Colour plate 1: *Bharati* Indian Research Base and *Ivan Papanin*

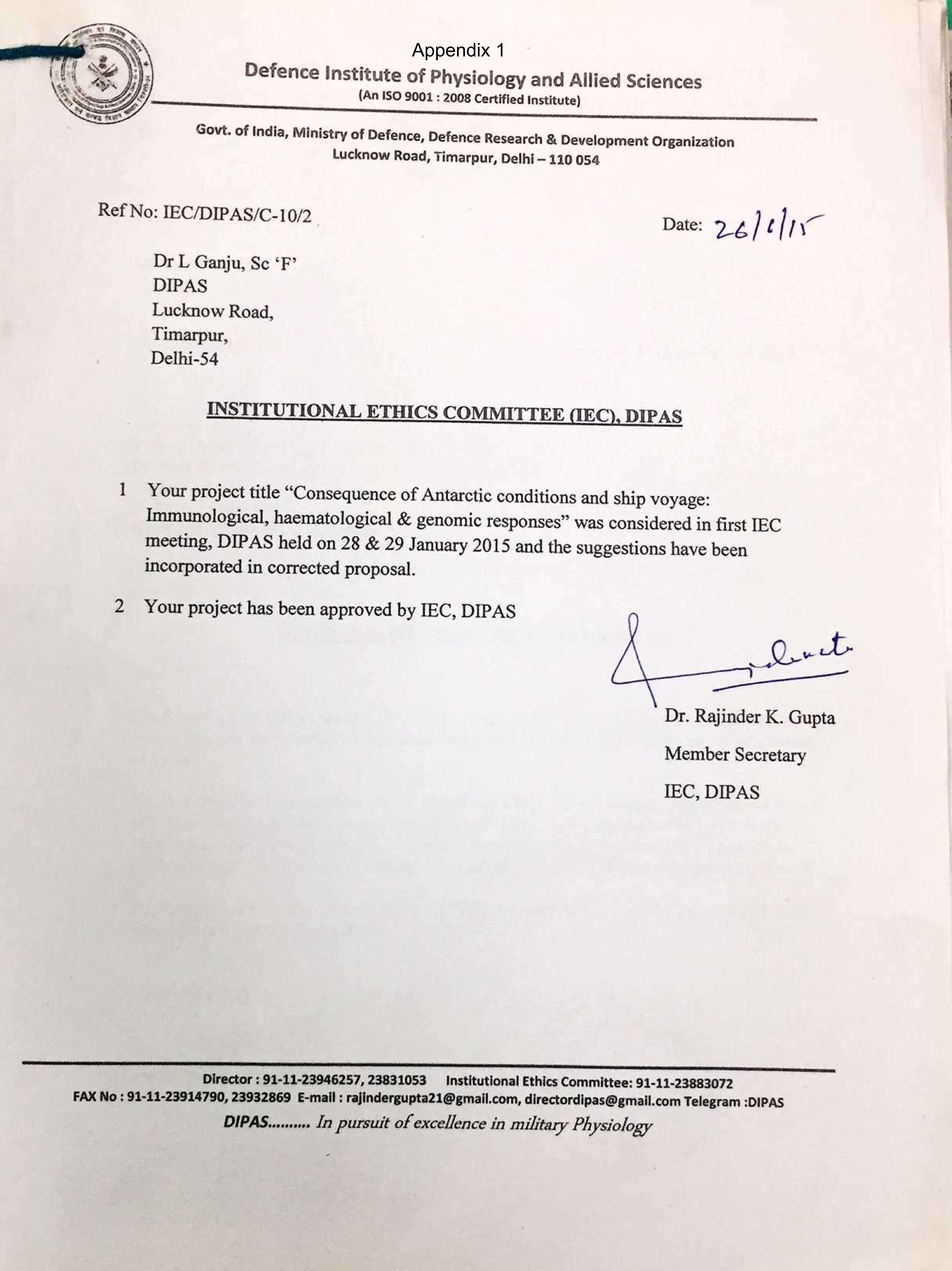
Colour plate 2: Yoga on Ship

Colour plate 3: Yoga on Ice Shelf

COLOUR PLATE 4: Members of the 35th Indian Scientific Expedition to Antarctica

Appendices

Appendix 1



Defence Institute of Physiology and Allied Sciences
(An ISO 9001 : 2008 Certified Institute)

Govt. of India, Ministry of Defence, Defence Research & Development Organization
Lucknow Road, Timarpur, Delhi – 110 054

Ref No: IEC/DIPAS/C-10/2

Date: 26/6/15

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INSTITUTIONAL ETHICS COMMITTEE (IEC), DIPAS

1 Your project title "Consequence of Antarctic conditions and ship voyage: Immunological, haematological & genomic responses" was considered in first IEC meeting, DIPAS held on 28 & 29 January 2015 and the suggestions have been incorporated in corrected proposal.

2 Your project has been approved by IEC, DIPAS

Dr. Rajinder K. Gupta
Member Secretary
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Appendix 2: Designing and Validation of Yoga modules

Yoga module for Antarctica

Even though Yoga practices are known to be beneficial for individuals irrespective of their health and disease states, it is essential to structure specific Yoga practices that are intended to provide most benefits. Yoga practices for Antarctica were designed with the following objectives:

a. To regulate mood and alleviate psychological stress caused due to isolation
b. To enhance physical wellness, overcome fatigue and regulate metabolism
c. To enable better thermoregulation
d. To enhance better sleep and promote interpersonal relationship

The objectives were listed based on the earlier reports on the psychological and physiological changes in Antarctic expeditioners. Practices identified were compiled together to promote calmness of mind and sleep, overcome stress and fatigue, promote overall endurance of the body, regulate digestion, metabolism and enable better pulmonary functions. We present here the data on the designing and validation of the Yoga module that was implemented in the expedition members. The details of the rationale for selecting yoga practices are mentioned in *table 10.2.1.*

Yoga module for sea voyage

A specific Yoga module was proposed to be performed during sea voyage – accounting to the difficulty in performing various asanas. The southern ocean, which has to be crossed by the Indian Voyage team has to undergo extensive pitching, rolling and yawing in the sea currents in the extreme weather making it difficult for most people.

The Yoga practices for Sea voyage were designed with the following objectives:

a. To minimise sea sickness
b. To promote digestion
c. To enhance mood states and alleviate anxiety
d. To promote relaxation

These objectives were listed based on the common problems that arise during sea voyage to Antarctica. Studies on motion sickness suggest diaphragmatic breathing as an effective non-pharmacological intervention[1]. Therefore, more emphasis was given to breathing practices in the Yoga module designed for Voyage.

Procedure adopted for selecting Yoga practices:

The classical and contemporary yoga texts were reviewed to develop the content of the Yoga module. Texts on *Yoga Sutras of Patanjali, Hatha Yoga Pradipika, Shiva Samhitha, Gheranda Samhita, Hatharathnavali, Bhagavad Gita, Upanishads, Yoga Vashishta and Yogic Sūkṣma vyāyāma* were reviewed [1–9]. Practices that might be difficult for the expeditioners to practice and those that are contra-indicated in common disorders such as hypertension and cardiovascular disorders were not included. Similarly, those practices that were difficult to objectively verify and certain *Sūkṣma vyāyāma* (loosening exercise) practices that might not be feasible to practice in group inside the Antarctic stations like *Jangha śakti vikāsaka* [9] were not included. The Yoga module that was designed consisted of postures with slow movements and breath awareness, loosening exercises, *sūryanamaskāra, āsanā, prāṇāyāma,* relaxation and *nādānusandhāna*. The duration of the entire practice is 1 hour.

The Yoga module was sent along with the objectives to forty yoga experts out of whom thirty responded with their scores and comments. The experts rated the usefulness of the module on a scale of 1 to 5 (1 not at all useful, 2 a little useful, 3 moderately useful, 4 very useful, 5 extremely useful). Content Validity Ratio (CVR) for suitability of items was calculated following Lawshe's method. Dichotomous (yes / no) responses were obtained to determine the duration of the individual practice and the entire yoga session.

Statistical Analysis of the response from experts:

Lawshe's CVR ratio was calculated (Lawshe, 1975) for each item in the module. Items with a CVR of 0.6 and above were considered beyond chance agreement ($p < 0.05$, one tailed) for 30 experts. Intra class correlation was calculated for inter-rater reliability (Harris, 1913).

Results

Thirty experts in Yoga therapy and research consented to contribute to the content validation of the Yoga module for extreme Antarctic environmental conditions. These Yoga experts had experience in various traditions of Yoga. The experts age ranged from 32 – 50 years (mean 36.3±4.17 years). The average experience following formal yoga training was 12.3 years ranging between 8 and 26 years. The scores obtained for the individual practices and the calculated CVR are shown in the *table 10.2.2*. One practice *Viparītakaraṇī* with CVR < 0.6 was excluded. The average CVR for the entire Yoga module for Antarctica was 0.89. Good agreement is noted for most practices listed in the yoga module. Intra Class Correlation for the entire module was 0.78.

All the experts opined on the need for practicing *Sūryanamaskāra* (sun salutation), relaxation and breath awareness based practices and *prāṇāyāma*. Most experts agreed on the duration of 1 hour for the Yoga practices. In addition to the practices that were asked to be scored by experts, seven experts made a positive remark to include *vāman dhauti kriya (*voluntarily induced vomiting after drinking saline water in empty stomach*)*. But, later it was not considered because of the space limitations and stringent procedures in treating waste water at Antarctic stations.

For the Yoga module to be practiced during sea voyage, it was considered to restrict asanas and provide emphasis on breathing and relaxation practices. The *Sūkṣma vyāyāma* practices involving neck, wrists, elbow, shoulders were included. *Supta Udarakarshanāsanā* was included to relax the back – which tends to get stiff with the jerky movements of the ship. The scores obtained for the individual Yoga practices of voyage are mentioned in *table 10.2.3*. The average of the entire module was 0.93.

Modifications adopted to the Yoga module for Voyage:

Despite considering the adverse sea conditions while designing Yoga module, the sea currents were much stronger for few of the practices to be performed. Instantaneously, a modified protocol was designed and administered to the voyage members. Due to the turbulent conditions throughout the sea voyage until reaching the destination, maintaining stability while sitting on the floor to practice Yoga was difficult. Hence, members were made to sit on chairs fixed to the floors. All *Sūkṣma vyāyāma* and *prāṇāyāma* practices recommended in the module were practiced while sitting on the chair. Quick Relaxation Technique and *Supta Udarakarshanāsanā* were not feasible to be practiced. Two modified postures (Modified Ardhakati chakrasana and supported lumbar twist) were practiced sitting in chair to facilitate strengthening the back.

Name of the practice	**Benefits**
Sūkṣma vyāyāma	
Grīvā śakti vikāsaka	Strengthens neck and is recommended for diseases concerned with organs in the neck
Aṅguli śakti vikāsaka	Strengthens fingers, wrist, elbows and hands
Maṇibandha śakti vikāsaka	
Kāraprastha śakti vikāsaka	
Kati śakti vikāsaka i & ii	Strengthens the entire back and improves pulmonary capacity. Maintenance of symmetry of the body
Jānu śakti vikāsaka	Recommended for prevention of pain in the knees and fatigue. Good in rheumatic conditions
Piṇḍali śakti vikāsaka	Strengthens lower half of the body and improves endurance
Gulpha – pāda – prastha – pāda – tala – śakti – vikāsaka	Relieves rheumatism of ankles and strengthens toes and the feet
Instant relaxation technique	Promotes relaxation
Sūryanamaskāra	Improves endurance
Quick relaxation technique	Promotes relaxation and increases self-awareness
Yogāsanāḥ	
Ardhakati cakrāsana	Relieve constipation and promote digestion
Trikoṇāsana	Stimulates nervous system, alleviates depression, improves digestion and peristalsis
Parivṛtta trikoṇāsana	Enhances endurance, alleviates depression
Pārśvakoṇāsana	Tones the muscles of back, thighs and arms
Vajrāsana	Prevents hernia, haemorrhoids and balances the digestive system. Might be beneficial in the management of hyperacidity and peptic ulcer
Uṣṭrāsana	Regulates heart, lungs and thyroid gland
Paścimottānāsana	Tones uro-genital system. Useful in the management of diseases involving liver, spleen and pancreas Stops / slows down / reverses ageing and cognitive decline
Vakrāsana	Toning of the nervous system
Arddha matsyendrāsana	Stops / slows down / reverses ageing and cognitive decline and destroys all types of diseases
Bhūnamanāsana	Improves metabolism and destroys all types of diseases
Cakki cālanā	Regulates digestion, improves lung function, endurance and prevents hernia
Bhūjaṅgāsana	Improves metabolism and destroys all types of diseases
Setubandhāsana	Regulates metabolism and strengthens back
Viparītakaraṇī	Stops / slows down / reverses ageing and cognitive decline
Prāṇāyāma	
Vibhāgīya śvasana	Enhances lung capacity. Improves self-awareness and promotes relaxation
Kapālabhāti kriyā	Promotes metabolism, circulation and helps overcome lethargy, fluid accumulation, depression.
Nāḍī śuddhi prāṇāyāma	Wards of stress, strain, fatigue and promotes mental calmness
Bhrāmarī	Restores equilibrium and regulates metabolism
Meditation	
Nādānusandhāna / AUM chanting	Calmness of mind, avoids negative thinking and helps overcome mental obstacles

Table 10.2.1: Rationale for selection of Yoga practices

S. No	**Practices**	**Experts**	**Score given by the experts**					**Content Validity Ratio**	**Remarks**
			5	**4**	**3**	**2**	**1**		
	Sūkṣma vyāyāma								
1.	Grīvā śakti vikāsaka	30	26	3	1	0	0	0.85	Retained
2.	Aṅguli śakti vikāsaka	30	25	4	1	0	0	0.80	Retained
3.	Maṇibandha śakti vikāsaka	30	26	2	2	0	0	0.85	Retained
4.	Kāraprastha śakti vikāsaka	30	25	2	3	0	0	0.80	Retained
5.	Kati śakti vikāsaka i & ii	30	26	3	1	0	0	0.85	Retained
6.	Jānu śakti vikāsaka	30	27	3	0	0	0	0.89	Retained
7.	Piṇḍali śakti vikāsaka	30	25	4	1	0	0	0.80	Retained
8.	Gulpha – pāda – prastha – pāda – tala – śakti – vikāsaka	30	27	2	1	0	0	0.89	Retained
9.	Instant relaxation technique	30	30	0	0	0	0	1.00	Retained
10.	Sūryanamaskāra	30	30	0	0	0	0	1.00	Retained
11.	Quick relaxation technique	30	30	0	0	0	0	1.00	Retained
	Yogāsanā								
12.	Ardhakati cakrāsana	30	26	4	0	0	0	0.85	Retained
13.	Trikoṇāsana	30	25	5	0	0	0	0.80	Retained
14.	Parivṛtta trikoṇāsana	30	24	4	2	0	0	0.75	Retained
15.	Pārśvakoṇāsana	30	26	3	1	0	0	0.85	Retained
16.	Vajrāsana	30	26	3	1	0	0	0.85	Retained
17.	Uṣṭrāsana	30	27	3	0	0	0	0.89	Retained
18.	Paścimottānāsana	30	28	2	0	0	0	0.93	Retained
19.	Vakrāsana	30	29	1	0	0	0	0.97	Retained
20.	Arddha matsyendrāsana	30	27	2	1	0	0	0.89	Retained
21.	Bhūnamanāsana	30	26	1	3	0	0	0.85	Retained
22.	Cakki cālanā	30	26	3	1	0	0	0.85	Retained
23.	Bhūjaṅgāsana	30	26	4	0	0	0	0.85	Retained
24.	Setubandhāsana	30	27	3	0	0	0	0.89	Retained
25.	Viparītakaraṇī	30	21	3	4	2	0	0.57	Deleted
	Prāṇāyāma								
26.	Vibhāgīya śvasana	30	30	0	0	0	0	1.00	Retained
27.	Kapālabhāti kriyā	30	28	2	0	0	0	0.93	Retained
28.	Nāḍī śuddhi prāṇāyāma	30	30	0	0	0	0	1.00	Retained
29.	Bhrāmarī	30	30	0	0	0	0	1.00	Retained
	Meditation								
30.	Nādānusandhāna / AUM chanting	30	28	2	0	0	0	0.93	Retained

Table 10.2.2: The list of Yoga practices proposed for Antarctica along with the scores given by the experts and the corresponding CV Ratio

S. No	Practices	Experts	Score given by the experts					Content Validity Ratio	Remarks
			5	4	3	2	1		
	Sūkṣma vyāyāma								
1.	Grīvā śakti vikāsaka	30	26	3	1	0	0	0.85	Retained
2.	Aṅguli śakti vikāsaka	30	25	4	1	0	0	0.80	Retained
3.	Maṇibandha śakti vikāsaka	30	26	2	2	0	0	0.85	Retained
4.	Kāraprastha śakti vikāsaka	30	25	2	3	0	0	0.80	Retained
5.	Kati śakti vikāsaka i & ii	30	26	3	1	0	0	0.85	Retained
6.	Jānu śakti vikāsaka	30	27	3	0	0	0	0.89	Retained
7.	Quick relaxation technique	30	30	0	0	0	0	1.00	Retained
	Yogāsanā								
8.	Supta Udarakarshanāsanā	30	30	0	0	0	0	1.00	Retained
	Prāṇāyāma								
9.	Vibhāgīya śvasana	30	30	0	0	0	0	1.00	Retained
10.	Kapālabhāti kriyā	30	28	2	0	0	0	0.93	Retained
11.	Nāḍī śuddhi prāṇāyāma	30	30	0	0	0	0	1.00	Retained
12.	Bhrāmarī	30	30	0	0	0	0	1.00	Retained
	Meditation								
13.	Nādānusandhāna / AUM chanting	30	28	2	0	0	0	0.93	Retained

Table 10.2.3: The list of Yoga practices proposed for Sea Voyage along with the scores given by the experts and their corresponding CV Ratio

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Appendix 3: Effect of Kunjal Kriya on Pulmonary Functions

Abstract:

Vomiting is an evolution conserved complex autonomic reflex orchestrated by several neurological centers in the brain. Vagus, the cranial nerve is understood to play a key role in regulation of vomiting. *Kunjal Kriya* (Voluntarily Induced Vomiting), is a yogic cleansing technique involving voluntarily inducing vomiting after drinking saline water (5%) in empty stomach. This study was designed with an objective to understand its effect on pulmonary functions in experienced practitioners and novices and derive its possible therapeutic applications.

Eighteen healthy individuals volunteered for the study of which nine subjects had experience of Voluntarily Induced Vomiting (ViV) and other nine subjects did not have prior experience of ViV. Pulmonary function tests were performed before and after ten minutes of rest following ViV. Analysis of Covariance was performed adjusted for gender and baseline values. No significant changes were observed across genders.

The results of the present study suggest a significant increase in SVC [$F_{(1,13)}$=5.699; p=0.03] and FEV1 [p=0.02] and reduction in ERV [$F_{(1,13)}$=5.029; p=0.04] and Respiratory Rate [$F_{(1,13)}$=3.244, p=0.09]. These changes suggest the possible role of ViV in enhancing the endurance of the respiratory muscles, decreased airway resistance, better emptying of lungs and vagal predominance respectively.

We conclude that ViV when practiced regularly enhances the endurance of the respiratory muscles and decrease the airway resistance. These findings also indicate need for scientific understanding of ViV in the management of motion sickness and restrictive pulmonary disorders like bronchitis and bronchial asthma.

Introduction

Yoga is a comprehensive lifestyle practice that involves practices for the body, mind and the intellect through physical postures (*asanas*), voluntary breath regulation (*pranayama*), cleansing practices (*kriya*) and meditation (*dhyana*). Yoga is being practiced in India since thousands of years. Studies have established the therapeutic benefit of Yoga practices irrespective of an individual being obese[1], hypertensive[2,3], diabetic[4] or even suffering from cancer[5,6]. Yoga practices are efficacious in not only regulating the autonomic nervous system but also beneficially regulating the gene expressions[7]. With all the available evidence to possibly suggest Yoga as a non-pharmacological intervention for several life-style diseases and non-communicable diseases, the basic underlying mechanism of several practices remains unexplored. This study aims to understand the physiological adaptation of pulmonary functions following *Kunjal Kriya* (voluntarily induced vomiting - ViV), a yogic cleansing technique in experienced and novice practitioners. There are no published scientific literature available documenting safety and psycho-physiological effects of ViV until date, making the present study as a novel effort. Despite the practice being observed as ‘involving considerable risk’ by the modern medical professionals, the safety of its practice is time tested and no complications have been reported.

Hatha Yoga Pradipika, an ancient Yoga scripture describes *Kunjal Kriya* (Voluntarily Induced Vomiting - ViV) as one of the six cleansing techniques to clean the body and regulate the mind[8]. Following practice of ViV, subjectively, an individual feels emptiness of stomach. Traditional practitioners suggest acute fever, visceral infection, hernia and cardio-vascular disorders as contra-indications for the practice. *Gherenda Samhita*, an ancient treatise on yoga claims that this practice when performed everyday can cure ailments of liver and spleen[9].

Vomiting, an evolution conserved survival mechanism in humans and in several organisms is understood to be one of the most complex autonomic reflex orchestrated by several neurological centers in the brain. The stimulus is manifested as an orderly response through excessive salivation, inhibition of normal gastric motility, retro-peristaltic movement, relaxation of lower esophageal sphincter, tachycardia, sweating, breath retention, contraction of abdominal and thoracic muscles. Despite vomiting being one of the most common clinical sign, understanding its neurobiology and relevance in maintaining is incomplete. Current understanding states, vagus as the key moderator of vomiting, manifested in strict co-ordination of nucleus tractus solitarius with area postrema, brainstem vestibular centers, sensory and emotional areas and several other areas of the brain[10].

Voluntarily induced vomiting is a common practice observed in patients suffering from bulimia apart from their laxative abuse, and diuretic abuse driven by distorted body-image perception. Complications of repeated voluntarily induced vomiting include dental erosion, discoloration of teeth. Due to the acidic contents coming in contact with the oesophagus, pharynx and oropharynx, symptoms of hoarseness, sore throat, dry cough, and difficulty in swallowing are reported[11].

Voluntarily induced Vomiting immediately after food has been viewed as a psychiatric illness. Ancient Yogic literature recommends practice of voluntary vomiting following consumption of saline water in empty stomach to be therapeutically beneficial. Hence, this study was designed with an objective to document the safety of its practice and possibly explore a mechanism of action of ViV from the perspective of Yoga practices.

Methods:

A flyer was displayed in the classrooms of the undergraduate naturopathy and yoga medical students regarding the study. Subjects were recruited following obtaining a written informed consent. Eighteen volunteers were recruited into two groups: Novices and Experienced group. All subjects were informed about the study and a written informed consent was obtained. All the volunteers recruited for the study reported to be healthy. Emergency medical treatment facility was available to address any unanticipated complications. The experimental and novices group consisted of nine individuals in each group with age of 19.2±0.9 years and 19.6±0.7 years respectively. Volunteers having experience of performing ViV for more than four times were recruited in the experienced group. There were 5 men and 4 women and 7 men and 2 women in the experienced and novices groups respectively.

The practice of ViV involves drinking warm saline water (5%) in the morning in empty stomach, sitting in squatting position until the individual feels a sense of fullness or nausea. The practitioner is then recommended to stand and bend forward from the low back and voluntarily trigger vomiting by gently touching the root of the tongue and uvula. It is observed that with practice, triggering the vomit may be required once or not at all whereas, in novices, it is required to trigger three to four times until all the consumed water is vomited out. The subjects rested in supine and voluntarily relaxed the entire body for ten minutes following vomiting. The pulmonary function tests were performed as per the standard guidelines[12] immediately before and after the practice of ViV using Schiller Spirovit SP-1 system.

Analysis of co-variance (ANCOVA) was performed to understand the between group changes, adjusted for the baseline values and gender. Body Mass Index was not considered as a covariate in our study as all the volunteers in both groups were having a BMI of 20.1±0.4 kg/m^2. There was no significant difference observed amongst the genders.

Results:

The slow vital capacity [$F_{(1,13)}$=5.699; p=0.03] increased in experienced group than in the novices. Within group comparison showed a contrasting change with a significant increase in slow vital capacity in experienced group (p=0.01) as compared to the significant reduction observed in the novices (p=0.02). Whereas, expiratory reserve volume [$F_{(1,13)}$=5.029; p=0.04] decreased significantly in novices as compared to experienced practitioners. Within group comparison indicate a significant reduction in expiratory reserve volume in novices (p=0.04). Whereas, no change was observed in the experienced group. A reduction in respiratory rate was observed in both experienced (p=0.01) and novices (p=0.03), with the extent of reduction being greater in the experienced group [$F_{(1,13)}$=3.244, p=0.09]. A significant increase in Forced Expiratory Volume was observed in experienced group (p=0.02) (*Table 1*).

Discussion:

The present study was designed with an objective to understand the role of ViV on pulmonary function. All the volunteers were healthy and did not report any clinical symptom following the intervention the entire day suggesting the safety of the intervention. This work is the first study conducted to understand the physiology of voluntarily induced vomiting as a standalone intervention in healthy human subjects.

The results of the present study suggest a significant increase in Slow Vital Capacity and Forced Inspiratory Volume (in the 1st second) and Respiratory Rate in the experienced group as compared to the significant reduction in the slow vital capacity and expiratory reserve volume in the novices group. The increase in slow vital capacity shall be attributed to better functioning of the diaphragm[13]. These changes suggest the possible role of ViV in enhancing the endurance of the respiratory muscles, decreased airway resistance, better emptying of lungs and vagal predominance respectively with practice suggesting adaptation of the pulmonary system. Reduced lung volume in the novices group shall be attributed to the psychological stress involved in practicing ViV for the first time. Both groups reported significant reduction in the respiratory rate. *Post hoc* analysis of our study showed a statistical power of 0.75, with an effect size of 1.32 and critical t = 2.119 indicating a strong evidence.

Vagus, the tenth cranial nerve orchestrates the vomiting reflex. Two distinct vagal afferent mechanoreceptors from the stomach: intra-ganglionic laminar ending (IGLE) and intramuscular array (IMA) respond to distension and smooth muscle contractions and also function as tension receptors[14]. These vagal afferents carry the mechanical information to the nucleus tractus solitarius [NTS] from stomach through jugular and nodose ganglion[15]. The NTS, located inside the blood brain barrier apart from its connections with mechanoreceptor vagal afferents from the stomach, also has intense neurological connections with: areas for control of respiration[16], sensory and emotional areas of brain, and the brainstem vestibular centers[17]. NTS is also connected with Area postrema that serves as the chemosensor, detecting any chemical change in the blood.

After distention of the stomach, NTS signals dorsal motor nucleus of vagus to initiate vomiting. The neuronal firing of vagal afferents decrease, resulting in relaxation of gastric wall tone and reduction of acid production[18 19]. NTS signals to increase the diaphragmatic functions through its mono-synaptic connections with the rostral and caudal ventral respiratory group[20]. Simultaneously NTS signals the respiratory smooth muscles, sub-mucosal glands and pulmonary vasculature[21] through nucleus ambiguous to alleviate airway resistance, facilitate better expiration mucosal clearance and better oxygen diffusion into the vasculature [22]. Interestingly, integration of the cardiac function also occurs at the nucleus ambiguous[23] – indicating a probable influence of ViV on the cardiac autonomic functions. As there are no chemicals sensed by the retro-trapezoid nucleus and the area postrema, the evolutionary survival mechanism of chemicals triggering vomiting will be conserved.

Studies on motion sickness suggest diaphragmatic breathing as an effective non-pharmacological intervention[24] . We speculate that the regular practice of ViV may enable the individual to control motion sickness associated symptoms through better diaphragmatic breathing. The results from the novices of the present study also indicate that vomiting might be an evolution conserved response to relieve the organism from an adverse stimuli (emotional, psychological shock or loss of equilibrium while at constant motion) and facilitate relaxation by promoting vagal predominance.

Earlier studies show that administering mild irritants like 2-5% sodium chloride increased the secretion of prostaglandins and other factors like nitric oxide, leptin, ghrelin, cholecystokinin and gastrin releasing peptide and facilitate 'adaptive cytoprotection' to protect gastric mucosa[25] [26]. Treatment with 5% sodium chloride enhanced mucosal blood flow, mucous secretion, mucosal proliferation and decreased acid secretion[27]. Also, the DNA content in the gastric juice was decreased indicating decreased mucosal damage and cell shredding[28]. Interestingly, following exposure to sodium chloride, histologically visible mucosal necrosis and plasma protein leakage into the gastric lumen were observed[29]. These distinct findings also point towards Kunjal Kriya as a potent ulcer protecting agent. However, studies on representative human subject is required to authenticate these preliminary findings.

Understanding the impact of ViV practice on biochemical changes, teeth, pharynx and oro-pharynx is beyond the scope of the present study and requires to be documented in the future studies. Further detailed studies are required to ascertain the psycho-physiological, biochemical changes following practice and the frequency for safe practice requires to be established.

From the above findings, we have conceptualized the probable mechanism of action of ViV and possible future directions for research (Fig1). Based on the findings from this study, we conclude that ViV when practiced regularly is expected to be a technique to enhance the endurance of the respiratory muscles and decrease the airway resistance. These findings also indicate the possibility of using the practice of ViV in the management of motion sickness and restrictive pulmonary disorders like bronchitis and bronchial asthma.

Appendix:

ViV – Voluntarily induced Vomiting

SVC – Slow Vital Capacity

ERV – Expiratory Reserve Volume

IRV – Inspiratory Reserve Volume

FVC – Forced Vital Capacity

PEF – Peak Expiratory Flow

FIVC – Forced Inspiratory Vital Capacity

FIV1 – Forced Inspiratory Vital Capacity in 1st Second

PIF – Peak Inspiratory Flow

RR – Respiratory Rate

TV – Tidal Volume

HRV – Heart Rate Variability

NTS – Nucleus Tractus Solitarius

Table 1

Variables	Experienced Group			Novices Group			df	F	Sig. (ANCOVA) p value	Partial Eta Squared
	Pre	Post	p value	Pre	Post	p value				
SVC	2.61±0.6	3.04±0.4	0.017 [a]	3.02±0.3	2.56±0.3	0.027 [a]	1,13	5.699	.033 [x]	.305
ERV	0.87±0.2	0.97±0.5	0.588	0.86±0.1	0.57±0.4	0.044 [a]	1,13	5.029	.043 [x]	.279
IRV	0.91±0.4	0.87±0.4	0.679	0.93±0.3	0.93±0.5	0.996	1,13	2.029	.178	.135
FVC	2.61±0.5	2.71±0.5	0.533	2.71±0.5	2.47±0.7	0.208	1,13	1.042	.326	.074
PEF	6.63±1.9	6.64±1.6	0.990	7.62±1.4	6.98±1.8	0.170	1,13	.172	.685	.013
FIVC	2.52±0.5	2.58±0.5	0.579	2.81±0.3	2.65±0.3	0.116	1,13	.390	.543	.029
FIV1	2.36±0.4	2.49±0.5	0.021 [a]	2.75±0.4	2.55±0.3	0.131	1,13	1.268	.280	.089
PIF	4.10±1.4	4.34±1.2	0.561	4.83±1.2	4.44±1.4	0.075	1,13	1.163	.300	.082
RR	15.28±4.3	10.69±2.7	0.01 [b]	16.36±5.0	13.44±2.3	0.032 [a]	1,13	3.244	.095	.200
TV	0.82±0.1	0.99±0.4	0.179	0.72±0.1	0.87±0.4	0.264	1,13	.041	.843	.003

Table 1: Table represents the Mean ± SD of the lung volumes measured in experienced and novices before and ten minutes after ViV.

