

iScience, Volume 25

Supplemental information

Changes in transcriptomic landscape in human end-stage heart failure with distinct etiology

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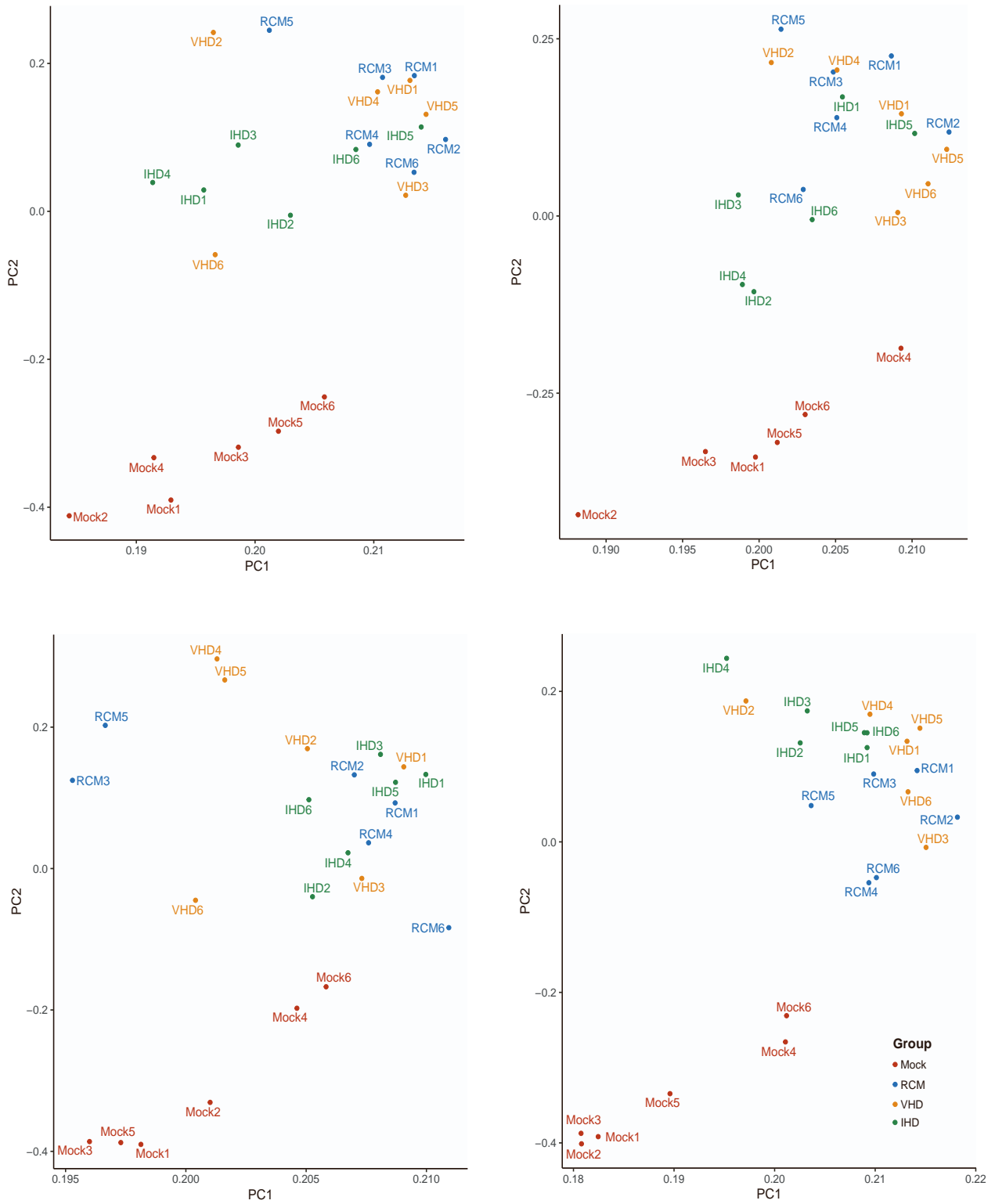


Figure S1. PCA plot of different expressed genes in each sample of mRNA, lncRNA, miRNA and circRNA. (related to Figure 1)

