GC	2	0.00548	5.33132
28	ID 28	TB Paru Aktif	0	0	0	TT	GG	GT	TT	3	1	2	1	GG	1	0.00325	1.38818
29	ID 29	KP BILATERAL	0	0	0	CC	GG	GG	TT	1	1	3	1	GC	2	0.01219	3.6828
30	ID 30	TB Aktif Pulmo DEXTRA, Dilatasi & Elongatio Aorta	0	0	0	TT	GG	GG	TT	3	1	3	1	GG	2	0.01044	16.0018
31	ID 31					CC	GA	GT	TC	1	2	2	2	GC	2	51.40337	71712.17171
32	ID 32					TT	GA	GT	TC	3	2	2	2	GG	1	24.55480	200.90766
33	ID 33					TC	GG	GT	TT	2	1	2	1	GG	1	130.72220	349.48901
34	ID 34					TC	GG	GT	TT	2	1	2	1	GC	2	0.00291	0.82965
35	ID 35	TB PARU LAMA AKTIF LESI LUAS DENGAN ATELEKTASIS LOBUS SUPERIOR PARU DEXTRA	1	0	0	CC	GG	GT	TT	1	1	2	1	GG	1	0.00423	3.27014
36	ID 36	TB PARU LAMA AKTIF LESI LUAS	0	0	0	TC	GG	GT	TT	2	1	2	1	GG	1	0.01979	9.5671
37	ID 37	TB PARU LAMA AKTIF LESI LUAS	0	0	0	TT	GA	GT	TC	3	2	2	2	GC	2	0.09182	6.77245
38	ID 38	TB PARU LAMA AKTIF LESI LUAS	0	0	0	TC	GG	TT	TT	2	1	1	1	GG	1	0.00697	276.16881
39	ID 39	TB Paru Aktif	0	0	0	TC	GG	GG	TT	2	1	3	1	GC	2	0.00719	331.50621
40	ID 40	TB PARU LAMA AKTIF LESI LUAS	0	0	0	TT	GA	GT	TC	3	2	2	2	GG	1	0.00248	49.38555
41	ID 41	TB Paru Aktif Lesi Luas	0	0	0	CC	AA	GG	TT	1	3	3	1	GC	2	0.00178	3.08195
42	ID 42					TC	GA	GT	TT	2	2	2	1	GG	1	0.00950	0.00519
43	ID 43					TC	GG	TT	TT	2	1	1	1	GC	2	0.01982	6.029
44	ID 44					TC	GG	GT	TT	2	1	2	1	GG	1	0.00596	781.68666
45	ID 45					CC	GG	GG	TT	1	1	3	1	GC	2	22.98570	1.03978
46	ID 46					TC	GG	TT	TT	2	1	1	1	GC	2	0.07298	0.11221
47	ID 47	TB PARU AKTIF LESI LUAS	0	0	0	TT	GG	TT	TC	3	1	1	2	GC	2	0.00063	0.3035
48	ID 48	TB PARU AKTIF LESI LUAS	0	0	0	TC	GA	GG	TT	2	2	3	1	GG	1	0.01096	0.05367
49	ID 49					CC	GA	GT	TC	1	2	2	2	GG	1	0.04758	526.43911
50	ID 50					TC	GG	TT	TT	2	1	1	1	GG	1	0.42836	0.13058
51	ID 51					TT	GG	GG	TT	3	1	3	1	CC	3	0.29316	69.74818
52	ID 52					TC	GG	GT	TT	2	1	2	1	GG	1	0.00342	280.08605
53	ID 53					TC	GA	GT	TT	2	2	2	1	GG	1	0.35627	8.65455
54	ID 54					TT	GG	GG	TT	3	1	3	1	GC	2	13.91429	0.07834
55	ID 55					TC	GG	GT	TC	2	1	2	2	GC	2	0.02597	1.92559
56	ID 56	TB Paru Aktif	0	0	0	TC	GG	GT	TT	2	1	2	1	GC	2	0.02069	1.66557
57	ID 57					TC	GA	GT	TT	2	2	2	1	GG	1	2.36288	28.64806



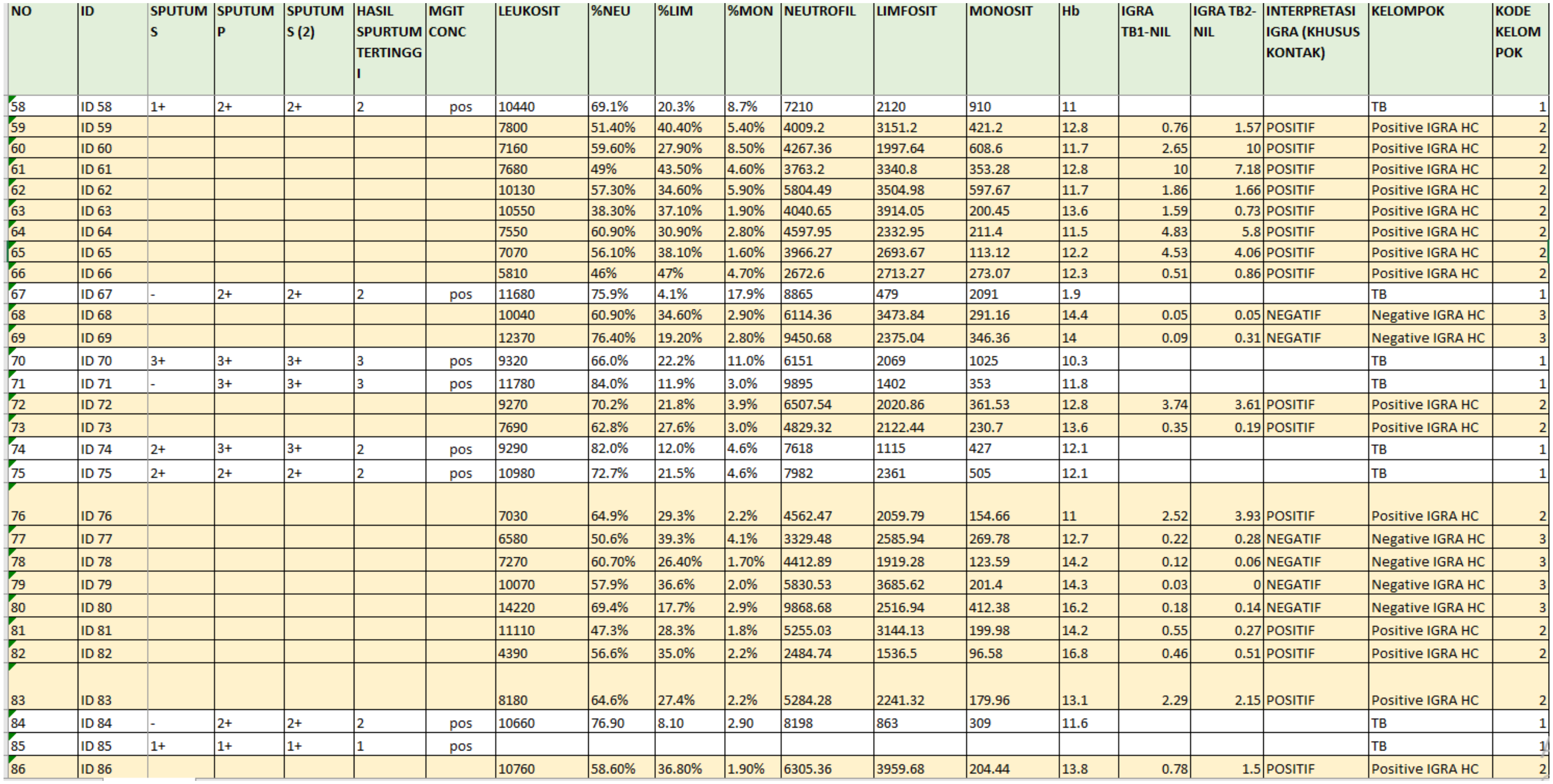
NO	ID	RM	UMUR	JENIS KELAMIN	kode jenis kelamin 1:Laki	bb(kg)	tb (cm)	BMI (KG/M2)	STATUS GIZI	RIWAYAT KONTAK	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK
58	ID 58	76741	59	Laki-Laki	1	55	165	20.20202	NORMAL	ADA		BAPAK
59	ID 59		38	Perempuan	2	58	155	24.14152	OVERWEIGHT	ADA	ISTRI	SUAMI
60	ID 60		36	Perempuan	2	67.5	165	24.79339	OVERWEIGHT	ADA	ISTRI	SUAMI
61	ID 61		55	Perempuan	2	49	150	21.77778	NORMAL	ADA	ISTRI	SUAMI
62	ID 62		29	Perempuan	2	66	150	29.33333	OBESE CLASS I	ADA	ISTRI	SUAMI
63	ID 63		45	Laki-Laki	1	65	170	22.49135	NORMAL	ADA	SUAMI	ISTRI
64	ID 64		43	Perempuan	2	40	154	16.86625	KURANG	ADA	anak	IBU
65	ID 65		62	Perempuan	2	49	150	21.77778	NORMAL	ADA	IBU	ANAK, SUAMI
66	ID 66		21	Perempuan	2	43.7	165	16.05142	KURANG	ADA	KEPONAKAN	TANTE
67	ID 67	76872	18	Perempuan	2	37	155	15.40062	KURANG	TIDAK ADA		
68	ID 68		29	Perempuan	2	70	148	31.95763	OBESE CLAS II	ADA	ANAK	BAPAK
69	ID 69		44	Perempuan	2	54	149	24.32323	OVERWEIGHT	ADA	ANAK	ANAK
70	ID 70	76922	50	Laki-Laki	1	40	160	15.625	KURANG	TIDAK ADA		
71	ID 71	76919	18	Laki-Laki	1	55	165	20.20202	NORMAL	TIDAK ADA		
72	ID 72		24	Perempuan	2	54	140	27.55102	OBESE CLASS I	ADA	ISTRI	SUAMI
73	ID 73		55	Laki-Laki	1	84	172	28.39373	OBESE CLASS I	ADA	ISTRI	ISTRI
74	ID 74	76941	41	Perempuan	2	55	148	25.10957	OBESE CLASS I	TIDAK ADA		
75	ID 75	76947	20	Perempuan	2	32	145	15.21998	KURANG	TIDAK ADA		
76	ID 76		46	Perempuan	2	53.7	148	24.51607	OVERWEIGHT	ADA	ISTRI	SUAMI
77	ID 77		55	Perempuan	2	41.3	155	17.19043	KURANG	ADA	SAUDARA KANDUNG	SAUDARA KANDUNG
78	ID 78		19	Perempuan	2	51	158	20.42942	NORMAL	ADA	KEPONAKAN	TANTE
79	ID 79		18	Perempuan	2	50.9	148	23.23776	OVERWEIGHT	ADA	SAUDARA KANDUNG	SAUDARA KANDUNG
80	ID 80		47	Laki-Laki	2	74.3	170	25.70934	OBESE CLASS I	ADA	AYAH MERTUA	MENANTU
81	ID 81		62	Laki-Laki	1	50	153	21.35931	NORMAL	ADA	SUAMI	ISTRI
82	ID 82		42	Laki-Laki	1	96	165	35.26171	OBESE CLAS II	ADA	SUAMI	ISTRI
83	ID 83		65	Perempuan	2	46	160	17.96875	KURANG	ADA	ISTRI	SUAMI
84	ID 84	77050	38	Perempuan	2	60	155	24.97399	OVERWEIGHT	TIDAK ADA		
85	ID 85	77055	62	Laki-Laki	1	51	163	19.1953	NORMAL	TIDAK ADA		
86	ID 86		40	Perempuan	2	55	145	26.15933	OBESE CLASS I	ADA	ISTRI	SUAMI



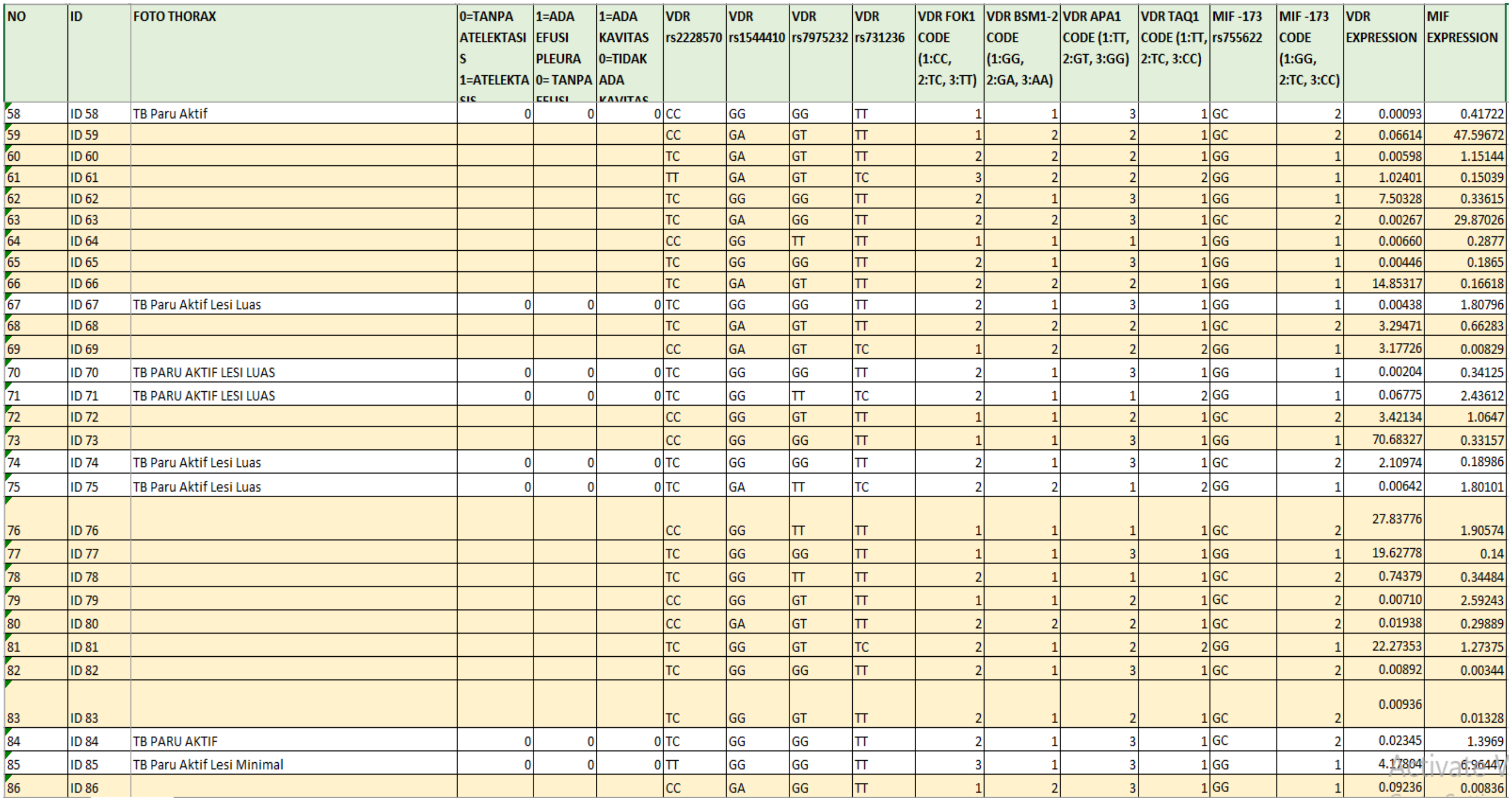
NO	ID	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK	BTA (tertinggi) kasus indeks 1=+1, 2=+2, 3=+3	LAMA TINGGAL DENGAN PENDERITA YANG KONTAK TERSEBUT (<6 BULAN/>=6BULAN)	SEKAMAR/TIDAK DENGAN PENDERITA TERSEBUT (YA/TIDAK\)	KODE SEKAMAR (1) TIDAK SEKAMAR (2)	JUMLAH ORANG YANG TINGGAL SERUMAH (1/2/3/4/ >=5 ORANG)	PERKIRAAN LUAS RUMAH (M2)	SINAR MATAHARI YANG MASUK DLM RUMAH (CUKUP/TIDAK CUKUP/TIDAK TAHU)
58	ID 58		BAPAK		>6BULAN	TIDAK		6	204	cukup
59	ID 59	ISTRI	SUAMI	1	>6 BULAN	YA	1	3	2,5X7	TIDAK CUKUP
60	ID 60	ISTRI	SUAMI	1	>6 BULAN	YA	1	6	4X9	TIDAK CUKUP
61	ID 61	ISTRI	SUAMI	1	>6 BULAN	YA	1	5	40	TIDAK CUKUP
62	ID 62	ISTRI	SUAMI	1	>6 BULAN	YA	1	5	5X7	TIDAK CUKUP
63	ID 63	SUAMI	ISTRI	1	>6 BULAN	YA	1	4	3X6	CUKUP
64	ID 64	anak	IBU	2	>6 BULAN	TIDAK	2	5	36	TIDAK CUKUP
65	ID 65	IBU	ANAK, SUAMI	2	>6 BULAN	YA	1	5	70	CUKUP
66	ID 66	KEPONAKAN	TANTE	1	>6 BULAN	TIDAK	2	3	48	TIDAK CUKUP
67	ID 67							5	60	CUKUP
68	ID 68	ANAK	BAPAK	3	>6 BULAN	TIDAK	2	4	48	CUKUP
69	ID 69	ANAK	ANAK	3	>6 BULAN	YA	1	3	150	CUKUP
70	ID 70							4	48	CUKUP
71	ID 71							3	150	CUKUP
72	ID 72	ISTRI	SUAMI	3	>6 BULAN	YA	1	7	120	CUKUP
73	ID 73	ISTRI	ISTRI	3	>6 BULAN	YA	1	4	48	CUKUP
74	ID 74							4	48	CUKUP
75	ID 75							3	150	CUKUP
76	ID 76	ISTRI	SUAMI	2	>6 BULAN	YA	1	7	60	CUKUP
77	ID 77	SAUDARA KANDUNG	SAUDARA KANDUNG	2	>6 BULAN	TIDAK	2	5	15	CUKUP
78	ID 78	KEPONAKAN	TANTE	1	>6 BULAN	TIDAK	2	3	150	CUKUP
79	ID 79	SAUDARA KANDUNG	SAUDARA KANDUNG	3	>6 BULAN	TIDAK	2	5	132	TIDAK CUKUP
80	ID 80	AYAH MERTUA	MENANTU	2	>6 BULAN	TIDAK	2	12	100	TIDAK CUKUP
81	ID 81	SUAMI	ISTRI	1	>6 BULAN	YA	1	7	64	TIDAK CUKUP
82	ID 82	SUAMI	ISTRI	2	>6 BULAN	YA	1	>5	10x20	CUKUP
83	ID 83	ISTRI	SUAMI	1	>6 BULAN	YA	1	3	8X7	CUKUP
84	ID 84							>5	10x20	CUKUP
85	ID 85							3	8x7	CUKUP
86	ID 86	ISTRI	SUAMI	1	>6 BULAN	YA	1	>5	8x12	CUKUP



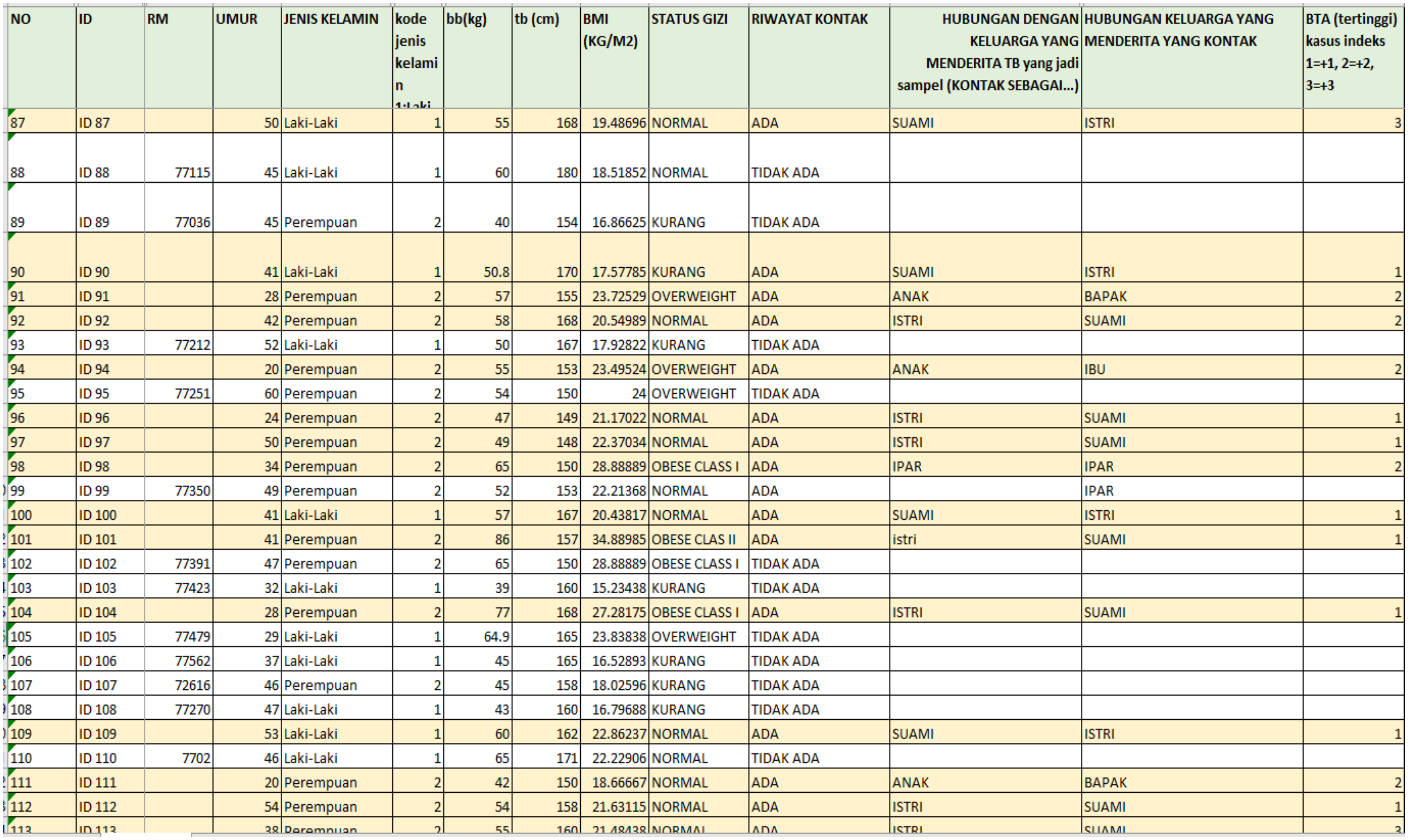
NO	ID	MEROKOK (TIDAK PERNAH / YA, SAAT INI BERHENTI / YA, HINGGA SAAT INI / TIDAK PERNAH)	RIWAYAT MEROKOK (1:PEROKOK; 2= BUKAN PEROKOK)	RIWAYAT MINUM ALKOHOL (1:PERNAH HINGGA SAAT INI , 2: PERNAH, SAAT INI BERHENTI, 3: TIDAK	ALKOHOL (YA, SERING/ YA, KADANG-KADANG/ TIDAK PERNAH	RIWAYAT NAPZA	BATUK (1: iya, 2:tidak)	HEMOPTOE (1: iya, 2:tidak)	SESAK (1: iya, 2:tidak)	NYERI DADA (1: IYA, 2 :TIDAK)	DEMAM (1:IYA , 2:TIDAK)	NAFSU MAKAN BERKURANG (1: iya	BB MENURUN (1: iya, 2:tidak)
58	ID 58	YA, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	1	1	1	1
59	ID 59	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
60	ID 60	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
61	ID 61	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
62	ID 62	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
63	ID 63	YA, HINGGA SAAT INI	1	1	YA	TIDAK PERNAH	2	2	2	2	2	2	2
64	ID 64	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
65	ID 65	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
66	ID 66	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
67	ID 67	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	1	2
68	ID 68	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
69	ID 69	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
70	ID 70	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
71	ID 71	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	2	2	1	1	2
72	ID 72	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
73	ID 73	YA, SAAT INI BERHENTI	1	2	BERHENTI	TIDAK PERNAH	2	2	2	2	2	2	2
74	ID 74	TIDAK PERNAH	0	3	TIDAK PERNAH		1	2	1	1	1	1	1
75	ID 75	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	2	1	1
76	ID 76	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
77	ID 77	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
78	ID 78	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
79	ID 79	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
80	ID 80	YA, SAAT INI BERHENTI	1	1	YA, SERING	TIDAK PERNAH	2	2	2	2	2	2	2
81	ID 81	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
82	ID 82	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
83	ID 83	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
84	ID 84	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	1	1
85	ID 85	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	2	1	1
86	ID 86	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2



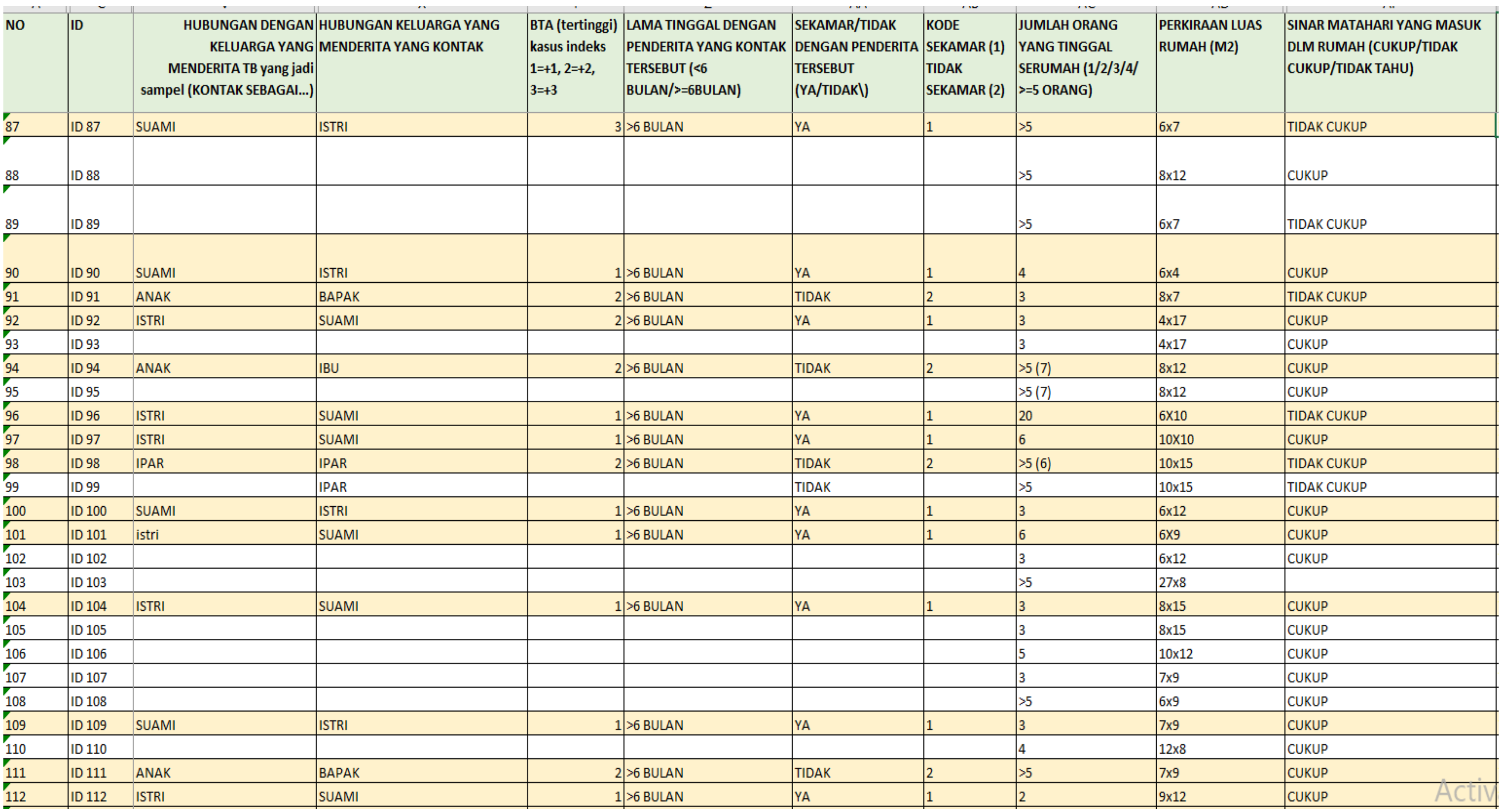
NO	ID	SPUTUM S	SPUTUM P	SPUTUM S (2)	HASIL SPURTUM TERTINGGI	MGIT CONC	LEUKOSIT	%NEU	%LIM	%MON	NEUTROFIL	LIMFOSIT	MONOSIT	Hb	IGRA TB1-NIL	IGRA TB2-NIL	INTERPRETASI IGRA (KHUSUS KONTAK)	KELOMPOK	KODE KELOMPOK
58	ID 58	1+	2+	2+	2	pos	10440	69.1%	20.3%	8.7%	7210	2120	910	11				TB	1
59	ID 59						7800	51.40%	40.40%	5.40%	4009.2	3151.2	421.2	12.8	0.76	1.57	POSITIF	Positive IGRA HC	2
60	ID 60						7160	59.60%	27.90%	8.50%	4267.36	1997.64	608.6	11.7	2.65	10	POSITIF	Positive IGRA HC	2
61	ID 61						7680	49%	43.50%	4.60%	3763.2	3340.8	353.28	12.8	10	7.18	POSITIF	Positive IGRA HC	2
62	ID 62						10130	57.30%	34.60%	5.90%	5804.49	3504.98	597.67	11.7	1.86	1.66	POSITIF	Positive IGRA HC	2
63	ID 63						10550	38.30%	37.10%	1.90%	4040.65	3914.05	200.45	13.6	1.59	0.73	POSITIF	Positive IGRA HC	2
64	ID 64						7550	60.90%	30.90%	2.80%	4597.95	2332.95	211.4	11.5	4.83	5.8	POSITIF	Positive IGRA HC	2
65	ID 65						7070	56.10%	38.10%	1.60%	3966.27	2693.67	113.12	12.2	4.53	4.06	POSITIF	Positive IGRA HC	2
66	ID 66						5810	46%	47%	4.70%	2672.6	2713.27	273.07	12.3	0.51	0.86	POSITIF	Positive IGRA HC	2
67	ID 67	-	2+	2+	2	pos	11680	75.9%	4.1%	17.9%	8865	479	2091	1.9				TB	1
68	ID 68						10040	60.90%	34.60%	2.90%	6114.36	3473.84	291.16	14.4	0.05	0.05	NEGATIF	Negative IGRA HC	3
69	ID 69						12370	76.40%	19.20%	2.80%	9450.68	2375.04	346.36	14	0.09	0.31	NEGATIF	Negative IGRA HC	3
70	ID 70	3+	3+	3+	3	pos	9320	66.0%	22.2%	11.0%	6151	2069	1025	10.3				TB	1
71	ID 71	-	3+	3+	3	pos	11780	84.0%	11.9%	3.0%	9895	1402	353	11.8				TB	1
72	ID 72						9270	70.2%	21.8%	3.9%	6507.54	2020.86	361.53	12.8	3.74	3.61	POSITIF	Positive IGRA HC	2
73	ID 73						7690	62.8%	27.6%	3.0%	4829.32	2122.44	230.7	13.6	0.35	0.19	POSITIF	Positive IGRA HC	2
74	ID 74	2+	3+	3+	2	pos	9290	82.0%	12.0%	4.6%	7618	1115	427	12.1				TB	1
75	ID 75	2+	2+	2+	2	pos	10980	72.7%	21.5%	4.6%	7982	2361	505	12.1				TB	1
76	ID 76						7030	64.9%	29.3%	2.2%	4562.47	2059.79	154.66	11	2.52	3.93	POSITIF	Positive IGRA HC	2
77	ID 77						6580	50.6%	39.3%	4.1%	3329.48	2585.94	269.78	12.7	0.22	0.28	NEGATIF	Negative IGRA HC	3
78	ID 78						7270	60.70%	26.40%	1.70%	4412.89	1919.28	123.59	14.2	0.12	0.06	NEGATIF	Negative IGRA HC	3
79	ID 79						10070	57.9%	36.6%	2.0%	5830.53	3685.62	201.4	14.3	0.03	0	NEGATIF	Negative IGRA HC	3
80	ID 80						14220	69.4%	17.7%	2.9%	9868.68	2516.94	412.38	16.2	0.18	0.14	NEGATIF	Negative IGRA HC	3
81	ID 81						11110	47.3%	28.3%	1.8%	5255.03	3144.13	199.98	14.2	0.55	0.27	POSITIF	Positive IGRA HC	2
82	ID 82						4390	56.6%	35.0%	2.2%	2484.74	1536.5	96.58	16.8	0.46	0.51	POSITIF	Positive IGRA HC	2
83	ID 83						8180	64.6%	27.4%	2.2%	5284.28	2241.32	179.96	13.1	2.29	2.15	POSITIF	Positive IGRA HC	2
84	ID 84	-	2+	2+	2	pos	10660	76.90	8.10	2.90	8198	863	309	11.6				TB	1
85	ID 85	1+	1+	1+	1	pos												TB	1
86	ID 86						10760	58.60%	36.80%	1.90%	6305.36	3959.68	204.44	13.8	0.78	1.5	POSITIF	Positive IGRA HC	2



NO	ID	FOTO THORAX	0=TANPA ATELEKTASIS 1=ATELEKTASIS	1=ADA EFUSI PLEURA 0= TANPA EFUSI	1=ADA KAVITAS 0=TIDAK ADA KAVITAS	VDR rs2228570	VDR rs1544410	VDR rs7975232	VDR rs731236	VDR FOK1 CODE (1:CC, 2:TC, 3:TT)	VDR BSM1-2 CODE (1:GG, 2:GA, 3:AA)	VDR APA1 CODE (1:TT, 2:GT, 3:GG)	VDR TAQ1 CODE (1:TT, 2:TC, 3:CC)	MIF -173 rs755622	MIF -173 CODE (1:GG, 2:TC, 3:CC)	VDR EXPRESSION	MIF EXPRESSION
58	ID 58	TB Paru Aktif	0	0	0	CC	GG	GG	TT	1	1	3	1	GC	2	0.00093	0.41722
59	ID 59					CC	GA	GT	TT	1	2	2	1	GC	2	0.06614	47.59672
60	ID 60					TC	GA	GT	TT	2	2	2	1	GG	1	0.00598	1.15144
61	ID 61					TT	GA	GT	TC	3	2	2	2	GG	1	1.02401	0.15039
62	ID 62					TC	GG	GG	TT	2	1	3	1	GG	1	7.50328	0.33615
63	ID 63					TC	GA	GG	TT	2	2	3	1	GC	2	0.00267	29.87026
64	ID 64					CC	GG	TT	TT	1	1	1	1	GG	1	0.00660	0.2877
65	ID 65					TC	GG	GG	TT	2	1	3	1	GG	1	0.00446	0.1865
66	ID 66					TC	GA	GT	TT	2	2	2	1	GG	1	14.85317	0.16618
67	ID 67	TB Paru Aktif Lesi Luas	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	0.00438	1.80796
68	ID 68					TC	GA	GT	TT	2	2	2	1	GC	2	3.29471	0.66283
69	ID 69					CC	GA	GT	TC	1	2	2	2	GG	1	3.17726	0.00829
70	ID 70	TB PARU AKTIF LESI LUAS	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	0.00204	0.34125
71	ID 71	TB PARU AKTIF LESI LUAS	0	0	0	TC	GG	TT	TC	2	1	1	2	GG	1	0.06775	2.43612
72	ID 72					CC	GG	GT	TT	1	1	2	1	GC	2	3.42134	1.0647
73	ID 73					CC	GG	GG	TT	1	1	3	1	GG	1	70.68327	0.33157
74	ID 74	TB Paru Aktif Lesi Luas	0	0	0	TC	GG	GG	TT	2	1	3	1	GC	2	2.10974	0.18986
75	ID 75	TB Paru Aktif Lesi Luas	0	0	0	TC	GA	TT	TC	2	2	1	2	GG	1	0.00642	1.80101
76	ID 76					CC	GG	TT	TT	1	1	1	1	GC	2	27.83776	1.90574
77	ID 77					TC	GG	GG	TT	1	1	3	1	GG	1	19.62778	0.14
78	ID 78					TC	GG	TT	TT	2	1	1	1	GC	2	0.74379	0.34484
79	ID 79					CC	GG	GT	TT	1	1	2	1	GC	2	0.00710	2.59243
80	ID 80					CC	GA	GT	TT	2	2	2	1	GC	2	0.01938	0.29889
81	ID 81					TC	GG	GT	TC	2	1	2	2	GG	1	22.27353	1.27375
82	ID 82					TC	GG	GG	TT	2	1	3	1	GC	2	0.00892	0.00344
83	ID 83					TC	GG	GT	TT	2	1	2	1	GC	2	0.00936	0.01328
84	ID 84	TB PARU AKTIF	0	0	0	TC	GG	GG	TT	2	1	3	1	GC	2	0.02345	1.3969
85	ID 85	TB Paru Aktif Lesi Minimal	0	0	0	TT	GG	GG	TT	3	1	3	1	GG	1	4.17804	6.96447
86	ID 86					CC	GA	GG	TT	1	2	3	1	GG	1	0.09236	0.00836