Levels of significance as understood from within group comparison using paired t test: [a] $p \leq 0.05$; [b] $p \leq 0.01$; [c] $p \leq 0.001$

Levels of significance as understood from between group comparison using Analysis of Covariance adjusted for Gender and baseline differences: [x] $p \leq 0.05$; [y] $p \leq 0.01$; [z] $p \leq 0.001$

SVC – Slow Vital Capacity; ERV – Expiratory Reserve Volume; IRV – Inspiratory Reserve Volume ; FVC – Forced Vital Capacity; PEF – Peak Expiratory Flow; FIVC – Forced Inspiratory Vital Capacity; FIV1 – Forced Inspiratory Volume in 1st Second; PIF – Peak Inspiratory Flow; RR – Respiratory Rate; TV - Tidal Volume

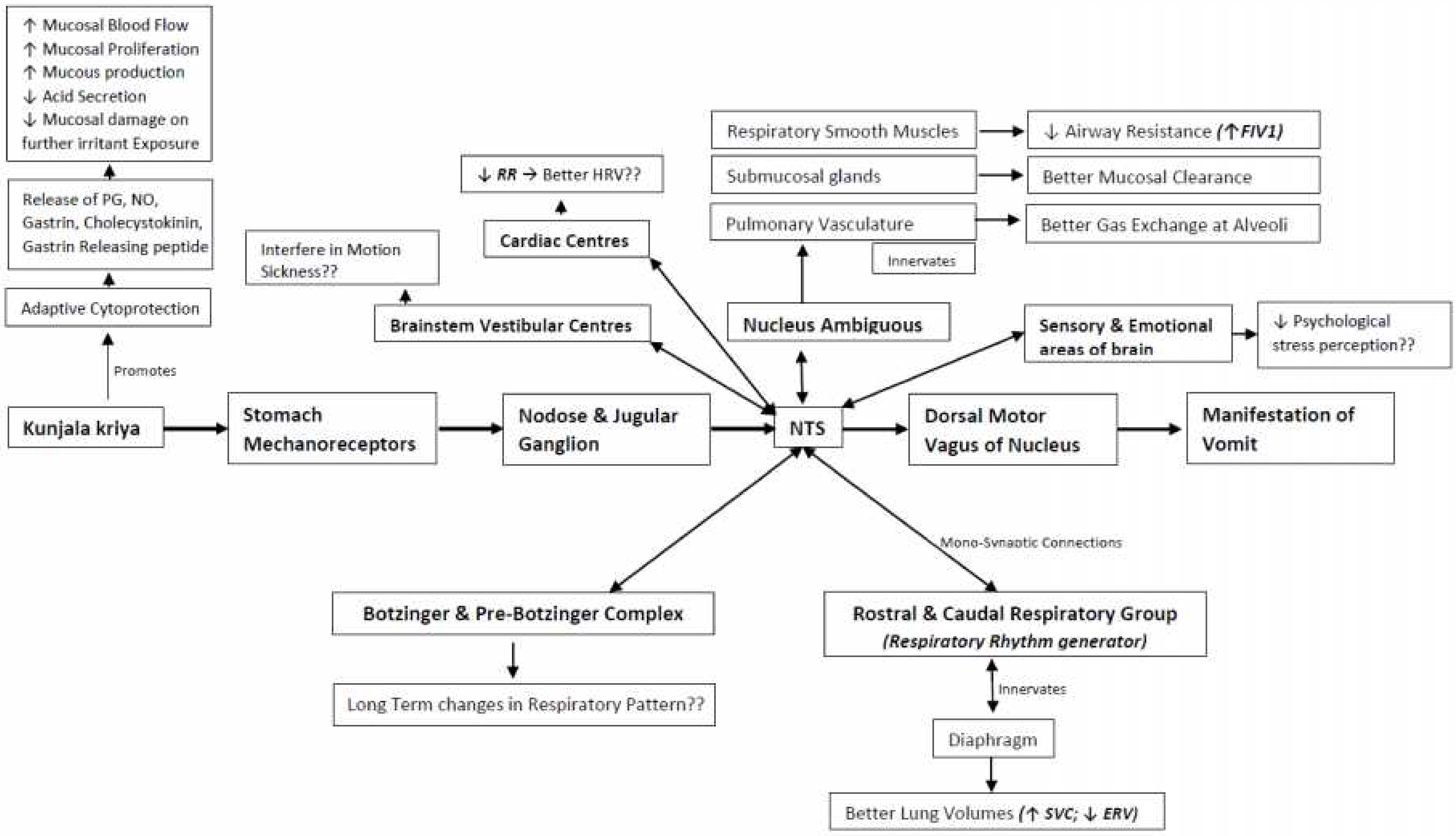

Fig 1: Probable Mechanism of Action of Voluntarily Induced Vomiting (Kunjala Kriya)

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Appendix 4: Scoring key for Psychological Assessments

Perseverative Thinking Questionnaire:

The 15 item self-reported questionnaire was administered to the subjects at the start of the expedition (at Cape Town) and before departing from Antarctica (Maitri). The questions were scored on a 5 point Likert scale from 0 to 4, where, 0=never, 1= rarely, 2=sometimes, 3=often, 4=almost always. Sum of all the questions provided the global perseverative cognition score. The subset scores were calculated as indicated below:

Sub scales	**Items / Questions**
Core Features of RNT	1+2+3+6+7+8+11+12+13
Unproductiveness of RNT	4+9+14
Mental capacity captured by RNT	5+10+15

Pittsburgh Sleep Quality Inventory

Pittsburgh Sleep Quality Inventory is a self-reported questionnaire used in to understand sleep quality both in clinical and research setting. A global score greater than 5 indicates poor quality of sleep and often associated with a pathology. Scores less than 5 indicates good quality of sleep. The minimum and maximum score can be 0 and 21 respectively. Duration of sleep, sleep disturbance, sleep latency, daytime dysfunction, sleep efficiency, need for medication and overall sleep quality can be estimated using PSQI.

The PSQI scores were estimated in SPSS from the raw data using the script below:

PSQIDURAT **DURATION OF SLEEP**

IF Q4 ≥ 7, THEN set value to 0
IF Q4 < 7 and ≥ 6, THEN set value to 1
IF Q4 < 6 and ≥ 5, THEN set value to 2
IF Q4 < 5, THEN set value to 3

Minimum Score = 0 (better); Maximum Score = 3 (worse)

PSQIDISTB SLEEP DISTURBANCE

IF Q5b + Q5c + Q5d + Q5e + Q5f + Q5g + Q5h + Q5i + Q5j (IF Q5JCOM is null or Q5j is null, set the value of Q5j to 0) = 0, THEN set value to 0

IF Q5b + Q5c + Q5d + Q5e + Q5f + Q5g + Q5h + Q5i + Q5j (IF Q5JCOM is null or Q5j is null, set the value of Q5j to 0) ≥ 1 and ≤ 9, THEN set value to 1

IF Q5b + Q5c + Q5d + Q5e + Q5f + Q5g + Q5h + Q5i + Q5j (IF Q5JCOM is null or Q5j is null, set the value of Q5j to 0) > 9 and ≤ 18, THEN set value to 2

IF Q5b + Q5c + Q5d + Q5e + Q5f + Q5g + Q5h + Q5i + Q5j (IF Q5JCOM is null or Q5j is null, set the value of Q5j to 0) > 18, THEN set value to 3

Minimum Score = 0 (better); Maximum Score = 3 (worse)

PSQILATEN SLEEP LATENCY

First, recode Q2 into Q2new thusly:

IF Q2 ≥ 0 and ≤ 15, THEN set value of Q2new to 0

IF Q2 > 15 and ≤ 30, THEN set value of Q2new to 1

IF Q2 > 30 and ≤ 60, THEN set value of Q2new to 2

IF Q2 > 60, THEN set value of Q2new to 3

Next

IF Q5a + Q2new = 0, THEN set value to 0

IF Q5a + Q2new ≥ 1 and ≤ 2, THEN set value to 1

IF Q5a + Q2new ≥ 3 and ≤ 4, THEN set value to 2

IF Q5a + Q2new ≥ 5 and ≤ 6, THEN set value to 3

Minimum Score = 0 (better); Maximum Score = 3 (worse)

PSQIDAYDYS DAY DYSFUNCTION DUE TO SLEEPINESS

IF Q8 + Q9 = 0, THEN set value to 0

IF Q8 + Q9 ≥ 1 and ≤ 2, THEN set value to 1

IF Q8 + Q9 ≥ 3 and ≤ 4, THEN set value to 2

IF Q8 + Q9 ≥ 5 and ≤ 6, THEN set value to 3

Minimum Score = 0 (better); Maximum Score = 3 (worse)

PSQIHSE **SLEEP EFFICIENCY**

Diffsec = Diff. in seconds between day and time of day Q1 & day Q3

Diffhour = Absolute value of diffsec / 3600

newtib =IF diffhour > 24, then newtib = diffhour – 24

IF diffhour ≤ 24, THEN newtib = diffhour

(NOTE, THE ABOVE JUST CALCULATES THE HOURS BETWEEN GNT (Q1) AND GMT (Q3))

tmphse = (Q4 / newtib) * 100

IF tmphse ≥ 85, THEN set value to 0

IF tmphse < 85 and ≥ 75, THEN set value to 1

IF tmphse < 75 and ≥ 65, THEN set value to 2

IF tmphse < 65, THEN set value to 3

Minimum Score = 0 (better); Maximum Score = 3 (worse)

PSQISLPQUAL **OVERALL SLEEP QUALITY**

Q6

Minimum Score = 0 (better); Maximum Score = 3 (worse)

PSQIMEDS **NEED MEDS TO SLEEP**

Q7

Minimum Score = 0 (better); Maximum Score = 3 (worse)

PSQI **TOTAL**

DURAT + DISTB + LATEN + DAYDYS + HSE + SLPQUAL + MEDS

Minimum Score = 0 (better); Maximum Score = 21 (worse)

Interpretation: TOTAL ≤ 5 associated with good sleep quality

TOTAL > 5 associated with poor sleep quality

Appendix 5: Protocol for Biochemistry tests

Liver function tests, Kidney Function Tests, Lipid Profile and Glucose estimation were performed in an automated bioanalyser (Mindray, PRC). The instrument was calibrated for the tests with calibrators (standards) and two controls (normal and pathological) were used to check the accuracy of calibration. All the reagents for the assessments were supplied by Mindray. The tests were run in duplicates to minimise the error.

Biochemical tests were conducted at three time points. The Baseline blood samples were not available with us for assessments.

Lab Protocol for Biochemical Tests

Lipid Profile:

Total Cholesterol:

Reaction Principle: Cholesterol Oxidase Peroxidase Method

By the catalysis of Cholesterol Esterase and Cholesterol Oxidase, Cholesterol Ester is catalysed to produce H_2O_2, which oxidises 4-Aminoantipyrine with phenol to form a coloured dye of Quinoneimine. The increase in absorbance is directly proportional to the concentration of Cholesterol.

Triglyceride:

Reaction Principle: Glycerokinase Peroxidase-Peroxidase method

Through a sequence of enzymatic catalysis steps by lipase, glycerokinase and glycerokinase peroxidase, triglycerides are catalysed to yield H_2O_2, which oxidise 4-Aminoantipyrinel to yield a coloured dye of Quinoneimine. The increase in absorbance is directly proportional to the concentration of triglycerides

High Density Lipoprotein (HDL):

Reaction Principle: Direct Method

The change in absorbance at 600nm is continuously monitored. The change is directly proportional to the concentration of the cholesterol in the sample and is used by the system to calculate and express the HDL cholesterol concentration.

Low Density Lipoprotein (LDL)

Reaction Principle: Direct Method

By the catalysis of Cholesterol Esterase and Cholesterol Oxidase, LDL is catalysed to produce H_2O_2 and Cholestenone. H_2O_2 oxidises 4-Aminoantipyrine to form a coloured dye of Quinoneimine. The increase in absorbance is directly proportional to the concentration of LDL.

Liver Function Tests:

Total Proteins:

Reaction Principle: Biuret Method

In an alkaline solution with a $pH > 12$, copper ions combine with proteins to produce a blue-violet colour complex. The increase in absorbance is directly proportional to the concentration of the proteins.

Albumins:

Reaction Principle: Bromcresol Green Method

In an acidic pH ($pH = 4.2$), serum albumin combines with bromcresol green to produce a glaucous complex. The increase in absorbance is directly proportional to the concentration of albumin

Total Bilirubin

Reaction Principle: Vanadiate Oxidating Method (VOX)

Vanadic acid at pH of 3.0, oxidates bilirubin into dehydrobilirubin. The reduction in absorbance at 450nm is directly proportional to the concentration of total bilirubin.

Gamma Glutamyltransferase (GGT)

Reaction Principle: Szasz Method

Gamma Glutamyltransferase transfers the Gamma Glutamyl group of gamma-glutamyl-3-carboxy-4-nitroanilide to glycyl-glycine with the production of p-nitroaniline. The amount of 5-amino-2-nitrobenzoate results in the elevated absorbance which is directly proportional to the activity of GGT in the sample.

Alanine Aminotransferase (ALT)

Reaction Principle: UV-assay without pyridoxal phosphate activation

Alanine Aminotransferase catalyses the reversible transamination of L-alanine and α-oxoglutarate to pyruvate and L-glutamate. The pyruvate is then reduced to lactate in the presence of lactate dehydrogenase (LDH) with the concurrent oxidation of reduced β-nicotinamide adenine dinucleotide (NADH) to β-nicotinamide adenine dinucleotide. This change in absorbance is directly proportional to the activity of ALT in the sample.

Serum Glutamic Oxaloacetic Transaminase (SGOT/AST)

Reaction Principle: UV assay without pyridoxal phosphate activation

Aspartate Aminotransferase catalyses the reversible transamination of L-aspartate and α-oxoglutarate to oxaloacetate and L-glutamate. The oxaloacetate is then reduced to malate in the presence of malate dehydrogenase with NADH being oxidised to NAD^+. The rate of reduction in NADH is directly proportional to the rate of formation of oxaloacetate and thus AST activity.

Renal Function Tests:

Urea

Reaction Principle: Urease glutamate dehydrogenase

Urea is hydrolysed by urease, and one of the products, ammonia, helps to convert NADH to NAD^+ with the catalysis of Glutamate Dehydrogenase. The reduction in absorbance is directly proportional to the concentration of Urea.

Uric Acid

Reaction Principle: Uricase-Peroxidase Method

By using ascorbic oxidase to eliminate the interference of ascorbic acid, the uric acid is catalysed to produce H_2O_2, which inturn oxidises 4-AAP to yield a coloured dye of Quinoneimine. The reduction in absorbance is directly proportional to the concentration of Uric acid.

Creatinine

Reaction Principle: JAFF method

Serum Glucose

Reaction Principle: Glucose oxidase – Peroxidase method

Through the catalysis of Glucose oxidase, glucose is oxidated to H_2O_2, and then in the presence of Peroxidase, H_2O_2 oxidates 4-aminoantipyrine with p-Hydroxybenzoic acid sodium to form a coloured dye of Quinoneimine. The increase in absorbance is directly proportional to the concentration of Glucose.

Appendix 6: Protocol for estimation of Biomarkers

We used a 96 well QPlex multiplex Chemiluminescence assay (Quansys Biosciences, USA) to quantify cortisol levels. IL-1, Il-2, Il-6, TNF-α, and C-Peptide were also assessed. Q-view software was used to quantify the Chemiluminescence spots. The standards were run in duplicates. Twelve subjects' serum samples were taken for assay. Biomarkers other than cortisol were below the detection limit of the kit. Two samples, one from each group were having Chemiluminescence intensities of Cortisol beyond detectable limits. The results of the biomarker Cortisol for ten subjects were considered for further analysis.

Assay procedure

a. The Calibrator along with the competitor was reconstituted as prescribed the product card
b. Serum samples were diluted at 1:2 ratio with sample diluent
c. 50 µl of samples and calibrator in duplicates were added to the 96 well plate
d. The plate was covered with the plate seal and was placed on a shaker incubator for two hours at room temperature (23ºC)
e. The 96 well plate was washed three times using wash buffer
f. Add 50µl per well detection mix, cover with a new seal and return to the shaker incubator for 1 hour at room temperature
g. Wash the plate three times with wash buffer
h. 50µl per well streptavidin –HRP 1X was added, the plate was covered and sealed with plate sealer and placed in the plate shaker at 500RPM for 15 minutes at room temperature
i. Fifteen minutes prior to use, mix substrate A and Substrate B and mix gently
j. Wash the plate with wash buffer 6 times
k. Add 50µl of the above mixed substrate and image immediately in chemidoc system
l. The images were analyses using Q-plex software (Quansys Biosciences).

Appendix 7: RNA extraction protocol

The PAXgene blood RNA tube was incubated at room temperature for 5 hours in order to achieve complete lysis of blood cells

1. Centrifuge the PAXgene Blood RNA Tube (BRT) for 10 minutes at 3000–5000 x *g* using a swing-out rotor.
2. Remove the supernatant from decanting or pipetting. Add 4 ml RNase-free water (RNFW) to the pellet, and close the tube using a fresh secondary BD Hemogard closure (supplied with the kit).

   If the supernatant is decanted, take care not to disturb the pellet, and dry the rim of the tube with a clean paper towel.
3. Vortex until the pellet is visibly dissolved, and centrifuge for 10 minutes at 3000–5000 x *g* using a swing-out rotor. Remove and discard the entire supernatant.
4. Add 350 µl resuspension buffer (BR1), and vortex until the pellet is visibly dissolved.
5. Pipet the sample into a 1.5 ml microcentrifuge tube (MCT). Add 300 µl binding buffer (BR2) and 40 µl proteinase K (PK). Mix by vortexing for 5 seconds, and incubate for 10 minutes at 55°C using a shaker–incubator at 400–1400 rpm. After incubation set the temperature of the shaker–incubator to 65°C (for step 20).
6. Pipet the lysate directly into a PAXgene Shredder spin column (PSC; lilac) placed in a 2 ml processing tube (PT), and centrifuge for 3 minutes at maximum speed (but not to exceed 20,000 x *g*).
7. Carefully transfer the entire supernatant of the flow-through fraction to a

fresh 1.5 ml microcentrifuge tube (MCT) without disturbing the pellet in the processing tube.

8. Add 350 µl ethanol (96–100%, purity grade p.a.). Mix by vortexing, and centrifuge briefly (1–2 seconds at 500–1000 x *g*) to remove drops from the inside of the tube lid.
9. Pipet 700 µl sample into the PAXgene RNA spin column (PRC; red) placed in a 2 ml processing tube (PT), and centrifuge for 1 minutes at 8000–20,000 x *g*. Place the spin column (PRC) in a new 2 ml processing tube (PT), and discard the old processing tube (PT) containing flow-through.
10. Pipet the remaining sample into the PAXgene RNA spin column (PRC), and centrifuge for 1 minutes at 8000–20,000 x *g*. Place the spin column (PRC) in a new 2 ml processing tube (PT), and discard the old processing tube (PT) containing flow-through.
11. Pipet 350 µl wash buffer 1 (BR3) into the PAXgene RNA spin column (PRC). Centrifuge for 1 minute at 8000–20,000 x *g*. Place the spin column (PRC) in a new 2 ml processing tube (PT), and discard the old processing tube (PT) containing flow-through.
12. Add 10 µl DNase I (RNFD) stock solution to 70 µl DNA digestion buffer (RDD) in a 1.5 ml microcentrifuge tube (MCT). Mix by gently flicking the tube, and centrifuge briefly to collect residual liquid from the sides of tube.
13. Pipet the DNase I (RNFD) incubation mix (80 µl) directly onto the PAXgene RNA spin column (PRC) membrane, and place on the benchtop (20–30°C) for 15 minutes.
14. Pipet 350 µl wash buffer 1 (BR3) into the PAXgene RNA spin column (PRC), and centrifuge for 1 minute at 8000–20,000 x *g*. Place the spin column (PRC)

in a new 2 ml processing tube (PT), and discard the old processing tube (PT) containing flow- through.

15. Pipet 500 µl wash buffer 2 (BR4) into the PAXgene RNA spin column (PRC), and centrifuge for 1 minute at 8000–20,000 x *g*. Place the spin column (PRC) in a new 2 ml processing tube (PT), and discard the old processing tube (PT) containing flow-through.
16. Add another 500 µl wash buffer 2 (BR4) to the PAXgene RNA spin column (PRC). Centrifuge for 3 minutes at 8000–20,000 x *g*.
17. Discard the processing tube (PT) containing the flow-through, and place the PAXgene RNA spin column (PRC) in a new 2 ml processing tube (PT). Centrifuge for 1 minute at 8000–20,000 x *g*.
18. Discard the processing tube (PT) containing the flow-through. Place the PAXgene RNA spin column (PRC) in a 1.5 ml microcentrifuge tube (MCT), and pipet 40 µl elution buffer (BR5) directly onto the PAXgene RNA spin column (PRC) membrane. Centrifuge for 1 minute at
    8000–20,000 x *g* to elute the RNA.
19. Repeat the elution step (step 18) as described, using 40 µl elution buffer (BR5) and the same microcentrifuge tube (MCT).
20. Incubate the eluate for 5 minutes at 65°C in the shaker–incubator (from step5) without shaking. After incubation, chill immediately on ice.
21. If the RNA samples will not be used immediately, store at –20°C or
    –70°C.

    An alliquot of the sample was used to measure the concentration of RNA using Spectrophotometer (Nanodrop 6000C).

Appendix 8: Bioanalyser Protocol

Decontaminating electrodes of Bioanalyser

- Slowly fill one of the wells of an electrode cleaner with 350 µl RNaseZAP
- Open the lid and place electrode cleaner in the Agilent 2100 bioanalyzer.
- Close the lid and leave it closed for about 1 minute.
- Open the lid and remove the electrode cleaner. Label the electrode cleaner and keep it for future use. You can reuse the electrode cleaner for all 25 chips in the kit.
- Slowly fill one of the wells of another electrode cleaner with 350 µl RNase- free water.
- Place electrode cleaner in the Agilent 2100 bioanalyzer.
- Close the lid and leave it closed for about 10 seconds.
- Open the lid and remove the electrode cleaner. Label it and keep it for further use.
- Wait another 10 seconds for the water on the electrodes to evaporate before closing the lid.

Preparing gel

- Allow all reagents to equilibrate to room temperature for 30 minutes before use.
- Place 550 µl of Agilent RNA 6000 Nano gel matrix (red) into the top receptacle of a spin filter.
- Place the spin filter in a microcentrifuge and spin for 10 minutes at 1500 g ± 20 % (for Eppendorf microcentrifuge, this corresponds to 4000 rpm).
- Aliquot 65 µl filtered gel into 0.5 ml RNase- free microfuge tubes that are included in the kit. Store the aliquots at 4 °C and use them within one month of preparation.

Preparing gel-Dye mix

- Allow all reagents to equilibrate to room temperature for 30 minutes before use. Protect the dye concentrate from light while bringing it to room temperature.
- Vortex RNA 6000 Nano dye concentrate (blue) for 10 seconds and spin down.
- Add 1 µl of RNA 6000 Nano dye concentrate (blue) to a 65 µl aliquot of filtered gel
- Cap the tube, vortex thoroughly and visually inspect proper mixing of gel and dye. Store the dye concentrate at 4 °C in the dark again.
- Spin tube for 10 minutes at room temperature at 13000 g

Loading the Gel-dye mix

- Allow the gel- dye mix to equilibrate to room temperature for 30 minutes before use and protect the gel- dye mix from light during this time.
- Take a new RNA Nano chip out of its sealed bag.
- Place the chip on the chip priming station.
- Pipette 9.0 µl of the gel- dye mix at the bottom of the well-marked and dispense the gel- dye mix.
- Set the timer to 30 seconds, make sure that the plunger is positioned at 1 ml and then close the chip priming station. The lock of the latch will click when the Priming Station is closed correctly
- Press the plunger of the syringe down until it is held by the clip.
- Wait for exactly 30 seconds and then release the plunger with the clip release mechanism.

- Visually inspect that the plunger moves back at least to the 0.3 ml mark.
- Wait for 5 seconds, then slowly pull back the plunger to the 1 ml position.
- Open the chip priming station.
- Pipette 9.0 µl of the gel- dye mix in each of the wells marked.

Loading RNA 6000 Nano marker

- Pipette 5 µl of the RNA 6000 Nano marker (green) into the well- marked with the ladder symbol and each of the 12 sample wells.

Loading ladder and samples

- Before use, thaw ladder aliquots and keep them on ice
- To minimize secondary structure, heat denature (70 °C, 2 minutes) the samples before loading on the chip.
- Pipette 1 µl of the RNA ladder into the well marked with the ladder symbol.
- Pipette 1 µl of each sample into each of the 12 sample wells.
- Set the timer to 60 seconds.
- Place the chip horizontally in the adapter of the IKA vortex mixer and make sure not to damage the buldge that fixes the chip during vortexing.
- Vortex for 60 seconds at 2400 rpm

Starting chip run

- Load the chip into the Bioanalyser providing appropriate identification to the Chip and sample location on the chip

- Inspect the ladder after run for normal pattern.
- Tabulate RIN numbers of the samples loaded

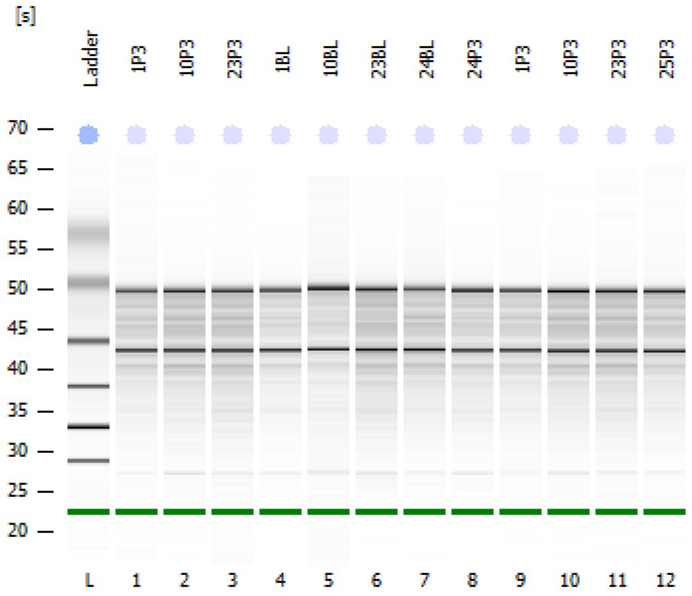
Appendix 8a: RNA Yield, Quality Control and Electropherogram

Group	Sample ID	RNA Conc (ng/Ul)	RIN Number
Control	1BL	267.7	7.2
Control	1P1	273.8	6.9
Control	1P3	87.2	7.3
Control	3BL	163.1	7.2
Control	3P1	95.4	8.2
Control	3P3	71.8	6.6
Control	5BL	337.2	7
Control	5P1	201	7.9
Control	5P3	229.8	7
Control	6BL	380.1	7.4
Control	6P1	237	8.1
Control	6P3	229.9	6.8
Control	10BL	79	8
Control	10P1	129	8.2
Control	10P3	131.9	6.7
Control	12BL	73.2	6.9
Control	12P1	151.7	7.7
Control	12P3	195.9	7.2
Yoga	14BL	89.4	7.1
Yoga	14P1	157.1	7.3
Yoga	14P3	132.6	7.2
Yoga	15BL	256	7.3
Yoga	15P1	167.9	7.4
Yoga	15P3	138.9	6.8
Yoga	19BL	85.1	6.8
Yoga	19P1	42.5	7
Yoga	19P3	161.8	6.6
Yoga	22BL	171.1	6.7
Yoga	22P1	186.5	8.3
Yoga	22P3	107.3	6.8
Yoga	23BL	150.2	6.5
Yoga	23P1	177.3	7.3
Yoga	23P3	88.4	6.9
Yoga	24BL	142.1	6.8
Yoga	24P1	161.1	7.8
Yoga	24P3	169.6	6.9

A representative electropherogram is mentioned below

Assay Class:	Eukaryote Total RNA Nano	Created:	12/6/2016 6:17:56 PM
Data Path:	C:\...Eukaryote Total RNA Nano_DE13806053_2016-12-06_18-17-56.xad	Modified:	12/6/2016 6:41:44 PM

Electrophoresis File Run Summary



Instrument Information:

Instrument Name:	DE13806053	Firmware:	C.01.069
Serial#:	DE13806053	Type:	G2939A

Assay Information:

Assay Origin Path:	C:\Program Files (x86)\Agilent\2100 bioanalyzer\2100 expert\assays\RNA\Eukaryote Total RNA Nano Series II.xsy
Assay Class:	Eukaryote Total RNA Nano
Version:	2.6
Assay Comments:	Total RNA Analysis ng sensitivity (Eukaryote)

Chip Information:

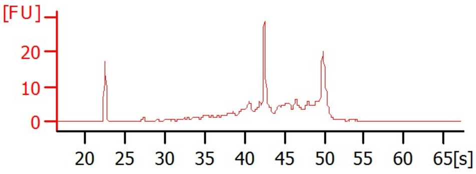
Chip Lot #:

Reagent Kit Lot #:

Chip Comments:

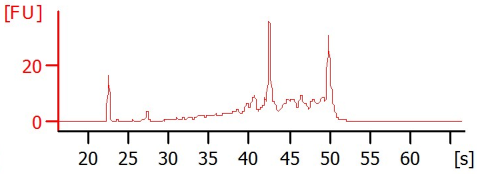
1P3

RIN: 7.30



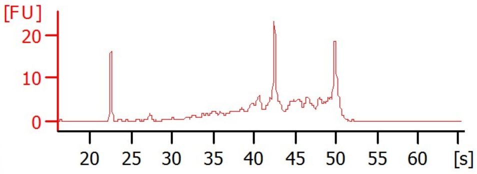
10P3

RIN: 6.70



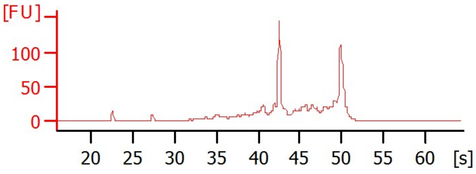
23P3

RIN: 6.90



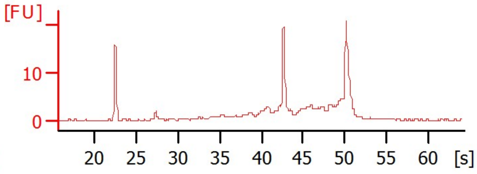
1BL

RIN: 7.20



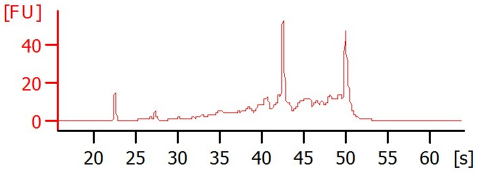
10BL

RIN:8



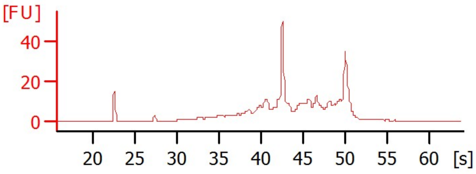
23BL

RIN: 6.40



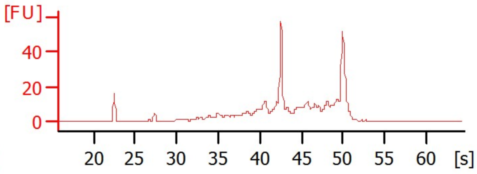
24BL

RIN: 6.80



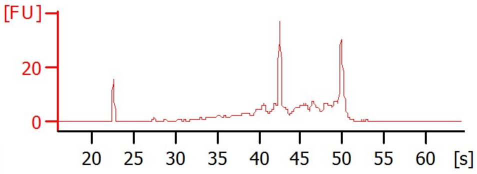
24P3

RIN: 6.90



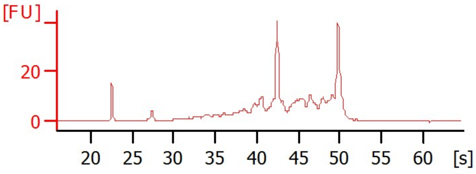
1P3

RIN:7



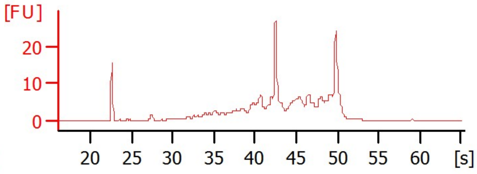
10P3

RIN: 6.70



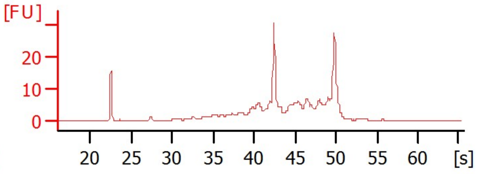
23P3

RIN: 6.60



25P3

RIN: 6.80



Appendix 9: Single Colour Gene Expression Protocol

Step 1: Creating Spike-In Mix

Mix (Vortex) the thawed Spikein Mix, spin & heat @ 37C for 5 min, vortex again & spin

1st Dilution (1S): 38µl Dilution buffer + 2 µl Spike stock mix (1:20) [Store upto 2 months]

Votex & Spin; proceed further

2nd Dilution (2S): 2µl of 1S + 48 µl Dilution buffer (1:25) [Discard immediately after use]

Votex & Spin; proceed further

3rd Dilution (3S): 2µl of 2S + 18µl Dilution Buffer (1:10) [Discard immediately after use]

Votex & Spin; proceed further

Step 2: Prelim step Readiness Check

1. Turn on PCR: Protocol 'Microarray/Denaturing' for ***Step 5***
2. Water bath set at 80 C
3. Place 5X First strand buffer @ 80 C for 3-4 mins, cool & place at RT until required

Step 3: Add 200ng sample + 2µl 3S *[Total Vol **3.5 µl**]*

ID	Conc/Ul	Volume Reqd for 200 ng	Rounded off Conc	Final Concentration	Water to be added
(1)	129	1.55	1.5	193.5	0
(2)	177.3	1.13	1.13	200.349	0.37
(3)	161.1	1.24	1.24	199.764	0.26
(4)	151.7	1.32	1.32	200.244	0.18
(5)	150.2	1.33	1.32	198.264	0.18
(6)	169.6	1.18	1.18	200.128	0.32
(7)	81.5	2.45	Conc		0
(8)	30.8	6.49	Conc		0

Step 4: Add T7 Primer Mix to sample

Samples: 8, Prep Rxn Vol: 9

Component	**Per sample (µl)**	**Per 9 samples (µl)**
T7 Primer	0.8	**7.2**
NF H2O	1	**9**
Total	**1.8**	16.2

Add 1.8µl T7 primer mix to each of 8 samples *Total vol 5.3µl*

Step 5: Heat denature in PCR @ 65C for 10 minutes & incubate on ice for 5 minutes

Step 6: Prepare cDNA master mix [First Strand Synthesis]

******* Keep **Affinity Script RNase Block Mix** (Violet cap) & **T7 RNA polymerase blend** (Red cap) **on ice** & other samples at RT *******

Prepare in 1.5 ml tube [**label: FSS**]

Component	**Vol per rxn** (µl)	**Vol per 9 rxn** (µl)
5X First Strand Buffer (Green cap)	2	**18**
0.1M DTT (White Cap)	1	**9**
10mM dNTP Mix (Green cap)	0.5	**4.5**
Affinity Script RNase Block Mix	1.2	**10.8**
Total	**4.7**	42.3

Briefly spin samples to remove droplets, continue keeping samples on ice

Add **4.7µl** of cDNA master mix into each of 8 samples *[Total Vol 10µl]*

Incubate samples in PCR protocol **First Strand Synthesis** [40C for 2 hours & 70C for 15 minutes]

Incubate samples on ice for 5 minutes

Note: Shift all reagents back to -20C and remove 30 mins prior to IVT

Step 7: In-Vitro Transcription

******* Keep **Affinity Script RNase Block Mix** (Violet cap) & **T7 RNA polymerase blend** (Red cap) **on ice** & other samples at RT *******

Prepare in 1.5 ml tube [**label: IVT**]

Component	**Vol per rxn** (µl)	**Vol per 9 rxn** (µl)
NF water (White Cap)	0.75	**6.75**
5X Transcription buffer (Blue Cap)	3.2	**28.8**
0.1M DTT (White Cap)	0.6	**5.4**
NTP Mix (Blue Cap)	1	**9**
T7 RNA Polymerase Blend (Red Cap)	0.21	**1.89**
Cyanine 3 CTP	0.24	**2.16**
Total	**6**	54

Add **6µl** Transcription master mix to the sample tube & gently mix by pipetting. [Total vol 16µl]

Incubate samples in PCR protocol **IVT [**40 C for 2 hours**]** & Incubate samples on Ice for 5 minutes

Step 8:

Ensure all reagents are shifted to -20 C

Switch on the Micro-centrifuge with temperature set to 4 C, 13000 rpm & 30 seconds

Step 9: Purify labelled / amplified RNA

1. Number 2 sets of 1.5 ml MCT according to sample ID [*one for processing & other for collecting elute(shall be taken from Kit)*]
2. Number new RNeasy Mini spin column according to sample ID
3. Set timer to 1 minute
4. Add 84µl of NF H2O to cRNA sample (to make up volume to 100 µl) in the PCR tube

5. Add 350 µl of Buffer RLT to each of the new 1.5 MCT
6. Transfer respective 100µl cRNA sample to MCT containing 350 µl RLT & mix well thro' pipetting
7. Add 250 µl 100% Ethanol & Mix thoroughly by pipetting *[Do Not Spin]*
8. Transfer 700 µl sample to RNeasy spin column & spin @ 4C, 13k rpm for 30 seconds
9. Transfer RNeasy column to new collection tube
10. Add 500µl of buffer RPE (with ethanol) to the column. Spin @ 4C, 13k rpm for 30 seconds
11. Discard flow through, reuse collection tube
12. Add 500µl of buffer RPE (with ethanol) to the column. Spin @ 4C, 13k rpm for 30 seconds
13. Discard flow through, reuse collection tube
14. Transfer RNeasy mini column to new 1.5ml MCT & spin @ 4C, 13k RPM for 30 seconds
15. Discard MCT & place in the fresh labelled MCT to collect elute
16. Add 30µl RNase free water directly on filer membrane, allow for 60 seconds
17. Elute @ 4C, 13k RPM for 30 seconds
18. Store sample on ice
19. Keep heating block @ 60 C & change the Centrifuge temperature setting to 21 C

Step 10: Quantify cRNA

1. Quantify with Nanodrop using microarray measurement option
2. Blank with nuclease free water
3. Calculate **concentration of cRNA** (using Quantification.xls sheet stored in D:/BRS)

   Formula:

   µg of cRNA = (Concentration of cRNA) X 30 µl (Elution Volume) / 1000

4. **Specific activity**

pmol Cy3 per µg cRNA = (Conc. of Cy3 / Conc. Of cRNA) X 1000

5. **Recommended Yield (> 0.825 µg) & Specific Activity (> 6)**

cRNA Yield & Specific Activity						
Sample ID	**Sp ID**	**Conc. Of cRNA (ng)**	**Elution Vol** (µl)	**Conc. Of Cy3 (ng)**	**Yield**	**Specific activity**
XX	1	196.2	30	2.6	5.886	13.3
XX	2	168	30	2.1	5.04	12.5
XX	3	220.5	30	3	6.615	13.6
XX	4	169.8	30	2	5.094	11.8
XX	5	147.2	30	1.4	4.416	9.5
XX	6	172.7	30	2.4	5.181	13.9
XX	7	164.4	30	2.5	4.932	15.2
XX	8	118.5	30	1.9	3.555	16.0

Step 11: Hybridisation:

Check if the heating block is set to 60C & ***switch on the Hyb oven @ 65 C & 10 RPM***

1. Label MCTs from 1 to 8

Sp.ID	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**
Sample ID	XX	XX	XX	XX	XX	XX	XX	XX

2. **Fragmentation Mix** (Calculate using Quantification.xls sheet stored in D:/BRS)

Sample ID	**SP. ID**	**Conc. Of cRNA (ng)**	**reqd vol for 600ng (µl)**	**Vol of 10X GE buffer** (µl)	**Vol of 25X Frag. Buffer** (µl)	**Vol of NF Water** (µl)	**Tot Vol** (25µl)
XX	1	196.2	3.1	5	1	15.9	25
XX	2	168	3.6	5	1	15.4	25
XX	3	220.5	2.7	5	1	16.3	25
XX	4	169.8	3.5	5	1	15.5	25
XX	5	147.2	4.1	5	1	14.9	25
XX	6	172.7	3.5	5	1	15.5	25
XX	7	164.4	3.6	5	1	15.4	25
XX	8	118.5	5.1	5	1	13.9	25

3. Mix well with vortexer

4. Incubate at 60 C for ***exactly*** 30 minutes to fragment RNA

   (use this time to prepare the hybridisation assembly)

5. Cool on ice for 1 minute

   ***** ## CARE##*****: Pipette & Mix 2X Hi-RPM Hybridisation buffer to the sample without inserting air bubbles. ***Do not Vortex***

6. Add **25 µl** of 2X Hi-RPM Hybridisation buffer to stop the fragmentation reaction

7. Spin for 1 min at RT, 13000 rpm – shift sample to ice & load on ASAP

Step 12: Preparing the Hybridisation assembly and loading slides

*****## CAUTION ##******Donot let the pipette tip or hybridisation solution touch the gasket walls***

1. Load clean Gasket slide into Hyb chamber lower surface

   Barcode label of gasket slide is to my left

2. Load samples left to right, from 1st row & then 2nd row
3. No air bubbles shall be introduced into the gasket wells
4. Load samples on the gasket slide. Put the active side of Agilent slide down in contact with gasket – positioned exactly parallel to each other

   "Agilent" Labelled Barcode side shall be facing down & numeric barcode side faces up
5. Fix the hyb chamber, tightly screw the chamber. Vertically rotate the assembled chamber to wet the gasket and assess mobility. Tap the assembly on hard surface to move stationary bubbles.
6. Place assembly in Hyb oven @ 65 C for 17 hours

Samples on slide

Sp.ID	**1**	**2**	**3**	**4**
Sample ID	XX	XX	XX	XX
Sp.ID	**5**	**6**	**7**	**8**
Sample ID	XX	XX	XX	XX

Preparation for Day 2

1. Add 0.005% (2 ml) Triton X-102 to gene expression wash buffer 1 & 2 (have done already)
2. Dispense 1 L of wash buffer 2 into a sterile storage bottle
3. Place in incubator with temperature preset @ 37 C for overnight pre-warming

Day 2

Step 1: Preparation

1. Clean three slide washing chambers, magnetic stirrer bars and slide racks profusely with milliQ water to ensure that there is no detergent sticking to the wall
2. Empty and dry the chambers

Step 2: Wash the Microarray Slides

1. Completely fill slide-staining dish #1 with Gene Expression Wash Buffer 1 at room temperature.
2. Put a slide rack into slide-staining dish #2. Add a magnetic stir bar. Fill slide-staining dish #2 with enough Gene Expression Wash Buffer 1 at room temperature to cover the slide rack. Put this dish on a magnetic stir plate.
3. Put the empty dish #3 on the stir plate and add a magnetic stir bar. Do not add the prewarmed (37°C) Gene Expression Wash Buffer 2 until the first wash step has begun.
4. Remove one hybridization chamber from incubator and record time. Record whether bubbles formed during hybridization and if all bubbles are rotating freely.
5. Prepare the hybridization chamber disassembly.
    a. Put the hybridization chamber assembly on a flat surface and loosen the thumbscrew, turning counter clockwise.
    b. Slide off the clamp assembly and remove the chamber cover.
    c. With gloved fingers, remove the array-gasket sandwich from the chamber base by grabbing the slides from their ends. Keep the microarray slide numeric barcode facing up as you quickly transfer the sandwich to slide-staining dish #1.
    d. Without letting go of the slides, submerge the array-gasket sandwich into slide-staining dish #1 containing Gene Expression Wash Buffer 1.
6. With the sandwich completely submerged in Gene Expression Wash Buffer 1, pry the sandwich open from the barcode end only:
    a. Slip one of the blunt ends of the forceps between the slides.
    b. Gently turn the forceps upwards or downwards to separate the slides.
    c. Let the gasket slide drop to the bottom of the staining dish.
    d. Grasp the top corner of the microarray slide, remove the slide, and then put it into the slide rack in the slide-staining dish #2 that contains Gene Expression Wash Buffer 1 at room temperature. Transfer the slide quickly so avoid premature drying of the slides. *Touch only the barcode portion of the microarray slide or its edges!*

    More effort is needed to separate the 4-pack and 8-pack sandwiched slides than the 1-pack and 2-pack sandwiched slides.
7. When all slides in the group are placed into the slide rack in slide-staining dish #2, stir using setting 4 for 1 minute.
8. During this wash step, remove Gene Expression Wash Buffer 2 from the 37°C water bath and pour into the slide-staining dish #3.
9. Transfer slide rack to slide-staining dish #3 that contains Gene Expression Wash Buffer 2 at elevated temperature. Stir using setting 4, or a moderate speed setting, for 1 minute.

10. Slowly remove the slide rack minimizing droplets on the slides. It should take 5 to 10 seconds to remove the slide rack. If liquid remains on the bottom edge of the slide, dab it on a cleaning tissue.
11. Discard used Gene Expression Wash Buffer 1 and Gene Expression Wash Buffer 2.
12. Repeat step 1 through step 12 for the next group of eight slides using fresh Gene Expression Wash Buffer 1 and Gene Expression Wash Buffer 2 pre-warmed to 37°C.
13. Put the slides in a slide holder.

Step 3: Scanning the slide:

1. Put assembled slide holders into the scanner cassette.
2. Select the appropriate scanner protocol: AgilentG3_HiSen_GX_1color (for G3 format, high-sensitivity mode)
3. Verify that the Scanner status in the main window says Scanner Ready.
4. Click Start Scan.
5. Save the .tif image with barcode and date of scan

Step 4: Extracting data using Feature Extraction:

1. Open the Agilent Feature Extraction (FE) program
2. Add the images (.tif) to be extracted to the FE Project.
    a. Click Add New Extraction Set(s) icon on the toolbar or right-click the Project Explorer and select Add Extraction...
    b. Browse to the location of the .tif files, select the .tif file(s) and click Open.
3. The FE program automatically assigns a default grid template and protocol for each extraction set, after the following conditions are set:

a. The default Single colour Gene Expression protocol must be specified in the FE Grid Template properties.

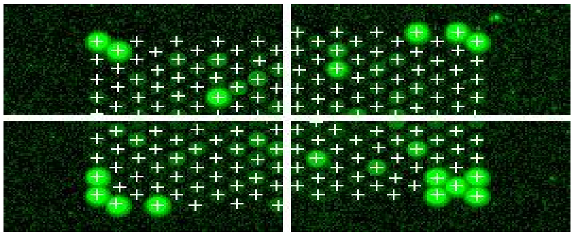
4. Complete Extraction
5. Check for QCs

Appendix 9a: Microarray QC Report

QC Report - Agilent Technologies : 1 Color Gene Expression

Date	Friday, December 09, 2016 - 13:25	Grid	072363_D_F_20150612
Image	SG14024373_257236314226_S001 [1_1]	BG Method	No Background
Protocol	GE1_1105_Oct12 (Read Only)	Background Detrend	On(FeatNCRange, LoPass)
User Name	admin	Multiplicative Detrend	True
FE Version	11.5.1.1	Additive Error	2(Green)
Sample(red/green)		Saturation Value	776621 (g)

Spot Finding of the Four Corners of the Array

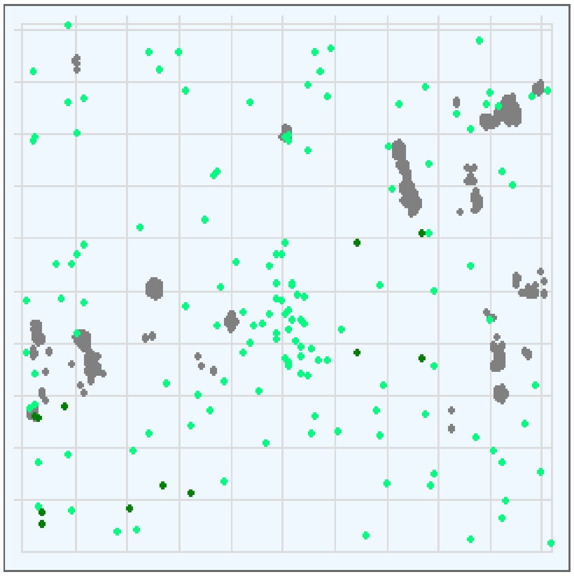


Grid Normal

	Feature Green	Local Background Green
Non Uniform	12	0
Population	139	581

Spatial Distribution of All Outliers on the Array

384 rows x 164 columns



FeatureNonUnif (Green) = 12(0.02%)

GeneNonUnif (Green) = 10 (0.017 %)

- ●BG NonUniform
- ●Green FeaturePopulation
- ●BG Population
- ●Green Feature NonUniform

Negative Control Stats

	Green
Average Net Signals	19.56
StdDev Net Signals	2.24
Average BG Sub Signal	-2.76
StdDev BG Sub Signal	2.03

Net Signal Statistics

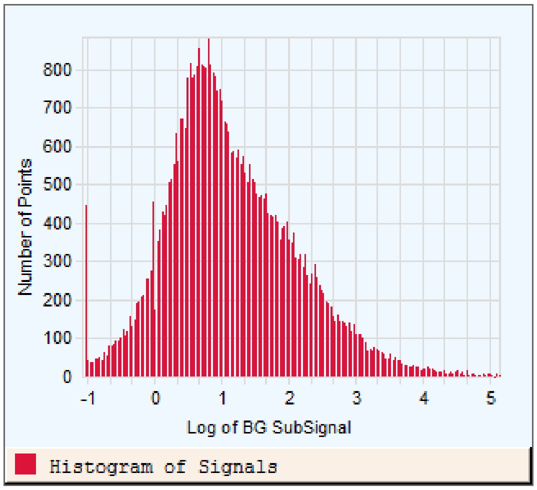
Agilent SpikeIns:

	Green
# Saturated Features	0
99% of Sig. Distrib.	94905
50% of Sig. Distrib.	14697
1% of Sig. Distrib.	1117

Non-Control probes:

	Green
# Saturated Features	0
99% of Sig. Distrib.	4090
50% of Sig. Distrib.	27
1% of Sig. Distrib.	17

Histogram of Signals Plot



Features (NonCtrl) with BGSubSignal < 0: 14325 (Green)

Local Bkg (inliers)

	Green
Number	62395
Avg	23.67
SD	1.60

Foreground Surface Fit

	Green
RMS_Fit	0.85
RMS_Resid	2.29
Avg_Fit	32.31

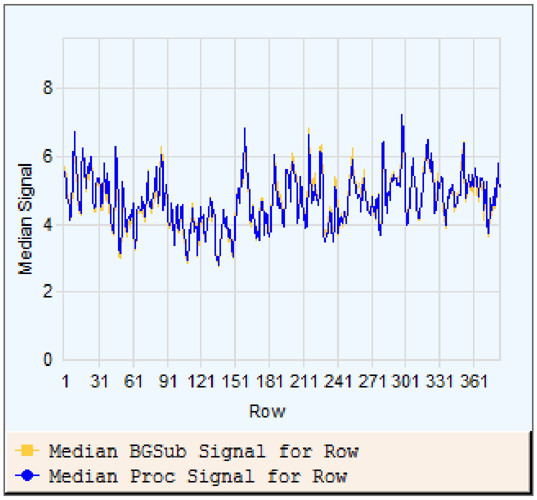
Multiplicative Surface Fit

	Green
RMS_Fit	0.07

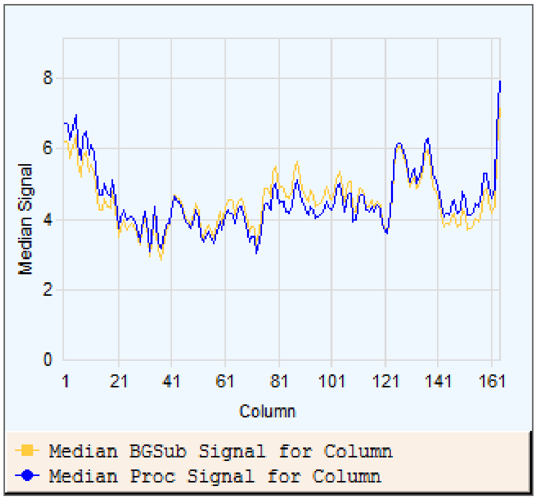
Reproducibility: %CV for Replicated Probes

	Median %CV Signal (inliers)	
	Non-Control probes Green	Agilent SpikeIns Green
BGSubSignal	11.45	9.37
ProcessedSignal	7.26	4.04

Spatial Distribution of Median Signals for each Row



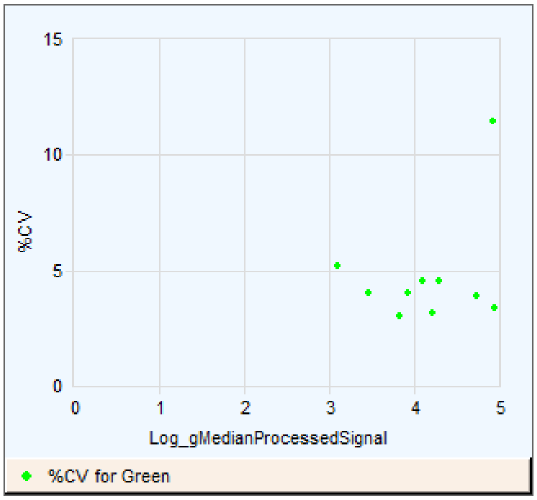
Spatial Distribution of Median Signals for each Column



Agilent SpikeIns Signal Statistics

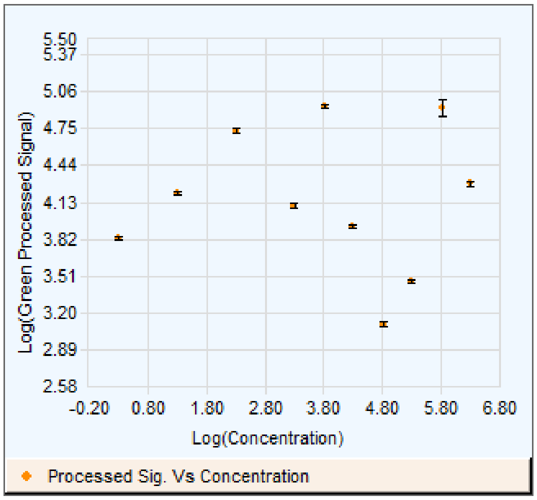
Probe Name	Log(Relative Conc.)	Median(Log Proc. Sig.)	% CV	StdDev
(+)E1A_r60_3	0.30	3.83	3.01	0.01
(+)E1A_r60_a104	1.30	4.22	3.18	0.01
(+)E1A_r60_a107	2.30	4.73	3.91	0.02
(+)E1A_r60_a135	3.30	4.10	4.54	0.02
(+)E1A_r60_a20	3.83	4.94	3.42	0.01
(+)E1A_r60_a22	4.30	3.93	4.04	0.02
(+)E1A_r60_a97	4.82	3.11	5.21	0.02
(+)E1A_r60_n11	5.30	3.47	4.05	0.02
(+)E1A_r60_n9	5.82	4.93	11.43	0.07
(+)E1A_r60_1	6.30	4.29	4.51	0.02

Agilent SpikeIns: %CV of Avg. Processed Signal Plot



Median %CV:4.04

Agilent SpikeIns: Log(Signal) vs. Log(Relative concentration) Plot



Agilent Spike-In Concentration-Response Statistics

Linear Range Statistics:

Low Signal	NA
High Signal	NA
Low Relative Concentration	NA
High Relative Concentration	NA
Slope	NA
R^2 Value	NA

Signal Detection Limit Statistics

Saturation Point	NA
Low Threshold	NA
Low Threshold Error	NA
Spike-In Detection Limit	NA

Evaluation Metrics for GE1_QCMT_Oct12
Good (8) ; Evaluate (2)

Metric Name	Value	Excellent	Good	Evaluate
IsGoodGrid	1.00		>1	<1
AnyColorPrcntFeatNonU...	0.02		<1	>1
gNegCtrlAveNetSig	19.56		<40	>40
gNegCtrlAveBGSubSig	-2.76		-10 to 5	<-10 or >5
gNegCtrlSDevBGSubSig	2.03		<10	>10
gSpatialDetrendRMSFil...	2.29		<15	>15
gNonCntrlMedCVProcSig...	7.26		0 to 8	<0 or >8
gE1aMedCVProcSignal	4.04		0 to 8	<0 or >8
absGE1E1aSlope	0.00		0.90 to 1.20	<0.90 or >1.20
DetectionLimit	-1.00		0.01 to 2	<0.01 or >2

• Excellent • Good • Evaluate

Annexure 10: Sample Location in Microarray slides with Code

257236314226	1_1 **1P3** *Ctrl*	1_2 **10P3** *Ctrl*	1_3 **23P3** *Yoga*	1_4 **1BL** *Ctrl*
	2_1 **10BL** *Ctrl*	2_2 **23BL** *Yoga*	2_3 **24BL** *Yoga*	2_4 **24P3** *Yoga*

257236314225	1_1 **3BL** *Ctrl*	1_2 **6BL** *Ctrl*	1_3 **15BL** *Yoga*	1_4 **22BL** *Yoga*
	2_1 **3P3** *Ctrl*	2_2 **6P3** *Ctrl*	2_3 **15P3** *Yoga*	2_4 **22P3** *Yoga*

257236314224	1_1 **5BL** *Ctrl*	1_2 **12BL** *Ctrl*	1_3 **14BL** *Yoga*	1_4 **19BL** *Yoga*
	2_1 **5P3** *Ctrl*	2_2 **12P3** *Ctrl*	2_3 **14P3** *Yoga*	2_4 **19P3** *Yoga*

257236316740	1_1 **1P1** *Ctrl*	1_2 **14P1** *Yoga*	1_3 **3P1** *Ctrl*	1_4 **5P1** *Ctrl*
	2_1 **15P1** *Yoga*	2_2 **19P1** *Yoga*	2_3 **22P1** *Yoga*	2_4 **6P1** *Ctrl*

257236316739	1_1 **10P1** *Ctrl*	1_2 **23P1** *Yoga*	1_3 **24P1** *Yoga*	1_4 **12P1** *Ctrl*
	2_1 **23BL** *Yoga (Rerun)*	2_2 **24P3** *Yoga (Rerun)*	2_3 **C1** *Another sample*	2_4 **Y11** *Another sample*

Appendix 11a: Significantly regulated pathways for timepoint comparison BL-P1

Pathway	**Source**	**External_id**	**p-value**	**q-value**
Metabolism	Reactome	R-HSA-1430728	2.96E-07	0.000991
Gene Expression	Reactome	R-HSA-74160	8.24E-07	0.001382
Signal Transduction	Reactome	R-HSA-162582	1.60E-05	0.01524
Immune System	Reactome	R-HSA-168256	1.88E-05	0.01524
Cell Cycle	Reactome	R-HSA-1640170	3.06E-05	0.01524
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	Reactome	R-HSA-975957	3.46E-05	0.01524
Nonsense-Mediated Decay (NMD)	Reactome	R-HSA-927802	3.46E-05	0.01524
The citric acid (TCA) cycle and respiratory electron transport	Reactome	R-HSA-1428517	3.64E-05	0.01524
Cell Cycle, Mitotic	Reactome	R-HSA-69278	5.43E-05	0.020246
SRP-dependent cotranslational protein targeting to membrane	Reactome	R-HSA-1799339	6.44E-05	0.021059
Cytoplasmic Ribosomal Proteins	Wikipathways	WP477	6.91E-05	0.021059
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	Reactome	R-HSA-975956	8.14E-05	0.022763
Metabolism of amino acids and derivatives	Reactome	R-HSA-71291	0.000116	0.029919
Antigen processing: Ubiquitination & Proteasome degradation	Reactome	R-HSA-983168	0.000128	0.030557
Cellular responses to stress	Reactome	R-HSA-2262752	0.000137	0.030694
Respiratory electron transport	Reactome	R-HSA-611105	0.000244	0.051225
Transcriptional Regulation by TP53	Reactome	R-HSA-3700989	0.000287	0.052609
Eukaryotic Translation Termination	Reactome	R-HSA-72764	0.000291	0.052609
Extension of Telomeres	Reactome	R-HSA-180786	0.000298	0.052609
Ribosome - Homo sapiens (human)	KEGG	path:hsa03010	0.000316	0.05299
Translation	Reactome	R-HSA-72766	0.000418	0.06027
Eukaryotic Translation Elongation	Reactome	R-HSA-156842	0.000426	0.06027
Class I MHC mediated antigen processing & presentation	Reactome	R-HSA-983169	0.00043	0.06027
Transmembrane transport of small molecules	Reactome	R-HSA-382551	0.000431	0.06027
DNA replication - Homo sapiens (human)	KEGG	path:hsa03030	0.000598	0.077408
Peptide chain elongation	Reactome	R-HSA-156902	0.000603	0.077408
Selenoamino acid metabolism	Reactome	R-HSA-2408522	0.00065	0.077408