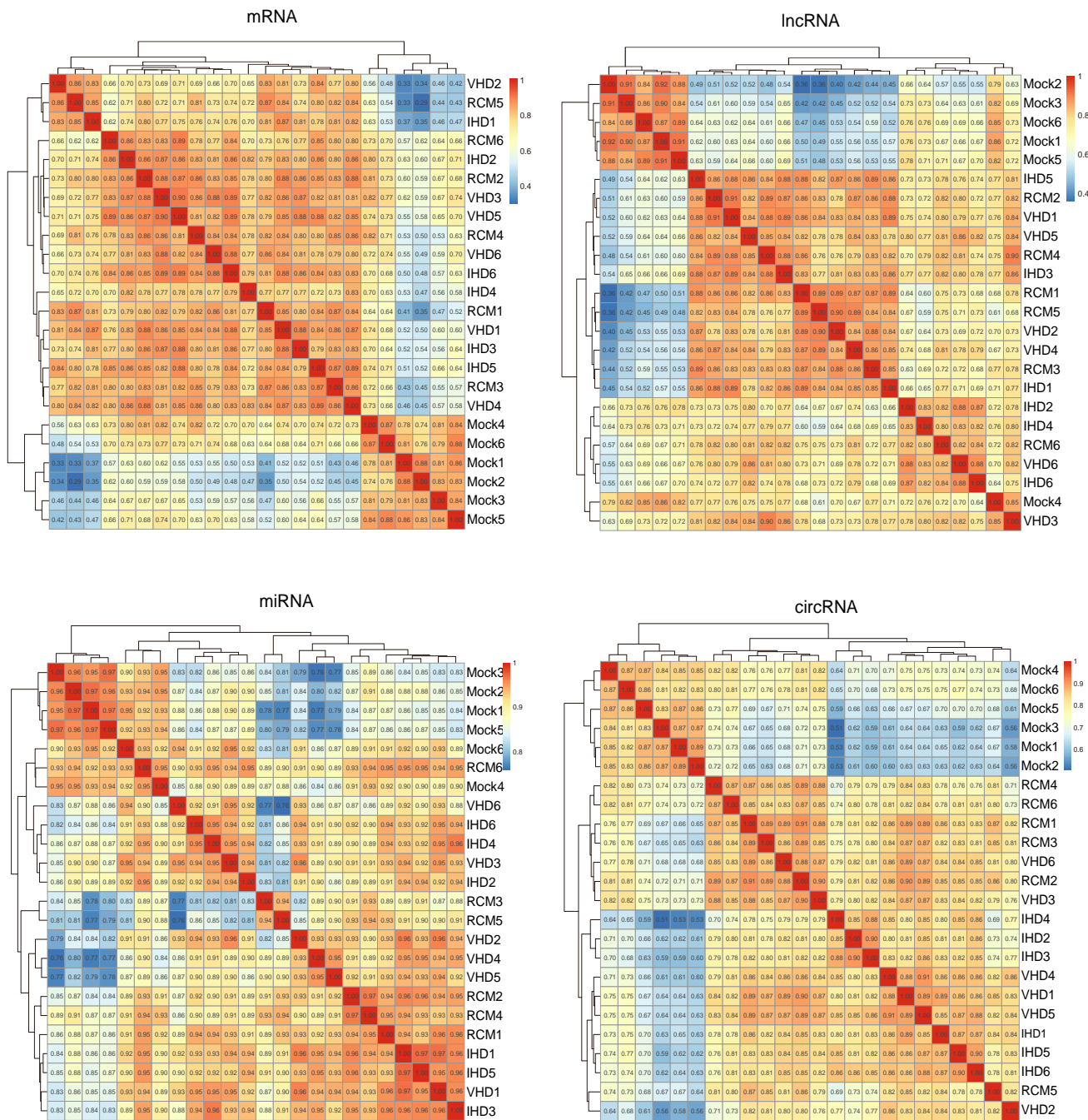


Figure S2. Correlation heatmap of different expressed genes in each sample of mRNA, lncRNA, miRNA and circRNA. (related to Figure 1)