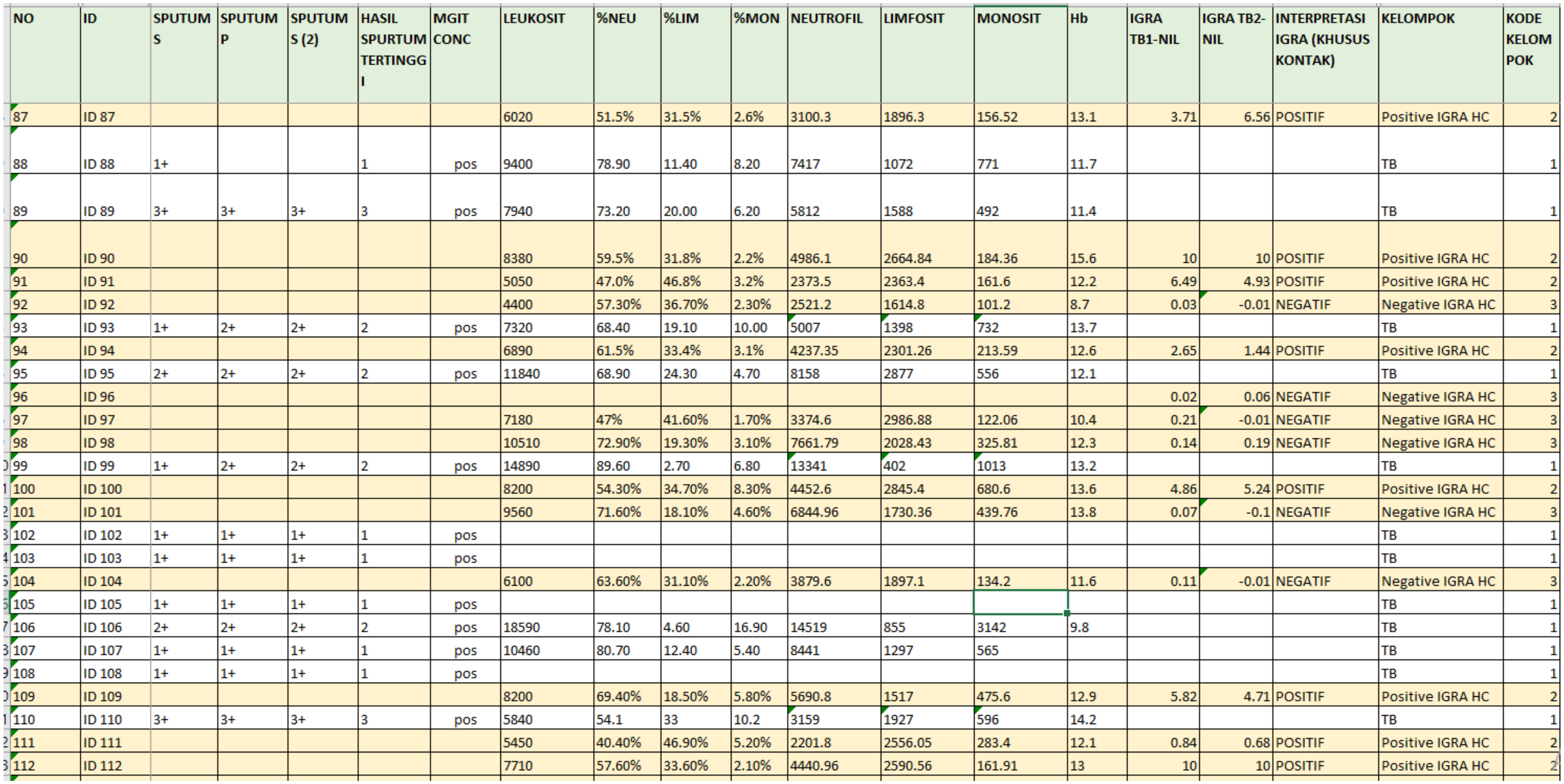


NO	ID	RM	UMUR	JENIS KELAMIN	kode jenis kelamin 1:Laki	bb(kg)	tb (cm)	BMI (KG/M2)	STATUS GIZI	RIWAYAT KONTAK	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK	BTA (tertinggi) kasus indeks 1=+1, 2=+2, 3=+3
87	ID 87		50	Laki-Laki	1	55	168	19.48696	NORMAL	ADA	SUAMI	ISTRI	3
88	ID 88	77115	45	Laki-Laki	1	60	180	18.51852	NORMAL	TIDAK ADA			
89	ID 89	77036	45	Perempuan	2	40	154	16.86625	KURANG	TIDAK ADA			
90	ID 90		41	Laki-Laki	1	50.8	170	17.57785	KURANG	ADA	SUAMI	ISTRI	1
91	ID 91		28	Perempuan	2	57	155	23.72529	OVERWEIGHT	ADA	ANAK	BAPAK	2
92	ID 92		42	Perempuan	2	58	168	20.54989	NORMAL	ADA	ISTRI	SUAMI	2
93	ID 93	77212	52	Laki-Laki	1	50	167	17.92822	KURANG	TIDAK ADA			
94	ID 94		20	Perempuan	2	55	153	23.49524	OVERWEIGHT	ADA	ANAK	IBU	2
95	ID 95	77251	60	Perempuan	2	54	150	24	OVERWEIGHT	TIDAK ADA			
96	ID 96		24	Perempuan	2	47	149	21.17022	NORMAL	ADA	ISTRI	SUAMI	1
97	ID 97		50	Perempuan	2	49	148	22.37034	NORMAL	ADA	ISTRI	SUAMI	1
98	ID 98		34	Perempuan	2	65	150	28.88889	OBESE CLASS I	ADA	IPAR	IPAR	2
99	ID 99	77350	49	Perempuan	2	52	153	22.21368	NORMAL	ADA		IPAR	
100	ID 100		41	Laki-Laki	1	57	167	20.43817	NORMAL	ADA	SUAMI	ISTRI	1
101	ID 101		41	Perempuan	2	86	157	34.88985	OBESE CLAS II	ADA	istri	SUAMI	1
102	ID 102	77391	47	Perempuan	2	65	150	28.88889	OBESE CLASS I	TIDAK ADA			
103	ID 103	77423	32	Laki-Laki	1	39	160	15.23438	KURANG	TIDAK ADA			
104	ID 104		28	Perempuan	2	77	168	27.28175	OBESE CLASS I	ADA	ISTRI	SUAMI	1
105	ID 105	77479	29	Laki-Laki	1	64.9	165	23.83838	OVERWEIGHT	TIDAK ADA			
106	ID 106	77562	37	Laki-Laki	1	45	165	16.52893	KURANG	TIDAK ADA			
107	ID 107	72616	46	Perempuan	2	45	158	18.02596	KURANG	TIDAK ADA			
108	ID 108	77270	47	Laki-Laki	1	43	160	16.79688	KURANG	TIDAK ADA			
109	ID 109		53	Laki-Laki	1	60	162	22.86237	NORMAL	ADA	SUAMI	ISTRI	1
110	ID 110	7702	46	Laki-Laki	1	65	171	22.22906	NORMAL	TIDAK ADA			
111	ID 111		20	Perempuan	2	42	150	18.66667	NORMAL	ADA	ANAK	BAPAK	2
112	ID 112		54	Perempuan	2	54	158	21.63115	NORMAL	ADA	ISTRI	SUAMI	1
113	ID 113		38	Perempuan	2	55	160	21.48438	NORMAL	ADA	ISTRI	SUAMI	3

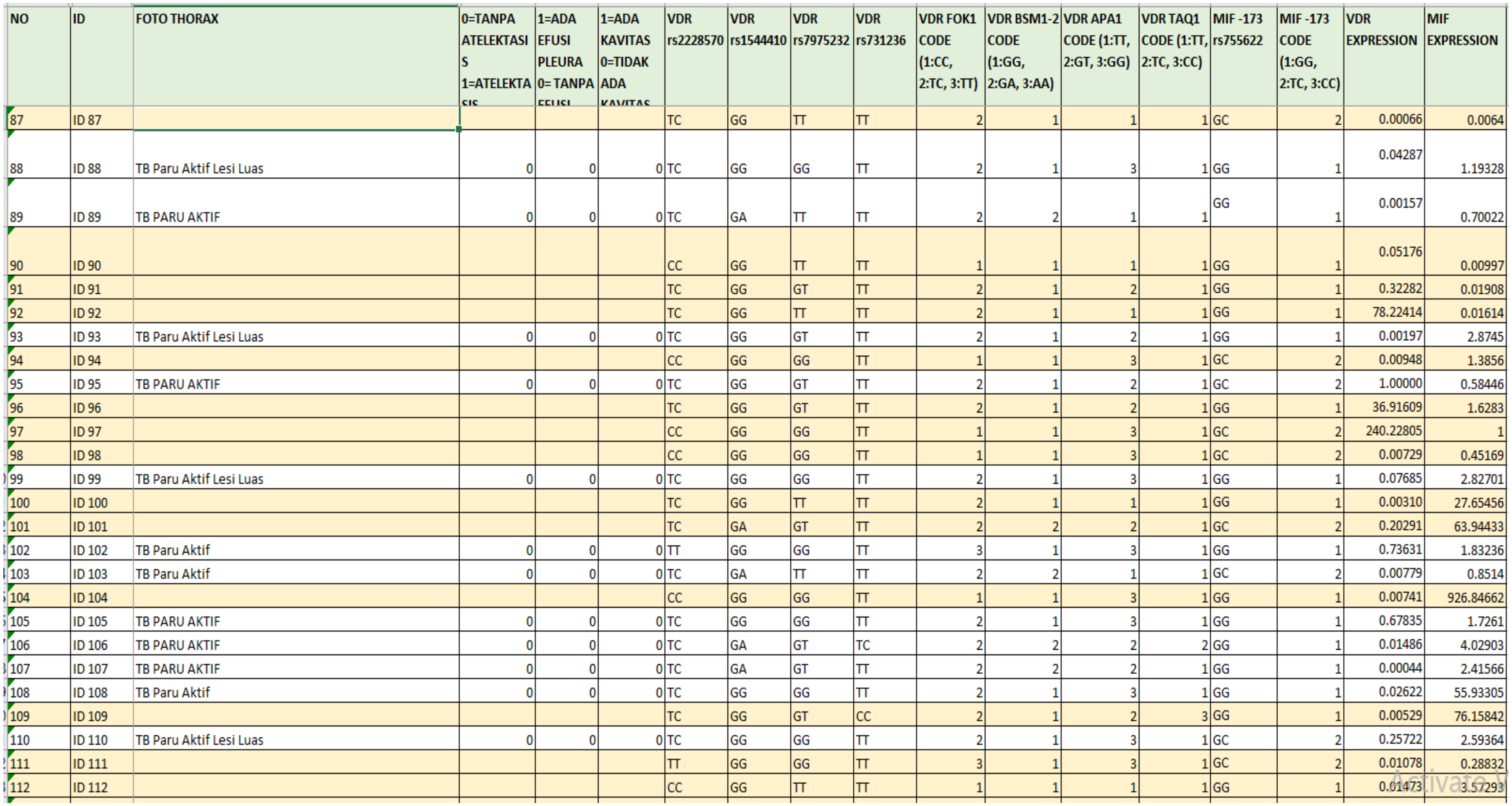


NO	ID	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK	BTA (tertinggi) kasus indeks 1=+1, 2=+2, 3=+3	LAMA TINGGAL DENGAN PENDERITA YANG KONTAK TERSEBUT (<6 BULAN/>=6BULAN)	SEKAMAR/TIDAK DENGAN PENDERITA TERSEBUT (YA/TIDAK\)	KODE SEKAMAR (1) TIDAK SEKAMAR (2)	JUMLAH ORANG YANG TINGGAL SERUMAH (1/2/3/4/ >=5 ORANG)	PERKIRAAN LUAS RUMAH (M2)	SINAR MATAHARI YANG MASUK DLM RUMAH (CUKUP/TIDAK CUKUP/TIDAK TAHU)
87	ID 87	SUAMI	ISTRI	3	>6 BULAN	YA	1	>5	6x7	TIDAK CUKUP
88	ID 88							>5	8x12	CUKUP
89	ID 89							>5	6x7	TIDAK CUKUP
90	ID 90	SUAMI	ISTRI	1	>6 BULAN	YA	1	4	6x4	CUKUP
91	ID 91	ANAK	BAPAK	2	>6 BULAN	TIDAK	2	3	8x7	TIDAK CUKUP
92	ID 92	ISTRI	SUAMI	2	>6 BULAN	YA	1	3	4x17	CUKUP
93	ID 93							3	4x17	CUKUP
94	ID 94	ANAK	IBU	2	>6 BULAN	TIDAK	2	>5 (7)	8x12	CUKUP
95	ID 95							>5 (7)	8x12	CUKUP
96	ID 96	ISTRI	SUAMI	1	>6 BULAN	YA	1	20	6X10	TIDAK CUKUP
97	ID 97	ISTRI	SUAMI	1	>6 BULAN	YA	1	6	10X10	CUKUP
98	ID 98	IPAR	IPAR	2	>6 BULAN	TIDAK	2	>5 (6)	10x15	TIDAK CUKUP
99	ID 99		IPAR			TIDAK		>5	10x15	TIDAK CUKUP
100	ID 100	SUAMI	ISTRI	1	>6 BULAN	YA	1	3	6x12	CUKUP
101	ID 101	istri	SUAMI	1	>6 BULAN	YA	1	6	6X9	CUKUP
102	ID 102							3	6x12	CUKUP
103	ID 103							>5	27x8	
104	ID 104	ISTRI	SUAMI	1	>6 BULAN	YA	1	3	8x15	CUKUP
105	ID 105							3	8x15	CUKUP
106	ID 106							5	10x12	CUKUP
107	ID 107							3	7x9	CUKUP
108	ID 108							>5	6x9	CUKUP
109	ID 109	SUAMI	ISTRI	1	>6 BULAN	YA	1	3	7x9	CUKUP
110	ID 110							4	12x8	CUKUP
111	ID 111	ANAK	BAPAK	2	>6 BULAN	TIDAK	2	>5	7x9	CUKUP
112	ID 112	ISTRI	SUAMI	1	>6 BULAN	YA	1	2	9x12	CUKUP

NO	ID	MEROKOK (TIDAK PERNAH / YA, SAAT INI BERHENTI / YA, HINGGA SAAT INI / TIDAK PERNAH)	RIWAYAT MEROKOK (1:PEROKOK; 2= BUKAN PEROKOK)	RIWAYAT MINUM ALKOHOL (1:PERNAH HINGGA SAAT INI , 2: PERNAH, SAAT INI BERHENTI , 3: TIDAK	ALKOHOL (YA, SERING/ YA, KADANG-KADANG/ TIDAK PERNAH	RIWAYAT NAPZA	BATUK (1: iya, 2:tidak)	HEMOPTOE (1: iya, 2:tidak)	SESAK (1: iya, 2:tidak)	NYERI DADA (1: IYA, 2 :TIDAK)	DEMAM (1:IYA , 2:TIDAK)	NAFSU MAKAN BERKURANG (1: iya	BB MENURUN (1: iya, 2:tidak)
87	ID 87	YA, HINGGA SAAR INI	1	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
88	ID 88	PERNAH SAAT INI BERHENTI	1	2	YA, KADANG-KADANG	TIDAK PERNAH	1	1	1	1	2	1	1
89	ID 89	PERNAH SAAT INI BERHENTI	1	2	YA, KADANG-KADANG	TIDAK PERNAH	1	2	1	1	1	1	1
90	ID 90	YA, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
91	ID 91	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
92	ID 92	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
93	ID 93	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	2	2	1	1
94	ID 94	TIDAK PERNAH	1	2	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
95	ID 95	PERNAH SAAT INI BERHENTI	1	2	YA, KADANG-KADANG	TIDAK PERNAH	1	2	2	1	1	1	1
96	ID 96	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
97	ID 97	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
98	ID 98	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
99	ID 99	PERNAH SAAT INI BERHENTI	1	2	YA, KADANG-KADANG	TIDAK PERNAH	1	2	1	2	1	1	1
100	ID 100	YA, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
101	ID 101	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
102	ID 102	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	2	2	2	2
103	ID 103	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	2	1	1
104	ID 104	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
105	ID 105	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
106	ID 106	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	2	1	1	1
107	ID 107	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	2	2	1	1
108	ID 108	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	2	1	1
109	ID 109	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
110	ID 110	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
111	ID 111	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
112	ID 112	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2

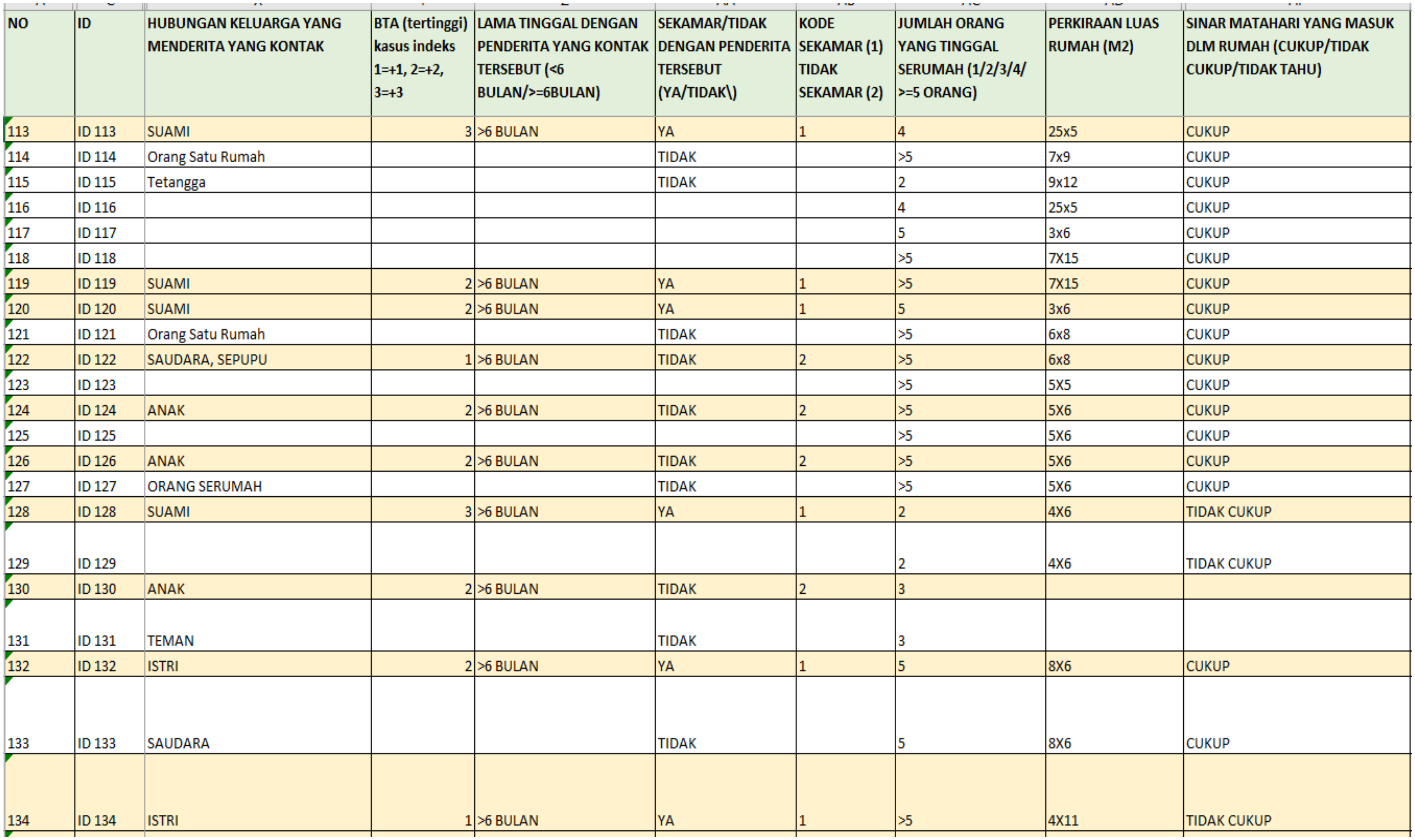


NO	ID	SPUTUM S	SPUTUM P	SPUTUM S (2)	HASIL SPURTUM TERTINGGI	MGIT CONC	LEUKOSIT	%NEU	%LIM	%MON	NEUTROFIL	LIMFOSIT	MONOSIT	Hb	IGRA TB1-NIL	IGRA TB2-NIL	INTERPRETASI IGRA (KHUSUS KONTAK)	KELOMPOK	KODE KELOMPOK
87	ID 87						6020	51.5%	31.5%	2.6%	3100.3	1896.3	156.52	13.1	3.71	6.56	POSITIF	Positive IGRA HC	2
88	ID 88	1+			1	pos	9400	78.90	11.40	8.20	7417	1072	771	11.7				TB	1
89	ID 89	3+	3+	3+	3	pos	7940	73.20	20.00	6.20	5812	1588	492	11.4				TB	1
90	ID 90						8380	59.5%	31.8%	2.2%	4986.1	2664.84	184.36	15.6	10	10	POSITIF	Positive IGRA HC	2
91	ID 91						5050	47.0%	46.8%	3.2%	2373.5	2363.4	161.6	12.2	6.49	4.93	POSITIF	Positive IGRA HC	2
92	ID 92						4400	57.30%	36.70%	2.30%	2521.2	1614.8	101.2	8.7	0.03	-0.01	NEGATIF	Negative IGRA HC	3
93	ID 93	1+	2+	2+	2	pos	7320	68.40	19.10	10.00	5007	1398	732	13.7				TB	1
94	ID 94						6890	61.5%	33.4%	3.1%	4237.35	2301.26	213.59	12.6	2.65	1.44	POSITIF	Positive IGRA HC	2
95	ID 95	2+	2+	2+	2	pos	11840	68.90	24.30	4.70	8158	2877	556	12.1				TB	1
96	ID 96														0.02	0.06	NEGATIF	Negative IGRA HC	3
97	ID 97						7180	47%	41.60%	1.70%	3374.6	2986.88	122.06	10.4	0.21	-0.01	NEGATIF	Negative IGRA HC	3
98	ID 98						10510	72.90%	19.30%	3.10%	7661.79	2028.43	325.81	12.3	0.14	0.19	NEGATIF	Negative IGRA HC	3
99	ID 99	1+	2+	2+	2	pos	14890	89.60	2.70	6.80	13341	402	1013	13.2				TB	1
100	ID 100						8200	54.30%	34.70%	8.30%	4452.6	2845.4	680.6	13.6	4.86	5.24	POSITIF	Positive IGRA HC	2
101	ID 101						9560	71.60%	18.10%	4.60%	6844.96	1730.36	439.76	13.8	0.07	-0.1	NEGATIF	Negative IGRA HC	3
102	ID 102	1+	1+	1+	1	pos												TB	1
103	ID 103	1+	1+	1+	1	pos												TB	1
104	ID 104						6100	63.60%	31.10%	2.20%	3879.6	1897.1	134.2	11.6	0.11	-0.01	NEGATIF	Negative IGRA HC	3
105	ID 105	1+	1+	1+	1	pos												TB	1
106	ID 106	2+	2+	2+	2	pos	18590	78.10	4.60	16.90	14519	855	3142	9.8				TB	1
107	ID 107	1+	1+	1+	1	pos	10460	80.70	12.40	5.40	8441	1297	565					TB	1
108	ID 108	1+	1+	1+	1	pos												TB	1
109	ID 109						8200	69.40%	18.50%	5.80%	5690.8	1517	475.6	12.9	5.82	4.71	POSITIF	Positive IGRA HC	2
110	ID 110	3+	3+	3+	3	pos	5840	54.1	33	10.2	3159	1927	596	14.2				TB	1
111	ID 111						5450	40.40%	46.90%	5.20%	2201.8	2556.05	283.4	12.1	0.84	0.68	POSITIF	Positive IGRA HC	2
112	ID 112						7710	57.60%	33.60%	2.10%	4440.96	2590.56	161.91	13	10	10	POSITIF	Positive IGRA HC	2

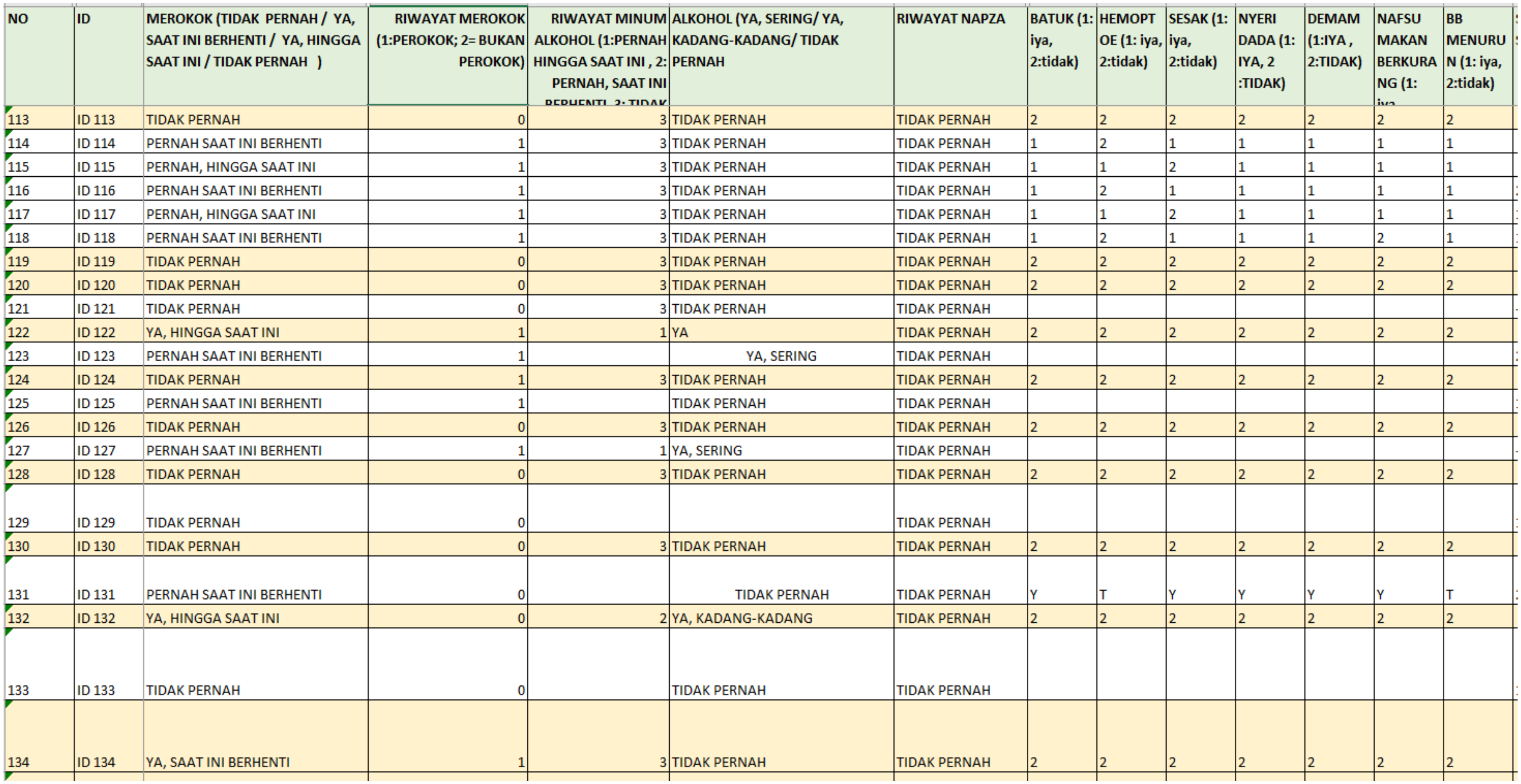


NO	ID	FOTO THORAX	0=TANPA ATELEKTASIS 1=ATELEKTA	1=ADA EFUSI PLEURA 0= TANPA	1=ADA KAVITAS 0=TIDAK ADA	VDR rs2228570	VDR rs1544410	VDR rs7975232	VDR rs731236	VDR FOK1 CODE (1:CC, 2:TC, 3:TT)	VDR BSM1-2 CODE (1:GG, 2:GA, 3:AA)	VDR APA1 CODE (1:TT, 2:GT, 3:GG)	VDR TAQ1 CODE (1:TT, 2:TC, 3:CC)	MIF -173 rs755622	MIF -173 CODE (1:GG, 2:TC, 3:CC)	VDR EXPRESSION	MIF EXPRESSION
87	ID 87					TC	GG	TT	TT	2	1	1	1	GC	2	0.00066	0.0064
88	ID 88	TB Paru Aktif Lesi Luas	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	0.04287	1.19328
89	ID 89	TB PARU AKTIF	0	0	0	TC	GA	TT	TT	2	2	1	1	GG	1	0.00157	0.70022
90	ID 90					CC	GG	TT	TT	1	1	1	1	GG	1	0.05176	0.00997
91	ID 91					TC	GG	GT	TT	2	1	2	1	GG	1	0.32282	0.01908
92	ID 92					TC	GG	TT	TT	2	1	1	1	GG	1	78.22414	0.01614
93	ID 93	TB Paru Aktif Lesi Luas	0	0	0	TC	GG	GT	TT	2	1	2	1	GG	1	0.00197	2.8745
94	ID 94					CC	GG	GG	TT	1	1	3	1	GC	2	0.00948	1.3856
95	ID 95	TB PARU AKTIF	0	0	0	TC	GG	GT	TT	2	1	2	1	GC	2	1.00000	0.58446
96	ID 96					TC	GG	GT	TT	2	1	2	1	GG	1	36.91609	1.6283
97	ID 97					CC	GG	GG	TT	1	1	3	1	GC	2	240.22805	1
98	ID 98					CC	GG	GG	TT	1	1	3	1	GC	2	0.00729	0.45169
99	ID 99	TB Paru Aktif Lesi Luas	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	0.07685	2.82701
100	ID 100					TC	GG	TT	TT	2	1	1	1	GG	1	0.00310	27.65456
101	ID 101					TC	GA	GT	TT	2	2	2	1	GC	2	0.20291	63.94433
102	ID 102	TB Paru Aktif	0	0	0	TT	GG	GG	TT	3	1	3	1	GG	1	0.73631	1.83236
103	ID 103	TB Paru Aktif	0	0	0	TC	GA	TT	TT	2	2	1	1	GC	2	0.00779	0.8514
104	ID 104					CC	GG	GG	TT	1	1	3	1	GG	1	0.00741	926.84662
105	ID 105	TB PARU AKTIF	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	0.67835	1.7261
106	ID 106	TB PARU AKTIF	0	0	0	TC	GA	GT	TC	2	2	2	2	GG	1	0.01486	4.02903
107	ID 107	TB PARU AKTIF	0	0	0	TC	GA	GT	TT	2	2	2	1	GG	1	0.00044	2.41566
108	ID 108	TB Paru Aktif	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	0.02622	55.93305
109	ID 109					TC	GG	GT	CC	2	1	2	3	GG	1	0.00529	76.15842
110	ID 110	TB Paru Aktif Lesi Luas	0	0	0	TC	GG	GG	TT	2	1	3	1	GC	2	0.25722	2.59364
111	ID 111					TT	GG	GG	TT	3	1	3	1	GC	2	0.01078	0.28832
112	ID 112					CC	GG	TT	TT	1	1	1	1	GG	1	0.01473	3.57293

NO	ID	RM	UMUR	JENIS KELAMIN	kode jenis kelamin 1:Laki	bb(kg)	tb (cm)	BMI (KG/M2)	STATUS GIZI	RIWAYAT KONTAK	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK
113	ID 113		38	Perempuan	2	55	160	21.48438	NORMAL	ADA	ISTRI	SUAMI
114	ID 114	77833	48	Laki-Laki	1	55	165	20.20202	NORMAL	ADA		Orang Satu Rumah
115	ID 115	77837	56	Laki-Laki	1	51	167	18.28678	KURANG	ADA		Tetangga
116	ID 116	77883	46	Laki-Laki	1	72	170	24.91349	OVERWEIGHT	TIDAK ADA		
117	ID 117	78458	50	Laki-Laki	1	50	150	22.22222	NORMAL			
118	ID 118	78454	44	Laki-Laki	1	45	155	18.73049	NORMAL			
119	ID 119		35	Perempuan	2	55	148	25.10957	OBESE CLASS I	ADA	ISTRI	SUAMI
120	ID 120		49	Perempuan	2	63	160	24.60938	OVERWEIGHT	ADA	ISTRI	SUAMI
121	ID 121	78492	19	Perempuan	2	37	150	16.44444	KURANG	ADA		Orang Satu Rumah
122	ID 122		24	Laki-Laki	1	65	165	23.87511	OVERWEIGHT	ADA	SAUDARA	SAUDARA, SEPUPU
123	ID 123	1119	40	Laki-Laki	1	45	165	16.52893	KURANG	TIDAK ADA		
124	ID 124		41	Perempuan	2	56	148	25.56611	OBESE CLASS I	ADA	IBU	ANAK
125	ID 125	78740	28	Laki-Laki	1	42	160	16.40625	KURANG	TIDAK ADA		
126	ID 126		50	Perempuan	2	70	154	29.51594	OBESE CLASS I	ADA	IBU	ANAK
127	ID 127	78763	21	Laki-Laki	1	46	170	15.91696	KURANG	ADA		ORANG SERUMAH
128	ID 128		39	Perempuan	2	48	148	21.91381	NORMAL	ADA	ISTRI	SUAMI
129	ID 129	78863	50	Laki-Laki	1	40	165	14.69238	KURANG	TIDAK ADA		
130	ID 130		53	Perempuan	2	45	148	20.54419	NORMAL	ADA	IBU	ANAK
131	ID 131	78919	19	Laki-Laki	1	54.5	164.5	20.14024	NORMAL	ADA		TEMAN
132	ID 132		32	Laki-Laki	1	55	170	19.03114	NORMAL	ADA	SUAMI	ISTRI
133	ID 133	78991	30	Perempuan	2	47	145	22.35434	NORMAL	ADA		SAUDARA
134	ID 134		39	Laki-Laki	1	54	165	19.83471	NORMAL	ADA	SUAMI	ISTRI

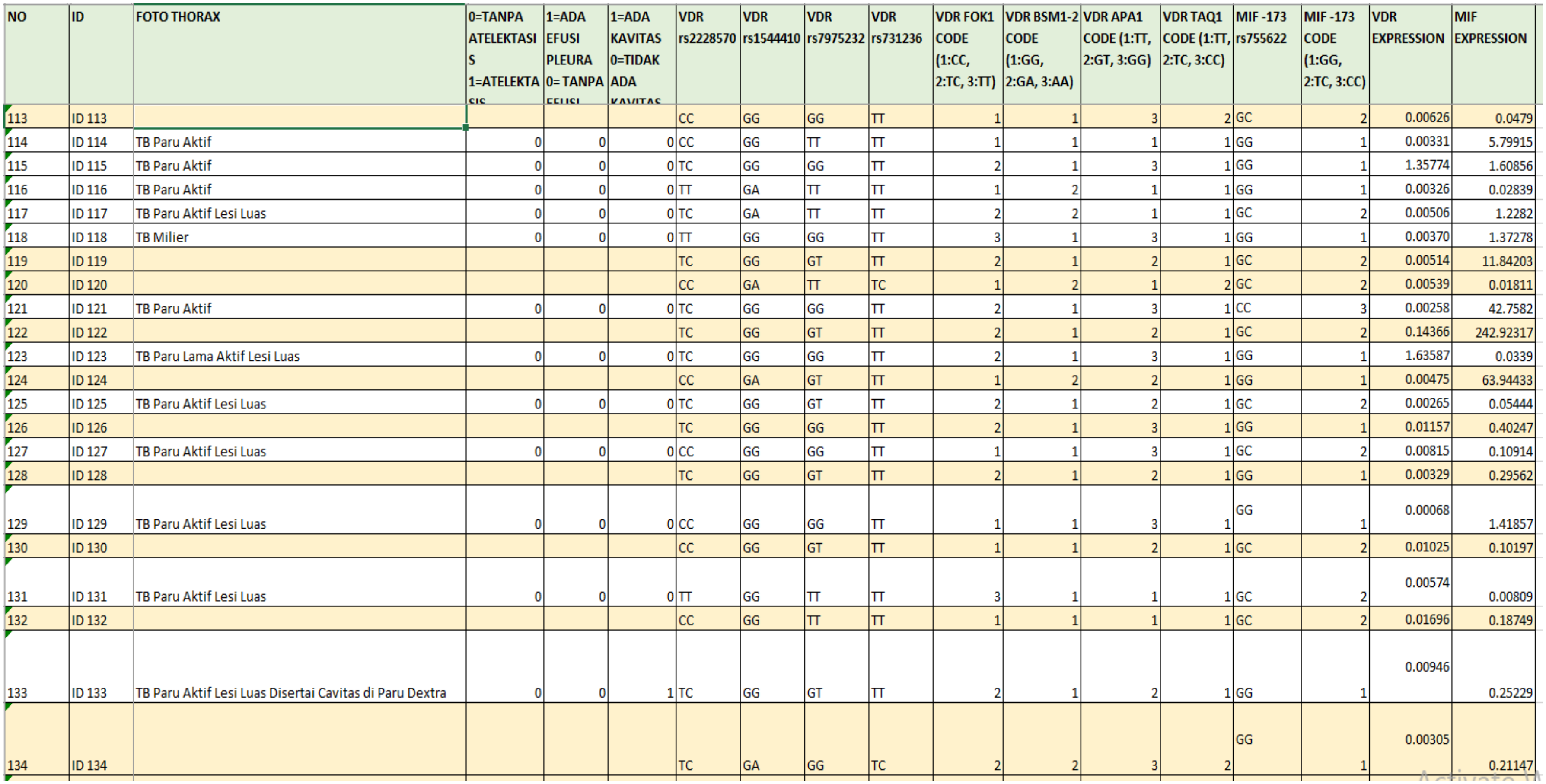


NO	ID	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK	BTA (tertinggi) kasus indeks 1=+1, 2=+2, 3=+3	LAMA TINGGAL DENGAN PENDERITA YANG KONTAK TERSEBUT (<6 BULAN/>=6BULAN)	SEKAMAR/TIDAK DENGAN PENDERITA TERSEBUT (YA/TIDAK\)	KODE SEKAMAR (1) TIDAK SEKAMAR (2)	JUMLAH ORANG YANG TINGGAL SERUMAH (1/2/3/4/ >=5 ORANG)	PERKIRAAN LUAS RUMAH (M2)	SINAR MATAHARI YANG MASUK DLM RUMAH (CUKUP/TIDAK CUKUP/TIDAK TAHU)
113	ID 113	SUAMI	3	>6 BULAN	YA	1	4	25x5	CUKUP
114	ID 114	Orang Satu Rumah			TIDAK		>5	7x9	CUKUP
115	ID 115	Tetangga			TIDAK		2	9x12	CUKUP
116	ID 116						4	25x5	CUKUP
117	ID 117						5	3x6	CUKUP
118	ID 118						>5	7X15	CUKUP
119	ID 119	SUAMI	2	>6 BULAN	YA	1	>5	7X15	CUKUP
120	ID 120	SUAMI	2	>6 BULAN	YA	1	5	3x6	CUKUP
121	ID 121	Orang Satu Rumah			TIDAK		>5	6x8	CUKUP
122	ID 122	SAUDARA, SEPUPU	1	>6 BULAN	TIDAK	2	>5	6x8	CUKUP
123	ID 123						>5	5X5	CUKUP
124	ID 124	ANAK	2	>6 BULAN	TIDAK	2	>5	5X6	CUKUP
125	ID 125						>5	5X6	CUKUP
126	ID 126	ANAK	2	>6 BULAN	TIDAK	2	>5	5X6	CUKUP
127	ID 127	ORANG SERUMAH			TIDAK		>5	5X6	CUKUP
128	ID 128	SUAMI	3	>6 BULAN	YA	1	2	4X6	TIDAK CUKUP
129	ID 129						2	4X6	TIDAK CUKUP
130	ID 130	ANAK	2	>6 BULAN	TIDAK	2	3		
131	ID 131	TEMAN			TIDAK		3		
132	ID 132	ISTRI	2	>6 BULAN	YA	1	5	8X6	CUKUP
133	ID 133	SAUDARA			TIDAK		5	8X6	CUKUP
134	ID 134	ISTRI	1	>6 BULAN	YA	1	>5	4X11	TIDAK CUKUP