DNA Replication	Reactome	R-HSA-69306	0.000654	0.077408
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	Reactome	R-HSA-163200	0.000669	0.077408
Formation of a pool of free 40S subunits	Reactome	R-HSA-72689	0.000694	0.077602
Huntington,s disease - Homo sapiens (human)	KEGG	path:hsa05016	0.000784	0.084878
Protein processing in endoplasmic reticulum - Homo sapiens (human)	KEGG	path:hsa04141	0.000817	0.085627
Fanconi anemia pathway - Homo sapiens (human)	KEGG	path:hsa03460	0.000872	0.088609
T helper 17 (Th17) targets (ROYAN institute)	Wikipathways	WP3536	0.000977	0.093583
Complement Activation	Wikipathways	WP545	0.000977	0.093583
Ubiquitin mediated proteolysis - Homo sapiens (human)	KEGG	path:hsa04120	0.001077	0.100368
M Phase	Reactome	R-HSA-68886	0.001144	0.103702
Selenocysteine synthesis	Reactome	R-HSA-2408557	0.00118	0.104192
L13a-mediated translational silencing of Ceruloplasmin expression	Reactome	R-HSA-156827	0.00125	0.10482
3, -UTR-mediated translational regulation	Reactome	R-HSA-157279	0.00125	0.10482
Cap-dependent Translation Initiation	Reactome	R-HSA-72737	0.00138	0.109698
Eukaryotic Translation Initiation	Reactome	R-HSA-72613	0.00138	0.109698
GTP hydrolysis and joining of the 60S ribosomal subunit	Reactome	R-HSA-72706	0.001406	0.109698
Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate - Homo sapiens (human)	KEGG	path:hsa00532	0.001465	0.111661
Complement and coagulation cascades - Homo sapiens (human)	KEGG	path:hsa04610	0.001548	0.115375
Telomere C-strand (Lagging Strand) Synthesis	Reactome	R-HSA-174417	0.001694	0.121809
Cellular Senescence	Reactome	R-HSA-2559583	0.001753	0.121809
Innate Immune System	Reactome	R-HSA-168249	0.001771	0.121809
Fanconi Anemia Pathway	Reactome	R-HSA-6783310	0.00178	0.121809
Endoderm Differentiation	Wikipathways	WP2853	0.001929	0.129394
Telomere Maintenance	Reactome	R-HSA-157579	0.002051	0.134886
APC/C-mediated degradation of cell cycle proteins	Reactome	R-HSA-174143	0.002248	0.142279
Regulation of mitotic cell cycle	Reactome	R-HSA-453276	0.002248	0.142279

IKK complex recruitment mediated by RIP1	Reactome	R-HSA-937041	0.002335	0.143657
Synthesis of DNA	Reactome	R-HSA-69239	0.002361	0.143657
The oncogenic action of L-2-hydroxyglutarate in Hydroxygluaricaciduria	SMPDB	SMP02358	0.002441	0.143657
The oncogenic action of D-2-hydroxyglutarate in Hydroxygluaricaciduria	SMPDB	SMP02359	0.002441	0.143657
Intra-Golgi and retrograde Golgi-to-ER traffic	Reactome	R-HSA-6811442	0.002665	0.1541
Oxidative phosphorylation - Homo sapiens (human)	KEGG	path:hsa00190	0.002755	0.15661
ATR signaling pathway	PID	atr_pathway	0.002838	0.158652
chondroitin sulfate biosynthesis	HumanCyc	PWY-6569	0.00293	0.161085
Fanconi anemia pathway	PID	fanconi_pathway	0.002992	0.161872
Parkinson,s disease - Homo sapiens (human)	KEGG	path:hsa05012	0.003192	0.169942
Gap-filling DNA repair synthesis and ligation in GG-NER	Reactome	R-HSA-5696397	0.003342	0.174688
role of brca1 brca2 and atr in cancer susceptibility	BioCarta	atrbrcapathway	0.003418	0.174688
COPI-dependent Golgi-to-ER retrograde traffic	Reactome	R-HSA-6811434	0.003711	0.174688
Organelle biogenesis and maintenance	Reactome	R-HSA-1852241	0.003776	0.174688
Chemokine receptors bind chemokines	Reactome	R-HSA-380108	0.003901	0.174688
eNOS activation and regulation	Reactome	R-HSA-203765	0.003906	0.174688
Metabolism of nitric oxide	Reactome	R-HSA-202131	0.003906	0.174688
dermatan sulfate biosynthesis	HumanCyc	PWY-6571	0.003906	0.174688
Malonyl-coa decarboxylase deficiency	SMPDB	SMP00502	0.003906	0.174688
Malonic Aciduria	SMPDB	SMP00198	0.003906	0.174688
Propanoate Metabolism	SMPDB	SMP00016	0.003906	0.174688
Methylmalonic Aciduria Due to Cobalamin-Related Disorders	SMPDB	SMP00201	0.003906	0.174688
Mitotic Metaphase and Anaphase	Reactome	R-HSA-2555396	0.003965	0.174985
Degradation of the extracellular matrix	Reactome	R-HSA-1474228	0.004077	0.177503
Complement cascade	Reactome	R-HSA-166658	0.004181	0.177503
Translesion Synthesis by POLH	Reactome	R-HSA-110320	0.004181	0.177503
Cell Cycle Checkpoints	Reactome	R-HSA-69620	0.004572	0.183037
p38 MAPK signaling pathway	PID	p38_mkk3_6pathway	0.004578	0.183037
Lagging Strand Synthesis	Reactome	R-HSA-69186	0.004639	0.183037

p53-Dependent G1 DNA Damage Response	Reactome	R-HSA-69563	0.004639	0.183037
p53-Dependent G1/S DNA damage checkpoint	Reactome	R-HSA-69580	0.004639	0.183037
G1/S DNA Damage Checkpoints	Reactome	R-HSA-69615	0.004639	0.183037
S Phase	Reactome	R-HSA-69242	0.004823	0.186102
Citrate cycle (TCA cycle) - Homo sapiens (human)	KEGG	path:hsa00020	0.004883	0.186102
The oncogenic action of 2-hydroxyglutarate	SMPDB	SMP02291	0.004883	0.186102
Vesicle-mediated transport	Reactome	R-HSA-5653656	0.005235	0.191222
Electron Transport Chain	Wikipathways	WP111	0.005274	0.191222
Pyruvate metabolism and Citric Acid (TCA) cycle	Reactome	R-HSA-71406	0.00533	0.191222
Membrane Trafficking	Reactome	R-HSA-199991	0.005333	0.191222
Vitamin D Receptor Pathway	Wikipathways	WP2877	0.005335	0.191222
Glycerolipid metabolism - Homo sapiens (human)	KEGG	path:hsa00561	0.005359	0.191222
Regulation of APC/C activators between G1/S and early anaphase	Reactome	R-HSA-176408	0.005579	0.194983
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	Reactome	R-HSA-174178	0.005581	0.194983
DNA Replication	Wikipathways	WP466	0.005649	0.195324
DNA Damage Bypass	Reactome	R-HSA-73893	0.005827	0.199418
Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	Reactome	R-HSA-110313	0.005995	0.203091
Mitotic Anaphase	Reactome	R-HSA-68882	0.006062	0.203328
Separation of Sister Chromatids	Reactome	R-HSA-2467813	0.006552	0.215004
Proteoglycan biosynthesis	EHMN	Proteoglycan biosynthesis metabolism	0.006577	0.215004
DNA Damage Response	Wikipathways	WP707	0.006603	0.215004
TP53 Regulates Metabolic Genes	Reactome	R-HSA-5628897	0.006891	0.222226
APC/C:Cdc20 mediated degradation of Securin	Reactome	R-HSA-174154	0.007145	0.228229
Methionine and cysteine metabolism	EHMN	Methionine and cysteine	0.007309	0.23127
Factors involved in megakaryocyte development and platelet production	Reactome	R-HSA-983231	0.007518	0.235668
classical complement pathway	BioCarta	classicpathway	0.007813	0.242622
APC/C:Cdc20 mediated degradation of Cyclin B	Reactome	R-HSA-174048	0.008232	0.253308

Development and heterogeneity of the ILC family	Wikipathways	WP3893	0.008362	0.254959
Oxidative Damage	Wikipathways	WP3941	0.008715	0.26188
Formation of the ternary complex, and subsequently, the 43S complex	Reactome	R-HSA-72695	0.008745	0.26188
TP53 Regulates Transcription of DNA Repair Genes	Wikipathways	WP3808	0.009277	0.275365
N-glycan trimming in the ER and Calnexin/Calreticulin cycle	Reactome	R-HSA-532668	0.009453	0.278112
integrin signaling pathway	BioCarta	integrinpathway	0.009635	0.281008
Regulation of TP53 Activity through Phosphorylation	Reactome	R-HSA-6804756	0.009831	0.284252

Appendix 11b: Significantly regulated pathways in timepoint comparison P1-P3

pathway	source	external_id	p-value	q-value
Ribosome - Homo sapiens (human)	KEGG	path:hsa03010	3.12376E-11	1.01022E-07
Selenocysteine synthesis	Reactome	R-HSA-2408557	3.95019E-10	6.38746E-07
Eukaryotic Translation Termination	Reactome	R-HSA-72764	8.14896E-10	8.78458E-07
Eukaryotic Translation Elongation	Reactome	R-HSA-156842	1.43809E-09	1.1627E-06
Peptide chain elongation	Reactome	R-HSA-156902	2.16489E-09	1.36852E-06
SRP-dependent cotranslational protein targeting to membrane	Reactome	R-HSA-1799339	2.53901E-09	1.36852E-06
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	Reactome	R-HSA-975956	3.20823E-09	1.4822E-06
Gene Expression	Reactome	R-HSA-74160	4.04392E-09	1.63475E-06
Formation of a pool of free 40S subunits	Reactome	R-HSA-72689	5.82124E-09	2.09176E-06
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	Reactome	R-HSA-975957	1.26449E-08	3.71761E-06
Nonsense-Mediated Decay (NMD)	Reactome	R-HSA-927802	1.26449E-08	3.71761E-06
Selenoamino acid metabolism	Reactome	R-HSA-2408522	1.49892E-08	3.98687E-06
GTP hydrolysis and joining of the 60S ribosomal subunit	Reactome	R-HSA-72706	1.60264E-08	3.98687E-06
L13a-mediated translational silencing of Ceruloplasmin expression	Reactome	R-HSA-156827	2.37638E-08	5.12348E-06
3, -UTR-mediated translational regulation	Reactome	R-HSA-157279	2.37638E-08	5.12348E-06
Translation	Reactome	R-HSA-72766	3.11561E-08	6.29742E-06
Cap-dependent Translation Initiation	Reactome	R-HSA-72737	4.4097E-08	7.92276E-06
Eukaryotic Translation Initiation	Reactome	R-HSA-72613	4.4097E-08	7.92276E-06
Metabolism	Reactome	R-HSA-1430728	6.36237E-08	1.08294E-05
Cytoplasmic Ribosomal Proteins	Wikipathways	WP477	2.3063E-07	3.68766E-05
Metabolism of proteins	Reactome	R-HSA-392499	2.39458E-07	3.68766E-05
Neutrophil degranulation	Reactome	R-HSA-6798695	2.26547E-06	0.000333025
Immune System	Reactome	R-HSA-168256	4.34885E-06	0.000611486
Innate Immune System	Reactome	R-HSA-168249	1.43602E-05	0.001935034
The citric acid (TCA) cycle and respiratory electron transport	Reactome	R-HSA-1428517	1.64031E-05	0.002121906
Oxidative phosphorylation - Homo sapiens (human)	KEGG	path:hsa00190	2.03058E-05	0.002447124
Electron Transport Chain	Wikipathways	WP111	2.04305E-05	0.002447124

Squalene and cholesterol biosynthesis	EHMN	Squalene and cholesterol biosynthesis	6.29425E-05	0.007269859
Metabolism of amino acids and derivatives	Reactome	R-HSA-71291	0.00012566	0.014014222
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	Reactome	R-HSA-163200	0.00013376	0.014419998
Formation of Incision Complex in GG-NER	Reactome	R-HSA-5696395	0.00013989	0.014593905
Complex I biogenesis	Reactome	R-HSA-6799198	0.00016353	0.016527527
Prostaglandin formation from dihomo gama-linoleic acid	EHMN	Prostaglandin formation from dihomo gama-linoleic acid	0.00020980	0.020561218
Formation of the ternary complex, and subsequently, the 43S complex	Reactome	R-HSA-72695	0.00023364	0.022223533
Dual incision in TC-NER	Reactome	R-HSA-6782135	0.00029913	0.027639617
Nucleotide Excision Repair	Reactome	R-HSA-5696398	0.00031372	0.028183351
B cell receptor signaling pathway - Homo sapiens (human)	KEGG	path:hsa04662	0.00034128	0.029830546
Gap-filling DNA repair synthesis and ligation in TC-NER	Reactome	R-HSA-6782210	0.00038589	0.032841769
Parkin-Ubiquitin Proteasomal System pathway	Wikipath ways	WP2359	0.00043054	0.035580765
Mitochondrial translation initiation	Reactome	R-HSA-5368286	0.00044008	0.035580765
Respiratory electron transport	Reactome	R-HSA-611105	0.00046594	0.036753045
Pentose phosphate pathway	EHMN	Pentose phosphate pathway	0.00050354	0.038772583
Mitochondrial translation	Reactome	R-HSA-5368287	0.00057839	0.043136307
tRNA processing	Reactome	R-HSA-72306	0.00058688	0.043136307
De novo fatty acid biosynthesis	EHMN	De novo fatty acid biosynthesis	0.00072097	0.05181427
Mitochondrial translation termination	Reactome	R-HSA-5419276	0.00078895	0.055467105
Mitochondrial translation elongation	Reactome	R-HSA-5389840	0.00084125	0.056066036
Cyclin D associated events in G1	Reactome	R-HSA-69231	0.00084948	0.056066036
G1 Phase	Reactome	R-HSA-69236	0.00084948	0.056066036
Ribosomal scanning and start codon recognition	Reactome	R-HSA-72702	0.00096862	0.062563912
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	Reactome	R-HSA-72662	0.00098662	0.062563912

Vitamin D3 (cholecalciferol) metabolism	EHMN	Vitamin D3 (cholecalciferol) metabolism	0.00100708	0.062632634
Host Interactions of HIV factors	Reactome	R-HSA-162909	0.00139073	0.083533521
Translation initiation complex formation	Reactome	R-HSA-72649	0.00141474	0.083533521
B cell receptor signaling	INOH	None	0.00142063	0.083533521
Generic Transcription Pathway	Reactome	R-HSA-212436	0.00159029	0.091839561
Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human)	KEGG	path:hsa04932	0.00165668	0.093356214
Purine metabolism	EHMN	Purine metabolism	0.00167429	0.093356214
Putative anti-Inflammatory metabolites formation from EPA	EHMN	Putative anti-Inflammatory metabolites formation from EPA	0.00177955	0.097543813
Hemostasis	Reactome	R-HSA-109582	0.00187751	0.100260417
Degradation of GLI2 by the proteasome	Reactome	R-HSA-5610783	0.00195312	0.100260417
Synthesis of glycosylphosphatidylinositol (GPI)	Reactome	R-HSA-162710	0.00195312	0.100260417
Translesion Synthesis by POLH	Reactome	R-HSA-110320	0.00195312	0.100260417
Vitamin B3 (nicotinate and nicotinamide) metabolism	EHMN	Vitamin B3 (nicotinate and nicotinamide) metabolism	0.00218153	0.109147453
Epstein-Barr virus infection - Homo sapiens (human)	KEGG	path:hsa05169	0.00219374	0.109147453
Basal cell carcinoma - Homo sapiens (human)	KEGG	path:hsa05217	0.00233459	0.114395142
Transcription-Coupled Nucleotide Excision Repair (TC-NER)	Reactome	R-HSA-6781827	0.00250052	0.120696991
Parkinson,s disease - Homo sapiens (human)	KEGG	path:hsa05012	0.00263741	0.125432542
Global Genome Nucleotide Excision Repair (GG-NER)	Reactome	R-HSA-5696399	0.00285026	0.133590457
Huntington,s disease - Homo sapiens (human)	KEGG	path:hsa05016	0.003297	0.152321394
Glycine, serine, alanine and threonine metabolism	EHMN	Glycine, serine, alanine and threonine metabolism	0.00351797	0.160241206
Phosphatidylinositol phosphate metabolism	EHMN	Phosphatidylinositol	0.00361135	0.162210029

		phosphate metabolism		
GLI3 is processed to GLI3R by the proteasome	Reactome	R-HSA-5610785	0.00390625	0.166106689
Constitutive Signaling by NOTCH1 HD Domain Mutants	Reactome	R-HSA-2691232	0.00390625	0.166106689
Signaling by NOTCH1 HD Domain Mutants in Cancer	Reactome	R-HSA-2691230	0.00390625	0.166106689
Sumoylation by RanBP2 regulates transcriptional repression	PID	ranbp2pathway	0.00390625	0.166106689
Notch	INOH	None	0.00395492	0.166106689
tRNA processing in the nucleus	Reactome	R-HSA-6784531	0.00407423	0.168924036
Ub-specific processing proteases	Reactome	R-HSA-5689880	0.00471362	0.192960149
Warburg Effect	SMPDB	SMP00654	0.00485134	0.193694291
Dual Incision in GG-NER	Reactome	R-HSA-5696400	0.00485134	0.193694291
Protein folding	Reactome	R-HSA-391251	0.00495237	0.195316682
Post-translational modification: synthesis of GPI-anchored proteins	Reactome	R-HSA-163125	0.00507447	0.197281216
HIV Infection	Reactome	R-HSA-162906	0.00512418	0.197281216
TLR p38	INOH	None	0.00544164	0.207038487
NOTCH1 Intracellular Domain Regulates Transcription	Reactome	R-HSA-2122947	0.00594034	0.223384711
Nuclear import of Rev protein	Reactome	R-HSA-180746	0.00612920	0.227837353
Alzheimer,s disease - Homo sapiens (human)	KEGG	path:hsa05010	0.00632598	0.232479749
TLR JNK	INOH	None	0.00663953	0.239058431
Activation of BH3-only proteins	Reactome	R-HSA-114452	0.00665283	0.239058431
endocytotic role of ndk phosphins and dynamin	BioCarta	ndkdynaminpathway	0.00683593	0.242938702
Hypoxic and oxygen homeostasis regulation of HIF-1-alpha	PID	hif1apathway	0.0078125	0.268783245
4-hydroxytamoxifen, Dexamethasone, and Retinoic Acids Regulation of p27 Expression	Wikipathways	WP3879	0.0078125	0.268783245
Passive transport by Aquaporins	Reactome	R-HSA-432047	0.0078125	0.268783245
Gap-filling DNA repair synthesis and ligation in GG-NER	Reactome	R-HSA-5696397	0.00805664	0.274265008
Influenza Viral RNA Transcription and Replication	Reactome	R-HSA-168273	0.00829844	0.277004124
Vitamin E metabolism	EHMN	Vitamin E metabolism	0.00830841	0.277004124
Deubiquitination	Reactome	R-HSA-5688426	0.00848117	0.279878862
Cellular responses to stress	Reactome	R-HSA-2262752	0.00865478	0.282723014
Hedgehog	INOH	None	0.00907005	0.293325457

ion channels and their functional role in vascular endothelium	BioCarta	raccpathway	0.00943565	0.298557223
Intrinsic Pathway for Apoptosis	Reactome	R-HSA-109606	0.00953640	0.298557223
Adaptive Immune System	Reactome	R-HSA-1280218	0.00955095	0.298557223
UCH proteinases	Reactome	R-HSA-5689603	0.00960109	0.298557223
BCR signaling pathway	PID	bcr_5pathway	0.00978948	0.301516068

Appendix 11c: Significantly regulated pathways for timepoint comparison BL-P3

Pathway	Source	External_id	p-value	q-value
Gene Expression	Reactome	R-HSA-74160	1.27E-34	4.15E-31
Metabolism of proteins	Reactome	R-HSA-392499	1.24E-30	2.03E-27
Immune System	Reactome	R-HSA-168256	6.57E-27	7.18E-24
Metabolism	Reactome	R-HSA-1430728	3.76E-26	3.08E-23
Signal Transduction	Reactome	R-HSA-162582	1.69E-23	1.11E-20
Post-translational protein modification	Reactome	R-HSA-597592	5.99E-18	3.27E-15
Innate Immune System	Reactome	R-HSA-168249	7.68E-18	3.59E-15
Vesicle-mediated transport	Reactome	R-HSA-5653656	7.60E-17	3.11E-14
Membrane Trafficking	Reactome	R-HSA-199991	1.00E-16	3.64E-14
Cell Cycle	Reactome	R-HSA-1640170	1.89E-16	6.19E-14
Cell Cycle, Mitotic	Reactome	R-HSA-69278	5.65E-14	1.68E-11
Cellular responses to stress	Reactome	R-HSA-2262752	6.32E-13	1.72E-10
Class I MHC mediated antigen processing & presentation	Reactome	R-HSA-983169	1.97E-12	4.96E-10
Generic Transcription Pathway	Reactome	R-HSA-212436	1.01E-11	2.24E-09
The citric acid (TCA) cycle and respiratory electron transport	Reactome	R-HSA-1428517	1.02E-11	2.24E-09
Neutrophil degranulation	Reactome	R-HSA-6798695	3.15E-11	6.44E-09
Organelle biogenesis and maintenance	Reactome	R-HSA-1852241	2.48E-10	4.79E-08
Transmembrane transport of small molecules	Reactome	R-HSA-382551	5.60E-10	1.02E-07
M Phase	Reactome	R-HSA-68886	8.45E-10	1.46E-07
miR-targeted genes in lymphocytes - TarBase	Wikipathways	WP2004	9.76E-10	1.60E-07
Ribosome - Homo sapiens (human)	KEGG	path:hsa03010	2.72E-09	4.23E-07
Antigen processing: Ubiquitination & Proteasome degradation	Reactome	R-HSA-983168	3.29E-09	4.82E-07
TNFalpha	NetPath	Pathway_TNFalpha	3.61E-09	4.82E-07
Adaptive Immune System	Reactome	R-HSA-1280218	3.65E-09	4.82E-07
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	Reactome	R-HSA-163200	3.68E-09	4.82E-07
Signaling by Rho GTPases	Reactome	R-HSA-194315	7.89E-09	9.93E-07
Huntington,s disease - Homo sapiens (human)	KEGG	path:hsa05016	9.07E-09	1.10E-06
Metabolism of lipids and lipoproteins	Reactome	R-HSA-556833	1.10E-08	1.29E-06
Metabolism of amino acids and derivatives	Reactome	R-HSA-71291	1.16E-08	1.31E-06
Toll-Like Receptors Cascades	Reactome	R-HSA-168898	1.37E-08	1.49E-06

Translation	Reactome	R-HSA-72766	1.49E-08	1.58E-06
miR-targeted genes in muscle cell - TarBase	Wikipathways	WP2005	3.57E-08	3.66E-06
Toll Like Receptor 4 (TLR4) Cascade	Reactome	R-HSA-166016	4.20E-08	4.17E-06
Respiratory electron transport	Reactome	R-HSA-611105	4.53E-08	4.36E-06
Disease	Reactome	R-HSA-1643685	8.25E-08	7.72E-06
Transcriptional Regulation by TP53	Reactome	R-HSA-3700989	8.72E-08	7.93E-06
Ubiquitin mediated proteolysis - Homo sapiens (human)	KEGG	path:hsa04120	1.23E-07	1.09E-05
Electron Transport Chain	Wikipathways	WP111	1.30E-07	1.12E-05
Alzheimer,s disease - Homo sapiens (human)	KEGG	path:hsa05010	1.45E-07	1.22E-05
Developmental Biology	Reactome	R-HSA-1266738	1.50E-07	1.23E-05
SRP-dependent cotranslational protein targeting to membrane	Reactome	R-HSA-1799339	1.55E-07	1.24E-05
Deubiquitination	Reactome	R-HSA-5688426	2.01E-07	1.57E-05
Cap-dependent Translation Initiation	Reactome	R-HSA-72737	2.38E-07	1.77E-05
Eukaryotic Translation Initiation	Reactome	R-HSA-72613	2.38E-07	1.77E-05
Alcoholism - Homo sapiens (human)	KEGG	path:hsa05034	2.77E-07	2.01E-05
Epigenetic regulation of gene expression	Reactome	R-HSA-212165	3.06E-07	2.06E-05
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	Reactome	R-HSA-975957	3.07E-07	2.06E-05
Nonsense-Mediated Decay (NMD)	Reactome	R-HSA-927802	3.07E-07	2.06E-05
Oxidative phosphorylation - Homo sapiens (human)	KEGG	path:hsa00190	3.14E-07	2.06E-05
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	Reactome	R-HSA-975956	3.14E-07	2.06E-05
Mitochondrial translation	Reactome	R-HSA-5368287	3.24E-07	2.08E-05
Parkinson,s disease - Homo sapiens (human)	KEGG	path:hsa05012	3.32E-07	2.09E-05
Signaling by GPCR	Reactome	R-HSA-372790	3.97E-07	2.45E-05
Cellular Senescence	Reactome	R-HSA-2559583	4.21E-07	2.55E-05
GTP hydrolysis and joining of the 60S ribosomal subunit	Reactome	R-HSA-72706	4.37E-07	2.60E-05
Purine metabolism	EHMN	Purine metabolism	4.88E-07	2.85E-05
Protein processing in endoplasmic reticulum - Homo sapiens (human)	KEGG	path:hsa04141	5.34E-07	3.07E-05
Mitochondrial translation initiation	Reactome	R-HSA-5368286	5.68E-07	3.15E-05
Mitochondrial translation elongation	Reactome	R-HSA-5389840	5.68E-07	3.15E-05
Activated TLR4 signalling	Reactome	R-HSA-166054	6.29E-07	3.43E-05
L13a-mediated translational silencing of Ceruloplasmin expression	Reactome	R-HSA-156827	6.99E-07	3.69E-05

3, -UTR-mediated translational regulation	Reactome	R-HSA-157279	6.99E-07	3.69E-05
Asparagine N-linked glycosylation	Reactome	R-HSA-446203	7.44E-07	3.87E-05
DNA Repair	Reactome	R-HSA-73894	7.56E-07	3.87E-05
Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human)	KEGG	path:hsa04932	8.65E-07	4.36E-05
Processing of Capped Intron-Containing Pre-mRNA	Reactome	R-HSA-72203	1.13E-06	5.61E-05
Intra-Golgi and retrograde Golgi-to-ER traffic	Reactome	R-HSA-6811442	1.18E-06	5.79E-05
Mitochondrial translation termination	Reactome	R-HSA-5419276	1.23E-06	5.91E-05
Mitotic Prophase	Reactome	R-HSA-68875	1.44E-06	6.67E-05
Chromatin modifying enzymes	Reactome	R-HSA-3247509	1.45E-06	6.67E-05
Chromatin organization	Reactome	R-HSA-4839726	1.45E-06	6.67E-05
Formation of a pool of free 40S subunits	Reactome	R-HSA-72689	1.47E-06	6.67E-05
Transcriptional misregulation in cancer - Homo sapiens (human)	KEGG	path:hsa05202	1.52E-06	6.82E-05
Eukaryotic Translation Termination	Reactome	R-HSA-72764	1.54E-06	6.82E-05
Neuronal System	Reactome	R-HSA-112316	1.76E-06	7.66E-05
Pathways in cancer - Homo sapiens (human)	KEGG	path:hsa05200	1.79E-06	7.72E-05
Endocytosis - Homo sapiens (human)	KEGG	path:hsa04144	2.11E-06	8.99E-05
Selenoamino acid metabolism	Reactome	R-HSA-2408522	2.64E-06	0.000111
RNA Polymerase I, RNA Polymerase III, and Mitochondrial Transcription	Reactome	R-HSA-504046	2.89E-06	0.00012
RHO GTPase Effectors	Reactome	R-HSA-195258	3.11E-06	0.000127
Senescence-Associated Secretory Phenotype (SASP)	Reactome	R-HSA-2559582	3.14E-06	0.000127
Cell Cycle Checkpoints	Reactome	R-HSA-69620	3.49E-06	0.000139
Cytoplasmic Ribosomal Proteins	Wikipathways	WP477	4.59E-06	0.000181
Glucocorticoid Receptor Pathway	Wikipathways	WP2880	5.69E-06	0.000222
Eukaryotic Translation Elongation	Reactome	R-HSA-156842	5.88E-06	0.000226
Selenocysteine synthesis	Reactome	R-HSA-2408557	6.89E-06	0.000262
PRC2 methylates histones and DNA	Reactome	R-HSA-212300	8.20E-06	0.000308
RNA transport - Homo sapiens (human)	KEGG	path:hsa03013	8.49E-06	0.000316
GPCR downstream signaling	Reactome	R-HSA-388396	8.69E-06	0.00032
Peptide chain elongation	Reactome	R-HSA-156902	9.61E-06	0.00035
Cytokine Signaling in Immune system	Reactome	R-HSA-1280215	1.02E-05	0.000366
RNA Polymerase I Transcription	Reactome	R-HSA-73864	1.14E-05	0.000405
HATs acetylate histones	Reactome	R-HSA-3214847	1.21E-05	0.000427
Oxidative Stress Induced Senescence	Reactome	R-HSA-2559580	1.29E-05	0.00045
Axon guidance	Reactome	R-HSA-422475	1.35E-05	0.000464
Apoptosis - Homo sapiens (human)	KEGG	path:hsa04210	1.44E-05	0.000492

Ribosomal scanning and start codon recognition	Reactome	R-HSA-72702	1.65E-05	0.000557
TRIF-mediated TLR3/TLR4 signaling	Reactome	R-HSA-937061	1.81E-05	0.000592
MyD88-independent TLR3/TLR4 cascade	Reactome	R-HSA-166166	1.81E-05	0.000592
Toll Like Receptor 3 (TLR3) Cascade	Reactome	R-HSA-168164	1.81E-05	0.000592
Programmed Cell Death	Reactome	R-HSA-5357801	1.82E-05	0.000592
EGFR1	NetPath	Pathway_EGFR 1	1.89E-05	0.000606
Signalling by NGF	Reactome	R-HSA-166520	1.91E-05	0.000608
TNF signaling pathway - Homo sapiens (human)	KEGG	path:hsa04668	1.97E-05	0.000621
MyD88:Mal cascade initiated on plasma membrane	Reactome	R-HSA-166058	2.13E-05	0.000646
Toll Like Receptor TLR1:TLR2 Cascade	Reactome	R-HSA-168179	2.13E-05	0.000646
Toll Like Receptor TLR6:TLR2 Cascade	Reactome	R-HSA-168188	2.13E-05	0.000646
Toll Like Receptor 2 (TLR2) Cascade	Reactome	R-HSA-181438	2.13E-05	0.000646
RNA Polymerase I Chain Elongation	Reactome	R-HSA-73777	2.15E-05	0.000647
Infectious disease	Reactome	R-HSA-5663205	2.17E-05	0.000647
Negative epigenetic regulation of rRNA expression	Reactome	R-HSA-5250941	2.22E-05	0.00065
NOD-like receptor signaling pathway - Homo sapiens (human)	KEGG	path:hsa04621	2.22E-05	0.00065
Separation of Sister Chromatids	Reactome	R-HSA-2467813	2.29E-05	0.000663
Ub-specific processing proteases	Reactome	R-HSA-5689880	2.61E-05	0.000749
Transmission across Chemical Synapses	Reactome	R-HSA-112315	2.65E-05	0.000755
Apoptosis	Reactome	R-HSA-109581	2.71E-05	0.000765
VEGFA-VEGFR2 Signaling Pathway	Wikipathways	WP3888	2.83E-05	0.000792
HIV Infection	Reactome	R-HSA-162906	3.02E-05	0.000838
RNA Polymerase I Promoter Clearance	Reactome	R-HSA-73854	3.14E-05	0.000864
Translation initiation complex formation	Reactome	R-HSA-72649	3.17E-05	0.000866
SUMOylation	Reactome	R-HSA-2990846	3.43E-05	0.000928
Progesterone-mediated oocyte maturation - Homo sapiens (human)	KEGG	path:hsa04914	3.54E-05	0.000943
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	Reactome	R-HSA-72662	3.54E-05	0.000943
Mitotic Anaphase	Reactome	R-HSA-68882	3.60E-05	0.000944
Mitotic Metaphase and Anaphase	Reactome	R-HSA-2555396	3.60E-05	0.000944
Intra-Golgi traffic	Reactome	R-HSA-6811438	3.77E-05	0.000973
Ribosome biogenesis in eukaryotes - Homo sapiens (human)	KEGG	path:hsa03008	3.77E-05	0.000973