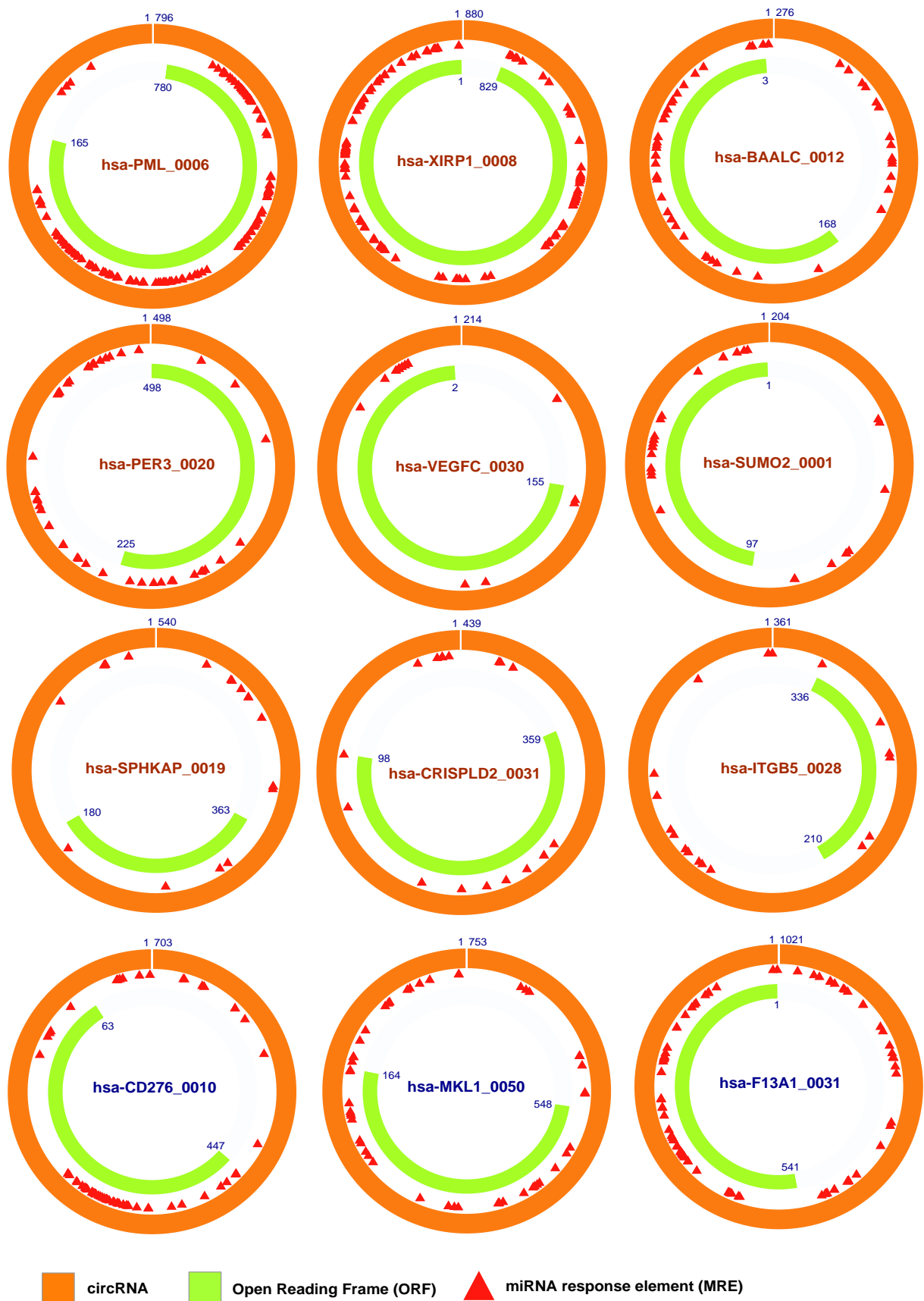


Figure S3. The structure of differentially expressed circRNAs which corresponding mRNA had been reported to be related to HF and more than 100bp in length. (related to Figure 5)

Table S1. Clinical information for non-failing hearts (transplant donor heart failed to implant after heart acquisition), RCM patients, IHD patients and VHD patients.

(related to experimental model and subject details section in STAR Methods)

	Age	Gender	BMI(kg/m ²)	Hypertension	Diabetes mellitus
Control (6)	26.2 (15-41)	5	22.67±2.10	0	0
	15	M	19.2	N	N
	18	M	21.8	N	N
	27	F	22.3	N	N
	41	M	25	N	N
	21	M	23.2	N	N
RCM (6)	18.3 (5-33)	2	22.15±1.30	0	0
	11	F	23.6	N	N
	24	M	20.1	N	N
	31	M	21.9	N	N
	6	M	23.5	N	N
	5	F	22.2	N	N
IHD (6)	46.3 (43-50)	6	22.08±1.64	2	4
	46	M	24.1	N	Y
	43	M	23.6	N	Y
	45	M	21	Y	Y
	47	M	22.9	N	N
	50	M	20.6	N	Y
VHD (6)	51.5 (30-65)	4	19.63±1.07	2	1
	47	M	20.3	Y	Y
	65	F	18.2	N	N
	38	M	20.7	Y	N
	30	M	20.3	N	N
	47	M	19.9	Y	N
	64	F	18.4	N	N
	65	M	20.3	N	Y
	History of cardiac surgery	IABP history	ECMO history	EF	
Control (6)	0	0	0	62.3±5.16	
	N	N	N	55	
	N	N	N	60	
	N	N	N	70	
	N	N	N	60	
	N	N	N	65	
RCM (6)	0	0	0	45.17±4.67	
	N	N	N	45	
	N	N	N	40	
	N	N	N	41	
	N	N	N	47	
	N	N	N	53	
IHD (6)	2	4	0	22.67±4.17	
	N	Y	N	20	
	Y	N	N	30	
	N	Y	N	22	
	N	N	N	20	
	N	Y	N	25	
VHD (6)	3	2	1	23.5±2.81	
	N	N	N	25	
	Y	Y	Y	27	
	Y	N	N	19	
	Y	Y	N	22	
	N	N	N	25	
	N	N	23		