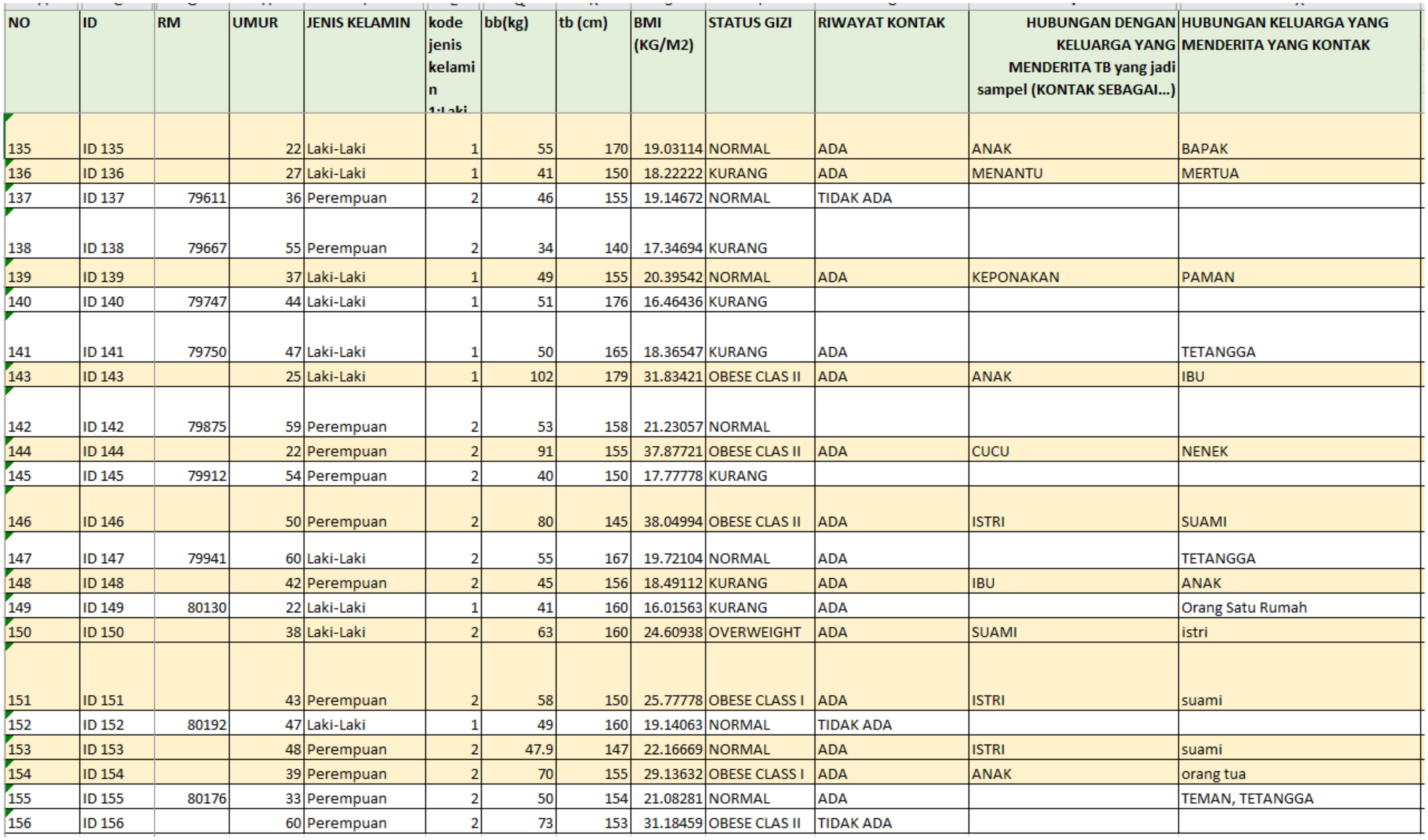


NO	ID	MEROKOK (TIDAK PERNAH / YA, SAAT INI BERHENTI / YA, HINGGA SAAT INI / TIDAK PERNAH)	RIWAYAT MEROKOK (1:PEROKOK; 2= BUKAN PEROKOK)	RIWAYAT MINUM ALKOHOL (1:PERNAH HINGGA SAAT INI , 2: PERNAH, SAAT INI BERHENTI, 3: TIDAK	ALKOHOL (YA, SERING/ YA, KADANG-KADANG/ TIDAK PERNAH	RIWAYAT NAPZA	BATUK (1: iya, 2:tidak)	HEMOPTOE (1: iya, 2:tidak)	SESAK (1: iya, 2:tidak)	NYERI DADA (1: IYA, 2 :TIDAK)	DEMAM (1:IYA , 2:TIDAK)	NAFSU MAKAN BERKURANG (1:	BB MENURUN (1: iya, 2:tidak)
113	ID 113	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
114	ID 114	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	1	1
115	ID 115	PERNAH, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	2	1	1	1	1
116	ID 116	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	1	1
117	ID 117	PERNAH, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	1	2	1	1	1	1
118	ID 118	PERNAH SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	2	1
119	ID 119	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
120	ID 120	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
121	ID 121	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH							
122	ID 122	YA, HINGGA SAAT INI	1	1	YA	TIDAK PERNAH	2	2	2	2	2	2	2
123	ID 123	PERNAH SAAT INI BERHENTI	1		YA, SERING	TIDAK PERNAH							
124	ID 124	TIDAK PERNAH	1	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
125	ID 125	PERNAH SAAT INI BERHENTI	1		TIDAK PERNAH	TIDAK PERNAH							
126	ID 126	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
127	ID 127	PERNAH SAAT INI BERHENTI	1	1	YA, SERING	TIDAK PERNAH							
128	ID 128	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
129	ID 129	TIDAK PERNAH	0			TIDAK PERNAH							
130	ID 130	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
131	ID 131	PERNAH SAAT INI BERHENTI	0		TIDAK PERNAH	TIDAK PERNAH	Y	T	Y	Y	Y	Y	T
132	ID 132	YA, HINGGA SAAT INI	0	2	YA, KADANG-KADANG	TIDAK PERNAH	2	2	2	2	2	2	2
133	ID 133	TIDAK PERNAH	0		TIDAK PERNAH	TIDAK PERNAH							
134	ID 134	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2

NO	ID	SPUTUM S	SPUTUM P	SPUTUM S (2)	HASIL SPURTUM TERTINGGI	MGIT CONC	LEUKOSIT	%NEU	%LIM	%MON	NEUTROFIL	LIMFOSIT	MONOSIT	Hb	IGRA TB1-NIL	IGRA TB2-NIL	INTERPRETASI IGRA (KHUSUS KONTAK)	KELOMPOK	KODE KELOMPOK
113	ID 113						7790	48.60%	38.40%	10.10%	3785.94	2991.36	786.79	12.4	10	10	POSITIF	Positive IGRA HC	2
114	ID 114		2+	2+	2	pos												TB	1
115	ID 115		1+	1+	1	pos												TB	1
116	ID 116	2+	3+	3+	3	pos	7880	79.8	13.5	5.5	6288	1064	433	14.5				TB	1
117	ID 117	1+	2+	2+	2	pos	13400	70.8	23.7	4	9487	3176	536	12				TB	1
118	ID 118	1+	2+	2+	2	pos	9370	94.7	2.8	1.4	8873	262	131	11.9				TB	1
119	ID 119						9480	53.90%	40.20%	3.60%	5109.72	3810.96	341.28	12.9	0.02	0.01	NEGATIF	Negative IGRA HC	3
120	ID 120						7080	59.70%	34.20%	1.90%	4226.76	2421.36	134.52	13	0.09	0.72	POSITIF	Positive IGRA HC	2
121	ID 121	-	1+	1+	1	pos	11650	78.5	18.5	2.2	9145	2155	256	13.2				TB	1
122	ID 122						9330	46.80%	41.70%	2.70%	4366.44	3890.61	251.91	15.6	2.22	10	POSITIF	Positive IGRA HC	2
123	ID 123	2+	2+	2+	2	pos	7570	63.4	30.8	20.9	4799	2332	1582	10.3				TB	1
124	ID 124						8410	65.40%	29.40%	2.60%	5500.14	2472.54	218.66	12.2	0.04	0.54	POSITIF	Positive IGRA HC	2
125	ID 125	1+	2+	2+	2	pos	7260	63.2	23	3.3	4588	1670	240	12.2				TB	1
126	ID 126						5440	32.70%	58.20%	1.80%	1778.88	3166.08	97.92	13.0	0.06	0.12	NEGATIF	Negative IGRA HC	3
127	ID 127	-	2+	2+	2	pos	7320	70.3	17.7	6.8	5146	1296	498	13.9				TB	1
128	ID 128						9260	64.10%	31.70%	2.70%	5935.66	2935.42	250.02	14.2	5.92	6.85	POSITIF	Positive IGRA HC	2
129	ID 129	1+	3+	3+	3	pos	15820	79.6	11.3	6.5	12593	1788	1028	10.1				TB	1
130	ID 130						8050	44.90%	48.10%	2.90%	3614.45	3872.05	233.45	12.3	0.87	2.99	POSITIF	Positive IGRA HC	2
131	ID 131	2+	2+	2+	2	pos	11530	75.90	17.8	5.1	8751	2052	588	9.2				TB	1
132	ID 132						7280	37.50%	52.50%	2.90%	2730	3822	211.12	13.4	3.33	5.72	POSITIF	Positive IGRA HC	2
133	ID 133	1+	2+	2+	2	pos	10110	78.60	15.3	5.8	7946	1547	586	10.6				TB	1
134	ID 134						6310	50.8%	37.5%	2.4%	3205.48	2366.25	151.44	13.7	3.37	6.89	POSITIF	Positive IGRA HC	2

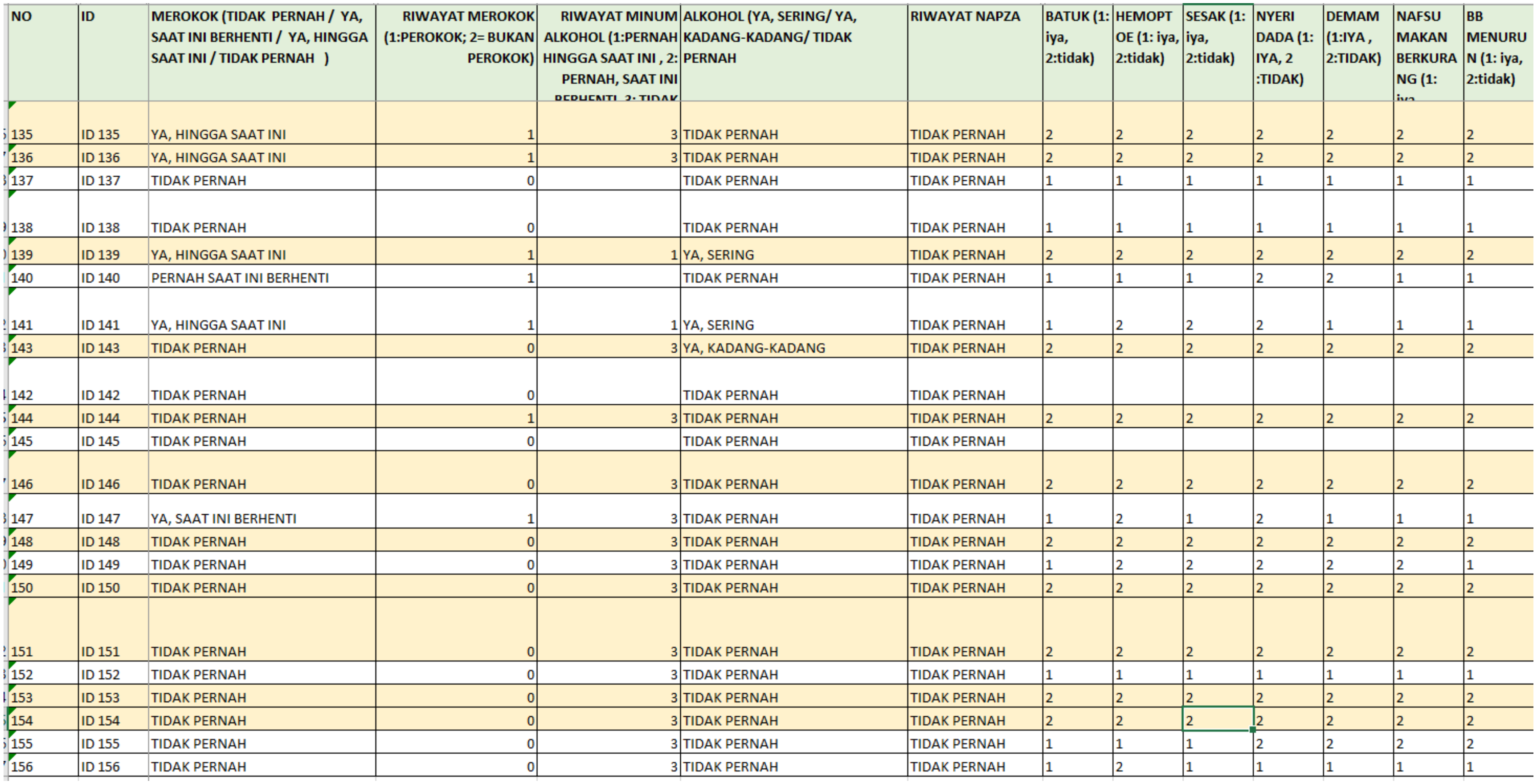


NO	ID	FOTO THORAX	0=TANPA ATELEKTASIS 1=ATELEKTASIS	1=ADA EFUSI PLEURA 0= TANPA EFUSI	1=ADA KAVITAS 0=TIDAK ADA KAVITAS	VDR rs2228570	VDR rs1544410	VDR rs7975232	VDR rs731236	VDR FOK1 CODE (1:CC, 2:TC, 3:TT)	VDR BSM1-2 CODE (1:GG, 2:GA, 3:AA)	VDR APA1 CODE (1:TT, 2:GT, 3:GG)	VDR TAQ1 CODE (1:TT, 2:TC, 3:CC)	MIF -173 rs755622	MIF -173 CODE (1:GG, 2:TC, 3:CC)	VDR EXPRESSION	MIF EXPRESSION
113	ID 113					CC	GG	GG	TT	1	1	3	2	GC	2	0.00626	0.0479
114	ID 114	TB Paru Aktif	0	0	0	CC	GG	TT	TT	1	1	1	1	GG	1	0.00331	5.79915
115	ID 115	TB Paru Aktif	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	1.35774	1.60856
116	ID 116	TB Paru Aktif	0	0	0	TT	GA	TT	TT	1	2	1	1	GG	1	0.00326	0.02839
117	ID 117	TB Paru Aktif Lesi Luas	0	0	0	TC	GA	TT	TT	2	2	1	1	GC	2	0.00506	1.2282
118	ID 118	TB Milier	0	0	0	TT	GG	GG	TT	3	1	3	1	GG	1	0.00370	1.37278
119	ID 119					TC	GG	GT	TT	2	1	2	1	GC	2	0.00514	11.84203
120	ID 120					CC	GA	TT	TC	1	2	1	2	GC	2	0.00539	0.01811
121	ID 121	TB Paru Aktif	0	0	0	TC	GG	GG	TT	2	1	3	1	CC	3	0.00258	42.7582
122	ID 122					TC	GG	GT	TT	2	1	2	1	GC	2	0.14366	242.92317
123	ID 123	TB Paru Lama Aktif Lesi Luas	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	1.63587	0.0339
124	ID 124					CC	GA	GT	TT	1	2	2	1	GG	1	0.00475	63.94433
125	ID 125	TB Paru Aktif Lesi Luas	0	0	0	TC	GG	GT	TT	2	1	2	1	GC	2	0.00265	0.05444
126	ID 126					TC	GG	GG	TT	2	1	3	1	GG	1	0.01157	0.40247
127	ID 127	TB Paru Aktif Lesi Luas	0	0	0	CC	GG	GG	TT	1	1	3	1	GC	2	0.00815	0.10914
128	ID 128					TC	GG	GT	TT	2	1	2	1	GG	1	0.00329	0.29562
129	ID 129	TB Paru Aktif Lesi Luas	0	0	0	CC	GG	GG	TT	1	1	3	1	GG	1	0.00068	1.41857
130	ID 130					CC	GG	GT	TT	1	1	2	1	GC	2	0.01025	0.10197
131	ID 131	TB Paru Aktif Lesi Luas	0	0	0	TT	GG	TT	TT	3	1	1	1	GC	2	0.00574	0.00809
132	ID 132					CC	GG	TT	TT	1	1	1	1	GC	2	0.01696	0.18749
133	ID 133	TB Paru Aktif Lesi Luas Disertai Cavitas di Paru Dextra	0	0	1	TC	GG	GT	TT	2	1	2	1	GG	1	0.00946	0.25229
134	ID 134					TC	GA	GG	TC	2	2	3	2	GG	1	0.00305	0.21147



NO	ID	RM	UMUR	JENIS KELAMIN	kode jenis kelamin 1:Laki	bb(kg)	tb (cm)	BMI (KG/M2)	STATUS GIZI	RIWAYAT KONTAK	HUBUNGAN DENGAN KELUARGA YANG MENDERITA TB yang jadi sampel (KONTAK SEBAGAI...)	HUBUNGAN KELUARGA YANG MENDERITA YANG KONTAK
135	ID 135		22	Laki-Laki	1	55	170	19.03114	NORMAL	ADA	ANAK	BAPAK
136	ID 136		27	Laki-Laki	1	41	150	18.22222	KURANG	ADA	MENANTU	MERTUA
137	ID 137	79611	36	Perempuan	2	46	155	19.14672	NORMAL	TIDAK ADA		
138	ID 138	79667	55	Perempuan	2	34	140	17.34694	KURANG			
139	ID 139		37	Laki-Laki	1	49	155	20.39542	NORMAL	ADA	KEPONAKAN	PAMAN
140	ID 140	79747	44	Laki-Laki	1	51	176	16.46436	KURANG			
141	ID 141	79750	47	Laki-Laki	1	50	165	18.36547	KURANG	ADA		TETANGGA
143	ID 143		25	Laki-Laki	1	102	179	31.83421	OBESE CLAS II	ADA	ANAK	IBU
142	ID 142	79875	59	Perempuan	2	53	158	21.23057	NORMAL			
144	ID 144		22	Perempuan	2	91	155	37.87721	OBESE CLAS II	ADA	CUCU	NENEK
145	ID 145	79912	54	Perempuan	2	40	150	17.77778	KURANG			
146	ID 146		50	Perempuan	2	80	145	38.04994	OBESE CLAS II	ADA	ISTRI	SUAMI
147	ID 147	79941	60	Laki-Laki	2	55	167	19.72104	NORMAL	ADA		TETANGGA
148	ID 148		42	Perempuan	2	45	156	18.49112	KURANG	ADA	IBU	ANAK
149	ID 149	80130	22	Laki-Laki	1	41	160	16.01563	KURANG	ADA		Orang Satu Rumah
150	ID 150		38	Laki-Laki	2	63	160	24.60938	OVERWEIGHT	ADA	SUAMI	istri
151	ID 151		43	Perempuan	2	58	150	25.77778	OBESE CLASS I	ADA	ISTRI	suami
152	ID 152	80192	47	Laki-Laki	1	49	160	19.14063	NORMAL	TIDAK ADA		
153	ID 153		48	Perempuan	2	47.9	147	22.16669	NORMAL	ADA	ISTRI	suami
154	ID 154		39	Perempuan	2	70	155	29.13632	OBESE CLASS I	ADA	ANAK	orang tua
155	ID 155	80176	33	Perempuan	2	50	154	21.08281	NORMAL	ADA		TEMAN, TETANGGA
156	ID 156		60	Perempuan	2	73	153	31.18459	OBESE CLAS II	TIDAK ADA		

NO	ID	BTA (tertinggi) kasus indeks 1=+1, 2=+2, 3=+3	LAMA TINGGAL DENGAN PENDERITA YANG KONTAK TERSEBUT (<6 BULAN/>=6BULAN)	SEKAMAR/TIDAK DENGAN PENDERITA TERSEBUT (YA/TIDAK\)	KODE SEKAMAR (1) TIDAK SEKAMAR (2)	JUMLAH ORANG YANG TINGGAL SERUMAH (1/2/3/4/ >=5 ORANG)	PERKIRAAN LUAS RUMAH (M2)	SINAR MATAHARI YANG MASUK DLM RUMAH (CUKUP/TIDAK CUKUP/TIDAK TAHU)
135	ID 135	1	>6 BULAN	TIDAK	2	>5	8X9	CUKUP
136	ID 136	3	>6 BULAN	TIDAK	2	>5	8X13	CUKUP
137	ID 137					>5	4X11	TIDAK CUKUP
138	ID 138					>5	8X9	CUKUP
139	ID 139	1	>6 BULAN	TIDAK	2	>5	8X12	CUKUP
140	ID 140					>5	8X13	CUKUP
141	ID 141			TIDAK		>5	8X12	CUKUP
143	ID 143	1	>6 BULAN	TIDAK	2	2	8X12	CUKUP
142	ID 142					2	8X12	CUKUP
144	ID 144	2	>6 BULAN	TIDAK	2	>5	8X12	CUKUP
145	ID 145					>5	8X12	CUKUP
146	ID 146	3	>6 BULAN	YA	1	3	8X16	CUKUP
147	ID 147			TIDAK		3	8X16	CUKUP
148	ID 148	1	>6 BULAN	TIDAK	2	4	9x6	CUKUP
149	ID 149			TIDAK		4	9x6	CUKUP
150	ID 150	1	>6 BULAN	YA	1	4	5x7	CUKUP
151	ID 151	1	>6 BULAN	YA	1	5	10x15	CUKUP
152	ID 152					4	5x7	CUKUP
153	ID 153	2	>6 BULAN	YA	1	>5	8X17	CUKUP
154	ID 154	2	>6 BULAN	TIDAK	2	>5	3,75x10	CUKUP
155	ID 155			TIDAK		5	10x15	CUKUP
156	ID 156					>5	3,75x10	CUKUP



NO	ID	MEROKOK (TIDAK PERNAH / YA, SAAT INI BERHENTI / YA, HINGGA SAAT INI / TIDAK PERNAH)	RIWAYAT MEROKOK (1:PEROKOK; 2= BUKAN PEROKOK)	RIWAYAT MINUM ALKOHOL (1:PERNAH HINGGA SAAT INI , 2: PERNAH, SAAT INI BERHENTI, 3: TIDAK	ALKOHOL (YA, SERING/ YA, KADANG-KADANG/ TIDAK PERNAH	RIWAYAT NAPZA	BATUK (1: iya, 2:tidak)	HEMOPTOE (1: iya, 2:tidak)	SESAK (1: iya, 2:tidak)	NYERI DADA (1: IYA, 2 :TIDAK)	DEMAM (1:IYA , 2:TIDAK)	NAFSU MAKAN BERKURANG (1: iya	BB MENURUN (1: iya, 2:tidak)
135	ID 135	YA, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
136	ID 136	YA, HINGGA SAAT INI	1	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
137	ID 137	TIDAK PERNAH	0		TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
138	ID 138	TIDAK PERNAH	0		TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
139	ID 139	YA, HINGGA SAAT INI	1	1	YA, SERING	TIDAK PERNAH	2	2	2	2	2	2	2
140	ID 140	PERNAH SAAT INI BERHENTI	1		TIDAK PERNAH	TIDAK PERNAH	1	1	1	2	2	1	1
141	ID 141	YA, HINGGA SAAT INI	1	1	YA, SERING	TIDAK PERNAH	1	2	2	2	1	1	1
143	ID 143	TIDAK PERNAH	0	3	YA, KADANG-KADANG	TIDAK PERNAH	2	2	2	2	2	2	2
142	ID 142	TIDAK PERNAH	0		TIDAK PERNAH	TIDAK PERNAH							
144	ID 144	TIDAK PERNAH	1	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
145	ID 145	TIDAK PERNAH	0		TIDAK PERNAH	TIDAK PERNAH							
146	ID 146	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
147	ID 147	YA, SAAT INI BERHENTI	1	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	2	1	1	1
148	ID 148	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
149	ID 149	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	2	2	2	2	1
150	ID 150	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
151	ID 151	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
152	ID 152	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	1	1	1	1
153	ID 153	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
154	ID 154	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	2	2	2	2	2	2	2
155	ID 155	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	1	1	2	2	2	2
156	ID 156	TIDAK PERNAH	0	3	TIDAK PERNAH	TIDAK PERNAH	1	2	1	1	1	1	1

NO	ID	SPUTUM S	SPUTUM P	SPUTUM S (2)	HASIL SPURTUM TERTINGGI	MGIT CONC	LEUKOSIT	%NEU	%LIM	%MON	NEUTROFIL	LIMFOSIT	MONOSIT	Hb	IGRA TB1-NIL	IGRA TB2-NIL	INTERPRETASI IGRA (KHUSUS KONTAK)	KELOMPOK	KODE KELOMPOK
135	ID 135						7730	54.4%	31.4%	9.3%	4205.12	2427.22	718.89	13.8	-0.02	-0.05	NEGATIF	Negative IGRA HC	3
136	ID 136						6640	40.6%	46.2%	5.3%	2695.84	3067.68	351.92	15.6	0.2	0.61	POSITIF	Positive IGRA HC	2
137	ID 137	1+	1+	1+	1	pos	19990	81.4	15	3.1	16272	2999	620	14				TB	1
138	ID 138	1+	1+	1+	1	pos	24150	86.9	7.9	4.4	20986	1908	1063	11.7				TB	1
139	ID 139						7410	58.0%	33.5%	2.6%	4297.8	2482.35	192.66	14.1	0.21	0.13	NEGATIF	Negative IGRA HC	3
140	ID 140	2+	3+	3+	3	pos												TB	1
141	ID 141	-	1+	1+	1	pos	12280	59.5	19.2	12.4	7307	2358	1523	12				TB	1
143	ID 143						9540	77.7%	15.1%	6.5%	7412.58	1440.54	620.1	15.2	-0.15	-0.2	NEGATIF	Negative IGRA HC	3
142	ID 142	-	1+	1+	1	pos	8350	75.6	15.4	7.3	6313	1286	610	11.9				TB	1
144	ID 144						11690	58.9%	35.0%	2.1%	6885.41	4091.5	245.49	12.2	0.04	-0.08	NEGATIF	Negative IGRA HC	3
145	ID 145	2+	2+	2+	2	pos	17600	84.4	8	7.1	14854	1408	1250	10.4				TB	1
146	ID 146						8230	56.3%	34.7%	2.2%	4633.49	2855.81	181.06	13.5	6.12	4.97	POSITIF	Positive IGRA HC	2
147	ID 147	3+	2+	2+	3	pos	11820	66.4	24.2	8	7848	2860	946	12.9				TB	1
148	ID 148						7920	63.4	30.4	3.5	502128	240768	27720	11.9	4.84	4.11	POSITIF	Positive IGRA HC	2
149	ID 149	1+	1+	1+	1	pos	9070	71.3	20.7	6.3	6467	1877	571	12.8				TB	1
150	ID 150						7630	51.70%	42.30%	2%	3944.71	3227.49	152.6	14.5	3.95	4.65	POSITIF	Positive IGRA HC	2
151	ID 151						5400	53.60%	36%	3.7	2894.4	1944	19980	14.8	0.09	0.06	NEGATIF	Negative IGRA HC	3
152	ID 152	1+	1+	1+	1	pos	20190	93.2	5.3	1.4	18817	1070	283	13.1				TB	1
153	ID 153						7050	75.20%	20.70%	1.70%	5301.6	1459.35	119.85	12.8	0.1	0.1	NEGATIF	Negative IGRA HC	3
154	ID 154						10060	81.70%	13.2	2.7	8219.02	132792	27162	13.5	0.21	0.18	NEGATIF	Negative IGRA HC	3
155	ID 155	-	1+	1+	1	pos	9520	66.8	24.4	6.9	6359	2323	657	13.4				TB	1
156	ID 156	1+	2+	2+	2	pos	10900	58.8	31.3	3.3	6409	3412	360	13.6				TB	1

NO	ID	KODE KELOMPOK	FOTO THORAX	0=TANPA ATELEKTASIS 1=ATELEKTASIS	1=ADA EFUSI PLEURA 0= TANPA EFUSI	1=ADA KAVITAS 0=TIDAK ADA KAVITAS	VDR rs2228570	VDR rs1544410	VDR rs7975232	VDR rs731236	VDR FOK1 CODE (1:CC, 2:TC, 3:TT)	VDR BSM1-2 CODE (1:GG, 2:GA, 3:AA)	VDR APA1 CODE (1:TT, 2:GT, 3:GG)	VDR TAQ1 CODE (1:TT, 2:TC, 3:CC)	MIF -173 rs755622	MIF -173 CODE (1:GG, 2:TC, 3:CC)	VDR EXPRESSION	MIF EXPRESSION
135	ID 135	3					CC	GA	GT	TT	1	2	2	1	GG	1	0.00031	0.16932
136	ID 136	2					CC	GA	GT	TT	1	2	2	1	GG	1	0.00427	0.39885
137	ID 137	1	KP Duplex Lama Aktif	0	0	0	TC	GG	GG	TT	2	1	3	1	GC	2	0.00462	147.25926
138	ID 138	1	TB Paru Aktif Lesi Luas	0	0	0	TT	GG	GT	TT	3	1	2	1	GG	1	0.00780	0.05286
139	ID 139	3					TT	GA	GT	TC	3	2	2	2	GG	1	0.00696	0.17545
140	ID 140	1	TB Paru Aktif Lesi Luas	0	0	0	TC	GG	TT	TT	2	1	1	1	GC	2	0.00337	9.03031
141	ID 141	1	TB Paru Duplex Lama Aktif	0	0	0	TC	GG	GG	TT	2	1	3	1	GC	2	0.00894	0.6695
143	ID 143	3					TC	GG	GT	TT	2	1	2	1	GC	2	0.00340	0.31772
142	ID 142	1	TB Paru Sanistra Aktif	0	0	0	TC	GG	GT	TT	2	1	2	1	GG	1	0.00104	0.80904
144	ID 144	3					TC	GG	GT	TT	2	1	2	1	GG	1	0.02619	0.62056
145	ID 145	1	TB Paru Aktif Lesi Luas	0	0	0	TC	GG	GT	TT	2	1	2	1	GG	1	0.00718	1.0689
146	ID 146	2					TC	GG	TT	TT	2	1	1	1	GC	2	0.00215	0.46283
147	ID 147	1	TB PARU AKTIF	0			TC	GA	GT	TC	2	2	2	2	CC	3	0.01838	170.17763
148	ID 148	2					TC	GG	GT	TT	2	1	2	1	CC	3	0.01061	0.3056
149	ID 149	1	TB Paru Aktif	0	0	0	CC	GG	GG	TT	1	1	3	1	GC	2	0.10772	3.68093
150	ID 150	2					CC	GG	GT	TT	1	1	2	1	GC	2	0.00505	1.4211
151	ID 151	3					CC	GG	GG	TT	1	1	3	1	GC	2	0.02570	0.22532
152	ID 152	1	TB Paru Aktif Lesi Luas	0	0	0	CC	GG	GG	TT	1	1	3	1	GC	2	0.04754	11.17292
153	ID 153	3					CC	GG	GG	TT	1	1	3	1	GG	1	0.00645	0.56018
154	ID 154	3					CC	GG	GG	TT	1	1	3	1	GG	1	0.00467	7.07716
155	ID 155	1	TB Paru Aktif Lesi Luas	0	0	0	CC	GG	GT	TT	1	1	2	1	GC	2	0.00411	9.86947
156	ID 156	1	KP Dextra Lama Aktif	0	0	0	TC	GG	GG	TT	2	1	3	1	GG	1	0.04590	0.14164

LAMPIRAN 3. POSISI PRIMER PADA GEN TARGET

A. PEMERIKSAAN POLIMORFISME

1. *VDR*

SNP	**Primer**	**Target**
***VDR* rs2228570**	F 5’-AGC TGG CCC TGG CAC TGA CTC TGC TCT-3’ R 5’-ATG GAA ACA CCT TGC TTC TTC TCC CTC-3’	267 bp
***VDR* rs1544410**	F 5’-AGT GTG CAG GCG ATT CGTA G-3’ R 5’-ATA GGC AGA ACC ATC TCTC AG-3’	191 bp
***VDR* rs7975232 dan *VDR* rs731236**	F 5'-CAG AGC ATG GAC AGG GAG CAA-3' R 5'-ACT TCG AGC ACA AGG GGC GTT AG-3'	500 bp
***MIF* -173 G/C rs755622**	F 5'-CTG ACT TCT CGG ACA CCA CT-3' R 5'-AAG GGT AAG GGG CCA TCT TC-3'	352 bp

Homo sapiens vitamin D receptor (VDR), RefSeqGene on chromosome 12

NCBI Reference Sequence: NG_008731.1

FASTA Graphics

Go to:

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LOCUS       NG_008731              70495 bp    DNA     linear   PRI 03-JUN-201
DEFINITION  Homo sapiens vitamin D receptor (VDR), RefSeqGene on chromosome 12.
ACCESSION   NG_008731
VERSION     NG_008731.1
KEYWORDS    RefSeq; RefSeqGene.
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 70495)
  AUTHORS   Loughran G, Jungreis I, Tzani I, Power M, Dmitriev RI, Ivanov IP,
            Kellis M and Atkins JF.
  TITLE     Stop codon readthrough generates a C-terminally extended variant of
            the human vitamin D receptor with reduced calcitriol response
  JOURNAL   J. Biol. Chem. 293 (12), 4434-4444 (2018)
   PUBMED   29386352
REFERENCE   2  (bases 1 to 70495)
  AUTHORS   Sunn KL, Cock TA, Crofts LA, Eisman JA and Gardiner EM.
  TITLE     Novel N-terminal variant of human VDR
  JOURNAL   Mol. Endocrinol. 15 (9), 1599-1609 (2001)
   PUBMED   11518809
REFERENCE   3  (bases 1 to 70495)
  AUTHORS   Crofts LA, Hancock MS, Morrison NA and Eisman JA.
  TITLE     Multiple promoters direct the tissue-specific expression of novel
            N-terminal variant human vitamin D receptor gene transcripts
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (18), 10529-10534 (1998)
   PUBMED   9724737
REFERENCE   4  (bases 1 to 70495)
  AUTHORS   Miyamoto K, Kesterson RA, Yamamoto H, Taketani Y, Nishiwaki E,
            Tatsumi S, Inoue Y, Morita K, Takeda E and Pike JW.
  TITLE     Structural organization of the human vitamin D receptor chromosomal
            gene and its promoter
  JOURNAL   Mol. Endocrinol. 11 (8), 1165-1179 (1997)
   PUBMED   9212063
COMMENT     REVIEWED REFSEQ: This record has been curated by NCBI staff. The
            reference sequence was derived from AC121338.6 and AC004466.1.
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            This sequence is a reference standard in the RefSeqGene project.

            Summary: This gene encodes vitamin D3 receptor, which is a member
            of the nuclear hormone receptor superfamily of ligand-inducible
            transcription factors. This receptor also functions as a receptor
            for the secondary bile acid, lithocholic acid. Downstream targets
            of vitamin D3 receptor are principally involved in mineral
            metabolism, though this receptor regulates a variety of other
            metabolic pathways, such as those involved in immune response and
            cancer. Mutations in this gene are associated with type II vitamin
            D-resistant rickets. A single nucleotide polymorphism in the
            initiation codon results in an alternate translation start site
            three codons downstream. Alternatively spliced transcript variants
            encoding different isoforms have been described for this gene. A
            recent study provided evidence for translational readthrough in
            this gene, and expression of an additional C-terminally extended
            isoform via the use of an alternative in-frame translation
            termination codon. [provided by RefSeq, Jun 2018].
            COMPLETENESS: full length.
PRIMARY     REFSEQ_SPAN         PRIMARY_IDENTIFIER PRIMARY_SPAN        COMP
            1-18898             AC121338.6         1997-20894          c
            18899-70495         AC004466.1         1-51597
FEATURES             Location/Qualifiers
ORIGIN
        1 ctggggcttg aggatgtggg agcaggtggg aaagacaaat accaaaagcc ccgaggaaga
       61 agacatgagc tgggctactg ggaatggagc cctggagcca gatggatttg gagtgaataa
      121 ctggtggtgc cctactcttt ctagggcagg ctgagtctgt gtgcattcac ttctcatggc
      181 attgcacagg actccttgga gctgttctgt tctgttctgg agcagtcaag atttctgaga
      241 tgccataggc atcatgaggc taaaagaacc ccccaaacct ggaaaatact tgtgagtggt
      301 aatatatcag ttgagtaaag gccacaaaag caaacattgg gtggatacat tctgcctcag
      361 … 29161
    29161 taatatatat taatatgtat ttatatattt aatgtatata ttatatatac attagagttt
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29221 agcaagtata aatctagctg tgaaagaaat tagcaatagt gtcactatta ctattaggat
29281 agttcaaaag taattgcgat ctttgccatt atttttgatg gccaaaacca caattacttt
29341 tgcaccaacc taatacatta aggtttccag gaaaagaaaa gctaaatgag gttagggaat
29401 ctccgaggtc tgtgaccggg attccctctg tccctttggg actgatgata acatattctt
29461 gcttatctgc accacttctt tcccttggtg tgaagctctt tggggaattt ttagaaagta
29521 tttgttttat tcatttggca gtagtggttt ctagacatat cttaaggttt gggcctctct
29581 gggcctcatt tgtaaagggg atgatgataa tagcatctac accatgaagt ggtatgaagg
29641 tgaaataaga cttaatgagc tttgatattc cacaccctag atcagagatc atgggcctag
29701 tcattgaaaa gtagctcaga gcctcccaag ggcccccaga atctgcctct gtcacccaag
29761 ggcaggagga aatggtaccc tggggtggag tgggttcttg tctcttgttt cctggctttc
29821 tctcttattt ttcttctgac aagaaggacc ctttgcctag ggtcaaaggg gtcactgaaa
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    63961 gggccacaga caggcctgcg cattcccaat actcaggctc tgctcttgcg tgaactgggc
                                                BSMI(2)   R 5’-ataggcagaaccatctctcag-3’ (64095-64075)
                                                          3’-tatccgtcttggtagagagtc-5’→
complementnya
                                                          5’-ctgaga
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Apa1 F 5’- cagagc atggacaggg agcaa (64765-64785) intron 8 **500 bp**
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Apa1 R 5’- acttcgagcacaaggggcgttag-3’ (65264-65242) **500 bp**
5’-ctaacgccc cttgtgctcg aagt-3’→ reverse complement
65221 cagcctgagt gcagcatgaa gctaacgccc cttgtgctcg aagtgtttgg caatgagatc
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ccaag
//

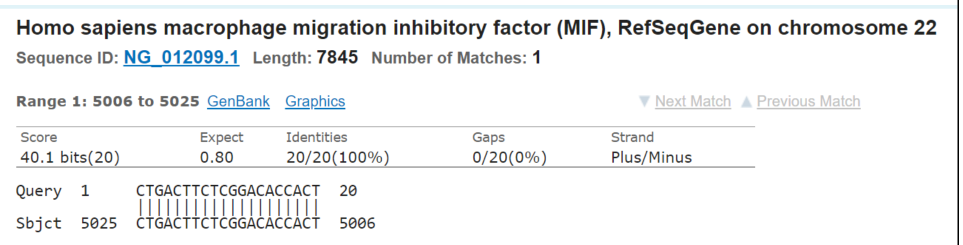
2. *MIF*

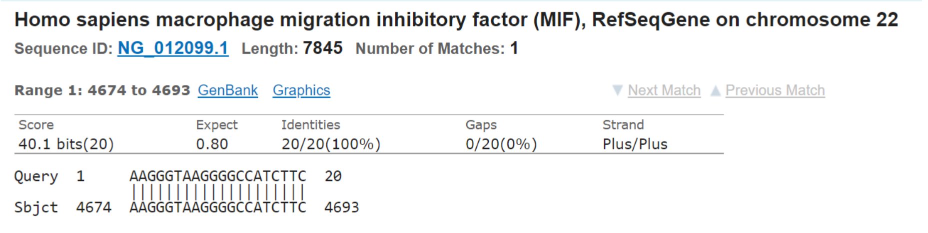
rs755622

Current Build 154
Released April 21, 2020

Organism	*Homo sapiens*	**Clinical Significance**	Not Reported in ClinVar
Position	chr22:23894205 (GRCh38.p12)	**Gene : Consequence**	MIF-AS1 : Non Coding Transcript Variant MIF : 2KB Upstream Variant
Alleles	G>C	**Publications**	75 citations LitVar 258
Variation Type	SNV Single Nucleotide Variation		
Frequency	C=0.254635 (31974/125568, TOPMED) C=0.30544 (24010/78608, PAGE_STUDY) C=0.25485 (7991/31356, GnomAD) (+ 12 more)	**Genomic View**	See rs on genome

SNP	Primer	Target

***MIF* -173 G/C rs755622**	F 5'-CTG ACT TCT CGG ACA CCA CT-3'
	
	Homo sapiens macrophage migration inhibitory factor (MIF), RefSeqGene on chromosome 22
	Sequence ID: NG_012099.1 Length: 7845 Number of Matches: 1
	Range 1: 5006 to 5025 GenBank Graphics ▼ Next Match ▲ Previous Match
	Score 40.1 bits(20) · Expect 0.80 · Identities 20/20(100%) · Gaps 0/20(0%) · Strand Plus/Minus
	`Query  1     CTGACTTCTCGGACACCACT  20`
	`             ||||||||||||||||||||`
	`Sbjct  5025  CTGACTTCTCGGACACCACT  5006`
	R 5'-AAG GGT AAG GGG CCA TCT TC-3'.
		352 bp

Homo sapiens macrophage migration inhibitory factor (MIF), RefSeqGene on chromosome 22

Sequence ID: NG_012099.1 Length: 7845 Number of Matches: 1

Range 1: 4674 to 4693 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
40.1 bits(20)	0.80	20/20(100%)	0/20(0%)	Plus/Plus

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Query  1     AAGGGTAAGGGGCCATCTTC  20
             ||||||||||||||||||||
Sbjct  4674  AAGGGTAAGGGGCCATCTTC  4693
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Homo sapiens macrophage migration inhibitory factor (MIF), RefSeqGene on chromosome 22

NCBI Reference Sequence: NG_012099.1

FASTA Graphics

Go to:

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LOCUS       NG_012099               7845 bp    DNA     linear   PRI 25-MAY-2020
DEFINITION  Homo sapiens macrophage migration inhibitory factor (MIF),
            RefSeqGene on chromosome 22.
ACCESSION   NG_012099
VERSION     NG_012099.1
KEYWORDS    RefSeq; RefSeqGene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
COMMENT     REVIEWED REFSEQ: This record has been curated by NCBI staff. The
```

```
            reference sequence was derived from AP000350.1.
            This sequence is a reference standard in the RefSeqGene project.