Formation of the ternary complex, and subsequently, the 43S complex	Reactome	R-HSA-72695	3.95E-05	0.00101
Meiosis	Reactome	R-HSA-1500620	4.26E-05	0.001081
NoRC negatively regulates rRNA expression	Reactome	R-HSA-427413	4.33E-05	0.00109
Gene Silencing by RNA	Reactome	R-HSA-211000	4.38E-05	0.001094
Pyruvate metabolism and Citric Acid (TCA) cycle	Reactome	R-HSA-71406	4.41E-05	0.001094
Gastrin-CREB signalling pathway via PKC and MAPK	Reactome	R-HSA-881907	4.75E-05	0.001169
Neurotransmitter Receptor Binding And Downstream Transmission In The Postsynaptic Cell	Reactome	R-HSA-112314	4.78E-05	0.001169
Apoptosis	Wikipathways	WP254	5.60E-05	0.001349
Apoptotic Signaling Pathway	Wikipathways	WP3639	5.60E-05	0.001349
Mitotic G1-G1/S phases	Reactome	R-HSA-453279	5.87E-05	0.001404
Late Phase of HIV Life Cycle	Reactome	R-HSA-162599	6.08E-05	0.001442
Complex I biogenesis	Reactome	R-HSA-6799198	6.51E-05	0.001533
Cell cycle - Homo sapiens (human)	KEGG	path:hsa04110	6.87E-05	0.001606
B-WICH complex positively regulates rRNA expression	Reactome	R-HSA-5250924	7.80E-05	0.001812
mTOR signaling pathway - Homo sapiens (human)	KEGG	path:hsa04150	8.35E-05	0.001926
Transcriptional regulation by small RNAs	Reactome	R-HSA-5578749	8.42E-05	0.001926
Apoptosis Modulation and Signaling	Wikipathways	WP1772	8.59E-05	0.001926
Apoptosis Modulation and Signaling	Wikipathways	WP3911	8.59E-05	0.001926
Apoptosis Modulation and Signaling	Wikipathways	WP3912	8.59E-05	0.001926
Antigen processing-Cross presentation	Reactome	R-HSA-1236975	8.66E-05	0.001929
miR-targeted genes in epithelium - TarBase	Wikipathways	WP2002	8.98E-05	0.001987
HIF-1 signaling pathway - Homo sapiens (human)	KEGG	path:hsa04066	9.18E-05	0.002018
mRNA Splicing - Major Pathway	Reactome	R-HSA-72163	9.99E-05	0.002182
Nuclear Receptors Meta-Pathway	Wikipathways	WP2882	0.000106	0.002309
Adrenergic signaling in cardiomyocytes - Homo sapiens (human)	KEGG	path:hsa04261	0.000109	0.002352
Positive epigenetic regulation of rRNA expression	Reactome	R-HSA-5250913	0.000125	0.002681
mRNA Splicing	Reactome	R-HSA-72172	0.000127	0.002685
Apoptosis - multiple species - Homo sapiens (human)	KEGG	path:hsa04215	0.000127	0.002685
Cell death signalling via NRAGE, NRIF and NADE	Reactome	R-HSA-204998	0.000128	0.002693
Amyloid fiber formation	Reactome	R-HSA-977225	0.000134	0.002784
HIV Life Cycle	Reactome	R-HSA-162587	0.000134	0.002784

DNA methylation	Reactome	R-HSA-5334118	0.000149	0.003062
SIRT1 negatively regulates rRNA Expression	Reactome	R-HSA-427359	0.000161	0.003288
TNF	INOH	None	0.000168	0.003409
Cilium Assembly	Reactome	R-HSA-5617833	0.000173	0.003505
Signaling events mediated by HDAC Class II	PID	hdac_classii_pathway	0.000177	0.003554
Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	Reactome	R-HSA-168643	0.000189	0.003771
Signaling Pathways in Glioblastoma	Wikipathways	WP2261	0.000192	0.003818
IL1	NetPath	Pathway_IL1	0.000203	0.003998
Condensation of Prophase Chromosomes	Reactome	R-HSA-2299718	0.000212	0.004158
IL-1 signaling pathway	Wikipathways	WP195	0.000233	0.004533
MyD88 dependent cascade initiated on endosome	Reactome	R-HSA-975155	0.000243	0.004653
Toll Like Receptor 7/8 (TLR7/8) Cascade	Reactome	R-HSA-168181	0.000243	0.004653
Butyrate Response Factor 1 (BRF1) binds and destabilizes mRNA	Reactome	R-HSA-450385	0.000244	0.004653
G alpha (q) signalling events	Reactome	R-HSA-416476	0.000244	0.004653
MyD88 cascade initiated on plasma membrane	Reactome	R-HSA-975871	0.000263	0.004928
Toll Like Receptor 10 (TLR10) Cascade	Reactome	R-HSA-168142	0.000263	0.004928
Toll Like Receptor 5 (TLR5) Cascade	Reactome	R-HSA-168176	0.000263	0.004928
Deadenylation-dependent mRNA decay	Reactome	R-HSA-429914	0.000268	0.004994
Oxidative phosphorylation	Wikipathways	WP623	0.00028	0.00518
superpathway of purine nucleotide salvage	HumanCyc	PWY66-409	0.000282	0.005194
Fatty acid, triacylglycerol, and ketone body metabolism	Reactome	R-HSA-535734	0.000286	0.005225
Generation of second messenger molecules	Reactome	R-HSA-202433	0.000293	0.005327
Transport to the Golgi and subsequent modification	Reactome	R-HSA-948021	0.000299	0.005407
Clathrin-mediated endocytosis	Reactome	R-HSA-8856828	0.000301	0.005414
Oocyte meiosis - Homo sapiens (human)	KEGG	path:hsa04114	0.000303	0.005418
Toll Like Receptor 9 (TLR9) Cascade	Reactome	R-HSA-168138	0.000305	0.005431
Intrinsic Pathway for Apoptosis	Reactome	R-HSA-109606	0.000316	0.005587
TP53 Regulates Metabolic Genes	Reactome	R-HSA-5628897	0.00032	0.005634
UCH proteinases	Reactome	R-HSA-5689603	0.000325	0.005698
TGF_beta_Receptor	NetPath	Pathway_TGF_beta_Receptor	0.00033	0.005745

SUMO E3 ligases SUMOylate target proteins	Reactome	R-HSA-3108232	0.000348	0.006014
RAB GEFs exchange GTP for GDP on RABs	Reactome	R-HSA-8876198	0.000349	0.006014
Mitotic G2-G2/M phases	Reactome	R-HSA-453274	0.000354	0.006068
Mesodermal Commitment Pathway	Wikipathways	WP2857	0.000357	0.006093
Spliceosome - Homo sapiens (human)	KEGG	path:hsa03040	0.000365	0.006196
Intracellular Signalling Through Adenosine Receptor A2a and Adenosine	SMPDB	SMP00320	0.000408	0.006852
Warburg Effect	SMPDB	SMP00654	0.000408	0.006852
TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	Reactome	R-HSA-975138	0.000411	0.006863
mtor signaling pathway	BioCarta	mtorpathway	0.00042	0.006976
Fanconi anemia pathway - Homo sapiens (human)	KEGG	path:hsa03460	0.000425	0.006981
APC/C-mediated degradation of cell cycle proteins	Reactome	R-HSA-174143	0.000426	0.006981
Regulation of mitotic cell cycle	Reactome	R-HSA-453276	0.000426	0.006981
Chemokine signaling pathway - Homo sapiens (human)	KEGG	path:hsa04062	0.000435	0.007081
MAP kinase activation in TLR cascade	Reactome	R-HSA-450294	0.000444	0.007166
Epstein-Barr virus infection - Homo sapiens (human)	KEGG	path:hsa05169	0.000444	0.007166
Focal Adhesion-PI3K-Akt-mTOR-signaling pathway	Wikipathways	WP3932	0.000446	0.007167
Signaling by Wnt	Reactome	R-HSA-195721	0.000486	0.007719
Regulation of Hypoxia-inducible Factor (HIF) by oxygen	Reactome	R-HSA-1234174	0.000488	0.007719
Cellular response to hypoxia	Reactome	R-HSA-2262749	0.000488	0.007719
Triglyceride Biosynthesis	Reactome	R-HSA-75109	0.00049	0.007719
rRNA modification in the nucleus and cytosol	Reactome	R-HSA-6790901	0.000499	0.007778
rRNA processing in the nucleus and cytosol	Reactome	R-HSA-8868773	0.000499	0.007778
Asthma - Homo sapiens (human)	KEGG	path:hsa05310	0.000504	0.007816
Sterol Regulatory Element-Binding Proteins (SREBP) signalling	Wikipathways	WP1982	0.000507	0.007835
rRNA processing	Reactome	R-HSA-72312	0.000513	0.007891
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	Reactome	R-HSA-174178	0.000534	0.008135
Pentose phosphate pathway - Homo sapiens (human)	KEGG	path:hsa00030	0.000534	0.008135
PKMTs methylate histone lysines	Reactome	R-HSA-3214841	0.000542	0.008216

Glycerophospholipid metabolism	EHMN	Glycerophospholipid metabolism	0.000548	0.008276
N-Glycan biosynthesis	EHMN	N-Glycan biosynthesis	0.000556	0.008359
Lysosome - Homo sapiens (human)	KEGG	path:hsa04142	0.000562	0.0084
G2/M Transition	Reactome	R-HSA-69275	0.000576	0.008582
Intracellular Signalling Through Adenosine Receptor A2b and Adenosine	SMPDB	SMP00321	0.000593	0.008783
N-glycan trimming in the ER and Calnexin/Calreticulin cycle	Reactome	R-HSA-532668	0.000607	0.008924
Translocation of ZAP-70 to Immunological synapse	Reactome	R-HSA-202430	0.00061	0.008924
Endosomal Sorting Complex Required For Transport (ESCRT)	Reactome	R-HSA-917729	0.00061	0.008924
TRAF6 Mediated Induction of proinflammatory cytokines	Reactome	R-HSA-168180	0.000624	0.009084
Brain-Derived Neurotrophic Factor (BDNF) signaling pathway	Wikipathways	WP2380	0.000631	0.009149
Meiotic recombination	Reactome	R-HSA-912446	0.000643	0.009231
RNA Polymerase I Promoter Opening	Reactome	R-HSA-73728	0.000643	0.009231
VEGF signaling pathway - Homo sapiens (human)	KEGG	path:hsa04370	0.000658	0.009404
O-linked glycosylation	Reactome	R-HSA-5173105	0.000715	0.010136
Synaptic vesicle cycle - Homo sapiens (human)	KEGG	path:hsa04721	0.000715	0.010136
tRNA processing	Reactome	R-HSA-72306	0.000723	0.010205
SUMOylation of DNA damage response and repair proteins	Reactome	R-HSA-3108214	0.000728	0.010239
ErbB1 downstream signaling	PID	erbb1_downstream_pathway	0.000755	0.010569
Retrograde transport at the Trans-Golgi-Network	Reactome	R-HSA-6811440	0.000759	0.010582
Ion channel transport	Reactome	R-HSA-983712	0.00079	0.010966
Small cell lung cancer - Homo sapiens (human)	KEGG	path:hsa05222	0.000833	0.011462
Neurotrophin signaling pathway - Homo sapiens (human)	KEGG	path:hsa04722	0.000833	0.011462
Chemokine signaling pathway	Wikipathways	WP3929	0.000843	0.011469
Regulation of TP53 Activity through Phosphorylation	Reactome	R-HSA-6804756	0.000845	0.011469
Regulation of APC/C activators between G1/S and early anaphase	Reactome	R-HSA-176408	0.000851	0.011469
MicroRNAs in cancer - Homo sapiens (human)	KEGG	path:hsa05206	0.000852	0.011469
Apoptosis Modulation by HSP70	Wikipathways	WP384	0.000854	0.011469
Caspase activation via extrinsic apoptotic signalling pathway	Reactome	R-HSA-5357769	0.000854	0.011469

ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression	Reactome	R-HSA-427389	0.000861	0.011498
Phospholipid metabolism	Reactome	R-HSA-1483257	0.000864	0.011498
Hemostasis	Reactome	R-HSA-109582	0.00088	0.011666
TGF-beta Signaling Pathway	Wikipathways	WP366	0.000927	0.01224
Degradation of the extracellular matrix	Reactome	R-HSA-1474228	0.000938	0.012335
Exercise-induced Circadian Regulation	Wikipathways	WP410	0.000952	0.012396
TNF alpha Signaling Pathway	Wikipathways	WP231	0.000961	0.012396
NGF signalling via TRKA from the plasma membrane	Reactome	R-HSA-187037	0.000961	0.012396
Propanoate metabolism - Homo sapiens (human)	KEGG	path:hsa00640	0.000965	0.012396
Nucleotide-binding Oligomerization Domain (NOD) pathway	Wikipathways	WP1433	0.000966	0.012396
Nicotinate and nicotinamide metabolism - Homo sapiens (human)	KEGG	path:hsa00760	0.000977	0.012396
Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	Reactome	R-HSA-1234176	0.000977	0.012396
CDP-diacylglycerol biosynthesis	HumanCyc	PWY-5667	0.000977	0.012396
Budding and maturation of HIV virion	Reactome	R-HSA-162588	0.000977	0.012396
p75 NTR receptor-mediated signalling	Reactome	R-HSA-193704	0.000987	0.012477
Synaptic Vesicle Pathway	Wikipathways	WP2267	0.001002	0.012529
Cyclin D associated events in G1	Reactome	R-HSA-69231	0.001002	0.012529
G1 Phase	Reactome	R-HSA-69236	0.001002	0.012529
Cholinergic synapse - Homo sapiens (human)	KEGG	path:hsa04725	0.001027	0.012741
Influenza Life Cycle	Reactome	R-HSA-168255	0.001027	0.012741
Signaling by Interleukins	Reactome	R-HSA-449147	0.001031	0.012741
FoxO family signaling	PID	foxopathway	0.00104	0.012788
p38 MAPK signaling pathway	PID	p38_mkk3_6pathway	0.001045	0.012788
Histone Modifications	Wikipathways	WP2369	0.001049	0.012788
Regulation of TP53 Activity	Reactome	R-HSA-5633007	0.00105	0.012788
Regulation of retinoblastoma protein	PID	rb_1pathway	0.001065	0.012861
DNA Damage Bypass	Reactome	R-HSA-73893	0.001065	0.012861
APC/C:Cdc20 mediated degradation of Securin	Reactome	R-HSA-174154	0.001068	0.012861
Cellular response to heat stress	Reactome	R-HSA-3371556	0.001093	0.013109
G2/M Checkpoints	Reactome	R-HSA-69481	0.001099	0.013136
Cardiac muscle contraction - Homo sapiens (human)	KEGG	path:hsa04260	0.001115	0.013282
Non-small cell lung cancer - Homo sapiens (human)	KEGG	path:hsa05223	0.001156	0.013712
Signaling by Insulin receptor	Reactome	R-HSA-74752	0.001221	0.014435

EGF-EGFR Signaling Pathway	Wikipathways	WP437	0.001267	0.01493
Mitotic Prometaphase	Reactome	R-HSA-68877	0.001285	0.015085
Hepatitis B - Homo sapiens (human)	KEGG	path:hsa05161	0.001292	0.015113
cGMP-PKG signaling pathway - Homo sapiens (human)	KEGG	path:hsa04022	0.001342	0.015594
Hedgehog ,on, state	Reactome	R-HSA-5632684	0.001343	0.015594
Pyrimidine metabolism	EHMN	Pyrimidine metabolism	0.001351	0.015637
Metalloprotease DUBs	Reactome	R-HSA-5689901	0.001374	0.015847
Glycerophospholipid metabolism - Homo sapiens (human)	KEGG	path:hsa00564	0.001397	0.016055
JAK STAT pathway and regulation	INOH	None	0.001408	0.016118
Signaling by Hedgehog	Reactome	R-HSA-5358351	0.00143	0.016304
Ras signaling pathway - Homo sapiens (human)	KEGG	path:hsa04014	0.001434	0.016304
TP53 Regulates Transcription of Cell Death Genes	Reactome	R-HSA-5633008	0.001444	0.016331
RIG-I-like Receptor Signaling	Wikipathways	WP3865	0.001446	0.016331
Direct p53 effectors	PID	p53downstreampathway	0.001459	0.016355
RNA degradation - Homo sapiens (human)	KEGG	path:hsa03018	0.001464	0.016355
Nanomaterial induced apoptosis	Wikipathways	WP2507	0.001465	0.016355
S Phase	Reactome	R-HSA-69242	0.001468	0.016355
ER to Golgi Anterograde Transport	Reactome	R-HSA-199977	0.00148	0.016435
Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	Reactome	R-HSA-5625886	0.001521	0.016786
Notch	NetPath	Pathway_Notch	0.001523	0.016786
ABC-family proteins mediated transport	Reactome	R-HSA-382556	0.001527	0.016786
PI3K-Akt signaling pathway - Homo sapiens (human)	KEGG	path:hsa04151	0.001539	0.016861
Global Genome Nucleotide Excision Repair (GG-NER)	Reactome	R-HSA-5696399	0.001561	0.01704
Golgi Associated Vesicle Biogenesis	Reactome	R-HSA-432722	0.00157	0.017084
PD-1 signaling	Reactome	R-HSA-389948	0.001579	0.017126
Clathrin derived vesicle budding	Reactome	R-HSA-421837	0.001596	0.01719
trans-Golgi Network Vesicle Budding	Reactome	R-HSA-199992	0.001596	0.01719
SLC-mediated transmembrane transport	Reactome	R-HSA-425407	0.001603	0.017209
Processing of DNA double-strand break ends	Reactome	R-HSA-5693607	0.001609	0.017222
Renal cell carcinoma - Homo sapiens (human)	KEGG	path:hsa05211	0.001635	0.01744
Regulation of PLK1 Activity at G2/M Transition	Reactome	R-HSA-2565942	0.001654	0.017557
Proteasome Degradation	Wikipathways	WP183	0.001673	0.017557

Phosphorylation of CD3 and TCR zeta chains	Reactome	R-HSA-202427	0.001678	0.017557
DroToll-like	INOH	None	0.001682	0.017557
adenosine ribonucleotides <i>de novo</i> biosynthesis	HumanCyc	PWY-7219	0.00169	0.017557
APC/C:Cdc20 mediated degradation of mitotic proteins	Reactome	R-HSA-176409	0.001694	0.017557
Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	Reactome	R-HSA-176814	0.001694	0.017557
Vitamin B3 (nicotinate and nicotinamide) metabolism	EHMN	Vitamin B3 (nicotinate and nicotinamide) metabolism	0.001694	0.017557
Viral carcinogenesis - Homo sapiens (human)	KEGG	path:hsa05203	0.001694	0.017557
Golgi-to-ER retrograde transport	Reactome	R-HSA-8856688	0.001814	0.018606
Transport of Mature mRNA Derived from an Intronless Transcript	Reactome	R-HSA-159231	0.001816	0.018606
Transport of Mature mRNAs Derived from Intronless Transcripts	Reactome	R-HSA-159234	0.001816	0.018606
COPI-mediated anterograde transport	Reactome	R-HSA-6807878	0.001818	0.018606
Rho GTPase cycle	Reactome	R-HSA-194840	0.001825	0.018616
VEGF	INOH	None	0.001839	0.018703
HDACs deacetylate histones	Reactome	R-HSA-3214815	0.001893	0.019134
Glycerophospholipid biosynthesis	Reactome	R-HSA-1483206	0.001894	0.019134
VEGFA-VEGFR2 Pathway	Reactome	R-HSA-4420097	0.001899	0.019134
Leukocyte transendothelial migration - Homo sapiens (human)	KEGG	path:hsa04670	0.001905	0.019134
G alpha (i) signalling events	Reactome	R-HSA-418594	0.001944	0.019267
AMPK signaling pathway - Homo sapiens (human)	KEGG	path:hsa04152	0.001951	0.019267
Malonyl-coa decarboxylase deficiency	SMPDB	SMP00502	0.001953	0.019267
Malonic Aciduria	SMPDB	SMP00198	0.001953	0.019267
Propanoate Metabolism	SMPDB	SMP00016	0.001953	0.019267
Methylmalonic Aciduria Due to Cobalamin-Related Disorders	SMPDB	SMP00201	0.001953	0.019267
Signaling by VEGF	Reactome	R-HSA-194138	0.002009	0.019754
cAMP signaling pathway - Homo sapiens (human)	KEGG	path:hsa04024	0.002021	0.019758
Resolution of Sister Chromatid Cohesion	Reactome	R-HSA-2500257	0.002021	0.019758
APC/C:Cdc20 mediated degradation of Cyclin B	Reactome	R-HSA-174048	0.00209	0.020376
The oncogenic action of D-2-hydroxyglutarate in Hydroxygluaricaciduria	SMPDB	SMP02359	0.002136	0.020699

Autodegradation of Cdh1 by Cdh1:APC/C	Reactome	R-HSA-174084	0.002136	0.020699
Hedgehog	INOH	None	0.00216	0.020837
G2/M DNA damage checkpoint	Reactome	R-HSA-69473	0.002163	0.020837
Nucleotide Excision Repair	Reactome	R-HSA-5696398	0.002178	0.020913
Factors involved in megakaryocyte development and platelet production	Reactome	R-HSA-983231	0.002185	0.020925
N-Glycan biosynthesis - Homo sapiens (human)	KEGG	path:hsa00510	0.002246	0.021443
DAP12 interactions	Reactome	R-HSA-2172127	0.002266	0.021575
Interleukin-1 signaling	Reactome	R-HSA-446652	0.00234	0.022214
G1/S Transition	Reactome	R-HSA-69206	0.002362	0.022359
TCF dependent signaling in response to WNT	Reactome	R-HSA-201681	0.00241	0.022744
Signal Transduction of S1P Receptor	Wikipathways	WP26	0.002441	0.022976
G alpha (12/13) signalling events	Reactome	R-HSA-416482	0.002485	0.023323
Insulin receptor signalling cascade	Reactome	R-HSA-74751	0.002535	0.023713
GPCR ligand binding	Reactome	R-HSA-500792	0.002541	0.023713
The oncogenic action of Succinate	SMPDB	SMP02292	0.002625	0.024349
The oncogenic action of Fumarate	SMPDB	SMP02295	0.002625	0.024349
Celecoxib Pathway, Pharmacodynamics	PharmGKB	PA152241951	0.002661	0.024615
Metabolism of carbohydrates	Reactome	R-HSA-71387	0.002711	0.025006
Insulin Signaling	Wikipathways	WP481	0.002742	0.025159
RHO GTPases activate PKNs	Reactome	R-HSA-5625740	0.002742	0.025159
Signaling by EGFR	Reactome	R-HSA-177929	0.002797	0.025589
HIF-1-alpha transcription factor network	PID	hif1_tfpathway	0.002833	0.025843
Cell Cycle	Wikipathways	WP179	0.002869	0.026102
Aminosugars metabolism	EHMN	Aminosugars metabolism	0.002901	0.026314
Ligand-dependent caspase activation	Reactome	R-HSA-140534	0.00293	0.026432
Nuclear Receptors in Lipid Metabolism and Toxicity	Wikipathways	WP299	0.00293	0.026432
TLR p38	INOH	None	0.002971	0.026659
IL-1 p38	INOH	None	0.002971	0.026659
TLR JNK	INOH	None	0.002992	0.026772
Conversion from APC/C:Cdc20 to APC/C:Cdh1 in late anaphase	Reactome	R-HSA-176407	0.003052	0.027233
Cargo recognition for clathrin-mediated endocytosis	Reactome	R-HSA-8856825	0.003103	0.027402
IRS-related events triggered by IGF1R	Reactome	R-HSA-2428928	0.003104	0.027402
IGF1R signaling cascade	Reactome	R-HSA-2428924	0.003104	0.027402
Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	Reactome	R-HSA-2404192	0.003104	0.027402

COPI-dependent Golgi-to-ER retrograde traffic	Reactome	R-HSA-6811434	0.00312	0.02747
APC-Cdc20 mediated degradation of Nek2A	Reactome	R-HSA-179409	0.003159	0.027585
Cdc20:Phospho-APC/C mediated degradation of Cyclin A	Reactome	R-HSA-174184	0.003159	0.027585
APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	Reactome	R-HSA-179419	0.003159	0.027585
Calcium Regulation in the Cardiac Cell	Wikipathways	WP536	0.00323	0.028135
Protein folding	Reactome	R-HSA-391251	0.00328	0.028492
Notch	INOH	None	0.003308	0.028611
DAP12 signaling	Reactome	R-HSA-2424491	0.003311	0.028611
Axon guidance - Homo sapiens (human)	KEGG	path:hsa04360	0.003328	0.028682
Platelet Aggregation Inhibitor Pathway, Pharmacodynamics	PharmGKB	PA154444041	0.003342	0.028705
FoxO signaling pathway - Homo sapiens (human)	KEGG	path:hsa04068	0.003353	0.028705
The oncogenic action of L-2-hydroxyglutarate in Hydroxygluaricaciduria	SMPDB	SMP02358	0.003357	0.028705
snRNP Assembly	Reactome	R-HSA-191859	0.003379	0.028745
Metabolism of non-coding RNA	Reactome	R-HSA-194441	0.003379	0.028745
Diseases of signal transduction	Reactome	R-HSA-5663202	0.00343	0.029105
NOD1/2 Signaling Pathway	Reactome	R-HSA-168638	0.003453	0.029217
Adipogenesis	Wikipathways	WP236	0.003462	0.029225
Metabolism of nucleotides	Reactome	R-HSA-15869	0.003475	0.029258
Glioma - Homo sapiens (human)	KEGG	path:hsa05214	0.003492	0.029324
Stimuli-sensing channels	Reactome	R-HSA-2672351	0.00352	0.029487
HTLV-I infection - Homo sapiens (human)	KEGG	path:hsa05166	0.003561	0.029753
G1 to S cell cycle control	Wikipathways	WP45	0.003589	0.029904
Tight junction - Homo sapiens (human)	KEGG	path:hsa04530	0.003611	0.029976
IRS-mediated signalling	Reactome	R-HSA-112399	0.003615	0.029976
Regulation of TP53 Expression and Degradation	Reactome	R-HSA-6806003	0.003654	0.030223
IL-1 JNK	INOH	None	0.003692	0.030458
Host Interactions of HIV factors	Reactome	R-HSA-162909	0.003719	0.030532
Transport of Mature Transcript to Cytoplasm	Reactome	R-HSA-72202	0.003725	0.030532
Mitochondrial protein import	Reactome	R-HSA-1268020	0.003803	0.030532
Validated targets of C-MYC transcriptional repression	PID	myc_represspathway	0.003803	0.030532
EPO signaling	INOH	None	0.003818	0.030532
Androgen receptor signaling pathway	Wikipathways	WP138	0.003831	0.030532

Senescence and Autophagy in Cancer	Wikipathways	WP615	0.003832	0.030532
NF-kappa B signaling pathway - Homo sapiens (human)	KEGG	path:hsa04064	0.003859	0.030532
Protein ubiquitination	Reactome	R-HSA-8852135	0.0039	0.030532
Retrograde neurotrophin signalling	Reactome	R-HSA-177504	0.003906	0.030532
Regulation of KIT signaling	Reactome	R-HSA-1433559	0.003906	0.030532
Mucin type O-glycan biosynthesis - Homo sapiens (human)	KEGG	path:hsa00512	0.003906	0.030532
mRNA decay by 3, to 5, exoribonuclease	Reactome	R-HSA-429958	0.003906	0.030532
Processing and activation of SUMO	Reactome	R-HSA-3215018	0.003906	0.030532
Pyruvate dehydrogenase deficiency (E3)	SMPDB	SMP00550	0.003906	0.030532
Pyruvate dehydrogenase deficiency (E2)	SMPDB	SMP00551	0.003906	0.030532
2-ketoglutarate dehydrogenase complex deficiency	SMPDB	SMP00549	0.003906	0.030532
Mitochondrial complex II deficiency	SMPDB	SMP00548	0.003906	0.030532
Fumarase deficiency	SMPDB	SMP00547	0.003906	0.030532
Congenital lactic acidosis	SMPDB	SMP00546	0.003906	0.030532
Citric Acid Cycle	SMPDB	SMP00057	0.003906	0.030532
Synthesis and interconversion of nucleotide di- and triphosphates	Reactome	R-HSA-499943	0.003906	0.030532
Fanconi Anemia Pathway	Reactome	R-HSA-6783310	0.003918	0.030549
TCR	NetPath	Pathway_TCR	0.003967	0.03086
Calnexin/calreticulin cycle	Reactome	R-HSA-901042	0.004005	0.031085
Regulation of toll-like receptor signaling pathway	Wikipathways	WP1449	0.004035	0.031185
Purine metabolism - Homo sapiens (human)	KEGG	path:hsa00230	0.004037	0.031185
CDC42 signaling events	PID	cdc42_pathway	0.004087	0.031496
Toll-like receptor signaling pathway - Homo sapiens (human)	KEGG	path:hsa04620	0.004278	0.032886
DNA Double-Strand Break Repair	Reactome	R-HSA-5693532	0.004364	0.033472
Fibroblast growth factor-1	NetPath	Pathway_Fibroblast__growth__factor-1	0.0045	0.03443
Regulation of nuclear SMAD2/3 signaling	PID	smad2_3nuclear pathway	0.004512	0.034447
Hepatitis C - Homo sapiens (human)	KEGG	path:hsa05160	0.004544	0.034607
Thyroid hormone signaling pathway - Homo sapiens (human)	KEGG	path:hsa04919	0.004601	0.034888
HDR through Homologous Recombination (HR) or Single Strand Annealing (SSA)	Reactome	R-HSA-5693567	0.004606	0.034888
Melanoma - Homo sapiens (human)	KEGG	path:hsa05218	0.004613	0.034888