Table S2. Sequencing information for miRNA-seq data of non-failing hearts (transplant donor heart failed to implant after heart acquisition), RCM patients, VHD patients and IHD patients
(related to transcriptome alignment section in STAR Methods)

Samples	Number of Reads	Number of Mapped reads	Mapped reads
Mock1	22034615	19045108	86.43%
Mock2	19948736	16193670	81.18%
Mock3	28705578	25312634	88.18%
Mock4	30878971	27157328	87.95%
Mock5	25969731	21634126	83.31%
Mock6	31678394	27377372	86.42%
RCM1	28781287	24900232	86.52%
RCM2	22449557	18499440	82.40%
RCM3	26348389	23227362	88.15%
RCM4	22472398	19760051	87.93%
RCM5	29789956	25266040	84.81%
RCM6	24485447	22078302	90.17%
VHD1	34025402	29317708	86.16%
VHD2	21483488	14836832	69.06%
VHD3	21664619	17917767	82.71%
VHD4	30324943	24255790	79.99%
VHD5	22664333	19245270	84.91%
VHD6	22325798	11949544	53.52%
IHD1	32629309	27807077	85.22%
IHD2	22241884	20167865	90.68%
IHD3	22086200	19348914	87.61%
IHD4	21937549	18898733	86.15%
IHD5	34694527	29792474	85.87%
IHD6	33125320	16678568	50.35%

Table S3. Sequencing information for circRNA-seq data of non-failing hearts (transplant donor heart failed to implant after heart acquisition), RCM patients, VHD patients and IHD patients
(related to transcriptome alignment section in STAR Methods)

Samples	Number of Reads	Number of Mapped reads	Mapped reads
Mock1	33688277	32237784	95.69%
Mock2	34257276	32833125	95.84%
Mock3	34163678	32974590	96.52%
Mock4	33712840	32719190	97.05%
Mock5	33778752	32756112	96.97%
Mock6	33789568	32778361	97.01%
RCM1	33593879	32245345	95.99%
RCM2	33466800	31988241	95.58%
RCM3	33553619	31917064	95.12%
RCM4	34009300	32689673	96.12%
RCM5	33934393	32706620	96.38%
RCM6	33813330	32176525	95.16%
VHD1	33711130	32553635	96.57%
VHD2	33689098	32255323	95.74%
VHD3	33916971	32541175	95.94%
VHD4	33577447	32088836	95.57%
VHD5	33342018	30292410	90.85%
VHD6	33639065	32550229	96.76%
IHD1	33265997	32021369	96.26%
IHD2	33875323	26744568	78.95%
IHD3	33527941	26081385	77.79%
IHD4	33861834	27489037	81.18%
IHD5	33796619	32165765	95.17%
IHD6	33659366	32101721	95.37%

Table S4. Sequencing information for mRNA-seq and lncRNA-seq data of non-failing hearts (transplant donor heart failed to implant after heart acquisition), RCM patients, VHD patients and IHD patients.
(related to transcriptome alignment section in STAR Methods)

Samples	Number of Reads	Number of Mapped reads	Mapped reads
Mock1	34213302	33726556	98.58%
Mock2	34288309	33842263	98.70%
Mock3	34274587	33847153	98.75%
Mock4	33568630	33096180	98.59%
Mock5	34270846	33547073	97.89%
Mock6	34221366	33827695	98.85%
RCM1	34304628	33840097	98.65%
RCM2	34280206	33825589	98.67%
RCM3	34309161	33881341	98.75%
RCM4	33521084	33019248	98.50%
RCM5	34194212	33738509	98.67%
RCM6	34129361	33692150	98.72%
VHD1	34189092	33761377	98.75%
VHD2	34270948	33847653	98.76%
VHD3	34269738	33874063	98.85%
VHD4	34271558	33778355	98.56%
VHD5	34365197	33886082	98.61%
VHD6	33587743	33109673	98.58%
IHD1	33620328	33013552	98.20%
IHD2	36793227	35626511	96.83%
IHD3	37365938	36314627	97.19%
IHD4	36727353	35259204	96.00%
IHD5	34279453	33718738	98.36%
IHD6	34398150	33860746	98.44%