            Summary: This gene encodes a lymphokine involved in cell-mediated
            immunity, immunoregulation, and inflammation. It plays a role in
            the regulation of macrophage function in host defense through the
            suppression of anti-inflammatory effects of glucocorticoids. This
            lymphokine and the JAB1 protein form a complex in the cytosol near
            the peripheral plasma membrane, which may indicate an additional
            role in integrin signaling pathways. [provided by RefSeq, Jul
            2008].
ORIGIN
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R 5’ – aagggta

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B. PEMERIKSAAN EKSPRESI GEN

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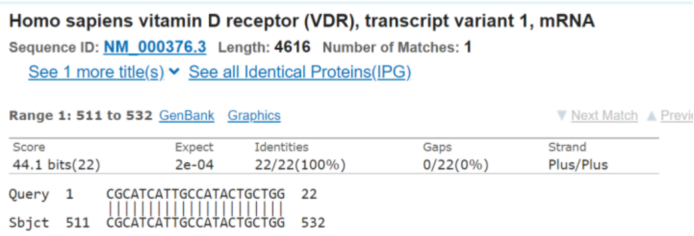
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Range 1: 511 to 532
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Query 1 CGCATCATTGCCATACTGCTGG 22
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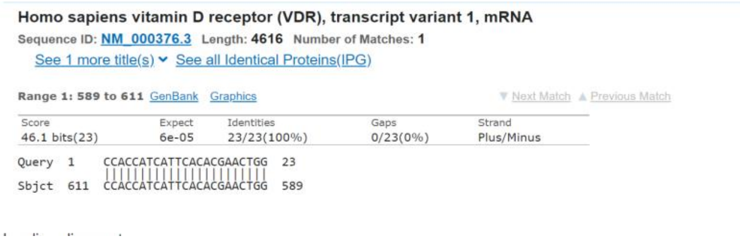
Sbjct 511 CGCATCATTGCCATACTGCTGG 532

Reverse 5’- CCA CCA TCA TTC ACA CGA ACT GG-3’

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Range 1: 589 to 611
Score 46.1 bits(23) Expect 6e-05 Identities 23/23(100%) Gaps 0/23(0%) Strand Plus/Minus
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Sbjct 611 CCACCATCATTCACACGAACTGG 589
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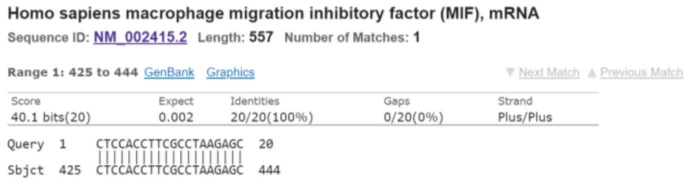
Homo sapiens macrophage migration inhibitory factor (MIF), mRNA
Sequence ID: NM_002415.2 Length: 557 Number of Matches: 1
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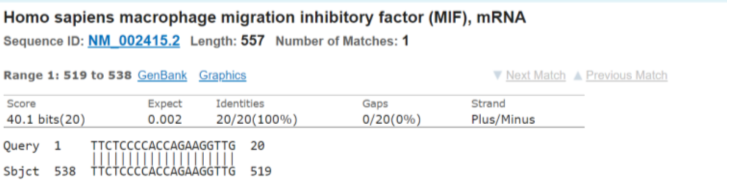
Sbjct 425 CTCCACCTTCGCCTAAGAGC 444

Reverse 5’- TTCTCCCCACCAGAAGGTTG-3’

Homo sapiens macrophage migration inhibitory factor (MIF), mRNA
Sequence ID: NM_002415.2 Length: 557 Number of Matches: 1
Range 1: 519 to 538
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Sbjct 538 TTCTCCCCACCAGAAGGTTG 519
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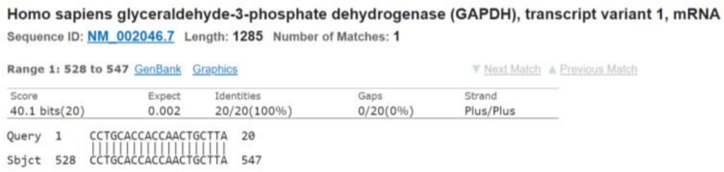
Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPDH), transcript variant 1, mRNA
Sequence ID: NM_002046.7 Length: 1285 Number of Matches: 1
Range 1: 528 to 547
Score 40.1 bits(20) Expect 0.002 Identities 20/20(100%) Gaps 0/20(0%) Strand Plus/Plus
Query 1 CCTGCACCACCAACTGCTTA 20
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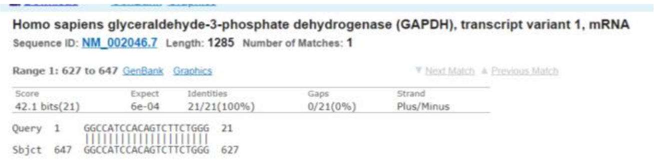
		Reverse (5’-GGC CAT CCA CAG TCT TCT GGG-3’)  Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPDH), transcript variant 1, mRNA Sequence ID: NM_002046.7 Length: 1285 Number of Matches: 1 Range 1: 627 to 647 GenBank Graphics ▼ Next Match ▲ Previous Match Score 42.1 bits(21) Expect 6e-04 Identities 21/21(100%) Gaps 0/21(0%) Strand Plus/Minus Query 1 GGCCATCCACAGTCTTCTGGG 21 ||||||||||||||||||||| Sbjct 647 GGCCATCCACAGTCTTCTGGG 627	

Homo sapiens vitamin D receptor (VDR), transcript variant 1, mRNA

NCBI Reference Sequence: NM_000376.3

FASTA Graphics

Go to:

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DEFINITION  Homo sapiens vitamin D receptor (VDR), transcript variant 1, mRNA.
ACCESSION   NM_000376
VERSION     NM_000376.3
KEYWORDS    RefSeq; MANE Select.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
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                                           reverse: ccaccatcattcacacgaactgg
                                                                cc agttcgtgtg
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aatgatggtg g (reverse complementer)

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721 tccagcttct ccaatctgga tctgagtgaa gaagattcag atgacccttc tgtgacccta
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Homo sapiens macrophage migration inhibitory factor (MIF), mRNA

NCBI Reference Sequence: NM_002415.2

FASTA Graphics

Go to:

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ACCESSION   NM_002415
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            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
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Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPDH), transcript variant 1, mRNA

NCBI Reference Sequence: NM_002046.7

FASTA Graphics

Go to:

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VERSION     NM_002046.7
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REFERENCE   1  (bases 1 to 1285)
  AUTHORS   Michielon A, Marchesani F, Faggiano S, Giaccari R, Campanini B,
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  TITLE     Human serine racemase is inhibited by glyceraldehyde 3-phosphate,
            but not by glyceraldehyde 3-phosphate dehydrogenase
  JOURNAL   Biochim Biophys Acta Proteins Proteom 1869 (1), 140544 (2021)
   PUBMED   32971286
  REMARK    GeneRIF: Human serine racemase is inhibited by glyceraldehyde
            3-phosphate, but not by glyceraldehyde 3-phosphate dehydrogenase.
REFERENCE   2  (bases 1 to 1285)
  AUTHORS   Liu P, Zhong Y, Cao T, Sheng X and Huang H.
  TITLE     A frequent somatic mutation in the 3'UTR of GAPDH facilitates the
            development of ovarian cancer by creating a miR125b binding site
  JOURNAL   Oncol Rep 44 (3), 887-896 (2020)
   PUBMED   32705257
  REMARK    GeneRIF: A frequent somatic mutation in the 3'UTR of GAPDH
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            binding site.
REFERENCE   10 (bases 1 to 1285)
  AUTHORS   Bruns,G.A. and Gerald,P.S.
  TITLE     Human glyceraldehyde-3-phosphate dehydrogenase in man-rodent
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  JOURNAL   Science 192 (4234), 54-56 (1976)
   PUBMED   176725
COMMENT     REVIEWED REFSEQ: This record has been curated by NCBI staff in
            collaboration with Francesco Amaldi. The reference sequence was
            derived from AK308198.1 and BC009081.1.
            This sequence is a reference standard in the RefSeqGene project.
            On Nov 23, 2018 this sequence version replaced NM_002046.6.

            Summary: This gene encodes a member of the
            glyceraldehyde-3-phosphate dehydrogenase protein family. The
            encoded protein has been identified as a moonlighting protein based
            on its ability to perform mechanistically distinct functions. The
```

product of this gene catalyzes an important energy-yielding step in carbohydrate metabolism, the reversible oxidative phosphorylation of glyceraldehyde-3-phosphate in the presence of inorganic phosphate and nicotinamide adenine dinucleotide (NAD). The encoded protein has additionally been identified to have uracil DNA glycosylase activity in the nucleus. Also, this protein contains a peptide that has antimicrobial activity against E. coli, P. aeruginosa, and C. albicans. Studies of a similar protein in mouse have assigned a variety of additional functions including nitrosylation of nuclear proteins, the regulation of mRNA stability, and acting as a transferrin receptor on the cell surface of macrophage. Many pseudogenes similar to this locus are present in the human genome. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Nov 2014].

Transcript Variant: This variant (1) encodes the longest isoform (1).

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

```
##Evidence-Data-START##
Transcript exon combination :: SRR5189661.97809.1,
                               SRR3476690.1051075.1 [ECO:0000332]
RNAseq introns              :: single sample supports all introns
                               SAMEA1965299, SAMEA1966682
                               [ECO:0000348]
##Evidence-Data-END##
```

```
##RefSeq-Attributes-START##
MANE Ensembl match                :: ENST00000229239.10/
                                     ENSP00000229239.5
multifunctional gene product(s)   :: PMID: 20727968
Protein has antimicrobial activity :: PMID: 22832495
RefSeq Select criteria            :: based on manual assertion,
                                     conservation, expression,
                                     longest protein
##RefSeq-Attributes-END##
```

```
            COMPLETENESS: full length.
ORIGIN
        1 gctctctgct cctcctgttc gacagtcagc cgcatcttct tttgcgtcgc cagccgagcc
       61 acatcgctca gacaccatgg ggaaggtgaa ggtcggagtc aacggatttg gtcgtattgg
      121 gcgcctggtc accagggctg cttttaactc tggtaaagtg gatattgttg ccatcaatga
      181 ccccttcatt gacctcaact acatggttta catgttccaa tatgattcca cccatggcaa
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      301 catcttccag gagcgagatc cctccaaaat caagtggggc gatgctggcg ctgagtacgt
      361 cgtggagtcc actggcgtct tcaccaccat ggagaaggct ggggctcatt tgcagggggg
      421 agccaaaagg gtcatcatct ctgccccctc tgctgatgcc cccatgttcg tcatgggtgt
                                                   forward cct gcaccaccaa
      481 gaaccatgag aagtatgaca acagcctcaa gatcatcagc aatgcctcct gcaccaccaa

          ctgctta
      541 ctgcttagca cccctggcca aggtcatcca tgacaacttt ggtatcgtgg aaggactcat
                            reverse ggcc atccacagtc ttctggg
                                    ccca gaagactgtg gatggcc
      601 gaccacagtc catgccatca ctgccaccca gaagactgtg gatggcccct ccgggaaact
      661 gtggcgtgat ggccgcgggg ctctccagaa catcatccct gcctctactg gcgctgccaa
      721 ggctgtgggc aaggtcatcc ctgagctgaa cgggaagctc actggcatgg ccttccgtgt
      781 ccccactgcc aacgtgtcag tggtggacct gacctgccgt ctagaaaaac ctgccaaata
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      901 ctacactgag caccaggtgg tctcctctga cttcaacagc gacacccact cctccacctt
      961 tgacgctggg gctggcattg ccctcaacga ccactttgtc aagctcattt cctggtatga
     1021 caacgaattt ggctacagca acagggtggt ggacctcatg gcccacatgg cctccaagga
     1081 gtaagacccc tggaccacca gccccagcaa gagcacaaga ggaagagaga gaccctcact
     1141 gctggggagt ccctgccaca ctcagtcccc caccacactg aatctcccct cctcacagtt
     1201 gccatgtaga ccccttgaag aggggagggg cctagggagc cgcaccttgt catgtaccat
     1261 caataaagta ccctgtgctc aacca
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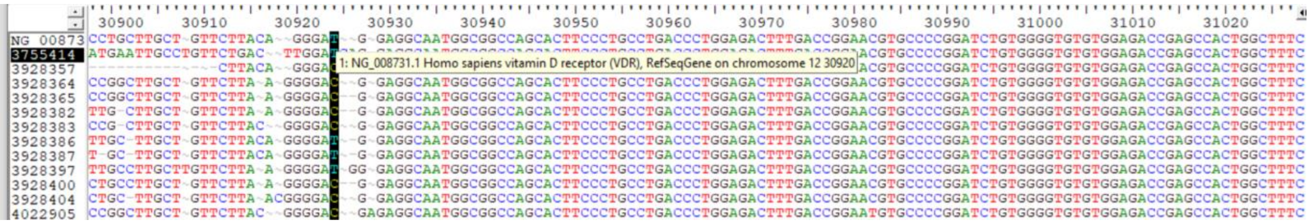
LAMPIRAN 4. HASIL PEMERIKSAAN POLIMORFISME

VDR rs2228570 NG_008731.1:g.30920T>C



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3755414  ATGAATTGCCTGTTCTGAC--TTGGAT                                                        ACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928357  --------------CTTACA--GGGAC 1: NG_008731.1 Homo sapiens vitamin D receptor (VDR), RefSeqGene on chromosome 12 30920 ACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928364  CCGGCTTGCT-GTTCTTA-A-GGGGAC--G-GAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928365  CCGGCTTGCT-GTTCTTA-A-GGGGAC--G-GAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928382  TTG-CTTGCT-GTTCTTA-A-GGGGAC--G-GAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928383  CCG-CTTGCT-GTTCTTAC--GGGGAC--G-GAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928386  TTGC-TTGCT-GTTCTTACA-GGGGAT--G-GAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928387  T-GC-TTGCT-GTTCTTACA-GGGGAT--G-GAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928397  TTGCCTTGCTTGTTCTTA-A-GGGGAT-GG-GAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928400  CTGCCTTGCT-GTTCTTA-A-GGGGAC--G-GAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
3928404  CTGC-TTGCT-GTTCTTA-ACGGGGAC--G-GAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
4022905  CCGGCTTGCT-GTTCTTAC--GGGGAC--GAGAGGCAATGGCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAATGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTC
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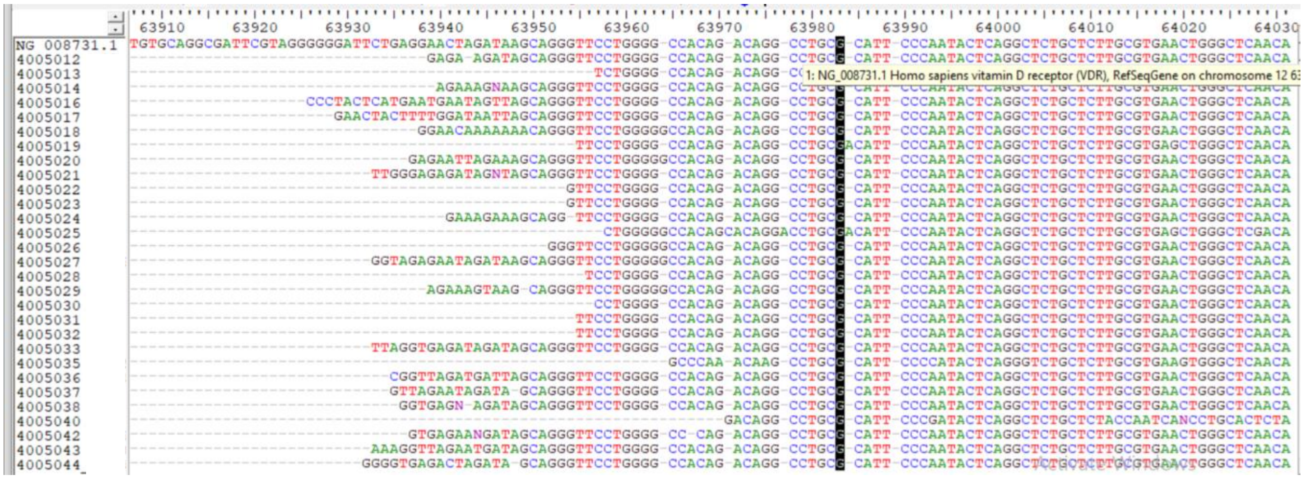
VDR rs 1544410 NG_008731.1:g.63980G>A



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4005012     --------------------------------GAGA-AGATAGCAGGGTTCCTGGGG-CCACAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
4005013     --------------------------------------------------TCTGGGG-CCACAG-ACAGG-CC 1: NG_008731.1 Homo sapiens vitamin D receptor (VDR), RefSeqGene on chromosome 12 63
4005014     ---------------------------------AGAAAGNAAGCAGGGTTCCTGGGG-CCACAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
4005016     -------------------CCCTACTCATGAATGAATAGTTAGCAGGGTTCCTGGGG-CCACAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
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4005018     -------------------------------GGAACAAAAAAACAGGGTTCCTGGGGGCCACAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
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4005020     ------------------------------GAGAATTAGAAAGCAGGGTTCCTGGGGGCCACAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
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4005025     ---------------------------------------------------CTGGGGGCCACAGCACAGGACCTGCGACATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAGCTGGGCTCGACA
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4005029     --------------------------------AGAAAGTAAG-CAGGGTTCCTGGGGGCCACAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
4005030     --------------------------------------------------CCTGGGG-CCACAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
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4005033     --------------------------TTAGGTGAGATAGATAGCAGGGTTCCTGGGG-CCACAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
4005035     ----------------------------------------------------------GCCCAA-ACAAG-CCTGCG-CATT-CCCCATACTCAGGGTCTGCTCTTGCGTGAAGTGGGCTCAACA
4005036     ----------------------------CGGTTAGATGATTAGCAGGGTTCCTGGGG-CCACAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
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4005040     ----------------------------------------------------------------GACAGG-CCTGCG-CATT-CCCGATACTCAGGCTCTGCTCTACCAATCANCCTGCACTCTA
4005042     ------------------------------GTGAGAANGATAGCAGGGTTCCTGGGG-CC-CAG-ACAGG-CCTGCG-CATT-CCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACA
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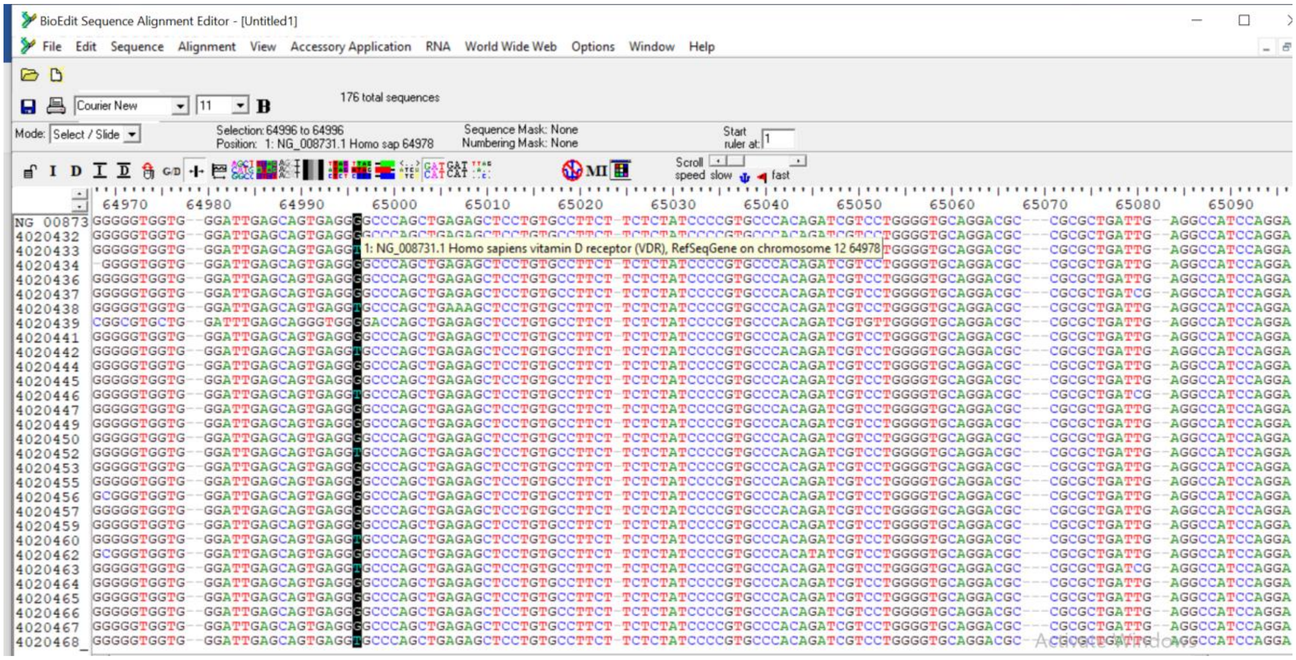
VDR rs7975232 NG_008731.1:g.64978G>T



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Selection: 64996 to 64996
Position: 1: NG_008731.1 Homo sap 64978
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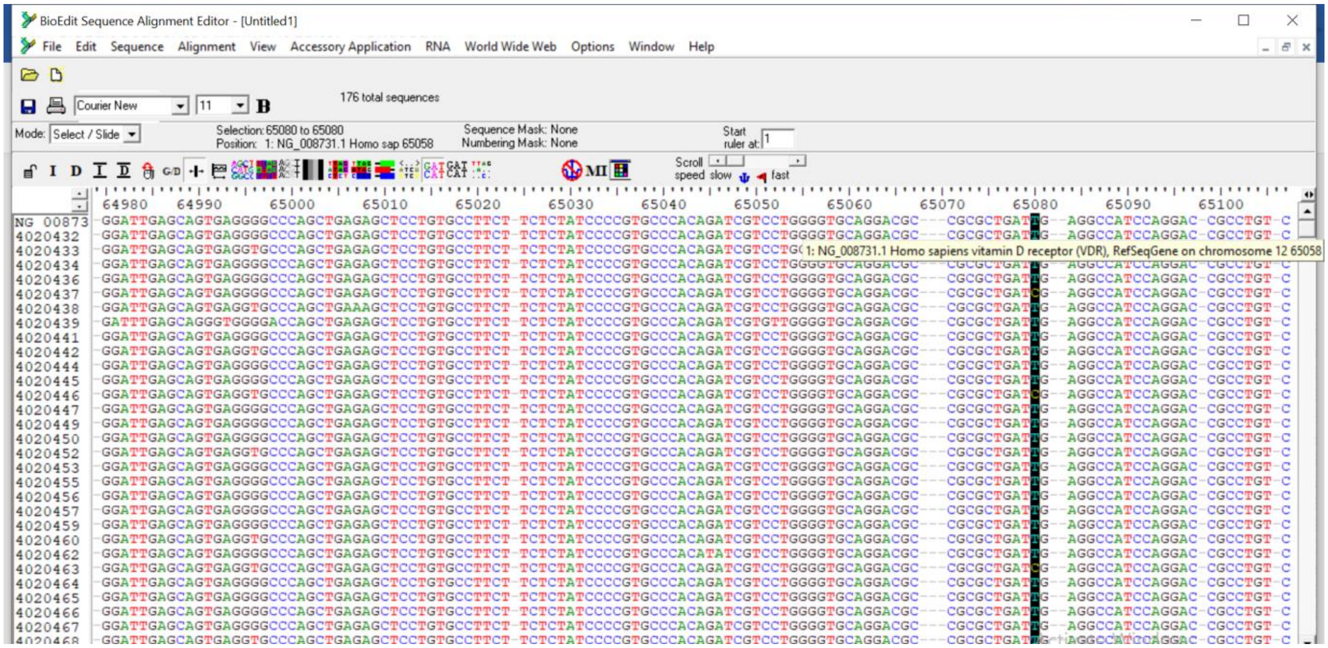
VDR rs731236 NG_008731.1:g.65058T>C



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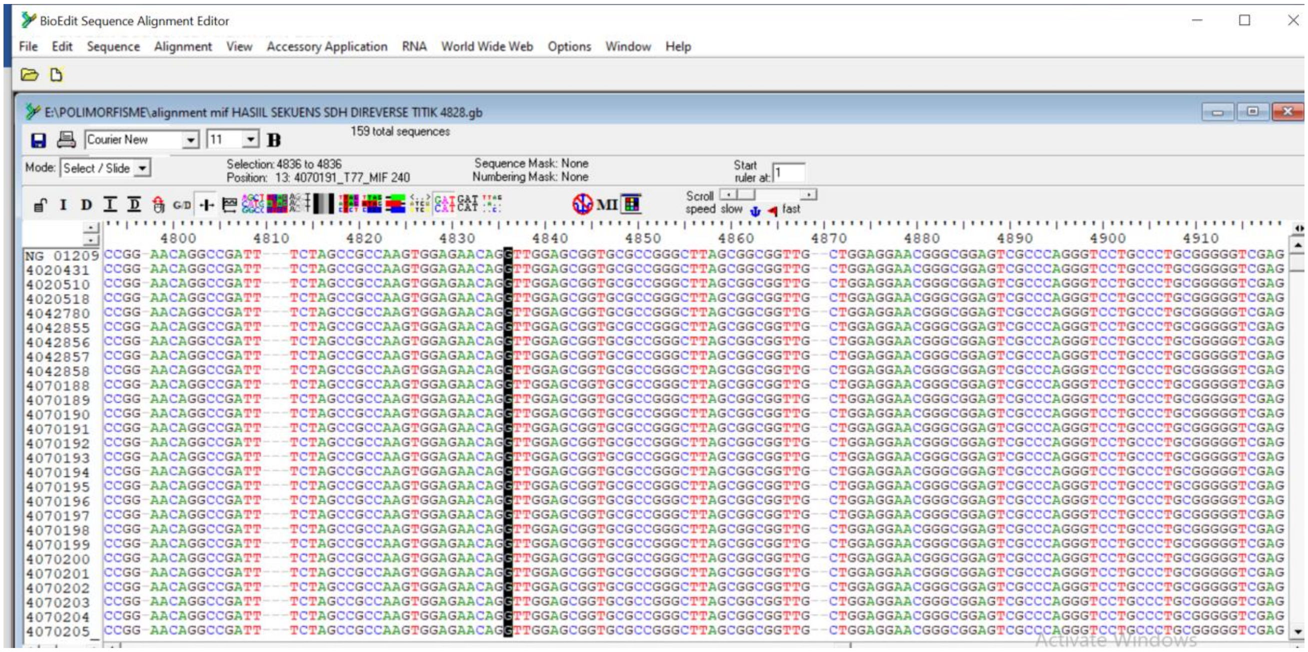
MIF -173 G/C rs755622



E:\POLIMORFISME\alignment mif HASIIL SEKUENS SDH DIREVERSE TITIK 4828.gb

Courier New 11

159 total sequences

Mode: Select / Slide

Selection: 4836 to 4836
Position: 13: 4070191_T77_MIF 240

Sequence Mask: None
Numbering Mask: None

Start ruler at: 1

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NG 01209 CCGG-AACAGGCCGATT---TCTAGCCGCCAAGTGGAGAACAGGTTGGAGCGGTGCGCCGGGCTTAGCGGCGGTTG--CTGGAGGAACGGGCGGAGTCGCCCAGGGTCCTGCCCTGCGGGGTCGAG
4020431  CCGG-AACAGGCCGATT---TCTAGCCGCCAAGTGGAGAACAGGTTGGAGCGGTGCGCCGGGCTTAGCGGCGGTTG--CTGGAGGAACGGGCGGAGTCGCCCAGGGTCCTGCCCTGCGGGGTCGAG
4020510  CCGG-AACAGGCCGATT---TCTAGCCGCCAAGTGGAGAACAGGTTGGAGCGGTGCGCCGGGCTTAGCGGCGGTTG--CTGGAGGAACGGGCGGAGTCGCCCAGGGTCCTGCCCTGCGGGGTCGAG
4020518  CCGG-AACAGGCCGATT---TCTAGCCGCCAAGTGGAGAACAGGTTGGAGCGGTGCGCCGGGCTTAGCGGCGGTTG--CTGGAGGAACGGGCGGAGTCGCCCAGGGTCCTGCCCTGCGGGGTCGAG
4042780  CCGG-AACAGGCCGATT---TCTAGCCGCCAAGTGGAGAACAGGTTGGAGCGGTGCGCCGGGCTTAGCGGCGGTTG--CTGGAGGAACGGGCGGAGTCGCCCAGGGTCCTGCCCTGCGGGGTCGAG
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LAMPIRAN 5. HASIL PEMERIKSAAN EKSPRESI GEN

VDR

Target	Sample	Control	Expression	Expression SEM	Corrected Expression SEM	Mean Cq	Cq SEM
GAPDH	ID_1					28.50	0.00000
GAPDH	ID_10					27.24	0.00000
GAPDH	ID_100					30.59	0.00000
GAPDH	ID_101					30.04	0.00000
GAPDH	ID_102					29.69	0.00000
GAPDH	ID_103					28.08	0.00000
GAPDH	ID_104					30.02	0.00000
GAPDH	ID_105					28.52	0.00000
GAPDH	ID_106					29.58	0.00000
GAPDH	ID_107					34.88	0.00000
GAPDH	ID_108					29.19	0.00000
GAPDH	ID_109					34.33	0.00000
GAPDH	ID_11					30.42	0.00000
GAPDH	ID_110					26.94	0.00000
GAPDH	ID_111					29.68	0.00000
GAPDH	ID_112					29.01	0.00000
GAPDH	ID_113					28.67	0.00000
GAPDH	ID_114					25.24	0.00000
GAPDH	ID_115					33.01	0.00000
GAPDH	ID_116					27.42	0.00000
GAPDH	ID_117					28.47	0.00000
GAPDH	ID_118					37.36	0.00000
GAPDH	ID_119					29.26	0.00000
GAPDH	ID_12					29.03	0.00000
GAPDH	ID_120					28.53	0.00000
GAPDH	ID_121					26.00	0.00000
GAPDH	ID_122					33.64	0.00000
GAPDH	ID_123					41.88	0.00000
GAPDH	ID_124					28.10	0.00000
GAPDH	ID_125					29.32	0.00000
GAPDH	ID_126					29.25	0.00000
GAPDH	ID_127					28.61	0.00000

GAPDH	ID_128					28.83	0.00000
GAPDH	ID_129					27.09	0.00000
GAPDH	ID_13					31.25	0.00000
GAPDH	ID_130					26.34	0.00000
GAPDH	ID_131					31.24	0.00000
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GAPDH	ID_133					32.14	0.00000
GAPDH	ID_134					33.17	0.00000
GAPDH	ID_135					34.77	0.00000
GAPDH	ID_136					32.39	0.00000
GAPDH	ID_137					27.60	0.00000
GAPDH	ID_138					32.71	0.00000
GAPDH	ID_139					33.57	0.00000
GAPDH	ID_14					28.31	0.00000
GAPDH	ID_140					35.37	0.00000
GAPDH	ID_141					28.27	0.00000
GAPDH	ID_142					31.39	0.00000
GAPDH	ID_143					34.02	0.00000
GAPDH	ID_144					34.73	0.00000
GAPDH	ID_145					31.83	0.00000
GAPDH	ID_146					35.16	0.00000
GAPDH	ID_147					28.35	0.00000
GAPDH	ID_148					33.54	0.00000
GAPDH	ID_149					36.43	0.00000
GAPDH	ID_15					30.33	0.00000
GAPDH	ID_150					33.13	0.00000
GAPDH	ID_151					33.12	0.00000
GAPDH	ID_152					28.78	0.00000
GAPDH	ID_153					33.36	0.00000
GAPDH	ID_154					30.19	0.00000
GAPDH	ID_155					31.22	0.00000
GAPDH	ID_156					30.75	0.00000
GAPDH	ID_16					28.82	0.00000
GAPDH	ID_17					29.91	0.00000
GAPDH	ID_18					38.04	0.00000
GAPDH	ID_19					28.23	0.00000
GAPDH	ID_2					33.90	0.00000
GAPDH	ID_20					28.06	0.00000
GAPDH	ID_21					28.34	0.00000
GAPDH	ID_22					28.39	0.00000

GAPDH	ID_23					27.90	0.00000
GAPDH	ID_24					31.15	0.00000
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GAPDH	ID_27					33.97	0.00000
GAPDH	ID_28					32.28	0.00000
GAPDH	ID_29					35.05	0.00000
GAPDH	ID_3					28.84	0.00000
GAPDH	ID_30					35.10	0.00000
GAPDH	ID_31					39.59	0.00000
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GAPDH	ID_34					29.05	0.00000
GAPDH	ID_35					26.70	0.00000
GAPDH	ID_36					33.51	0.00000
GAPDH	ID_37					36.69	0.00000
GAPDH	ID_38					33.77	0.00000
GAPDH	ID_39					28.76	0.00000
GAPDH	ID_4					27.90	0.00000
GAPDH	ID_40					30.22	0.00000
GAPDH	ID_41					30.56	0.00000
GAPDH	ID_42					28.61	0.00000
GAPDH	ID_43					30.52	0.00000
GAPDH	ID_44					30.52	0.00000
GAPDH	ID_45					36.13	0.00000
GAPDH	ID_46					33.29	0.00000
GAPDH	ID_47					26.48	0.00000
GAPDH	ID_48					34.97	0.00000
GAPDH	ID_49					34.33	0.00000
GAPDH	ID_5					28.30	0.00000
GAPDH	ID_50					32.95	0.00000
GAPDH	ID_51					28.26	0.00000
GAPDH	ID_52					32.67	0.00000
GAPDH	ID_53					28.36	0.00000
GAPDH	ID_54					35.68	0.00000
GAPDH	ID_55					31.24	0.00000
GAPDH	ID_56					35.59	0.00000
GAPDH	ID_57					32.45	0.00000
GAPDH	ID_58					35.52	0.00000
GAPDH	ID_59					29.57	0.00000

GAPDH	ID_6					28.37	0.00000
GAPDH	ID_60					28.65	0.00000
GAPDH	ID_61					30.49	0.00000
GAPDH	ID_62					33.17	0.00000
GAPDH	ID_63					28.10	0.00000
GAPDH	ID_64					27.90	0.00000
GAPDH	ID_65					28.09	0.00000
GAPDH	ID_66					33.80	0.00000
GAPDH	ID_67					34.35	0.00000
GAPDH	ID_68					31.80	0.00000
GAPDH	ID_69					30.99	0.00000
GAPDH	ID_7					30.24	0.00000
GAPDH	ID_70					35.58	0.00000
GAPDH	ID_71					33.13	0.00000
GAPDH	ID_72					32.24	0.00000
GAPDH	ID_73					33.38	0.00000
GAPDH	ID_74					31.50	0.00000
GAPDH	ID_75					28.40	0.00000
GAPDH	ID_76					31.36	0.00000
GAPDH	ID_77					35.61	0.00000
GAPDH	ID_78					33.58	0.00000
GAPDH	ID_79					28.92	0.00000
GAPDH	ID_8					27.31	0.00000
GAPDH	ID_80					30.84	0.00000
GAPDH	ID_81					34.45	0.00000
GAPDH	ID_82					29.78	0.00000
GAPDH	ID_83					30.35	0.00000
GAPDH	ID_84					27.06	0.00000
GAPDH	ID_85					29.54	0.00000
GAPDH	ID_86					31.48	0.00000
GAPDH	ID_87					28.01	0.00000
GAPDH	ID_88					29.47	0.00000
GAPDH	ID_89					26.59	0.00000
GAPDH	ID_9					30.99	0.00000
GAPDH	ID_90					31.42	0.00000
GAPDH	ID_91					34.69	0.00000
GAPDH	ID_92					38.65	0.00000
GAPDH	ID_93					27.97	0.00000
GAPDH	ID_94					30.46	0.00000
GAPDH	ID_95					30.18	0.00000