RIPK1-mediated regulated necrosis	Reactome	R-HSA-5213460	0.004639	0.034923
Regulated Necrosis	Reactome	R-HSA-5218859	0.004639	0.034923
Pyrimidine metabolism - Homo sapiens (human)	KEGG	path:hsa00240	0.004678	0.034928
Sphingolipid signaling pathway - Homo sapiens (human)	KEGG	path:hsa04071	0.00468	0.034928
Bladder cancer - Homo sapiens (human)	KEGG	path:hsa05219	0.004685	0.034928
Transport of glucose and other sugars, bile salts and organic acids, metal ions and amine compounds	Reactome	R-HSA-425366	0.004693	0.034928
TLR NFkB	INOH	None	0.004693	0.034928
IL4	NetPath	Pathway_IL4	0.004719	0.034982
Dopaminergic synapse - Homo sapiens (human)	KEGG	path:hsa04728	0.004721	0.034982
MAPK signaling pathway - Homo sapiens (human)	KEGG	path:hsa04010	0.004742	0.035003
Bladder Cancer	Wikipathways	WP2828	0.004745	0.035003
mRNA Processing	Wikipathways	WP411	0.004758	0.035013
RIG-I-like receptor signaling pathway - Homo sapiens (human)	KEGG	path:hsa04622	0.004852	0.035536
TRAIL signaling pathway	PID	trail_pathway	0.00486	0.035536
O-linked glycosylation of mucins	Reactome	R-HSA-913709	0.004879	0.035536
apoptotic signaling in response to dna damage	BioCarta	chemicalpathway	0.004883	0.035536
mRNA decay by 5, to 3, exoribonuclease	Reactome	R-HSA-430039	0.004883	0.035536
Methionine and cysteine metabolism	EHMN	Methionine and cysteine metabolism	0.004895	0.035546
Fc epsilon receptor (FCERI) signaling	Reactome	R-HSA-2454202	0.004956	0.035907
FAS (CD95) signaling pathway	PID	faspathway	0.005023	0.036317
Regulation of Androgen receptor activity	PID	ar_tf_pathway	0.005086	0.036692
RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways	Reactome	R-HSA-168928	0.005146	0.037042
Fatty Acyl-CoA Biosynthesis	Reactome	R-HSA-75105	0.00516	0.037058
p53 signaling pathway - Homo sapiens (human)	KEGG	path:hsa04115	0.005187	0.037174
ER Quality Control Compartment (ERQC)	Reactome	R-HSA-901032	0.005249	0.037452
RNA Polymerase I Transcription Termination	Reactome	R-HSA-73863	0.005249	0.037452
IL-7 signaling	INOH	None	0.005263	0.037453
L1CAM interactions	Reactome	R-HSA-373760	0.005322	0.037453
Regulation of TP53 Degradation	Reactome	R-HSA-6804757	0.005329	0.037453
Processing of Capped Intronless Pre-mRNA	Reactome	R-HSA-75067	0.005329	0.037453

Post-Elongation Processing of Intronless pre-mRNA	Reactome	R-HSA-112297	0.005329	0.037453
DNA Replication Pre-Initiation	Reactome	R-HSA-69002	0.005329	0.037453
M/G1 Transition	Reactome	R-HSA-68874	0.005329	0.037453
Nanoparticle triggered autophagic cell death	Wikipathways	WP2509	0.005371	0.037667
Export of Viral Ribonucleoproteins from Nucleus	Reactome	R-HSA-168274	0.005581	0.039054
Pentose Phosphate Pathway	SMPDB	SMP00031	0.005859	0.040656
Glucose-6-phosphate dehydrogenase deficiency	SMPDB	SMP00518	0.005859	0.040656
Ribose-5-phosphate isomerase deficiency	SMPDB	SMP00519	0.005859	0.040656
Transaldolase deficiency	SMPDB	SMP00520	0.005859	0.040656
IL-1 NFkB	INOH	None	0.006096	0.042171
TLR ECSIT MEKK1 JNK	INOH	None	0.006104	0.042171
Interleukin-7 signaling	Reactome	R-HSA-1266695	0.006287	0.043345
Human Thyroid Stimulating Hormone (TSH) signaling pathway	Wikipathways	WP2032	0.006372	0.043839
Intestinal immune network for IgA production - Homo sapiens (human)	KEGG	path:hsa04672	0.006451	0.04429
TP53 Regulates Transcription of Cell Death Genes	Wikipathways	WP3802	0.006577	0.044871
Pink/Parkin Mediated Mitophagy	Reactome	R-HSA-5205685	0.006577	0.044871
Mitophagy	Reactome	R-HSA-5205647	0.006577	0.044871
RNA Polymerase III Transcription Initiation From Type 3 Promoter	Reactome	R-HSA-76071	0.006653	0.045297
Signaling events mediated by Hepatocyte Growth Factor Receptor (c-Met)	PID	met_pathway	0.006676	0.045336
Metabolism of polyamines	Reactome	R-HSA-351202	0.006714	0.045336
RNA Polymerase I Promoter Escape	Reactome	R-HSA-73772	0.006714	0.045336
MAPK Cascade	Wikipathways	WP422	0.006714	0.045336
Inflammatory mediator regulation of TRP channels - Homo sapiens (human)	KEGG	path:hsa04750	0.006743	0.045442
Tristetraprolin (TTP, ZFP36) binds and destabilizes mRNA	Reactome	R-HSA-450513	0.006836	0.045971
mTOR signaling pathway	PID	mtor_4pathway	0.006955	0.046666
tRNA processing in the nucleus	Reactome	R-HSA-6784531	0.006968	0.046666
Carbohydrate digestion and absorption - Homo sapiens (human)	KEGG	path:hsa04973	0.007101	0.047364
Synthesis of active ubiquitin: roles of E1 and E2 enzymes	Reactome	R-HSA-8866652	0.007101	0.047364
Proteoglycan biosynthesis	EHMN	Proteoglycan biosynthesis	0.007145	0.047464
Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding	Reactome	R-HSA-6814122	0.007145	0.047464

Pancreatic cancer - Homo sapiens (human)	KEGG	path:hsa05212	0.007383	0.048944
Toll-like Receptor Signaling Pathway	Wikipathways	WP75	0.007417	0.049003
PDGFR-beta signaling pathway	PID	pdgfrbpathway	0.007422	0.049003
SUMOylation of DNA replication proteins	Reactome	R-HSA-4615885	0.007443	0.049036
TNF related weak inducer of apoptosis (TWEAK) Signaling Pathway	Wikipathways	WP2036	0.007456	0.049036
Death Receptor Signalling	Reactome	R-HSA-73887	0.00756	0.04952
Nuclear Envelope Breakdown	Reactome	R-HSA-2980766	0.00756	0.04952
Alzheimers Disease	Wikipathways	WP2059	0.007594	0.04952
Downregulation of SMAD2/3:SMAD4 transcriptional activity	Reactome	R-HSA-2173795	0.007629	0.04952
Recycling pathway of L1	Reactome	R-HSA-437239	0.007629	0.04952
Fatty acid elongation - Homo sapiens (human)	KEGG	path:hsa00062	0.007629	0.04952
MAPK Signaling Pathway	Wikipathways	WP382	0.007658	0.04952
ABC transporters - Homo sapiens (human)	KEGG	path:hsa02010	0.00769	0.04952
O-Glycan biosynthesis	EHMN	O-Glycan biosynthesis	0.00769	0.04952
Choline metabolism in cancer - Homo sapiens (human)	KEGG	path:hsa05231	0.007727	0.04952
Natural killer cell mediated cytotoxicity - Homo sapiens (human)	KEGG	path:hsa04650	0.007751	0.04952
Pentose phosphate pathway (hexose monophosphate shunt)	Reactome	R-HSA-71336	0.007813	0.04952
TCA cycle	HumanCyc	PWY66-398	0.007813	0.04952
Citric acid cycle (TCA cycle)	Reactome	R-HSA-71403	0.007813	0.04952
Hypoxic and oxygen homeostasis regulation of HIF-1-alpha	PID	hif1apathway	0.007813	0.04952
Steroid biosynthesis - Homo sapiens (human)	KEGG	path:hsa00100	0.007813	0.04952
carm1 and regulation of the estrogen receptor	BioCarta	carmerpathway	0.007813	0.04952
heparan sulfate biosynthesis	HumanCyc	PWY-6564	0.007813	0.04952
Extracellular matrix organization	Reactome	R-HSA-1474244	0.007817	0.04952
Recognition of DNA damage by PCNA-containing replication complex	Reactome	R-HSA-110314	0.007904	0.049973
purine nucleotides <i>de novo</i> biosynthesis	HumanCyc	PWY-841	0.007938	0.049973
Glutamatergic synapse - Homo sapiens (human)	KEGG	path:hsa04724	0.007961	0.049973
p38 mapk signaling pathway	BioCarta	p38mapkpathway	0.00801	0.049973
Sudden Infant Death Syndrome (SIDS) Susceptibility Pathways	Wikipathways	WP706	0.008024	0.049973

Citrate cycle (TCA cycle) - Homo sapiens (human)	KEGG	path:hsa00020	0.008057	0.049973
The oncogenic action of 2-hydroxyglutarate	SMPDB	SMP02291	0.008057	0.049973
Trafficking of AMPA receptors	Reactome	R-HSA-399719	0.008057	0.049973
Glutamate Binding, Activation of AMPA Receptors and Synaptic Plasticity	Reactome	R-HSA-399721	0.008057	0.049973
TLR ECSIT MEKK1 p38	INOH	None	0.008057	0.049973
Pentose phosphate cycle	INOH	None	0.008057	0.049973
AndrogenReceptor	NetPath	Pathway_AndrogenReceptor	0.008174	0.050607
Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human)	KEGG	path:hsa04961	0.008316	0.051144
Activation of BH3-only proteins	Reactome	R-HSA-114452	0.008316	0.051144
Basal transcription factors - Homo sapiens (human)	KEGG	path:hsa03022	0.008316	0.051144
Influenza Infection	Reactome	R-HSA-168254	0.008338	0.051144
Angiopoietin Like Protein 8 Regulatory Pathway	Wikipathways	WP3915	0.008339	0.051144
p75(NTR)-mediated signaling	PID	p75ntrpathway	0.008474	0.051823
Citrate cycle	INOH	None	0.008545	0.051823
Biosynthesis of unsaturated fatty acids - Homo sapiens (human)	KEGG	path:hsa01040	0.008545	0.051823
Inactivation of APC/C via direct inhibition of the APC/C complex	Reactome	R-HSA-141430	0.008545	0.051823
Inhibition of the proteolytic activity of APC/C required for the onset of anaphase by mitotic spindle checkpoint components	Reactome	R-HSA-141405	0.008545	0.051823
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis - Homo sapiens (human)	KEGG	path:hsa00563	0.008545	0.051823
Phospholipase D signaling pathway - Homo sapiens (human)	KEGG	path:hsa04072	0.008671	0.052434
Signaling events mediated by HDAC Class I	PID	hdac_classi_pathway	0.008678	0.052434
Transcriptional regulation of white adipocyte differentiation	Reactome	R-HSA-381340	0.008715	0.052562
IKK complex recruitment mediated by RIP1	Reactome	R-HSA-937041	0.008965	0.053968
Homology Directed Repair	Reactome	R-HSA-5693538	0.009123	0.05482
Post-translational modification: synthesis of GPI-anchored proteins	Reactome	R-HSA-163125	0.009141	0.054828
Propanoate metabolism	EHMN	Propanoate metabolism	0.009277	0.055343

hypoxia and p53 in the cardiovascular system	BioCarta	p53hypoxiapathway	0.009277	0.055343
Acyl chain remodelling of PE	Reactome	R-HSA-1482839	0.009277	0.055343
HDR through Homologous Recombination (HRR)	Reactome	R-HSA-5685942	0.00934	0.055613
Nongenotropic Androgen signaling	PID	ar_nongenomic_pathway	0.009453	0.055982
Detoxification of Reactive Oxygen Species	Reactome	R-HSA-3299685	0.009453	0.055982
NEP/NS2 Interacts with the Cellular Export Machinery	Reactome	R-HSA-168333	0.009453	0.055982
Valine, leucine and isoleucine degradation - Homo sapiens (human)	KEGG	path:hsa00280	0.009609	0.056479
Regulation of HSF1-mediated heat shock response	Reactome	R-HSA-3371453	0.009612	0.056479
AGE-RAGE pathway	Wikipathways	WP2324	0.009638	0.056479
Cleavage of Growing Transcript in the Termination Region	Reactome	R-HSA-109688	0.009645	0.056479
RNA Polymerase II Transcription Termination	Reactome	R-HSA-73856	0.009645	0.056479
Post-Elongation Processing of the Transcript	Reactome	R-HSA-76044	0.009645	0.056479
Nonhomologous End-Joining (NHEJ)	Reactome	R-HSA-5693571	0.009658	0.056479
TGF-Ncore	Signalink	None	0.009932	0.057971
Peptide ligand-binding receptors	Reactome	R-HSA-375276	0.009948	0.057971

Appendix 12: Differentially regulated Transcription Factors							
BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
100507290	3.3441941	100288687	4.474784581	100288687	-2.624873379	100288687	-4.108962112
100289678	-2.4212012	100131017	2.38493995	100131017	-2.140939	100131017	2.5045984
100288687	2.806607086	731220	2.446578	730394	2.261837	731220	-2.0194137
100131390	-5.649724	730394	-2.3506892	503835	-3.281106533	730394	2.2867298
643641	2.5974908	644168	2.8104866	503834	-3.2084398	644168	-2.0152318
503835	4.081317067	503835	2.966424475	503582	-5.647336	503835	-5.90893215
503834	3.8467283	503582	2.311642625	440695	-4.659726	503582	-2.9610077
503582	3.010131967	440695	4.3288965	399823	-2.0281576	440695	-3.2904613
440695	2.11237085	404281	2.0256715	390010	-3.33522535	404281	-2.282308
404281	2.3181877	390010	3.6027913	375287	2.199268	401262	-2.3846934
401262	-2.044922	389524	-2.6187859	374655	-2.791009	399823	-2.7515528
399823	2.7805586	389136	2.64408	347862	-2.0201554	390010	-5.8744291
390010	3.5017946	347853	-3.3423915	347853	-2.56193065	389136	-2.20101895
389524	-2.5800345	344167	2.18022	344167	-2.3248248	340260	-2.68712725
389136	7.580889	344022	3.3488623	344022	-2.877663	339745	2.7489673
375287	2.6369226	340543	-2.1689909	340260	6.9111375	339488	-2.4042754
374655	-2.681257	340260	2.95022436	339745	2.884564	284119	-2.2145677
347862	4.254357	339745	-2.4590814	339559	2.208701	257397	3.0428936
347853	2.9195073	257397	-2.2113261	338323	-5.8967353	255313	-2.97089505
344167	2.2464328	256643	-3.1705103	285550	2.5494177	253639	-2.5369537
342909	-2.032523	256380	-4.18829655	285267	-2.6084564	221833	-2.490439233
342538	3.5777478	255313	2.29451045	284119	-2.203634	221830	2.72638455
339745	-2.0047035	255101	3.8134367	257397	3.3738883	221037	2.1801325
339665	2.2354722	221937	-2.0700836	256380	2.1505609	219409	-3.4626174
339559	-2.489365	221833	2.37664492	255313	-2.144042	201501	-2.121782833
339488	2.0901012	171568	-2.2120038	255101	-2.7895179	171568	2.3100834
338323	5.8038563	171389	-2.3264337	253639	-3.30642075	163081	2.3376808
284390	2.077376	170302	2.6085582	221833	3.3806515	163050	2.0957055

BL-P1-C	Fold Change	BL-P1-Y	Fold Change	P1-P3-C	Fold Change	P1-P3-Y	Fold Change
257397	-2.457138	170082	-3.133631	221037	2.4643534	162972	4.60792525
256536	2.4359329	163081	-2.5262386	219749	2.71527425	159296	-17.0962155
255313	2.6884378	163050	-2.1180065	219409	-3.1472604	158431	2.407508867
255101	2.8663202	162972	-2.1436337	201501	-3.2784502	158405	-2.9288425
253639	2.6155539	159296	4.5900858	170302	-2.706868	155054	2.1154118
221833	2.18675715	158431	-2.1135634	170082	2.016163	149628	2.8279734
221830	-3.0029957	157848	3.05276315	168620	-5.22857	148398	-5.870256767
221037	-2.90365445	154150	2.88439375	163081	3.14608	148254	3.128990625
219749	-2.9738648	153527	2.0057793	163050	2.4725976	148156	2.7561155
219409	3.0508735	149628	-3.245898	162972	4.9345048	135935	-3.0578719
201501	2.1327497	148398	4.1121929	159296	-3.32677275	133522	2.473732
200186	4.6906886	148254	-2.39083748	158431	2.7465737	128611	2.572625833
197358	3.50373705	148156	-2.7981231	158405	-5.0453615	128553	2.0489204
196513	3.44554125	146198	-2.8216474	157848	-2.652678533	128408	-2.49021615
171568	-2.20251	135935	2.139309033	154150	-2.9163554	127540	-2.75626865
170082	2.4800284	128611	-2.597277	153527	-2.1868348	124411	2.3873572
168620	4.132373	128553	-3.078488	148398	-3.454183367	123811	2.968621533
163081	-2.57277515	128408	6.803141	148254	3.63099435	121551	2.0929184
163050	-2.3138514	127540	2.537067733	148156	2.621736567	121340	-2.7079515
163033	2.9605947	127428	2.648678	138715	-4.906601	116113	-3.20162475
162993	-2.4871483	124411	-2.167533733	138474	-2.1832806	116039	-2.0165403
162972	-3.21289435	121340	2.5233378	135935	-2.0777224	114991	2.2019155
159296	4.128619117	116113	4.9538233	133522	2.5348525	114781	-2.1473513
158800	-2.3466184	116039	3.1889656	128611	2.4405878	114548	-3.0947184
158431	-2.431508467	114548	2.69392445	128408	7.3226505	112885	-4.321043
158405	3.4125957	112885	2.846125167	127540	-2.73708355	112464	-3.2841032
157848	2.4594027	94104	-2.31199664	127428	-2.3435295	93953	2.870325
154150	2.9534978	93953	-2.0735627	124411	2.1622797	91408	2.28102675
148398	3.797219067	90843	-2.3053894	123811	3.2517746	90853	-2.646297875

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
148254	-2.88079495	90668	3.014404133	121340	-2.47958	90594	3.4038947
146198	2.73427785	85474	2.5744147	116151	2.0205994	89857	-2.3254058
138715	4.4462066	85446	2.4287956	116113	-2.542181967	85446	-2.3135755
138474	2.532541	84913	4.95485405	116039	-4.8362026	84913	-3.67460065
135935	2.1481946	84733	2.1178334	114826	2.0603204	84733	-2.4557037
133522	-3.208796	84726	5.04760408	114548	-2.124434	84726	-7.97964358
128611	2.5376885	84717	2.6714658	112885	-2.3152611	84717	-2.5826773
128408	-3.374366433	84460	-2.619372125	94104	2.2460454	84460	2.625018075
127540	2.8869431	84441	-2.1517727	93953	2.2172775	84289	2.7651094
127428	2.0106623	84306	-2.4814517	92002	-2.06854235	84246	2.1143105
124641	2.2348924	84289	-2.5440282	90853	-2.892984633	84159	2.0694833
124411	-2.180542275	84225	2.001415	90668	-2.8423278	83463	-2.0847309
121340	2.1985024	83746	-2.0261762	90594	4.6403394	81857	-3.821665933
116225	-2.0252564	83463	2.13313745	90378	-2.1908891	80790	-2.116969
116151	2.1356307	81857	2.302495433	85446	-2.8148293	80712	-2.4451828
116113	2.909459	81848	2.122617	84913	-5.5092607	80320	-2.5437157
116039	2.3921447	80712	3.28741	84807	2.1277459	80110	2.1942198
114548	3.4307973	80325	2.029288	84726	-3.432546883	80012	3.7192662
112885	3.1972843	80320	7.5673547	84717	-2.913367567	79977	-3.9528917
112464	2.0830681	80012	-2.0144367	84527	2.94173235	79898	2.673071767
94104	-2.151824067	79977	5.45119865	84460	2.79465685	79891	2.4742873
93953	2.50531885	79898	-2.5071883	84246	2.313735	79816	-4.497044767
92002	2.2768118	79816	2.5991819	84232	4.5315042	79673	-3.508368
90853	2.783551767	79673	4.275829767	84166	2.020134	79184	2.18634324
90843	-3.0656496	79184	-2.129723175	81848	-2.5891464	79158	2.1459513
90594	-2.1701431	79175	3.4049406	81669	2.480772933	64763	-2.11429275
90135	3.2929223	65988	2.5250355	80790	-2.3064418	64344	-2.917809433
89857	3.813826	64919	-2.7042112	80320	-11.423474	64127	2.0888577
85364	-2.0967166	64763	2.746903733	80110	2.0415292	59348	2.614660767

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
84969	2.902861	64344	3.4212434	80012	3.85922595	59269	2.188629
84954	-4.393433	64127	2.9664207	79960	2.460937967	58492	2.5453973
84913	4.430951167	60529	2.638585	79921	2.0405793	58486	3.2620292
84733	2.0880506	59348	-2.5837596	79898	4.678721	57763	2.2554734
84726	3.1291982	59269	-2.8393977	79816	-2.3092558	57713	-2.055546
84717	2.69032175	58486	-2.297303	79673	-2.2111683	57711	2.3751395
84527	-3.123301	57721	-2.0696754	79184	2.281612	57649	-2.5196733
84460	-2.53158464	57711	-2.046722	79158	2.6326778	57621	2.3128228
84246	-2.0434215	57649	-2.227671	64864	2.5463238	57209	-2.321735
84232	-11.410292	57616	2.9635327	64763	-2.8787322	57187	2.320966433
84225	2.6986985	57594	-2.253146	64236	2.2921459	57157	5.5326513
84148	2.8326812	57332	-2.1396618	64127	-2.0998895	56980	2.572369267
81848	2.507252	57187	-2.38343105	63976	2.4490933	56978	2.1693156
81628	-5.4591618	57157	-2.3181105	63929	2.163041967	56950	2.1122332
80790	-2.0288138	57018	-2.0853567	60529	3.618128	55854	3.124902267
80325	2.35305165	56950	-2.276246	59348	2.5864606	55818	2.3362343
80320	8.705113	56731	-2.2715921	59269	-3.128735033	55810	-2.1560817
79960	2.2311785	55854	-2.52207075	58492	2.0233543	55806	-6.658296367
79898	-3.341166	55832	2.2053561	58486	3.380062733	55802	2.1153233
79816	3.5334991	55806	3.58088558	57763	4.5431995	55734	2.1748736
79750	2.35717405	55734	12.840887	57713	2.0040405	55634	3.60153935
79673	2.06741525	55689	2.3235443	57711	3.00478055	55553	-3.2736976
79230	3.7464292	55634	-2.2975708	57649	-2.0357614	55534	-2.332036
79184	-2.613745	55553	2.468498	57621	3.531676	55290	2.209518
79158	2.1628458	55274	-2.3817124	57616	-2.4071863	55274	2.84404025
65988	2.8289218	55175	-2.426565	57594	2.2293773	55249	-2.1765306
64784	-4.1749973	54897	2.6550746	57332	-2.2446048	55175	2.2136931
64763	2.3631845	54799	-2.1829178	57157	3.467663933	54897	-2.552544
64236	-8.653165	54738	3.7921495	56980	4.2743416	54856	-2.2479472

BL-P1-C	Fold Change	BL-P1-Y	Fold Change	P1-P3-C	Fold Change	P1-P3-Y	Fold Change
64127	3.3859174	54700	-2.18297255	56978	2.6125867	54799	2.382567175
63929	2.9034255	53635	-2.3867986	55854	3.822999967	54738	-2.1482544
63925	-2.0475929	53335	-2.0730193	55832	-3.2506654	54700	2.758414567
59269	2.29849995	51773	-2.321940833	55818	5.5955634	54556	2.045815
58525	2.8814614	51742	-2.208038	55806	-3.73647625	53339	2.5600822
58492	-2.0620582	51513	2.07841765	55802	2.3883722	53335	-2.1390235
58486	-3.3614986	51385	-3.8002682	55734	2.10961	51742	2.688532267
57763	-3.7297869	51317	2.4782674	55689	-3.664379533	51621	-3.18675582
57721	-2.30464765	51315	-2.7436701	55655	-2.435226	51385	3.372702
57713	-2.3270271	51119	-2.56958598	55643	2.2198222	51317	-3.533841
57711	-2.4643831	51105	-2.0509706	55634	2.670644267	51315	2.72912915
57621	2.361914	50674	4.77316322	55553	-3.3801544	51222	-3.1995327
57616	4.3488204	30062	2.5881693	55534	-2.7572984	51119	3.434338275
57594	-2.5017006	29969	-2.03262245	55290	3.1245162	51105	2.37500154
57332	-2.4777794	29933	3.254138533	55205	2.1295998	50674	-10.492475
57157	-3.4802237	29911	-2.3037996	54962	3.2436926	30062	-2.3885999
56731	2.8653126	29883	-3.1886368	54897	-2.2299826	30011	-2.020544
55854	-3.7704421	28990	-2.066099	54799	6.0999265	30009	-2.3368986
55832	2.4844916	27154	2.4035397	54700	3.29565785	29969	2.8529789
55818	-2.62464145	26998	4.139130833	54556	2.1581535	29965	-2.3484073
55813	-2.0420158	26152	-2.170270533	54107	2.1577911	29883	3.2111808
55806	2.709763086	26009	-2.703623433	53335	-2.7294908	29115	-2.0865128
55802	3.3982678	25946	2.0123045	51773	2.4668777	29068	-2.0368187
55734	2.680125	25934	-2.0265164	51742	2.5763304	27287	-2.7931297
55689	3.11968865	25917	-2.3011905	51621	-2.949808833	27164	-3.13410485
55553	3.862352	25879	-2.624019133	51513	-17.893866	27125	2.60981495
55249	2.6421142	25844	2.152514325	51317	-2.94424485	26998	-2.937932767
54962	-2.1462493	25839	-2.343752	51315	4.3789399	26292	2.1219037
54870	-2.2365682	25821	-2.17861385	51222	-2.53187405	26253	2.3461046

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
54856	2.31524825	25803	4.0270066	51119	3.112558	26191	3.8255637
54799	-4.8636365	23762	3.54786025	50943	-2.083398	26121	2.258328367
54700	-2.327362675	23522	2.28161734	50674	-3.23186	26009	2.9873989
54556	2.9829261	23492	2.4072768	30812	-2.0493319	25946	-3.3533621
54108	2.115189	23468	-2.6887279	30011	-2.243058933	25934	2.6834543
54107	2.0082688	23373	4.39285884	29969	3.33534495	25917	2.481601
53335	2.2496374	23361	-2.109704	29965	-2.206937	25879	2.7858863
51742	-2.5358478	23173	-2.3171966	29883	2.89406184	25844	-3.508065867
51616	-2.512661	23066	3.2359164	28990	2.2214626	25839	2.6299238
51513	6.169353	23036	-2.55953515	27287	-2.017469	25821	2.779819175
51460	3.1533225	23019	-2.085158	27164	-2.57303765	25803	-3.1639419
51317	3.65763605	22938	-2.6346498	26253	-2.1100233	23762	-2.280739467
51315	-3.426106067	22938	-2.6346498	26191	2.860353975	23522	-2.9030799
51222	2.58493975	22900	-3.7239063	26152	2.32839325	23492	-3.568661233
51147	-3.0267184	22807	-2.4724276	26013	-4.354654	23480	-2.1344078
51105	2.6383745	22806	-3.331298	26009	3.18874146	23440	2.118375775
50674	2.6944422	22797	-2.4398022	25946	-2.057488	23373	-6.8736148
30812	2.7410662	11335	-2.33069335	25844	-2.31309915	23269	-2.53491405
30011	2.790691	11262	-2.2192688	25821	-114.7688445	23125	-2.0440733
30009	5.482832	11200	-2.3152441	25803	-3.9133813	23118	2.841660367
29965	2.29499815	11198	2.1883569	23761	2.7147925	23114	-7.1409235
29950	2.8388934	11198	2.1883569	23522	-2.7968875	23081	2.0963993
29911	-2.1226058	11194	-2.1218033	23492	-2.99215595	23051	-3.6862098
29068	-3.136526	11193	-2.1450868	23480	-2.1785781	23036	3.3057767
27287	5.3154964	11168	-2.36675155	23469	-2.0830696	23035	2.8940792
27125	-3.2478223	11155	3.9357545	23468	-2.1838981	23030	-2.27943065
27089	-3.0242026	11083	-2.22013865	23440	2.0848271	22944	2.5072486
27044	2.3573873	11063	3.1607823	23373	-2.2726568	22938	2.242896
27023	2.12433005	10987	-2.3403568	23269	-4.063180367	22938	2.242896

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
26998	3.452744667	10865	4.14031075	23215	-2.2339492	22900	2.41868105
26253	3.17769245	10771	-2.4562125	23173	2.5548913	22882	-2.138205
26013	2.72789275	10743	2.2346258	23118	2.8648971	22797	3.508277833
25988	-3.2209818	10669	4.51801028	23114	-3.232669833	11335	2.9405948
25946	2.5038931	10660	2.6142488	23081	2.2486384	11317	2.2849038
25937	2.0644941	10629	2.061096	23051	-2.8187156	11244	2.4082992
25879	-3.026111925	10581	2.6351469	23030	-2.1114042	11200	2.2799678
25841	2.2295618	10580	4.8154197	22978	2.2232132	11196	2.6838922
25821	-2.58432925	10499	-2.2149956	22944	2.918498	11194	2.7634423
25803	3.5883257	10479	-2.3387754	22938	2.5207496	11193	3.4783309
23762	2.710010657	10477	2.544988267	22936	2.2017162	11179	2.56604325
23761	-15.173828	10403	-3.6471213	22882	-3.3572216	11168	3.757848133
23729	2.529614	10320	-2.4060451	22861	2.674437	11155	-2.7233355
23567	2.27943335	10260	-2.671614	22807	3.00293595	11137	2.0208251
23522	3.2085066	10251	3.494138133	22797	2.75260105	11137	2.0208251
23492	2.8795681	10213	-2.6812565	11335	3.59032605	11104	2.314584
23480	3.7330253	10153	-2.703409867	11262	-2.55359565	11063	-2.4670172
23469	2.2601833	9988	-2.2957151	11196	2.9698994	10988	2.1963924
23466	2.637877	9987	-2.605401	11193	3.9588022	10987	2.7446473
23429	2.72335575	9975	-2.241126467	11189	-8.3520852	10943	2.2342854
23373	2.74521395	9891	-4.304141	11179	3.2161212	10890	2.233694
23309	2.3719103	9886	-2.391782	11155	-2.2550995	10865	-3.604358133
23269	2.316213586	9852	-2.9599695	11104	2.7282875	10781	2.1445663
23261	2.9076056	9819	-2.24307215	10988	2.5318782	10743	-2.1418576
23215	-2.038222	9794	2.831764333	10987	3.252471	10669	-9.304900433
23140	2.4415324	9774	-2.2300813	10943	2.7808113	10660	-2.2626706
23135	-2.198439	9702	-2.185215	10915	3.4373102	10625	2.600059967
23113	4.5990667	9643	-2.1895297	10892	2.9885849	10589	-2.033126
23099	2.5815082	9603	-4.390893	10890	2.5650854	10581	-2.856491