GAPDH	ID_96					34.70	0.00000
GAPDH	ID_97					39.53	0.00000
GAPDH	ID_98					28.13	0.00000
GAPDH	ID_99					28.47	0.00000
VDR	ID_1		0.00297	0.00000	0.00000	33.04	0.00000
VDR	ID_10		0.25182	0.00000	0.00000	25.37	0.00000
VDR	ID_100		0.00310	0.00000	0.00000	35.08	0.00000
VDR	ID_101		0.20291	0.00000	0.00000	28.49	0.00000
VDR	ID_102		0.73631	0.00000	0.00000	26.28	0.00000
VDR	ID_103		0.00779	0.00000	0.00000	31.23	0.00000
VDR	ID_104		0.00741	0.00000	0.00000	33.24	0.00000
VDR	ID_105		0.67835	0.00000	0.00000	25.23	0.00000
VDR	ID_106		0.01486	0.00000	0.00000	31.80	0.00000
VDR	ID_107		0.00044	0.00000	0.00000	42.16	0.00000
VDR	ID_108		0.02622	0.00000	0.00000	30.59	0.00000
VDR	ID_109		0.00529	0.00000	0.00000	38.04	0.00000
VDR	ID_11		0.00927	0.00000	0.00000	33.32	0.00000
VDR	ID_110		0.25722	0.00000	0.00000	25.05	0.00000
VDR	ID_111		0.01078	0.00000	0.00000	32.36	0.00000
VDR	ID_112		0.01473	0.00000	0.00000	31.25	0.00000
VDR	ID_113		0.00626	0.00000	0.00000	32.13	0.00000
VDR	ID_114		0.00331	0.00000	0.00000	29.63	0.00000
VDR	ID_115		1.35774	0.00000	0.00000	28.72	0.00000
VDR	ID_116		0.00326	0.00000	0.00000	31.83	0.00000
VDR	ID_117		0.00506	0.00000	0.00000	32.25	0.00000
VDR	ID_118		0.00370	0.00000	0.00000	41.58	0.00000
VDR	ID_119		0.00514	0.00000	0.00000	33.02	0.00000
VDR	ID_12		0.00218	0.00000	0.00000	34.02	0.00000
VDR	ID_120		0.00539	0.00000	0.00000	32.22	0.00000
VDR	ID_121		0.00258	0.00000	0.00000	30.75	0.00000
VDR	ID_122		0.14366	0.00000	0.00000	32.59	0.00000
VDR	ID_123		1.63587	0.00000	0.00000	37.32	0.00000
VDR	ID_124		0.00475	0.00000	0.00000	31.97	0.00000
VDR	ID_125		0.00265	0.00000	0.00000	34.03	0.00000
VDR	ID_126		0.01157	0.00000	0.00000	31.83	0.00000
VDR	ID_127		0.00815	0.00000	0.00000	31.69	0.00000
VDR	ID_128		0.00329	0.00000	0.00000	33.22	0.00000
VDR	ID_129		0.00068	0.00000	0.00000	33.76	0.00000
VDR	ID_13		1.04459	0.00000	0.00000	27.34	0.00000
VDR	ID_130		0.01025	0.00000	0.00000	29.10	0.00000

VDR	ID_131		0.00574	0.00000	0.00000	34.84	0.00000
VDR	ID_132		0.01696	0.00000	0.00000	28.46	0.00000
VDR	ID_133		0.00946	0.00000	0.00000	35.01	0.00000
VDR	ID_134		0.00305	0.00000	0.00000	37.68	0.00000
VDR	ID_135		0.00031	0.00000	0.00000	42.56	0.00000
VDR	ID_136		0.00427	0.00000	0.00000	36.41	0.00000
VDR	ID_137		0.00462	0.00000	0.00000	31.50	0.00000
VDR	ID_138		0.00780	0.00000	0.00000	35.86	0.00000
VDR	ID_139		0.00696	0.00000	0.00000	36.88	0.00000
VDR	ID_14		0.29758	0.00000	0.00000	26.21	0.00000
VDR	ID_140		0.00337	0.00000	0.00000	39.73	0.00000
VDR	ID_141		0.00894	0.00000	0.00000	31.23	0.00000
VDR	ID_142		0.00104	0.00000	0.00000	37.45	0.00000
VDR	ID_143		0.00340	0.00000	0.00000	38.37	0.00000
VDR	ID_144		0.02619	0.00000	0.00000	36.14	0.00000
VDR	ID_145		0.00718	0.00000	0.00000	35.10	0.00000
VDR	ID_146		0.00215	0.00000	0.00000	40.17	0.00000
VDR	ID_147		0.01838	0.00000	0.00000	30.27	0.00000
VDR	ID_148		0.01061	0.00000	0.00000	36.25	0.00000
VDR	ID_149		0.10772	0.00000	0.00000	35.79	0.00000
VDR	ID_15		0.00305	0.00000	0.00000	34.84	0.00000
VDR	ID_150		0.00505	0.00000	0.00000	36.91	0.00000
VDR	ID_151		0.02570	0.00000	0.00000	34.55	0.00000
VDR	ID_152		0.04754	0.00000	0.00000	29.32	0.00000
VDR	ID_153		0.00645	0.00000	0.00000	36.78	0.00000
VDR	ID_154		0.00467	0.00000	0.00000	34.08	0.00000
VDR	ID_155		0.00411	0.00000	0.00000	35.29	0.00000
VDR	ID_156		0.04590	0.00000	0.00000	31.34	0.00000
VDR	ID_16		2.48874	0.00000	0.00000	23.65	0.00000
VDR	ID_17		0.00983	0.00000	0.00000	32.73	0.00000
VDR	ID_18		84.33926	0.00000	0.00000	27.79	0.00000
VDR	ID_19		0.00723	0.00000	0.00000	31.49	0.00000
VDR	ID_2		0.00041	0.00000	0.00000	41.29	0.00000
VDR	ID_20		0.00605	0.00000	0.00000	31.58	0.00000
VDR	ID_21		0.00948	0.00000	0.00000	31.21	0.00000
VDR	ID_22		0.00833	0.00000	0.00000	31.44	0.00000
VDR	ID_23		0.00943	0.00000	0.00000	30.78	0.00000
VDR	ID_24		0.00007	0.00000	0.00000	41.01	0.00000
VDR	ID_25		0.00030	0.00000	0.00000	40.37	0.00000
VDR	ID_26		0.00369	0.33437	0.33437	36.79	1.55378

VDR	ID_27		0.00548	0.00000	0.00000	37.63	0.00000
VDR	ID_28		0.00325	0.00000	0.00000	36.70	0.00000
VDR	ID_29		0.01219	0.00000	0.00000	37.56	0.00000
VDR	ID_3		0.26646	0.00000	0.00000	26.90	0.00000
VDR	ID_30		0.01044	0.00000	0.00000	37.83	0.00000
VDR	ID_31		51.40337	0.00000	0.00000	30.06	0.00000
VDR	ID_32		24.55480	0.00000	0.00000	26.94	0.00000
VDR	ID_33		130.72220	0.00000	0.00000	26.44	0.00000
VDR	ID_34		0.00291	0.00000	0.00000	33.62	0.00000
VDR	ID_35		0.00423	0.00000	0.00000	30.73	0.00000
VDR	ID_36		0.01979	0.00000	0.00000	35.32	0.00000
VDR	ID_37		0.09182	0.00000	0.00000	36.29	0.00000
VDR	ID_38		0.00697	0.00000	0.00000	37.08	0.00000
VDR	ID_39		0.00719	0.00000	0.00000	32.03	0.00000
VDR	ID_4		1.20200	0.00000	0.00000	23.78	0.00000
VDR	ID_40		0.00248	0.00000	0.00000	35.02	0.00000
VDR	ID_41		0.00178	0.00000	0.00000	35.85	0.00000
VDR	ID_42		0.00950	0.00000	0.00000	31.48	0.00000
VDR	ID_43		0.01982	0.00000	0.00000	32.33	0.00000
VDR	ID_44		0.00596	0.00000	0.00000	34.06	0.00000
VDR	ID_45		22.98570	0.00000	0.00000	27.75	0.00000
VDR	ID_46		0.07298	0.00000	0.00000	33.21	0.00000
VDR	ID_47		0.00063	0.00000	0.00000	33.26	0.00000
VDR	ID_48		0.01096	0.00000	0.00000	37.63	0.00000
VDR	ID_49		0.04758	0.00000	0.00000	34.87	0.00000
VDR	ID_5		0.27095	0.00000	0.00000	26.33	0.00000
VDR	ID_50		0.42836	0.00000	0.00000	30.32	0.00000
VDR	ID_51		0.29316	0.00000	0.00000	26.18	0.00000
VDR	ID_52		0.00342	0.00000	0.00000	37.01	0.00000
VDR	ID_53		0.35627	0.00000	0.00000	26.00	0.00000
VDR	ID_54		13.91429	0.00000	0.00000	28.03	0.00000
VDR	ID_55		0.02597	0.00000	0.00000	32.65	0.00000
VDR	ID_56		0.02069	0.00000	0.00000	37.33	0.00000
VDR	ID_57		2.36288	0.00000	0.00000	27.36	0.00000
VDR	ID_58		0.00093	0.00000	0.00000	41.74	0.00000
VDR	ID_59		0.06614	0.00000	0.00000	29.64	0.00000
VDR	ID_6		0.09879	0.00000	0.00000	27.86	0.00000
VDR	ID_60		0.00598	0.00000	0.00000	32.18	0.00000
VDR	ID_61		1.02401	0.00000	0.00000	26.60	0.00000
VDR	ID_62		7.50328	0.00000	0.00000	26.41	0.00000

VDR	ID_63		0.00267	0.00000	0.00000	32.80	0.00000
VDR	ID_64		0.00660	0.00000	0.00000	31.29	0.00000
VDR	ID_65		0.00446	0.00000	0.00000	32.05	0.00000
VDR	ID_66		14.85317	0.00000	0.00000	26.06	0.00000
VDR	ID_67		0.00438	0.00000	0.00000	38.33	0.00000
VDR	ID_68		3.29471	0.00000	0.00000	26.23	0.00000
VDR	ID_69		3.17726	0.00000	0.00000	25.47	0.00000
VDR	ID_7		1.12827	0.00000	0.00000	26.21	0.00000
VDR	ID_70		0.00204	0.00000	0.00000	40.67	0.00000
VDR	ID_71		0.06775	0.00000	0.00000	33.16	0.00000
VDR	ID_72		3.42134	0.00000	0.00000	26.62	0.00000
VDR	ID_73		70.68327	0.00000	0.00000	23.38	0.00000
VDR	ID_74		2.10974	0.00000	0.00000	26.57	0.00000
VDR	ID_75		0.00642	0.00000	0.00000	31.83	0.00000
VDR	ID_76		27.83776	0.00000	0.00000	22.71	0.00000
VDR	ID_77		19.62778	0.00000	0.00000	27.47	0.00000
VDR	ID_78		0.74379	0.00000	0.00000	30.16	0.00000
VDR	ID_79		0.00710	0.00000	0.00000	32.21	0.00000
VDR	ID_8		0.11901	0.00000	0.00000	26.53	0.00000
VDR	ID_80		0.01938	0.00000	0.00000	32.68	0.00000
VDR	ID_81		22.27353	0.00000	0.00000	26.12	0.00000
VDR	ID_82		0.00892	0.00000	0.00000	32.74	0.00000
VDR	ID_83		0.00936	0.00000	0.00000	33.24	0.00000
VDR	ID_84		0.02345	0.00000	0.00000	28.62	0.00000
VDR	ID_85		4.17804	0.00000	0.00000	23.62	0.00000
VDR	ID_86		0.09236	0.00000	0.00000	31.06	0.00000
VDR	ID_87		0.00066	0.00000	0.00000	34.73	0.00000
VDR	ID_88		0.04287	0.00000	0.00000	30.17	0.00000
VDR	ID_89		0.00157	0.00000	0.00000	32.05	0.00000
VDR	ID_9		3.79971	0.00000	0.00000	25.21	0.00000
VDR	ID_90		0.05176	0.00000	0.00000	31.84	0.00000
VDR	ID_91		0.32282	0.00000	0.00000	32.47	0.00000
VDR	ID_92		78.22414	0.00000	0.00000	28.51	0.00000
VDR	ID_93		0.00197	0.00000	0.00000	33.11	0.00000
VDR	ID_94		0.00948	0.00000	0.00000	33.33	0.00000
VDR	ID_95		1.00000	0.00000	0.00000	26.32	0.00000
VDR	ID_96		36.91609	0.00000	0.00000	25.64	0.00000
VDR	ID_97		240.22805	0.00000	0.00000	27.77	0.00000
VDR	ID_98		0.00729	0.00000	0.00000	31.38	0.00000
VDR	ID_99		0.07685	0.00000	0.00000	28.32	0.00000

Perbedaan Ekspresi Gen *VDR* berdasarkan kelompok (TB aktif, Kontak serumah IGRA positi dan negatif)

Target	Biological Group	Control	Expression	Expression 95% CI Low	Expression 95% CI High	P-Value
GAPDH	(-) IGRA HC					
GAPDH	(+) IGRA HC					
GAPDH	ACTIVE TB	C				
VDR	(-) IGRA HC		5.06714	1.14939	22.33879	0.013560
VDR	(+) IGRA HC		3.99362	1.44320	11.05109	0.011396
VDR	ACTIVE TB	C	1.00000	0.56434	1.77200	

Target	df	P-Value ANOVA	Contrast	Ratio	Lower Bound (95%)	Upper Bound (95%)	P-Value Tukey	Significant
VDR	2	0.01295						Yes
			(-) IGRA HC - (+) IGRA HC	1.26881	0.219354	7.339183	0.944792	No
			(-) IGRA HC - ACTIVE TB	5.06714	1.040700	24.671749	0.043109	Yes
			(+) IGRA HC - ACTIVE TB	3.99362	1.016427	15.691208	0.046636	Yes

EKSPRESI GEN *MIF*

Target	Sample	Control	Expression	Expression SEM	Corrected Expression SEM	Mean Cq	Cq SEM
GAPDH	ID 1					37.14	0.00000
GAPDH	ID 10					27.56	0.00000
GAPDH	ID 100					30.75	0.00000
GAPDH	ID 101					27.35	0.00000
GAPDH	ID 102					30.21	0.00000

GAPDH	ID 103					28.39	0.00000
GAPDH	ID 104					32.51	0.00000
GAPDH	ID 105					28.90	0.00000
GAPDH	ID 106					30.10	0.00000
GAPDH	ID 107					26.31	0.00000
GAPDH	ID 108					29.50	0.00000
GAPDH	ID 109					29.92	0.00000
GAPDH	ID 11					30.79	0.00000
GAPDH	ID 110					27.25	0.00000
GAPDH	ID 111					30.63	0.00000
GAPDH	ID 112					27.30	0.00000
GAPDH	ID 113					28.71	0.00000
GAPDH	ID 114					24.27	0.00000
GAPDH	ID 115					23.77	0.00000
GAPDH	ID 116					25.97	0.00000
GAPDH	ID 117					26.39	0.00000
GAPDH	ID 118					26.64	0.00000
GAPDH	ID 119					27.76	0.00000
GAPDH	ID 12					29.32	0.00000
GAPDH	ID 120					35.04	0.00000
GAPDH	ID 121					24.29	0.00000
GAPDH	ID 122					25.79	0.00000
GAPDH	ID 123					26.73	0.00000
GAPDH	ID 124					32.45	0.00000
GAPDH	ID 125					27.54	0.00000
GAPDH	ID 126					31.56	0.00000
GAPDH	ID 127					27.30	0.00000
GAPDH	ID 128					28.87	0.00000
GAPDH	ID 129					28.18	0.00000
GAPDH	ID 13					31.58	0.00000
GAPDH	ID 130					27.78	0.00000
GAPDH	ID 131					29.26	0.00000
GAPDH	ID 132					27.45	0.00000
GAPDH	ID 133					29.54	0.00000
GAPDH	ID 134					38.49	0.00000
GAPDH	ID 135					36.10	0.00000
GAPDH	ID 136					30.70	0.00000
GAPDH	ID 137					26.10	0.00000
GAPDH	ID 138					37.92	0.00000
GAPDH	ID 139					33.55	0.00000

GAPDH	ID 14					28.66	0.00000
GAPDH	ID 140					34.34	0.00000
GAPDH	ID 141					28.87	0.00000
GAPDH	ID 142					38.26	0.00000
GAPDH	ID 143					31.20	0.00000
GAPDH	ID 144					29.12	0.00000
GAPDH	ID 145					39.38	0.00000
GAPDH	ID 146					33.35	0.00000
GAPDH	ID 147					24.95	0.00000
GAPDH	ID 148					33.48	0.00000
GAPDH	ID 149					30.01	0.00000
GAPDH	ID 15					30.87	0.00000
GAPDH	ID 150					30.59	0.00000
GAPDH	ID 151					30.59	0.00000
GAPDH	ID 152					25.14	0.00000
GAPDH	ID 153					31.24	0.00000
GAPDH	ID 154					28.25	0.00000
GAPDH	ID 155					29.45	0.00000
GAPDH	ID 156					28.03	0.00000
GAPDH	ID 16					29.16	0.00000
GAPDH	ID 17					30.22	0.00000
GAPDH	ID 18					38.36	0.00000
GAPDH	ID 19					35.07	0.00000
GAPDH	ID 2					36.99	0.00000
GAPDH	ID 20					39.96	0.00000
GAPDH	ID 21					32.03	0.00000
GAPDH	ID 22					39.04	0.00000
GAPDH	ID 23					32.72	0.00000
GAPDH	ID 24					37.36	0.00000
GAPDH	ID 25					38.41	0.00000
GAPDH	ID 26					37.51	0.00000
GAPDH	ID 27					31.31	0.00000
GAPDH	ID 28					36.57	0.00000
GAPDH	ID 29					30.79	0.00000
GAPDH	ID 3					29.18	0.00000
GAPDH	ID 30					32.92	0.00000
GAPDH	ID 31					29.37	0.00000
GAPDH	ID 32					35.77	0.00000
GAPDH	ID 33					37.67	0.00000
GAPDH	ID 34					31.99	0.00000

GAPDH	ID 35					27.47	0.00000
GAPDH	ID 36					36.86	0.00000
GAPDH	ID 37					28.42	0.00000
GAPDH	ID 38					29.34	0.00000
GAPDH	ID 39					30.35	0.00000
GAPDH	ID 4					28.20	0.00000
GAPDH	ID 40					37.31	0.00000
GAPDH	ID 41					36.38	0.00000
GAPDH	ID 42					27.11	0.00000
GAPDH	ID 43					26.02	0.00000
GAPDH	ID 44					28.19	0.00000
GAPDH	ID 45					36.43	0.00000
GAPDH	ID 46					30.37	0.00000
GAPDH	ID 47					37.75	0.00000
GAPDH	ID 48					35.50	0.00000
GAPDH	ID 49					25.90	0.00000
GAPDH	ID 5					28.63	0.00000
GAPDH	ID 50					33.26	0.00000
GAPDH	ID 51					28.36	0.00000
GAPDH	ID 52					30.92	0.00000
GAPDH	ID 53					28.46	0.00000
GAPDH	ID 54					36.06	0.00000
GAPDH	ID 55					31.73	0.00000
GAPDH	ID 56					35.16	0.00000
GAPDH	ID 57					32.55	0.00000
GAPDH	ID 58					36.09	0.00000
GAPDH	ID 59					29.68	0.00000
GAPDH	ID 6					28.72	0.00000
GAPDH	ID 60					28.75	0.00000
GAPDH	ID 61					30.60	0.00000
GAPDH	ID 62					33.27	0.00000
GAPDH	ID 63					30.12	0.00000
GAPDH	ID 64					31.93	0.00000
GAPDH	ID 65					31.64	0.00000
GAPDH	ID 66					33.96	0.00000
GAPDH	ID 67					27.75	0.00000
GAPDH	ID 68					31.92	0.00000
GAPDH	ID 69					31.07	0.00000
GAPDH	ID 7					30.58	0.00000
GAPDH	ID 70					38.72	0.00000

GAPDH	ID 71					33.44	0.00000
GAPDH	ID 72					32.39	0.00000
GAPDH	ID 73					33.49	0.00000
GAPDH	ID 74					31.87	0.00000
GAPDH	ID 75					29.00	0.00000
GAPDH	ID 76					31.47	0.00000
GAPDH	ID 77					35.78	0.00000
GAPDH	ID 78					33.69	0.00000
GAPDH	ID 79					29.03	0.00000
GAPDH	ID 8					27.66	0.00000
GAPDH	ID 80					30.96	0.00000
GAPDH	ID 81					34.55	0.00000
GAPDH	ID 82					32.00	0.00000
GAPDH	ID 83					34.21	0.00000
GAPDH	ID 84					27.37	0.00000
GAPDH	ID 85					29.92	0.00000
GAPDH	ID 86					31.59	0.00000
GAPDH	ID 87					27.66	0.00000
GAPDH	ID 88					29.85	0.00000
GAPDH	ID 89					26.98	0.00000
GAPDH	ID 9					31.30	0.00000
GAPDH	ID 90					31.53	0.00000
GAPDH	ID 91					34.83	0.00000
GAPDH	ID 92					28.08	0.00000
GAPDH	ID 93					28.27	0.00000
GAPDH	ID 94					34.05	0.00000
GAPDH	ID 95					33.12	2.62088
GAPDH	ID 96					30.16	0.00000
GAPDH	ID 97					36.26	0.00000
GAPDH	ID 98					30.48	0.00000
GAPDH	ID 99					28.85	0.00000
MIF	ID 1		242.92317	0.00000	0.00000	31.46	0.00000
MIF	ID 10		0.17545	0.00000	0.00000	32.32	0.00000
MIF	ID 100		0.05444	0.00000	0.00000	37.20	0.00000
MIF	ID 101		0.08501	0.00000	0.00000	33.15	0.00000
MIF	ID 102		1.27375	0.00000	0.00000	32.10	0.00000
MIF	ID 103		0.34484	0.00000	0.00000	32.17	0.00000
MIF	ID 104		7.02379	0.00000	0.00000	31.95	0.00000
MIF	ID 105		0.33157	0.00000	0.00000	32.74	0.00000
MIF	ID 106		1.90574	0.00000	0.00000	31.42	0.00000

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MIF	ID 108		2.59243	0.00000	0.00000	30.37	0.00000
MIF	ID 109		0.10914	0.00000	0.00000	35.36	0.00000
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MIF	ID 110		0.29889	0.00000	0.00000	31.24	0.00000
MIF	ID 111		1.41857	0.00000	0.00000	32.37	0.00000
MIF	ID 112		0.00809	0.00000	0.00000	36.50	0.00000
MIF	ID 113		0.25229	0.00000	0.00000	32.94	0.00000
MIF	ID 114		0.00519	0.00000	0.00000	34.11	0.00000
MIF	ID 115		0.00344	0.00000	0.00000	34.20	0.00000
MIF	ID 116		0.01328	0.00000	0.00000	34.45	0.00000
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MIF	ID 123		0.01908	0.00000	0.00000	34.68	0.00000
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MIF	ID 125		1.38560	0.00000	0.00000	29.32	0.00000
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MIF	ID 130		0.80904	0.00000	0.00000	30.33	0.00000
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MIF	ID 87		0.02839	0.00000	0.00000	35.04	0.00000
MIF	ID 88		0.16618	0.00000	0.00000	34.68	0.00000
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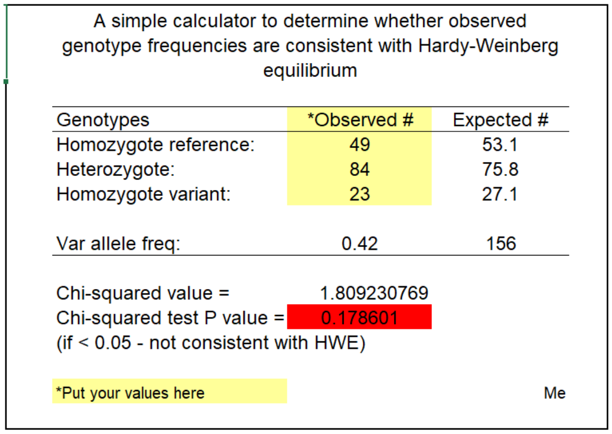
MIF	ID 90		1.22820	0.00000	0.00000	33.48	0.00000
MIF	ID 91		1.37278	0.00000	0.00000	36.62	0.00000
MIF	ID 92		0.06673	0.00000	0.00000	34.23	0.00000
MIF	ID 93		0.00829	0.00000	0.00000	37.43	0.00000
MIF	ID 94		42.75820	0.00000	0.00000	30.87	0.00000
MIF	ID 95		0.82965	1.06084	1.06084	35.63	0.54841
MIF	ID 96		1.02519	0.00000	0.00000	32.37	0.00000
MIF	ID 97		62.31722	0.00000	0.00000	32.54	0.00000
MIF	ID 98		1.33991	0.00000	0.00000	32.30	0.00000
MIF	ID 99		1.06470	0.00000	0.00000	31.00	0.00000

PERBEDAAN EKSPRESI GEN *MIF*

Target	Biological Group	Control	Expression	Expression 95% CI Low	Expression 95% CI High	P-Value
GAPDH	(-) IGRA HC					
GAPDH	(+) IGRA HC					
GAPDH	ACTIVE TB	C				
MIF	(-) IGRA HC		0.66493	0.31496	1.40375	0.533617
MIF	(+) IGRA HC		0.84813	0.43864	1.63990	0.765311
MIF	ACTIVE TB	C	1.00000	0.48289	2.07087	

LAMPIRAN 6. ANALISIS STATISTIK

Pengecekan HWE



A simple calculator to determine whether observed genotype frequencies are consistent with Hardy-Weinberg equilibrium

Genotypes	*Observed #	Expected #
Homozygote reference:	49	53.1
Heterozygote:	84	75.8
Homozygote variant:	23	27.1
Var allele freq:	0.42	156

Chi-squared value = 1.809230769

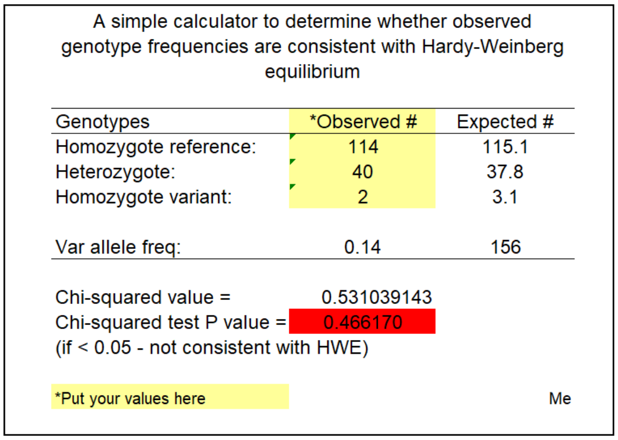
Chi-squared test P value = 0.178601

(if < 0.05 - not consistent with HWE)

*Put your values here

Me

VDR rs2228570



A simple calculator to determine whether observed genotype frequencies are consistent with Hardy-Weinberg equilibrium

Genotypes	*Observed #	Expected #
Homozygote reference:	114	115.1
Heterozygote:	40	37.8
Homozygote variant:	2	3.1
Var allele freq:	0.14	156

Chi-squared value = 0.531039143

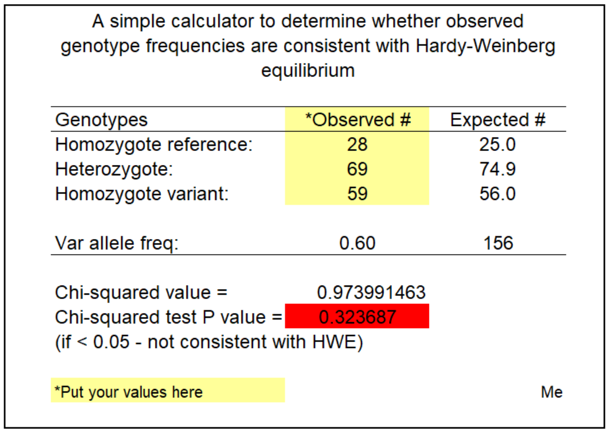
Chi-squared test P value = 0.466170

(if < 0.05 - not consistent with HWE)

*Put your values here

Me

VDR rs1544410



A simple calculator to determine whether observed genotype frequencies are consistent with Hardy-Weinberg equilibrium

Genotypes	*Observed #	Expected #
Homozygote reference:	28	25.0
Heterozygote:	69	74.9
Homozygote variant:	59	56.0
Var allele freq:	0.60	156

Chi-squared value = 0.973991463

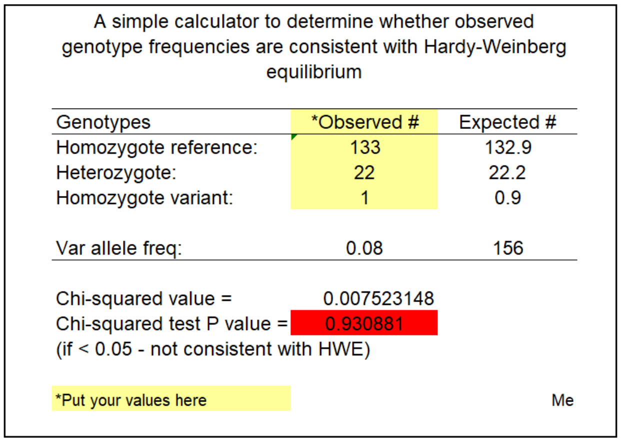
Chi-squared test P value = 0.323687

(if < 0.05 - not consistent with HWE)

*Put your values here

Me

VDR rs7975232



A simple calculator to determine whether observed genotype frequencies are consistent with Hardy-Weinberg equilibrium

Genotypes	*Observed #	Expected #
Homozygote reference:	133	132.9
Heterozygote:	22	22.2
Homozygote variant:	1	0.9
Var allele freq:	0.08	156

Chi-squared value = 0.007523148

Chi-squared test P value = 0.930881

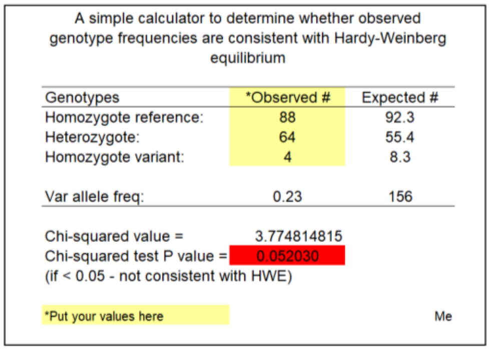
(if < 0.05 - not consistent with HWE)

*Put your values here

Me

VDR rs731236

MIF -173 G/C rs755622



A simple calculator to determine whether observed genotype frequencies are consistent with Hardy-Weinberg equilibrium

Genotypes	*Observed #	Expected #
Homozygote reference:	88	92.3
Heterozygote:	64	55.4
Homozygote variant:	4	8.3
Var allele freq:	0.23	156

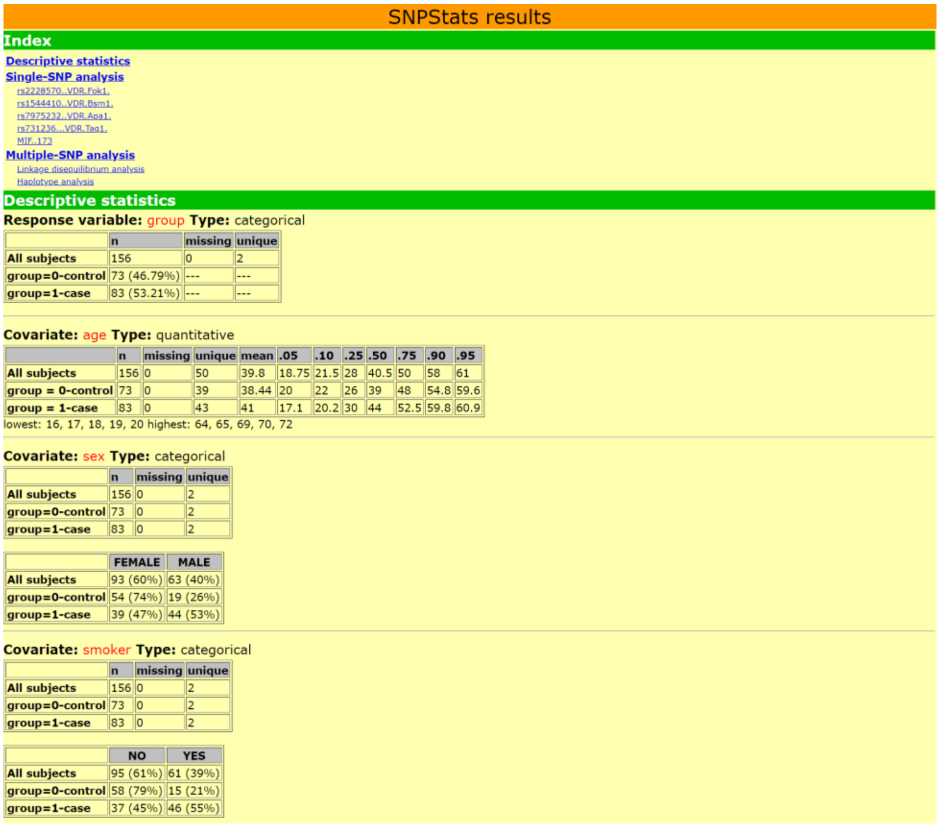
Chi-squared value = 3.774814815
Chi-squared test P value = 0.052030
(if < 0.05 - not consistent with HWE)

*Put your values here

Me

Polimorfisme *VDR*

Case: TB paru aktif Control: Kontak serumah



SNPStats results

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Descriptive statistics
Single-SNP analysis
rs2228570..VDR.Fok1.
rs1544410..VDR.Bsm1.
rs7975232..VDR.Apa1.
rs731236...VDR.Taq1.
MIF..173
Multiple-SNP analysis
Linkage disequilibrium analysis
Haplotype analysis

Descriptive statistics

Response variable: group **Type:** categorical

	n	missing	unique
All subjects	156	0	2
group=0-control	73 (46.79%)	---	---
group=1-case	83 (53.21%)	---	---

Covariate: age **Type:** quantitative

	n	missing	unique	mean	.05	.10	.25	.50	.75	.90	.95
All subjects	156	0	50	39.8	18.75	21.5	28	40.5	50	58	61
group = 0-control	73	0	39	38.44	20	22	26	39	48	54.8	59.6
group = 1-case	83	0	43	41	17.1	20.2	30	44	52.5	59.8	60.9

lowest: 16, 17, 18, 19, 20 highest: 64, 65, 69, 70, 72

Covariate: sex **Type:** categorical

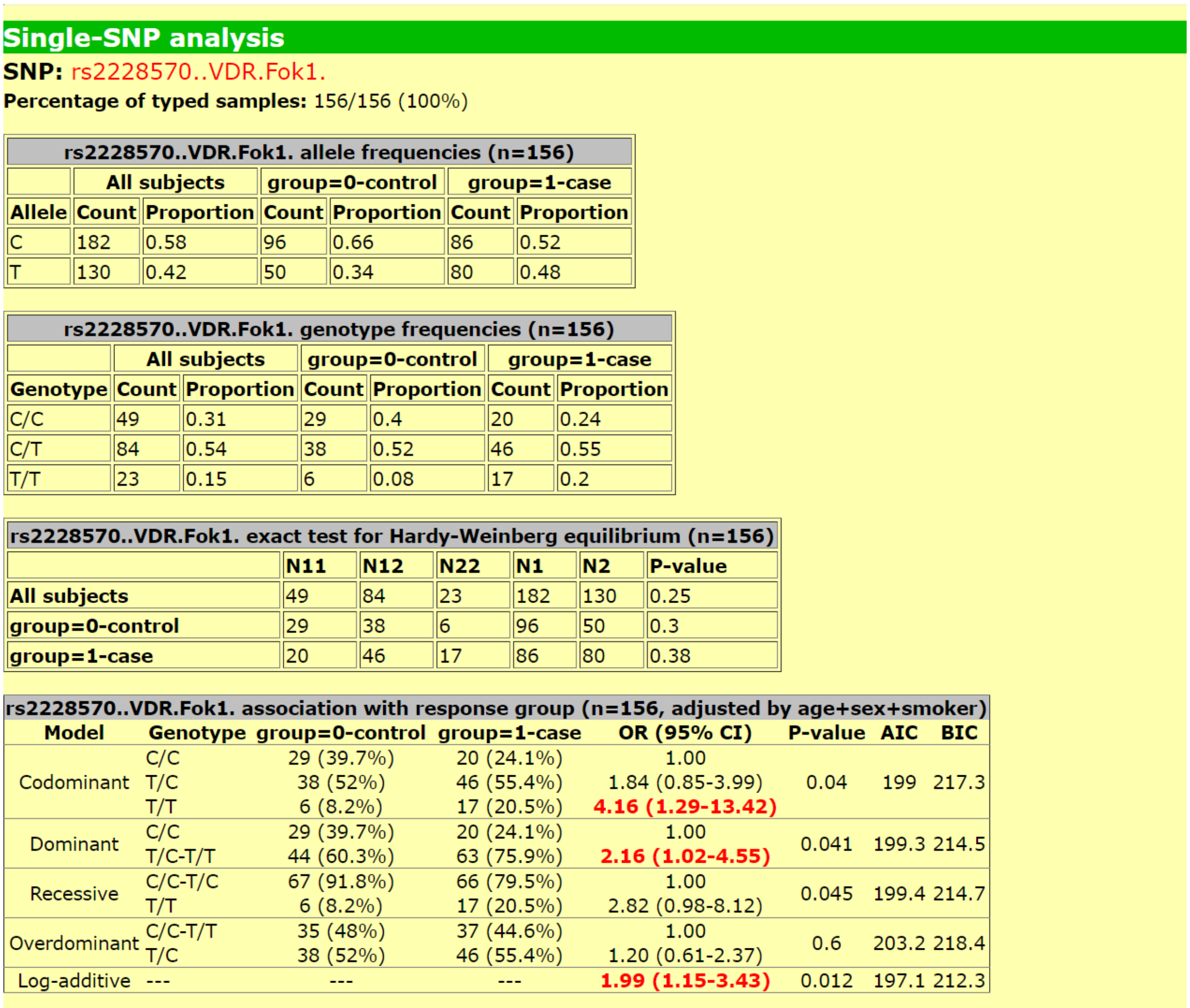
	n	missing	unique
All subjects	156	0	2
group=0-control	73	0	2
group=1-case	83	0	2

	FEMALE	MALE
All subjects	93 (60%)	63 (40%)
group=0-control	54 (74%)	19 (26%)
group=1-case	39 (47%)	44 (53%)

Covariate: smoker **Type:** categorical

	n	missing	unique
All subjects	156	0	2
group=0-control	73	0	2
group=1-case	83	0	2

	NO	YES
All subjects	95 (61%)	61 (39%)
group=0-control	58 (79%)	15 (21%)
group=1-case	37 (45%)	46 (55%)



Single-SNP analysis

SNP: rs2228570..VDR.Fok1.

Percentage of typed samples: 156/156 (100%)

rs2228570..VDR.Fok1. allele frequencies (n=156)

	All subjects		group=0-control		group=1-case	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
C	182	0.58	96	0.66	86	0.52
T	130	0.42	50	0.34	80	0.48

rs2228570..VDR.Fok1. genotype frequencies (n=156)

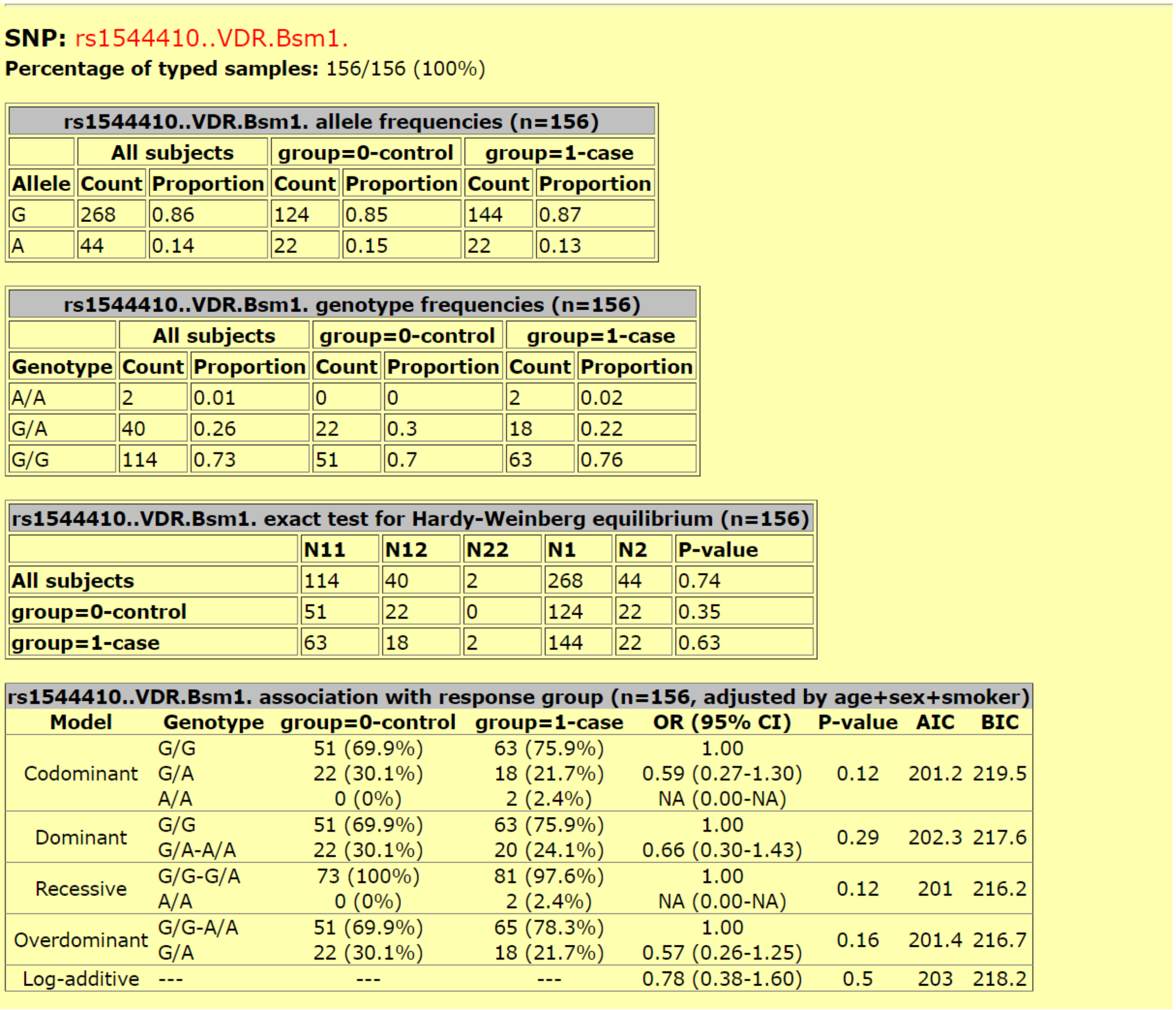
	All subjects		group=0-control		group=1-case	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
C/C	49	0.31	29	0.4	20	0.24
C/T	84	0.54	38	0.52	46	0.55
T/T	23	0.15	6	0.08	17	0.2

rs2228570..VDR.Fok1. exact test for Hardy-Weinberg equilibrium (n=156)

	N11	N12	N22	N1	N2	P-value
All subjects	49	84	23	182	130	0.25
group=0-control	29	38	6	96	50	0.3
group=1-case	20	46	17	86	80	0.38

rs2228570..VDR.Fok1. association with response group (n=156, adjusted by age+sex+smoker)

Model	Genotype	group=0-control	group=1-case	OR (95% CI)	P-value	AIC	BIC
Codominant	C/C	29 (39.7%)	20 (24.1%)	1.00	0.04	199	217.3
	T/C	38 (52%)	46 (55.4%)	1.84 (0.85-3.99)			
	T/T	6 (8.2%)	17 (20.5%)	**4.16 (1.29-13.42)**			
Dominant	C/C	29 (39.7%)	20 (24.1%)	1.00	0.041	199.3	214.5
	T/C-T/T	44 (60.3%)	63 (75.9%)	**2.16 (1.02-4.55)**			
Recessive	C/C-T/C	67 (91.8%)	66 (79.5%)	1.00	0.045	199.4	214.7
	T/T	6 (8.2%)	17 (20.5%)	2.82 (0.98-8.12)			
Overdominant	C/C-T/T	35 (48%)	37 (44.6%)	1.00	0.6	203.2	218.4
	T/C	38 (52%)	46 (55.4%)	1.20 (0.61-2.37)			
Log-additive	---	---	---	**1.99 (1.15-3.43)**	0.012	197.1	212.3



SNP: rs1544410..VDR.Bsm1.

Percentage of typed samples: 156/156 (100%)

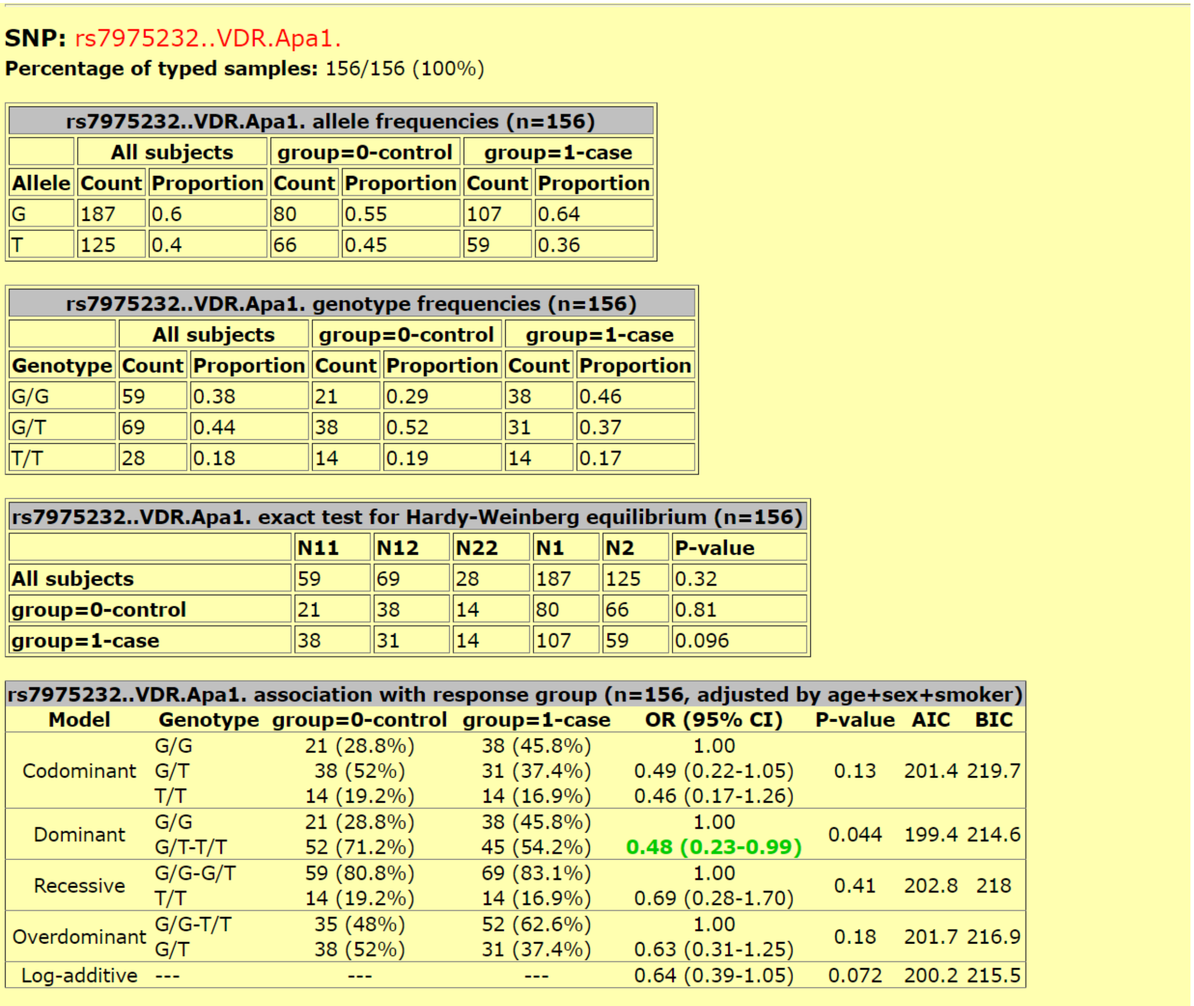
rs1544410..VDR.Bsm1. allele frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G	268	0.86	124	0.85	144	0.87
A	44	0.14	22	0.15	22	0.13

rs1544410..VDR.Bsm1. genotype frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A/A	2	0.01	0	0	2	0.02
G/A	40	0.26	22	0.3	18	0.22
G/G	114	0.73	51	0.7	63	0.76

rs1544410..VDR.Bsm1. exact test for Hardy-Weinberg equilibrium (n=156)						
	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	114	40	2	268	44	0.74
group=0-control	51	22	0	124	22	0.35
group=1-case	63	18	2	144	22	0.63

rs1544410..VDR.Bsm1. association with response group (n=156, adjusted by age+sex+smoker)

Model	Genotype	group=0-control	group=1-case	OR (95% CI)	P-value	AIC	BIC
Codominant	G/G	51 (69.9%)	63 (75.9%)	1.00	0.12	201.2	219.5
	G/A	22 (30.1%)	18 (21.7%)	0.59 (0.27-1.30)			
	A/A	0 (0%)	2 (2.4%)	NA (0.00-NA)			
Dominant	G/G	51 (69.9%)	63 (75.9%)	1.00	0.29	202.3	217.6
	G/A-A/A	22 (30.1%)	20 (24.1%)	0.66 (0.30-1.43)			
Recessive	G/G-G/A	73 (100%)	81 (97.6%)	1.00	0.12	201	216.2
	A/A	0 (0%)	2 (2.4%)	NA (0.00-NA)			
Overdominant	G/G-A/A	51 (69.9%)	65 (78.3%)	1.00	0.16	201.4	216.7
	G/A	22 (30.1%)	18 (21.7%)	0.57 (0.26-1.25)			
Log-additive	---	---	---	0.78 (0.38-1.60)	0.5	203	218.2



SNP: rs7975232..VDR.Apa1.

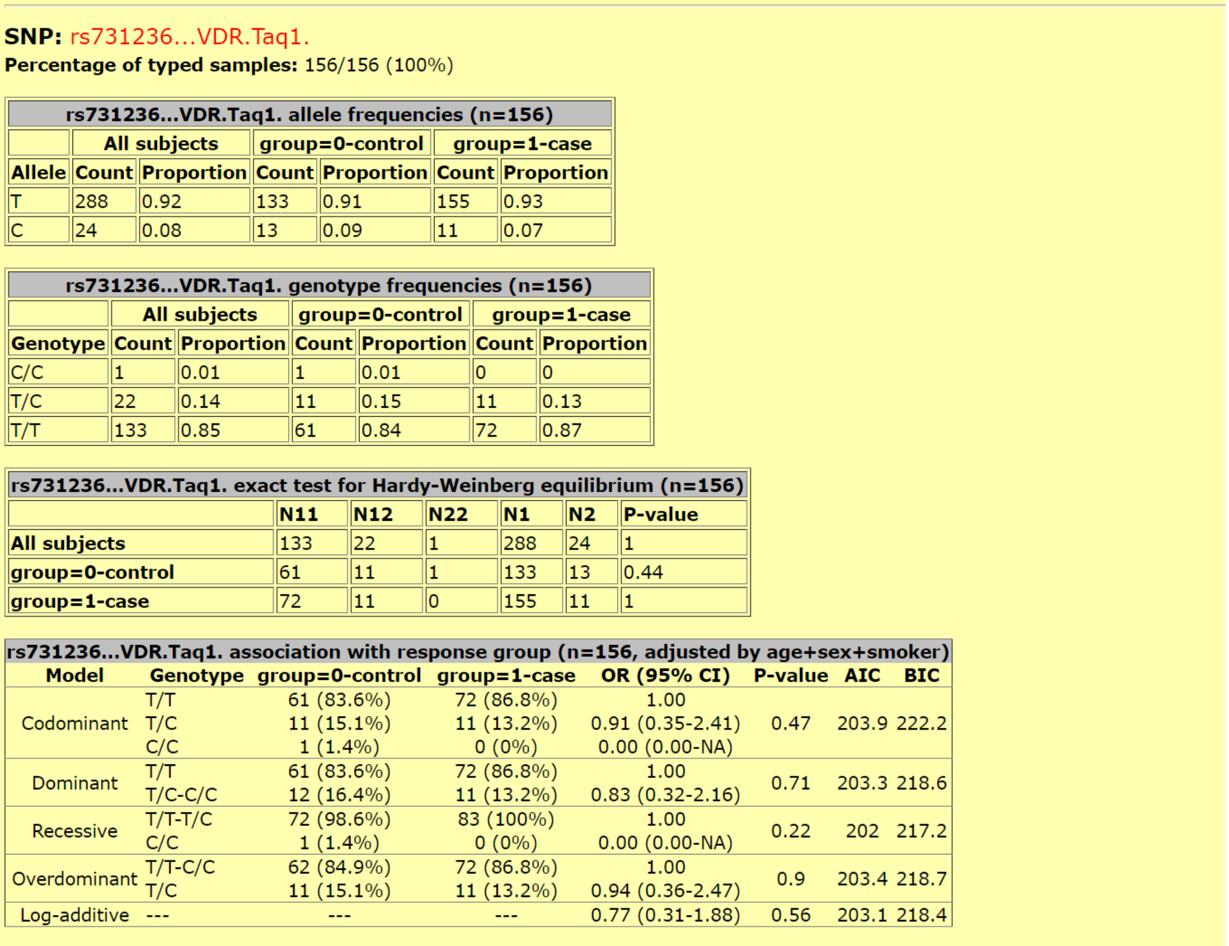
Percentage of typed samples: 156/156 (100%)

rs7975232..VDR.Apa1. allele frequencies (n=156)						
	All subjects		**group=0-control**		**group=1-case**	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G	187	0.6	80	0.55	107	0.64
T	125	0.4	66	0.45	59	0.36

rs7975232..VDR.Apa1. genotype frequencies (n=156)						
	All subjects		**group=0-control**		**group=1-case**	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G/G	59	0.38	21	0.29	38	0.46
G/T	69	0.44	38	0.52	31	0.37
T/T	28	0.18	14	0.19	14	0.17

rs7975232..VDR.Apa1. exact test for Hardy-Weinberg equilibrium (n=156)					
	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	59	69	28	187	125	0.32
group=0-control	21	38	14	80	66	0.81
group=1-case	38	31	14	107	59	0.096

rs7975232..VDR.Apa1. association with response group (n=156, adjusted by age+sex+smoker)							
Model	**Genotype**	**group=0-control**	**group=1-case**	**OR (95% CI)**	**P-value**	**AIC**	**BIC**
Codominant	G/G	21 (28.8%)	38 (45.8%)	1.00	0.13	201.4	219.7
	G/T	38 (52%)	31 (37.4%)	0.49 (0.22-1.05)			
	T/T	14 (19.2%)	14 (16.9%)	0.46 (0.17-1.26)			
Dominant	G/G	21 (28.8%)	38 (45.8%)	1.00	0.044	199.4	214.6
	G/T-T/T	52 (71.2%)	45 (54.2%)	**0.48 (0.23-0.99)**			
Recessive	G/G-G/T	59 (80.8%)	69 (83.1%)	1.00	0.41	202.8	218
	T/T	14 (19.2%)	14 (16.9%)	0.69 (0.28-1.70)			
Overdominant	G/G-T/T	35 (48%)	52 (62.6%)	1.00	0.18	201.7	216.9
	G/T	38 (52%)	31 (37.4%)	0.63 (0.31-1.25)			
Log-additive	---	---	---	0.64 (0.39-1.05)	0.072	200.2	215.5



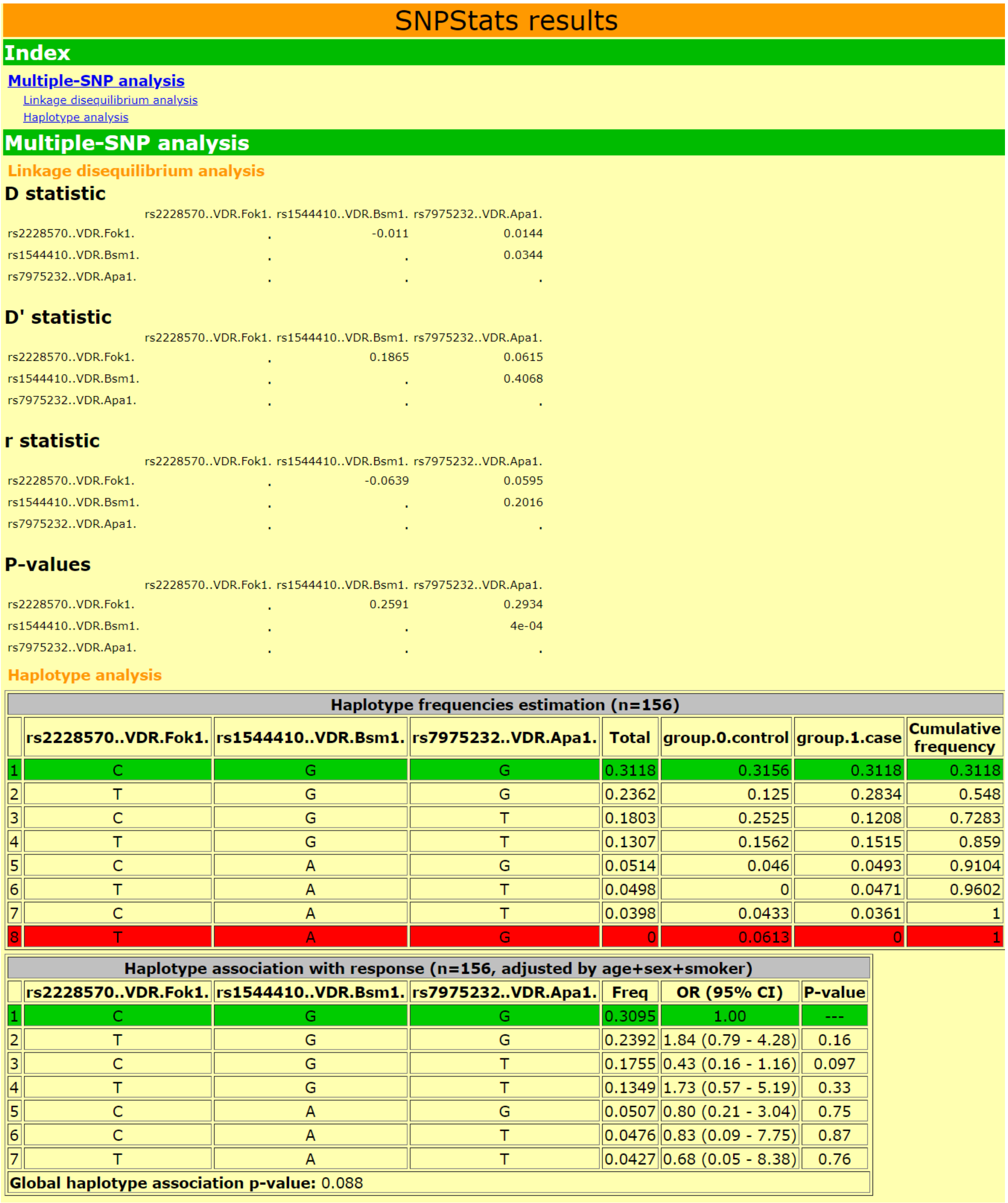
SNP: rs731236...VDR.Taq1.
Percentage of typed samples: 156/156 (100%)

rs731236...VDR.Taq1. allele frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
T	288	0.92	133	0.91	155	0.93
C	24	0.08	13	0.09	11	0.07

rs731236...VDR.Taq1. genotype frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
C/C	1	0.01	1	0.01	0	0
T/C	22	0.14	11	0.15	11	0.13
T/T	133	0.85	61	0.84	72	0.87

rs731236...VDR.Taq1. exact test for Hardy-Weinberg equilibrium (n=156)						
	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	133	22	1	288	24	1
group=0-control	61	11	1	133	13	0.44
group=1-case	72	11	0	155	11	1

rs731236...VDR.Taq1. association with response group (n=156, adjusted by age+sex+smoker)							
Model	**Genotype**	**group=0-control**	**group=1-case**	**OR (95% CI)**	**P-value**	**AIC**	**BIC**
Codominant	T/T	61 (83.6%)	72 (86.8%)	1.00	0.47	203.9	222.2
	T/C	11 (15.1%)	11 (13.2%)	0.91 (0.35-2.41)			
	C/C	1 (1.4%)	0 (0%)	0.00 (0.00-NA)			
Dominant	T/T	61 (83.6%)	72 (86.8%)	1.00	0.71	203.3	218.6
	T/C-C/C	12 (16.4%)	11 (13.2%)	0.83 (0.32-2.16)			
Recessive	T/T-T/C	72 (98.6%)	83 (100%)	1.00	0.22	202	217.2
	C/C	1 (1.4%)	0 (0%)	0.00 (0.00-NA)			
Overdominant	T/T-C/C	62 (84.9%)	72 (86.8%)	1.00	0.9	203.4	218.7
	T/C	11 (15.1%)	11 (13.2%)	0.94 (0.36-2.47)			
Log-additive	---	---	---	0.77 (0.31-1.88)	0.56	203.1	218.4



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Multiple-SNP analysis

Linkage disequilibrium analysis

D statistic

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.
rs2228570..VDR.Fok1.	.	-0.011	0.0144
rs1544410..VDR.Bsm1.	.	.	0.0344
rs7975232..VDR.Apa1.	.	.	.

D' statistic

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.
rs2228570..VDR.Fok1.	.	0.1865	0.0615
rs1544410..VDR.Bsm1.	.	.	0.4068
rs7975232..VDR.Apa1.	.	.	.

r statistic

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.
rs2228570..VDR.Fok1.	.	-0.0639	0.0595
rs1544410..VDR.Bsm1.	.	.	0.2016
rs7975232..VDR.Apa1.	.	.	.

P-values

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.
rs2228570..VDR.Fok1.	.	0.2591	0.2934
rs1544410..VDR.Bsm1.	.	.	4e-04
rs7975232..VDR.Apa1.	.	.	.

Haplotype analysis

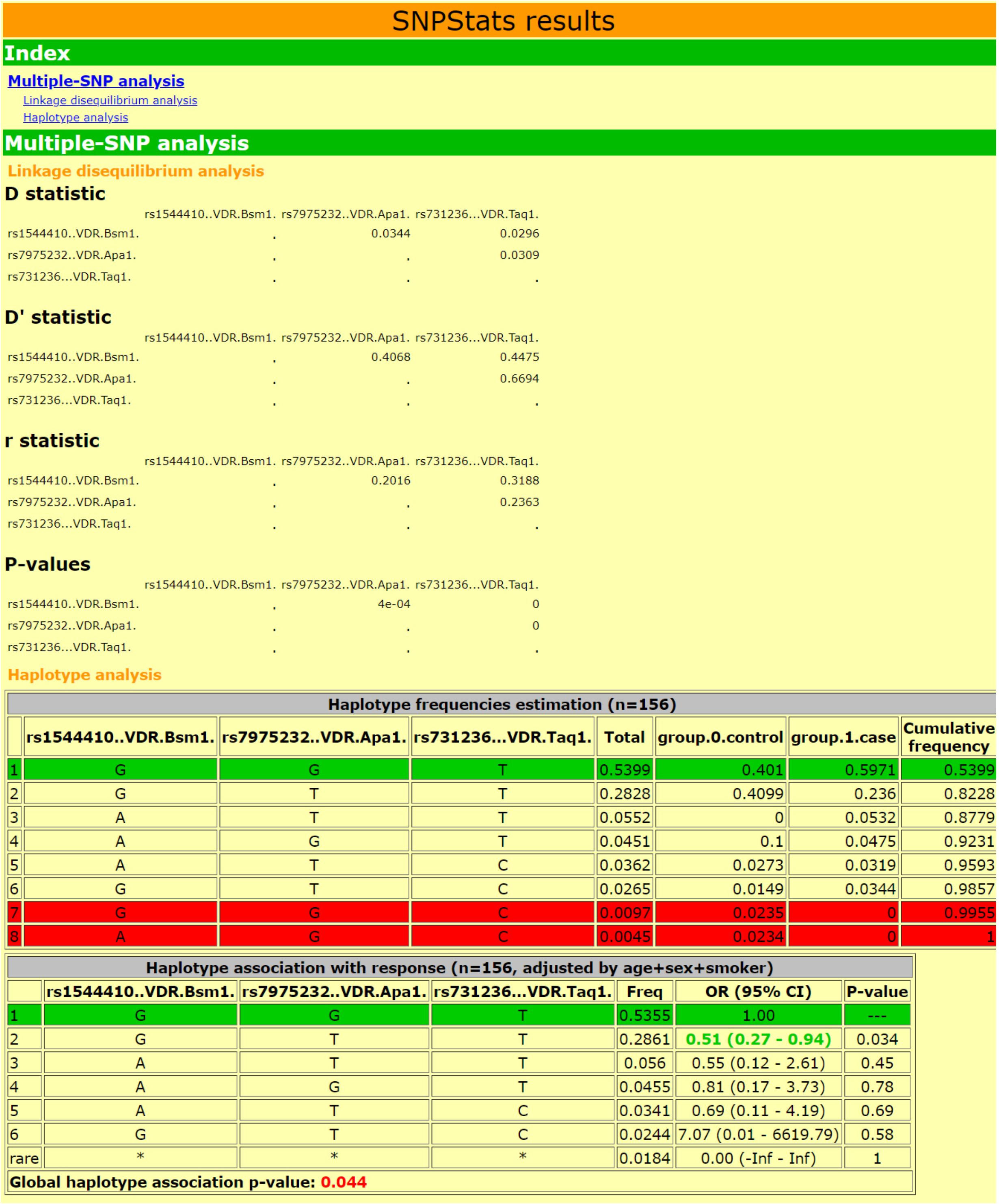
Haplotype frequencies estimation (n=156)

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	Total	group.0.control	group.1.case	Cumulative frequency
1	C	G	G	0.3118	0.3156	0.3118	0.3118
2	T	G	G	0.2362	0.125	0.2834	0.548
3	C	G	T	0.1803	0.2525	0.1208	0.7283
4	T	G	T	0.1307	0.1562	0.1515	0.859
5	C	A	G	0.0514	0.046	0.0493	0.9104
6	T	A	T	0.0498	0	0.0471	0.9602
7	C	A	T	0.0398	0.0433	0.0361	1
8	T	A	G	0	0.0613	0	1

Haplotype association with response (n=156, adjusted by age+sex+smoker)

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	Freq	OR (95% CI)	P-value
1	C	G	G	0.3095	1.00	---
2	T	G	G	0.2392	1.84 (0.79 - 4.28)	0.16
3	C	G	T	0.1755	0.43 (0.16 - 1.16)	0.097
4	T	G	T	0.1349	1.73 (0.57 - 5.19)	0.33
5	C	A	G	0.0507	0.80 (0.21 - 3.04)	0.75
6	C	A	T	0.0476	0.83 (0.09 - 7.75)	0.87
7	T	A	T	0.0427	0.68 (0.05 - 8.38)	0.76

Global haplotype association p-value: 0.088



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Linkage disequilibrium analysis

D statistic

	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.
rs1544410..VDR.Bsm1.	.	0.0344	0.0296
rs7975232..VDR.Apa1.	.	.	0.0309
rs731236...VDR.Taq1.	.	.	.

D' statistic

	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.
rs1544410..VDR.Bsm1.	.	0.4068	0.4475
rs7975232..VDR.Apa1.	.	.	0.6694
rs731236...VDR.Taq1.	.	.	.

r statistic

	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.
rs1544410..VDR.Bsm1.	.	0.2016	0.3188
rs7975232..VDR.Apa1.	.	.	0.2363
rs731236...VDR.Taq1.	.	.	.

P-values

	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.
rs1544410..VDR.Bsm1.	.	4e-04	0
rs7975232..VDR.Apa1.	.	.	0
rs731236...VDR.Taq1.	.	.	.

Haplotype analysis

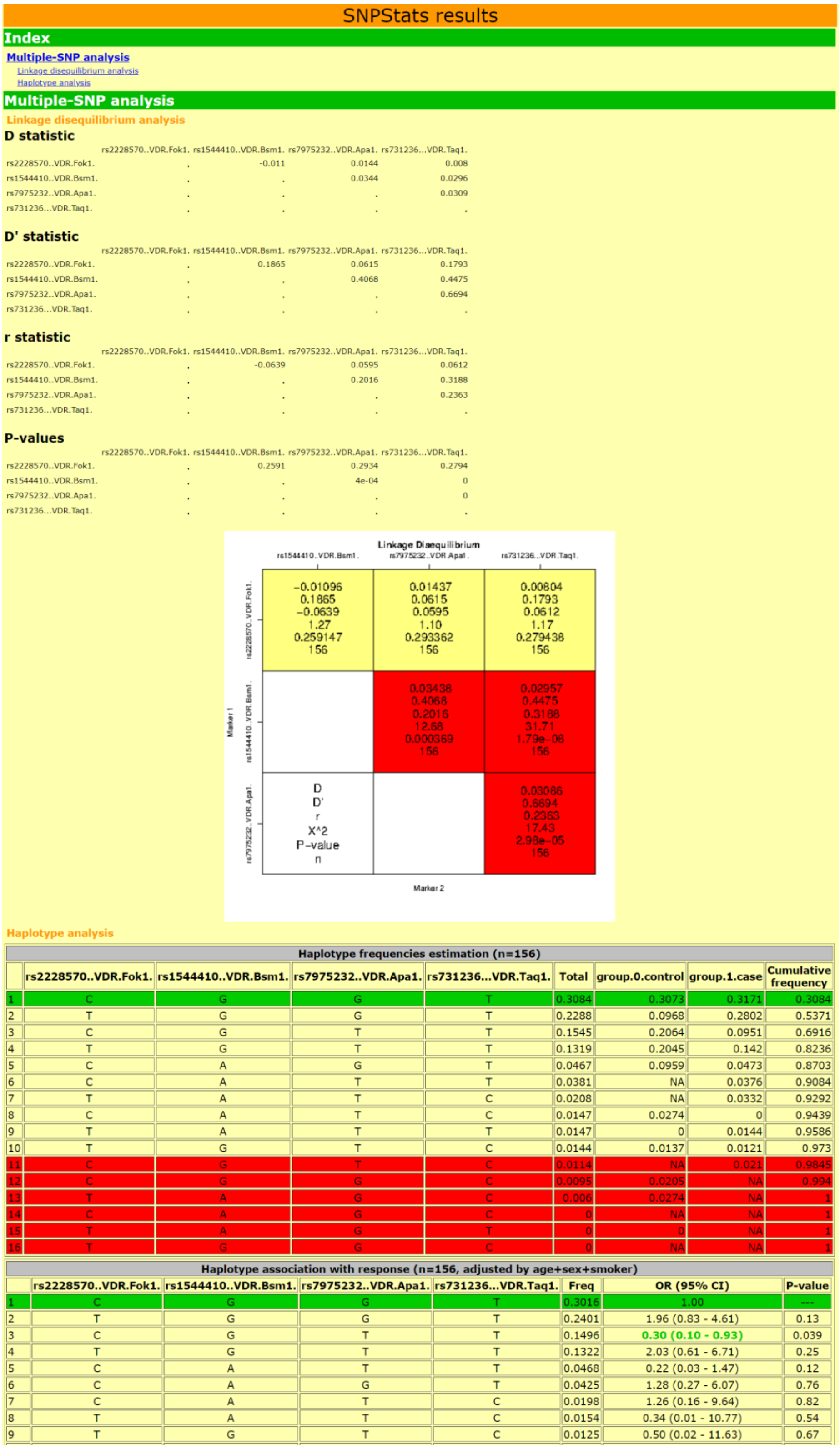
Haplotype frequencies estimation (n=156)

	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.	Total	group.0.control	group.1.case	Cumulative frequency
1	G	G	T	0.5399	0.401	0.5971	0.5399
2	G	T	T	0.2828	0.4099	0.236	0.8228
3	A	T	T	0.0552	0	0.0532	0.8779
4	A	G	T	0.0451	0.1	0.0475	0.9231
5	A	T	C	0.0362	0.0273	0.0319	0.9593
6	G	T	C	0.0265	0.0149	0.0344	0.9857
7	G	G	C	0.0097	0.0235	0	0.9955
8	A	G	C	0.0045	0.0234	0	1

Haplotype association with response (n=156, adjusted by age+sex+smoker)

	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.	Freq	OR (95% CI)	P-value
1	G	G	T	0.5355	1.00	---
2	G	T	T	0.2861	**0.51 (0.27 - 0.94)**	0.034
3	A	T	T	0.056	0.55 (0.12 - 2.61)	0.45
4	A	G	T	0.0455	0.81 (0.17 - 3.73)	0.78
5	A	T	C	0.0341	0.69 (0.11 - 4.19)	0.69
6	G	T	C	0.0244	7.07 (0.01 - 6619.79)	0.58
rare	*	*	*	0.0184	0.00 (-Inf - Inf)	1

Global haplotype association p-value: 0.044



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Multiple-SNP analysis

Linkage disequilibrium analysis

D statistic

```
                    rs2228570..VDR.Fok1. rs1544410..VDR.Bsm1. rs7975232..VDR.Apa1. rs731236...VDR.Taq1.
rs2228570..VDR.Fok1.                    .               -0.011               0.0144                0.008
rs1544410..VDR.Bsm1.                    .                    .               0.0344               0.0296
rs7975232..VDR.Apa1.                    .                    .                    .               0.0309
rs731236...VDR.Taq1.                    .                    .                    .                    .
```

D' statistic

```
                    rs2228570..VDR.Fok1. rs1544410..VDR.Bsm1. rs7975232..VDR.Apa1. rs731236...VDR.Taq1.
rs2228570..VDR.Fok1.                    .               0.1865               0.0615               0.1793
rs1544410..VDR.Bsm1.                    .                    .               0.4068               0.4475
rs7975232..VDR.Apa1.                    .                    .                    .               0.6694
rs731236...VDR.Taq1.                    .                    .                    .                    .
```

r statistic

```
                    rs2228570..VDR.Fok1. rs1544410..VDR.Bsm1. rs7975232..VDR.Apa1. rs731236...VDR.Taq1.
rs2228570..VDR.Fok1.                    .              -0.0639               0.0595               0.0612
rs1544410..VDR.Bsm1.                    .                    .               0.2016               0.3188
rs7975232..VDR.Apa1.                    .                    .                    .               0.2363
rs731236...VDR.Taq1.                    .                    .                    .                    .
```

P-values

```
                    rs2228570..VDR.Fok1. rs1544410..VDR.Bsm1. rs7975232..VDR.Apa1. rs731236...VDR.Taq1.
rs2228570..VDR.Fok1.                    .               0.2591               0.2934               0.2794
rs1544410..VDR.Bsm1.                    .                    .                4e-04                    0
rs7975232..VDR.Apa1.                    .                    .                    .                    0
rs731236...VDR.Taq1.                    .                    .                    .                    .
```

	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.
rs2228570..VDR.Fok1.	−0.01096 0.1865 −0.0639 1.27 0.259147 156	0.01437 0.0615 0.0595 1.10 0.293362 156	0.00804 0.1793 0.0612 1.17 0.279438 156
rs1544410..VDR.Bsm1.		0.03438 0.4068 0.2016 12.68 0.000369 156	0.02957 0.4475 0.3188 31.71 1.79e−08 156
rs7975232..VDR.Apa1.	D D' r X^2 P−value n		0.03086 0.6694 0.2363 17.43 2.98e−05 156

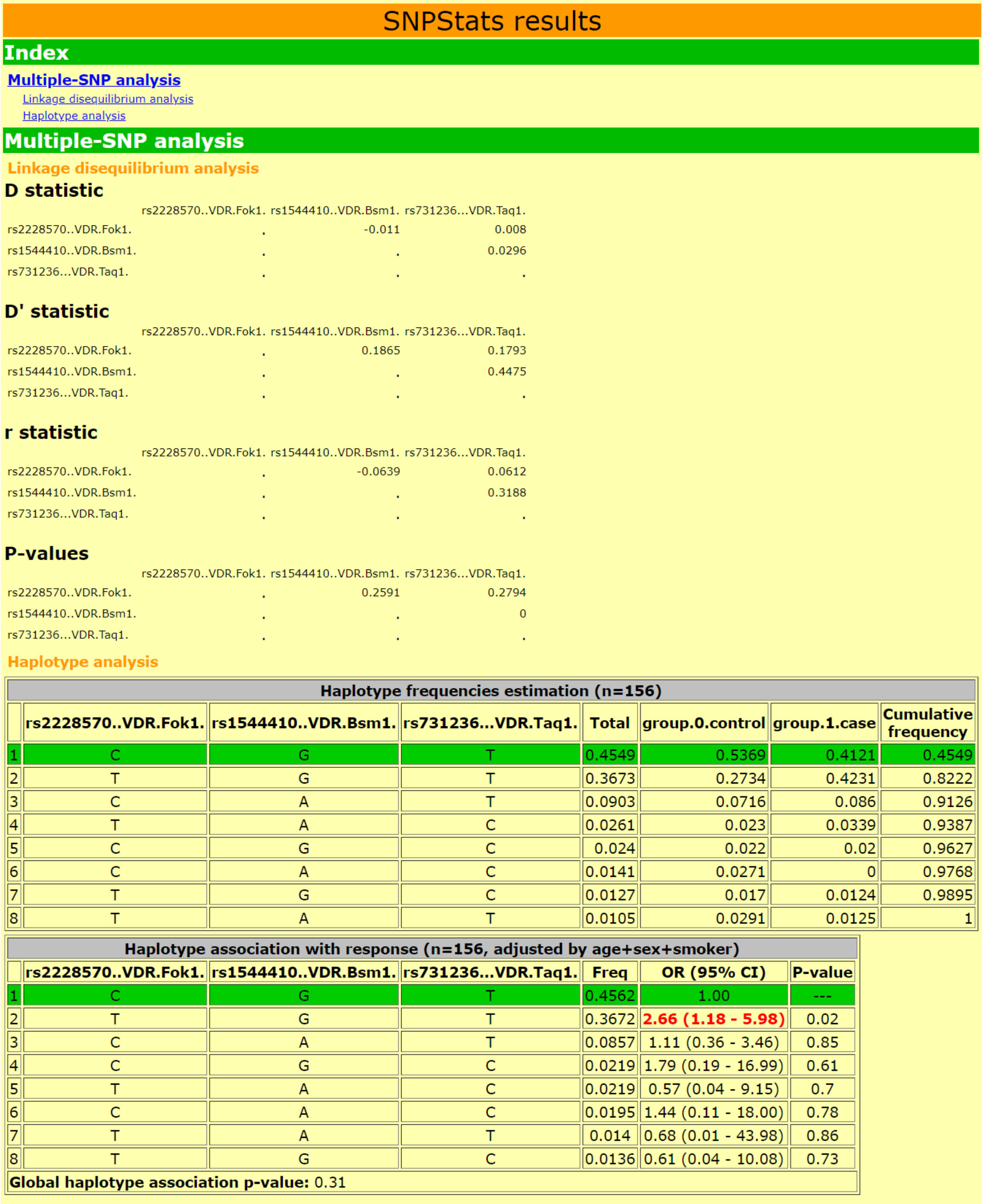
Haplotype analysis

Haplotype frequencies estimation (n=156)

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.	Total	group.0.control	group.1.case	Cumulative frequency
1	C	G	G	T	0.3084	0.3073	0.3171	0.3084
2	T	G	G	T	0.2288	0.0968	0.2802	0.5371
3	C	G	T	T	0.1545	0.2064	0.0951	0.6916
4	T	G	T	T	0.1319	0.2045	0.142	0.8236
5	C	A	G	T	0.0467	0.0959	0.0473	0.8703
6	C	A	T	T	0.0381	NA	0.0376	0.9084
7	T	A	T	C	0.0208	NA	0.0332	0.9292
8	C	A	T	C	0.0147	0.0274	0	0.9439
9	T	A	T	T	0.0147	0	0.0144	0.9586
10	T	G	T	C	0.0144	0.0137	0.0121	0.973
11	C	G	T	C	0.0114	NA	0.021	0.9845
12	C	G	G	C	0.0095	0.0205	NA	0.994
13	T	A	G	C	0.006	0.0274	NA	1
14	C	A	G	C	0	NA	NA	1
15	T	A	G	T	0	0	NA	1
16	T	G	G	C	0	NA	NA	1

Haplotype association with response (n=156, adjusted by age+sex+smoker)

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.	Freq	OR (95% CI)	P-value
1	C	G	G	T	0.3016	1.00	---
2	T	G	G	T	0.2401	1.96 (0.83 - 4.61)	0.13
3	C	G	T	T	0.1496	**0.30 (0.10 - 0.93)**	0.039
4	T	G	T	T	0.1322	2.03 (0.61 - 6.71)	0.25
5	C	A	T	T	0.0468	0.22 (0.03 - 1.47)	0.12
6	C	A	G	T	0.0425	1.28 (0.27 - 6.07)	0.76
7	C	A	T	C	0.0198	1.26 (0.16 - 9.64)	0.82
8	T	A	T	C	0.0154	0.34 (0.01 - 10.77)	0.54
9	T	G	T	C	0.0125	0.50 (0.02 - 11.63)	0.67



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Multiple-SNP analysis

Linkage disequilibrium analysis

D statistic

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs731236...VDR.Taq1.
rs2228570..VDR.Fok1.	.	-0.011	0.008
rs1544410..VDR.Bsm1.	.	.	0.0296
rs731236...VDR.Taq1.	.	.	.