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
23087	2.8295856	9586	2.1260567	10865	-3.1090428	10580	-2.88621515
23081	-2.3555524	9516	2.0447652	10781	2.9175904	10526	2.2115788
23051	2.656883367	9459	-2.5257114	10771	-2.1598303	10479	3.1120908
23036	-3.04525555	9455	2.6266775	10669	-3.093675425	10477	-2.82772065
23030	2.4155775	9444	2.1294386	10660	2.3942313	10449	2.3607962
22982	2.578620925	9400	3.614003	10657	2.3584855	10438	2.22952825
22955	-2.027441	9338	-2.2282403	10629	2.3922482	10403	3.39260725
22936	2.876398	9330	-2.07455745	10625	3.36367	10379	-2.3949356
22887	3.353636	9260	2.0760376	10608	4.0922084	10320	2.4364192
22861	-3.0915182	9235	-2.27109885	10581	-2.49670505	10252	-2.3907385
22807	-2.5515926	9232	-2.0568612	10580	-6.710091467	10251	-3.84135255
22797	-2.6596243	9208	-2.0516677	10479	3.022258	10213	2.52725825
11335	-3.7651525	9205	-2.9823709	10403	2.383477933	10153	3.915770833
11315	2.10891	9204	-2.685994325	10379	-3.7069142	9988	2.3024083
11270	-2.1862876	9203	-2.0337458	10362	-3.75396892	9987	2.69120245
11244	-2.038924	9194	-2.2368999	10320	-2.3162026	9975	3.03553795
11200	2.0606334	9143	7.8324947	10260	2.2827501	9886	-2.9427524
11196	-2.1519978	9139	2.29374895	10251	-2.9723818	9878	2.2705264
11194	2.2449565	9095	-2.6731248	10214	-2.2298545	9852	2.7249286
11189	9.276996	8994	6.987851	10213	3.09576905	9819	2.7917633
11155	2.2776783	8939	2.8805609	10153	3.634609333	9794	-2.5714882
11143	-3.0972776	8928	3.241961125	9988	2.2480364	9774	4.7077671
11137	3.5666378	8846	-2.090152	9987	2.488407167	9702	2.6328709
11063	-3.5782068	8805	-2.0301373	9975	3.00609765	9678	2.20980225
10987	-2.7491713	8725	-2.3416629	9935	-2.57748495	9658	-2.2642791
10943	-2.0040376	8648	2.0550747	9886	-2.5547166	9643	2.3929506
10933	-4.468965	8621	-2.5162276	9878	2.6962886	9603	3.4398459
10915	-3.498116	8615	2.4077132	9866	-2.5020362	9580	2.0613563
10892	-2.3722939	8550	-2.4621623	9852	2.126669	9519	2.1167116

BL-P1-C	Fold Change	BL-P1-Y	Fold Change	P1-P3-C	Fold Change	P1-P3-Y	Fold Change
10890	-2.1343343	8522	-2.0595393	9819	2.807795833	9459	2.1095145
10865	2.6439571	8456	3.296821533	9794	-2.53047375	9442	2.0776026
10771	2.508531	8202	-2.524362	9774	3.57209845	9412	2.450578
10725	3.4897068	8193	3.107977	9678	2.1848812	9337	2.418541833
10660	2.627881	8111	-2.286101	9643	2.9102629	9330	2.05526635
10657	4.3409677	8089	2.2151203	9611	-2.1371622	9325	2.0286832
10625	2.0850265	8028	2.4651327	9603	3.1660278	9282	2.1278634
10620	2.5656695	8022	4.96803008	9586	-3.4112306	9260	-2.560377767
10611	2.3486257	7942	2.224755475	9519	2.3109715	9236	2.938299
10580	5.246019675	7916	-2.1620653	9480	-3.8289816	9205	2.78499055
10541	-3.291042	7775	-2.2837524	9412	2.0718849	9204	3.500339233
10524	-2.9161038	7771	4.474130775	9325	2.8146615	9194	2.4203242
10524	-2.9161038	7769	-2.013676467	9205	3.2878528	9139	-2.39471345
10471	-2.2131262	7764	-2.086158567	9204	3.29329705	9111	2.0583184
10467	2.288217	7764	-2.086158567	9143	-2.7665648	8994	2.2177584
10449	3.4644833	7750	-2.229902	8994	-5.51989775	8928	-5.66945065
10403	-2.10703315	7678	-2.1385968	8812	-3.0829756	8805	2.7020873
10362	3.937517338	7629	-2.2387038	8805	3.371107	8725	2.6872246
10251	2.490832633	7565	-2.16283605	8648	-2.0731227	8648	-2.8497467
10213	-2.7657769	7545	2.547256	8622	-2.4842024	8615	2.5717282
10155	-3.03323	7404	-2.3140585	8615	2.0992317	8522	-3.1615117
10153	-3.25580155	7392	-2.1222277	8521	-3.117259	8456	-3.940009925
10138	2.7842903	7392	-2.1222277	8464	-2.8671105	8436	-3.6360173
9988	-2.0848279	7391	2.2511116	8436	-2.4983462	8202	2.1442647
9985	2.50984905	7391	2.2511116	8242	-2.3103018	8139	2.5476756
9984	-3.4594018	7376	-2.4847748	8193	-2.83960965	8089	2.629456667
9975	-3.3365664	7270	-2.4099578	8089	4.711567	7994	-2.2694228
9935	3.1101387	7161	2.7640466	7994	-2.0384836	7942	-2.7908542
9886	4.4656687	7091	4.383612	7942	-2.0460694	7804	2.49642335

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
9878	2.5280426	7090	2.055034	7916	2.8699107	7803	2.1395335
9866	3.4022045	7089	-2.8739615	7804	2.473468	7776	2.52131345
9852	-2.0172718	7088	4.19647594	7781	-2.6221166	7776	2.52131345
9794	2.6072763	7030	2.77739985	7776	2.3872492	7771	-5.671455633
9678	-2.05055975	7029	4.74233848	7776	2.3872492	7769	2.476482033
9643	-2.74834055	7020	7.9464693	7775	2.4618618	7763	2.1912884
9612	2.06025	7014	-2.0569203	7771	-4.022035933	7752	2.08948395
9611	-2.6318803	7005	4.781314	7769	2.1204185	7750	3.634109933
9586	2.3967412	7003	4.37185464	7752	2.64574645	7678	2.1576014
9580	3.3121202	6938	-2.105233	7750	3.60409215	7629	2.0948935
9519	2.8411366	6928	2.399794333	7693	2.1926951	7568	2.4915483
9516	-6.379445	6920	-3.5435297	7692	2.6052177	7565	2.87090375
9441	2.1315405	6919	-2.306117	7584	2.1949196	7559	2.831587867
9397	2.3075871	6917	-2.6803451	7568	3.9458482	7556	-2.620041
9337	-2.8670687	6899	2.3050823	7565	3.12197485	7556	-2.620041
9330	-2.1264446	6887	2.890674	7559	3.088104267	7555	2.0617652
9282	3.1563432	6882	-2.393944	7556	2.688118	7553	2.04005535
9260	-2.6910198	6880	-2.29808345	7556	2.688118	7534	-2.9668257
9235	-3.30317	6879	-2.5448077	7536	-2.461355	7528	2.1701827
9232	3.8531458	6872	-2.74897155	7528	3.1125083	7403	2.214965
9205	-2.1040192	6775	-2.55567625	7511	-2.9867404	7392	-2.596029
9204	-2.3389888	6772	2.2655787	7421	-2.0996737	7392	-2.596029
9191	-2.8364491	6772	2.2655787	7343	2.5424771	7376	2.036966
9143	2.3455226	6758	2.9184519	7270	3.347085	7342	2.45147485
8994	4.984619633	6757	2.2212386	7188	3.2284575	7270	2.4717275
8896	-2.215097	6720	6.7558352	7182	-3.4534757	7161	-2.61861435
8848	3.2131643	6703	3.7307577	7161	-3.17578435	7138	-3.1292239
8812	4.08076275	6688	2.928922	7091	-2.940853125	7091	-4.7480437
8805	3.5540805	6667	2.0994828	7090	-2.0431533	7090	-2.6854649

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
8667	3.6722424	6643	-2.2923717	7089	2.0731542	7088	-8.237028
8543	-2.3856094	6297	-2.18471075	7030	-3.1626441	7067	-2.1851506
8521	2.67126515	6129	-3.585738971	7029	-2.344395	7030	-3.36931865
8464	2.1845548	6120	-2.7764435	7024	2.0996146	7029	-6.346211833
8456	2.012839525	6095	-3.2698652	7020	-2.7167059	7027	-2.0448234
8436	4.917165	6050	2.7740731	7014	-2.2862878	7013	2.003322
8405	4.455766	5990	2.9228246	7005	-3.5354168	7005	-3.9920199
8284	-2.1585176	5989	2.0902464	7003	-4.97992	7003	-4.423597
8193	2.79673605	5977	2.1901057	6942	-2.3660502	6942	-2.0532117
8110	2.089441	5916	3.2315999	6928	-2.08203815	6928	-4.02169235
8028	2.481985	5914	5.548597633	6925	-2.2417808	6925	-2.0146823
8022	2.9588124	5724	3.09292496	6917	2.1116302	6924	2.0956068
7994	2.82393505	5395	-2.317241283	6908	-2.5618277	6920	2.080777
7942	2.3313664	5360	2.0999373	6899	-2.3273327	6917	2.0135872
7862	-2.9114013	5309	3.73804592	6887	-2.9333551	6899	-2.3834832
7776	-3.0289161	5307	2.5106918	6882	2.83587825	6882	2.671349767
7776	-3.0289161	5136	2.3339822	6880	3.2155471	6881	-2.2995524
7771	3.4483429	5134	-2.0857537	6873	2.7328389	6880	2.4626161
7769	-2.3589081	5134	-2.0857537	6777	-2.3629923	6879	2.954631467
7764	-3.6787943	5111	-2.3883421	6775	2.3617024	6873	2.5162113
7764	-3.6787943	5108	-2.5230483	6772	-6.7717743	6872	2.28944265
7752	2.0634558	5083	-2.2869701	6772	-6.7717743	6777	-2.4628735
7733	-2.2714076	5078	2.72735625	6767	-2.1202805	6775	2.3976896
7693	2.576966	5026	-2.4797804	6758	-2.4487283	6772	-2.4576466
7678	-2.1147889	5024	3.836134933	6721	-4.368646	6772	-2.4576466
7584	-2.1454725	5003	2.1653886	6720	-5.5789107	6767	2.0796375
7568	-2.44738995	5001	-2.11302875	6703	-2.8195602	6758	-2.8008256
7567	2.6758208	5000	-2.1644184	6688	-2.2036643	6720	-15.241721
7566	2.1701624	4849	5.18002256	6671	2.7755301	6689	-2.6944659

BL-P1-C	Fold Change	BL-P1-Y	Fold Change	P1-P3-C	Fold Change	P1-P3-Y	Fold Change
7565	-4.085078	4824	2.2049851	6668	-2.5317912	6688	-5.074251
7559	-2.73978025	4808	2.72442614	6667	-2.3551297	6672	-2.3521447
7556	-2.0233858	4783	-2.4156907	6658	-5.59248915	6671	3.791626467
7556	-2.0233858	4782	2.3459241	6653	-2.4784902	6670	3.112648167
7534	2.366686	4778	2.37296485	6643	2.98956095	6668	-2.6746192
7512	2.5458844	4774	2.3584807	6605	2.6430236	6667	-2.8735874
7421	3.1423192	4773	-3.0218644	6601	-6.231128	6653	-2.0654893
7404	-2.18149315	4659	-2.0415056	6532	-2.2240117	6643	3.2006402
7403	-2.5635853	4656	4.771868	6473	-7.197808	6605	2.5328161
7392	2.6310923	4656	4.771868	6304	-3.6292887	6601	-2.5057412
7392	2.6310923	4603	-2.18555415	6257	3.498093	6533	-2.5989107
7270	-2.5869353	4332	2.2513528	6239	-2.3435924	6204	2.2373927
7182	2.733761	4303	2.3287425	6204	3.6779944	6129	2.66733408
7181	-2.0039191	4287	-2.148749	6196	-2.529487	6119	2.5455294
7161	2.7821406	4200	2.6126926	6132	-2.3895574	6118	2.0188124
7157	-2.1927574	4185	13.525626	6129	4.482980413	6095	2.9177535
7139	2.99164845	4173	-2.3139153	6122	2.16267275	6018	2.87176095
7136	2.78538355	4093	2.413712	6118	2.6243056	5990	-3.6269803
7091	4.82056792	4090	2.816017625	6018	4.7249968	5977	-2.242888
7090	-2.44117635	4066	2.2616928	5991	-2.309348	5925	2.965890633
7089	-2.9116452	4010	2.1124926	5989	-2.0164812	5914	-15.83816988
7088	2.0443402	4004	3.113526925	5934	2.0586812	5467	2.63298
7030	2.4160145	3899	-2.4504633	5932	3.24924645	5395	2.071775633
7024	2.6574848	3823	-4.042444	5925	2.652966875	5309	-5.606284
7014	-2.2028131	3818	3.4997745	5914	-2.437663929	5138	-2.033258
7013	-2.2799735	3817	3.1115344	5814	2.006181	5134	2.0625954
7005	2.577414367	3816	-2.0809624	5467	-2.365431	5134	2.0625954
7003	2.94519945	3811	-4.782237	5360	-3.64209	5108	2.7149277
6942	2.8805957	3805	5.1649074	5309	-2.219030367	5078	-2.6717477

BL-P1-C	Fold Change	BL-P1-Y	Fold Change	P1-P3-C	Fold Change	P1-P3-Y	Fold Change
6938	-2.1713843	3803	-2.59317	5187	2.11729625	5024	-8.4173619
6928	2.0404726	3801	7.318825675	5184	2.0595522	5019	3.070828333
6920	-2.297094	3430	2.115524	5140	3.7512577	5013	2.8059118
6917	2.4244123	3338	3.00078294	5134	2.6280969	5004	-2.3679287
6887	3.8968036	3320	-2.810043257	5134	2.6280969	5001	2.4872875
6882	-2.487589	3223	2.2971864	5119	-2.3199668	4928	2.3177166
6880	-3.1123376	3221	-2.289024	5108	2.5924724	4920	-2.0319545
6878	2.6629834	3212	-2.1187913	5083	-7.8195567	4849	-7.96336286
6873	-2.48151565	3206	6.3139821	5080	-9.653018	4824	-2.0499804
6827	2.9233994	3205	3.805483325	5078	-4.8709044	4808	-6.3089371
6778	4.4188237	3201	2.406193	5026	2.036684	4802	-2.0221355
6777	5.8904533	3183	-2.132188	5000	3.31604945	4782	2.0568151
6776	-2.5218496	3171	3.0574869	4901	2.235133	4778	-2.0382276
6776	-2.5218496	3167	5.7511459	4856	2.3908438	4774	-2.587427433
6775	-2.1740875	3146	-2.4867568	4850	2.0449734	4772	-2.2940478
6773	2.94325055	3142	2.7823796	4849	-2.46496358	4659	3.58333126
6772	2.8422048	3118	2.0582273	4848	-2.4051497	4656	-6.7329189
6772	2.8422048	3083	4.20285904	4808	-9.5832833	4656	-6.7329189
6767	4.6375957	3068	4.056567425	4807	2.251795	4648	-2.5451145
6758	2.560315767	2972	3.2294264	4799	3.0565604	4605	-2.045987
6757	2.3738003	2963	-2.2573836	4782	-2.13255975	4603	4.6781784
6749	2.3596058	2919	2.0400574	4775	2.4321603	4332	-2.02324215
6721	3.41958465	2908	-4.6558256	4774	-2.0175965	4331	3.0695796
6720	4.89168836	2623	2.2324178	4659	3.15835528	4303	-2.5733027
6702	3.1662195	2516	3.87431	4656	-2.569735733	4298	-2.0390847
6689	2.0216763	2348	2.4801179	4656	-2.569735733	4286	-2.0220044
6671	-2.7714651	2301	3.6844864	4603	3.405690467	4185	-2.540494
6670	-2.396428067	2275	-2.0083332	4601	2.074986225	4173	2.4982054
6667	2.9839282	2130	-2.7776072	4332	-4.0613256	4093	-2.1790586

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
6658	2.4564893	2128	5.31462994	4331	5.2979364	4090	-6.6564078
6653	3.1495551	2120	-2.4249518	4302	-2.2829108	4089	3.9675617
6643	-3.0157063	2117	2.0069144	4298	3.1233919	4087	2.101163
6642	3.118725	2116	2.1013641	4286	-2.202181	4084	-2.210284167
6605	2.58291135	2115	2.8446894	4185	-4.1806373	4066	-2.5559032
6473	5.2851753	2114	-2.0201402	4084	-2.989108967	4010	-3.08321405
6132	2.2972522	2113	-2.5674274	4066	4.31009605	4010	-3.08321405
6129	-3.531139125	2103	4.34192454	4010	-2.045843	4004	-4.077734767
6122	-2.026148	2101	-2.43816375	4010	-2.045843	3821	2.888287417
6118	-2.1286309	2077	-2.1882114	3975	-2.58669875	3818	-2.1473951
6117	2.566937	2020	4.2945094	3821	3.006784625	3816	-2.2462783
6097	4.1800246	2016	2.73496685	3817	-2.4302261	3811	2.2957964
6018	2.6561007	1911	3.10577025	3809	2.13754265	3805	-2.119408617
5993	2.5025362	1870	2.275684	3805	-5.03270315	3803	2.199824
5990	2.7634788	1836	-2.6130168	3801	-4.550729	3801	-3.212821633
5989	2.6620455	1628	-2.12926915	3735	-2.8064969	3665	-2.6069214
5914	4.1779397	1602	2.1519446	3727	5.1192203	3663	-2.5889719
5813	3.422878	1600	3.5652341	3702	2.476750667	3660	2.1368215
5626	2.4078796	1487	-2.2681015	3622	2.2383158	3622	2.162509
5360	3.2811665	1482	2.5780907	3607	-2.3411908	3607	-2.3139935
5309	2.296705	1397	-2.5779748	3430	2.0354123	3430	-2.4009893
5187	-4.3608418	1386	-2.16941815	3398	2.6099164	3399	2.1128387
5140	-2.5685444	1102	-2.0783546	3321	-4.734723275	3398	2.4788216
5138	2.9448326	1052	2.63294185	3320	3.0873703	3321	-3.6214608
5134	-2.3433708	955	3.4869415	3212	2.2747513	3320	3.20131785
5134	-2.3433708	954	2.270571533	3206	-7.752714433	3212	2.295712
5130	-2.0389283	953	2.79395135	3202	-2.3644102	3206	-8.710235933
5127	4.5948033	951	2.1531472	3201	2.0392635	3205	-3.543620667
5125	2.8555217	741	3.26569628	3171	-4.9453313	3201	-2.0025935

BL-P1-C	Fold Change	BL-P1-Y	Fold Change	P1-P3-C	Fold Change	P1-P3-Y	Fold Change
5119	2.667822	463	2.31441555	3146	2.0890281	3183	2.2255871
5111	-2.4920306	394	-2.0809646	3120	2.007944	3171	-2.7534901
5078	3.431915667	360	-3.239249633	3118	-2.51290735	3167	-5.1608311
5026	-2.82625565			3096	-2.8608725	3146	2.4919994
5024	3.592164			3083	-4.287228033	3142	-2.0053165
5004	3.2725556			3081	-2.29275965	3113	-2.0156362
5003	-2.4458923			2972	-3.9926825	3083	-13.5143635
5000	-2.808458967			2965	2.3912878	3081	-2.453007
4928	4.0930627			2963	2.5496335	3059	-2.1603131
4901	2.1153536			2960	4.5429794	2965	3.1113008
4849	2.917115371			2959	3.1975821	2963	2.60262075
4848	3.8456216			2914	-2.6220794	2960	3.5208814
4783	3.093244			2649	-2.1162942	2919	2.0122101
4778	2.97606415			2647	2.7854621	2908	2.866890867
4775	-6.312746			2624	-5.088971733	2625	2.0824473
4774	7.051526			2551	2.718336133	2624	-4.46529546
4666	4.155369			2516	-3.0766683	2623	-3.1414676
4656	3.547835917			2313	2.7940447	2551	3.698690667
4656	3.547835917			2308	2.2735348	2348	-3.90552665
4648	-2.6067991			2296	-5.055044	2313	2.2515055
4605	2.1460528			2275	-2.3678966	2301	-3.9875755
4603	-3.2428007			2274	-2.4135199	2274	-2.2490768
4335	2.099933933			2128	-3.6390871	2130	-2.34573885
4332	4.098679			2120	-3.864239533	2128	-8.050899475
4306	-2.3252637			2115	-3.5783026	2120	-2.30050095
4298	2.441003			2114	2.3145123	2116	-2.023389
4287	3.51944525			2113	2.8536026	2115	-4.6912036
4286	2.338776			2104	-3.0304964	2114	2.0860963
4261	2.59865			2103	-2.306341267	2113	2.3498774

BL-P1-C	Fold Change	BL-P1-Y	Fold Change	P1-P3-C	Fold Change	P1-P3-Y	Fold Change
4174	-4.729988			2099	-3.0811499	2103	-3.721222
4170	-2.2814386			2079	2.958995	2101	2.4874742
4093	2.464701			2077	2.253809	2079	2.2656658
4087	2.355926			2016	-2.85462098	2020	-2.8777514
4084	2.26071052			1871	3.027777	1997	2.0596259
4010	2.127045			1870	-2.93360375	1876	2.37730115
3817	2.057582			1808	-3.4786632	1875	2.2345579
3815	-2.585674			1806	2.326341	1874	2.443453
3811	-2.3108737			1743	2.0974035	1871	2.9255826
3809	-2.2820703			1600	-3.1320554	1870	-3.5084503
3735	3.0158687			1537	-2.6320698	1836	3.960604
3659	-4.362641			1523	-3.3690276	1831	-2.355634
3622	-2.0280397			1482	18.365227	1820	-2.5113258
3621	-3.5471542			1337	2.1776862	1806	2.4186829
3607	3.2984111			1102	4.215007	1600	-3.49443885
3516	3.20392985			1052	2.058741	1482	-2.44119835
3431	2.183916			1051	-3.526489	1317	-3.2998517
3430	-8.783458			954	-2.420144533	1052	-2.625182867
3400	4.0132265			953	3.1665841	1051	-2.0145879
3399	-4.386596			951	-2.9901905	954	-2.587462025
3398	3.11640425			902	3.7857594	951	-2.5543271
3394	7.006136			861	2.098971	902	2.23351775
3321	6.84168465			860	-2.5756574	861	-2.0728356
3320	-3.213245088			786	-2.9454029	860	-2.4486232
3221	2.886623			777	-3.8273985	741	-8.0288365
3212	2.0725384			741	-2.752521533	644	2.1121788
3206	4.90464475			740	2.0850506	406	2.136432667
3202	2.3545843			738	-3.1212816	405	-2.3566604
3201	2.6735435			689	2.2862246	394	2.3622959

BL-P1-C	Fold Change	BL-P1-Y	Fold Change	P1-P3-C	Fold Change	P1-P3-Y	Fold Change
3182	-2.5493014			406	2.621261	360	2.668655467
3171	4.3629404			394	3.3197142	307	2.7289026
3170	2.2867427			360	2.338832		
3146	-2.3354764			348	-2.606355633		
3120	-3.5590122			346	-2.1932974		
3118	2.9286072			257	-2.7085714		
3115	-4.83592195						
3113	-3.2740962						
3097	2.8895087						
3091	2.688652933						
3083	4.191385825						
3081	2.6640294						
2972	2.526251933						
2969	2.843679167						
2968	-2.3086414						
2965	-2.1838621						
2963	-2.50889175						
2961	-2.6402225						
2960	-2.51858465						
2957	2.1404579						
2908	2.123581525						
2649	2.874072675						
2647	-2.1974928						
2625	3.658768						
2551	-2.7827976						
2516	3.9606307						
2495	2.937950767						
2313	-2.0990555						
2309	2.20633192						

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
2275	-6.511479						
2274	6.5110507						
2273	2.2462087						
2130	2.1635313						
2128	2.57459756						
2118	2.7485662						
2116	2.1965468						
2115	3.6067238						
2114	-2.133797						
2104	2.47978						
2103	4.13678806						
2099	2.4833051						
2079	-2.5394365						
2077	-2.3885435						
2063	2.0724766						
2034	2.2040126						
2017	2.99025895						
2000	2.66657						
1997	-2.1599759						
1912	3.8010403						
1870	3.67476256						
1831	4.1671886						
1820	3.50687						
1806	-2.088272						
1743	2.322732						
1628	-2.5933123						
1602	2.6359345						
1600	2.349774783						
1536	2.7342854						

BL-P1-C	**Fold Change**	**BL-P1-Y**	**Fold Change**	**P1-P3-C**	**Fold Change**	**P1-P3-Y**	**Fold Change**
1523	2.691792						
1487	2.7075417						
1397	-2.13816635						
1396	2.5960131						
1386	-2.09830165						
1053	3.7726332						
1052	2.261047						
1051	3.4653996						
1050	-2.737651						
954	3.534273267						
951	-3.9472315						
904	2.5233736						
863	2.2400203						
860	3.56238985						
741	2.7747604						
689	-2.6791178						
463	2.9973847						
394	-2.397195925						
307	2.8956063						
257	2.5639458						
196	-2.2570311						

BL-P3-C	**Fold Change**	**BL-P3-Y**	**Fold Change**
100289678	-2.394133	100507290	-2.1148493
100288687	3.174767991	503834	2.897875433
100131390	-6.8683043	503582	3.1823869
643641	2.9319215	401262	-2.2693311
503835	3.2003756	399823	-2.8359702
503834	3.00413695	390010	2.0782728
401262	-2.196376	389692	2.7472565
390010	2.4020038	347862	2.0737476
389136	4.0891128	347853	-2.233146
375287	2.68918385	344167	3.3090553
374655	-7.4834123	344022	3.28403135
353274	2.1120036	340784	2.5513452
347862	2.3410103	340543	-2.8323076
344167	2.0503287	340260	-2.3046732
344022	3.6195577	339559	2.658385
342909	2.7500901	285550	2.2444324
342538	2.5557148	284119	-2.5408443
340260	10.480807	257397	-2.34377465
339745	2.6522925	256643	-2.730415
285550	-2.0828974	256380	-2.36551875
284390	2.1340046	255101	2.6667542
256643	-2.3503067	253639	-2.6072464
256380	3.010374167	221937	-2.3973897
255313	-2.2415895	221833	2.3237128
253639	-2.0886257	221037	2.315712
221833	2.7572906	200186	-2.2898035
219749	2.425281	171389	-2.1545935
219409	2.1512468	170302	2.1033227

BL-P3-C	**Fold Change**	**BL-P3-Y**	**Fold Change**
200186	3.1886325	169841	-2.2064688
196513	3.1724741	162972	2.523618
170082	2.15471385	159296	2.1506798
163033	2.199633	158431	2.357247
162993	-2.081183	155054	2.0297701
162972	2.1682339	152518	3.1716428
159296	6.2045607	149628	-2.8824842
153527	2.2942495	148398	2.5825527
152518	2.06136165	127540	2.5116339
149628	-2.3068497	127428	2.7094543
148398	2.32934535	121551	2.9764597
148156	4.606136	114991	2.0354667
138474	-2.0318196	114781	-2.4342
133522	-2.24222935	114548	-2.01145
128611	3.811184	94104	-5.041649
128553	-2.4919524	92002	-2.6886213
128408	5.6453855	91408	-2.5000205
127540	2.001478	90843	-2.8479981
126208	-2.3274837	90668	3.3126426
124641	2.050884	90594	2.3851776
123811	8.5496435	89857	-2.4993248
116039	-2.0217018	85446	-2.0306947
114826	2.3110845	84922	-2.499799
112885	2.90394085	84913	3.72946205
94104	2.2688725	84733	2.5757825
93953	3.47658775	84460	-2.248292
92002	-2.2459214	84166	2.338926
91662	-2.0166883	81669	-3.3363323
91408	5.2201347	80712	2.476127

BL-P3-C	**Fold Change**	**BL-P3-Y**	**Fold Change**
90668	2.4414711	80320	2.9749217
90594	2.4803214	80012	2.8368993
90135	3.4896193	79977	-2.2767663
89857	3.12908115	79960	-2.512856
85364	-2.2366695	79891	2.6126456
84969	2.6292727	79184	-3.359426
84954	-2.4532974	65988	3.6009151
84913	3.2236013	64919	2.1109374
84733	2.1021054	64864	-2.1854093
84717	-2.156073	64393	2.176781
84460	-3.8296041	64375	2.1337225
84441	-2.3307152	64332	-2.681672
84306	2.7606542	64210	-2.1947775
84232	2.8289945	63934	-2.0871344
84148	2.2080328	60529	2.332529633
83463	-3.2035453	59348	-2.23823055
81857	-2.2540696	57721	-2.2970002
81628	-3.352399	57713	-2.4226296
80790	-2.56402735	57616	-2.0606627
80325	3.0810144	57209	-2.1964765
80012	4.1735196	57187	-2.1435397
79960	3.8453186	57157	3.0722289
79921	2.7598932	55818	3.7534914
79898	2.101653	55810	-2.0016468
79891	2.0936925	55802	-2.147445
79816	4.34166215	55734	16.360588
79673	-2.8200903	55643	-2.843883
79230	3.8747237	55634	2.2509704
79158	5.67492	55534	2.137748

BL-P3-C	Fold Change	BL-P3-Y	Fold Change
65988	2.4424937	55274	-3.0149608
64864	5.866691	55175	-2.0475671
64784	-2.38767335	54897	-2.8084002
64754	2.2566063	54856	-2.7485952
64236	-3.7600648	54799	2.3107011
64127	4.548278	54700	-2.072122
63976	2.830637	53339	2.0279472
63929	3.42857395	51773	-2.342824
60529	3.8956227	51742	4.3095813
59269	-2.0344055	51460	-2.0109117
58525	2.5960934	51317	-2.643656
58492	3.870182	51222	-3.5760608
58486	4.13312	50674	2.161616075
57721	-2.5293348	30011	-2.1421006
57713	-2.1077394	30009	-2.8964744
57711	3.145925	29997	-2.0527
57621	8.341515	29950	-2.012542
57616	7.26271	29889	-2.0611567
57332	-2.0407271	29115	-2.5145168
57209	2.11077295	29068	-2.7492812
56980	8.140796	27287	-3.6777096
56731	2.006065	27154	2.6551027
56655	2.3590553	27023	2.103455
55893	-2.0109549	26998	2.0722718
55832	-2.1821916	26338	2.419846767
55810	-2.0517423	26152	-2.6633224
55806	2.522495	26121	-2.71346855
55802	3.28484475	26013	-2.0408263
55734	2.6413023	25879	-2.4357154

BL-P3-C	Fold Change	BL-P3-Y	Fold Change
55689	3.5981069	25844	2.7723453
55655	-2.435817	25839	-2.5597246
55553	2.4743192	23762	2.6059882
55290	2.1468437	23533	-2.0156362
55249	2.226758	23440	2.79264035
54870	-2.7800274	23373	2.09529915
54856	2.112581	23309	-2.036913
54799	-2.797621	23269	-2.164193
54556	3.420514	23261	-2.135385
54107	3.297285	23118	2.3139744
53339	4.6058636	23066	2.607735
51616	-2.457653	23036	-2.0979373
51513	-2.9004443	22900	2.2688873
51460	3.4211183	22807	-2.5990777
51193	2.2924433	22797	2.6581445
51119	2.7375705	11336	-2.2892678
51105	2.536938425	11311	-2.2298232
50674	2.094962733	11262	-2.685291067
30812	2.2407866	11155	2.2668986
30011	-2.335238975	11083	-5.3957453
30009	4.61285	10988	2.2165792
29969	5.5453768	10951	-2.5296563
29883	3.7214595	10781	2.1056156
29068	2.0375621	10771	-2.5824751
28971	2.0269473	10660	-2.7414134
27154	-2.0999544	10629	2.0150547
27125	-3.5585911	10625	2.3076336
27089	2.6224744	10611	-2.2602348
27044	2.1139193	10580	2.5567035

BL-P3-C	Fold Change	BL-P3-Y	Fold Change
26338	3.52861265	10527	-2.1722465
26253	3.9526012	10524	-2.0256515
26191	3.76277245	10524	-2.0256515
26009	3.8461928	10479	-2.0370343
26007	2.5720092	10477	2.178862833
25988	-2.344336	10473	2.164331
25821	-245.2170282	10449	-2.4431365
23762	2.93975985	10403	-2.1113288
23567	2.510706233	10362	2.14764242
23480	2.3865929	10322	2.0876648
23469	3.0488696	10320	-2.1916032
23440	2.2409433	10260	-3.2904146
23361	-2.49459185	10251	2.53557725
23309	2.3969495	10214	2.031113267
23261	2.2193818	10155	-2.1843188
23215	-2.3805604	9988	-2.94245765
23135	-2.3349583	9702	4.6492143
23118	7.28261735	9701	2.2445292
23113	3.1867805	9678	-2.1060374
23087	3.015207	9612	-2.2179453
23081	2.9136326	9611	-2.0624113
23035	3.4683743	9527	-2.0936828
23030	2.2045662	9337	2.57271065
22936	4.82554	9325	-2.189869
22887	4.1691008	9282	-2.157481
22882	-3.1828348	9260	-2.11136535
22861	-2.2434878	9209	-2.1762335
22807	4.9722095	9208	-2.5861633
11336	-2.1017504	9204	-2.1753008

BL-P3-C	**Fold Change**	**BL-P3-Y**	**Fold Change**
11335	4.1221757	9143	8.238421
11335	4.1221757	9139	2.78409685
11315	2.5120523	9095	-2.2842567
11311	-2.9188097	8994	3.831383
11270	-2.5296023	8928	2.7231606
11262	-2.282137467	8846	-2.029754
11198	-2.13794215	8812	4.5255084
11198	-2.13794215	8805	-2.802852
11194	3.4744563	8667	-2.0248442
11193	3.6909635	8615	3.7500541
11189	-2.0353656	8521	3.584844
11179	5.1804757	8456	2.3621365
11143	-2.9457028	8436	-4.0909214
11137	3.6933284	8089	3.931783767
10933	-3.0558064	7803	2.9260085
10890	2.8478863	7771	2.11760225
10745	3.7581465	7767	-2.1915236
10725	2.959184	7764	-2.4535402
10660	2.3686285	7764	-2.4535402
10657	2.16191205	7750	2.3469028
10625	4.0332513	7629	-2.077826
10620	2.7022207	7568	2.3316703
10581	-2.1372591	7556	-4.2396855
10527	2.3169255	7556	-4.2396855
10479	5.529865	7404	-2.6460373
10478	-2.3939898	7403	-2.1107788
10477	-2.2436657	7391	2.5376196
10449	4.595681	7391	2.5376196
10438	5.2606263	7182	-2.177453

BL-P3-C	**Fold Change**	**BL-P3-Y**	**Fold Change**
10379	-4.6272316	7181	-2.8606365
10322	-2.0124223	7181	-2.8606365
10251	2.1463664	7106	2.5720835
10155	-2.90809935	7088	2.10643724
10153	3.4880002	7067	2.2541225
10138	2.0814455	7067	2.2541225
10042	3.6928518	7030	2.1928978
10020	3.041841	7029	2.043163825
9894	2.4921072	7024	-2.597982
9886	3.7174094	7020	2.528630825
9878	4.957741	7019	-2.0043154
9819	3.887608	7014	-2.2074301
9792	2.08499	7005	2.597057
9774	2.241954333	6942	-2.1845167
9767	2.3146834	6925	-2.052628
9701	-2.3116205	6917	-2.4362307
9658	4.3074455	6872	-2.7802857
9611	-2.126205	6777	-2.447297
9603	2.0095546	6775	-2.3637942
9586	-2.2301035	6773	-2.0608802
9527	3.8618975	6773	-2.0608802
9519	4.8073397	6689	-2.2643585
9516	-5.3494404	6672	-2.03948995
9480	-2.1766722	6671	2.63132835
9444	-3.2634257	6658	-2.5679336
9440	5.462452	6654	2.1061509
9412	3.764483	6601	-2.4226685
9400	-2.929646	6595	-2.5690825
9337	-3.575331	6533	-2.22577405

BL-P3-C	Fold Change	BL-P3-Y	Fold Change
9325	4.7489896	6257	-2.0167744
9282	3.9706838	6204	-2.0938573
9235	-2.4690629	6196	-2.083124
9209	2.8460656	6120	-2.6622205
9208	-4.050718	6095	-2.1069336
9202	2.354665	6050	2.225119
9111	6.409346	5925	2.015136
8928	2.68665	5916	2.221814567
8864	3.2120059	5612	2.025308
8848	2.9416068	5465	-2.2999728
8805	4.45961	5307	5.59119115
8667	3.2406354	5187	-2.2972453
8622	-2.0661304	5140	2.12462995
8621	-2.0489333	5127	-2.3237264
8615	3.604225	5078	2.6377952
8550	2.7286255	5026	-2.348206
8543	-2.0678272	5024	2.7339977
8456	2.7310587	5004	-2.26346345
8405	4.18924	4856	3.3961658
8320	2.2836883	4850	-2.115197
8284	-3.650455	4848	-2.441083
8178	-2.7817516	4802	-2.278725
8111	2.199966	4800	-2.60684965
8089	3.5650253	4783	2.4514558
7988	2.2139354	4782	2.1806993
7979	3.5565753	4774	-2.5064054
7965	-2.442083	4773	-2.0333493
7942	-2.829697	4656	3.1661239
7862	-2.1376063	4656	3.1661239

BL-P3-C	Fold Change	BL-P3-Y	Fold Change
7771	2.5059752	4648	-3.1398358
7769	2.26080465	4647	2.2416773
7764	-2.443816233	4605	-2.003284
7764	-2.443816233	4603	2.97423255
7752	4.6071334	4601	2.378141925
7750	2.7276256	4335	2.6902096
7693	4.4815097	4302	-2.7238977
7567	2.4522865	4200	2.18435955
7566	2.8624406	4185	12.820031
7536	-2.0774646	4093	2.8137383
7534	4.724902	4089	2.0937839
7528	2.736285	4088	-2.1024973
7512	2.03016	4084	-2.4027648
7511	-4.1205997	3899	-2.054534
7421	2.4246535	3818	2.1909933
7403	-2.6114464	3816	-3.418248
7392	3.116518	3811	-2.0830407
7392	3.116518	3805	2.24523495
7391	2.1999514	3803	-2.573945
7391	2.1999514	3801	2.4400151
7188	5.3446665	3703	-2.3274736
7182	-2.0219035	3662	-2.3177474
7161	2.1881723	3660	2.017524
7135	2.4896614	3490	-2.3048127
7090	-2.931641067	3398	-2.8281608
7089	-3.9131675	3320	-2.929249167
7088	2.37555635	3212	2.548681
7029	3.5694561	3205	2.977983675
7024	2.8216166	3201	2.8656373

BL-P3-C	**Fold Change**	**BL-P3-Y**	**Fold Change**
7014	-5.0362644	3183	-2.4073143
7013	-2.9038851	3167	2.9488065
7008	-2.0746598	3146	-2.069521
7005	2.032007	3142	-2.0154603
7003	4.94926065	3113	-2.0241597
6942	-2.5988584	2965	-2.4196844
6936	3.7862657	2960	2.145659133
6926	-2.386294	2957	-2.191079
6925	-2.8977058	2649	-2.9070542
6924	-2.3365493	2624	-2.48893145
6917	2.0825635	2551	2.81297135
6908	-2.0859563	2516	2.1948855
6887	-2.3234518	2130	-2.17703525
6884	-2.0650685	2128	2.39880478
6882	2.231702	2120	-2.54615465
6879	8.295122	2116	-2.2171237
6878	2.1550393	2114	2.0536427
6827	2.1954277	2103	3.233721
6778	2.5753524	2079	-2.2770184
6777	3.9201365	2020	-2.6842563
6776	-3.8479548	2017	-2.6217163
6776	-3.8479548	2005	-2.1552558
6775	-2.2289178	1911	3.40525205
6773	4.1803503	1876	-2.0754495
6772	-2.382578	1820	-2.648146
6772	-2.382578	1805	2.328509775
6749	2.3020277	1743	-2.023573
6689	-2.740472	1555	-3.3934314
6670	2.6609986	1488	3.03516925

BL-P3-C	Fold Change	BL-P3-Y	Fold Change
6668	-2.652588	1487	2.6653583
6667	-2.159632	1482	-3.4025128
6658	-3.6924033	1397	-2.2355773
6653	-2.0589752	1396	-2.0087986
6643	3.64294	1386	-2.071789
6642	3.7345395	1317	-2.5308719
6641	3.979643	1051	-2.2964597
6601	-15.250524	955	3.65397215
6599	2.1266339	951	-2.36136915
6595	-3.301117533	860	-2.2344995
6399	4.0517287	777	-2.36456
6399	4.0517287	740	2.0501614
6129	5.4479647	644	-2.12599
6117	2.8141425	406	-2.0140812
6097	3.9329054	405	-2.7279673
6018	4.9135805	394	-3.217109
5925	5.6771073	326	-2.0021296
5914	2.12319378		
5436	2.971374		
5395	-2.65743755		
5360	2.0344732		
5307	2.4755404		
5184	2.235612		
5134	2.2892563		
5134	2.2892563		
5133	2.1322875		
5130	-2.3530748		
5127	2.8252943		
5118	2.041834		

BL-P3-C	**Fold Change**	**BL-P3-Y**	**Fold Change**
5116	2.495428		
5108	2.9426277		
5023	-2.1418116		
5013	-2.9892309		
4928	2.1353978		
4901	2.0953596		
4848	2.227456		
4802	-3.67645345		
4800	3.609104		
4775	-2.581797		
4774	3.495013		
4656	7.68081465		
4656	7.68081465		
4647	-2.403426		
4609	-4.5205337		
4603	3.467677533		
4298	2.6741197		
4185	-2.330116		
4174	-2.7956011		
4171	2.062986		
4170	2.1028504		
4090	2.73760565		
4089	2.8009694		
4087	2.5286694		
3975	-2.6216252		
3823	2.6962352		
3818	2.3536582		
3817	-2.2283533		
3815	-3.1539078		

BL-P3-C	Fold Change	BL-P3-Y	Fold Change
3811	-2.4114778		
3809	-2.0684009		
3805	-3.9740436		
3801	-2.310795		
3659	-2.305326		
3621	-3.1187685		
3607	3.4472985		
3490	2.960123		
3400	2.0311441		
3399	-2.2042434		
3398	6.525315		
3394	2.31255385		
3340	2.6488016		
3221	4.2420177		
3212	3.1863444		
3202	2.2967293		
3201	2.6634901		
3120	-2.86895095		
3119	-3.50986705		
3118	-2.2831848		
3113	-2.5731955		
3097	2.3409283		
3096	-2.606773		
3091	5.459194233		
2963	3.1343892		
2960	2.542802433		
2908	5.272537233		
2799	3.4129572		
2647	-2.1944323		

BL-P3-C	**Fold Change**	**BL-P3-Y**	**Fold Change**
2551	2.3849325		
2495	2.28355		
2313	2.0580552		
2309	2.85726474		
2275	-6.518067		
2274	3.9245816		
2130	2.336461		
2128	2.290708625		
2113	2.8441472		
2103	2.822695733		
2101	2.6142201		
2077	-2.47906925		
2067	-2.0823963		
2034	3.2244956		
2020	5.934926		
1997	-2.2432914		
1871	8.140347		
1870	3.47144215		
1831	5.305002		
1808	-2.3891704		
1806	2.5950332		
1805	3.43522335		
1628	-2.1298575		
1536	3.0127344		
1523	-2.3023802		
1487	3.7552373		
1482	18.2944554		
1396	-3.1076813		
1387	2.4036477		

BL-P3-C	**Fold Change**	**BL-P3-Y**	**Fold Change**
1051	3.1145728		
951	-4.5196915		
902	3.826593		
864	2.1842372		
861	2.9729511		
777	-2.2453356		
741	2.3906121		
740	-2.0030935		
738	-2.1738675		
689	-2.230091		
468	2.1158855		
360	2.2146847		
166	-2.3907235		

Appendix 13: List of Transcription factors from stringent protocol

EnterezID	BL_P1_Control	EnterezID	BL_P1_Yoga	EnterezID	P1_P3_Control
6129	-2.7520688	3320	-7.2985836	4808	-2.67187
3320	-2.4397025	84460	-2.1761644	2624	-2.63677
84460	-2.2687688	25879	-2.0430315	10362	-2.58809
51315	-2.230613	6129	-2.0043588	23269	-2.37638
4609	-2.136164	90668	2.0295343	6720	-2.37391
7003	2.0198367	5916	2.0375316	3083	-2.32321
23373	2.0304697	10084	2.0436366	6601	-2.24355
148398	2.0349584	9767	2.0484185	2017	-2.12757
3068	2.0366325	26338	2.0576887	90853	-2.12106
503835	2.0459917	10865	2.0706108	7771	-2.03542
10214	2.0571172	1052	2.0710902	84726	-2.02241
8928	2.0624564	84717	2.0725396	3167	-2.01641
100288687	2.0851083	4808	2.0782814	1044	-2.013
5024	2.1414437	154150	2.0921955	1482	2.024859
7545	2.1450512	23051	2.0997634	29883	2.09205
50674	2.1480439	503582	2.1171746	22807	2.106957
55806	2.2155902	1600	2.1227207	80012	2.119315
23145	2.2163582	23492	2.1323445	3320	2.193378
1600	2.2502067	953	2.1446042	2960	2.38972
10669	2.2975426	337968	2.1455271	9774	2.39651
5914	2.3708181	112885	2.1652234	4603	2.814789
3083	2.3745396	221833	2.176905	128408	2.856074
4808	2.4363165	51621	2.217427	6129	4.559765
84726	2.4408154	7030	2.273556		
3167	2.546256	4090	2.276788		
7771	2.582966	340260	2.3131275		
6720	2.7141767	1488	2.3512254		
159296	2.7260537	5724	2.3553872		
4656	2.7396097	340784	2.3589532		
4656	2.7396097	10251	2.37742		
1870	3.0286238	2016	2.4037404		
10362	3.260056	390010	2.4125695		
		8928	2.4154396		
		503835	2.4430993		
		27023	2.450749		
		23613	2.471625		
		3338	2.5357566		
		79673	2.606502		
		23269	2.621923		
		197358	2.728601		
		3805	2.79309		
		64344	2.8001287		
		6703	2.8128395		
		3205	2.834104		
		741	2.8578207		
		55806	2.9129226		

EnterezID	BL_P1_Control	EnterezID	BL_P1_Yoga	EnterezID	P1_P3_Control
		3801	2.9230816		
		7771	2.9346364		
		148398	2.9357421		
		5309	2.9737546		
		3068	3.0552368		
		348	3.1412349		
		7003	3.2709804		
		10669	3.4038024		
		7029	3.4087808		
		3083	3.4477324		
		10214	3.5104065		
		7088	3.5148108		
		23373	3.550432		
		5024	3.5888212		
		84726	3.7136376		
		3167	3.7508411		
		50674	3.804648		
		4656	3.830724		
		4656	3.830724		
		4849	3.9503505		
		2128	4.136806		
		159296	4.232178		
		6720	4.307993		
		5914	4.8821425		
		10362	5.153313		
		100288687	15.3873591		

EnterezID	P1_P3_Yoga	EnterezID	BL_P3_Control	EnterezID	BL_P3_Yoga
23145	-4.39166	6601	-2.40019	NIL	NIL
2624	-3.42235	25821	-2.3847		
10362	-2.90583	2275	-2.00292		
6720	-2.89124				
5914	-2.70796				
3083	-2.56647				
159296	-2.44089				
1.00E+08	-2.40737				
84726	-2.4046				
10669	-2.38014				
3167	-2.32418				
23269	-2.29341				
10214	-2.26772				
340260	-2.25177				
50674	-2.24115				
741	-2.22876				
5024	-2.22516				
3801	-2.2035				
6703	-2.18043				
2128	-2.17746				
4849	-2.16584				
7771	-2.11371				
23373	-2.09454				
148398	-2.0905				
90853	-2.0787				
197358	-2.05657				
27023	-2.04987				
4656	-2.03015				
4656	-2.03015				
79673	-2.02927				
7029	-2.0273				
55806	-2.02501				
84717	-2.00524				
80012	2.004606				
25821	2.014629				
2960	2.052008				
3320	2.136399				
9774	2.406471				

Appendix 14: Biochemistry Tests Raw Data

ID	Group	TG_P1	HDL_P1	LDL_P1	VLDL_P1	Glucose_P1	Urea_P1	UricAcid_P1	Total_Cholesterol_P1	ALT_P1	AST_P1
1	Control	91	46	82	18	101	27	8	142	29	47
3	Control	124	30	119	25	83	29	4	178	17	53
7	Control	76	34	82	15	95	30	8	138	11	27
9	Control	120	54	138	24	85	29	6	229	6	37
8	Control	79	67	78	16	101	19	4	159	14	38
10	Control	129	48	186	26	107	31	8	334	26	38
12	Control	89	58	122	18	95	21	5	198	24	28
14	Yoga	106	52	120	21	86	31	7	202	6	49
16	Yoga	117	42	106	23	76	27	4	172	15	38
17	Yoga	118	38	131	24	89	21	6	195	14	37
28	Yoga	109	50	96	22	97	31	6	172	26	45
29	Yoga	74	37	78	15	79	16	5	127	8	22
20	Yoga	43	62	66	9	69	14	3	138	11	39
22	Yoga	113	46	120	23	105	36	6	194	11	33
24	Yoga	108	29	91	22	89	29	6	137	19	27
23	Yoga	103	34	102	21	85	22	6	156	33	52
25	Yoga	101	47	116	20	85	21	7	186	14	27

ID	Group	ALP_P1	GGT_P1	Bilirubin_P1	Total_Protein_P1	Albumin_P1	Corr_Creatinine_P1		TG_P2	HDL_P2	LDL_P2
1	Control	1	44	0	71	47	0.9		124	46	90
3	Control	-2	33	0	73	45	1		103	34	130
7	Control	-2	23	0	85	52	1.3		91	36	100
9	Control	-1	33	1	74	46	0.9		111	61	157
8	Control	-2	38	0	72	46	0.8		117	70	146
10	Control	-2	36	0	86	65	1.4		120	47	131
12	Control	-2	22	1	74	47	0.8		82	50	148
14	Yoga	-1	41	0	83	52	1		73	56	114
16	Yoga	0	26	0	88	53	1.1		174	39	117
17	Yoga	0	32	0	78	49	1.3		105	36	152
28	Yoga	-2	25	1	84	51	0.6		147	53	110
29	Yoga	0	17	0	70	41	0.8		114	41	113
20	Yoga	-3	17	1	76	48	0.7		54	64	86
22	Yoga	-2	32	1	76	48	1		133	48	172
24	Yoga	-2	27	1	83	50	1.1		127	34	108
23	Yoga	-1	20	0	75	50	0.8		125	39	126
25	Yoga	-4	23	1	76	49	0.7		128	50	125

ID	Group	VLDL_P2	Glucose_P2	Urea_P2	UricAcid_P2	Total_Cholesterol_P2	ALT_P2	AST_P2	ALP_P2	GGT_P2	Bilirubin_P2
1	Control	25	101	25	7	155	34	35	0	39	0
3	Control	21	96	31	4	193	13	21	-2	22	1
7	Control	18	94	31	7	162	9	22	0	16	0
9	Control	22	97	34	6	250	10	20	-2	23	1
8	Control	23	103	27	5	245	20	28	-1	49	0
10	Control	24	104	28	6	208	8	25	0	24	1
12	Control	16	100	44	6	227	5	29	-1	23	1
14	Yoga	15	85	35	6	192	10	20	-2	20	0
16	Yoga	35	87	30	4	185	12	29	-1	21	0
17	Yoga	21	97	35	6	222	18	31	-3	27	1
28	Yoga	29	106	23	5	187	25	38	1	24	1
29	Yoga	23	88	21	6	177	27	34	0	26	0
20	Yoga	11	85	14	3	168	5	23	-1	14	0
22	Yoga	27	101	31	7	268	28	49	0	32	0
24	Yoga	25	94	31	6	166	22	34	-1	27	0
23	Yoga	25	86	17	7	193	19	29	0	16	1
25	Yoga	26	85	20	7	200	16	24	-3	17	1

ID	Group	Total_Protein_P2	Albumin_P2	Corr_Creatinine_P2
1	Control	70	46	0.8
3	Control	72	46	0.9
7	Control	85	51	1
9	Control	77	49	1
8	Control	75	47	0.8
10	Control	74	46	1
12	Control	78	49	0.9
14	Yoga	81	53	1
16	Yoga	82	51	1
17	Yoga	76	48	1.2
28	Yoga	81	50	0.8
29	Yoga	76	45	0.8
20	Yoga	73	47	0.7
22	Yoga	87	56	1.1
24	Yoga	76	47	1.1
23	Yoga	81	55	1
25	Yoga	75	48	0.8

ID	Group	TG_P1	HDL_P1	LDL_P1	VLDL_P1	Glucose_P1	Urea_P1	UricAcid_P1	Total_Cholesterol_P1	ALT_P1	AST_P1
6	Control	59	53	99	12	88	12	5	165	14	20
12	Control	89	58	122	18	95	21	5	198	24	28
1	Control	91	46	82	18	101	27	8	142	29	47
10	Control	129	48	186	26	107	31	8	334	26	38
5	Control	94	43	121	19	83	29	3	205	15	57
3	Control	124	30	119	25	83	29	4	178	17	53
9	Control	120	54	138	24	85	29	6	229	6	37
20	Yoga	43	62	66	9	69	14	3	138	11	39
24	Yoga	108	29	91	22	89	29	6	137	19	27
25	Yoga	101	47	116	20	85	21	7	186	14	27
22	Yoga	113	46	120	23	105	36	6	194	11	33
17	Yoga	118	38	131	24	89	21	6	195	14	37
14	Yoga	106	52	120	21	86	31	7	202	6	49
15	Yoga	88	43	135	18	92	30	6	210	16	29
19	Yoga	74	37	78	15	79	16	5	127	8	22
23	Yoga	103	34	102	21	85	22	6	156	33	52

ID	**Group**	**ALP_P1**	**GGT_P1**	**Bilirubin_P1**	**Total_Protein_P1**	**Albumin_P1**	**Corr_Creatinine_P1**	**TG_P3**	**HDL_P3**	**LDL_P3**
6	Control	0	30	0	67	45	0.8	62	63	116
12	Control	-2	22	1	74	47	0.8	78	59	143
1	Control	1	44	0	71	47	0.9	91	49	82
10	Control	-2	36	0	86	65	1.4	100	57	158
5	Control	1	27	1	88	53	0.9	103	52	121
3	Control	-2	33	0	73	45	1	129	38	140
9	Control	-1	33	1	74	46	0.9	167	70	172
20	Yoga	-3	17	1	76	48	0.7	55	68	80
24	Yoga	-2	27	1	83	50	1.1	76	37	120
25	Yoga	-4	23	1	76	49	0.7	88	53	123
22	Yoga	-2	32	1	76	48	1	95	63	194
17	Yoga	0	32	0	78	49	1.3	102	46	168
14	Yoga	-1	41	0	83	52	1	105	55	147
15	Yoga	-1	39	0	80	50	1.1	106	42	209
19	Yoga	0	17	0	70	41	0.8	110	45	124
23	Yoga	-1	20	0	75	50	0.8	116	39	141

ID	Group	VLDL_P3	Glucose_P3	Urea_P3	UricAcid_P3	Total_Chol	ALT_P3	AST_P3	ALP_P3	GGT_P3
6	Control	12	83	11	6	194	0	24	-1	32
12	Control	16	96	31	6	218	23	28	-1	22
1	Control	18	92	21	7	142	34	43	0	43
10	Control	20	107	27	6	241	9	29	-2	31
5	Control	21	80	27	3	196	14	50	1	29
3	Control	26	102	29	4	206	30	46	1	39
9	Control	33	109	26	6	272	19	48	-1	31
20	Yoga	11	83	14	3	161	8	32	-1	16
24	Yoga	15	94	29	6	171	35	39	-1	31
25	Yoga	18	80	19	7	187	5	25	-1	19
22	Yoga	19	93	25	6	289	10	59	-2	36
17	Yoga	20	96	35	6	239	21	54	-3	34
14	Yoga	21	92	27	6	233	24	35	-2	24
15	Yoga	21	104	21	6	291	8	20	-2	27
19	Yoga	22	90	19	5	190	30	60	-1	46
23	Yoga	23	83	16	7	194	28	32	-3	18

ID	Group	TG_P2	HDL_P2	LDL_P2	VLDL_P2	Glucose_P2	Urea_P2	UricAcid_P2	Total_Cholesterol_P2	ALT_P2	AST_P2
1	Control	124	46	90	25	101	25	7	155	34	35
3	Control	103	34	130	21	96	31	4	193	13	21
9	Control	111	61	157	22	97	34	6	250	10	20
10	Control	120	47	131	24	104	28	6	208	8	25
12	Control	82	50	148	16	100	44	6	227	5	29
14	Yoga	73	56	114	15	85	35	6	192	10	20
17	Yoga	105	36	152	21	97	35	6	222	18	31
19	Yoga	114	41	113	23	88	21	6	177	27	34
20	Yoga	54	64	86	11	85	14	3	168	5	23
22	Yoga	133	48	172	27	101	31	7	268	28	49
24	Yoga	127	34	108	25	94	31	6	166	22	34
23	Yoga	125	39	126	25	86	17	7	193	19	29
25	Yoga	128	50	125	26	85	20	7	200	16	24

ID	Group	ALP_P2	GGT_P2	Bilirubin_P2	Total_Protein_P2	Albumin_P2	Corr_Creatinine_P2	TG_P3	HDL_P3	LDL_P3
1	Control	0	39	0	70	46	0.8	91	49	82
3	Control	-2	22	1	72	46	0.9	129	38	140
9	Control	-2	23	1	77	49	1	167	70	172
10	Control	0	24	1	74	46	1	100	57	158
12	Control	-1	23	1	78	49	0.9	78	59	143
14	Yoga	-2	20	0	81	53	1	105	55	147
17	Yoga	-3	27	1	76	48	1.2	102	46	168
19	Yoga	0	26	0	76	45	0.8	110	45	124
20	Yoga	-1	14	0	73	47	0.7	55	68	80
22	Yoga	0	32	0	87	56	1.1	95	63	194
24	Yoga	-1	27	0	76	47	1.1	76	37	120
23	Yoga	0	16	1	81	55	1	116	39	141
25	Yoga	-3	17	1	75	48	0.8	88	53	123

ID	Group	VLDL_P3	Glucose_P3	Urea_P3	UricAcid_P3	Total_Chol	ALT_P3	AST_P3	ALP_P3	GGT_P3	Bilirubin_P3
1	Control	18	92	21	7	142	34	43	0	43	0
3	Control	26	102	29	4	206	30	46	1	39	0
9	Control	33	109	26	6	272	19	48	-1	31	0
10	Control	20	107	27	6	241	9	29	-2	31	0
12	Control	16	96	31	6	218	23	28	-1	22	0
14	Yoga	21	92	27	6	233	24	35	-2	24	0
17	Yoga	20	96	35	6	239	21	54	-3	34	0
19	Yoga	22	90	19	5	190	30	60	-1	46	0
20	Yoga	11	83	14	3	161	8	32	-1	16	0
22	Yoga	19	93	25	6	289	10	59	-2	36	0
24	Yoga	15	94	29	6	171	35	39	-1	31	0
23	Yoga	23	83	16	7	194	28	32	-3	18	0
25	Yoga	18	80	19	7	187	5	25	-1	19	0

ID	Group	Total_Protein_P3	Albumin_P3	Corr_Creatinine_P3
1	Control	71	49	0.9
3	Control	73	46	0.9
9	Control	78	49	0.9
10	Control	74	46	1
12	Control	73	48	1
14	Yoga	77	49	0.9
17	Yoga	72	45	1.3
19	Yoga	74	42	0.8
20	Yoga	72	46	0.7
22	Yoga	85	55	1.1
24	Yoga	73	45	1.1
23	Yoga	71	49	0.7
25	Yoga	71	45	0.8

Appendix 15: Psychology Tests Raw Data

ID	**Group**	Age	Gender	Diet	Height	Height(m)	Weight	BMI	PTQ_Pre	Core_RNT_pre	Unprod_pre	Mental_RNT_Pre	Weight_post
14	Yoga	32	1	2	170	1.7	67	23.183	8	8	0	0	68
15	Yoga	46	1	2	175	1.75	85	27.755	22	13	4	5	82
17	Yoga	40	1	2	174	1.74	84	27.745	23	18	2	3	81
19	Yoga	52	1	1	169	1.69	70	24.509	5	2	0	3	69
22	Yoga	27	1	2	170	1.7	73	25.26	20	12	3	5	72
23	Yoga	28	1	1	178	1.78	72	22.724	4	3	0	1	74
24	Yoga	34	1	2	161	1.61	65	25.076	17	10	5	2	67
20	Yoga	27	2	1	157	1.57	48	19.473	19	11	3	5	46
21	Yoga	29	1	2	165	1.65	62	22.773	4	1	0	3	63
25	Yoga	26	1	2	174	1.74	85	28.075	27	18	5	4	87
1	Control	34	1	2	180	1.8	92	28.395	30	18	4	8	95
2	Control	36	1	2	166	1.66	82	29.758	29	17	6	6	86
5	Control	36	1	2	172	1.72	65	21.971	20	11	4	5	68
6	Control	43	1	2	172	1.72	70	23.661	18	14	3	1	74
9	Control	40	1	2	174	1.74	80	26.424	13	8	3	2	79
10	Control	32	1	2	174	1.74	99	32.699	13	9	2	2	102
12	Control	32	1	2	168	1.68	68	24.093	18	15	2	1	74
8	Control	49	1	1	169	1.69	76	26.61	4	0	1	3	79
11	Control	27	1	2	162	1.62	72	27.435	8	6	2	0	80

ID	**Group**	PTQ_Post	Core_RNT_	Unprod_RNT_pre	Mental_Cap_RNT_Pre
14	Yoga	0	0	0	0
15	Yoga	14	10	1	3
17	Yoga	20	12	5	3
19	Yoga	1	1	0	0
22	Yoga	11	6	3	2
23	Yoga	0	0	0	0
24	Yoga	20	11	5	4
20	Yoga	8	4	3	1
21	Yoga	2	1	1	0
25	Yoga	23	14	4	5
1	Control	33	18	7	8
2	Control	32	19	7	6
5	Control	19	12	3	4
6	Control	22	15	3	4
9	Control	24	14	6	4
10	Control	16	9	4	3
12	Control	20	15	4	1
8	Control	8	2	3	3
11	Control	14	9	2	3