D' statistic

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs731236...VDR.Taq1.
rs2228570..VDR.Fok1.	.	0.1865	0.1793
rs1544410..VDR.Bsm1.	.	.	0.4475
rs731236...VDR.Taq1.	.	.	.

r statistic

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs731236...VDR.Taq1.
rs2228570..VDR.Fok1.	.	-0.0639	0.0612
rs1544410..VDR.Bsm1.	.	.	0.3188
rs731236...VDR.Taq1.	.	.	.

P-values

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs731236...VDR.Taq1.
rs2228570..VDR.Fok1.	.	0.2591	0.2794
rs1544410..VDR.Bsm1.	.	.	0
rs731236...VDR.Taq1.	.	.	.

Haplotype analysis

Haplotype frequencies estimation (n=156)

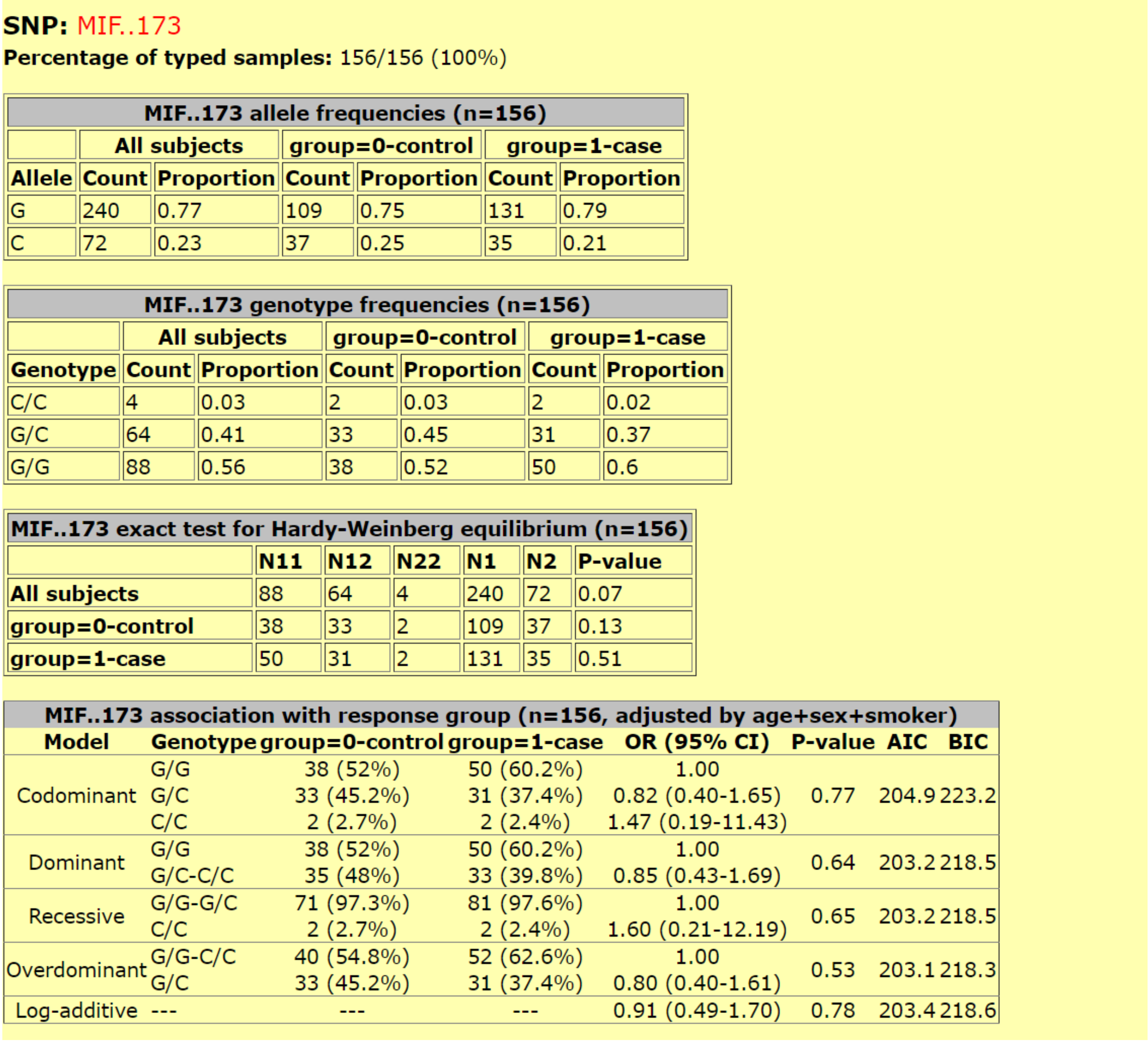
	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs731236...VDR.Taq1.	Total	group.0.control	group.1.case	Cumulative frequency
1	C	G	T	0.4549	0.5369	0.4121	0.4549
2	T	G	T	0.3673	0.2734	0.4231	0.8222
3	C	A	T	0.0903	0.0716	0.086	0.9126
4	T	A	C	0.0261	0.023	0.0339	0.9387
5	C	G	C	0.024	0.022	0.02	0.9627
6	C	A	C	0.0141	0.0271	0	0.9768
7	T	G	C	0.0127	0.017	0.0124	0.9895
8	T	A	T	0.0105	0.0291	0.0125	1

Haplotype association with response (n=156, adjusted by age+sex+smoker)

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs731236...VDR.Taq1.	Freq	OR (95% CI)	P-value
1	C	G	T	0.4562	1.00	---
2	T	G	T	0.3672	**2.66 (1.18 - 5.98)**	0.02
3	C	A	T	0.0857	1.11 (0.36 - 3.46)	0.85
4	C	G	C	0.0219	1.79 (0.19 - 16.99)	0.61
5	T	A	C	0.0219	0.57 (0.04 - 9.15)	0.7
6	C	A	C	0.0195	1.44 (0.11 - 18.00)	0.78
7	T	A	T	0.014	0.68 (0.01 - 43.98)	0.86
8	T	G	C	0.0136	0.61 (0.04 - 10.08)	0.73

Global haplotype association p-value: 0.31

MIF -173 G/C rs755622



SNP: MIF..173

Percentage of typed samples: 156/156 (100%)

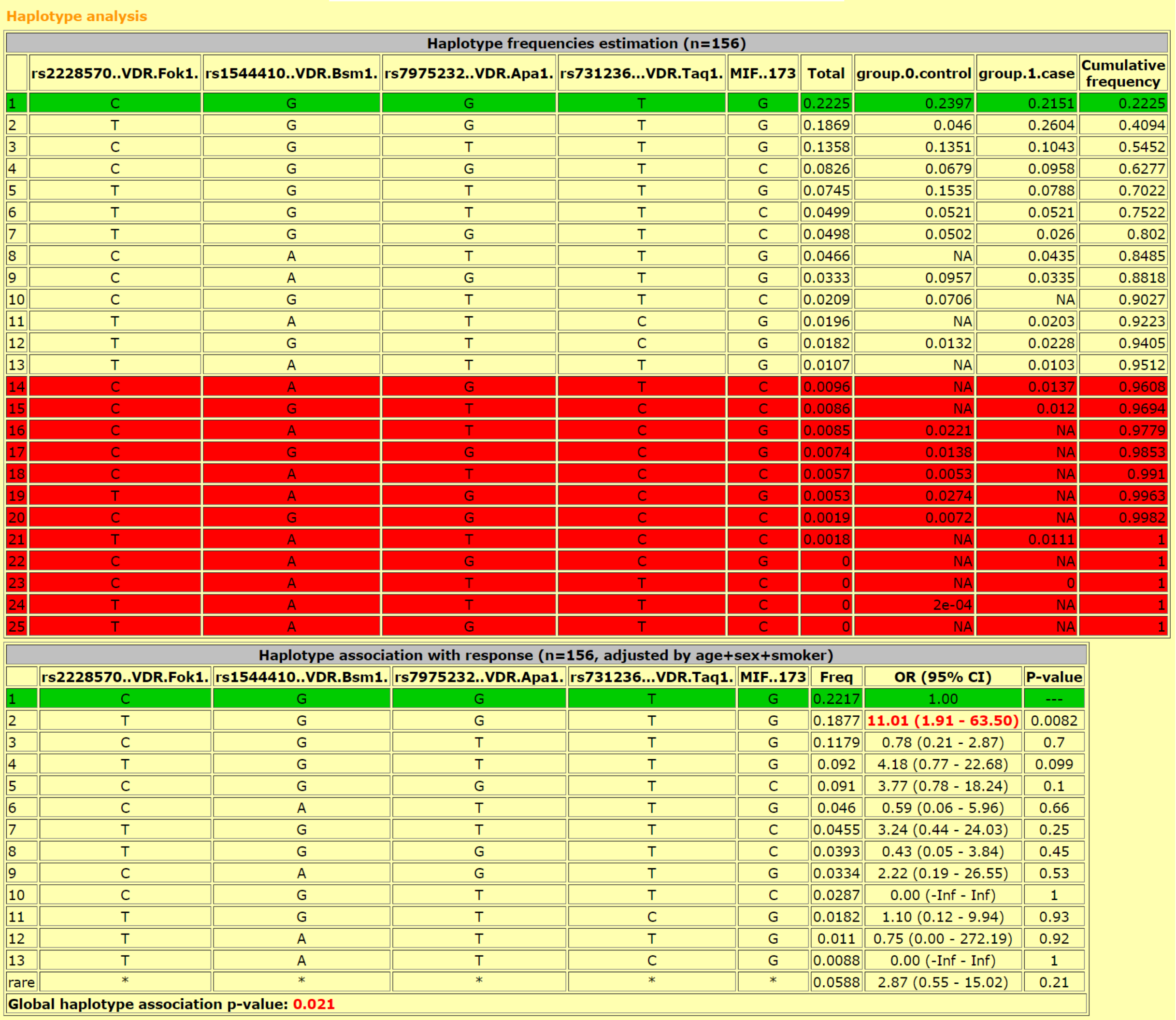
MIF..173 allele frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G	240	0.77	109	0.75	131	0.79
C	72	0.23	37	0.25	35	0.21

MIF..173 genotype frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
C/C	4	0.03	2	0.03	2	0.02
G/C	64	0.41	33	0.45	31	0.37
G/G	88	0.56	38	0.52	50	0.6

MIF..173 exact test for Hardy-Weinberg equilibrium (n=156)						
	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	88	64	4	240	72	0.07
group=0-control	38	33	2	109	37	0.13
group=1-case	50	31	2	131	35	0.51

MIF..173 association with response group (n=156, adjusted by age+sex+smoker)

Model	Genotype	group=0-control	group=1-case	OR (95% CI)	P-value	AIC	BIC
Codominant	G/G	38 (52%)	50 (60.2%)	1.00	0.77	204.9	223.2
	G/C	33 (45.2%)	31 (37.4%)	0.82 (0.40-1.65)			
	C/C	2 (2.7%)	2 (2.4%)	1.47 (0.19-11.43)			
Dominant	G/G	38 (52%)	50 (60.2%)	1.00	0.64	203.2	218.5
	G/C-C/C	35 (48%)	33 (39.8%)	0.85 (0.43-1.69)			
Recessive	G/G-G/C	71 (97.3%)	81 (97.6%)	1.00	0.65	203.2	218.5
	C/C	2 (2.7%)	2 (2.4%)	1.60 (0.21-12.19)			
Overdominant	G/G-C/C	40 (54.8%)	52 (62.6%)	1.00	0.53	203.1	218.3
	G/C	33 (45.2%)	31 (37.4%)	0.80 (0.40-1.61)			
Log-additive	---	---	---	0.91 (0.49-1.70)	0.78	203.4	218.6



Haplotype analysis

Haplotype frequencies estimation (n=156)

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.	MIF..173	Total	group.0.control	group.1.case	Cumulative frequency
1	C	G	G	T	G	0.2225	0.2397	0.2151	0.2225
2	T	G	G	T	G	0.1869	0.046	0.2604	0.4094
3	C	G	T	T	G	0.1358	0.1351	0.1043	0.5452
4	C	G	G	T	C	0.0826	0.0679	0.0958	0.6277
5	T	G	T	T	G	0.0745	0.1535	0.0788	0.7022
6	T	G	T	T	C	0.0499	0.0521	0.0521	0.7522
7	T	G	G	T	C	0.0498	0.0502	0.026	0.802
8	C	A	T	T	G	0.0466	NA	0.0435	0.8485
9	C	A	G	T	G	0.0333	0.0957	0.0335	0.8818
10	C	G	T	T	C	0.0209	0.0706	NA	0.9027
11	T	A	T	C	G	0.0196	NA	0.0203	0.9223
12	T	G	T	C	G	0.0182	0.0132	0.0228	0.9405
13	T	A	T	T	G	0.0107	NA	0.0103	0.9512
14	C	A	G	T	C	0.0096	NA	0.0137	0.9608
15	C	G	T	C	C	0.0086	NA	0.012	0.9694
16	C	A	T	C	G	0.0085	0.0221	NA	0.9779
17	C	G	G	C	G	0.0074	0.0138	NA	0.9853
18	C	A	T	C	C	0.0057	0.0053	NA	0.991
19	T	A	G	C	G	0.0053	0.0274	NA	0.9963
20	C	G	G	C	C	0.0019	0.0072	NA	0.9982
21	T	A	T	C	C	0.0018	NA	0.0111	1
22	C	A	G	C	G	0	NA	NA	1
23	C	A	T	T	C	0	NA	0	1
24	T	A	T	T	C	0	2e-04	NA	1
25	T	A	G	T	C	0	NA	NA	1

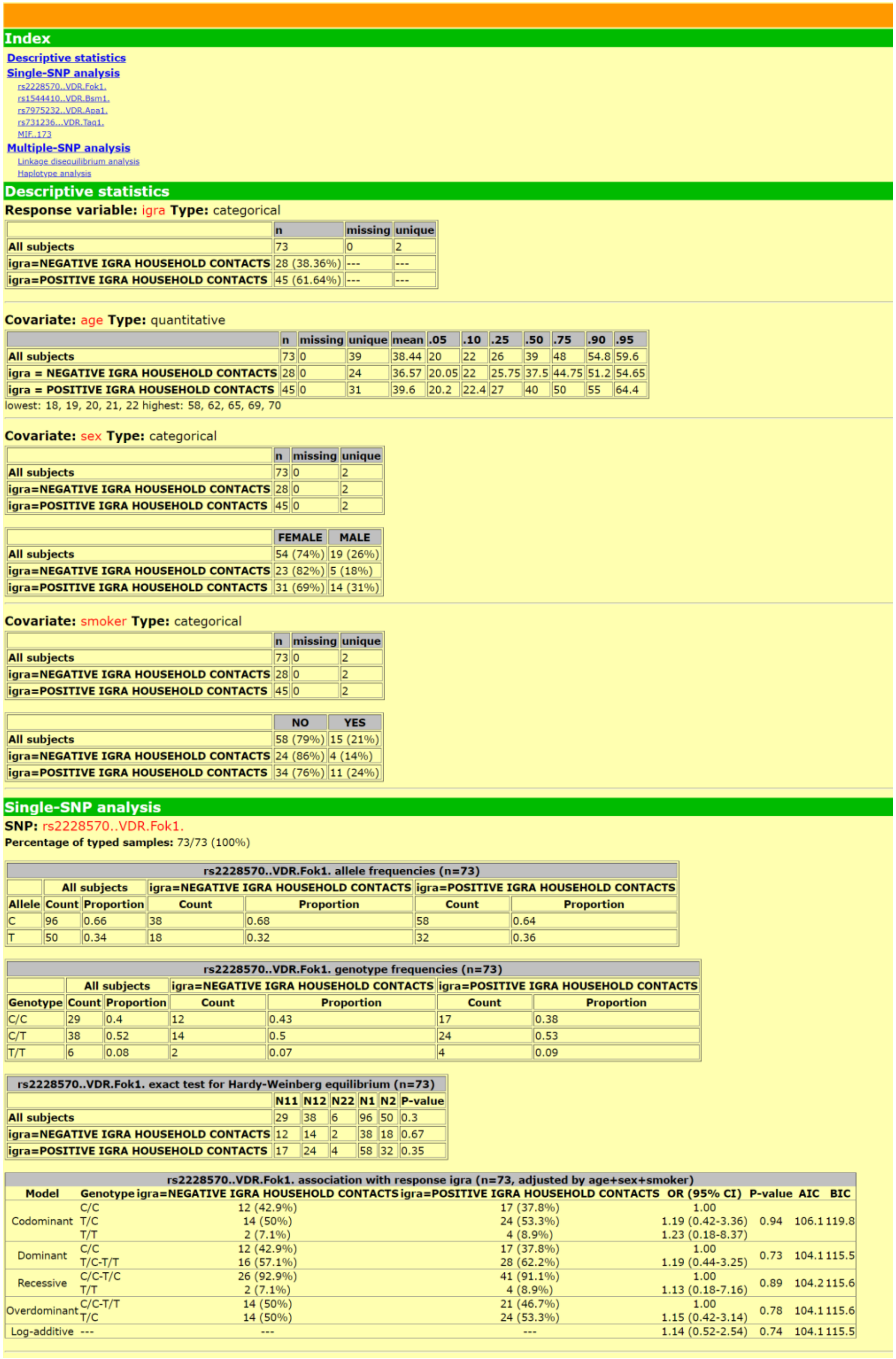
Haplotype association with response (n=156, adjusted by age+sex+smoker)

	rs2228570..VDR.Fok1.	rs1544410..VDR.Bsm1.	rs7975232..VDR.Apa1.	rs731236...VDR.Taq1.	MIF..173	Freq	OR (95% CI)	P-value
1	C	G	G	T	G	0.2217	1.00	---
2	T	G	G	T	G	0.1877	**11.01 (1.91 - 63.50)**	0.0082
3	C	G	T	T	G	0.1179	0.78 (0.21 - 2.87)	0.7
4	T	G	T	T	G	0.092	4.18 (0.77 - 22.68)	0.099
5	C	G	G	T	C	0.091	3.77 (0.78 - 18.24)	0.1
6	C	A	T	T	G	0.046	0.59 (0.06 - 5.96)	0.66
7	T	G	T	T	C	0.0455	3.24 (0.44 - 24.03)	0.25
8	T	G	G	T	C	0.0393	0.43 (0.05 - 3.84)	0.45
9	C	A	G	T	G	0.0334	2.22 (0.19 - 26.55)	0.53
10	C	G	T	T	C	0.0287	0.00 (-Inf - Inf)	1
11	T	G	T	C	G	0.0182	1.10 (0.12 - 9.94)	0.93
12	T	A	T	T	G	0.011	0.75 (0.00 - 272.19)	0.92
13	T	A	T	C	G	0.0088	0.00 (-Inf - Inf)	1
rare	*	*	*	*	*	0.0588	2.87 (0.55 - 15.02)	0.21

Global haplotype association p-value: 0.021

Polimorfisme VDR

Case: Kontak serumah IGRA positif   Control: Kontak serumah IGRA negatif



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- **Multiple-SNP analysis**
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  - Haplotype analysis

Descriptive statistics

Response variable: igra **Type:** categorical

	n	missing	unique
All subjects	73	0	2
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	28 (38.36%)	---	---
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	45 (61.64%)	---	---

Covariate: age **Type:** quantitative

	n	missing	unique	mean	.05	.10	.25	.50	.75	.90	.95
All subjects	73	0	39	38.44	20	22	26	39	48	54.8	59.6
igra = NEGATIVE IGRA HOUSEHOLD CONTACTS	28	0	24	36.57	20.05	22	25.75	37.5	44.75	51.2	54.65
igra = POSITIVE IGRA HOUSEHOLD CONTACTS	45	0	31	39.6	20.2	22.4	27	40	50	55	64.4

lowest: 18, 19, 20, 21, 22 highest: 58, 62, 65, 69, 70

Covariate: sex **Type:** categorical

	n	missing	unique
All subjects	73	0	2
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	28	0	2
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	45	0	2

	FEMALE	MALE
All subjects	54 (74%)	19 (26%)
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	23 (82%)	5 (18%)
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	31 (69%)	14 (31%)

Covariate: smoker **Type:** categorical

	n	missing	unique
All subjects	73	0	2
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	28	0	2
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	45	0	2

	NO	YES
All subjects	58 (79%)	15 (21%)
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	24 (86%)	4 (14%)
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	34 (76%)	11 (24%)

Single-SNP analysis

SNP: rs2228570..VDR.Fok1.

Percentage of typed samples: 73/73 (100%)

rs2228570..VDR.Fok1. allele frequencies (n=73)

	All subjects		igra=NEGATIVE IGRA HOUSEHOLD CONTACTS		igra=POSITIVE IGRA HOUSEHOLD CONTACTS	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
C	96	0.66	38	0.68	58	0.64
T	50	0.34	18	0.32	32	0.36

rs2228570..VDR.Fok1. genotype frequencies (n=73)

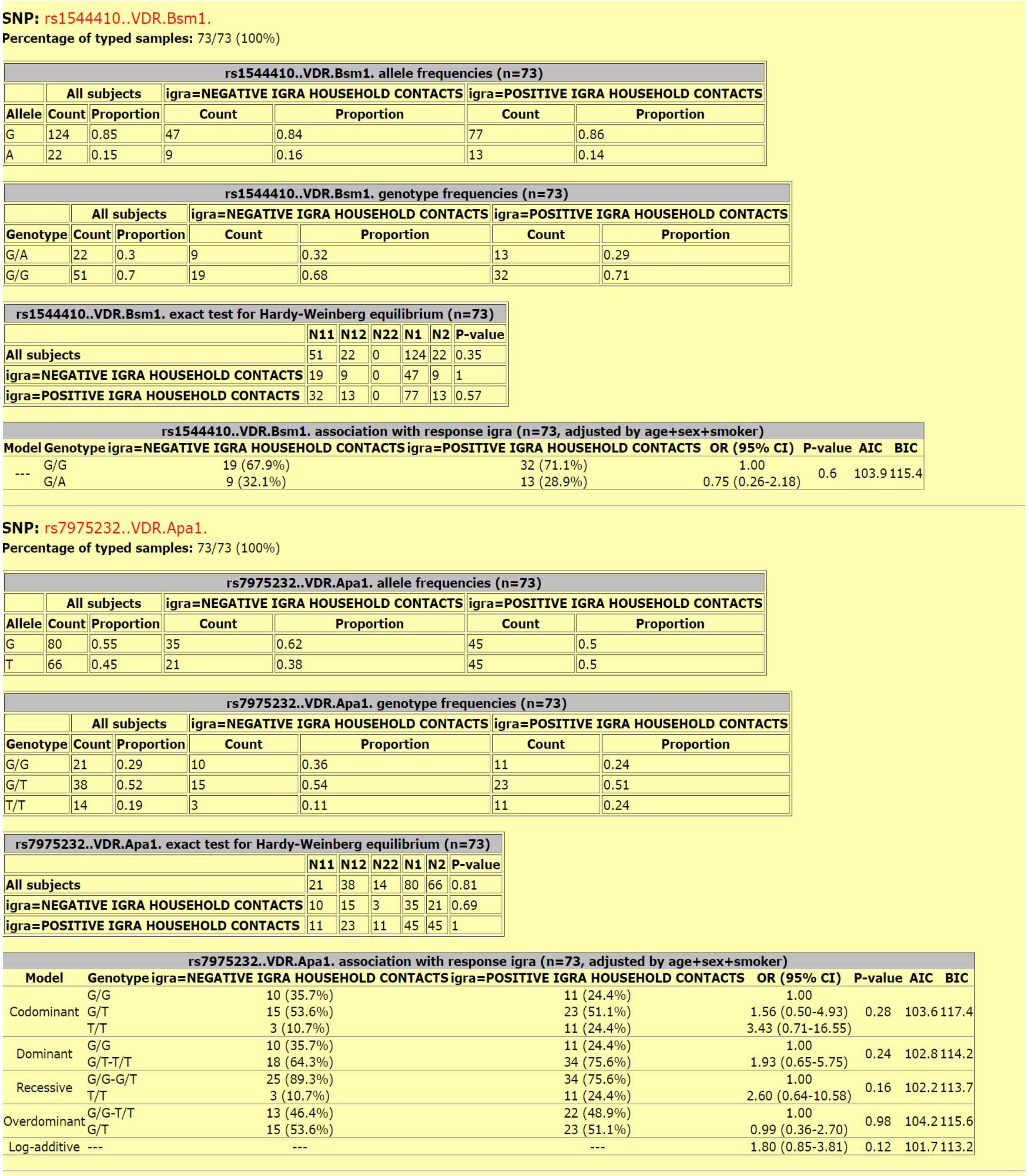
	All subjects		igra=NEGATIVE IGRA HOUSEHOLD CONTACTS		igra=POSITIVE IGRA HOUSEHOLD CONTACTS	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
C/C	29	0.4	12	0.43	17	0.38
C/T	38	0.52	14	0.5	24	0.53
T/T	6	0.08	2	0.07	4	0.09

rs2228570..VDR.Fok1. exact test for Hardy-Weinberg equilibrium (n=73)

	N11	N12	N22	N1	N2	P-value
All subjects	29	38	6	96	50	0.3
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	12	14	2	38	18	0.67
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	17	24	4	58	32	0.35

rs2228570..VDR.Fok1. association with response igra (n=73, adjusted by age+sex+smoker)

Model	Genotype	igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	igra=POSITIVE IGRA HOUSEHOLD CONTACTS	OR (95% CI)	P-value	AIC	BIC
Codominant	C/C	12 (42.9%)	17 (37.8%)	1.00	0.94	106.1	119.8
	T/C	14 (50%)	24 (53.3%)	1.19 (0.42-3.36)			
	T/T	2 (7.1%)	4 (8.9%)	1.23 (0.18-8.37)			
Dominant	C/C	12 (42.9%)	17 (37.8%)	1.00	0.73	104.1	115.5
	T/C-T/T	16 (57.1%)	28 (62.2%)	1.19 (0.44-3.25)			
Recessive	C/C-T/C	26 (92.9%)	41 (91.1%)	1.00	0.89	104.2	115.6
	T/T	2 (7.1%)	4 (8.9%)	1.13 (0.18-7.16)			
Overdominant	C/C-T/T	14 (50%)	21 (46.7%)	1.00	0.78	104.1	115.6
	T/C	14 (50%)	24 (53.3%)	1.15 (0.42-3.14)			
Log-additive	---	---	---	1.14 (0.52-2.54)	0.74	104.1	115.5



SNP: rs1544410..VDR.Bsm1.

Percentage of typed samples: 73/73 (100%)

rs1544410..VDR.Bsm1. allele frequencies (n=73)

	All subjects		igra=NEGATIVE IGRA HOUSEHOLD CONTACTS		igra=POSITIVE IGRA HOUSEHOLD CONTACTS	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G	124	0.85	47	0.84	77	0.86
A	22	0.15	9	0.16	13	0.14

rs1544410..VDR.Bsm1. genotype frequencies (n=73)

	All subjects		igra=NEGATIVE IGRA HOUSEHOLD CONTACTS		igra=POSITIVE IGRA HOUSEHOLD CONTACTS	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G/A	22	0.3	9	0.32	13	0.29
G/G	51	0.7	19	0.68	32	0.71

rs1544410..VDR.Bsm1. exact test for Hardy-Weinberg equilibrium (n=73)

	N11	N12	N22	N1	N2	P-value
All subjects	51	22	0	124	22	0.35
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	19	9	0	47	9	1
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	32	13	0	77	13	0.57

rs1544410..VDR.Bsm1. association with response igra (n=73, adjusted by age+sex+smoker)

Model	Genotype	igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	igra=POSITIVE IGRA HOUSEHOLD CONTACTS	OR (95% CI)	P-value	AIC	BIC
---	G/G	19 (67.9%)	32 (71.1%)	1.00	0.6	103.9	115.4
	G/A	9 (32.1%)	13 (28.9%)	0.75 (0.26-2.18)			

SNP: rs7975232..VDR.Apa1.

Percentage of typed samples: 73/73 (100%)

rs7975232..VDR.Apa1. allele frequencies (n=73)

	All subjects		igra=NEGATIVE IGRA HOUSEHOLD CONTACTS		igra=POSITIVE IGRA HOUSEHOLD CONTACTS	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G	80	0.55	35	0.62	45	0.5
T	66	0.45	21	0.38	45	0.5

rs7975232..VDR.Apa1. genotype frequencies (n=73)

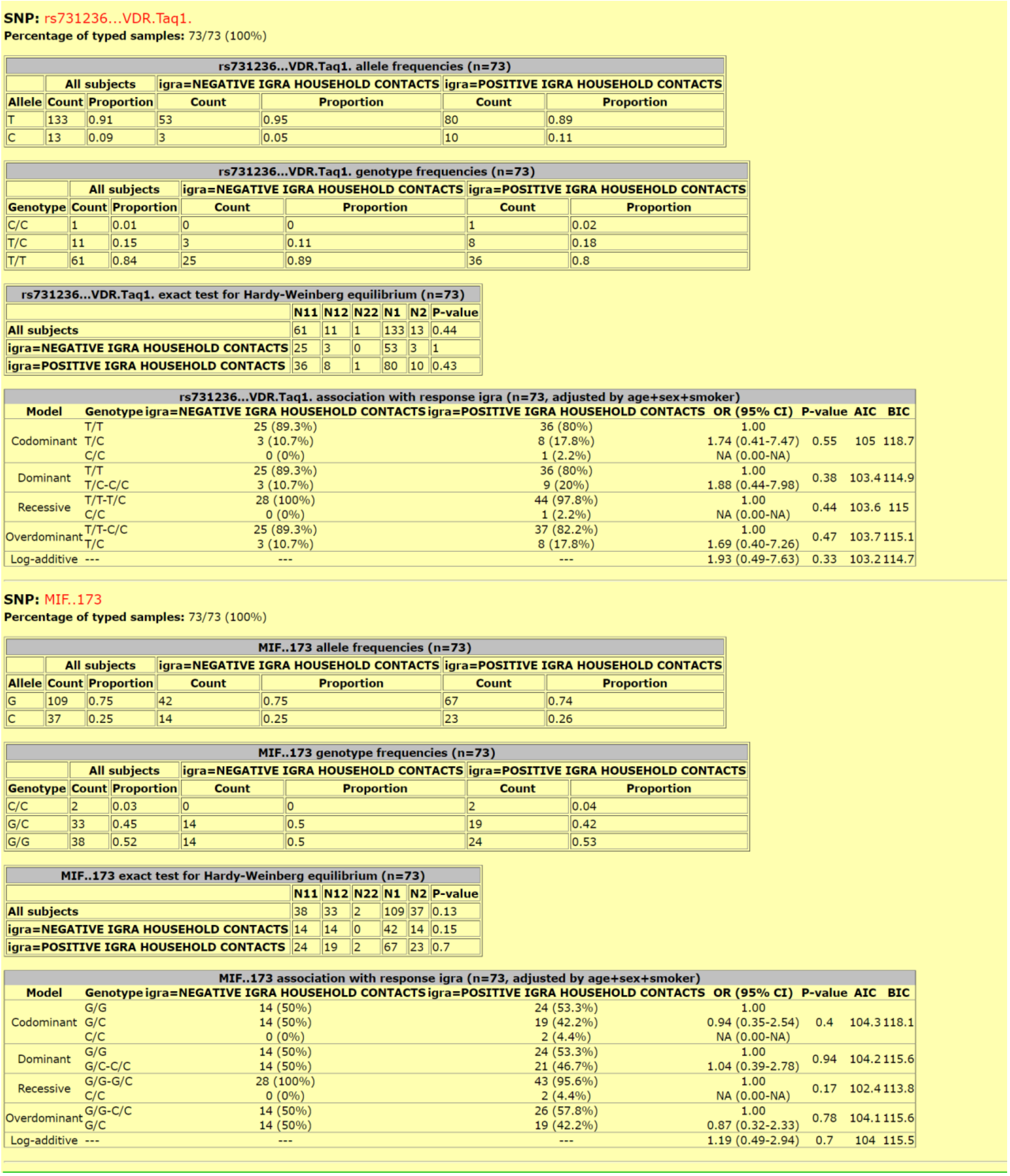
	All subjects		igra=NEGATIVE IGRA HOUSEHOLD CONTACTS		igra=POSITIVE IGRA HOUSEHOLD CONTACTS	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G/G	21	0.29	10	0.36	11	0.24
G/T	38	0.52	15	0.54	23	0.51
T/T	14	0.19	3	0.11	11	0.24

rs7975232..VDR.Apa1. exact test for Hardy-Weinberg equilibrium (n=73)

	N11	N12	N22	N1	N2	P-value
All subjects	21	38	14	80	66	0.81
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	10	15	3	35	21	0.69
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	11	23	11	45	45	1

rs7975232..VDR.Apa1. association with response igra (n=73, adjusted by age+sex+smoker)

Model	Genotype	igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	igra=POSITIVE IGRA HOUSEHOLD CONTACTS	OR (95% CI)	P-value	AIC	BIC
Codominant	G/G	10 (35.7%)	11 (24.4%)	1.00	0.28	103.6	117.4
	G/T	15 (53.6%)	23 (51.1%)	1.56 (0.50-4.93)			
	T/T	3 (10.7%)	11 (24.4%)	3.43 (0.71-16.55)			
Dominant	G/G	10 (35.7%)	11 (24.4%)	1.00	0.24	102.8	114.2
	G/T-T/T	18 (64.3%)	34 (75.6%)	1.93 (0.65-5.75)			
Recessive	G/G-G/T	25 (89.3%)	34 (75.6%)	1.00	0.16	102.2	113.7
	T/T	3 (10.7%)	11 (24.4%)	2.60 (0.64-10.58)			
Overdominant	G/G-T/T	13 (46.4%)	22 (48.9%)	1.00	0.98	104.2	115.6
	G/T	15 (53.6%)	23 (51.1%)	0.99 (0.36-2.70)			
Log-additive	---	---	---	1.80 (0.85-3.81)	0.12	101.7	113.2



SNP: rs731236...VDR.Taq1.

Percentage of typed samples: 73/73 (100%)

rs731236...VDR.Taq1. allele frequencies (n=73)

	All subjects		**igra=NEGATIVE IGRA HOUSEHOLD CONTACTS**		**igra=POSITIVE IGRA HOUSEHOLD CONTACTS**	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
T	133	0.91	53	0.95	80	0.89
C	13	0.09	3	0.05	10	0.11

rs731236...VDR.Taq1. genotype frequencies (n=73)

	All subjects		**igra=NEGATIVE IGRA HOUSEHOLD CONTACTS**		**igra=POSITIVE IGRA HOUSEHOLD CONTACTS**	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
C/C	1	0.01	0	0	1	0.02
T/C	11	0.15	3	0.11	8	0.18
T/T	61	0.84	25	0.89	36	0.8

rs731236...VDR.Taq1. exact test for Hardy-Weinberg equilibrium (n=73)

	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	61	11	1	133	13	0.44
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	25	3	0	53	3	1
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	36	8	1	80	10	0.43

rs731236...VDR.Taq1. association with response igra (n=73, adjusted by age+sex+smoker)

Model	**Genotype**	**igra=NEGATIVE IGRA HOUSEHOLD CONTACTS**	**igra=POSITIVE IGRA HOUSEHOLD CONTACTS**	**OR (95% CI)**	**P-value**	**AIC**	**BIC**
Codominant	T/T	25 (89.3%)	36 (80%)	1.00	0.55	105	118.7
	T/C	3 (10.7%)	8 (17.8%)	1.74 (0.41-7.47)			
	C/C	0 (0%)	1 (2.2%)	NA (0.00-NA)			
Dominant	T/T	25 (89.3%)	36 (80%)	1.00	0.38	103.4	114.9
	T/C-C/C	3 (10.7%)	9 (20%)	1.88 (0.44-7.98)			
Recessive	T/T-T/C	28 (100%)	44 (97.8%)	1.00	0.44	103.6	115
	C/C	0 (0%)	1 (2.2%)	NA (0.00-NA)			
Overdominant	T/T-C/C	25 (89.3%)	37 (82.2%)	1.00	0.47	103.7	115.1
	T/C	3 (10.7%)	8 (17.8%)	1.69 (0.40-7.26)			
Log-additive	---	---	---	1.93 (0.49-7.63)	0.33	103.2	114.7

SNP: MIF..173

Percentage of typed samples: 73/73 (100%)

MIF..173 allele frequencies (n=73)

	All subjects		**igra=NEGATIVE IGRA HOUSEHOLD CONTACTS**		**igra=POSITIVE IGRA HOUSEHOLD CONTACTS**	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G	109	0.75	42	0.75	67	0.74
C	37	0.25	14	0.25	23	0.26

MIF..173 genotype frequencies (n=73)

	All subjects		**igra=NEGATIVE IGRA HOUSEHOLD CONTACTS**		**igra=POSITIVE IGRA HOUSEHOLD CONTACTS**	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
C/C	2	0.03	0	0	2	0.04
G/C	33	0.45	14	0.5	19	0.42
G/G	38	0.52	14	0.5	24	0.53

MIF..173 exact test for Hardy-Weinberg equilibrium (n=73)

	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	38	33	2	109	37	0.13
igra=NEGATIVE IGRA HOUSEHOLD CONTACTS	14	14	0	42	14	0.15
igra=POSITIVE IGRA HOUSEHOLD CONTACTS	24	19	2	67	23	0.7

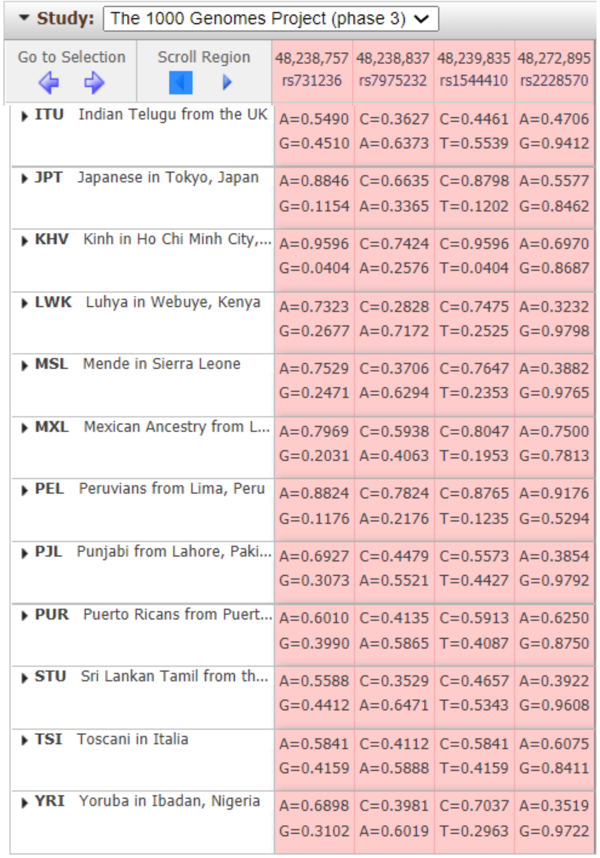
MIF..173 association with response igra (n=73, adjusted by age+sex+smoker)

Model	**Genotype**	**igra=NEGATIVE IGRA HOUSEHOLD CONTACTS**	**igra=POSITIVE IGRA HOUSEHOLD CONTACTS**	**OR (95% CI)**	**P-value**	**AIC**	**BIC**
Codominant	G/G	14 (50%)	24 (53.3%)	1.00	0.4	104.3	118.1
	G/C	14 (50%)	19 (42.2%)	0.94 (0.35-2.54)			
	C/C	0 (0%)	2 (4.4%)	NA (0.00-NA)			
Dominant	G/G	14 (50%)	24 (53.3%)	1.00	0.94	104.2	115.6
	G/C-C/C	14 (50%)	21 (46.7%)	1.04 (0.39-2.78)			
Recessive	G/G-G/C	28 (100%)	43 (95.6%)	1.00	0.17	102.4	113.8
	C/C	0 (0%)	2 (4.4%)	NA (0.00-NA)			
Overdominant	G/G-C/C	14 (50%)	26 (57.8%)	1.00	0.78	104.1	115.6
	G/C	14 (50%)	19 (42.2%)	0.87 (0.32-2.33)			
Log-additive	---	---	---	1.19 (0.49-2.94)	0.7	104	115.5

Perbandingan proporsi alel SNP *VDR* dan *MIF* pada studi ini dengan populasi lain

Study: The 1000 Genomes Project (phase 3)

	48,238,757 rs731236	48,238,837 rs7975232	48,239,835 rs1544410	48,272,895 rs2228570
Populations / Samples	A=0.7234 G=0.2766	C=0.4846 A=0.5154	C=0.7041 T=0.2959	A=0.3285 G=0.6715
ACB African Carribbeans in Ba...	A=0.6510 G=0.3490	C=0.3281 A=0.6719	C=0.6875 T=0.3125	A=0.1771 G=0.8229
ASW Americans of African An...	A=0.7541 G=0.2459	C=0.3689 A=0.6311	C=0.7295 T=0.2705	A=0.1967 G=0.8033
BEB Bengali from Bangladesh	A=0.6802 G=0.3198	C=0.4012 A=0.5988	C=0.5407 T=0.4593	A=0.3605 G=0.6395
CDX Chinese Dai in Xishuang...	A=0.9247 G=0.0753	C=0.6559 A=0.3441	C=0.9409 T=0.0591	A=0.5215 G=0.4785
CEU Utah Residents (CEPH) w...	A=0.5303 G=0.4697	C=0.4040 A=0.5960	C=0.5303 T=0.4697	A=0.4293 G=0.5707
CHB Han Chinese in Bejing, C...	A=0.9612 G=0.0388	C=0.7184 A=0.2816	C=0.9563 T=0.0437	A=0.4223 G=0.5777
CHS Southern Han Chinese	A=0.9333 G=0.0667	C=0.7619 A=0.2381	C=0.9429 T=0.0571	A=0.3857 G=0.6143
CLM Colombians from Medelli...	A=0.7447 G=0.2553	C=0.4947 A=0.5053	C=0.7500 T=0.2500	A=0.4096 G=0.5904
ESN Esan in Nigeria	A=0.7071 G=0.2929	C=0.4242 A=0.5758	C=0.6869 T=0.3131	A=0.1919 G=0.8081
FIN Finnish in Finland	A=0.6616 G=0.3384	C=0.4545 A=0.5455	C=0.6616 T=0.3384	A=0.3636 G=0.6364
GBR British in England and Sc...	A=0.6648 G=0.3352	C=0.5385 A=0.4615	C=0.6538 T=0.3462	A=0.3901 G=0.6099
GIH Gujarati Indian from Hou...	A=0.6845 G=0.3155	C=0.4854 A=0.5146	C=0.5728 T=0.4272	A=0.2913 G=0.7087
GWD Gambian in Western Di...	A=0.7345 G=0.2655	C=0.3451 A=0.6549	C=0.7788 T=0.2212	A=0.1947 G=0.8053
IBS Iberian Population in Spain	A=0.5701 G=0.4299	C=0.4299 A=0.5701	C=0.5607 T=0.4393	A=0.3271 G=0.6729

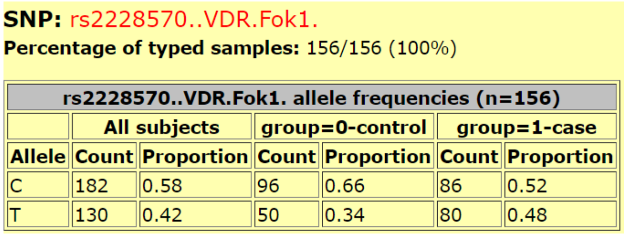


Study: The 1000 Genomes Project (phase 3)

	48,238,757 rs731236	48,238,837 rs7975232	48,239,835 rs1544410	48,272,895 rs2228570
ITU Indian Telugu from the UK	A=0.5490 G=0.4510	C=0.3627 A=0.6373	C=0.4461 T=0.5539	A=0.4706 G=0.9412
JPT Japanese in Tokyo, Japan	A=0.8846 G=0.1154	C=0.6635 A=0.3365	C=0.8798 T=0.1202	A=0.5577 G=0.8462
KHV Kinh in Ho Chi Minh City,...	A=0.9596 G=0.0404	C=0.7424 A=0.2576	C=0.9596 T=0.0404	A=0.6970 G=0.8687
LWK Luhya in Webuye, Kenya	A=0.7323 G=0.2677	C=0.2828 A=0.7172	C=0.7475 T=0.2525	A=0.3232 G=0.9798
MSL Mende in Sierra Leone	A=0.7529 G=0.2471	C=0.3706 A=0.6294	C=0.7647 T=0.2353	A=0.3882 G=0.9765
MXL Mexican Ancestry from L...	A=0.7969 G=0.2031	C=0.5938 A=0.4063	C=0.8047 T=0.1953	A=0.7500 G=0.7813
PEL Peruvians from Lima, Peru	A=0.8824 G=0.1176	C=0.7824 A=0.2176	C=0.8765 T=0.1235	A=0.9176 G=0.5294
PJL Punjabi from Lahore, Paki...	A=0.6927 G=0.3073	C=0.4479 A=0.5521	C=0.5573 T=0.4427	A=0.3854 G=0.9792
PUR Puerto Ricans from Puert...	A=0.6010 G=0.3990	C=0.4135 A=0.5865	C=0.5913 T=0.4087	A=0.6250 G=0.8750
STU Sri Lankan Tamil from th...	A=0.5588 G=0.4412	C=0.3529 A=0.6471	C=0.4657 T=0.5343	A=0.3922 G=0.9608
TSI Toscani in Italia	A=0.5841 G=0.4159	C=0.4112 A=0.5888	C=0.5841 T=0.4159	A=0.6075 G=0.8411
YRI Yoruba in Ibadan, Nigeria	A=0.6898 G=0.3102	C=0.3981 A=0.6019	C=0.7037 T=0.2963	A=0.3519 G=0.9722

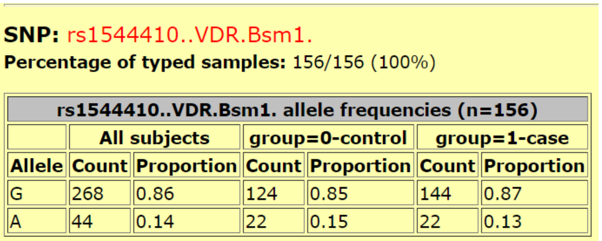
(National Center for Biotechnology Information, 2021)

Pada penelitian ini:



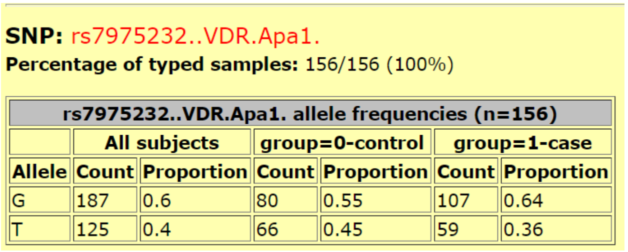
SNP: rs2228570..VDR.Fok1.
Percentage of typed samples: 156/156 (100%)

rs2228570..VDR.Fok1. allele frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Allele	Count	Proportion	Count	Proportion	Count	Proportion
C	182	0.58	96	0.66	86	0.52
T	130	0.42	50	0.34	80	0.48



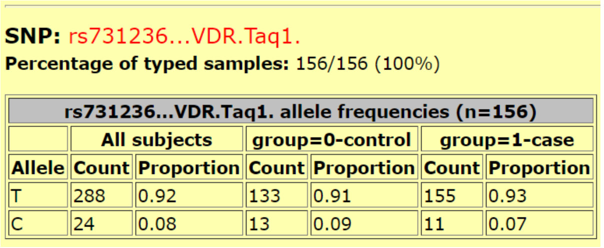
SNP: rs1544410..VDR.Bsm1.
Percentage of typed samples: 156/156 (100%)

rs1544410..VDR.Bsm1. allele frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Allele	Count	Proportion	Count	Proportion	Count	Proportion
G	268	0.86	124	0.85	144	0.87
A	44	0.14	22	0.15	22	0.13



SNP: rs7975232..VDR.Apa1.
Percentage of typed samples: 156/156 (100%)

rs7975232..VDR.Apa1. allele frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Allele	Count	Proportion	Count	Proportion	Count	Proportion
G	187	0.6	80	0.55	107	0.64
T	125	0.4	66	0.45	59	0.36



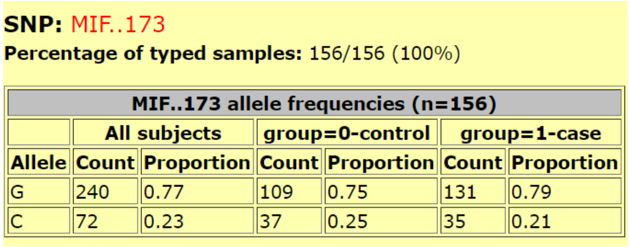
SNP: rs731236...VDR.Taq1.
Percentage of typed samples: 156/156 (100%)

rs731236...VDR.Taq1. allele frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Allele	Count	Proportion	Count	Proportion	Count	Proportion
T	288	0.92	133	0.91	155	0.93
C	24	0.08	13	0.09	11	0.07

MIF -173 rs755622

Populations / Samples	24,236,392 rs755622
	G=0.9209 C=0.4545
ACB African Carribbeans in Ba...	G=0.8333 C=0.6250
ASW Americans of African An...	G=0.8852 C=0.6721
BEB Bengali from Bangladesh	G=0.9651 C=0.5116
CDX Chinese Dai in Xishuang...	G=0.9785 C=0.3226
CEU Utah Residents (CEPH) w...	G=0.9798 C=0.3232
CHB Han Chinese in Bejing, C...	G=0.9709 C=0.3398
CHS Southern Han Chinese	G=0.9429 C=0.4000
CLM Colombians from Medelli...	G=0.9362 C=0.4362
ESN Esan in Nigeria	G=0.8788 C=0.6061
FIN Finnish in Finland	G=0.9798 C=0.3535
GBR British in England and Sc...	G=0.9670 C=0.3626
GIH Gujarati Indian from Hou...	G=0.9126 C=0.4272
GWD Gambian in Western Di...	G=0.8230 C=0.7257
IBS Iberian Population in Spain	G=0.9533 C=0.3364

Pada penelitian ini:



SNP: MIF..173
Percentage of typed samples: 156/156 (100%)

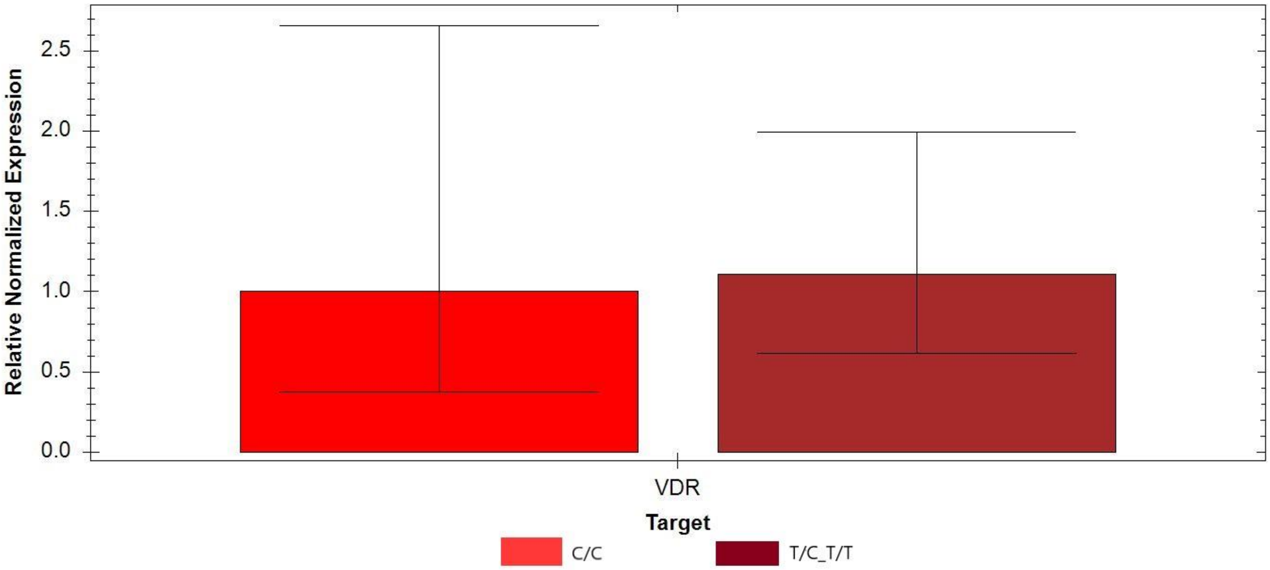
MIF..173 allele frequencies (n=156)						
	All subjects		group=0-control		group=1-case	
Allele	Count	Proportion	Count	Proportion	Count	Proportion
G	240	0.77	109	0.75	131	0.79
C	72	0.23	37	0.25	35	0.21

(National Center for Biotechnology Information, 2021)

Perbedaan Ekspresi Gen *VDR* sesuai genotipe *VDR*

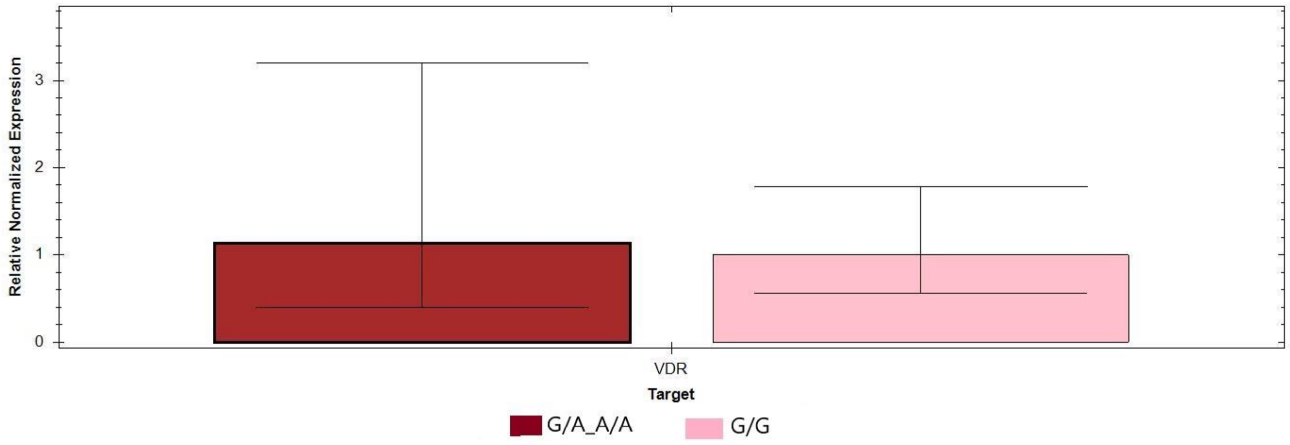
VDR 228570

Target	Biological Group	Control	Expression	Expression 95% CI Low	Expression 95% CI High	P-Value
GAPDH	C/C	C				
GAPDH	T/C_T/T					
VDR	C/C	C	1.00000	0.37658	2.65548	
VDR	T/C_T/T		1.10767	0.61455	1.99649	0.852312



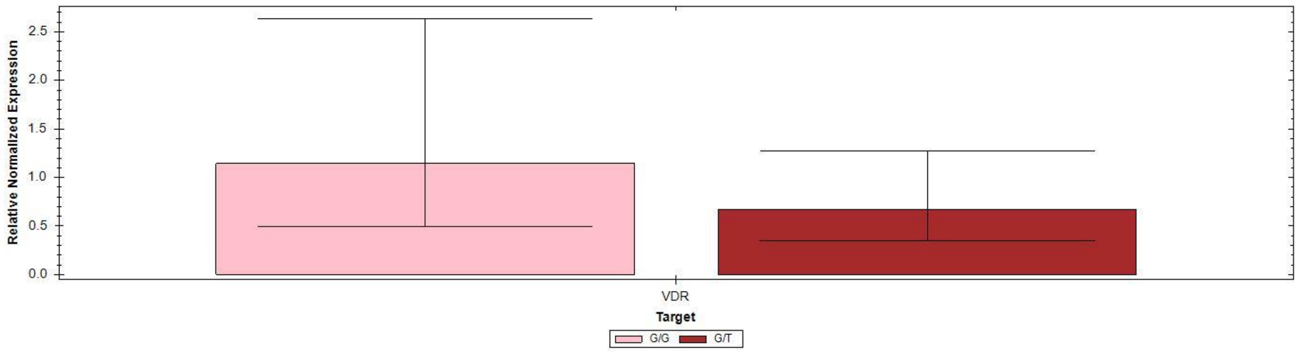
VDR rs1544410

Target	Biological Group	Control	Expression	Expression 95% CI Low	Expression 95% CI High	P-Value
GAPDH	G/A_A/A					
GAPDH	G/G	C				
VDR	G/A_A/A		1.13172	0.39958	3.20533	0.829547
VDR	G/G	C	1.00000	0.56069	1.78351	



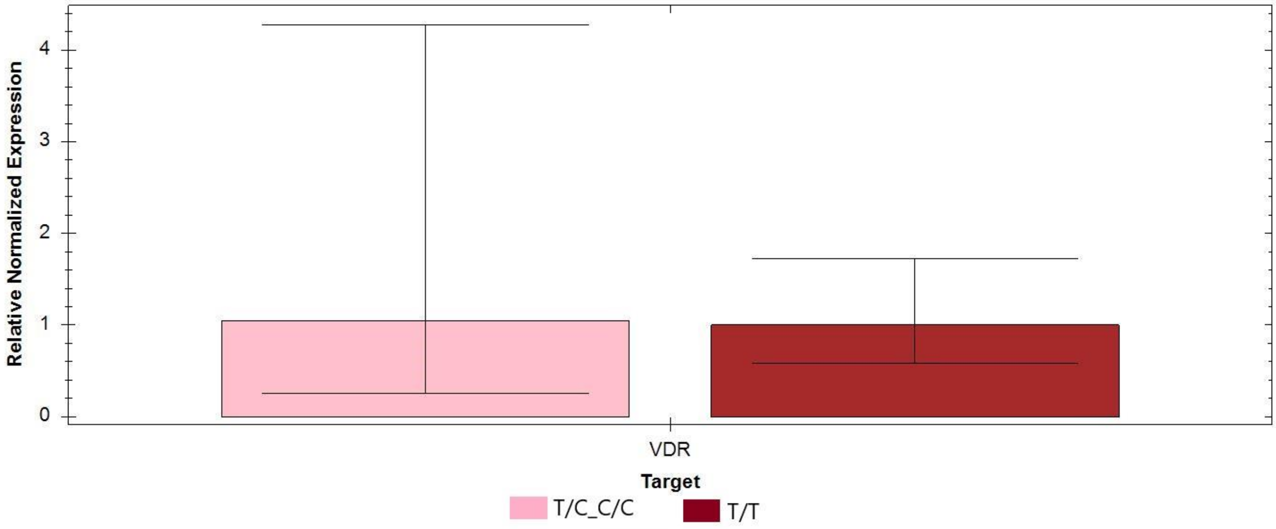
VDR rs7975232

Target	Biological Group	Control	Expression	Expression 95% CI Low	Expression 95% CI High	P-Value
GAPDH	G/G					
GAPDH	G/T_T/T					
VDR	G/G		1.14342	0.49686	2.63136	
VDR	G/T_T/T		0.66885	0.35241	1.26942	



VDR rs731236

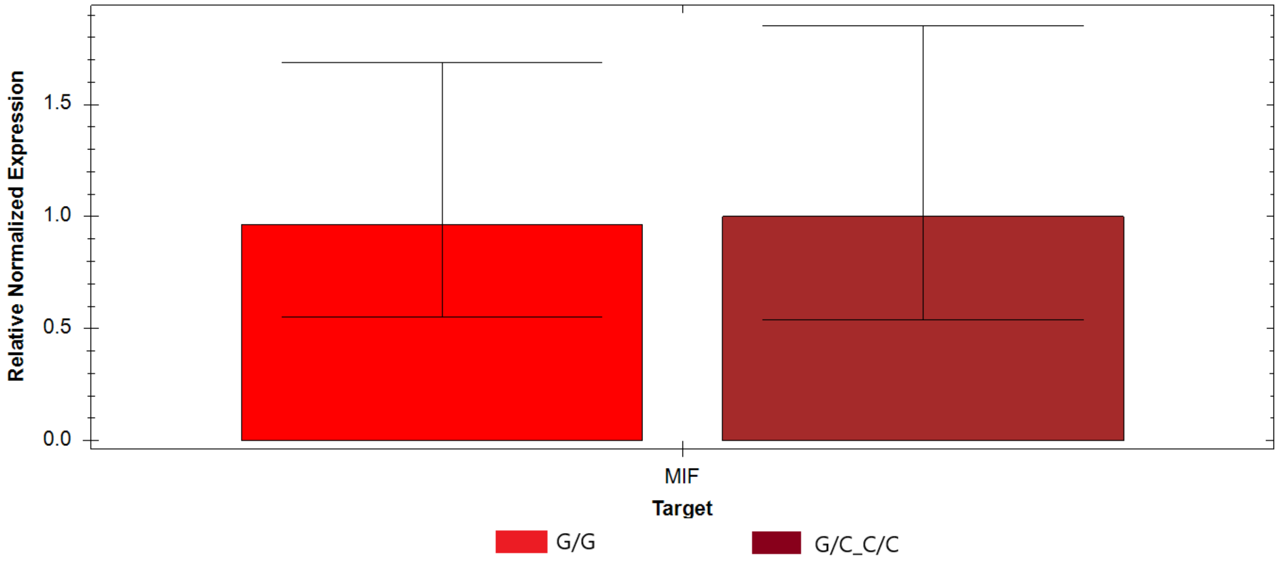
Target	Biological Group	Control	Expression	Expression 95% CI Low	Expression 95% CI High	P-Value
GAPDH	T/C_T/T					
GAPDH	T/T	C				
VDR	T/C_T/T		1.05086	0.25826	4.27598	0.945005
VDR	T/T	C	1.00000	0.58075	1.72190	



Perbedaan Ekspresi Gen *MIF* berdasarkan genotipe *MIF*

MIF -173 G/C rs755622

Target	Biological Group	Control	Expression	Expression 95% CI Low	Expression 95% CI High	P-Value
GAPDH	G/C_C/C	C				
GAPDH	G/G					
MIF	G/C_C/C	C	1.03529	0.54006	1.85163	0.935779
MIF	G/G		1.00000	0.55308	1.68689	


Relative Normalized Expression
0.0
0.5
1.0
1.5
MIF
Target
G/G
G/C_C/C

Analisis hubungan genotipe *VDR* dengan ekspresi gen *VDR*

Parameter Estimates

			95% Wald Confidence Interval		Hypothesis Test				95% Wald Confidence Interval for Exp(B)	
Parameter	B	Std. Error	Lower	Upper	Wald Chi-Square	df	Sig.	Exp(B)	Lower	Upper
(Intercept)	-1.317	.2325	-1.772	-.861	32.070	1	.000	.268	.170	.423
[C/C=.00]	.077	.2377	-.389	.543	.104	1	.747	1.080	.678	1.720
[C/C=1.00]	0[a]	.	.	.	.	.	.	1	.	.
[G/G=.00]	.118	.2656	-.402	.639	.198	1	.656	1.126	.669	1.895
[G/G=1.00]	0[a]	.	.	.	.	.	.	1	.	.
[VDR_A_GG=.00]	-.323	.2398	-.793	.147	1.818	1	.178	.724	.452	1.158
[VDR_A_GG=1.00]	0[a]	.	.	.	.	.	.	1	.	.
[VDR_T_TT=.00]	.084	.3304	-.563	.732	.065	1	.799	1.088	.569	2.079
[VDR_T_TT=1.00]	0[a]	.	.	.	.	.	.	1	.	.
(Scale)	1.861[b]	.2107	1.491	2.323						

Dependent Variable: EXPVDR1L

Model: (Intercept), C/C, G/G, VDR_A_GG, VDR_T_TT

a. Set to zero because this parameter is redundant.

b. Maximum likelihood estimate.

Analisis hubungan genotipe *MIF* dengan ekspresi gen *MIF*

Parameter Estimates

			95% Wald Confidence Interval		Hypothesis Test				95% Wald Confidence Interval for Exp(B)	
Parameter	B	Std. Error	Lower	Upper	Wald Chi-Square	df	Sig.	Exp(B)	Lower	Upper
(Intercept)	.106	.1301	-.149	.361	.668	1	.414	1.112	.862	1.435
[MIF_GG=.00]	.011	.1956	-.373	.394	.003	1	.957	1.011	.689	1.483
[MIF_GG=1.00]	0[a]	.	.	.	.	.	.	1	.	.
(Scale)	1.473[b]	.1668	1.180	1.839						

Dependent Variable: Relative MIF Gene Expression

Model: (Intercept), MIF_GG

a. Set to zero because this parameter is redundant.

b. Maximum likelihood estimate.

Analisis multivariat

Parameter Estimates

			95% Wald Confidence Interval		Hypothesis Test				95% Wald Confidence Interval for Exp(B)	
Parameter	B	Std. Error	Lower	Upper	Wald Chi-Square	df	Sig.	Exp(B)	Lower	Upper
(Intercept)	5.902	1.6642	2.640	9.164	12.577	1	.000	365.693	14.014	9542.841
[GENDER=1.00]	.132	.6015	-1.047	1.311	.048	1	.826	1.141	.351	3.711

[GENDER=2.00]	0[a]	.	.	.	.	.	.	1	.	.
[C/C=.00]	1.262	.4764	.328	2.196	7.014	1	.008	3.532	1.388	8.985
[C/C=1.00]	0[a]	.	.	.	.	.	.	1	.	.
[G/G=.00]	-.364	.5136	-1.370	.643	.501	1	.479	.695	.254	1.902
[G/G=1.00]	0[a]	.	.	.	.	.	.	1	.	.
[VDR_A_GG=.00]	-1.189	.5144	-2.198	-.181	5.344	1	.021	.304	.111	.834
[VDR_A_GG=1.00]	0[a]	.	.	.	.	.	.	1	.	.
[VDR_T_TT=.00]	-.268	.6279	-1.499	.963	.182	1	.670	.765	.223	2.619
[VDR_T_TT=1.00]	0[a]	.	.	.	.	.	.	1	.	.
[MIF_GG=.00]	-.033	.4509	-.917	.851	.005	1	.941	.967	.400	2.341
[MIF_GG=1.00]	0[a]	.	.	.	.	.	.	1	.	.
[SMOKER=.00]	-1.046	.5878	-2.198	.106	3.166	1	.075	.351	.111	1.112
[SMOKER=1.00]	0[a]	.	.	.	.	.	.	1	.	.
AGE	.022	.0163	-.010	.054	1.754	1	.185	1.022	.990	1.055
BMI	-.307	.0615	-.427	-.186	24.887	1	.000	.736	.652	.830
EXPVDR1L	-.395	.1763	-.741	-.050	5.032	1	.025	.673	.477	.951
Relative MIF Gene Expression	.039	.2044	-.361	.440	.037	1	.848	1.040	.697	1.553
(Scale)	1[b]									

Dependent Variable: TB_NONTB

Model: (Intercept), GENDER, C/C, G/G, VDR_A_GG, VDR_T_TT, MIF_GG, SMOKER, AGE, BMI, EXPVDR1L, Relative MIF Gene Expression

a. Set to zero because this parameter is redundant.

b. Fixed at the displayed value.

Variabel	**OR^a (95% CI)**	**Nilai p^a**
Umur	1.02 (0.99-1.06)	0.19
Jenis kelamin Laki-laki	1.14 (0.35-3.71)	0.83
Indeks massa tubuh	**0.74 (0.65-0.83)**	**<0.0001***
Bukan Perokok	0.35 (0.11-1.11)	0.08
rs2228570 (VDR FokI) T/C-T/T (CC ref.)	**3.53 (1.39-8.99)**	**0.008***
rs1544410 (VDR BsmI) G/A-AA (GG ref.)	0.7 (0.25-1.9)	0.48
rs7975232 (VDR ApaI) T/G-T/T (GG ref.)	**0.3 (0.11-0.83)**	**0.02***
rs731236 (VDR TaqI) T/C-C/C (TT ref.)	0.77 (0.22-2.62)	0.67
rs755622 (MIF -173 G/C) G/C-C/C (GG ref.)	0.97 (0.4-2.34)	0.94
Ekspresi Gen VDR (Log)	**0.67 (0.48-0.95)**	**0.03***
Ekspresi Gen MIF (Log)	1.04 (0.7-1.55)	0.85

* Nilai p signifikan

[a] Analisis disesuaikan dengan umur, jenis kelamin, IMT, status perokok/riwayat perokok, polimorfisme rs2228570 (VDR FokI), rs1544410 (VDR BsmI), rs7975232 (VDR ApaI), rs731236 (VDR TaqI), rs755622 (MIF -173 G/C), Ekspresi Gen VDR (Log), dan Ekspresi Gen MIF (Log) dengan menggunakan kontak serumah sebagai referensi.

Parameter Estimates

			95% Wald Confidence Interval		Hypothesis Test			Exp(B)	95% Wald Confidence Interval for Exp(B)	
Parameter	B	Std. Error	Lower	Upper	Wald Chi-Square	df	Sig.		Lower	Upper
(Intercept)	5.223	2.5587	.208	10.238	4.167	1	.041	185.548	1.232	27952.758
[GENDER=1.00]	-.397	.8877	-2.137	1.343	.200	1	.655	.672	.118	3.830
[GENDER=2.00]	0^a	.	.	.	.	.	.	1	.	.
[C/C=.00]	1.462	.8353	-.175	3.099	3.063	1	.080	4.314	.839	22.175
[C/C=1.00]	0^a	.	.	.	.	.	.	1	.	.
[G/G=.00]	-1.037	.7680	-2.543	.468	1.824	1	.177	.354	.079	1.597
[G/G=1.00]	0^a	.	.	.	.	.	.	1	.	.
[VDR_A_GG=.00]	.833	.8249	-.784	2.450	1.020	1	.312	2.301	.457	11.587
[VDR_A_GG=1.00]	0^a	.	.	.	.	.	.	1	.	.
[VDR_T_TT=.00]	.689	1.0032	-1.278	2.655	.471	1	.492	1.991	.279	14.223
[VDR_T_TT=1.00]	0^a	.	.	.	.	.	.	1	.	.
[MIF_GG=.00]	.094	.6590	-1.198	1.385	.020	1	.887	1.098	.302	3.996
[MIF_GG=1.00]	0^a	.	.	.	.	.	.	1	.	.
[SMOKER=.00]	-1.474	1.0242	-3.481	.534	2.071	1	.150	.229	.031	1.705
[SMOKER=1.00]	0^a	.	.	.	.	.	.	1	.	.
AGE	.007	.0277	-.048	.061	.060	1	.807	1.007	.954	1.063
BMI	-.244	.0821	-.405	-.083	8.844	1	.003	.783	.667	.920
EXPVDR1L	-.267	.2178	-.693	.160	1.498	1	.221	.766	.500	1.174
Relative MIF Gene Expression	.326	.4058	-.469	1.121	.645	1	.422	1.385	.625	3.069
[afb_index_case=1.00]	-1.086	1.0739	-3.191	1.019	1.022	1	.312	.338	.041	2.771
[afb_index_case=2.00]	-1.378	1.1323	-3.598	.841	1.482	1	.223	.252	.027	2.318

[afb_index_case=3.00]	0[a]	.	.	.	.	.	.	1	.	.
[relationshipwithindexcase=1.00]	1.340	.9202	-.464	3.143	2.120	1	.145	3.819	.629	23.182
[relationshipwithindexcase=2.00]	3.058	1.0573	.986	5.130	8.365	1	.004	21.286	2.680	169.070
[relationshipwithindexcase=3.00]	0[a]	.	.	.	.	.	.	1	.	.
(Scale)	1[b]									

Dependent Variable: IGRA

Model: (Intercept), GENDER, C/C, G/G, VDR_A_GG, VDR_T_TT, MIF_GG, SMOKER, AGE, BMI, EXPVDR1L, Relative MIF Gene Expression, afb_index_case, relationshipwithindexcase

a. Set to zero because this parameter is redundant.

b. Fixed at the displayed value.

Variabel	**OR[a] (95% CI)**	**Nilai p[a]**
Umur	1.01 (0.96-1.06)	0.81
Jenis kelamin		
Laki-laki	0.67 (0.12-1.38)	0.66
Perempuan	1	
Indeks massa tubuh	**0.78 (0.67-0.92)**	**0.003***
BTA kasus indeks:		
1+	0.34 (0.04-2.77)	0.31
2+	0.25 (0.03-2.32)	0.22
3+	1	
Hubungan dengan kasus indeks		
Orang tua/anak	3.82 (0.63-23.18)	0.15
Istri	21.29 (2.68-169.07)	0.004
Lainnya	1	
Status perokok		0.15

Bukan Perokok	0.23 (0.03-1.7)	
Perokok	1	
rs2228570 (VDR FokI)		
T/C-T/T	4.31 (0.84-22.18)	0.08
CC	1	
rs1544410 (VDR BsmI)		
G/A-AA	0.35 (0.08-1.6)	0.18
GG	1	
rs7975232 (VDR ApaI)		
G/T-T/T	2.3 (0.46-11.59)	0.31
GG	1	
rs731236 (VDR TaqI)		
T/C-C/C	1.99 (0.28-14.22)	0.49
TT	1	
rs755622 (MIF -173 G/C)		
G/C-C/C	1.1 (0.3-4)	0.89
GG	1	
Ekspresi Gen VDR (Log)	0.77 (0.5-1.17)	0.22
Ekspresi Gen MIF (Log)	1.39 (0.63-3.07)	0.42

* Nilai p signifikan

[a] Analisis disesuaikan dengan umur, jenis kelamin, IMT, status perokok/riwayat perokok, polimorfisme rs2228570 (VDR FokI), rs1544410 (VDR BsmI), rs7975232 (VDR ApaI), rs731236 (VDR TaqI), rs755622 (MIF -173 G/C), Ekspresi Gen VDR (Log) dan Ekspresi Gen MIF (Log) dengan menggunakan kontak serumah IGRA negatif sebagai referensi.